Package ‘RecordLinkage’

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Description Provides functions for linking and de-duplicating data sets. Methods based on a stochastic approach are implemented as well as classification algorithms from the machine learning domain.
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genSamples.r strcmp.r compare.r getPairs.r summary.r
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**classifySupv**

**Supervised Classification**

**Description**

Supervised classification of record pairs based on a trained model.

**Usage**

```r
classifySupv(model, newdata, ...)
```

```r
## S4 method for signature 'RecLinkClassif,RecLinkData'
classifySupv(model, newdata,
             convert.na = TRUE, ...)
```

```r
## S4 method for signature 'RecLinkClassif,RLBigData'
classifySupv(model, newdata,
             convert.na = TRUE, withProgressBar = (sink.number()==0), ...)
```

**Arguments**

- `model` Object of class `RecLinkClassif`. The calibrated model. See `trainSupv`.
- `newdata` Object of class "`RecLinkData`" or "`RLBigData`". The data to classify.
- `convert.na` Logical. Whether to convert missing values in the comparison patterns to 0.
- `withProgressBar` Whether to display a progress bar
- `...` Further arguments for the `predict` method.

**Details**

The record pairs in `newdata` are classified by calling the appropriate `predict` method for `model$model`.

By default, the "`RLBigDataDedup`" method displays a progress bar unless output is diverted by `sink`, e.g. when processing a Sweave file.

**Value**

For the "`RecLinkData`" method, a S3 object of class "`RecLinkResult`" that represents a copy of `newdata` with element `rpairs$prediction`, which stores the classification result, as addendum.

For the "`RLBigData`" method, a S4 object of class "`RLResult`".

**Author(s)**

Andreas Borg, Murat Sariyar
classifyUnsup

See Also
trainSupv for training of classifiers, classifyUnsup for unsupervised classification.

Examples

# Split data into training and validation set, train and classify with rpart
data(RLdata500)
pairs=compare.dedup(RLdata500, identity=identity.RLdata500, blockfld=list(1,3,5,6,7))
l=splitData(pairs, prop=0.5, keep.mprop=TRUE)
model=trainSupv(l$train, method="rpart", minsplit=5)
result=classifySupv(model=model, newdata=l$valid)
summary(result)

classifyUnsup  Unsupervised Classification

Description

Classify record pairs with unsupervised clustering methods.

Usage

classifyUnsup(rpairs, method, ...)

Arguments

rpairs Object of type RecLinkData. The data to classify.
method The classification method to use. One of "kmeans", "bclust".
... Further arguments for the classification method

Details

A clustering algorithm is applied to find clusters in the comparison patterns. In the case of two clusters (the default), the cluster further from the origin (i.e. representing higher similarity values) is interpreted as the set of links, the other as the set of non-links.

Supported methods are:

- kmeans  K-means clustering, see kmeans.
- bclust  Bagged clustering, see bclust.

Value

An object of class "RecLinkResult" that represents a copy of newdata with element rpairs$prediction, which stores the classification result, as addendum.
Author(s)
Andreas Borg, Murat Sariyar

See Also
trainSupv and classifySupv for supervised classification.

Examples
# Classification with bclust
data(RLdata500)
rpairs=compare.dedup(RLdata500, identity=identity.RLdata500,
blockfld=list(1,3,5,6,7))
result=classifyUnsup(rpairs,method="bclust")
summary(result)

close
Serialization of record linkage object.

Description
Saving, loading and deep copying of record linkage objects for big data sets.

Usage
clone(object, ...)
saveRLObject(object, file, ...)
loadRLObject(file)

Arguments
object Object of class "RLBigData". The object to save.
file The name of the file to save to or load from.
... Optional arguments for possible additions, currently not used.

Details
The classes for big data sets make use of file-backed data structures from the ff package, therefore the load and save mechanism of R is not sufficient for persistent storage of these objects. Also, assignment via <- does not duplicate the ff data structures.
clone makes a deep copy of an object by duplicating the underlying files.
saveRLObject saves an object to zip file containing a dump of the R object as well as the associated ff files.
loadRLObject loads an object from a file saved by saveRLObject.
clone and saveRLObject are generic functions with methods for "RLBigData" and "RLResult".
compare

If `loadRLObject` is called with `inPlace = FALSE` (the default), a working copy of the database is made in a temporary file and the original file left untouched. Calling with `inPlace = TRUE` sets the provided file as working copy and changes made to the database are persistent. This option is useful when working with large files in order to prevent disk usage overhead. `saveRLObject` and `loadRLObject` require working zip/unzip programs.

Value

c `clone` returns a deep copy of object.
loadRLObject returns the loaded object.
saveRLOObject is used for its side effects.

Note

Objects loaded with `inPlace = TRUE` must be saved again after changes have been made to the object (e.g. calculation of weights).

Author(s)

Andreas Borg, Murat Sariyar

---

**compare**  
*Compare Records*

**Description**

Builds comparison patterns of record pairs for deduplication or linkage.

**Usage**

```r
closeup.dedup (dataset, blockfld = FALSE, phonetic = FALSE,  
phonfun = pho_h, strcmp = FALSE, strcmpfun = jarowinkler, exclude = FALSE,  
identity = NA, n_match = NA, n_non_match = NA)

closeup.linkage (dataset1, dataset2, blockfld = FALSE,  
phonetic = FALSE, phonfun = pho_h, strcmp = FALSE,  
strcmpfun = jarowinkler, exclude = FALSE, identity1 = NA, identity2 = NA,  
n_match = NA, n_non_match = NA)
```

**Arguments**

- `dataset`  
  Table of records to be deduplicated. Either a data frame or a matrix.
- `dataset1`, `dataset2`  
  Two data sets to be linked.
- `blockfld`  
  Blocking field definition. A list of integer or character vectors with column indices or FALSE to disable blocking. See details and examples.
compare

**phonetic**
Determines usage of a phonetic code. If FALSE, no phonetic code will be used; if TRUE, the phonetic code will be used for all columns; if a numeric or character vector is given, the phonetic code will be used for the specified columns.

**phonfun**
Function for phonetic code. See details.

**strpos**
Determines usage of a string metric. Used in the same manner as phonetic

**strmpfun**
User-defined function for string metric. See details.

**exclude**
Columns to be excluded. A numeric or character vector specifying the columns which should be excluded from comparison

**identity, identity1, identity2**
Optional numerical vectors for identifying matches and non-matches. In a deduplication process, two records dataset[i,] and dataset[j,] are a true match if and only if identity[i,]==identity[j,]. In a linkage process, two records datasetQ[i,] and datasetR[j,] are a true match if and only if identityQ[i,]==identityR[j,].

**n_match, n_non_match**
Number of desired matches and non-matches in the result.

### Details

These functions build record pairs and finally comparison patterns by which these pairs are later classified as links or non-links. They make up the initial stage in a Record Linkage process after possibly normalizing the data. Two general scenarios are reflected by the two functions: compare.dedup works on a single data set which is to be deduplicated, compare.linkage is intended for linking two data sets together.

Data sets are represented as data frames or matrices (typically of type character), each row representing one record, each column representing one field or attribute (like first name, date of birth...). Row names are not retained in the record pairs. If an identifier other than row number is needed, it should be supplied as a designated column and excluded from comparison (see note on exclude below).

Each element of blockfld specifies a set of columns in which two records must agree to be included in the output. Each blocking definition in the list is applied individually, the sets obtained thereby are combined by a union operation. If blockfld is FALSE, no blocking will be performed, which leads to a large number of record pairs \( \frac{n(n-1)}{2} \) where \( n \) is the number of records.

As an alternative to blocking, a determined number of n_match matches and n_non_match non-matches can be drawn if identity or identity1 and identity2 are supplied. This is relevant for generating training sets for the supervised classifiers (see trainsup).

Fields can be excluded from the linkage process by supplying their column index in the vector exclude, which is especially useful for external identifiers. Excluded fields can still be used for blocking, also with phonetic code.

Phonetic codes and string similarity measures are supported for enhanced detection of misspellings. Applying a phonetic code leads to a binary values, where 1 denotes equality of the generated phonetic code. A string comparator leads to a similarity value in the range \([0,1]\). String comparison is not allowed on a field for which a phonetic code is generated. For phonetic encoding functions included in the package, see phonetics. For the included string comparators, see jarowinkler and levenshteinSim. Please note that phonetic code and string metrics can slow down the generation of comparison patterns significantly.
User-defined functions for phonetic code and string comparison can be supplied via the arguments `phonfun` and `strcmpfun`. `phonfun` is expected to have a single character argument (the string to be transformed) and must return a character value with the encoded string. `strcmpfun` must have as arguments the two strings to be compared and return a similarity value in the range $[0, 1]$, with 0 denoting the lowest and 1 denoting the highest degree of similarity. Both functions must be fully vectorized to work on matrices.

**Value**

An object of class `RecLinkPairs` with the following components:

- `data` Copy of the records, converted to a data frame.
- `pairs` Generated comparison patterns.
- `frequencies` For each column included in `pairs`, the average frequency of values (reciprocal of number of distinct values).

**Author(s)**

Andreas Borg, Murat Sariyar

**See Also**

`ReclinkData` for the format of returned objects,

**Examples**

```r
data(RLdata500)
data(RLdata10000)

# deduplication without blocking, use string comparator on names
# Not run: rpairs=compare.dedup(RLdata500, strcmp=1:4)
# linkage with blocking on first name and year of birth, use phonetic
# code on first components of first and last name
rpairs=compare.linkage(RLdata500, RLdata10000, blockfld=c(1,7), phonetic=c(1,3))
# deduplication with blocking on either last name or complete date of birth,
# use string comparator on all fields, include identity information
rpairs=compare.dedup(RLdata500, identity=identity.RLdata500, strcmp=TRUE,  
blockfld=list(1,c(5,6,7)))
# Draw 100 matches and 1000 non-matches
# Not run: rpairs=compare.dedup(RLdata10000, identity=identity.RLdata10000, n_match=100,  
n_non_match=10000)
# End(Not run)
```
deleteNULLs  

Remove NULL Values

Description
Removes all NULL elements from a list or vector.

Usage
deleteNULLs(x)

Arguments
x  A vector or list

Value
A copy of x with NULL values removed.

Note
This function is internally used for simple lists and vectors. The behaviour for nested lists and vectors embedded in lists is not thoroughly tested.

References

editMatch  

Edit Matching Status

Description
Allows editing the matching status of record pairs.

Usage
editMatch(rpairs)

Arguments
rpairs  A “RecLinkData” or “RLBigData” object. The record pairs to edit.
Details

This function pops up an editor (via `edit`) where each record pair in `rpairs` is printed in two consecutive lines, pairs separated by blank lines. The matching status is printed and can be edited in the last column following the first respective record. A match is denoted by 1, a non-match by 0. NAs are possible to mark pairs with unknown status. Changes in other fields are ignored.

Manual editing of the matching status is useful for clerical review in general and in particular to label training sets. In conjunction with `getMinimalTrain`, good results can be obtained with a manageable effort of manual review.

Value

A copy of `rpairs` with edited matching status.

Author(s)

Andreas Borg

See Also

`getMinimalTrain`

---

**emClassify**

*Weight-based Classification of Data Pairs*

**Description**

Classifies data pairs to which weights were assigned by `emWeights`. Based on user-defined thresholds or predefined error rates.

**Usage**

```r
emClassify(rpairs, threshold.upper = Inf,
            threshold.lower = threshold.upper, my = Inf, ny = Inf, ...)
```

```r
## S4 method for signature 'RecLinkData,ANY,ANY'
emClassify(rpairs, threshold.upper = Inf,
            threshold.lower = threshold.upper, my = Inf, ny = Inf)
```

```r
## S4 method for signature 'RLBigData,ANY,ANY'
emClassify(rpairs, threshold.upper = Inf,
            threshold.lower = threshold.upper, my = Inf, ny = Inf,
            withProgressBar = (sink.number()==0))
```
Arguments

rpairs  
ReclinkData object with weight information.

my  
A probability. Error bound for false positives.

ny  
A probability. Error bound for false negatives.

threshold.upper  
A numeric value. Threshold for links.

threshold.lower  
A numeric value. Threshold for possible links.

withProgressBar  
Whether to display a progress bar

...  
Placeholder for method-specific arguments.

Details

Two general approaches are implemented. The classical procedure by Fellegi and Sunter (see references) minimizes the number of possible links with given error levels for false links (my) and false non-links (ny).

The second approach requires thresholds for links and possible links to be set by the user. A pair with weight $w$ is classified as a link if $w \geq \text{threshold.upper}$, as a possible link if $\text{threshold.upper} \geq w \geq \text{threshold.lower}$ and as a non-link if $w < \text{threshold.lower}$.

If threshold.upper or threshold.lower is given, the threshold-based approach is used, otherwise, if one of the error bounds is given, the Fellegi-Sunter model. If only my is supplied, links are chosen to meet the error bound and all other pairs are classified as non-links (the equivalent case holds if only ny is specified). If no further arguments than rpairs are given, a single threshold of 0 is used.

Value

For the “ReclinkData” method, a S3 object of class “ReclinkResult” that represents a copy of newdata with element rpairs$prediction, which stores the classification result, as addendum.

For the “RLBigData” method, a S4 object of class “RLResult”.

Note

The quality of classification of the Fellegi-Sunter method relies strongly on reasonable estimations of m- and u-probabilities. The results should be evaluated critically.

Author(s)

Andreas Borg, Murat Sariyar

References

See Also

getPairs to produce output from which thresholds can be determined conveniently.

emWeights

Calculate weights

Description

Calculates weights for Record Linkage based on an EM algorithm.

Usage

edmWeights(rpairs, cutoff = 0.95, ...)

## S4 method for signature 'RecLinkData'
edmWeights(rpairs, cutoff = 0.95, ...)

## S4 method for signature 'RLBigData'
edmWeights(rpairs, cutoff = 0.95,
        verbose = TRUE, ...)

Arguments

rpairs The record pairs for which to compute weights. See details.
cutoff Either a numeric value in the range [0,1] or a vector with the same length as the number of attributes in the data. Cutoff value for string comparator.
verbose Logical. Whether to print progress messages.
... Additional arguments passed to mygllm.

Details

Since package version 0.3, this is a generic functions with methods for S3 objects of class "RecLinkData" as well as S4 objects of classes "RLBigDataDedup" and "RLBigDataLinkage".

The weight of a record pair is calculated by \( \log_2 \frac{M}{U} \), where \( M \) and \( U \) are estimated m- and u-probabilities for the present comparison pattern. If a string comparator is used, weights are first calculated based on a binary table where all comparison values greater or equal \( \text{cutoff} \) are set to one, all other to zero. The resulting weight is adjusted by adding for every pair \( \log_2 \left( \prod_{j:s_{ij} \geq \text{cutoff}} s_{ij} \right) \), where \( s_{ij} \) is the value of the string metric for attribute \( j \) in data pair \( i \).

The appropriate value of \( \text{cutoff} \) depends on the choice of string comparator. The default is adjusted to jarowinkler, a lower value (e.g. 0.7) is recommended for levenshteinSim.

Estimation of \( M \) and \( U \) is done by an EM algorithm, implemented by mygllm. For every comparison pattern, the estimated numbers of matches and non-matches are used to compute the corresponding probabilities. Estimations based on the average frequencies of values and given error rates are taken as initial values. In our experience, this increases stability and performance of the EM algorithm.
Some progress messages are printed to the message stream (see `message` if `verbose` \( \Rightarrow \) TRUE. This includes progress bars, but these are suppressed if output is diverted by `sink` to avoid cluttering the output file.

**Value**

A copy of `rpairs` with the weights attached. See the class documentation ("`RecLinkData`", "`RLBigDataDedup`" and "`RLBigDataLinkage`") on how weights are stored.

**Side effects**

The "`RLBigData`" method writes to a disk file containing a `ffvector` that contains the calculated weights. belonging to object

**Author(s)**

Andreas Borg, Murat Sariyar

**References**


**See Also**

`emclassify` for classification of weighted pairs. `epiWeights` for a different approach for weight calculation.

### epiClassify

**Classify record pairs with EpiLink weights**

**Description**

Classifies record pairs as link, non-link or possible link based on weights computed by `epiWeights` and the thresholds passed as arguments.

**Usage**

```r
epiClassify(rpairs, threshold.upper, threshold.lower = threshold.upper, 
...)
```

```r
## S4 method for signature 'RecLinkData'
epiClassify(rpairs, threshold.upper, threshold.lower = threshold.upper)

## S4 method for signature 'RLBigData'
epiClassify(rpairs, threshold.upper, threshold.lower = threshold.upper, 
  e = 0.01, f = getFrequencies(rpairs), withProgressBar = (sink.number() == 0))
```
Arguments

- **rpairs**: `RecLinkData` object. Record pairs to be classified.
- **threshold.upper**: A numeric value between 0 and 1.
- **threshold.lower**: A numeric value between 0 and 1 lower than `threshold.upper`
- **e**: Numeric vector. Estimated error rate(s).
- **f**: Numeric vector. Average frequency of attribute values.
- **withProgressBar**: Logical. Whether to display a progress bar.
- **...**: Placeholder for optional arguments

Details

All record pairs with weights greater or equal `threshold.upper` are classified as links. Record pairs with weights smaller than `threshold.upper` and greater or equal `threshold.lower` are classified as possible links. All remaining records are classified as non-links.

For the "ReclinkData" method, weights must have been calculated for `rpairs` using `epiWeights`. A progress bar is displayed by the "RLBigData" method only if weights are calculated on the fly and, by default, unless output is diverted by `sink` (e.g. in a Sweave script).

Value

For the "ReclinkData" method, a S3 object of class "RecLinkResult" that represents a copy of `newdata` with element `rpairs$prediction`, which stores the classification result, as addendum.

For the "RLBigData" method, a S4 object of class "RLResult".

Author(s)

Andreas Borg, Murat Sariyar

See Also

- `epiWeights`

Examples

```r
# generate record pairs
data(RLdata500)
p=compare.dedup(RLdata500, strcmp=TRUE ,strcmpfun=levenshteinSim,
  identity=identity.RLdata500, blockfld=list("by", "bm", "bd"))

# calculate weights
p=epiWeights(p)

# classify and show results
summary(epiClassify(p,0.6))
```
epiWeights

**Calculate EpiLink weights**

### Description
Calculates weights for record pairs based on the EpiLink approach (see references).

### Usage
```r
epiWeights(rpairs, e = 0.01, f, ...)
```

```r
## S4 method for signature 'RecLinkData'
epiWeights(rpairs, e = 0.01, f = rpairs$frequencies)
```

```r
## S4 method for signature 'RLBigData'
epiWeights(rpairs, e = 0.01, f = getFrequencies(rpairs),
            withProgressbar = (sink.number()==0))
```

### Arguments
- **rpairs**: The record pairs for which to compute weights. See details.
- **e**: Numeric vector. Estimated error rate(s).
- **f**: Numeric vector. Average frequency of attribute values.
- **withProgressbar**: Whether to display a progress bar
- **...**: Placeholder for method-specific arguments.

### Details
This function calculates weights for record pairs based on the approach used by Contiero et al. in the EpiLink record linkage software (see references).

Since package version 0.3, this is a generic function with methods for S3 objects of class "RecLinkData" as well as S4 objects of classes "RLBigDataDedup" and "RLBigDataLinkage".

The weight for a record pair \((x^1, x^2)\) is computed by the formula

\[
\frac{\sum_i w_i s(x^1_i, x^2_i)}{\sum_i w_i}
\]

where \(s(x^1_i, x^2_i)\) is the value of a string comparison of records \(x^1\) and \(x^2\) in the \(i\)-th field and \(w_i\) is a weighting factor computed by

\[
w_i = \log_2(1 - e_i)/f_i
\]

where \(f_i\) denotes the average frequency of values and \(e_i\) the estimated error rate for field \(i\).

String comparison values are taken from the record pairs as they were generated with `compare.dedup` or `compare.linkage`. The use of binary patterns is possible, but in general yields poor results.
The average frequency of values is by default taken from the object rpairs. Both frequency and error rate \( e \) can be set to a single value, which will be recycled, or to a vector with distinct error rates for every field.

The error rate(s) and frequency(s) must satisfy \( e_i \leq 1 - f_i \) for all \( i \), otherwise the functions fails. Also, some other rare combinations can result in weights with illegal values (NaN, less than 0 or greater than 1). In this case a warning is issued.

By default, the "RLBigDataDedup" method displays a progress bar unless output is diverted by sink, e.g. when processing a Sweave file.

**Value**

A copy of rpairs with the weights attached. See the class documentation ("ReclinkData", "RLBigDataDedup" and "RLBigDataLinkage") on how weights are stored.

For the "RLBigData" method, the returned object is only a shallow copy in the sense that it links to the same ff data files as database file as rpairs.

**Side effects**

The "RLBigData" method creates a "ffvector" object, for which a disk file is created.

**Author(s)**

Andreas Borg, Murat Sariyar

**References**


**See Also**

epiclassify for classification based on EpiLink weights. emWeights for a different approach for weight calculation.

**Examples**

```r
# generate record pairs
data(RLdata500)
p<-compare.dedup(RLdata500,strcmp=TRUE ,strcmpfun=levenshteinSim,
                 identity=identity,RLdata500, blockfld=list("by", "bm", "bd"))

# calculate weights
p<-'piWeights(p)

# classify and show results
summary(epiclassify(p,0.6))
```
ffdf-class

Class “ffdf”

Description

S4 representation of S3 class "ffdf", created by setOldClass. See ffdf for documentation of the underlying S3 class.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

.S3Class: Object of class "character"

Extends

Class "oldClass", directly.

Methods

No methods defined with class "ffdf" in the signature.

ff_vector-class

Class “ff_vector”

Description

S4 representation of S3 class "ff_vector", created by setOldClass. See ff for documentation of the underlying S3 class.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

.S3Class: Object of class "character"

Extends

Class "oldClass", directly.

Methods

No methods defined with class "ff_vector" in the signature.
**genSamples**

*Generate Training Set*

---

**Description**

Generates training data by unsupervised classification.

**Usage**

```r
genSamples(dataset, num.non, des.mprop = 0.1)
```

**Arguments**

- `dataset` Object of class `ReclinkData`. Data pairs from which to sample.
- `num.non` Positive Integer. Number of desired non-links in the training set.
- `des.mprop` Real number in the range [0,1]. Ratio of number of links to number of non-links in the training set.

**Details**

The application of supervised classifiers (via `classifySupv`) requires a training set of record pairs with known matching status. Where no such data are available, `genSamples` can be used to generate training data. The matching status is determined by unsupervised clustering with `bclust`. Subsequently, the desired number of links and non-links are sampled.

If the requested numbers of matches or non-matches is not feasible, a warning is issued and the maximum possible number is considered.

**Value**

A list of "ReclinkResult" objects.

- `train` The sampled training data.
- `valid` All other record pairs

Record pairs are split into the respective pairs components. The prediction components represent the clustering result. If weights are present in `dataset`, the corresponding values of `wdata` are stored to `train` and `valid`. All other components are copied from `dataset`.

**Note**

Unsupervised clustering may lead to a poor quality of classification, all subsequent results should be evaluated critically.

**Author(s)**

Andreas Borg, Murat Sariyar
**getErrMeasures-methods**

**See Also**

*splitData* for splitting data sets without clustering.

---

**getErrMeasures-methods**

*Calculate Error Measures*

---

**Description**

Computes various error measures for the classification of a data set.

**Details**

Let $TP$ be the number of correctly classified matches (true positives), $TN$ the number of correctly classified non-matches (true negatives), $FP$ and $FN$ the number of misclassified non-matches and matches (false positives and false negatives). The calculated error measures are:

- **alpha error** $\frac{FN}{TP+FN}$
- **beta error** $\frac{FP}{TN+FP}$
- **accuracy** $\frac{TP+TN}{TP+TN+FP+FN}$
- **precision** $\frac{TP}{TP+FP}$
- **sensitivity** $\frac{TP}{TP+FN}$
- **specificity** $\frac{TN}{TN+FP}$
- **ppv** Positive predictive value: $\frac{TP}{TP+FP}$
- **npv** Negative predictive value: $\frac{TN}{TN+FN}$

**Value**

A list with components alpha, beta, accuracy, precision, sensitivity, specificity, ppv and npv, each a number in the range $[0, 1]$.

**Methods**

signature(object = "RecLinkResult") Method for S3 result objects of class "RecLinkResult"

signature(object = "RLResult") Method for S4 objects of class "RLResult", from classification of big data objects (see "RLBigData", "RLBigDataDedup", "RLBigDataLinkage")

A wrapper function errMMeasures(result) exists for compatibility with package version 0.2.

**Note**

Record pairs with unknown true matching status (e.g. due to missing values in the argument identity to *RLBigDataDedup*) and possible links are not counted, which can distort the values returned by this function.
getExpectedSize

Description
Estimates the total number of record pairs generated by a dataset and specified blocking conditions.

Usage
getExpectedSize(object, ...)

    ## S4 method for signature 'RLBigDataDedup'
    getExpectedSize(object)

    ## S4 method for signature 'RLBigDataLinkage'
    getExpectedSize(object)

    ## S4 method for signature 'data.frame'
    getExpectedSize(object, blockfld = list())

Arguments
object Either a record linkage object or a dataset.
blockfld A blocking definition, such as in compare.dedup
... Placeholder for additional arguments.

Details
The "RLBigData*" methods are only left for backward compability. Since version 0.4, all record pairs for such objects are generated and stored in a disk file. The methods return the true number of record pairs.

For the "data.frame" method, estimation is based on the assumption that agreement or disagreement of one attribute is independent of the other attributes.

blockfld is a blocking definition such as for RLBigDataDedup.

Value
The expected number of record pairs.

Author(s)
Andreas Borg, Murat Sariyar
getFrequencies-methods

Get attribute frequencies

Description

Returns the average frequencies of attribute values for a Record Linkage object, which is $1 / \text{unique}(c)$, for every data column $c$.

Methods

signature(x = "RLBigData")

getMinimalTrain Create a minimal training set

Description

Samples a subset of the provided data (comparison patterns) so that every comparison pattern in $rpairs$ is represented in the subset at least once.

Usage

getMinimalTrain(rpairs, nEx = 1)

Arguments

rpairs A "RecLinkData" or "RLBigData" object. The data set from which to create a minimal training set.

nEx The desired number of examples per comparison pattern.

Details

Our internal research has given indication that in the context of Record Linkage with supervised classification procedures small training sets are often sufficient, provided they cover the whole range of present comparison patterns. By default, this function creates a minimal training set that is a subset of the record pairs to be classified in which every present comparison pattern is represented by exactly one training example. By this approach, the work to classify a training set by clerical review can be minimized while keeping a good classification performance.

Larger training sets can be obtained by setting nEx to a higher number. Up to nEx examples for every comparison pattern are randomly selected, limited by the total number of record pairs with that pattern.
getPairs

Value

An object of the same class as \texttt{rpairs}, representing a minimal comprehensive training set. The appropriate subset of comparison patterns (and weights, if present) is taken, all other components are copied.

Note

Application is only advisable for binary comparison patterns (i.e. only 0 and 1 appear as agreement values). For patterns with string comparison values, the size of the returned set can be too large for a manual review. A warning is issued if fuzzy agreement values (> 0 and < 1) are present in the data.

Note

Due to the small size of the resulting training set, outliers can have a relatively high impact on further classification results. Stable methods such as Bagging or Support-Vector-Machines should be used in conjunction with minimal training sets to minimize this risk.

Author(s)

Andreas Borg, Murat Sariyar

See Also

\texttt{editMatch} for manually setting the matching status of the training pairs.

Examples

data(RLdata500)
p <- compare.dedup(RLdata500,blockfld=list(1,3),identity=identity.RLdata500)
train <- getMinimalTrain(p)
classif <- trainSupv(train,method="bagging")
summary(classifySupv(classif,newdata=p))
getPairs

Usage

## S4 method for signature 'RecLinkData'
getPairs(object, max.weight = Inf, min.weight = -Inf,
         single.rows = FALSE, show = "all", sort = !is.null(object$Wdata))

## S4 method for signature 'RLBigData'
getPairs(object, max.weight = Inf, min.weight = -Inf,
         filter.match = c("match", "unknown", "nonmatch"),
         withWeight = hasWeights(object), withMatch = TRUE, single.rows = FALSE,
         sort = withWeight)

## S4 method for signature 'RLResult'
getPairs(object, filter.match = c("match", "unknown", "nonmatch"),
         filter.link = c("nonlink", "possible", "link"), max.weight = Inf,
         min.weight = -Inf, withMatch = TRUE, withClass = TRUE,
         withWeight = hasWeights(object@data), single.rows = FALSE, sort = withWeight)

gETFalsePos(object, single.rows = FALSE)
gETFalsenEG(object, single.rows = FALSE)
gETFalsoH(object, single.rows = FALSE)

Arguments

*object*    The data or result object from which to extract record pairs.

*max.weight*, *min.weight*
    Real numbers. Upper and lower weight threshold.

*filter.match*
    Character vector, a nonempty subset of c("match", "nonmatch", "unknown")
    denoting which pairs to allow in the output.

*filter.link*
    Character vector, a nonempty subset of c("link", "nonlink", "unknown")
    denoting which pairs to allow in the output.

*withWeight*
    Logical. Whether to include linkage weights in the output.

*withMatch*
    Logical. Whether to include matching status in the output.

*withClass*
    Logical. Whether to include classification result in the output.

*single.rows*
    Logical. Whether to print record pairs in one row instead of two consecutive rows.

*show*
    Character. Selects which records to show, one of "links", "nonlinks", "possible", "all".

*sort*
    Logical. Whether to sort descending by weight.

Details

These methods extract record pairs from "RecLinkData", or "RecLinkResult", "RLBigData" and "RLResult" objects. Possible applications are retrieving a linkage result for further processing, conducting a manual review in order to determine classification thresholds or inspecting misclassified pairs.

The various arguments can be grouped by the following purposes:
getPairs

1. Controlling which record pairs are included in the output: min.weight and max.weight, filter.match, filter.link, show.

2. Controlling which information is shown: withWeight, withMatch, withClass.

3. Controlling the overall structure of the result: sort, single.rows.

The weight limits are inclusive, i.e. a record pair with weight w is included only if \( w \geq \text{min.weight} \) AND \( w \leq \text{max.weight} \).

If single.rows is not TRUE, pairs are output on two consecutive lines in a more readable format. All data are converted to character, which can lead to a loss of precision for numeric values. Therefore, this format should be used for printing only.

getFalsePos, getFalseNeg and getFalse are shortcuts (currently for objects of class "RLResult" only) to retriive false positives (links that are non-matches in fact), false negatives (non-links that are matches in fact) or all falsely classified pairs, respectively.

**Value**

A data frame. If single.rows is TRUE, each row holds (in this order) id and data fields of the first record, id and data fields of the second record and possibly matching status, classification result and/or weight.

If single.rows is not TRUE, the result holds for each resulting record pair consecutive rows of the following format:

1. ID and data fields of the first record followed by as many empty fields to match the length of the following line.
2. ID and data fields of the second record, possibly followed by matching status, classification result and/or weight.
3. A blank line to separate record pairs.

**Note**

When non-matches are included in the output and blocking is permissive, the result object can be very large, possibly leading to memory problems.

**Author(s)**

Andreas Borg, Murat Sariyar

**Examples**

data(RLdata500)

# create record pairs and calculate epilink weights rpairs <- RLBigDataDedup(RLdata500, identity = identity.RLdata500, blockfld=list(1,3,5,6,7)) rpairs <- epiWeights(rpairs)

# show all record pairs with weights between 0.5 and 0.6 getPairs(rpairs, min.weight=0.5, max.weight=0.6)
getParetoThreshold

```
# show only matches with weight <= 0.5
getPairs(rpairs, max.weight=0.5, filter.match="match")

# classify with one threshold
result <- epiClassify(rpairs, 0.5)

# show all links, do not show classification in the output
getPairs(result, filter.link="link", withClass = FALSE)

# see wrongly classified pairs
getFalsePos(result)
getFalseNeg(result)
```

---

**getParetoThreshold**  
*Estimate Threshold from Pareto Distribution*

**Description**

Calculates a classification threshold based on a generalized Pareto distribution (GPD) fitted to the weights distribution of the given data pairs.

**Usage**

```
getParetoThreshold(rpairs, quantil = 0.95, interval = NA)
## S4 method for signature 'RecLinkData'
getParetoThreshold(rpairs, quantil = 0.95, interval = NA)
## S4 method for signature 'RLBigData'
getParetoThreshold(rpairs, quantil = 0.95, interval = NA)
```

**Arguments**

- `rpairs` A "RecLinkData" or "RLBigData" object with weights. The data for which to compute a threshold.
- `quantil` A real number between 0 and 1. The quantil which to compute.
- `interval` A numeric vector denoting the interval on which to fit a GPD.

**Details**

This threshold calculation is based on the assumption that the distribution of weights exhibit a ‘fat tail’ which can be fitted by a generalized Pareto distribution (GPD). The limits of the interval which is subject to the fitting are usually determined by reviewing a mean residual life plot of the data. If the limits are not externally supplied, a MRL plot is displayed from which the endpoints can be selected by mouse input. If only one endpoint is selected or supplied, the greater endpoint is set to the maximum weight.

A suitable interval is characterized by a relatively long, approximately linear segment of the plot.
Value

A classification threshold.

Note

The quality of matching varies, poor results can occur in some cases. Evaluate carefully before applying to a real case.

Author(s)

Andreas Borg, Murat Sariyar

References


See Also

emWeights and epiWeights for calculating weights, emClassify and epiClassify for classifying with the returned threshold.

Examples

data(RLdata500)
rpairs=compare.dedup(RLdata500, identity=identity.RLdata500, strcmp=TRUE,
blockfld=list(1,3,5:7))
rpairs=epiWeights(rpairs)
# leave out argument interval to choose from plot
## Not run: threshold=getParetoThreshold(rpairs,interval=c(0.68, 0.79))
## Not run: summary(epiClassify(rpairs,threshold))
**gpdEst**

*Estimate Threshold from Pareto Distribution*

**Description**

Fits a Pareto distribution to the distribution of weights and calculates a quantile on the fitted model as classification threshold.

**Usage**

```r
gpdEst(wdata, thresh = -Inf, quantil = 0.95)
```

**Arguments**

- `wdata` A numeric vector representing weights of record pairs.
- `thresh` Threshold for exceedances.
- `quantil` A real number between 0 and 1. The desired quantil.

**Details**

The weights that exceed `thresh` are fitted to a generalized Pareto distribution (GPD). The estimated parameters `shape` and `scale` are used to calculate a classification threshold by the formula

\[
\text{thresh} + \frac{\text{scale}}{\text{shape}} \left( \frac{n}{k (1 - \text{quantil})^{\text{shape}}} - 1 \right)
\]

where \( n \) is the total number of weights and \( k \) the number of exceedances.

**Value**

A real number representing the resulting classification threshold. It is assured that the threshold lies in a reasonable range.

**Author(s)**

Murat Sariyar

**See Also**

`getParetoThreshold` for user-level function
### mygl1m  
*Generalized Log-Linear Fitting*

**Description**  
Fits a log-linear model for collapsed contingency tables.

**Usage**  
mygl1m(y, s, X, maxit = 1000, tol = 1e-05, E = rep(1, length(s)))

**Arguments**
- **y**: Vector of observed cell frequencies.
- **s**: Scatter matrix. s[i] is the cell in the observed array that corresponds to cell i in the full array.
- **X**: Design matrix.
- **maxit**: Maximum number of iterations.
- **tol**: Convergence parameter.
- **E**: Full contingency table. Should be initialized with either ones or a priori estimates.
Details

This is an implementation and extension of the algorithm published by Haber (1984). It also incorporates ideas of David Duffy (see references).

A priori estimates of the full contingency table can be given as start values by argument E. This can reduce execution time significantly.

Value

Estimated full contingency table.

Author(s)

Andreas Borg, Murat Sariyar

References


David Duffy: glim: Generalised log-linear model. R package version 0.31. see http://www.qimr.edu.au/davidD/#loglin

See Also

emWeights, which makes use of log-linear fitting for weight calculation.

optimalThreshold  Optimal Threshold for Record Linkage

Description

Calculates the optimal threshold for weight-based Record Linkage.

Usage

optimalThreshold(rpairs, my = NaN, ny = NaN)
## S4 method for signature 'RecLinkData'
optimalThreshold(rpairs, my = NaN, ny = NaN)
## S4 method for signature 'RLBigData'
optimalThreshold(rpairs, my = NaN, ny = NaN)

Arguments

rpairs  Record pairs for which to calculate a threshold.
my  A real value in the range [0,1]. Error bound for false positives.
ny  A real value in the range [0,1]. Error bound for false negatives.
Details

Weights must have been calculated for rpairs, for example by *emWeights* or *epiWeights*. The true match result must be known for rpairs, mostly this is provided through the identity argument of *compare.*

For the following, it is assumed that all records with weights greater than or equal to the threshold are classified as links, the remaining as non-links. If no further arguments are given, a threshold which minimizes the absolute number of misclassified record pairs is returned. If my is supplied (ny is ignored in this case), a threshold is picked which maximizes the number of correctly classified links while keeping the ratio of false links to the total number of links below or equal my. If ny is supplied, the number of correct non-links is maximized under the condition that the ratio of falsely classified non-links to the total number of non-links does not exceed ny.

Two separate runs of *optimalThreshold* with values for my and ny respectively allow for obtaining a lower and an upper threshold for a three-way classification approach (yielding links, non-links and possible links).

Value

A numeric value, the calculated threshold.

Author(s)

Andreas Borg, Murat Sariyar

See Also

*emWeights* *emClassify* *epiWeights* *epiClassify*

Examples

```r
# create record pairs
data(RLdata500)
p=compare.dedup(RLdata500,identity=identity.RLdata500, strcmp=TRUE, strcmpfun=levenshteinSim)

# calculate weights
p=epiWeights(p)

# split record pairs in two sets
l=splitData(dataset=p, prop=0.5, keep.mprop=TRUE)

# get threshold from training set
threshold=optimalThreshold(l$train)

# classify remaining data
summary(epiClassify(l$valid,threshold))
```
phonetics

---

**Phonetic Code**

<table>
<thead>
<tr>
<th>phonetics</th>
</tr>
</thead>
</table>

**Description**

Interface to phonetic coding functions.

**Usage**

```r
pho_h(str)
soundex(str)
```

**Arguments**

- `str`: A character vector or matrix. Factors are converted to character.

**Details**

Translates its argument to a phonetic code. `pho_h` by Jörg Michael (see references) is intended for German language and normalizes umlauts and accent characters. `soundex` is a widespread algorithm for English names. This implementation can only handle common characters. Both algorithms strip off non-alphabetical characters, with the exception that numbers are left unchanged by `pho_h`.

The C code for `soundex` was taken from PostgreSQL 8.3.6.

**Value**

A character vector or matrix with the same size and dimensions as `str`, containing its phonetic encoding.

**Author(s)**

Andreas Borg (R interface only)

**References**


**See Also**

- `jarowinkler`
- `levenshteinSim` for string comparison.
**RecLinkClassif-class**

**Class** "RecLinkClassif"

**Description**

S4 wrapper for S3 class with the same name, which has the same structure as a RecLinkData object plus the following components:

- prediction Linkage result. Coded as a factor with levels "N" for non-links, "P" for possible links and "L" for links.
- attrNames Column names of the set of comparison patterns.

**Objects from the Class**

Objects of the S3 class are created by classification functions, such as classifySupv or emClassify

**Slots**

- .S3Class: Object of class "character".

**Extends**

Class "oldClass", directly.

**Methods**

- classifySupv signature(model = "RecLinkClassif", newdata = "RecLinkData")
- classifySupv signature(model = "RecLinkClassif", newdata = "RLBigData")

**Author(s)**

Andreas Borg, Murat Sariyar

**Examples**

showClass("RecLinkClassif")
RecLinkData-class

Class "RecLinkData"

Description

S4 wrapper for S3 class "RecLinkData".

Objects from the Class

Objects of the S3 class are created by the comparison functions `compare.*`. The S4 class is virtual and exists solely for internal usage in method signatures.

Slots

`.S3Class`: Internal slot.

See "RecLinkData" for the structure of the S3 class.

Extends

Class "oldClass", directly.

Methods

Use `getMethods(classes = "RecLinkData")` to list the methods defined for this class.

Author(s)

Andreas Borg, Murat Sariyar

See Also

"RecLinkData" for the structure of the S3 class. `compare.dedup`, which creates objects of this class. "RLBigData", an alternative data structure suitable for big data sets.

Examples

`showClass("RecLinkData")`
RecLinkData.object  
Record Linkage Data Object

Description

S3 class representing information about record pairs for Record Linkage, as returned by functions compare.dedup and compare.linkage.

Value

A list with at least the following elements:

data (for type = "deduplication"): Object of class "data.frame". Data frame of original records.

data1, data2 (for type = "linkage"): Objects of class "data.frame". Data frames of original records.

pairs: Object of class "data.frame" Data frame of data pairs. Each row represents the comparison pattern of two records, identified by columns id1 and id2. The other columns contain for each considered attribute a real number in the range [0..1] representing the degree of similarity. These columns are named according to the respective columns in data. The last column contains the matching status of the pair, coded as 1 for a match or 0 for a non-match.

frequencies: Object of class "numeric" Numeric vector with average frequency of values for each column included in pairs (reciprocal of number of distinct values).

type: Object of class "character" Identifies whether a linkage ("linkage") or a deduplication ("deduplication") project is represented.

.S3class: Internal slot.

The following elements are optional:

M: Object of class "numeric" Vector of m-probabilities as calculated by emWeights.

U: Object of class "numeric" Vector of u-probabilities as calculated by emWeights.

W: Object of class "numeric" Vector of log-likelihood weights as calculated by emWeights, corresponding to binary comparison patterns as created by bincombinations.

Wdata: Object of class "numeric" Vector of log-likelihood weights as calculated by emWeights, corresponding to the rows of pairs.

Author(s)

Andreas Borg, Murat Sariyar

See Also

"ReclinkData" for the S4 representation. compare.dedup, which creates objects of this class. "RLBigData", an alternative data structure suitable for big data sets.
RecLinkResult-class

Description
S4 wrapper for S3 class "RecLinkResult".

Objects from the Class
Object of the S3 class are created by classification functions, such as classifySupv and emClassify. The S4 class is virtual and exists solely for internal usage in method signatures.

Slots
.S3Class: Internal slot.
See "RecLinkResult" for the structure of the S3 class.

Extends
Class "RecLinkData", directly. Class "oldClass", by class "RecLinkData", distance 2.

Methods
%append% signature(x = "RecLinkResult", y = "RecLinkResult")
getErrorMeasures signature(object="RecLinkResult")
getTable signature(object="RecLinkResult")

Author(s)
Andreas Borg, Murat Sariyar

See Also
"RecLinkResult" for the structure of the S3 class. "RLResult", the equivalent data structure for big data sets.

Examples
showClass("RecLinkResult")
ReclinkResult.object  Record Linkage Result Object

Description

S3 class representing information about the classification result of a Record Linkage procedure and the data from which this result is derived.

Value

A list with all mandatory and optional elements of class "ReclinkData" plus the following:

prediction: Object of class "factor" Classification of each record, corresponding to the record pairs stored in component pairs. Levels are:
"N" for non-links.
"P" for possible links,
"L" for links.

Author(s)

Andreas Borg, Murat Sariyar

See Also

"ReclinkResult" for the S4 representation. "ReclinkData" for the superclass. "RLResult", the equivalent data structure for big data sets.

resample  Safe Sampling

Description

Performs sampling without replacement while avoiding undesired behaviour if x has length 1. See documentation of sample.

Usage

resample(x, size, ...)

Arguments

x  A vector from which to sample.
size  A non-negative number giving the size of the sample.
...  Further arguments to sample.
Description

Abstract class for big data sets.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots in "RLBigData"

- **frequencies**: Object of class "numeric". Average frequency of values for each column of the underlying data (1 / of number of distinct values)
- **blockFld**: Object of class "list". Blocking definition. See documentation for constructor functions for details.
- **excludeFld**: Object of class "numeric". Indices of attributes which are not considered for comparison.
- **strcmpFld**: Object of class "numeric". Indices of attributes on which a string comparator is executed.
- **strcmpFun**: Object of class "character". String representing the string comparison function.
- **phanteticFld**: Object of class "numeric". Indices of attributes on which a phonetic code is generated.
- **phanteticFun**: Object of class "character". String representing the phonetic coding function.
- **drv**: Object of class "DBIDriver". Database driver.
- **con**: Object of class "DBIConnection". Database connection.

Methods

- **begin** signature(x = "RLBigData")
- **classifySupv** signature(model = "RecLinkClassif", newdata = "RLBigData")
- **clear** signature(x = "RLBigData")
- **clone** signature(object = "RLBigData")
- **emClassify** signature(rpairs = "RLBigData")
- **emWeights** signature(rpairs = "RLBigData")
- **epiClassify** signature(rpairs = "RLBigData")
- **epiWeights** signature(rpairs = "RLBigData")
- **getDbFile** signature(object = "RLBigData")
- **getFrequencies** signature(x = "RLBigData")
- **getMatchCount** signature(object = "RLBigData")
getNACount signature(object = "RLBigData")
getPairs signature(object = "RLBigData")
getPatternCounts signature(x = "RLBigData")
getSQLStatement signature(object = "RLBigData")
nextPairs signature(x = "RLBigData")
saveRLObject signature(object = "RLBigData")
show signature(object = "RLBigData")

Author(s)
Andreas Borg

See Also
Non-abstract subclasses "RLBigDataDedup" and "RLBigDataLinkage" with constructors RLBigDataDedup and RLBigDataLinkage.

Examples
showClass("RLBigData")

---

**RLBigDataDedup**

*Constructors for big data objects.*

**Description**
These are constructors which initialize a record linkage setup for big datasets, either deduplication of one (RLBigDataDedup) or linkage of two datasets (RLBigDataLinkage).

**Usage**

RLBigDataDedup(dataset, identity = NA, blockfld = list(), exclude = numeric(0),
strcmp = numeric(0), strcmpfun = "jarowinkler", phonetic = numeric(0),
phonfun = "pho_h")

RLBigDataLinkage(dataset1, dataset2, identity1 = NA, identity2 = NA,
blockfld = list(), exclude = numeric(0), strcmp = numeric(0),
strcmpfun = "jarowinkler", phonetic = numeric(0), phonfun = "pho_h")
Arguments

- **dataset, dataset1, dataset2**
  Table of records to be deduplicated or linked. Either a data frame or a matrix.

- **identity, identity1, identity2**
  Optional vectors (are converted to factors) for identifying true matches and non-matches. In a deduplication process, two records dataset[i,] and dataset[j,] are a true match if and only if identity[i,] == identity[j,]. In a linkage process, two records dataset1[i,] and dataset2[j,] are a true match if and only if identity1[i,] == identity2[j,].

- **blockfld**
  Blocking field definition. A numeric or character vector or a list of several such vectors, corresponding to column numbers or names. See details and examples.

- **exclude**
  Columns to be excluded. A numeric or character vector corresponding to columns of dataset or dataset1 and dataset2 which should be excluded from comparison.

- **strcmp**
  Determines usage of string comparison. If FALSE, no string comparison will be used; if TRUE, string comparison will be used for all columns; if a numeric or character vector is given, the string comparison will be used for the specified columns.

- **strcmpfun**
  Character string representing the string comparison function. Possible values are "jaro_winkler" and "levenshtein".

- **phonetic**
  Determines usage of phonetic code. Used in the same manner as strcmp.

- **phonfun**
  Character string representing the phonetic function. Currently, only "pho_h" is supported (see pho_h).

Details

These functions act as constructors for the S4 classes "RLBigDataDedup" and "RLBigDataLinkage". They make up the initial stage in a Record Linkage process using large data sets (>= 1.000.000 record pairs) after possibly normalizing the data. Two general scenarios are reflected by the two functions: RLBigDataDedup works on a single data set which is to be deduplicated, RLBigDataLinkage is intended for linking two data sets together. Their usage follows the functions compare.dedup and compare.linkage, which are recommended for smaller amounts of data, e.g. training sets.

Datasets are represented as data frames or matrices (typically of type character), each row representing one record, each column representing one attribute (like first name, date of birth,...). Row names are not retained in the record pairs. If an identifier other than row number is needed, it should be supplied as a designated column and excluded from comparison (see note on exclude below).

In case of RLBigDataLinkage, the two datasets must have the same number of columns and it is assumed that their column classes and semantics match. If present, the column names of dataset1 are assigned to dataset2 in order to enforce a matching format. Therefore, column names used in blockfld or other arguments refer to dataset1.

Each element of blockfld specifies a set of columns in which two records must agree to be included in the output. Each blocking definition in the list is applied individually, the sets obtained thereby are combined by a union operation. If blockfld is FALSE, no blocking will be performed, which leads to a large number of record pairs (\( \frac{n(n-1)}{2} \) where \( n \) is the number of records).

Fields can be excluded from the linkage process by supplying their column index in the vector exclude, which is especially useful for external identifiers. Excluded fields can still be used for blocking, also with phonetic code.
Phonetic codes and string similarity measures are supported for enhanced detection of misspellings. Applying a phonetic code leads to binary similarity values, where 1 denotes equality of the generated phonetic code. A string comparator leads to a similarity value in the range $[0, 1]$. Using string comparison on a field for which a phonetic code is generated is possible, but issues a warning.

In contrast to the `compare.*` functions, phonetic coding and string comparison is not carried out in R, but by database functions. Supported functions are "pho_h" for phonetic coding and "jarowinkler" and "levenshtein" for string comparison. See the documentation for their R equivalents (phonetic functions, string comparison) for further information.

**Value**

An object of class "RLBigDataDedup" or "RLBigDataLinkage", depending on the called function.

**Side effects**

The RSQLite database driver is initialized via `dbDriver("SQLite")` and a connection established and stored in the returned object. Extension functions for phonetic code and string comparison are loaded into the database. The records in `dataset` or `datasetQ` and `datasetR` are stored in tables "data" or "data1" and "data2", respectively, and indices are created on all columns involved in blocking.

**Author(s)**

Andreas Borg, Murat Sariyar

**See Also**

"RLBigDataDedup", "RLBigDataLinkage", `compare.dedup`, `compare.linkage`, the vignette "Classes for record linkage of big data sets".

**Examples**

```r
data(RLdata500)
data(RLdata10000)
# deduplication without blocking, use string comparator on names
rpairs <- RLBigDataDedup(RLdata500, strcmp = 1:4)
# linkage with blocking on first name and year of birth, use phonetic
# code on first components of first and last name
rpairs <- RLBigDataLinkage(RLdata500, RLdata10000, blockfld = c(1, 7),
                           phonetic = c(1, 3))
# deduplication with blocking on either last name or complete date of birth,
# use string comparator on all fields, include identity information
rpairs <- RLBigDataDedup(RLdata500, identity = identity.RLdata500, strcmp=TRUE,
                        blockfld = list(1, c(5, 6, 7)))
```
Description

Represents a record linkage setup where a single dataset is to be deduplicated.

Objects from the Class

Objects should be created using the constructor function `RLBigDataDedup`, which does some essential error checking, conversion and initialization.

Slots

See also "RLBigData" for inherited slots.

data: Object of class "data.frame" Data set.
identity: Object of class "factor" True ID of records in data

Extends

Class "RLBigData", directly.

Methods

getColumnNames signature(object = "RLBigDataDedup")
getExpectedSize signature(object = "RLBigDataDedup")
See also RLBigData-class for inherited methods.

Author(s)

Andreas Borg

See Also

RLBigDataDedup, RLBigData-class

Examples

showClass("RLBigDataDedup")
Description

Represents a record linkage setup with two datasets which are to be linked together.

Objects from the Class

Objects should be created using the constructor function `RLBigDataLinkage`, which does some essential error checking, conversion and initialization.

Slots

See also "RLBigData" for inherited slots.

data1: Object of class "data.frame" First data set.
data2: Object of class "data.frame" Second data set.
identity1: Object of class "factor" True ID of records in data1
identity2: Object of class "factor" True ID of records in data2

Extends

Class "RLBigData", directly.

Methods

`getColumnNames` signature(object = "RLBigDataLinkage")
`getExpectedSize` signature(object = "RLBigDataLinkage")
See also `RLBigData-class` for inherited methods.

Author(s)

Andreas Borg

See Also

"RLBigData", `RLBigDataLinkage`

Examples

`showClass("RLBigDataLinkage")`
Description

These tables contain artificial personal data for the evaluation of Record Linkage procedures. Some records have been duplicated with randomly generated errors. \texttt{RLdata500} contains 50 duplicates, \texttt{RLdata10000} 1000 duplicates.

Usage

\begin{verbatim}
RLdata500
RLdata10000
identity.RLdata500
identity.RLdata10000
\end{verbatim}

Format

\texttt{RLdata500} and \texttt{RLdata10000} are character matrices with 500 and 10000 records. Each row represents one record, with the following columns:

- \texttt{fname\_c1} First name, first component
- \texttt{fname\_c2} First name, second component
- \texttt{lname\_c1} Last name, first component
- \texttt{lname\_c2} Last name, second component
- \texttt{by} Year of birth
- \texttt{bm} Month of birth
- \texttt{bd} Day of birth

\texttt{identity.RLdata500} and \texttt{identity.RLdata10000} are integer vectors representing the true record ids of the two data sets. Two records are duplicates, if and only if their corresponding values in the identity vector agree.

Author(s)

Andreas Borg

Source

Generated with the data generation component of Febrl (Freely Extensible Biomedical Record Linkage), version 0.3. See \url{http://datamining.anu.edu.au/projects/linkage.html} for details. The following data sources were used (all relate to Germany):

- \url{http://www.beliebte-vornamen.de/760-alle_jahre.htm}, a list of the 100 most popular first names since 1890. The frequencies found in the source above were extrapolated to fit this list.
http://www.peter-doerling.de/Geneal/Nachnamen_100.htm, a list of the 100 most frequent family names with frequencies.


Web links as of October 2009.

---

**RLResult-class**

Class "RLResult"

**Description**

A class that represents the result of a record linkage procedure with big data sets.

**Objects from the Class**

Objects from this class are created by the classification functions in this package, e.g. `classifySupv`. Directly creating instances by calling `new` is neither necessary nor recommended.

**Slots**

data: Object of class "RLBigData". The data set which was classified.
prediction: Object of class "ff". A vector with classification result for every record pair, coded by levels "N" for a non-link, "P" for a possible link and "L" for a link.

**Methods**

`clone` signature(object = "RLResult")
`getDbFile` signature(object = "RLResult")
`getErrorMeasures` signature(object = "RLResult")
`getPairs` signature(object = "RLResult")
`getTable` signature(object = "RLResult")
`saveRLObject` signature(object = "RLResult")

**Note**

The slot data uses a database to store data and create comparison patterns, thus assignment of a "RLResult" object to a different variable can lead to undesired results. Use `clone` to make a distinct copy. Similarly, the standard save mechanism does not work; `saveRLObject` and `loadRLObject` are provided to make objects persistent over different R sessions.

**Author(s)**

Andreas Borg, Murat Sariyar

**See Also**

`classifySupv`, `emClassify` and `epiClassify` create objects of this type.
**Description**

Shows summarized information on a "RLBigData" object.

**Usage**

```r
## S4 method for signature 'RLBigData'
show(object)
```

**Arguments**

- `object` The object for which to show a summary.

**Details**

The printed information consists of the type of linkage procedure (deduplication or linkage) and the number of records and the approximate number of record pairs as calculated by `getExpectedSize`. More information is obtained by the `summary` methods for these classes.

**Value**

`show` returns an invisible NULL and is used for its side effect.

**Author(s)**

Andreas Borg, Murat Sariyar

**See Also**

`show`

**Examples**

```r
data(RLdata500)
rpairs <- RLBigDataDedup(RLdata500)
rpairs
```
splitData

**Split Data**

**Description**

Splits a data set into two sets with desired proportions.

**Usage**

```r
splitData(dataset, prop, keep.mprop = FALSE, num.non = 0, des.mprop = 0,
use.pred = FALSE)
```

**Arguments**

- `dataset`: Object of class `ReclinkData`. Data pairs to split.
- `prop`: Real number between 0 and 1. Proportion of data pairs to form the training set.
- `keep.mprop`: Logical. Whether the ratio of matches should be retained.
- `num.non`: Positive Integer. Desired number on non-matches in the training set.
- `des.mprop`: Real number between 0 and 1. Desired proportion of matches to non-matches in the training set.
- `use.pred`: Logical. Whether to apply match ratio to previous classification results instead of true matching status.

**Value**

A list of `ReclinkData` objects.

- `train`: The sampled training data.
- `valid`: All other record pairs.

The sampled data are stored in the `pairs` attributes of `train` and `valid`. If present, the attributes `prediction` and `wdata` are split and the corresponding values saved. All other attributes are copied to both data sets.

If the number of desired matches or non-matches is higher than the number actually present in the data, the maximum possible number is chosen and a warning issued.

**Author(s)**

Andreas Borg, Murat Sariyar

**See Also**

- `genSamples` for generating training data based on unsupervised classification.
Examples

```r
data(RLdata500)
pairs=compare.dedup(RLdata500, identity=identity.RLdata500, blockfld=list(1,3,5,6,7))

# split into halves, do not enforce match ratio
l=splitData(pairs, prop=0.5)
summary(l$train)
summary(l$valid)

# split into 1/3 and 2/3, retain match ratio
l=splitData(pairs, prop=1/3, keep.mprop=TRUE)
summary(l$train)
summary(l$valid)

# generate a training set with 100 non-matches and 10 matches
l=splitData(pairs, num.non=100, des.mprop=0.1, keep.mprop=TRUE)
summary(l$train)
summary(l$valid)
```

Description

Methods for stochastic record linkage following the framework of Fellegi and Sunter.

Usage

```r
## S4 method for signature 'RecLinkData'
fsWeights(rpairs, m = 0.95, u = rpairs$frequencies, cutoff = 1)
## S4 method for signature 'RLBigData'
fsWeights(rpairs, m=0.95, u=getfrequencies(rpairs),
          cutoff=1, withProgressBar = (sink.number()==0))
## S4 method for signature 'RecLinkData'
fsClassify(rpairs, ...)
## S4 method for signature 'RLBigData'
fsClassify(rpairs, threshold.upper, threshold.lower=threshold.upper,
           m=0.95, u=getfrequencies(rpairs), withProgressBar = (sink.number()==0), cutoff=1)
```

Arguments

- `rpairs` The record pairs to be classified.
threshold.upper
A numeric value between 0 and 1.

threshold.lower
A numeric value between 0 and 1 lower than threshold.upper.

m, u
Numeric vectors. m- and u-probabilities of matching variables, see Details.

withProgressBar
Logical. Whether to display a progress bar.

cutoff
Numeric value. Threshold for converting string comparison values to binary values.

... Arguments passed to emClassify.

Details
These methods perform stochastic record linkage following the framework of Fellegi and Sunter (see reference).

fsWeights calculates matching weights on an object based on the specified m- and u-probabilities. Each of m and u can be a numeric vector or a single number in the range \([0, 1]\).

fsClassify performs classification based on the calculated weights. All record pairs with weights greater or equal threshold.upper are classified as links. Record pairs with weights smaller than threshold.upper and greater or equal threshold.lower are classified as possible links. All remaining records are classified as non-links.

The "ReclinkData" method is a shortcut for emClassify.

The "RLBigData" method checks if weights are present in the underlying database. If this is the case, classification is based on the existing weights. If not, weights are calculated on the fly during classification, but not stored. The latter behaviour might be preferable when a very large dataset is to be classified and disk space is limited. A progress bar is displayed only if weights are calculated on the fly and, by default, unless output is diverted by sink (e.g. in a Sweave script).

For a general introduction to weight based record linkage, see the vignette "Weight-based deduplication".

Value
fsWeights returns a copy of the object with the calculated weights added. Note that "RLBigData" objects have some reference-style semantics, see clone for more information.

For the "ReclinkData" method, fsClassify returns a S3 object of class "ReclinkResult" that represents a copy of newdata with element rpairs$prediction, which stores the classification result, as addendum.

For the "RLBigData" method, fsClassify returns a S4 object of class "RLResult".

Author(s)
Andreas Borg, Murat Sarıyar

References


**See Also**

- `epiWeights`

**Examples**

```r
# generate record pairs
data(RLdata500)
rpairs <- compare.dedup(RLdata500, blockfld=list(1,3,5,6,7), identity=identity.RLdata500)

# calculate weights
rpairs <- fsWeights(rpairs)

# classify and show results
summary(fsClassify(rpairs, 0))
```

---

**Description**

Functions for computation of the similarity between two strings.

**Usage**

```r
jarowinkler(str1, str2, W_1=1/3, W_2=1/3, W_3=1/3, r=0.5)
levenshteinSim(str1, str2)
levenshteinDist(str1, str2)
```

**Arguments**

- `str1`, `str2` Two character vectors to compare.
- `W_1`, `W_2`, `W_3` Adjustable weights.
- `r` Maximum transposition radius. A fraction of the length of the shorter string.

**Details**

String metrics compute a similarity value in the range \([0, 1]\) for two strings, with 1 denoting the highest (usually equality) and 0 denoting the lowest degree of similarity. In the context of Record Linkage, string similarities can improve the discernibility between matches and non-matches.

`jarowinkler` is an implementation of the algorithm by Jaro and Winkler (see references). For the meaning of `W_1`, `W_2`, `W_3` and `r` see the referenced article. For most applications, the default values are reasonable.

`levenshteinDist` returns the Levenshtein distance, which cannot be directly used as a valid string comparator. `levenshteinSim` is a similarity function based on the Levenshtein distance, calculated by \(1 - \frac{d(str_1, str_2)}{\max(A,B)}\), where `d` is the Levenshtein distance function and `A` and `B` are the lengths of the strings.

Arguments `str1` and `str2` are expected to be of type "character". Non-alphabetical characters can be processed. Valid format combinations for the arguments are:
• Two arrays with the same dimensions.
• Two vectors. The shorter one is recycled as necessary.

Value
A numeric vector with similarity values in the interval \([0, 1]\). For \texttt{levenshteinDist}, the edit distance as an integer vector.

Note
String comparison is case-sensitive, which means that for example "R" and "r" have a similarity of 0. If this behaviour is undesired, strings should be normalized before processing.

Author(s)
Andreas Borg, Murat Sariyar

References

Examples
```r
# compare two strings:
jarowinkler("Andreas","Anreas")
# compare one string with several others:
levenshteinSim("Andreas",c("Anreas","Andea"))
# compare two vectors of strings:
jarowinkler(c("Andreas","Borg"),c("Andreas","Bork"))
```

---

subset

Subset operator for record linkage objects

Description
Extracts a subset of a "ReclinkData" or "ReclinkResult" object.

Usage
```r
## S3 method for class 'ReclinkData'
x[i]
## S3 method for class 'ReclinkResult'
x[i]
## S3 method for class 'RLBigData'
x[i]
## S3 method for class 'RLResult'
x[i]
```
Arguments

- **x**: The object which to index.
- **i**: Indeces of pairs to include in the subset.

Value

A copy of x with only the pairs with indices specified by x.

Author(s)

Andreas Borg, Murat Sariyar

Examples

```r
## Samples a subset of pairs

data(RL.data500)
rpairs <- compare.dedup(RL.data500, identity = identity.RL.data500,
  blockfld = list(1,3,5,6,7))
nPairs <- nrow(rpairs$pairs)
s <- sample(nPairs, nPairs / 2)
samp <- rpairs[s]
```

Description

Prints information on `RecLinkData` and "`RecLinkResult" objects.

Usage

```r
## S3 method for class 'RecLinkData'
summary(object,...)

## S3 method for class 'RecLinkResult'
summary(object,...)
```

Arguments

- **object**: The object for which to print a summary.
- **...**: Additional arguments from the generic, silently ignored.
Details

(The following information is probably outdated as of Nov 17, 2011.)

The printed information for RecLinkData objects includes:

- The number of records.
- The number of record pairs.
- The number of true matches, true non-matches and pairs with unknown status.
- If weights have been calculated for this object, a textual histogram of the weight distribution.

Information on "RecLinkResult" objects includes all of the above and the following:

- The number of detected links, non-links and possible links.
- The following error measures, if the true matching status of all record pairs is known: Alpha error (ratio of false links to matches), beta error (ratio of false non-links to non-matches) and accuracy (ratio of correctly classified pairs to the total number of pairs).
- A cross-classified table counting true matching status against classification. The true matching status is represented as logical values, possibly including NA for unknown status. Classification results are represented by:
  - "L" for links,
  - "P" for possible links
  - "N" for non-links

Value

Returns an invisible NULL and is used for its side effect.

Author(s)

Andreas Borg

See Also

RecLinkData,"RecLinkResult"

summary.RLBigData summary methods for "RLBigData" objects.

Description

Shows summarized information on a "RLBigDataDup" or "RLBigDataDup" object.
Usage

```r
## S3 method for class 'RLBigDataDedup'
summary(object, ...)
## S3 method for class 'RLBigDataLinkage'
summary(object, ...)
## S3 method for class 'summaryRLBigDataDedup'
print(x, ...)
## S3 method for class 'summaryRLBigDataLinkage'
print(x, ...)
```

Arguments

- `object` The object for which to show a summary.
- `x` Return value of the summary function.
- `...` Additional arguments from the generic function are ignored.

Details

The `summary` methods return a list of the format shown below. The `print` method displays this information on the console in a user-friendly format.

Blocking fields are displayed in a style like `[attr1, [attr2, attr3]]`, where `attr1` etc. are column names and attributes within brackets represent one blocking iteration. See `compare.dedup` or `RLBigDataDedup` for an explanation of blocking criteria.

Value

For `summary`, a list with components:

- `nData` Only for the "RLBigDataDedup" method: Number of records in the dataset.
- `nData1` Only for the "RLBigDataLinkage" method: Number of records in dataset 1.
- `nData2` Only for the "RLBigDataLinkage" method: Number of records in dataset 2.
- `attributes` Column names of dataset(s).
- `blockFld` Blocking definition as a list of character vectors, representing column names.
- `nPairs` Number of record pairs
- `nMatches` Number of matches in the set of record pairs.
- `nNonMatches` Number of non-matches in the set of record pairs.
- `nUnknown` Number of record pairs with unknown matching status.
- `weightHist` Only if weights have been calculated for `object`: a summary of the weights in histogram style.

Author(s)

Andreas Borg, Murat Sariyar
See Also

`summary "RLBigData"`, `RLBigDataDedup`, `RLBigDataLinkage`

Examples

```r
data(RLdata500)
rpairs <- RLBigDataDedup(RLdata500, identity = identity.RLdata500,
  blockfld=list(1,3,5:7))
rpairs <- epiWeights(rpairs)
summary(rpairs)
```

---

**summary.RLResult**

*Summary method for "RLResult" objects.*

Description

Get summarized information on a "RLResult" object.

Usage

```r
## S4 method for signature 'RLResult'
summary(object)
## S3 method for class 'summaryRLResult'
print(x, ...)
```

Arguments

- `object` The object for which to show a summary.
- `x` Return value of the summary function.
- `...` Additional arguments from the generic function are ignored.

Details

The summary methods return a list of the format shown below. The print method displays this information on the console in a user-friendly format.

Value

For summary, a list with components

- `nPairs` Number of record pairs.
- `nLinks` Number of detected links.
- `nPossibleLinks` Number of detected possible links.

Author(s)

Andreas Borg, Murat Sariyar
**trainSupv**

See Also

summary "RLResult"

Examples

```r
data(RL.data500)
rpairs <- RLBigDataDedup(RL.data500, blockfld=list(1,3,5:7),
                       identity = identity.RL.data500)
rpairs <- epiWeights(rpairs)
result <- epiClassify(rpairs, 0.7)
summary(result)
```

### Description

Trains a classifier for supervised classification of record pairs.

### Usage

```r
trainSupv(rpairs, method, use.pred = FALSE, omit.possible = TRUE,
          convert.na = TRUE, include.data = FALSE, ...)
```

### Arguments

- **rpairs**: Object of class `RecLinkData`. Training data.
- **method**: A character vector. The classification method to use.
- **use.pred**: Logical. Whether to use results of an unsupervised classification instead of true matching status.
- **omit.possible**: Logical. Whether to remove pairs labeled as possible links or with unknown status.
- **convert.na**: Logical. Whether to convert NAs to 0 in the comparison patterns.
- **include.data**: Logical. Whether to include training data in the result object.
- **...**: Further arguments to the training method.

### Details

The given dataset is used as training data for a supervised classification. Either the true matching status has to be known for a sufficient number of data pairs or the data must have been classified previously, e.g. by using `emClassify` or `classifyUnsup`. In the latter case, argument `use.pred` has to be set to `TRUE`.

A classifying method has to be provided as a character string (factors are converted to character) through argument `method`. The supported classifiers are:

- "svm" Support vector machine, see `svm`. 
"rpart" Recursive partitioning tree, see \texttt{rpart}.
"ada" Stochastic boosting model, see \texttt{ada}.
"bagging" Bagging with classification trees, see \texttt{bagging}.
"nnet" Single-hidden-layer neural network, see \texttt{nnet}.
"bumping" A bootstrap based method using classification trees, see details.

Arguments in ... are passed to the corresponding function.

Most classifiers cannot handle NAs in the data, so by default these are converted to 0 before training.

By \texttt{omit.possible = TRUE}, possible links or pairs with unknown status are excluded from the trainings set. Setting this argument to FALSE allows three-class-classification (links, non-links and possible links), but the results tend to be poor.

Leaving \texttt{include.data=FALSE} saves memory, setting it to TRUE can be useful for saving the classifier while keeping track of the underlying training data.

**BUMPING**, (acronym for “Bootstrap umbrella of model parameters”), is an ensemble method described by Tibshirani and Knight, 1999. Such as in bagging, multiple classifiers are trained on bootstrap samples of the training set. The key difference is that not the aggregated decision of all classifiers (e.g. by majority vote) is used to classify new data, but only the single model that performs best on the whole training set. In combination with classification trees as underlying classifiers this approach allows good interpretability of the trained model while being more stable against outliers than traditionally induced decision trees. The number of bootstrap samples to use can be controlled by supplying the argument \texttt{n.bootstrap}, which defaults to 25.

**Value**

An object of class \texttt{RecLinkClassif} with the following components:

- \texttt{train} If \texttt{include.data} is TRUE, a copy of \texttt{rpairs}, otherwise an empty data frame with the same column names.
- \texttt{model} The model returned by the underlying training function.
- \texttt{method} A copy of the argument method.

**Author(s)**

Andreas Borg, Murat Sariyar

**References**


**See Also**

\texttt{classifySupv} for classifying with the trained model, \texttt{classifyUnsup} for unsupervised classification
Examples

# Train a rpart decision tree with additional parameter minsplit
data(RLdata500)
pairs=compare.dedup(RLdata500, identity=identity.RLdata500,
                     blockfld=list(1:3,5,6,7))
model=trainSupv(pairs, method="rpart", minsplit=5)
summary(model)

# create unordered pairs of \{1,2,3\}: \{1,2\},\{1,3\} and (2,3)
unorderedPairs(3)

# create unordered pairs of \{"a","b","c"\}: \{"a","b"\}, \{"a","c"\},\{"b","c"\}
unorderedPairs(c("a","b","c"))

unorderedPairs

Create Unordered Pairs

Description

Creates all unordered pairs of some objects or of the first x natural numbers.

Usage

unorderedPairs(x)

Arguments

x

Either an arbitrary vector of literals or a natural number

Details

If x has length one, all unordered pairs of the first x natural numbers are created. If x has more than one element, all unordered pairs of the elements of x are created.

Value

A matrix with two rows, each column holding one pair.

Author(s)

Andreas Borg

Examples

# create unordered pairs of \{1,2,3\}: \{1,2\},\{1,3\} and (2,3)
unorderedPairs(3)

# create unordered pairs of \{"a","b","c"\}: \{"a","b"\}, \{"a","c"\},\{"b","c"\}
unorderedPairs(c("a","b","c"))
%append%-methods

Concatenate comparison patterns or classification results

Description

Combines two object of class "RecLinkData" or "RecLinkResult" by concatenating comparison patterns and, if available, weights and classification results.

Usage

```r
x %append% y
```

```r
## S4 method for signature 'RecLinkData,RecLinkData'
x %append% y
```

```r
## S4 method for signature 'RecLinkResult,RecLinkResult'
x %append% y
```

Arguments

- `x, y` The objects to combine.

Value

An object with class corresponding to the input objects which represents the concatenation of `x` and `y`. Its component `pairs` is `rbind(x$pairs, y$pairs)`. If both `x` and `y` have weights stored in component `wdata`, the result gets `c(x$wdata, y$wdata)` as component `wdata`. For the "RecLinkResult" method, the result also includes the concatenation of the predicted classes in `x` and `y` as component `prediction`.

Note

The methods perform only a minimum of integrity checks, so the user has to make sure that the underlying data, the formats of comparison patterns (e.g. excluded columns) and the type of weights (method and parameters of weight calculation) match.

Author(s)

Andreas Borg, Murat Sariyar

Examples

```r
data(RLdata500)
rpairs1=compare.dedup(RLdata500, blockfld=1, identity = identity.RLdata500)

summary(rpairs1)
```
summary(rpairs2)
summary(rpairs1 %append% rpairs2)
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