Package ‘gdata’

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Description Various R programming tools for data manipulation
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Author Gregory R. Warnes, Ben Bolker, Gregor Gorjanc, Gabor
Grothendieck, Ales Korosec, Thomas Lumley, Don MacQueen, Arni
Magnusson, Jim Rogers, and others
Maintainer Gregory R. Warnes <greg@warner.net>
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Description

The gdata package provides various R programming tools for data manipulation.

Details

The following are sources of information on gdata package:

- DESCRIPTION file: `library(help="gdata")`
- This file: `package?gdata`
Description

The function returns the value of the last evaluated top-level expression, which is always assigned to .Last.value (in package:base).

Usage

ans()

Details

This function retrieves .Last.value. For more details see .Last.value.

Value

.Last.value

Author(s)

Liviu Andronic

See Also

.Last.value, eval

Examples

2+2  # Trivial calculation...
ans()  # See the answer again

gamma(1:15)  # Some intensive calculation...
fac14 <- ans()  # store the results into a variable

rnorm(20)  # Generate some standard normal values
ans()^2  # Convert to Chi-square(1) values...
stem(ans())  # Now show a stem-and-leaf table
**Description**

Display function argument names and corresponding default values, formatted in two columns for easy reading.

**Usage**

```r
Args(name, sort=FALSE)
```

**Arguments**

- `name`: a function or function name.
- `sort`: whether arguments should be sorted.

**Value**

A data frame with named rows and a single column called `value`, containing the default value of each argument.

**Note**

Primitive functions like `sum` and `all` have no formal arguments. See the `formals` help page.

**Author(s)**

Arni Magnusson

**See Also**

`Args` is a verbose alternative to `args`, based on `formals`. `help` also describes function arguments.

**Examples**

```r
Args(g1n)
Args(scan)
Args(legend, sort=TRUE)
```
bindData

Bind two data frames into a multivariate data frame

Description

Usually data frames represent one set of variables and one needs to bind/join them for multivariate analysis. When `merge` is not the appropriate solution, `bindData` might perform an appropriate binding for two data frames. This is especially useful when some variables are measured once, while others are repeated.

Usage

```r
bindData(x, y, common)
```

Arguments

- `x` data.frame
- `y` data.frame
- `common` character, list of column names that are common to both input data frames

Details

Data frames are joined in such a way that the new data frame has \( c + (n_1 - c) + (n_2 - c) \) columns, where \( c \) is the number of common columns, and \( n_1 \) and \( n_2 \) are the number of columns in the first and in the second data frame, respectively.

Value

A data frame.

Author(s)

Gregor Grojanc

See Also

`merge`, `wideByFactor`

Examples

```r
n1 <- 6
n2 <- 12
n3 <- 4
## Single trait 1
num <- c(5:n1, 10:13)
(tmp1 <- data.frame(y1=rnorm(n=n1),
                      f1=factor(rep(c("A", "B"), n1/2)),
                      ch=letters[num],
                      y2=rnorm(n=n2),
                      f2=factor(rep(c("A", "B"), n2/2)),
                      ch=letters[num],
                      y3=rnorm(n=n3),
                      f3=factor(rep(c("A", "B"), n3/2)),
                      ch=letters[num]),
bindData(x=tmp1, y=tmp2, common=c("f1", "y1", "y2", "y3")))
```
case

Map elements of a vector according to the provided `cases`

Description

Map elements of a vector according to the provided `cases`. This function is useful for mapping discrete values to factor labels and is the vector equivalent to the switch function.

Usage

case(x, ..., default = NA)

Arguments

x Vector to be converted

... Map of alternatives, specified as "name"=value

default Value to be assigned to elements of x not matching any of the alternatives. Defaults to NA.
cbindx

Details
This function is to switch what if else is to if, and is a convenience wrapper for factor.

Value
A factor variables with each element of x mapped into the corresponding level of specified in the mapping.

Author(s)
Gregory R. Warnes <greg@warnes.net>

See Also
factor, switch, ifelse

Examples
```r
## default = NA
case( c(1,1,4,3), "a"=1, "b"=2, "c"=3)

## default = "foo"
case( c(1,1,4,3), "a"=1, "b"=2, "c"=3, default="foo" )
```

Description

cbindx column-binds objects with different number of rows.

Usage

```r
cbindX(...)
```

Arguments

... matrix and data.frame objects

Details
First the object with maximal number of rows is found. Other objects that have less rows get (via rbind) additional rows with NA values. Finally, all objects are column-binded (via cbind).

Value
See details
Author(s)

Gregor Gorjanc

See Also

Regular \texttt{cbind} and \texttt{rbind}

Examples

df1 <- data.frame(a=1:3, b=c("A", "B", "C"))
df2 <- data.frame(c=as.character(1:5), a=5:1)

ma1 <- matrix(as.character(1:4), nrow=2, ncol=2)
ma2 <- matrix(1:6, nrow=3, ncol=2)

cbindX(df1, df2)
cbindX(ma1, ma2)

Details

Function to center text strings for display on the text console by prepending the necessary number of spaces to each element.

Value

Vector of character strings.
Combine R Objects With a Column Labeling the Source

Author(s)
Gregory R. Warnes <greg@warnes.net>

See Also
strwrap

Examples

```r
cat(centerText("One Line Test"), "\n\n")

mText <- c("This", "is an example", "of a multiline text ", "with ", "leading", "and trailing ", "spaces.")
cat("\n", centerText(mText), "\n", sep="\n")
```

Description
Take a sequence of vector, matrix or data frames and combine into rows of a common data frame with an additional column source indicating the source object.

Usage

```r
combine(..., names=NULL)
```

Arguments

... vectors or matrices to combine.

names character vector of names to use when creating source column.

Details

If there are several matrix arguments, they must all have the same number of columns. The number of columns in the result will be one larger than the number of columns in the component matrixes. If all of the arguments are vectors, these are treated as single column matrixes. In this case, the column containing the combineinated vector data is labeled data.

When the arguments consist of a mix of matrices and vectors the number of columns of the result is determined by the number of columns of the matrix arguments. Vectors are considered row vectors and have their values recycled or subsetted (if necessary) to achieve this length.

The source column is created as a factor with levels corresponding to the name of the object from which the each row was obtained. When the names argument is ommitted, the name of each object is obtained from the specified argument name in the call (if present) or from the name of the object. See below for examples.
**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

`rbind`, `merge`

**Examples**

```r
a <- matrix(rnorm(12), ncol=4, nrow=3)
b <- 1:4
combine(a,b)

combine(x=a,b)
combine(x=a,y=b)
combine(a,b, names=c("one","two"))

c <- 1:6
combine(b,c)
```

---

**Description**

Convert medical measurements between International Standard (SI) and US 'Conventional' Units.

**Usage**

```r
ConvertMedUnits(x, measurement, abbreviation,
    to = c("Conventional", "SI", "US"),
    exact = !missing(abbreviation))
```

**Arguments**

- `x` Vector of measurement values
- `measurement` Name of the measurement
- `abbreviation` Measurement abbreviation
- `to` Target units
- `exact` Logical indicating whether matching should be exact
Details

Medical laboratories and practitioners in the United States use one set of units (the so-called 'Conventional' units) for reporting the results of clinical laboratory measurements, while the rest of the world uses the International Standard (SI) units. It often becomes necessary to translate between these units when participating in international collaborations.

This function converts between SI and US 'Conventional' units.

If `exact=FALSE`, `grep` will be used to do a case-insensitive sub-string search for matching measurement names. If more than one match is found, an error will be generated, along with a list of the matching entries.

Value

Returns a vector of converted values. The attribute 'units' will contain the target units converted.

Author(s)

Gregory R. Warnes <greg@warnes.net>

References

http://www.globalrph.com/conv_si.htm

See Also

The data set `MedUnits` provides the conversion factors.

Examples

data(MedUnits)

# show available conversions
MedUnits$Measurement

# Convert SI Glucose measurement to 'Conventional' units
GlucoseSI = c(5, 5.4, 5, 5.1, 5.6, 5.1, 4.9, 5.2, 5.5) # in SI Units
GlucoseUS = ConvertMedUnits( GlucoseSI, "Glucose", to="US" )
cbind(GlucoseSI,GlucoseUS)

## Not run:
# See what happens when there is more than one match
ConvertMedUnits( 27.5, "Creatin", to="US")

## End(Not run)

# To solve the problem do:
ConvertMedUnits( 27.5, "Creatinine", to="US", exact=TRUE)
**drop.levels**

*Drop unused factor levels*

**Description**

Drop unused levels in a factor

**Usage**

```r
drop.levels(x, reorder=TRUE, ...)
```

**Arguments**

- `x`  
  object to be processed
- `reorder`  
  should factor levels be reordered using `reorder.factor`?
- `...`  
  additional arguments to `reorder.factor`

**Details**

`drop.levels` is a generic function, where default method does nothing, while method for factors drops all unused levels. Drop is done with `x[, drop=TRUE]`.

There are also convenient methods for `list` and `data.frame`, where all unused levels are dropped in all factors (one by one) in a `list` or a `data.frame`.

**Value**

Input object without unused levels.

**Author(s)**

Jim Rogers <james.a.rogers@pfizer.com> and Gregor Gorjanc

**Examples**

```r
f <- factor(c("A", "B", "C", "D"))[1:3]
drop.levels(f)

l <- list(f=f, i=1:3, c=c("A", "B", "D"))
drop.levels(l)

df <- as.data.frame(l)
str(df)
str(drop.levels(df))
```
duplicated2

**Determine Duplicate Elements**

**Description**

duplicated2() determines which elements of a vector or data frame are duplicates, and returns a logical vector indicating which elements (rows) are duplicates.

**Usage**

duplicated2(x, bothWays=TRUE, ...)

**Arguments**

- **x**: a vector or a data frame or an array or NULL.
- **bothWays**: if TRUE (the default), duplication should be considered from both sides. For more information see the argument fromLast to the function duplicated.
- **...**: further arguments passed down to duplicated() and its methods.

**Details**

The standard duplicated function (in package:base) only returns TRUE for the second and following copies of each duplicated value (second-to-last and earlier when fromLast=TRUE). This function returns all duplicated elementes, including the first (last) value.

When bothWays is FALSE, duplicated2() defaults to a duplicated call. When bothWays is TRUE, the following call is being executed: duplicated(x, ...) | duplicated(x, fromLast=TRUE, ...)

**Value**

For a vector input, a logical vector of the same length as x. For a data frame, a logical vector with one element for each row. For a matrix or array, and when MARGIN = 0, a logical array with the same dimensions and dimnames.

For more details see duplicated.

**Author(s)**

Liviu Andronic

**See Also**

duplicated, unique

**Examples**

data(iris)
iris[duplicated(iris), ] # 2nd duplicated value
iris[duplicated(iris, fromLast=TRUE), ] # 1st duplicated value
iris[duplicated2(iris), ] # both duplicated values
Display Information about Elements in a Given Object

Description

This function is depreciated. Please use \code{ll} instead.

Display name, class, size, and dimensions of each element in a given object.

Usage

\dontrun{
  elem(object=1, unit=c("KB","MB","bytes"), digits=0,
       dimensions=FALSE)
}

Arguments

- **object**: object containing named elements, perhaps a model or data frame.
- **unit**: required unit for displaying element size: "KB", "MB", "bytes", or first letter.
- **digits**: number of decimals to display when rounding element size.
- **dimensions**: whether element dimensions should be returned.

Details

A verbose alternative to \code{names()}.  

Value

A data frame with named rows and the following columns:

- **Class**: element class.
- **KB**: element size (see notes).
- **Dim**: element dimensions (optional).

Note

The name of the element size column is the same as the unit used.

Elements of class \code{classRepresentation}, \code{ClassUnionRepresentation}, and \code{grob} do not have a defined size, so 0 bytes are assumed for those.

Author(s)

Arni Magnusson <arnima@u.washington.edu>

See Also

\code{names}, \code{str}, and \code{summary} display different information about object elements.

\code{ll} and \code{env} are related to \code{elem}.  

**Examples**

```r
## Not run:
data(infert)
elem(infert)
model <- glm(case~spontaneous+induced, family=binomial, data=infert)
elem(model, dim=TRUE)
elem(model$family)

## End(Not run)
```

---

**Description**

Display name, number of objects, and size of all loaded environments.

**Usage**

```r
env(unit="KB", digits=0)
```

**Arguments**

- `unit` unit for displaying environment size: "bytes", "KB", "MB", or first letter.
- `digits` number of decimals to display when rounding environment size.

**Value**

A data frame with the following columns:

- **Environment** environment name.
- **Objects** number of objects in environment.
- **KB** environment size (see notes).

**Note**

The name of the environment size column is the same as the unit used.

**Author(s)**

Arni Magnusson

**See Also**

- `env` is a verbose alternative to `search`.
- `ll` is a related function that describes objects in an environment.
Examples

### Not run:
```
env()
```

### End(Not run)

---

frameApply

*Subset analysis on data frames*

Description

Apply a function to row subsets of a data frame.

Usage

```
frameApply(x, by=NULL, on=by[1], fun=function(xi) c(Count=nrow(xi)),
           subset=TRUE, simplify=TRUE, byvar.sep="\$\@\$", ...)
```

Arguments

- **x**: a data frame
- **by**: names of columns in x specifying the variables to use to form the subgroups. None of the by variables should have the name "sep" (you will get an error if one of them does; a bit of laziness in the code). Unused levels of the by variables will be dropped. Use by = NULL (the default) to indicate that all of the data is to be treated as a single (trivial) subgroup.
- **on**: names of columns in x specifying columns over which fun is to be applied. These can include columns specified in by, (as with the default) although that is not usually the case.
- **fun**: a function that can operate on data frames that are row subsets of x[on]. If simplify = TRUE, the return value of the function should always be either a try-error (see `try`), or a vector of fixed length (i.e. same length for every subset), preferably with named elements.
- **subset**: logical vector (can be specified in terms of variables in data). This row subset of x is taken before doing anything else.
- **simplify**: logical. If TRUE (the default), return value will be a data frame including the by columns and a column for each element of the return vector of fun. If FALSE, the return value will be a list, sometimes necessary for less structured output (see description of return value below).
- **byvar.sep**: character. This can be any character string not found anywhere in the values of the by variables. The by variables will be pasted together using this as the separator, and the result will be used as the index to form the subgroups.
- **...**: additional arguments to fun.
Details

This function accomplishes something similar to `by`. The main difference is that `frameApply` is designed to return data frames and lists instead of objects of class 'by'. Also, `frameApply` works only on the unique combinations of the `by` that are actually present in the data, not on the entire cartesian product of the `by` variables. In some cases this results in great gains in efficiency, although `frameApply` is hardly an efficient function.

Value

A data frame if `simplify = TRUE` (the default), assuming there is sufficiently structured output from `fun`. If `simplify = FALSE` and `by` is not NULL, the return value will be a list with two elements. The first element, named "by", will be a data frame with the unique rows of `x[by]`, and the second element, named "result" will be a list where the ith component gives the result for the ith row of the "by" element.

Author(s)

Jim Rogers <james.a.rogers@pfizer.com>

Examples

data(ELISA, package="gtools")

# Default is slightly unintuitive, but commonly useful:
frameApply(ELISA, by = c("PlateDay", "Read"))

# Wouldn't actually recommend this model! Just a demo:
frameApply(ELISA, on = c("Signal", "Concentration"), by = c("PlateDay", "Read"),
fun = function(dat) coef(lm(Signal ~ Concentration, data = dat)))

frameApply(ELISA, on = "Signal", by = "Concentration",
fun = function(dat, ...) {
  x <- dat[[1]]
  out <- c(Mean = mean(x, ...),
           SD = sd(x, ...),
           N = sum(!is.na(x))
  },
  na.rm = TRUE,
  subset = !is.na(Concentration))

---

gdata-defunct

Defunct Functions in Package 'gdata'

Description

The functions or variables listed here are no longer part of 'gdata'.

getYear

Usage

aggregate.table(x, by1, by2, FUN=mean, ...)

Arguments

x data to be summarized
by1 first grouping factor.
by2 second grouping factor.
FUN a scalar function to compute the summary statistics which can be applied to all
data subsets. Defaults to mean.
... Optional arguments for FUN.

Details

aggregate.table(x, by1, by2, FUN=mean, ...) should be replaced by tapply(X=x, INDEX=list(by1, by2), FUN=...)

getYear

Get date/time parts from date and time objects

Description

get* functions provide an *experimental* approach for extracting the date/time parts from objects
of a date/time class. They are designed to be intuitive and thus lowering the learning curve for work
with date and time classes in R.

Usage

getYear(x, format, ...)
getMonth(x, format, ...)
getDay(x, format, ...)
getHour(x, format, ...)
getMin(x, format, ...)
getSec(x, format, ...)

Arguments

x generic, date/time object
format character, format
... arguments passed to other methods

Value

Character
**humanReadable**

**Author(s)**
Gregor Gorjanc

**See Also**
- Date
- DateTimeClasses
- strftime

**Examples**

```r
## --- Date class ---
tmp <- Sys.Date()
tmp

getYear(tmp)
getMonth(tmp)
getDay(tmp)

## --- POSIXct class ---
tmp <- as.POSIXct(tmp)

getYear(tmp)
getMonth(tmp)
getDay(tmp)

## --- POSIXlt class ---
tmp <- as.POSIXlt(tmp)

getYear(tmp)
getMonth(tmp)
getDay(tmp)
```

**humanReadable**

*Print byte size in human readable format*

**Description**

humanReadable converts byte size in human readable format such as kB, MB, GB, etc.

**Usage**

```r
humanReadable(x, standard="SI", digits=1, width=3, sep=" ")
```
Arguments

x integer, byte size

standard character, "SI" for powers of 1000 or anything else for powers of 1024, see details
digits integer, number of digits after decimal point
width integer, width of number string
sep character, separator between number and unit

Details

Basic unit used to store information in computers is a bit. Bits are represented as zeroes and ones - binary number system. Although, the binary number system is not the same as the decimal number system, decimal prefixes for binary multiples such as kilo and mega are often used. In the decimal system kilo represent 1000, which is close to $2^{10} = 1024$ in the binary system. This sometimes causes problems as it is not clear which powers (2 or 10) are used in a notation like 1 kB. To overcome this problem International Electrotechnical Commission (IEC) has provided the following solution to this problem:

<table>
<thead>
<tr>
<th>Name</th>
<th>System</th>
<th>Symbol</th>
<th>Size</th>
<th>Conversion</th>
</tr>
</thead>
<tbody>
<tr>
<td>byte</td>
<td>binary</td>
<td>B</td>
<td>$2^3$</td>
<td>8 bits</td>
</tr>
<tr>
<td>kilobyte</td>
<td>decimal</td>
<td>kB</td>
<td>$10^3$</td>
<td>1000 bytes</td>
</tr>
<tr>
<td>kibibyte</td>
<td>binary</td>
<td>KiB</td>
<td>$2^{10}$</td>
<td>1024 bytes</td>
</tr>
<tr>
<td>megabyte</td>
<td>decimal</td>
<td>MB</td>
<td>$(10^3)^2$</td>
<td>1000 kilobytes</td>
</tr>
<tr>
<td>mebibyte</td>
<td>binary</td>
<td>MiB</td>
<td>$(2^{10})^2$</td>
<td>1024 kibibytes</td>
</tr>
<tr>
<td>gigabyte</td>
<td>decimal</td>
<td>GB</td>
<td>$(10^3)^3$</td>
<td>1000 megabytes</td>
</tr>
<tr>
<td>gibibyte</td>
<td>binary</td>
<td>GiB</td>
<td>$(2^{10})^3$</td>
<td>1024 mebibytes</td>
</tr>
<tr>
<td>terabyte</td>
<td>decimal</td>
<td>TB</td>
<td>$(10^3)^4$</td>
<td>1000 gigabytes</td>
</tr>
<tr>
<td>tebibyte</td>
<td>binary</td>
<td>TiB</td>
<td>$(2^{10})^4$</td>
<td>1024 gibibytes</td>
</tr>
<tr>
<td>petabyte</td>
<td>decimal</td>
<td>PB</td>
<td>$(10^3)^5$</td>
<td>1000 terabytes</td>
</tr>
<tr>
<td>pebibyte</td>
<td>binary</td>
<td>PiB</td>
<td>$(2^{10})^5$</td>
<td>1024 pebibytes</td>
</tr>
<tr>
<td>exabyte</td>
<td>decimal</td>
<td>EB</td>
<td>$(10^3)^6$</td>
<td>1000 petabytes</td>
</tr>
<tr>
<td>exbibyte</td>
<td>binary</td>
<td>EiB</td>
<td>$(2^{10})^6$</td>
<td>1024 exbibytes</td>
</tr>
<tr>
<td>zettabyte</td>
<td>decimal</td>
<td>ZB</td>
<td>$(10^3)^7$</td>
<td>1000 exabytes</td>
</tr>
<tr>
<td>zebibyte</td>
<td>binary</td>
<td>ZiB</td>
<td>$(2^{10})^7$</td>
<td>1024 zebibytes</td>
</tr>
<tr>
<td>yottabyte</td>
<td>decimal</td>
<td>YB</td>
<td>$(10^3)^8$</td>
<td>1000 zettabytes</td>
</tr>
<tr>
<td>yebibyte</td>
<td>binary</td>
<td>YiB</td>
<td>$(2^{10})^8$</td>
<td>1024 zebibytes</td>
</tr>
</tbody>
</table>

where Zi and Yi are GNU extensions to IEC. To get the output in the decimal system (powers of 1000) use standard="SI". Otherwise IEC standard (powers of 1024) is used.

For printout both digits and width can be specified. If width is NULL, all values have given number of digits. If width is not NULL, output is rounded to a given width and formatted similar to human readable format of ls, df or du shell commands.
installXLSXsupport

Value

Byte size in human readable format as character with proper unit symbols added at the end of the string.

Author(s)

Ales Korosec and Gregor Gorjanc

References

http://en.wikipedia.org/wiki/Binary_prefix


See Also

object.size, ll

Examples

baseSI <- 10
powerSI <- seq(from=3, to=27, by=3)
SI0 <- (baseSI)^powerSI
k <- length(SI0) - 1
SI1 <- SI0 - SI0 / c(2, runif(n=k, min=1.01, max=5.99))
SI2 <- SI0 + SI0 / c(2, runif(n=k, min=1.01, max=5.99))

baseIEC <- 2
powerIEC <- seq(from=10, to=90, by=10)
IEC0 <- (baseIEC)^powerIEC
IEC1 <- IEC0 - IEC0 / c(2, runif(n=k, min=1.01, max=5.99))
IEC2 <- IEC0 + IEC0 / c(2, runif(n=k, min=1.01, max=5.99))

cbind(humanReadable(x=SI1, width=NULL, digits=3),
       humanReadable(x=SI0, width=NULL, digits=2),
       humanReadable(x=SI2, width=NULL, digits=1),
       humanReadable(x=IEC1, standard="IEC", width=7, digits=3),
       humanReadable(x=IEC0, standard="IEC", width=7, digits=2),
       humanReadable(x=IEC2, standard="IEC", width=7, digits=1))
Usage

installXLSXsupport(perl = "perl", verbose = FALSE)

Arguments

perl          Path to perl interpreter (optional).
verbose       If TRUE, show additional messages during processing.

Details

This function calls the perl script 'install_modules.pl' located in the perl subdirectory of the gdata package directory (or inst/perl in the source package). This perl script attempts to use the perl 'CPAN' package, which should be included as part of most perl installations, to automatically download, compile, and install the Compress::Raw::Zlib and Spreadsheet::XLSX perl modules needed for read.xls to support support Excel 2007+ XLSX files into the gdata perl subdirectory.

Since the perl modules are installed into the gdata installation directory, the perl modules will be available until the gdata package is replaced or removed. Since this occurs each time a new version of gdata is installed, installXLSXsupport will need to be run each time a new version of the gdata package is installed.

Further, the binary Compress::Raw::Zlib package installed by installXLSXsupport is tied to the particular version of perl used to compile it, therefore, you will need to re-run installXLSXsupport if you install a different perl distribution.

This installation process will fail if 1) perl is not available on the search path and the perl argument is not used to specify the path of the perl executable, 2) the perl installation is not properly configured for installing binary packages*, 3) if the CPAN module is not present, or 4) if the C compiler specified by the perl installation is not present.

In particular, installXLSXsupport will fail for the version of perl included with the current RTools.zip package, which is not correctly configured to allow installation of additional perl packages. (The RTools version of perl is installed in a different directory than the perl configuration files expect.)

The function xlsFormats can be used to see whether XLS and XLSX formats are supported by the currently available perl modules.

Value

Either TRUE indicating that the necessary perl modules have been successfully installed, or FALSE indicating that an error has occurred.

See Also

read.xls, xls2csv, xlsFormats

Examples

```r
## Not run:
installXLSXsupport()
```

## End(Not run)
Interleave Rows of Data Frames or Matrices

Description

Interleave rows of data frames or Matrices.

Usage

interleave(..., append.source=TRUE, sep=" ", drop=FALSE)

Arguments

... objects to be interleaved
append.source Boolean Flag. When TRUE (the default) the argument name will be appended to
the row names to show the source of each row.
sep Separator between the original row name and the object name.
drop boolean flag - When TRUE, matrices containing one column will be converted
to vectors.

Details

This function creates a new matrix or data frame from its arguments.
The new object will have all of the rows from the source objects interleaved. IE, it will contain row
1 of object 1, followed by row 1 of object 2, ... row 1 of object 'n', row 2 of object 1, row 2 of object
2, ... row 2 of object 'n' ...

Value

Matrix containing the interleaved rows of the function arguments.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

cbind, rbind, combine

Examples

# Simple example
a <- matrix(1:10, ncol=2, byrow=TRUE)
b <- matrix(letters[1:10], ncol=2, byrow=TRUE)
c <- matrix(LETTERS[1:10], ncol=2, byrow=TRUE)
interleave(a,b,c)
# Useful example:
# Create a 2-way table of means, standard errors, and # obs

g1 <- sample(letters[1:5], 1000, replace=TRUE)
g2 <- sample(LETTERS[1:3], 1000, replace=TRUE)
dat <- rnorm(1000)

stderr <- function(x) sqrt(var(x, na.rm=TRUE) / nobs(x))

means <- tapply(dat, list(g1, g2), mean)
stderrs <- tapply(dat, list(g1, g2), stderr)
ns <- tapply(dat, list(g1, g2), nobs)
blanks <- matrix(" ", nrow=5, ncol=3)

tab <- interleave("Mean"=round(means,2),
                 "Std Err"=round(stderrs,2),
                 "N"=ns, " " = blanks, sep=" ")

print(tab, quote=FALSE)

# Using drop to control coercion to a lower dimensions:

m1 <- matrix(1:4)
m2 <- matrix(5:8)

interleave(m1, m2, drop=TRUE) # This will be coerced to a vector
interleave(m1, m2, drop=FALSE) # This will remain a matrix

---

**is.what**

*Run Multiple is.* Tests on a Given Object*

**Description**

Run multiple is.* tests on a given object: is.na, is.numeric, and many others.

**Usage**

is.what(object, verbose=FALSE)

**Arguments**

- **object**: any R object.
- **verbose**: whether negative tests should be included in output.
Value

A character vector containing positive tests, or when `verbose` is `TRUE`, a data frame showing all test results.

Note

The following procedure is used to look for valid tests:

1. Find all objects named `is.*` in all loaded environments.
2. Discard objects that are not functions.
3. Include test result only if it is of class "logical", not an `NA`, and of length 1.

Author(s)

Arni Magnusson, inspired by `demo(is.things)`.

See Also

`is.na` and `is.numeric` are commonly used tests.

Examples

```r
is.what(pi)
is.what(NA, verbose=TRUE)
is.what(lm(1:1))
is.what(is.what)
```

---

**keep**

*Remove All Objects, Except Those Specified*

Description

Remove all objects from the user workspace, except those specified.

Usage

```
keep(..., list=character(0), all=FALSE, sure=FALSE)
```

Arguments

- `...` objects to be kept, specified one by one, quoted or unquoted.
- `list` character vector of object names to be kept.
- `all` whether hidden objects (beginning with a `.`) should be removed, unless explicitly kept.
- `sure` whether to perform the removal, otherwise return names of objects that would have been removed.
Details

Implemented with safety caps: objects whose name starts with a `.` are not removed unless `all=TRUE`, and an explicit `sure=TRUE` is required to remove anything.

Value

A character vector containing object names, or `NULL` when `sure` is `TRUE`.

Author(s)

Arni Magnusson

See Also

`keep` is a convenient interface to `rm` when removing most objects from the user workspace.

Examples

```r
data(women, cars)
keep(cars)
## To remove all objects except cars, run:
## keep(cars, sure=TRUE)
```

Describe Objects or Elements

Display name, class, size, and dimensions of each object in a given environment. Alternatively, if the main argument is a list-like object, its elements are listed and described.

Usage

```r
ll(pos=1, unit="KB", digits=0, dim=FALSE, sort=FALSE, class=NULL,
invert=FALSE, ...)
```

Arguments

- `pos` environment position number, environment name, data frame, list, model, or any object that is list.
- `unit` unit for displaying object size: "bytes", "KB", "MB", or first letter.
- `digits` number of decimals to display when rounding object size.
- `dim` whether object dimensions should be returned.
- `sort` whether elements should be sorted by name.
- `class` character vector for limiting the output to specified classes.
- `invert` whether to invert the class filter, so specified classes are excluded.
- `...` passed to `ls`.
**Value**

A data frame with named rows and the following columns:

- **Class**: object class.
- **KB**: object size *(see note)*.
- **Dim**: object dimensions *(optional)*.

**Note**

The name of the object size column is the same as the unit used.

**Author(s)**

Arni Magnusson, with a contribution by Jim Rogers

**See Also**

- `ll` is a verbose alternative to `ls` (objects in an environment) and `names` (elements in a list-like object).
- `str` and `summary` also describe elements in a list-like objects.
- `env` is a related function that describes all loaded environments.

**Examples**

```r
ll()  # all=TRUE
ll("package:base")
ll("package:base", class="function", invert=TRUE)

data(infert)
ll(infert)
model <- glm(case~spontaneous+induced, family=binomial, data=infert)
ll(model, dim=TRUE)
ll(model, sort=TRUE)
ll(model$family)
```

---

**Description**

Return a character vector giving the names of function objects in the specified environment.

**Usage**

```r
ls.funs(...)```
Arguments

Arguments passed to `ls`. See the help for `ls` for details.

Details

This function calls `ls` and then returns a character vector containing only the names of only function objects.

Value

character vector

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

`ls`, `is.function`

Examples

```r
## List functions defined in the global environment:
ls.funs()

## List functions available in the base package:
ls.funs("package:base")
```

Description

`mapLevels` produces a map with information on levels and/or internal integer codes. As such can be conveniently used to store level mapping when one needs to work with internal codes of a factor and later transform back to factor or when working with several factors that should have the same levels and therefore the same internal coding.

Usage

```r
mapLevels(x, codes=TRUE, sort=TRUE, drop=FALSE, combine=FALSE, ...)
mapLevels(x) <- value
```
**mapLevels**

**Arguments**

- **x**  
  object whose levels will be mapped, look into details

- **codes**  
  boolean, create integer levelsMap (with internal codes) or character levelsMap (with level names)

- **sort**  
  boolean, sort levels of character x, look into details

- **drop**  
  boolean, drop unused levels

- **combine**  
  boolean, combine levels, look into details

- **...**  
  additional arguments for sort

- **value**  
  levelsMap or listLevelsMap, output of mapLevels methods or constructed by user, look into details

**Value**

`mapLevels()` returns “levelsMap” or “listLevelsMap” objects as described in levelsMap and listLevelsMap section.

Result of `mapLevels<-` is always a factor with remapped levels or a “list/data.frame” with remapped factors.

**mapLevels**

The `mapLevels` function was written primarily for work with “factors”, but is generic and can also be used with “character”, “list” and “data.frame”, while “default” method produces error. Here the term levels is also used for unique character values.

When `codes=TRUE` integer “levelsMap” with information on mapping internal codes with levels is produced. Output can be used to transform integer to factor or remap factor levels as described below. With `codes=FALSE` character “levelsMap” is produced. The later is useful, when one would like to remap factors or combine factors with some overlap in levels as described in `mapLevels<-` section and shown in examples.

The `sort` argument provides possibility to sort levels of “character” x and has no effect when x is a “factor”.

Argument `combine` has effect only in “list” and “data.frame” methods and when `codes=FALSE` i.e. with character “levelsMaps”. The later condition is necessary as it is not possible to combine maps with different mapping of level names and integer codes. It is assumed that passed “list” and “data.frame” have all components for which methods exist. Otherwise error is produced.

**levelsMap and listLevelsMap**

Function `mapLevels` returns a map of levels. This map is of class “levelsMap”, which is actually a list of length equal to number of levels and with each component of length 1. Components need not be of length 1. There can be either integer or character “levelsMap”. **Integer “levelsMap”** (when `codes=TRUE`) has names equal to levels and components equal to internal codes. **Character “levelsMap”** (when `codes=FALSE`) has names and components equal to levels. When `mapLevels` is applied to “list” or “data.frame”, result is of class “listLevelsMap”, which is a list of “levelsMap” components described previously. If `combine=TRUE`, result is a “levelsMap” with all levels in x components.
For ease of inspection, print methods unlists “levelsMap” with proper names. mapLevels<- methods are fairly general and therefore additional convenience methods are implemented to ease the work with maps: is.levelsMap and is.listLevelsMap; as.levelsMap and as.listLevelsMap for coercion of user defined maps; generic “[“ and “c” for both classes (argument recursive can be used in “c” to coerce “listLevelsMap” to “levelsMap”) and generic unique and sort (generic from R 2.4) for “levelsMap”.

mapLevels<-

Workhorse under mapLevels<- methods is levels<-. mapLevels<- just control the assignment of “levelsMap” (integer or character) or “listLevelsMap” to x. The idea is that map values are changed to map names as indicated in levels examples. Integer “levelsMap” can be applied to “integer” or “factor”, while character “levelsMap” can be applied to “character” or “factor”. Methods for “list” and “data.frame” can work only on mentioned atomic components/columns and can accept either “levelsMap” or “listLevelsMap”. Recycling occurs, if length of value is not the same as number of components/columns of a “list/data.frame”.

Author(s)

Gregor Gorjanc

See Also

factor, levels and unclass

Examples

```r
## --- Integer levelsMap ---

(f <- factor(sample(letters, size=20, replace=TRUE)))
(mapInt <- mapLevels(f))

## Integer to factor

(int <- as.integer(f))
(mapLevels(int) <- mapInt)
all.equal(int, f)

## Remap levels of a factor

(fac <- factor(as.integer(f)))
(mapLevels(fac) <- mapInt) # the same as levels(fac) <- mapInt
all.equal(fac, f)

## --- Character levelesMap ---

f1 <- factor(letters[1:10])
f2 <- factor(letters[5:14])

## Internal codes are the same, but levels are not

as.integer(f1)
as.integer(f2)
```
## Description

This function allows easy selection of the column names of an object using a set of inclusion and exclusion criteria.

## Usage

```r
matchcols(object, with, without, method=c("and","or"), ...)```

## Arguments

- **object**: Matrix or dataframe
- **with, without**: Vector of regular expression patterns
- **method**: One of "and" or "or"
- **...**: Optional arguments to `grep`

## Value

Vector of column names which match all (method="and") or any (method="or") of the patterns specified in with, but none of the patterns specified in without.
Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

grep

Examples

# create a matrix with a lot of named columns
x <- matrix( ncol=30, nrow=5 )
colnames(x) <- c("AffyID","Overall Group Means: Control",
                "Overall Group Means: Moderate",
                "Overall Group Means: Marked",
                "Overall Group Means: Severe",
                "Overall Group StdDev: Control",
                "Overall Group StdDev: Moderate",
                "Overall Group StdDev: Marked",
                "Overall Group StdDev: Severe",
                "Overall Group CV: Control",
                "Overall Group CV: Moderate",
                "Overall Group CV: Marked",
                "Overall Group CV: Severe",
                "Overall Model P-value",
                "Overall Model: (Intercept): Estimate",
                "Overall Model: Moderate: Estimate",
                "Overall Model: Marked: Estimate",
                "Overall Model: Severe: Estimate",
                "Overall Model: (Intercept): Std. Error",
                "Overall Model: Moderate: Std. Error",
                "Overall Model: Marked: Std. Error",
                "Overall Model: Severe: Std. Error",
                "Overall Model: (Intercept): t value",
                "Overall Model: Moderate: t value",
                "Overall Model: Marked: t value",
                "Overall Model: Severe: t value",
                "Overall Model: (Intercept): Pr(>|t|)",
                "Overall Model: Moderate: Pr(>|t|)",
                "Overall Model: Marked: Pr(>|t|)",
                "Overall Model: Severe: Pr(>|t|)"
)

# Get the columns which give estimates or p-values
# only for marked and severe groups
matchcols(x, with=c("Pr", "Std. Error"),
             without=c("Intercept","Moderate"),
             method="or"
)

# Get just the column which give the p-value for the intercept
matchcols(x, with=c("Intercept", "Pr") )
Table of conversions between International Standard (SI) and US 'Conventional' Units for common medical measurements.

Description

Table of conversions between International Standard (SI) and US 'Conventional' Units for common medical measurements.

Usage

data(MedUnits)

Format

A data frame with the following 5 variables.

- **Abbreviation**: Common Abbreviation (mostly missing)
- **Measurement**: Measurement Name
- **ConventionalUnit**: Conventional Unit
- **Conversion**: Conversion factor
- **SIUnit**: SI Unit

Details

Medical laboratories and practitioners in the United States use one set of units (the so-called 'Conventional' units) for reporting the results of clinical laboratory measurements, while the rest of the world uses the International Standard (SI) units. It often becomes necessary to translate between these units when participating in international collaborations.

This data set provides constants for converting between SI and US 'Conventional' units.

To perform the conversion from SI units to US 'Conventional' units do:

- Measurement in ConventionalUnit = (Measurement in SIUnit) / Conversion

To perform conversion from 'Conventional' to SI units do:

- Measurement in SIUnit = (Measurement in ConventionalUnit) * Conversion

Source

http://www.globalrph.com/conv_si.htm

See Also

The function ConvertMedUnits automates the conversion task.
Examples

```r
data(MedUnits)

# show available conversions
MedUnits$Measurement

# utility function
matchUnits <- function(X) MedUnits[ grep(X, MedUnits$Measurement),]

# Convert SI Glucose measurement to 'Conventional' units
GlucoseSI = c(5, 5.4, 5, 5.1, 5.6, 5.1, 4.9, 5.2, 5.5) # in SI Units
GlucoseUS = GlucoseSI / matchUnits("Glucose")$Conversion
cbind(GlucoseSI,GlucoseUS)

# also consider using ConvertMedUnits()
ConvertMedUnits( GlucoseSI, "Glucose", to="US" )
```

---

`nobs`

**Compute the Number of Non-missing Observations**

Description

Compute the number of non-missing observations. Provides a 'default' method to handle vectors, and a method for data frames.

Usage

```r
nobs(object, ...)
```

## Default S3 method:

```r
nobs(object, ...)
```

## S3 method for class 'data.frame'

```r
nobs(object, ...)
```

## S3 method for class 'lm'

```r
nobs(object, ...)
```

Arguments

- `object` Target Object
- `...` Optional parameters (currently ignored)

Details

Calculate the number of observations in `object`.

- For numeric vectors, this is simply the number of non-NA elements, as computed by `sum(!is.na(object))`.
- For dataframe objects, the result is a vector containing the number of non-NA elements of each column.
The `nobs` and `nobs.lm` functions defined in gtools are simply aliases for the functions in the base R `stats` package, provided for backwards compatibility.

**Value**

Either single numeric value (for vectors) or a vector of numeric values (for data.frames) giving the number of non-missing values.

**Note**

The base R package `stats` now provides a S3 dispatch function for `nobs`, and methods for for objects of classes "lm", "glm", "nls" and "logLik", as well as a default method.

Since they provided a subset of the functionality, the base method dispatch (`nobs` function and method for "lm" objects (`nobs.lm`) are, as of gdata version 2.10.1, simply aliases for the equivalent functions in the base R `stats` package.

Since gdata's default method (`nobs.default`) processes vectors and hands any other data/object types to `stats:::nobs.default`.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

`is.na`, `length`

**Examples**

```r
x <- c(1, 2, 3, 5, NA, 6, 7, 1, NA)
length(x)
nobs(x)

df <- data.frame(x=rnorm(100), y=rnorm(100))
df[1, 1] <- NA
df[1, 2] <- NA
df[2, 1] <- NA

nobs(df)

fit <- lm(y ~ x, data=df)
nobs(fit)
```
nPairs

**Number of variable pairs**

### Description

*nPairs* counts the number of pairs between variables.

### Usage

nPairs(x, margin=FALSE, names=TRUE, abbrev=TRUE, ...)

### Arguments

- **x**  
  data.frame or a matrix
- **margin**  
  logical, calculate the cumulative number of “pairs”
- **names**  
  logical, add row/col-names to the output
- **abbrev**  
  logical, abbreviate names
- **...**  
  other arguments passed to `abbreviate`

### Details

The class of returned matrix is `nPairs` and matrix. There is a summary method, which shows the opposite information - counts how many times each variable is known, while the other variable of a pair is not. See examples.

### Value

Matrix of order $k$, where $k$ is the number of columns in $x$. Values in a matrix represent the number of pairs between columns/variables in $x$. If `margin=TRUE`, the number of columns is $k + 1$ and the last column represents the cumulative number of pairing all variables.

### Author(s)

Gregor Gorjanc

### See Also

`abbreviate`

### Examples

```r
## Test data
test <- data.frame(V1=c(1, 2, 3, 4, 5),
                    V2=c(NA, 2, 3, 4, 5),
                    V3=c(1, NA, NA, NA, NA),
                    V4=c(1, 2, 3, NA, NA))
```
## Description

Provides an estimate of the memory that is being used to store an R object.

## Usage

```r
object.size(...)
```

## Arguments

- `...`
  - `object.size`: R objects; `print` arguments to be passed to or from other methods.
  - `x`: output from `object.size`
  - `quote`: logical, indicating whether or not the result should be printed with surrounding quotes.
  - `humanReadble`: logical, use the "human readable" format.

## Details

This is a modified copy from the utils package in R as for 2008-12-15.

Exactly which parts of the memory allocation should be attributed to which object is not clear-cut. This function merely provides a rough indication: it should be reasonably accurate for atomic vectors, but does not detect if elements of a list are shared, for example. (Sharing amongst elements of a character vector is taken into account, but not that between character vectors in a single object.)
The calculation is of the size of the object, and excludes the space needed to store its name in the symbol table.

Associated space (e.g. the environment of a function and what the pointer in a EXTPTSRSP points to) is not included in the calculation.

Object sizes are larger on 64-bit platforms than 32-bit ones, but will very likely be the same on different platforms with the same word length and pointer size.

Class of returned object is c("byte", "numeric") with appropriate print and c methods.

By default object.size outputs size in bytes, but human readable format similar to ls, df or du shell commands can be invoked with options(humanReadable=TRUE).

Value

An object of class "object.size" with a length-one double value, an estimate of the memory allocation attributable to the object in bytes.

See Also

Memory-limits for the design limitations on object size. humanReadable for human readable format.

Examples

object.size(letters)
object.size(ls)
## find the 10 largest objects in the base package
z <- sapply(ls("package:base"), function(x)
  object.size(get(x, envir = baseenv())))
(tmp <- as.matrix(rev(sort(z))[1:10]))

as.object.size(14567567)
options(humanReadable=TRUE)
(z <- object.size(letters, c(letters, letters), rep(letters, 100), rep(letters, 10000)))
is.object.size(z)
as.object.size(14567567)

Description

Read Excel files

Read a Microsoft Excel file into a data frame
Usage

```r
read.xls(xls, sheet=1, verbose=FALSE, pattern, na.strings=c("NA","INT/0"),
  ... , method=c("csv","tsv","tab"), perl="perl")
```

```r
xls2csv(xls, sheet=1, verbose=FALSE, blank.lines.skip=TRUE, ... , perl="perl")
```

```r
xls2tab(xls, sheet=1, verbose=FALSE, blank.lines.skip=TRUE, ... , perl="perl")
```

```r
xls2tsv(xls, sheet=1, verbose=FALSE, blank.lines.skip=TRUE, ... , perl="perl")
```

```r
xls2sep(xls, sheet=1, verbose=FALSE, blank.lines.skip=TRUE, ... ,
  method=c("csv","tsv","tab"), perl="perl")
```

Arguments

- **xls**: path to the Microsoft Excel file. Supports "http://", "https://", and "ftp://" URLs.
- **sheet**: name or number of the worksheet to read
- **verbose**: logical flag indicating whether details should be printed as the file is processed.
- **pattern**: if specified, them skip all lines before the first containing this string
- **perl**: name of the perl executable to be called.
- **method**: intermediate file format, "csv" for comma-separated and "tab" for tab-separated
- **na.strings**: a character vector of strings which are to be interpreted as 'NA' values. See `read.table` for details.
- **blank.lines.skip**: logical flag indicating whether blank lines in the original file should be ignored.
- ... additional arguments to read.table. The defaults for read.csv() are used.

Details

This function works translating the named Microsoft Excel file into a temporary .csv or .tab file, using the xls2csv or xls2tab Perl script installed as part of this (gdata) package.

Caution: In the conversion to csv, strings will be quoted. This can be problem if you are trying to use the `comment.char` option of `read.table` since the first character of all lines (including comment lines) will be "\"" after conversion.

If you have quotes in your data which confuse the process you may wish to use `read.xls(...)`, `quote = '\'`). This will cause the quotes to be regarded as data and you will have to then handle the quotes yourself after reading the file in.

Caution: If you call "xls2csv" directly, is your responsibility to close and delete the file after using it.

Value

- "read.xls" returns a data frame.
- "xls2sep" returns a temporary file in the specified format. "xls2csv" and "xls2tab" are simply wrappers for "xls2sep" specifying method as "csv" or "tab", respectively.

Note

Either a working version of Perl must be present in the executable search path, or the exact path of the perl executable must be provided via the perl argument. See the examples below for an illustration.
Author(s)

Gregory R. Warnes <greg@warnes.net>, Jim Rogers <james.a.rogers@pfizer.com>, and Gabor Grothendieck <ggrothendieck@gmail.com>.

References

http://www.analytics.washington.edu/statcomp/downloads/xls2csv

See Also

read.csv

Examples

# iris.xls is included in the gregmisc package for use as an example
xlsfile <- file.path(path.package('gdata'), 'xls', 'iris.xls')
xlsfile

iris <- read.xls(xlsfile) # defaults to csv format
iris <- read.xls(xlsfile.method="csv") # specify csv format
iris <- read.xls(xlsfile.method="tab") # specify tab format

head(iris) # look at the top few rows

## Not run:
## Example specifying exact Perl path for default MS-Windows install of
## ActiveState perl
iris <- read.xls(xlsfile, perl="C:\perl\bin\perl.exe")

## End(Not run)

## Not run:
## Example specifying exact Perl path for Unix systems
iris <- read.xls(xlsfile, perl="/usr/bin/perl")

## finding perl
## (read.xls automatically calls findPerl so this is rarely needed)
perl <- gdata:::findPerl("perl")
iris <- read.xls(xlsfile, perl=perl)

## End(Not run)

## Not run:
## read xls file from net
nba.url <- "http://mgtclass.mgt.unm.edu/Bose/Excel/Tutorial.05/Cases/NBA.xls"
nba <- read.xls(nba.url)

## End(Not run)
rename.vars

## Not run:
## read xls file ignoring all lines prior to first containing State
crime.url <- "http://www.jrsainfo.org/jabg/state_data2/Tribal_Data00.xls"
crime <- read.xls(crime.url, pattern = "State")

## use of xls2csv - open con, print two lines, close con
con <- xls2csv(crime.url)
print(readLines(con, 2))
file.remove(summary(con)$description)

## End(Not run)

## Examples demonstrating selection of specific 'sheets'
## from the example XLS file 'ExampleExcelFile.xls'
exampleFile <- file.path(path.package('gdata'), 'xls',
                          'ExampleExcelFile.xls')
exampleFile2007 <- file.path(path.package('gdata'), 'xls',
                          'ExampleExcelFile.xlsx')

## see the number and names of sheets:
sheetCount(exampleFile)
if( 'XLSX' %in% xlsFormats() ) ## if XLSX is supported..
    sheetCount(exampleFile2007)

## show names of sheets in the file
sheetNames(exampleFile)
if( 'XLSX' %in% xlsFormats() ) ## if XLSX is supported..
    sheetNames(exampleFile2007)

data <- read.xls(exampleFile) ## default is first worksheet
data <- read.xls(exampleFile, sheet=2) ## second worksheet by number
data <- read.xls(exampleFile, sheet="Sheet Second",v=TRUE) ## and by name

## load the third worksheet, skipping the first two non-data lines...
if( 'XLSX' %in% xlsFormats() ) ## if XLSX is supported..
    data <- read.xls(exampleFile2007, sheet="Sheet with initial text", skip=2)

## load a file containing data and column names using latin-1
## characters
latinFile <- file.path(path.package('gdata'), 'xls', 'latin-1.xls')
latin1 <- read.xls(latinFile, fileEncoding="latin1")
colnames(latin1)

rename.vars

Remove or rename variables in a dataframe
rename.vars

Description

Remove or rename variables in a data frame.

Usage

rename.vars(data, from="", to="", info=TRUE)
remove.vars(data, names="", info=TRUE)

Arguments

data dataframe to be modified.
from character vector containing the current name of each variable to be renamed.
to character vector containing the new name of each variable to be renamed.
names character vector containing the names of variables to be removed.
info boolean value indicating whether to print details of the removal/renaming. Defaults to TRUE.

Value

The updated data frame with variables listed in from renamed to the corresponding element of to.

Author(s)

Code by Don MacQueen <macq@llnl.gov>. Documentation by Gregory R. Warnes <greg@warne.net>

See Also

names, colnames, data.frame

Examples

data <- data.frame(x=1:10, y=1:10, z=1:10)
names(data)
data <- rename.vars(data, c("x","y","z"), c("first","second","third"))
names(data)
data <- remove.vars(data, "second")
names(data)
### Description

Reorder the levels of a factor

### Usage

```r
## S3 method for class 'factor'
reorder(x, 
X, 
FUN, 
..., 
order=is.ordered(x), 
new.order, 
sort=mixedsort)
```

### Arguments

- **x**: factor
- **X**: auxiliary data vector
- **FUN**: function to be applied to subsets of `X` determined by `x`, to determine factor order
- **...**: optional parameters to `FUN`
- **order**: logical value indicating whether the returned object should be an `ordered` factor
- **new.order**: a vector of indexes or a vector of label names giving the order of the new factor levels
- **sort**: function to use to sort the factor level names, used only when `new.order` is missing

### Details

This function changes the order of the levels of a factor. It can do so via three different mechanisms, depending on whether, `X` and `FUN`, `new.order` or `sort` are provided.

If `X` and `FUN` are provided: The data in `X` is grouped by the levels of `x` and `FUN` is applied. The groups are then sorted by this value, and the resulting order is used for the new factor level names.

If `new.order` is provided: For a numeric vector, the new factor level names are constructed by reordering the factor levels according to the numeric values. For vectors, `new.order` gives the list of new factor level names. In either case levels omitted from `new.order` will become missing (`NA`) values.

If `sort` is provided (as it is by default): The new factor level names are generated by applying the supplied function to the existing factor level names. With `sort=mixedsort` the factor levels are sorted so that combined numeric and character strings are sorted in according to character rules on the character sections (including ignoring case), and the numeric rules for the numeric sections. See `mixedsort` for details.
Value

A new factor with reordered levels

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

factor and reorder

Examples

# Create a 4 level example factor
trt <- factor(sample(c("PLACEBO", "300 MG", "600 MG", "1200 MG"), 100, replace=TRUE ))
summary(trt)
# Note that the levels are not in a meaningful order.

# Change the order to something useful
# default "mixedsort" ordering
trt2 <- reorder(trt)
summary(trt2)
# using indexes:
trt3 <- reorder(trt, new.order=c(4, 2, 3, 1))
summary(trt3)
# using label names:
trt4 <- reorder(trt, new.order=c("PLACEBO", "300 MG", "600 MG", "1200 MG"))
summary(trt4)
# using frequency
trt5 <- reorder(trt, X=as.numeric(trt), FUN=length)
summary(trt5)

# drop out the '300 MG' level
trt6 <- reorder(trt, new.order=c("PLACEBO", "600 MG", "1200 MG"))
summary(trt6)

resample

Consistent Random Samples and Permutations

Description

resample takes a sample of the specified size from the elements of x using either with or without replacement.

Usage

resample(x, size, replace = FALSE, prob = NULL)
**Arguments**

- **x**: A numeric, complex, character or logical vector from which to choose.
- **size**: Non-negative integer giving the number of items to choose.
- **replace**: Should sampling be with replacement?
- **prob**: A vector of probability weights for obtaining the elements of the vector being sampled.

**Details**

resample differs from the S/R sample function in resample always considers x to be a vector of elements to select from, while sample treats a vector of length one as a special case and samples from 1:x. Otherwise, the functions have identical behavior.

**Value**

Vector of the same length as the input, with the elements permuted.

**Author(s)**

Gregory R. Warnes <greg@warnes.net>

**See Also**

sample

**Examples**

```r
## sample behavior differs if first argument is scalar vs vector
sample( c(10) )
sample( c(10,10) )

## resample has the consistent behavior for both cases
resample( c(10) )
resample( c(10,10) )
```

---

**sheetCount**  
*Count or list sheet names in Excel spreadsheet files.*

**Description**

Count or list sheet names in Excel spreadsheet files.

**Usage**

```r
sheetCount(xls, verbose = FALSE, perl = "perl")
sheetNames(xls, verbose = FALSE, perl = "perl")
```
**Arguments**

- **xls**: File path to spreadsheet. Supports "http://", "https://", and "ftp://" URLs.
- **verbose**: If TRUE, show additional messages during processing.
- **perl**: Path to perl interpreter.

**Value**

- `sheetCount` returns the number of sheets in the spreadsheet. `sheetNames` returns the names of sheets in the spreadsheet.

**See Also**

- `read.xls`, `xls2csv`.

**Examples**

```r
xlsfile <- system.file("xls", "iris.xls", package = "gdata")
xlsfile

sheetCount(xlsfile)

exampleFile <- file.path(path.package("gdata"), "xls", 'ExampleExcelFile.xls')
exampleFile2007 <- file.path(path.package("gdata"), "xls", 'ExampleExcelFile.xlsx')

sheetCount(exampleFile)

if( 'XLSX' %in% xlsFormats() ) # if XLSX is supported.
  sheetNames(exampleFile2007)
```

---

**startsWith**

*Determine if a character string "starts with" with the specified characters.*

**Description**

Determine if a character string "starts with" with the specified characters.

**Usage**

`startsWith(str, pattern, trim=FALSE, ignore.case=FALSE)`
trim

Arguments

str character vector to test
pattern characters to check for
trim Logical flag indicating whether leading whitespace should be removed from str before testing for a match.
ignore.case Logical flag indicating whether case should be ignored when testing for a match.

Details

This function returns TRUE for each element of the vector str where pattern occurs at the beginning of the string. If trim is TRUE, leading whitespace is removed from the elements of str before the test is performed. If ignore.case is TRUE, character case is ignored.

Value

Boolean vector of the same length as str.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

substr, trim

Examples

## simplest example:
startsWith( 'Testing', 'Test')

## vector examples
s <- c('Testing', ' Testing', 'testing', 'Texting')
names(s) <- s
startsWith(s, 'Test')  # 'Testing', 'testing', and 'Texting' do not match
startsWith(s, 'Test', trim=TRUE)  # Now 'Testing' matches
startsWith(s, 'Test', ignore.case=TRUE)  # Now 'testing' matches

trim Remove leading and trailing spaces from character strings

Description

Remove leading and trailing spaces from character strings and other related objects.

Usage

trim(s, recode.factor=TRUE, ...)

## simplest example:
startsWith( 'Testing', 'Test')

## vector examples
s <- c('Testing', ' Testing', 'testing', 'Texting')
names(s) <- s
startsWith(s, 'Test')  # 'Testing', 'testing', and 'Texting' do not match
startsWith(s, 'Test', trim=TRUE)  # Now 'Testing' matches
startsWith(s, 'Test', ignore.case=TRUE)  # Now 'testing' matches

trim Remove leading and trailing spaces from character strings

Description

Remove leading and trailing spaces from character strings and other related objects.

Usage

trim(s, recode.factor=TRUE, ...)

## simplest example:
startsWith( 'Testing', 'Test')

## vector examples
s <- c('Testing', ' Testing', 'testing', 'Texting')
names(s) <- s
startsWith(s, 'Test')  # 'Testing', 'testing', and 'Texting' do not match
startsWith(s, 'Test', trim=TRUE)  # Now 'Testing' matches
startsWith(s, 'Test', ignore.case=TRUE)  # Now 'testing' matches

trim Remove leading and trailing spaces from character strings

Description

Remove leading and trailing spaces from character strings and other related objects.

Usage

trim(s, recode.factor=TRUE, ...)
Arguments

s      object to be processed
recode.factor should levels of a factor be recoded, see below
... arguments passed to other methods, currently only to reorder.factor for factors

Details

trim is a generic function, where default method does nothing, while method for character s trims its elements and method for factor s trims levels. There are also methods for list and data.frame.

Trimming character strings can change the sort order in some locales. For factors, this can affect the coding of levels. By default, factor levels are recoded to match the trimmed sort order, but this can be disabled by setting recode.factor=FALSE. Recoding is done with reorder.factor.

Value

s with all leading and trailing spaces removed in its elements.

Author(s)

Gregory R. Warnes <greg@warnes.net> with contributions by Gregor Gorjanc

See Also

sub, gsub as well as argument strip.white in read.table and reorder.factor

Examples

s <- " this is an example string   "
trim(s)

f <- factor(c(s, s, " A", " B ", " C ", "D ")
levels(f)

trim(f)
levels(trim(f))

trim(f, recode.factor=FALSE)
levels(trim(f, recode.factor=FALSE))

l <- list(s=rep(s, times=6), f=f, i=1:6)
trim(l)

df <- as.data.frame(l)
trim(df)
trimSum

Trim a vector such that the last/first value represents the sum of trimmed values

Description
trimSum trims (shortens) a vector in such a way that the last or first value represents the sum of trimmed values. User needs to specify the desired length of a trimmed vector.

Usage
trimSum(x, n, right=TRUE, na.rm=FALSE, ...)

Arguments
x numeric, a vector of numeric values
n numeric, desired length of the output
right logical, trim on the right/bottom or the left/top side
na.rm logical, remove NA values when applying a function
... arguments passed to other methods - currently not used

Value
Trimmed vector with a last/first value representing the sum of trimmed values

Author(s)
Gregor Gorjanc

See Also
trim

Examples
x <- 1:10
trimSum(x, n=5)
trimSum(x, n=5, right=FALSE)

x[9] <- NA
trimSum(x, n=5)
trimSum(x, n=5, na.rm=TRUE)
unknownToNA  

Change unknown values to NA and vice versa

**Description**

Unknown or missing values (NA in R) can be represented in various ways (as 0, 999, etc.) in different programs. `isUnknown`, `unknownToNA`, and `NAToUnknown` can help to change unknown values to NA and vice versa.

**Usage**

```r
isUnknown(x, unknown=NA, ...)  
unknownToNA(x, unknown, warning=FALSE, ...)  
NAToUnknown(x, unknown, force=FALSE, call.=FALSE, ...)
```

**Arguments**

- `x`: generic, object with unknown value(s)
- `unknown`: generic, value used instead of NA
- `warning`: logical, issue warning if `x` already has NA
- `force`: logical, force to apply already existing value in `x`
- `...`: arguments pased to other methods (as.character for POSIXlt in case of `isUnknown`)
- `call.`: logical, look in `warning`

**Details**

This functions were written to handle different variants of “other NA” like representations that are usually used in various external data sources. `unknownToNA` can help to change unknown values to NA for work in R, while `NAToUnknown` is meant for the opposite and would usually be used prior to export of data from R. `isUnknown` is utility function for testing for unknown values.

All functions are generic and the following classes were tested to work with latest version: “integer”, “numeric”, “character”, “factor”, “Date”, “POSIXct”, “POSIXlt”, “list”, “data.frame” and “matrix”. For others default method might work just fine.

`unknownToNA` and `isUnknown` can cope with multiple values in `unknown`, but those should be given as a “vector”. If not, coercing to vector is applied. Argument `unknown` can be feed also with “list” in “list” and “data.frame” methods.

If named “list” or “vector” is passed to argument `unknown` and `x` is also named, matching of names will occur.

Recycling occurs in all “list” and “data.frame” methods, when `unknown` argument is not of the same length as `x` and `unknown` is not named.
Argument **unknown** in `NAToUnknown` should hold value that is not already present in `x`. If it does, error is produced and one can bypass that with `force=TRUE`, but be warned that there is no way to distinguish values after this action. Use at your own risk! Anyway, warning is issued about new value in `x`. Additionally, caution should be taken when using `NAToUnknown` on factors as additional level (value of `unknown`) is introduced. Then, as expected, `unknownToNA` removes defined level in `unknown`. If `unknown="NA"`, then "NA" is removed from factor levels in `unknownToNA` due to consistency with conversions back and forth.

Unknown representation in `unknown` should have the same class as `x` in `NAToUnknown`, except in factors, where `unknown` value is coerced to character anyway. Silent coercion is also applied, when “integer” and “numeric” are in question. Otherwise warning is issued and coercing is tried. If that fails, `R` introduces `NA` and the goal of `NAToUnknown` is not reached.

`NAToUnknown` accepts only single value in `unknown` if `x` is atomic, while “list” and “data.frame” methods accept also “vector” and “list”.

“list/data.frame” methods can work on many components/columns. To reduce the number of needed specifications in `unknown` argument, default `unknown` value can be specified with component ".default". This matches component/column ".default" as well as all other undefined components/columns! Look in examples.

**Value**

`unknownToNA` and `NAToUnknown` return modified `x`. `isUnknown` returns logical values for object `x`.

**Author(s)**

Gregor Gorjanc

**See Also**

`is.na`

**Examples**

```r
xInt <- c(0, 1, 0, 5, 6, 7, 8, 9, NA)
isUnknown(x=xInt, unknown=0)
isUnknown(x=xInt, unknown=c(0, NA))
(xInt <- unknownToNA(x=xInt, unknown=0))
(xInt <- NAToUnknown(x=xInt, unknown=0))

xFac <- factor(c("0", 1, 2, 3, NA, "NA"))
isUnknown(x=xFac, unknown=0)
isUnknown(x=xFac, unknown=c(0, NA))
isUnknown(x=xFac, unknown=c(0, "NA"))
isUnknown(x=xFac, unknown=c(0, "NA", NA))
(xFac <- unknownToNA(x=xFac, unknown="NA"))
(xFac <- NAToUnknown(x=xFac, unknown="NA"))

xList <- list(xFac=xFac, xInt=xInt)
isUnknown(xList, unknown=c("NA", 0))
isUnknown(xList, unknown=list("NA", 0))
```
unmatrix

Convert a matrix into a vector, with appropriate names

Description

Convert a matrix into a vector, with element names constructed from the row and column names of the matrix.

Usage

unmatrix(x, byrow=FALSE)

Arguments

x

matrix

byrow

Logical. If FALSE, the elements within columns will be adjacent in the resulting vector, otherwise elements within rows will be adjacent.

Value

A vector with names constructed from the row and column names from the matrix. If the the row or column names are missing, ('r1', 'r2', ...) or ('c1', 'c2', ...) will be used as appropriate.

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also

as.vector

Examples

# simple, useless example
m <- matrix(letters[1:10], ncol=5)
m
unmatrix(m)

# unroll model output
upper Triangle

Description

Extract or replace the upper/lower triangular portion of a matrix

Usage

upperTriangle(x, diag=FALSE)
upperTriangle(x, diag=FALSE) <- value
lowerTriangle(x, diag=FALSE)
lowerTriangle(x, diag=FALSE) <- value

Arguments

x Matrix
diag Logical. If TRUE, include the matrix diagonal.
value Either a single value or a vector of length equal to that of the current upper/lower triangular. Should be of a mode which can be coerced to that of x.

Value

upperTriangle(x) and lowerTriangle(x) return the upper or lower triangle of matrix x, respectively. The assignment forms replace the upper or lower triangular area of the matrix with the provided value(s).

Author(s)

Gregory R. Warnes <greg@warnes.net>

See Also
diag

Examples

x <- matrix(1:25, nrow=5, ncol=5)
x
upperTriangle(x)
upperTriangle(x, diag=TRUE)
lowerTriangle(x)
wideByFactor(x, factor, common, sort=TRUE, keepFactor=TRUE)

Arguments

x    data frame
factor    character, column name of a factor by which variables will be divided
common    character, column names of (common) columns that should not be divided
sort    logical, sort resulting data frame by factor levels
keepFactor    logical, keep the ‘factor’ column

Details

Given data frame is modified in such a way, that output represents a data frame with $c + f + n \times v$ columns, where $c$ is a number of common columns for all levels of a factor, $f$ is a factor column, $n$ is a number of levels in factor $f$ and $v$ is a number of variables that should be divided for each level of a factor. Number of rows stays the same!

Value

A data frame where divided variables have sort of “diagonalized” structure
write.fwf

Author(s)
Gregor Gorjanc

See Also
reshape in the stats package, melt and cast in the reshape package

Examples
```r
n <- 10
f <- 2
tmp <- data.frame(y1=rnorm(n=n),
                  y2=rnorm(n=n),
                  f1=factor(rep(letters[1:f], n/2)),
                  f2=factor(c(rep("M", n/2), rep(c("M", c("F"), n/2))),
                  c1=1:n),
                  c2=2*(1:n))

wideByFactor(x=tmp, factor="f1", common=c("c1", "c2", "f2"))
wideByFactor(x=tmp, factor="f1", common=c("c1", "c2"))
```

write.fwf

Write object in fixed width format

Description
write.fwf writes object in fixed width format.

Usage
```r
write.fwf(x, file=", append=FALSE, quote=FALSE, sep=" ", na="",
rownames=FALSE, colnames=TRUE, rowCol=NULL, justify="left",
formatInfo=FALSE, quoteInfo=TRUE, width=NULL, eol="\n",
qmethod=c("escape", "double"), ...)
```

Arguments
- **x**: data.frame or matrix, the object to be written
- **file**: character, name of file or connection, look in write.table for more
- **append**: logical, append to existing data in file
- **quote**: logical, quote data in output
- **na**: character, the string to use for missing values i.e. NA in the output
- **sep**: character, separator between columns in output
- **rownames**: logical, print row names
colnames logical, print column names
rowCol character, rownames column name
justify character, alignment of character columns; see format
formatInfo logical, return information on number of levels, widths and format
quoteInfo logical, should formatInfo account for quotes
width numeric, width of the columns in the output
eol the character(s) to print at the end of each line (row). For example, 'eol="\r\n"' will produce Windows' line endings on a Unix-alike OS, and 'eol="\r"' will produce files as expected by Mac OS Excel 2004.
qmethod a character string specifying how to deal with embedded double quote characters when quoting strings. Must be one of "escape" (default), in which case the quote character is escaped in C style by a backslash, or "double", in which case it is doubled. You can specify just the initial letter.

... further arguments to format.info and format

Details

*Fixed *width *format is not used widely anymore. Use some other format (say *comma separated *values; see read.csv) if you can. However, if you need fixed width format then write.fwf can help you.

Output is similar to print(x) or format(x). Formatting is done completely by format on a column basis. Columns in the output are by default separated with a space i.e. empty column with a width of one character, but that can be changed with sep argument as passed to write.table via ....

As mentioned formatting is done completely by format. Arguments can be passed to format via ... to further modify the output. However, note that the returned formatInfo might not properly account for this, since format.info (which is used to collect information about formatting) lacks the arguments of format.

quote can be used to quote fields in the output. Since all columns of x are converted to character (via format) during the output, all columns will be quoted! If quotes are used, read.table can be easily used to read the data back into R. Check examples. Do read the details about quoteInfo argument.

Use only *true* character, i.e., avoid use of tabs, i.e., "\t", or similar separators via argument sep. Width of the separator is taken as the number of characters evaluated via nchar(sep).

Use argument na to convert missing/unknown values. Only single value can be specified. Use NToUnknown prior to export if you need greater flexibility.

If rowCol is not NULL and rownames=TRUE, rownames will also have column name with rowCol value. This is mainly for flexibility with tools outside R. Note that (at least in R 2.4.0) it is not "easy" to import data back to R with read.fwf if you also export rownames. This is the reason, that default is rownames=FALSE.

Information about format of output will be returned if formatInfo=TRUE. Returned value is described in value section. This information is gathered by format.info and care was taken to handle numeric properly. If output contains rownames, values account for this. Additionally, if rowCol is not NULL returned values contain also information about format of rownames.
If quote=TRUE, the output is of course wider due to quotes. Return value (with formatInfo=TRUE) can account for this in two ways; controlled with argument quoteInfo. However, note that there is no way to properly read the data back to R if quote=TRUE & quoteInfo=FALSE arguments were used for export. quoteInfo applies only when quote=TRUE. Assume that there is a file with quoted data as shown below (column numbers in first three lines are only for demonstration of the values in the output).

123456789 12345678 # for position
123 1234567 123456 # for width with quoteInfo=TRUE
1 12345 1234 # for width with quoteInfo=FALSE
"a" "hsgh" " 9"
" " " "bb" " 123"

With quoteInfo=TRUE write.fwf will return

colname position width
V1 1 3
V2 5 7
V3 13 6

or (with quoteInfo=FALSE)

colname position width
V1 2 1
V2 6 5
V3 14 4

Argument width can be used to increase the width of the columns in the output. This argument is passed to the width argument of format function. Values in width are recycled if there is less values than the number of columns. If the specified width is to short in comparison to the "width" of the data in particular column, error is issued.

Value

Besides its effect to write/export data write.fwf can provide information on format and width. A data.frame is returned with the following columns:

colname name of the column
nlevels number of unique values (unused levels of factors are dropped), 0 for numeric column
position starting column number in the output
width width of the column
digits number of digits after the decimal point
exp width of exponent in exponential representation; 0 means there is no exponential representation, while 1 represents exponent of length one i.e. 1e+6 and 2 1e+06 or 1e+16
Author(s)

Gregor Gorjanc

See Also

format.info, format, NAnToUnknown, write.table, read.fwf, read.table and trim

Examples

```r
## Some data
data <- round(c(733070.345678, 1214213.78765456, 553823.79876567, 1005022.8876545678, 571063.88765456, 606718.3876545678, 1053686.6, 971024.187656, 631193.398765456, 879431.1), digits=3)

testData <- data.frame(num1=c(1:10, NA),
                        num2=c(NA, seq(from=1, to=5.5, by=0.5)),
                        num3=c(NA, num),
                        int1=c(as.integer(1:4), NA, as.integer(4:9)),
                        fac1=factor(c(NA, letters[1:9], "hjh")),
                        fac2=factor(c(letters[6:15], NA)),
                        cha1=c(letters[17:26], NA),
                        cha2=c(NA, "longer", letters[25:17]),
                        stringsAsFactors=FALSE)
levels(testData$fac1) <- c(levels(testData$fac1), "unusedLevel")
testData$Date <- as.Date("1900-1-1")
testData$Date[2] <- NA
testData$POSIXt <- as.POSIXct(strptime("1900-1-1 01:01:01", format="%Y-%m-%d %H:%M:%S"))
testData$POSIXt[5] <- NA

## Default
write.fwf(x=testData)

## NA should be -
write.fwf(x=testData, na="-")
## NA should be ~NA~
write.fwf(x=testData, na="~NA~")

## Some other separator than space
write.fwf(x=testData[, 1:4], sep="-mySep-")

## Force wider columns
write.fwf(x=testData[, 1:5], width=20)

## Write to file and report format and fixed width information
file <- tempfile()
formatInfo <- write.fwf(x=testData, file=file, formatInfo=TRUE)

## Read exported data back to R (note +1 due to separator)
## ... without header
```
read.fwf(file=file, widths=formatInfo$width + 1, header=FALSE, skip=1, strip.white=TRUE)

## ... with header - via postimport modification
tmp <- read.fwf(file=file, widths=formatInfo$width + 1, skip=1, strip.white=TRUE)
colnames(tmp) <- read.table(file=file, nrow=1, as.is=TRUE)

tmp

## ... with header - persuading read.fwf to accept header properly
## (thanks to Marc Schwartz)
read.fwf(file=file, widths=formatInfo$width + 1, strip.white=TRUE, skip=1, col.names=read.table(file=file, nrow=1, as.is=TRUE))

## ... with header - with the use of quotes
write.fwf(x=testData, file=file, quote=TRUE)
read.table(file=file, header=TRUE, strip.white=TRUE)

## Tidy up
unlink(file)

---

**xlsFormats**

Check which file formats are supported by read.xls

### Description

Check which file formats are supported by read.xls

### Usage

```r
xlsFormats(perl = "perl", verbose = FALSE)
```

### Arguments

- **perl**
  - Path to perl interpreter (optional).
- **verbose**
  - If TRUE, show additional messages during processing.

### Value

Vector of supported formats, possible elements are 'XLS' and 'XLSX'.

### See Also

- `read.xls`, `xls2csv`

### Examples

```r
xlsFormats()
```
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