

Package ‘StatMatch’

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Type Package

Title Statistical Matching

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Suggests MASS, Hmisc

Description Integration of two data sources referred to the same target population which share a number of common variables (aka data fusion). Some functions can also be used to impute missing values in data sets through hot deck imputation methods. Methods to perform statistical matching when dealing with data from complex sample surveys are available too.

License GPL (>= 2)

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StatMatch-package	<i>Statistical Matching or Data Fusion</i>
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Description

Functions to perform statistical matching (aka data fusion), i.e. the integration of two data sources. Some functions can also be used to impute missing values in data sets through hot deck imputation methods.

Details

Package: StatMatch
 Type: Package
 Version: 1.2-1
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Statistical matching (aka data fusion) aims at integrating two data sources referred to same target population and sharing a number of variables in common. The final objective is that of studying the relationship of variables not jointly observed in a single data sources. The integration can be performed at micro (a synthetic of fused file is the output) or macro level (estimates of correlations, regression coefficients, contingency tables are required). Nonparametric hot deck imputation methods (random, rank and nearest neighbour donor) can be used to derive the synthetic data set. In alternative it is possible to use a mixed (parametric–nonparametric) procedure based on predictive mean matching. Methods to perform statistical matching when dealing with data from complex sample surveys are available too. Finally some functions can be used to explore the uncertainty due to the typical matching framework. For major details see D’Orazio et al. (2006) or the package vignette.

Author(s)

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References

D’Orazio M., Di Zio M., Scanu M. (2006) *Statistical Matching, Theory and Practice*. Wiley, Chichester.

 comb.samples

Statistical Matching of data from complex sample surveys

Description

This function permits to cross-tabulate two categorical variables, Y and Z, observed separately in two independent surveys (Y is collected in survey A and Z is collected in survey B) carried out on the same target population. The two surveys share a number of common variables X. When it is available a third survey C, carried on the same population, in which both Y and Z are collected, these data are used as a source of auxiliary information.

The statistical matching is performed by carrying out calibration of the survey weights, as suggested in Renssen (1998).

It is possible also to use the function to derive the estimates that units present a given category of the target variable (estimation are based on Linear Probability Models and are obtained as a by-product of the Renssen’s method).

Usage

```
comb.samples(svy.A, svy.B, svy.C=NULL, y.lab, z.lab, form.x,
             estimation=NULL, micro=FALSE, ...)
```

Arguments

- | | |
|-------|---|
| svy.A | A svydesign R object that stores the data collected in the survey A and all the information concerning the sampling design. This object can be created by using the function svydesign in the package survey . All the variables specified in form.x and by y.lab must be available in svy.A. |
| svy.B | A svydesign R object that stores the data collected in the survey B and all the information concerning the sampling design. This object can be created by using the function svydesign in the package survey . All the variables specified in form.x and by z.lab must be available in svy.B. |
| svy.C | <p>A svydesign R object that stores the data collected in the the survey C and all the information concerning the sampling design. This object can be created by using the function svydesign in the package survey.</p> <p>When svy.C=NULL (default), i.e. no auxiliary information is available, the function returns an estimate of the contingency table of Y vs. Z under the Conditional Independence assumption (CIA) (see Details for major information).</p> <p>When svy.C is available, if estimation="incomplete" then it must contain at least y.lab and z.lab variables. On the contrary, when estimation="synthetic" all the variables specified in form.x, y.lab and z.lab must be available in svy.C.</p> |

y.lab	A string providing the name of the Y variable, collected in survey A and in survey C (if available). The Y variable must be a categorical variable (factor or integer in R).
z.lab	A string providing the name of the Z variable collected in survey B and in survey C (if available). The Z variable must be a categorical variable (factor or integer in R).
form.x	<p>A R formula specifying the matching variables (subset of the X variables) collected in all the surveys, and how have to be considered in combining samples. For instance <code>form.x=~x1+x2</code> means that the variables <code>x1</code> and <code>x2</code> have to be considered marginally without taking into account their cross-tabulation; just their marginal distribution is considered. In order to skip the intercept the formula has to be written as <code>form.x=~x1+x2-1</code>.</p> <p>When dealing with categorical variables, if the formula is written as <code>form.x=~x1:x2-1</code>, it means that the joint distribution of the two variables (table of <code>x1</code> vs. <code>x2</code>) has to be considered.</p> <p>To better understand the usage of <code>form.x</code> see model.matrix (see also formula).</p> <p>Due to weights calibration features, it is preferable to work with categorical X variables. In some cases, procedure may be successful when a single continuous variable is considered jointly with one or more categorical variables, but in most of the cases, it may be necessary to categorize the continuous variable (see Details).</p>
estimation	A character string that identifies the method to be used to estimate the table of Y vs. Z when data from survey C are available. As suggested in Renssen (1998), two alternative methods are available: (i) Incomplete Two-Way Stratification (<code>estimation="incomplete"</code> , or <code>estimation="ITWS"</code> , the default one) and (ii) Synthetic Two-Way Stratification (<code>estimation="synthetic"</code> or <code>estimation="STWS"</code>). In the first case (<code>estimation="incomplete"</code>) only Y and Z variables must be available in <code>svy.C</code> . On the contrary, when <code>estimation="synthetic"</code> the survey C must contain all the X variables specified via <code>form.x</code> , the Y variable and the Z variable. See Details for further information.
micro	Predictions of Z in A and of Y in B are provided. In particular when Y and Z are both categorical variables it is provided the estimated probability that a unit presents a category of the given variable. These probabilities are estimated as a by-product of the whole procedure by considering Linear Probability Models, as suggested in Renssen (1998) (see Details)
...	<p>Further arguments that may be necessary for calibration. In particular, the argument <code>calfun</code> allows to specify the calibration function:</p> <ul style="list-style-type: none"> (i) <code>calfun="linear"</code> for linear calibration (default); (ii) <code>calfun="raking"</code> to rake the survey weights; and (iii) <code>calfun="logit"</code> for logit calibration. See calibrate for major details. <p>Note that when <code>calfun="linear"</code> there is the chance of having negative calibrated weights. This drawback can be avoided by requiring that the final weights lie in a given interval specified via the argument <code>bounds</code> of the function calibrate. Generally speaking, in sample surveys one expects that weights are greater than or equal to 1, i.e. <code>bounds=c(1, Inf)</code>.</p>

The number of iterations used in calibration can be modified by using the argument `maxit` (by default `maxit=50`).

See [calibrate](#) for further details.

Details

This function estimates the contingency table of Y vs. Z by performing a series of calibrations of the survey weights. In practice the estimation is carried out on data in survey C by exploiting all the information from surveys A and B . When survey C is not available the table of Y vs. Z is estimated under the assumption of Conditional Independence (CIA), i.e. $p(Y, Z) = p(Y|\mathbf{X}) \times p(Z|\mathbf{X}) \times p(\mathbf{X})$.

When data from survey C are available (Renssen, 1998), the table of Y vs. Z can be estimated by: Incomplete Two-Way Stratification (ITWS) or Synthetic Two-Way Stratification (STWS). In the first case (ITWS) the weights of the units in survey C are calibrated so that the new weights allow to reproduce the marginal distributions of Y estimated on survey A , and that of Z estimated on survey B . Note that the distribution of the \mathbf{X} variables in survey A and in survey B , must be harmonized before performing ITWS (see [harmonize.x](#)).

The Synthetic Two-Way Stratification allows to estimate the table of Y vs. Z by considering also the \mathbf{X} variables observed in C . This method consists in correcting the table of Y vs. Z estimated under the CIA according to the relationship between Y and Z observed in survey C (for major details see Renssen, 1998).

When the argument `micro` is set to `TRUE` the function provides also $Z.A$ and $Y.B$. The first data.frame has the same rows as `svy.A` and the number of columns equals the number of categories of the Z variable specified via `z.lab`. Each row provides the estimated probabilities of assuming a value in the various categories. The same happens for $Y.B$ which presents the estimated probabilities of assuming a category of `y.lab` for each unit in B .

The estimated probabilities are obtained by applying the linear probability models (for major details see Renssen, 1998). Unfortunately, such models may provide estimated probabilities less than 0 or greater than 1. Much caution should be used in using such predictions for practical purposes.

Value

A R list with the results of the calibration procedure according to the input arguments.

<code>yz.CIA</code>	The table of Y (<code>y.lab</code>) vs. Z (<code>z.lab</code>) estimated under the Conditional Independence Assumption (CIA).
<code>cal.C</code>	The survey object <code>svy.C</code> after the calibration. Only when <code>svy.C</code> is provided.
<code>yz.est</code>	The table of Y (<code>y.lab</code>) vs. Z (<code>z.lab</code>) estimated under the method specified via estimation argument. Only when <code>svy.C</code> is provided.
<code>Z.A</code>	Only when <code>micro=TRUE</code> . It is a data frame with the same rows as in <code>svy.A</code> and the number of columns is equal to the number of categories of the variable <code>z.lab</code> . Each row provides the estimated probabilities for that unit of presenting the various categories of <code>z.lab</code> .
<code>Y.B</code>	Only when <code>micro=TRUE</code> . It is a data frame with the same rows as in <code>svy.B</code> and the number of columns is equal to the number of categories of <code>y.lab</code> . Each row provides the estimated probabilities for that unit of presenting the various categories of <code>y.lab</code> .

call Stores the call to this function with all the values specified for the various arguments (call=match.call()).

Author(s)

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References

D’Orazio, M., Di Zio, M. and Scanu, M. (2006). *Statistical Matching: Theory and Practice*. Wiley, Chichester.

Renssen, R.H. (1998) “Use of Statistical Matching Techniques in Calibration Estimation”. *Survey Methodology*, **24**, pp. 171–183.

See Also

[calibrate](#), [svydesign](#), [harmonize.x](#)

Examples

```
data(quine, package="MASS") #loads quine from MASS
str(quine)
quine$c.Days <- cut(quine$Days, c(-1, seq(0,20,10),100))
table(quine$c.Days)

# split quine in two subsets
set.seed(124)
lab.A <- sample(nrow(quine), 70, replace=TRUE)
quine.A <- quine[lab.A, c("Eth", "Sex", "Age", "Lrn")]
quine.B <- quine[-lab.A, c("Eth", "Sex", "Age", "c.Days")]

# create svydesign objects
require(survey)
quine.A$f <- 70/nrow(quine) # sampling fraction
quine.B$f <- (nrow(quine)-70)/nrow(quine)
svy.qA <- svydesign(~1, fpc=~f, data=quine.A)
svy.qB <- svydesign(~1, fpc=~f, data=quine.B)

# Harmonization wrt the joint distribution
# of ('Sex' x 'Age' x 'Eth')

# vector of population total known
# estimated from the full data set
# note the formula!
tot.m <- colSums(model.matrix(~Eth:Sex:Age-1, data=quine))
tot.m

out.hz <- harmonize.x(svy.A=svy.qA, svy.B=svy.qB, x.tot=tot.m,
  form.x=~Eth:Sex:Age-1, cal.method="linear")
```

```

# estimation of 'Lrn' vs. 'c.Days' under the CIA

svy.qA.h <- out.hz$cal.A
svy.qB.h <- out.hz$cal.B

out.1 <- comb.samples(svy.A=svy.qA.h, svy.B=svy.qB.h,
                     svy.C=NULL, y.lab="Lrn", z.lab="c.Days",
                     form.x=~Eth:Sex:Age-1)

out.1$yz.CIA
addmargins(out.1$yz.CIA)

#
# incomplete two-way stratification

# select a sample C from quine
# and define a survey object

set.seed(4321)
lab.C <- sample(nrow(quine), 50, replace=TRUE)
quine.C <- quine[lab.C, c("Lrn", "c.Days")]
quine.C$f <- 50/nrow(quine) # sampling fraction
svy.qC <- svydesign(~1, fpc=~f, data=quine.C)

# call comb.samples
out.2 <- comb.samples(svy.A=svy.qA.h, svy.B=svy.qB.h,
                     svy.C=svy.qC, y.lab="Lrn", z.lab="c.Days",
                     form.x=~Eth:Sex:Age-1, estimation="incomplete",
                     calfun="linear", maxit=100)

summary(weights(out.2$cal.C))
out.2$yz.est # estimated table of 'Lrn' vs. 'c.Days'
# difference wrt the table 'Lrn' vs. 'c.Days' under CIA
addmargins(out.2$yz.est)-addmargins(out.2$yz.CIA)

# synthetic two-way stratification
# only macro estimation

quine.C <- quine[lab.C, ]
quine.C$f <- 50/nrow(quine) # sampling fraction
svy.qC <- svydesign(~1, fpc=~f, data=quine.C)

out.3 <- comb.samples(svy.A=svy.qA.h, svy.B=svy.qB.h,
                     svy.C=svy.qC, y.lab="Lrn", z.lab="c.Days",
                     form.x=~Eth:Sex:Age-1, estimation="synthetic",
                     calfun="linear", bounds=c(.5, Inf), maxit=100)

summary(weights(out.3$cal.C))

out.3$yz.est # estimated table of 'Lrn' vs. 'c.Days'
# difference wrt the table of 'Lrn' vs. 'c.Days' under CIA
addmargins(out.3$yz.est)-addmargins(out.3$yz.CIA)
# diff wrt the table of 'Lrn' vs. 'c.Days' under incomplete 2ws

```

```

addmargins(out.3$yz.est)-addmargins(out.2$yz.CIA)

# synthetic two-way stratification
# with micro predictions

out.4 <- comb.samples(svy.A=svy.qA.h, svy.B=svy.qB.h,
  svy.C=svy.qC, y.lab="Lrn", z.lab="c.Days",
  form.x=~Eth:Sex:Age-1, estimation="synthetic",
  micro=TRUE, calfun="linear", bounds=c(.5,Inf),
  maxit=100)

head(out.4$Z.A)
head(out.4$Y.B)

```

 comp.prop

Compares two distributions of categorical variables

Description

This function compares two distributions of the same categorical variable(s).

Usage

```
comp.prop(p1, p2, n1, n2=NULL, ref=FALSE)
```

Arguments

p1	A vector or an array containing relative or absolute frequencies for one or more categorical variables. Usually it is the output of the function <code>xtabs</code> or <code>table</code> .
p2	A vector or an array containing relative or absolute frequencies for one or more categorical variables. Usually it is the output of the function <code>xtabs</code> or <code>table</code> . If <code>ref=FALSE</code> then p2 is a further estimate of the distribution of the categorical variable(s) being considered. On the contrary (<code>ref=TRUE</code>) it is the 'reference' distribution (the distribution considered true).
n1	The sample size of the sample of the sample on which p1 has been estimated.
n2	The sample size of the sample of the sample on which p2 has been estimated, required just when <code>ref=FALSE</code> (p2 is estimated on another sample and is not the reference distribution).
ref	Logical. Denotes whether p2 is the reference distribution (true distribution when <code>ref=TRUE</code>) or just another estimate (<code>ref=FALSE</code>) of the distribution derived from another sample with sample size n2.

Details

This function computes some similarity or dissimilarity measures among marginal (joint) distribution of categorical variables(s). The following measures are considered:

Dissimilarity index or total variation distance:

$$\Delta_{12} = \frac{1}{2} \sum_{j=1}^J |p_{1,j} - p_{2,j}|$$

where $p_{s,j}$ are the relative frequencies ($0 \leq p_{s,j} \leq 1$). The dissimilarity index ranges from 0 (minimum dissimilarity) to 1. It can be interpreted as the smallest fraction of units that need to be reclassified in order to make the distributions equal. When p_2 is the reference distribution (true or expected distribution under a given hypothesis) then, following the Agresti's rule of thumb (Agresti 2002, pp. 329–330), values of $\Delta_{12} < 0.03$ denotes that the estimated distribution p_1 follow the true or expected pattern quite closely.

Overlap between two distributions:

$$O_{12} = \sum_{j=1}^J \min(p_{1,j}, p_{2,j})$$

It is a measure of similarity which ranges from 0 to 1 (the distributions are equal). It is worth noting that $O_{12} = 1 - \Delta_{12}$.

Bhattacharyya coefficient:

$$B_{12} = \sum_{j=1}^J \sqrt{p_{1,j} \times p_{2,j}}$$

It is a measure of similarity and ranges from 0 to 1 (the distributions are equal).

Hellinger's distance:

$$d_{H,12} = \sqrt{1 - B_{1,2}}$$

It is a dissimilarity measure which ranges from 0 (distributions are equal) to 1 (max dissimilarity). It satisfies all the properties of a distance measure ($0 \leq d_{H,12} \leq 1$; symmetry and triangle inequality). Hellinger's distance is related to the dissimilarity index, and it is possible to show that:

$$d_{H,12}^2 \leq \Delta_{12} \leq d_{H,12} \sqrt{2}$$

Alongside with those similarity/dissimilarity measures the Pearson's Chi-squared is computed. Two formulas are considered. When p_2 is the reference distribution (true or expected under some hypothesis, ref=TRUE):

$$\chi_P^2 = n_1 \sum_{j=1}^J \frac{(p_{1,j} - p_{2,j})^2}{p_{2,j}}$$

When p_2 is a distribution estimated on a second sample then:

$$\chi_P^2 = \sum_{i=1}^2 \sum_{j=1}^J n_i \frac{(p_{i,j} - p_{+,j})^2}{p_{+,j}}$$

where $p_{+,j}$ is the expected frequency for category j , obtained as follows:

$$p_{+,j} = \frac{n_1 p_{1,j} + n_2 p_{2,j}}{n_1 + n_2}$$

The Chi-Square value can be used to test the hypothesis that two distributions are equal (df=J-1). Unfortunately such a test would not be useful when the distribution are estimated from samples selected from finite population using complex selection schemes (stratification, clustering, etc.). In such a case different alternative corrected Chi-square tests are available (cf. Sarndal et al., 1992, Sec. 13.5). One possibility consist in dividing the Pearson's Chi-square test by the *generalised design effect* of both the surveys. Its estimation is not simple (sampling design variables need to be available). The generalised design effect is smaller than 1 in the presence of stratified random sampling designs. It exceeds 1 the presence of a two stage cluster sampling design. For the purposes of analysis it is reported the value of the generalised design effect g that would determine the acceptance of the null hypothesis (equality of distributions) in the case of $\alpha=0.05$ (df=J-1), i.e. values of g such that

$$\frac{\chi_P^2}{g} \leq \chi_{J-1,0.05}^2$$

Value

A list object with two or three components depending on the argument `ref`.

<code>meas</code>	A vector with the measures of similarity/dissimilarity between the distributions: dissimilarity index (" <code>tvd</code> "), overlap (" <code>overlap</code> "), Bhattacharyya coefficient (" <code>Bhatt</code> ") and Hellinger's distance (" <code>Hell</code> ").
<code>chi.sq</code>	A vector with the following values: Pearson's Chi-square (" <code>Pearson</code> "), the degrees of freedom (" <code>df</code> "), the percentile of a Chi-squared distribution (" <code>q0.05</code> ") and the largest admissible value of the generalised design effect that would determine the acceptance of H_0 (equality of distributions).
<code>p.exp</code>	When <code>ref=FALSE</code> it is reported the value of the reference distribution $p_{+,j}$ estimated used in deriving the Chi-square statistic and also the dissimilarity index. On the contrary (<code>ref=TRUE</code>) it is set equal to the argument <code>p2</code> .

Author(s)

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References

- Agresti A (2002) *Categorical Data Analysis. Second Edition*. Wiley, new York.
 Sarndal CE, Swensson B, Wretman JH (1992) *Model Assisted Survey Sampling*. Springer-Verlag, New York.

Examples

```

data(quine, package="MASS") #loads quine from MASS
str(quine)

# split quine in two subsets
set.seed(124)
lab.A <- sample(nrow(quine), 70, replace=TRUE)
quine.A <- quine[lab.A, c("Eth", "Sex", "Age")]
quine.B <- quine[-lab.A, c("Eth", "Sex", "Age")]

# compare est. distributions from 2 samples
# 1 variable
tt.A <- xtabs(~Age, data=quine.A)
tt.B <- xtabs(~Age, data=quine.B)
comp.prop(p1=tt.A, p2=tt.B, n1=nrow(quine.A), n2=nrow(quine.B), ref=FALSE)

# joint distr. of more variables
tt.A <- xtabs(~Eth+Sex+Age, data=quine.A)
tt.B <- xtabs(~Eth+Sex+Age, data=quine.B)
comp.prop(p1=tt.A, p2=tt.B, n1=nrow(quine.A), n2=nrow(quine.B), ref=FALSE)

# compare est. distr. with a one considered as reference
tt.A <- xtabs(~Eth+Sex+Age, data=quine.A)
tt.all <- xtabs(~Eth+Sex+Age, data=quine)
comp.prop(p1=tt.A, p2=tt.all, n1=nrow(quine.A), n2=NULL, ref=TRUE)

```

create.fused

Creates a matched (synthetic) dataset

Description

Creates a *synthetic* data frame after the statistical matching of two data sources at *micro* level.

Usage

```

create.fused(data.rec, data.don, mtc.ids,
             z.vars, dup.x=FALSE, match.vars=NULL)

```

Arguments

data.rec	A matrix or data frame that plays the role of <i>recipient</i> in the statistical matching application.
data.don	A matrix or data frame that that plays the role of <i>donor</i> in the statistical matching application.

mtc.ids	A matrix with two columns. Each row must contain the name or the index of the recipient record (row) in data.don and the name or the index of the corresponding donor record (row) in data.don. Note that this type of matrix is returned by the functions NND.hotdeck , RANDwNND.hotdeck , rankNND.hotdeck , and mixed.mtc .
z.vars	A character vector with the names of the variables available only in data.don that should be “donated” to data.rec.
dup.x	Logical. When TRUE the values of the matching variables in data.don are also “donated” to data.rec. The names of the matching variables have to be specified with the argument match.vars. To avoid confusion, the matching variables added to data.rec are renamed by adding the suffix “don”. By default dup.x=FALSE.
match.vars	A character vector with the names of the matching variables. It has to be specified only when dup.x=TRUE.

Details

This function allows to create the synthetic (or fused) data set after the application of a statistical matching in a *micro* framework. For details see D’Orazio *et al.* (2006).

Value

The data frame data.rec with the z.vars filled in and, when dup.x=TRUE, with the values of the matching variables match.vars observed on the donor records.

Author(s)

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References

D’Orazio, M., Di Zio, M. and Scanu, M. (2006). *Statistical Matching: Theory and Practice*. Wiley, Chichester.

See Also

[NND.hotdeck](#) [RANDwNND.hotdeck](#) [rankNND.hotdeck](#)

Examples

```
lab <- c(1:15, 51:65, 101:115)
iris.rec <- iris[lab, c(1:3,5)] # recipient data.frame
iris.don <- iris[-lab, c(1:2,4:5)] # donor data.frame

# Now iris.rec and iris.don have the variables
# "Sepal.Length", "Sepal.Width" and "Species"
# in common.
# "Petal.Length" is available only in iris.rec
# "Petal.Width" is available only in iris.don
```

```
# find the closest donors using NND hot deck;
# distances are computed on "Sepal.Length" and "Sepal.Width"

out.NND <- NND.hotdeck(data.rec=iris.rec, data.don=iris.don,
  match.vars=c("Sepal.Length", "Sepal.Width"),
  don.class="Species")

# create synthetic data.set, without the
# duplication of the matching variables

fused.0 <- create.fused(data.rec=iris.rec, data.don=iris.don,
  mtc.ids=out.NND$mtc.ids, z.vars="Petal.Width")

# create synthetic data.set, with the "duplication"
# of the matching variables

fused.1 <- create.fused(data.rec=iris.rec, data.don=iris.don,
  mtc.ids=out.NND$mtc.ids, z.vars="Petal.Width",
  dup.x=TRUE, match.vars=c("Sepal.Length", "Sepal.Width"))
```

fact2dummy

Transforms a categorical variable in a set of dummy variables

Description

Transforms a factor or more factors contained in a data frame in a set of dummy variables.

Usage

```
fact2dummy(data, all=TRUE, lab="x")
```

Arguments

data	A factor or a data frame that contains one or more factors (columns whose class is “factor” or “ordered”) that have to be substituted by dummy variables.
all	Logical. When all=TRUE (default) the output matrix will contain as many dummy variables as the number of the levels of the factor variable. On the contrary, when all=FALSE, the dummy variable related to the last level of the factor is dropped.
lab	A character string with the name of the variable to be pasted with its levels. This is used only when data is a factor. By default it is set to “x”.

Details

This function substitutes categorical variables in the input data frame (columns whose class is “factor” or “ordered”) with the corresponding dummy variables.

Value

A matrix with the dummy variables instead of initial factor variables.

Author(s)

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See Also

[gower.dist](#)

Examples

```
x <- runif(5)
y <- factor(c(1,2,1,2,2))
z <- ordered(c(1,2,3,2,2))
xyz <- data.frame(x,y,z)
fact2dummy(xyz)

fact2dummy(xyz, all=FALSE)

#example with iris data frame
str(iris)
ir.mat <- fact2dummy(iris)
```

Fbwidths.by.x

Computes the Frechet bounds of cells in a contingency table by considering all the possible subsets of the common variables.

Description

This function permits to compute the bounds for cell probabilities in the contingency table **Y** vs. **Z** starting from the marginal tables (**X** vs. **Y**), (**X** vs. **Z**) and the joint distribution of the **X** variables, by considering all the possible subsets of the **X** variables. In this manner it is possible to identify which subset of the **X** variables produces the major reduction of the uncertainty.

Usage

```
Fbwidths.by.x(tab.x, tab.xy, tab.xz)
```

Arguments

- `tab.x` A R table crossing the **X** variables. This table must be obtained by using the function `xtabs` or `table`, e.g.
`tab.x <- xtabs(~x1+x2+x3, data=data.all).`
- `tab.xy` A R table of **X** vs. **Y** variable. This table must be obtained by using the function `xtabs` or `table`, e.g.
`table.xy <- xtabs(~x1+x2+x3+y, data=data.A).`
 A single categorical **Y** variables is allowed. One or more categorical variables can be considered as **X** variables (common variables). Obviously, the same **X** variables in `tab.x` must be available in `tab.xy`. Moreover, it is assumed that the joint distribution of the **X** variables computed from `tab.xy` is equal to `tab.x`; a warning is produced if this is not true.
- `tab.xz` A R table of **X** vs. **Z** variable. This table must be obtained by using the function `xtabs` or `table`, e.g.
`tab.xz <- xtabs(~x1+x2+x3+z, data=data.B).`
 A single categorical **Z** variable is allowed. One or more categorical variables can be considered as **X** variables (common variables). The same **X** variables in `tab.x` must be available in `tab.xz`. Moreover, it is assumed that the joint distribution of the **X** variables computed from `tab.xz` is equal to `tab.x`; a warning is produced if this is not true.

Details

This function permits to compute the Frechet bounds for the frequencies in the contingency table of **Y** vs. **Z**, starting from the conditional distributions $P(Y|X)$ and $P(Z|X)$ (for details see [Frechet.bounds.cat](#)), by considering all the possible subsets of the **X** variables. In this manner it is possible to identify the subset of the **X** variables, with highest association with both **Y** and **Z**, that permits to reduce the uncertainty concerning the distribution of **Y** vs. **Z**.

The uncertainty is measured by the average of the widths of the bounds for the cells in the table of **Y** vs. **Z** it is also reported:

$$\bar{d} = \frac{1}{J \times K} \sum_{j,k} (p_{Y=j,Z=k}^{(up)} - p_{Y=j,Z=k}^{(low)})$$

For details see [Frechet.bounds.cat](#).

Value

A list with the estimated estimated bounds for the cells in the table of **Y** vs. **Z** for each possible subset of the **X** variables. The final component `sum.unc` is a data.frame that summarizes the findings for each subset of the **X** variables and measures of the uncertainty are reported. In particular the data frame reports the no. of **X** variables ("`x.vars`"), the number of cells in the joint distribution of the **X** variables ("`x.cells`"), the number of cells in joint distribution of the **X** variables with frequency equal to 0 ("`x.freq0`"), the average widths of the uncertainty intervals ("`av.widths`").

Author(s)

Marcello D'Orazio <madorazi@istat.it>

References

Ballin, M., D’Orazio, M., Di Zio, M., Scanu, M. and Torelli, N. (2009) “Statistical Matching of Two Surveys with a Common Subset”. *Working Paper*, **124**. Dip. Scienze Economiche e Statistiche, Univ. di Trieste, Trieste.

D’Orazio, M., Di Zio, M. and Scanu, M. (2006). *Statistical Matching: Theory and Practice*. Wiley, Chichester.

See Also

[Frechet.bounds.cat](#), [harmonize.x](#)

Examples

```
data(quine, package="MASS") #loads quine from MASS
str(quine)
quine$c.Days <- cut(quine$Days, c(-1, seq(0,50,10),100))
table(quine$c.Days)

# split quine in two subsets
set.seed(4567)
lab.A <- sample(nrow(quine), 70, replace=TRUE)
quine.A <- quine[lab.A, 1:4]
quine.B <- quine[-lab.A, c(1:3,6)]

# compute the tables required by Fbwidths.by.x()
freq.x <- xtabs(~Eth+Sex+Age, data=quine.A)
freq.xy <- xtabs(~Eth+Sex+Age+Lrn, data=quine.A)
freq.xz <- xtabs(~Eth+Sex+Age+c.Days, data=quine.B)

# apply Fbwidths.by.x()
bounds.yz <- Fbwidths.by.x(tab.x=freq.x, tab.xy=freq.xy,
                           tab.xz=freq.xz)

bounds.yz$sum.unc
```

Frechet.bounds.cat *Frechet bounds of cells in a contingency table*

Description

This function permits to derive the bounds for cell probabilities of the table Y vs. Z starting from the marginal tables (**X** vs. Y), (**X** vs. Z) and the joint distribution of the **X** variables.

Usage

```
Frechet.bounds.cat(tab.x, tab.xy, tab.xz, print.f="tables", tol= 0.0001)
```


Arguments

tab.x	<p>A R table crossing the X variables. This table must be obtained by using the function <code>xtabs</code> or <code>table</code>, e.g.</p> <pre>tab.x <- xtabs(~x1+x2+x3, data=data.all).</pre> <p>When <code>tab.x = NULL</code> then <code>tab.xy</code> and <code>tab.xz</code> must be supplied.</p>
tab.xy	<p>A R table of X vs. Y variable. This table must be obtained by using the function <code>xtabs</code> or <code>table</code>, e.g.</p> <pre>table.xy <- xtabs(~x1+x2+x3+y, data=data.A).</pre> <p>A single categorical Y variable is allowed. One or more categorical variables can be considered as X variables (common variables). Obviously, the same X variables in <code>tab.x</code> must be available in <code>tab.xy</code>. Moreover, it is assumed that the joint distribution of the X variables computed from <code>tab.xy</code> is equal to <code>tab.x</code>; a warning appears if this is not true (see argument <code>tol</code>).</p> <p>When <code>tab.x = NULL</code> then <code>tab.xy</code> should be a one-dimensional table providing the marginal distribution of the Y variable.</p>
tab.xz	<p>A R table of X vs. Z variable. This table must be obtained by using the function <code>xtabs</code> or <code>table</code>, e.g.</p> <pre>tab.xz <- xtabs(~x1+x2+x3+z, data=data.B).</pre> <p>A single categorical Z variable is allowed. One or more categorical variables can be considered as X variables (common variables). The same X variables in <code>tab.x</code> must be available in <code>tab.xz</code>. Moreover, it is assumed that the joint distribution of the X variables computed from <code>tab.xz</code> is equal to <code>tab.x</code>; a warning appears if this is not true (see argument <code>tol</code>).</p> <p>When <code>tab.x = NULL</code> then <code>tab.xz</code> should be a one-dimensional table providing the marginal distribution of the Z variable.</p>
print.f	<p>A string: when <code>print.f="tables"</code> (default) all the cells' estimates will be saved as tables in a list. On the contrary, if <code>print.f="data.frame"</code>, they will be saved as columns of a data.frame.</p>
tol	<p>Tolerance used in comparing joint distributions as far as X variables are considered (default <code>tol= 0.0001</code>); the joint distribution of the X variables computed from <code>tab.xy</code> and <code>tab.xz</code> should be equal to that in <code>tab.x</code>.</p>

Details

This function permits to compute the Frechet bounds for the relative frequencies in the contingency table of **Y** vs. **Z**, starting from the distributions $P(Y|X)$, $P(Z|X)$ and $P(X)$. The bounds for the relative frequencies $p_{j,k}$ in the table **Y** vs. **Z** are:

$$p_{Y=j,Z=k}^{(low)} = \sum_i p_{X=i} \max(0; p_{Y=j|X=i} + p_{Z=k|X=i} - 1)$$

$$p_{Y=j,Z=k}^{(up)} = \sum_i p_{X=i} \min(p_{Y=j|X=i}; p_{Z=k|X=i})$$

The relative frequencies $p_{X=i} = n_i/n$ are computed from the frequencies in `tab.x`; the relative frequencies $p_{Y=j|X=i} = n_{ij}/n_{i+}$ are computed from the `tab.xy`, finally, $p_{Z=k|X=i} = n_{ik}/n_{k+}$ are derived from `tab.xy`.

It is assumed that the marginal distribution of the \mathbf{X} variables is the same in all the input tables: `tab.x`, `tab.xy` and `tab.xz`. If this is not true a warning message will appear.

Note that the cells bounds for the relative frequencies in the contingency table of Y vs. Z are computed also without considering the \mathbf{X} variables:

$$\max\{0; p_{Y=j} + p_{Z=k} - 1\} \leq p_{Y=j, Z=k} \leq \min\{p_{Y=j}; p_{Z=k}\}$$

These bounds represent the unique output when `tab.x = NULL`.

Finally, the contingency table of Y vs. Z estimated under the Conditional Independence Assumption (CIA) is obtained by considering:

$$p_{Y=j, Z=k} = p_{Y=j|X=i} \times p_{Z=k|X=i} \times p_{X=i}$$

When `tab.x = NULL` then it is also provided the expected table under the assumption of independence between Y and Z :

$$p_{Y=j, Z=k} = p_{Y=j} \times p_{Z=k}$$

Value

When `print.f="tables"` (default) a list with the following components:

<code>low.u</code>	The estimated lower bounds for the relative frequencies in the table Y vs. Z without conditioning on the \mathbf{X} variables.
<code>up.u</code>	The estimated upper bounds for the relative frequencies in the table Y vs. Z without conditioning on the \mathbf{X} variables.
<code>CIA</code>	The estimated relative frequencies in the table Y vs. Z under the Conditional Independence Assumption (CIA).
<code>low.cx</code>	The estimated lower bounds for the relative frequencies in the table Y vs. Z when conditioning on the \mathbf{X} variables.
<code>up.cx</code>	The estimated upper bounds for the relative frequencies in the table Y vs. Z when conditioning on the \mathbf{X} variables.
<code>uncertainty</code>	The uncertainty associated to input data, summarized in terms of average width of uncertainty bounds with and without conditioning on the \mathbf{X} variables

When `print.f="data.frame"` the output list contains just two components:

<code>bounds</code>	A <code>data.frame</code> whose columns reports the estimated uncertainty bounds.
<code>uncertainty</code>	The uncertainty associated to input data, summarized in terms of average width of uncertainty bounds with and without conditioning on the \mathbf{X} variables

Author(s)

Marcello D'Orazio <madorazi@istat.it>

References

Ballin, M., D’Orazio, M., Di Zio, M., Scanu, M. and Torelli, N. (2009) “Statistical Matching of Two Surveys with a Common Subset”. *Working Paper*, **124**. Dip. Scienze Economiche e Statistiche, Univ. di Trieste, Trieste.

D’Orazio, M., Di Zio, M. and Scanu, M. (2006). *Statistical Matching: Theory and Practice*. Wiley, Chichester.

See Also

[Fbwidths.by.x](#), [harmonize.x](#)

Examples

```
data(quine, package="MASS") #loads quine from MASS
str(quine)

# split quine in two subsets
set.seed(7654)
lab.A <- sample(nrow(quine), 70, replace=TRUE)
quine.A <- quine[lab.A, 1:3]
quine.B <- quine[-lab.A, 2:4]

# compute the tables required by Frechet.bounds.cat()
freq.x <- xtabs(~Sex+Age, data=quine.A)
freq.xy <- xtabs(~Sex+Age+Eth, data=quine.A)
freq.xz <- xtabs(~Sex+Age+Lrn, data=quine.B)

# apply Frechet.bounds.cat()
bounds.yz <- Frechet.bounds.cat(tab.x=freq.x, tab.xy=freq.xy,
                              tab.xz=freq.xz, print.f="data.frame")
bounds.yz

#compare marg. distribution of Xs in A and B
comp.prop(p1=margin.table(freq.xy,c(1,2)), p2=margin.table(freq.xz,c(1,2)),
          n1=nrow(quine.A), n2=nrow(quine.B))

# harmonize distr. of Sex vs. Age before applying
# Frechet.bounds.cat()

N <- nrow(quine)
quine.A$pop <- N
quine.A$f <- N/70 # reciprocal sampling fraction
quine.B$pop <- N
quine.B$f <- N/(N-70)

# derive the table of Sex vs. Age related to the whole data set
tot.sex.age <- colSums(model.matrix(~Sex*Age-1, data=quine))
tot.sex.age

# use hamonize.x() to harmonize the Sex vs. Age between
```

```

# quine.A and quine.B

# create svydesign objects
require(survey)
svy.qA <- svydesign(~1, weights=~f, fpc=~pop, data=quine.A)
svy.qB <- svydesign(~1, weights=~f, fpc=~pop, data=quine.B)

# apply harmonize.x
out.hz <- harmonize.x(svy.A=svy.qA, svy.B=svy.qB, form.x=~Sex*Age-1, x.tot=tot.sex.age)

# compute the new tables required by Frechet.bounds.cat()
freq.x <- xtabs(out.hz$weights.A~Sex+Age, data=quine.A)
freq.xy <- xtabs(out.hz$weights.A~Sex+Age+Eth, data=quine.A)
freq.xz <- xtabs(out.hz$weights.B~Sex+Age+Lrn, data=quine.B)

#compare marg. distribution of Xs in A and B
comp.prop(p1=margin.table(freq.xy,c(1,2)), p2=margin.table(freq.xz,c(1,2)),
          n1=nrow(quine.A), n2=nrow(quine.B))

# apply Frechet.bounds.cat()
bounds.yz <- Frechet.bounds.cat(tab.x=freq.x, tab.xy=freq.xy,
                               tab.xz=freq.xz, print.f="data.frame")
bounds.yz

```

gower.dist

Computes the Gower's Distance

Description

This function computes the Gower's distance (dissimilarity) among units in a dataset or among observations in two distinct datasets.

Usage

```
gower.dist(data.x, data.y=data.x, rngs=NULL, KR.corr=TRUE)
```

Arguments

data.x	<p>A matrix or a data frame containing variables that should be used in the computation of the distance.</p> <p>Columns of mode <code>numeric</code> will be considered as interval scaled variables; columns of mode <code>character</code> or class <code>factor</code> will be considered as categorical nominal variables; columns of class <code>ordered</code> will be considered as categorical ordinal variables and, columns of mode <code>logical</code> will be considered as binary asymmetric variables (see <code>Details</code> for further information).</p> <p>Missing values (NA) are allowed.</p> <p>If only <code>data.x</code> is supplied, the dissimilarities between rows of <code>data.x</code> will be computed.</p>
--------	--

<code>data.y</code>	A numeric matrix or data frame with the same variables, of the same type, as those in <code>data.x</code> . Dissimilarities between rows of <code>data.x</code> and rows of <code>data.y</code> will be computed. If not provided, by default it is assumed equal to <code>data.x</code> and only dissimilarities between rows of <code>data.x</code> will be computed.
<code>rngs</code>	A vector with the ranges to scale the variables. Its length must be equal to number of variables in <code>data.x</code> . In correspondence of nonnumeric variables, just put 1 or NA. When <code>rngs=NULL</code> (default) the range of a numeric variable is estimated by jointly considering the values for the variable in <code>data.x</code> and those in <code>data.y</code> . Therefore, assuming <code>rngs=NULL</code> , if a variable "X1" is considered: <pre>rngs["X1"] <- max(data.x[, "X1"], data.y[, "X1"]) - min(data.x[, "X1"], data.y[, "X1"])</pre>
<code>KR.corr</code>	When TRUE (default) the extension of the Gower's dissimilarity measure proposed by Kaufman and Rousseeuw (1990) is used. Otherwise, when <code>KR.corr=FALSE</code> , the Gower's (1971) formula is considered.

Details

This function computes distances among records when variables of different type (categorical and continuous) have been observed. In order to handle different types of variables, the Gower's dissimilarity coefficient (Gower, 1971) is used. By default (`KR.corr=TRUE`) the Kaufman and Rousseeuw (1990) extension of the Gower's dissimilarity coefficient is used.

The final dissimilarity between the i th and j th unit is obtained as a weighted sum of dissimilarities for each variable:

$$d(i, j) = \frac{\sum_k \delta_{ijk} d_{ijk}}{\sum_k \delta_{ijk}}$$

In particular, d_{ijk} represents the distance between the i th and j th unit computed considering the k th variable. It depends on the nature of the variable:

- logical columns are considered as asymmetric binary variables, for such case $d_{ijk} = 0$ if $x_{ik} = x_{jk} = \text{TRUE}$, 1 otherwise;
- factor or character columns are considered as categorical nominal variables and $d_{ijk} = 0$ if $x_{ik} = x_{jk}$, 1 otherwise;
- numeric columns are considered as interval-scaled variables and

$$d_{ijk} = \frac{|x_{ik} - x_{jk}|}{R_k}$$

being R_k the range of the k th variable. The range is the one supplied with the argument `rngs` (`rngs[k]`) or the one computed on available data (when `rngs=NULL`);

- ordered columns are considered as categorical ordinal variables and the values are substituted with the corresponding position index, r_{ik} in the factor levels. When `KR.corr=FALSE` these position indexes (that are different from the output of the R function `rank`) are transformed in the following manner

$$z_{ik} = \frac{(r_{ik} - 1)}{\max(r_{ik}) - 1}$$

These new values, z_{ik} , are treated as observations of an interval scaled variable.

As far as the weight δ_{ijk} is concerned:

- $\delta_{ijk} = 0$ if $x_{ik} = \text{NA}$ or $x_{jk} = \text{NA}$;
- $\delta_{ijk} = 0$ if the variable is asymmetric binary and $x_{ik} = x_{jk} = 0$ or $x_{ik} = x_{jk} = \text{FALSE}$;
- $\delta_{ijk} = 1$ in all the other cases.

In practice, NAs and couple of cases with $x_{ik} = x_{jk} = \text{FALSE}$ do not contribute to distance computation.

Value

A matrix object with distances among rows of data .x and those of data .y.

Author(s)

Marcello D’Orazio <madorazi@istat.it>

References

Gower, J. C. (1971), “A general coefficient of similarity and some of its properties”. *Biometrics*, **27**, 623–637.

Kaufman, L. and Rousseeuw, P.J. (1990), *Finding Groups in Data: An Introduction to Cluster Analysis*. Wiley, New York.

See Also

[daisy.dist](#)

Examples

```
x1 <- as.logical(rbinom(10,1,0.5))
x2 <- sample(letters, 10, replace=TRUE)
x3 <- rnorm(10)
x4 <- ordered(cut(x3, -4:4, include.lowest=TRUE))
xx <- data.frame(x1, x2, x3, x4, stringsAsFactors = FALSE)

# matrix of distances among observations in xx
gower.dist(xx)

# matrix of distances among first obs. in xx
# and the remaining ones
gower.dist(data.x=xx[1:3,], data.y=xx[4:10,])
```

harmonize.x	<i>Harmonizes the marginal (joint) distribution of a set of variables observed independently in two sample surveys referred to the same target population</i>
-------------	---

Description

This function permits to harmonize the marginal or the joint distribution of a set of variables observed independently in two sample surveys carried out on the same target population. This harmonization is carried out by using the calibration of the survey weights of the sample units in both the surveys according to the procedure suggested by Renssen (1998).

Usage

```
harmonize.x(svy.A, svy.B, form.x, x.tot=NULL,
            cal.method="linear", ...)
```

Arguments

svy.A	A svydesign R object that stores the data collected in the the survey A and all the information concerning the sampling design. This object can be created by using the function svydesign in the package survey .
svy.B	A svydesign R object that stores the data collected in the the survey B and all the information concerning the sampling design. This object can be created by using the function svydesign in the package survey .
form.x	<p>A R formula specifying which of the variables, common to both the surveys, have to be considered, and how have to be considered. For instance <code>form.x=~x1+x2</code> means that the marginal distribution of the variables <code>x1</code> and <code>x2</code> have to be harmonized and there is also an 'Intercept'. In order to skip the intercept the formula has to be written in the following manner <code>form.x=~x1+x2-1</code>.</p> <p>When dealing with categorical variables, if the formula is written in the following manner <code>form.x=~x1:x2-1</code> it means that the harmonization has to be carried out by considering the joint distribution of the two variables (<code>x1</code> vs. <code>x2</code>). To better understand how <code>form.x</code> works see model.matrix (see also formula).</p> <p>Due to weights calibration features, it is preferable to work with categorical X variables. In some cases, the procedure may be successful when a single continuous variable is considered jointly with one or more categorical variables. When dealing with several continuous variable it may be preferable to categorize them.</p>
x.tot	A vector or table with known population totals for the X variables. A vector is required when <code>cal.method="linear"</code> or <code>cal.method="raking"</code> . The names and the length of the vector depends on the way it is specified the argument <code>form.x</code> (see model.matrix). A contingency table is required when <code>cal.method="poststratify"</code> (for details see postStratify).

When `x.tot` is not provided (i.e. `x.tot=NULL`) then the vector of totals is estimated as a weighted average of the totals estimated on the two surveys. The weight assigned to the totals estimated from A is $\lambda = n_A / (n_A + n_B)$; $1 - \lambda$ is the weight assigned to **X** totals estimated from survey B (n_A and n_B are the number of units in A and B respectively).

`cal.method` A string that specifies how the calibration of the weights in `svy.A` and `svy.B` has to be carried out. By default `cal.method="linear"` linear calibration is performed. In particular, the calibration is carried out by mean of the function `calibrate` in the package `survey`.

Alternatively, it is possible to rake the origin survey weights by specifying `cal.method="raking"`. Finally, it is possible to perform a simple post-stratification by setting `cal.method="poststratify"`. Note that in this case the weights adjustments are carried out by considering the function `postStratify` in the package `survey`.

`...` Further arguments that may be necessary for calibration or post-stratification. In particular, when `cal.method="linear"` there is the chance of having negative weights. This drawback can be avoided by requiring that the final weights lie in a given interval specified via `bounds` argument (an argument of `calibrate`). In sample surveys one expects that weights are greater than or equal to 1, i.e. `bounds=c(1, Inf)`.

The number of iterations used in calibration can be modified too by using the argument `maxit` (by default `maxit=50`).

See `calibrate` for further details.

Details

This function harmonizes the totals of the **X** variables, observed in both survey A and survey B, to be equal to given known totals specified via `x.tot`. When these totals are not known (`x.tot=NULL`) they are estimated by combining the estimates derived from the two separate surveys. The harmonization is carried out according to a procedure suggested by Renssen (1998) based on calibration of survey weights (for major details on calibration see Sarndal and Lundstrom, 2005). The procedure is particularly suited to deal with categorical **X** variables, in this case it permits to harmonize the joint or the marginal distribution of the categorical variables being considered. Note that an incomplete crossing of the **X** variables can be considered: i.e. harmonisation wrt to the joint distribution of $X_1 \times X_2$ and the marginal distribution of X_3).

The calibration procedure may not produce the final result due to convergence problems. In this case an error message appears. In order to reach convergence it may be necessary to launch the procedure with less constraints (i.e a reduced number of population totals) by joining adjacent categories or by discarding some variables.

In some limited cases it could be possible to consider both categorical and continuous variables. In this situation it may happen that calibration is not successful. In order to reach convergence it may be necessary to categorize the continuous **X** variables.

Post-stratification is a special case of calibration; all the weights of the units in a given post-stratum are modified so the reproduce the known total for that post-stratum. Post-stratification avoids problems of convergence but, on the other hand it may produce final weights with a higher variability than those derived from the calibration.

Value

A R with list the results of calibration procedures carried out on survey A and survey B, respectively. In particular the following components will be provided:

cal.A	The survey object <code>svy.A</code> after the calibration; in particular, the weights now are calibrated with respect to the totals of the X variables.
cal.B	The survey object <code>svy.B</code> after the calibration; in particular, the weights now are calibrated with respect to the totals of the X variables.
weights.A	The new calibrated weights associated to the the units in <code>svy.A</code> .
weights.B	The new calibrated weights associated to the the units in <code>svy.B</code> .
call	Stores the call to this function with all the values specified for the various arguments (<code>call=match.call()</code>).

Author(s)

Marcello D’Orazio <mdorazi@istat.it>

References

D’Orazio, M., Di Zio, M. and Scanu, M. (2006). *Statistical Matching: Theory and Practice*. Wiley, Chichester.

Renssen, R.H. (1998) “Use of Statistical Matching Techniques in Calibration Estimation”. *Survey Methodology*, N. **24**, pp. 171–183.

Sarndal, C.E. and Lundstrom, S. (2005) *Estimation in Surveys with Nonresponse*. Wiley, Chichester.

See Also

[comb.samples](#), [calibrate](#), [svydesign](#), [postStratify](#),

Examples

```
data(quine, package="MASS") #loads quine from MASS
str(quine)

# split quine in two subsets
set.seed(7654)
lab.A <- sample(nrow(quine), 70, replace=TRUE)
quine.A <- quine[lab.A, c("Eth", "Sex", "Age", "Lrn")]
quine.B <- quine[-lab.A, c("Eth", "Sex", "Age", "Days")]

# create svydesign objects
require(survey)
quine.A$f <- 70/nrow(quine) # sampling fraction
quine.B$f <- (nrow(quine)-70)/nrow(quine)
svy.qA <- svydesign(~1, fpc=~f, data=quine.A)
svy.qB <- svydesign(~1, fpc=~f, data=quine.B)

#-----
```

```

# example (1)
# Harmonization of the distr. of Sex vs. Age
# usign poststratification

# (1.a) known population totals
# the population toatal are computed on the full data frame
tot.sex.age <- xtabs(~Sex+Age, data=quine)
tot.sex.age

out.hz <- harmonize.x(svy.A=svy.qA, svy.B=svy.qB, form.x=~Sex+Age,
  x.tot=tot.sex.age, cal.method="poststratify")

tot.A <- xtabs(out.hz$weights.A~Sex+Age, data=quine.A)
tot.B <- xtabs(out.hz$weights.B~Sex+Age, data=quine.B)

tot.sex.age-tot.A
tot.sex.age-tot.B

# (1.b) unknown population totals (x.tot=NULL)
# the population total is estimated by combining totals from the
# two surveys

out.hz <- harmonize.x(svy.A=svy.qA, svy.B=svy.qB, form.x=~Sex+Age,
  x.tot=NULL, cal.method="poststratify")

tot.A <- xtabs(out.hz$weights.A~Sex+Age, data=quine.A)
tot.B <- xtabs(out.hz$weights.B~Sex+Age, data=quine.B)

tot.A
tot.A-tot.B

#-----
# example (2)
# Harmonization wrt the maginal distribution
# of 'Eth', 'Sex' and 'Age'
# using linear calibration

# (2.a) vector of population total known
# estimated from the full data set
# note the formula! only marginal distribution of the
# variables are considered
tot.m <- colSums(model.matrix(~Eth+Sex+Age-1, data=quine))
tot.m

out.hz <- harmonize.x(svy.A=svy.qA, svy.B=svy.qB, x.tot=tot.m,
  form.x=~Eth+Sex+Age-1, cal.method="linear")

summary(out.hz$weights.A) #check for negative weights
summary(out.hz$weights.B) #check for negative weights

tot.m
svytable(formula=~Eth, design=out.hz$cal.A)
svytable(formula=~Eth, design=out.hz$cal.B)

```

```

svytable(formula=~Sex, design=out.hz$cal.A)
svytable(formula=~Sex, design=out.hz$cal.B)

# Note: margins are equal but joint distributions are not!
svytable(formula=~Sex+Age, design=out.hz$cal.A)
svytable(formula=~Sex+Age, design=out.hz$cal.B)

# (2.b) vector of population total unknown
out.hz <- harmonize.x(svy.A=svy.qA, svy.B=svy.qB, x.tot=NULL,
  form.x=~Eth+Sex+Age-1, cal.method="linear")
svytable(formula=~Eth, design=out.hz$cal.A)
svytable(formula=~Eth, design=out.hz$cal.B)

svytable(formula=~Sex, design=out.hz$cal.A)
svytable(formula=~Sex, design=out.hz$cal.B)

#-----
# example (3)
# Harmonization wrt the joint distribution of 'Sex' vs. 'Age'
# and the marginal distribution of 'Eth'
# using raking

# vector of population total known
# estimated from the full data set
# note the formula!
tot.m <- colSums(model.matrix(~Eth+(Sex:Age)-1, data=quine))
tot.m

out.hz <- harmonize.x(svy.A=svy.qA, svy.B=svy.qB, x.tot=tot.m,
  form.x=~Eth+(Sex:Age)-1, cal.method="raking")

summary(out.hz$weights.A) #check for negative weights
summary(out.hz$weights.B) #check for negative weights

tot.m
svytable(formula=~Eth, design=out.hz$cal.A)
svytable(formula=~Eth, design=out.hz$cal.B)

svytable(formula=~Sex+Age, design=out.hz$cal.A)
svytable(formula=~Sex+Age, design=out.hz$cal.B)

#-----
# example (4)
# Harmonization wrt the joint distribution
# of ('Sex' x 'Age' x 'Eth')

# vector of population total known
# estimated from the full data set
# note the formula!
tot.m <- colSums(model.matrix(~Eth:Sex:Age-1, data=quine))
tot.m

```

```

out.hz <- harmonize.x(svy.A=svy.qA, svy.B=svy.qB, x.tot=tot.m,
                    form.x=~Eth:Sex:Age-1, cal.method="linear")
tot.m
svytable(formula=~Eth+Sex+Age, design=out.hz$cal.A)
svytable(formula=~Eth+Sex+Age, design=out.hz$cal.B)

```

mahalanobis.dist	<i>Computes the Mahalanobis Distance</i>
------------------	--

Description

This function computes the Mahalanobis distance among units in a dataset or among observations in two distinct datasets.

Usage

```
mahalanobis.dist(data.x, data.y=NULL, vc=NULL)
```

Arguments

data.x	A matrix or a data frame containing variables that should be used in the computation of the distance. Only continuous variables are allowed. Missing values (NA) are not allowed. When only data.x is supplied, the distances between rows of data.x is computed.
data.y	A numeric matrix or data frame with the same variables, of the same type, as those in data.x (only continuous variables are allowed). Dissimilarities between rows of data.x and rows of data.y will be computed. If not provided, by default it is assumed data.y=data.x and only dissimilarities between rows of data.x will be computed.
vc	Covariance matrix that should be used in distance computation. If it is not supplied (vc=NULL) it is estimated from the input data. In particular, when vc=NULL and only data.x is supplied then the covariance matrix is estimated from data.x (var(data.x)). On the contrary when vc=NULL and both data.x and data.y are available then the covariance matrix is estimated on the joined data sets (i.e. var(rbind(data.x, data.y))).

Details

This function computes the Mahalanobis distance:

$$d(i, j) = \sqrt{(x_i - x_j)^T S^{-1} (x_i - x_j)}$$

When vc=NULL the covariance matrix S is estimated from the available data (see argument vc for details) otherwise the one supplied via the argument vc is used.

Value

A matrix object with distances among rows of `data.x` and those of `data.y`.

Author(s)

Marcello D’Orazio <madorazi@istat.it>

References

Mahalanobis, P C (1936) “On the generalised distance in statistics”. Proceedings of the National Institute of Sciences of India 2, pp. 49-55.

See Also

[mahalanobis](#)

Examples

```
md1 <- mahalanobis.dist(iris[1:6,1:4])
md2 <- mahalanobis.dist(data.x=iris[1:6,1:4], data.y=iris[51:60, 1:4])

vv <- var(iris[,1:4])
md1a <- mahalanobis.dist(data.x=iris[1:6,1:4], vc=vv)
md2a <- mahalanobis.dist(data.x=iris[1:6,1:4], data.y=iris[51:60, 1:4], vc=vv)
```

maximum.dist

Computes the Maximum Distance

Description

This function computes the Maximum distance (or L^∞ norm) among units in a dataset or among observations in two distinct datasets.

Usage

```
maximum.dist(data.x, data.y=data.x, rank=FALSE)
```

Arguments

`data.x` A matrix or a data frame containing variables that should be used in the computation of the distance. Only continuous variables are allowed. Missing values (NA) are not allowed.

When only `data.x` is supplied, the distances between rows of `data.x` is computed.

data.y	A numeric matrix or data frame with the same variables, of the same type, as those in data.x (only continuous variables are allowed). Dissimilarities between rows of data.x and rows of data.y will be computed. If not provided, by default it is assumed data.y=data.x and only dissimilarities between rows of data.x will be computed.
rank	Logical, when TRUE the original values are substituted by their ranks divided by the number of values plus one (following suggestion in Kovar et al. 1988). This rank transformation permits to remove the effect of different scales on the distance computation. When computing ranks the tied observations assume the average of their position (ties.method = "average" in calling the rank function).

Details

This function computes the L^∞ distance also know as minimax distance. In practice the distance among two records is the maximum of the absolute differences among the observed variables:

$$d(i, j) = \max(|x_{1i} - x_{1j}|, |x_{2i} - x_{2j}|, \dots, |x_{Ki} - x_{Kj}|)$$

When rank=TRUE the original values are substituted by their ranks divided by the number of values plus one (following suggestion in Kovar et al. 1988).

Value

A matrix object with distances among rows of data.x and those of data.y.

Author(s)

Marcello D’Orazio <madorazi@istat.it>

References

Kovar, J.G., MacMillan, J. and Whitridge, P. (1988). “Overview and strategy for the Generalized Edit and Imputation System”. Statistics Canada, Methodology Branch Working Paper No. BSMD 88-007 E/F.

See Also

[rank](#),

Examples

```
md1 <- maximum.dist(iris[1:10,1:4])
md2 <- maximum.dist(iris[1:10,1:4], rank=TRUE)

md3 <- maximum.dist(data.x=iris[1:50,1:4], data.y=iris[51:100,1:4])
md4 <- maximum.dist(data.x=iris[1:50,1:4], data.y=iris[51:100,1:4], rank=TRUE)
```

 mixed.mtc

Statistical Matching via Mixed Methods

Description

This function implements some mixed methods to perform statistical matching between two data sources.

Usage

```
mixed.mtc(data.rec, data.don, match.vars, y.rec, z.don, method="ML",
          rho.yz=NULL, micro=FALSE, constr.alg="Hungarian")
```

Arguments

- | | |
|------------|---|
| data.rec | A matrix or data frame that plays the role of <i>recipient</i> in the statistical matching application. This data set must contain all variables (columns) that should be used in statistical matching, i.e. the variables called by the arguments <code>match.vars</code> and <code>y.rec</code> . Note that continuous variables are expected, if there are some categorical variables they are recoded into dummies. Missing values (NA) are not allowed. |
| data.don | A matrix or data frame that plays the role of <i>donor</i> in the statistical matching application. This data set must contain all the numeric variables (columns) that should be used in statistical matching, i.e. the variables called by the arguments <code>match.vars</code> and <code>z.don</code> . Note that continuous variables are expected, if there are some categorical variables they are recoded into dummies. Missing values (NA) are not allowed. |
| match.vars | A character vector with the names of the common variables (the columns in both the data frames) to be used as matching variables (\mathbf{X}). |
| y.rec | A character vector with the name of the target variable Y that is observed only for units in <code>data.rec</code> . Only one continuous variable is allowed. |
| z.don | A character vector with the name of the target variable Z that is observed only for units in <code>data.don</code> . Only one continuous variable is allowed. |
| method | A character vector that identifies the method that should be used to estimate the parameters of the regression models: Y vs. \mathbf{X} and Z vs. \mathbf{X} . Maximum Likelihood method is used when <code>method="ML"</code> (default); on the contrary, when <code>method="MS"</code> the parameters are estimated according to approach proposed by Moriarity and Scheuren (2001 and 2003). See Details for further information. |
| rho.yz | A numeric value representing a guess for the correlation among the Y (<code>y.rec</code>) and the Z variable (<code>z.don</code>) that are not jointly observed. When <code>method="MS"</code> then the argument <code>cor.yz</code> must specify the value of the correlation coefficient ρ_{YZ} ; on the contrary, when <code>method="ML"</code> , it must specify the <i>partial correlation coefficient</i> among Y and Z given \mathbf{X} ($\rho_{YZ \mathbf{X}}$). |

	By default (<code>rho.yz=NULL</code>). In practice, in absence of auxiliary information concerning the correlation coefficient or the partial correlation coefficient, the statistical matching is carried out under the assumption of independence among Y and Z given \mathbf{X} (Conditional Independence Assumption, CIA), i.e. $\rho_{YZ \mathbf{X}} = 0$.
<code>micro</code>	Logical. When <code>micro=FALSE</code> (default) only the parameter estimates are returned. On the contrary, when <code>micro=TRUE</code> the function returns also <code>data.rec</code> filled in with the values for the variable Z . The donors for filling in Z in <code>data.rec</code> are identified using a constrained distance hot deck method. In this case, the number of units (rows) in <code>data.don</code> must be greater or equal to the number of units (rows) in <code>data.rec</code> . See next argument and Details for further information.
<code>constr.alg</code>	A string that has to be specified when <code>micro=TRUE</code> , in order to solve the transportation problem involved by the constrained distance hot deck method. Two choices are available: “lpSolve” and “Hungarian”. In the first case, <code>constr.alg="lpSolve"</code> , the transportation problem is solved by means of the function <code>lp.transport</code> available in the package <code>lpSolve</code> . When <code>constr.alg="Hungarian"</code> (default) the transportation problem is solved using the Hungarian method implemented in the function <code>solve_LSAP</code> available in the package <code>clue</code> (Hornik, 2012). Note that Hungarian algorithm is more efficient and requires less processing time.

Details

This function implements some mixed methods to perform statistical matching. A mixed method consists of two steps:

- (1) adoption of a parametric model for the joint distribution of (\mathbf{X}, Y, Z) and estimation of its parameters;
- (2) derivation of a complete “synthetic” data set (recipient data set filled in with values for the Z variable) using a nonparametric approach.

In this case, as far as (1) is concerned, it is assumed that (\mathbf{X}, Y, Z) follows a multivariate normal distribution. Please note that if some of the \mathbf{X} are categorical, then they are recoded into dummies before starting with the estimation. In such a case the assumption of multivariate normal distribution may be questionable.

The whole procedure is based on the imputation method known as *predictive mean matching*. The procedure consists of three steps:

step 1a) Regression step: the two linear regression models Y vs. \mathbf{X} and Z vs. \mathbf{X} are considered and their parameters are estimated.

step 1b) Computation of intermediate values. For the units in `data.rec` the following intermediate values are derived:

$$\tilde{z}_a = \hat{\alpha}_Z + \hat{\beta}_{Z\mathbf{X}}\mathbf{x}_a + e_a$$

for each $a = 1, \dots, n_A$, being n_A the number of units in `data.rec` (rows of `data.rec`). Note that, e_a is a random draw from the multivariate normal distribution with zero mean and estimated residual variance $\hat{\sigma}_{Z|\mathbf{X}}$.

Similarly, for the units in `data.don` the following intermediate values are derived:

$$\tilde{y}_b = \hat{\alpha}_Y + \hat{\beta}_{Y\mathbf{X}}\mathbf{x}_b + e_b$$

for each $b = 1, \dots, n_B$, being n_B the number of units in `data.don` (rows of `data.don`). e_b is a random draw from the multivariate normal distribution with zero mean and estimated residual variance $\hat{\sigma}_{Y|\mathbf{X}}$.

step 2) Matching step. For each observation (row) in `data.rec` a donor is chosen in `data.don` through a nearest neighbor constrained distance hot deck procedure. The distances are computed between (y_a, \tilde{z}_a) and (\tilde{y}_b, z_b) using Mahalanobis distance.

For further details see Sections 2.5.1 and 3.6.1 in D’Orazio *et al.* (2006).

In step 1a) the parameters of the regression model can be estimated by means of the Maximum Likelihood method (`method="ML"`) (see D’Orazio *et al.*, 2006, pp. 19–23,73–75) or, using the Moriarity and Scheuren (2001 and 2003) approach (`method="MS"`) (see also D’Orazio *et al.*, 2006, pp. 75–76). The two estimation methods are compared in D’Orazio *et al.* (2005).

When `method="MS"`, if the value specified for the argument `rho.yz` is not compatible with the other correlation coefficients estimated from the data, then it is substituted with the closest value compatible with the other estimated coefficients.

When `micro=FALSE` only the estimation of the parameters is performed (step 1a). Otherwise, (`micro=TRUE`) the whole procedure is carried out.

Value

A list with a varying number of components depending on the values of the arguments `method` and `rho.yz`.

<code>mu</code>	The estimated mean vector.
<code>vc</code>	The estimated variance–covariance matrix.
<code>cor</code>	The estimated correlation matrix.
<code>res.var</code>	A vector with estimates of the residual variances $\sigma_{Y Z\mathbf{X}}$ and $\sigma_{Z Y\mathbf{X}}$.
<code>start.prho.yz</code>	It is the initial guess for the partial correlation coefficient $\rho_{YZ \mathbf{X}}$ passed in input via the <code>rho.yz</code> argument when <code>method="ML"</code> .
<code>rho.yz</code>	Returned in output only when <code>method="MS"</code> . It is a vector with four values: the initial guess for ρ_{YZ} ; the lower and upper bounds for $\hat{\rho}_{YZ}$ in the statistical matching framework given the correlation coefficients among Y and \mathbf{X} and the correlation coefficients among Z and \mathbf{X} estimated from the available data; and, finally, the closest admissible value used in computations instead of the initial <code>rho.yz</code> that resulted not coherent with the others correlation coefficients estimated from the available data.
<code>phi</code>	When <code>method="MS"</code> . Estimates of the ϕ terms introduced by Moriarity and Scheuren (2001 and 2003).
<code>filled.rec</code>	The <code>data.rec</code> filled in with the values of Z. It is returned only when <code>micro=TRUE</code> .

mtc.ids	when micro=TRUE. This is a matrix with the same number of rows of data.rec and two columns. The first column contains the row names of the data.rec and the second column contains the row names of the corresponding donors selected from the data.don. When the input matrices do not contain row names, a numeric matrix with the indexes of the rows is provided.
dist.rd	A vector with the distances among each recipient unit and the corresponding donor, returned only in case micro=TRUE.
call	How the function has been called.

Author(s)

Marcello D’Orazio <madorazi@istat.it>

References

- D’Orazio, M., Di Zio, M. and Scanu, M. (2005). “A comparison among different estimators of regression parameters on statistically matched files through an extensive simulation study”, *Contributi*, **2005/10**, Istituto Nazionale di Statistica, Rome.
- D’Orazio, M., Di Zio, M. and Scanu, M. (2006). *Statistical Matching: Theory and Practice*. Wiley, Chichester.
- Hornik K. (2012). clue: Cluster ensembles. R package version 0.3-45. <http://CRAN.R-project.org/package=clue>.
- Moriarity, C., and Scheuren, F. (2001). “Statistical matching: a paradigm for assessing the uncertainty in the procedure”. *Journal of Official Statistics*, **17**, 407–422. <http://www.jos.nu/Articles/abstract.asp?article=173407>
- Moriarity, C., and Scheuren, F. (2003). “A note on Rubin’s statistical matching using file concatenation with adjusted weights and multiple imputation”, *Journal of Business and Economic Statistics*, **21**, 65–73.

See Also

[NND.hotdeck](#), [mahalanobis.dist](#)

Examples

```
# reproduce the statistical matching framework
# starting from the iris data.frame
set.seed(98765)
pos <- sample(1:150, 50, replace=FALSE)
ir.A <- iris[pos,c(1,3:5)]
ir.B <- iris[-pos, 2:5]

xx <- intersect(colnames(ir.A), colnames(ir.B))
xx # common variables

# ML estimation method under CIA ((rho_YZ|X=0));
# only parameter estimates (micro=FALSE)
# only continuous matching variables
```

```

xx.mtc <- c("Petal.Length", "Petal.Width")
mtc.1 <- mixed.mtc(data.rec=ir.A, data.don=ir.B, match.vars=xx.mtc,
                  y.rec="Sepal.Length", z.don="Sepal.Width")

# estimated correlation matrix
mtc.1$cor

# ML estimation method under CIA ((rho_YZ|X=0));
# only parameter estimates (micro=FALSE)
# categorical variable 'Species' used as matching variable

xx.mtc <- xx
mtc.2 <- mixed.mtc(data.rec=ir.A, data.don=ir.B, match.vars=xx.mtc,
                  y.rec="Sepal.Length", z.don="Sepal.Width")

# estimated correlation matrix
mtc.2$cor

# ML estimation method with partial correlation coefficient
# set equal to 0.5 (rho_YZ|X=0.5)
# only parameter estimates (micro=FALSE)

mtc.3 <- mixed.mtc(data.rec=ir.A, data.don=ir.B, match.vars=xx.mtc,
                  y.rec="Sepal.Length", z.don="Sepal.Width",
                  rho.yz=0.5)

# estimated correlation matrix
mtc.3$cor

# ML estimation method with partial correlation coefficient
# set equal to 0.5 (rho_YZ|X=0.5)
# with imputation step (micro=TRUE)

mtc.4 <- mixed.mtc(data.rec=ir.A, data.don=ir.B, match.vars=xx.mtc,
                  y.rec="Sepal.Length", z.don="Sepal.Width",
                  rho.yz=0.5, micro=TRUE, constr.alg="Hungarian")

# first rows of data.rec filled in with z
head(mtc.4$filled.rec)

#
# Moriarity and Scheuren estimation method under CIA;
# only with parameter estimates (micro=FALSE)
mtc.5 <- mixed.mtc(data.rec=ir.A, data.don=ir.B, match.vars=xx.mtc,
                  y.rec="Sepal.Length", z.don="Sepal.Width",
                  method="MS")

# the starting value of rho.yz and the value used
# in computations
mtc.5$rho.yz

# estimated correlation matrix

```

```

mtc.5$cor

# Moriarity and Scheuren estimation method
# with correlation coefficient set equal to -0.15 (rho_YZ=-0.15)
# with imputation step (micro=TRUE)

mtc.6 <- mixed.mtc(data.rec=ir.A, data.don=ir.B, match.vars=xx.mtc,
                  y.rec="Sepal.Length", z.don="Sepal.Width",
                  method="MS", rho.yz=-0.15,
                  micro=TRUE, constr.alg="lpSolve")

# the starting value of rho.yz and the value used
# in computations
mtc.6$rho.yz

# estimated correlation matrix
mtc.6$cor

# first rows of data.rec filled in with z imputed values
head(mtc.6$filled.rec)

```

NND.hotdeck

Distance Hot Deck method.

Description

This function implements the distance hot deck method to match the records of two data sources that share some variables.

Usage

```

NND.hotdeck(data.rec, data.don, match.vars,
            don.class=NULL, dist.fun="Manhattan",
            constrained=FALSE, constr.alg="Hungarian",
            keep.t=FALSE, ...)

```

Arguments

data.rec	A matrix or data frame that plays the role of <i>recipient</i> . This data frame must contain the variables (columns) that should be used, directly or indirectly, in the matching application (specified via <code>match.vars</code> and eventually <code>don.class</code>). Missing values (NA) are allowed.
data.don	A matrix or data frame that plays the role of <i>donor</i> . The variables (columns) involved, directly or indirectly, in the computation of distance must be the same and of the same type as those in <code>data.rec</code> (specified via <code>match.vars</code> and eventually <code>don.class</code>).

<code>match.vars</code>	A character vector with the names of the matching variables (the columns in both the data frames) that have to be used to compute distances among records (rows) in <code>data.rec</code> and those in <code>data.don</code> .
<code>don.class</code>	A character vector with the names of the variables (columns in both the data frames) that have to be used to identify the donation classes. In this case the computation of distances is limited to those units of <code>data.rec</code> and <code>data.doc</code> that belong to the same donation class. The case of empty donation classes should be avoided. It would be preferable that variables used to form donation classes are defined as factor. When not specified (default) no donation classes are used. This should require more memory to store the distance matrix and a higher computational effort.
<code>dist.fun</code>	A string with the name of the distance function that has to be used. The following distances are allowed: “Manhattan” (aka “City block”; default), “Euclidean”, “Mahalanobis”, “exact” or “exact matching”, “Gower”, “minimax” or one of the distance functions available in the package proxy . Note that the distance is computed using the function <code>dist</code> of the package proxy with the exception of the “Gower” (see function <code>gower.dist</code> for details), “Mahalanobis” (function <code>mahalanobis.dist</code>) and “minimax” (see <code>maximum.dist</code>) cases. When <code>dist.fun="Manhattan"</code> , “Euclidean”, “Mahalanobis” or “minimax” all the non numeric variables in <code>data.rec</code> and <code>data.don</code> will be converted to numeric. On the contrary, when <code>dist.fun="exact"</code> or <code>dist.fun="exact matching"</code> , all the variables in <code>data.rec</code> and <code>data.don</code> will be converted to character and, as far as the distance computation is concerned, they will be treated as categorical nominal variables, i.e. distance is 0 if a couple of units present the same response category and 1 otherwise.
<code>constrained</code>	Logical. When <code>constrained=FALSE</code> (default) each record in <code>data.don</code> can be used as a donor more than once. On the contrary, when <code>constrained=TRUE</code> each record in <code>data.don</code> can be used as a donor only once. In this case, the set of donors is selected by solving a transportation problem, in order to minimize the overall matching distance. See description of the argument <code>constr.alg</code> for details.
<code>constr.alg</code>	A string that has to be specified when <code>constrained=TRUE</code> . Two choices are available: “lpSolve” and “hungarian”. In the first case, <code>constr.alg="lpSolve"</code> , the transportation problem is solved by means of the function <code>lp.transport</code> available in the package lpSolve . When <code>constr.alg="hungarian"</code> (default) the transportation problem is solved using the Hungarian method, implemented in function <code>solve_LSAP</code> available in the package clue . Note that Hungarian algorithm is faster and more efficient if compared to <code>constr.alg="lpSolve"</code> .
<code>keep.t</code>	Logical, when donation classes are used by setting <code>keep.t=TRUE</code> prints information on the donation classes being processed (by default <code>keep.t=FALSE</code>).
<code>...</code>	Additional arguments that may be required by <code>gower.dist</code> , or by <code>maximum.dist</code> , or by <code>dist</code> .

Details

This function finds a donor record in `data.don` for each record in `data.rec`. In the unconstrained case, it searches for the closest donor record in `data.don` for each record in the recipient data set,

according to the chosen distance function. When for a given recipient record there are more donors available at the minimum distance, one of them is picked at random.

In the constrained case the set of donors is chosen in order to minimize the overall matching distance. In this case the number of units (rows) in the donor data set has to be larger or equal to the number of units of the recipient data set. When the donation classes are used, this condition must be satisfied in each donation class. For further details on nearest neighbor distance hot deck refer to Chapter 2 in D’Orazio *et al.* (2006).

This function can also be used to impute missing values in a data set using the nearest neighbor distance hot deck. In this case `data.rec` is the part of the initial data set that contains missing values; on the contrary, `data.don` is the part of the data set without missing values. See R code in the Examples for details.

Value

A R list with the following components:

<code>mtc.ids</code>	A matrix with the same number of rows of <code>data.rec</code> and two columns. The first column contains the row names of the <code>data.rec</code> and the second column contains the row names of the corresponding donors selected from the <code>data.don</code> . When the input matrices do not contain row names, a numeric matrix with the indexes of the rows is provided.
<code>dist.rd</code>	A vector with the distances among each recipient unit and the corresponding donor.
<code>noad</code>	When <code>constrained=FALSE</code> , it reports the number of available donors at the minimum distance for each recipient unit.
<code>call</code>	How the function has been called.

Author(s)

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References

- D’Orazio, M., Di Zio, M. and Scanu, M. (2006). *Statistical Matching: Theory and Practice*. Wiley, Chichester.
- Hornik K. (2012). `clue`: Cluster ensembles. R package version 0.3-45. <http://CRAN.R-project.org/package=clue>.
- Rodgers, W.L. (1984). “An evaluation of statistical matching”. *Journal of Business and Economic Statistics*, **2**, 91–102.
- Singh, A.C., Mantel, H., Kinack, M. and Rowe, G. (1993). “Statistical matching: use of auxiliary information as an alternative to the conditional independence assumption”. *Survey Methodology*, **19**, 59–79.

See Also

[RANDwNND.hotdeck](#)

Examples

```

# reproduce the classical matching framework
lab <- c(1:15, 51:65, 101:115)
iris.rec <- iris[lab, c(1:3,5)] # recipient data.frame
iris.don <- iris[-lab, c(1:2,4:5)] #donor data.frame

# Now iris.rec and iris.don have the variables
# "Sepal.Length", "Sepal.Width" and "Species"
# in common.
# "Petal.Length" is available only in iris.rec
# "Petal.Width" is available only in iris.don

# Find the closest donors computing distance
# on "Sepal.Length" and "Sepal.Width"
# unconstrained case, Euclidean distance

out.NND.1 <- NND.hotdeck(data.rec=iris.rec, data.don=iris.don,
                        match.vars=c("Sepal.Length", "Sepal.Width") )

# create the synthetic data.set:
# fill in "Petal.Width" in iris.rec

fused.1 <- create.fused(data.rec=iris.rec, data.don=iris.don,
                       mtc.ids=out.NND.1$mtc.ids, z.vars="Petal.Width")

# Find the closest donors computing distance
# on "Sepal.Length", "Sepal.Width" and Species;
# unconstrained case, Gower's distance

out.NND.2 <- NND.hotdeck(data.rec=iris.rec, data.don=iris.don,
                        match.vars=c("Sepal.Length", "Sepal.Width", "Species"),
                        dist.fun="Gower")

# find the closest donors using "Species" to form donation classes
# and "Sepal.Length" and "Sepal.Width" to compute distance;
# unconstrained case.

out.NND.3 <- NND.hotdeck(data.rec=iris.rec, data.don=iris.don,
                        match.vars=c("Sepal.Length", "Sepal.Width"),
                        don.class="Species")

# find the donors using "Species" to form donation classes
# and "Sepal.Length" and "Sepal.Width" to compute distance;
# constrained case, "Hungarian" algorithm

library(clue)
out.NND.4 <- NND.hotdeck(data.rec=iris.rec, data.don=iris.don,

```

```

match.vars=c("Sepal.Length", "Sepal.Width"),
don.class="Species", constrained=TRUE,
constr.alg="Hungarian")

# Example of Imputation of missing values.
# Introducing missing values in iris
ir.mat <- iris
miss <- rbinom(nrow(iris), 1, 0.3)
ir.mat[miss==1,"Sepal.Length"] <- NA
iris.rec <- ir.mat[miss==1,-1]
iris.don <- ir.mat[miss==0,]

#search for NND donors
imp.NND <- NND.hotdeck(data.rec=iris.rec, data.don=iris.don,
                      match.vars=c("Sepal.Width", "Petal.Length", "Petal.Width"),
                      don.class="Species")

# imputing missing values
iris.rec.imp <- create.fused(data.rec=iris.rec, data.don=iris.don,
                            mtc.ids=imp.NND$mtc.ids, z.vars="Sepal.Length")

# rebuild the imputed data.frame
final <- rbind(iris.rec.imp, iris.don)

```

pw.assoc

Pairwise association measure between categorical variables

Description

This function computes some association measures between a categorical nominal variable and each of the other available predictors (also categorical variables).

Usage

```
pw.assoc(formula, data, weights=NULL, freq0c=NULL)
```

Arguments

formula	A formula of the type $y \sim x_1 + x_2$ where y denotes the name of the categorical variable (a factor in R) which plays the role of the dependent variable while x_1 and x_2 are the name of the predictors (both categorical variables). Numeric variables are not allowed; eventual numerical variables should be categorized (see function cut) before being passed to <code>pw.assoc</code> .
data	The data frame which contains the variables called by formula.
weights	The name of the eventual variable in data which provides the units' weights. Weights are used to estimate frequencies (a cell frequency is estimated by summing the weights of the units which present the given characteristics). Default is NULL (no weights available, each unit counts 1).

freq0c A small number which is substituted to eventual cells with zero frequencies in order to avoid computation failures. When NULL (default) a cell with zero frequency is substitutes with $1/N^2$, being N the sample size.

Details

This function computes some association measures among the response variable and each of the predictors specified in the formula. The following association measure are considered:

Cramer's V:

$$V = \sqrt{\frac{\chi^2}{N \times \min [I - 1, J - 1]}}$$

N is the sample size, I is the number of rows and J is the number of columns. Cramer's V ranges from 0 to 1.

Goodman-Kruskal $\lambda(R|C)$:

$$\lambda(R|C) = \frac{\sum_{j=1}^J \max_i(p_{ij}) - \max_i(p_{i+})}{1 - \max_i(p_{i+})}$$

It ranges from 0 to 1, and denotes how much the knowledge of the column variable (predictor) helps in reducing the prediction error of the values of the row variable.

Goodman-Kruskal $\tau(R|C)$:

$$\tau(R|C) = \frac{\sum_{i=1}^I \sum_{j=1}^J p_{ij}^2 / p_{+j} - \sum_{i=1}^I p_{i+}^2}{1 - \sum_{i=1}^I p_{i+}^2}$$

It takes values in the interval [0,1] and has the same PRE meaning of the lambda.

Theil's Uncertainty coefficient:

$$U(R|C) = \frac{\sum_{i=1}^I \sum_{j=1}^J p_{ij} \log(p_{ij}/p_{+j}) - \sum_{i=1}^I p_{i+} \log p_{i+}}{-\sum_{i=1}^I p_{i+} \log p_{i+}}$$

It takes values in the interval [0,1] and measure the reduction of uncertainty in the row variable due to knowing the column variable.

It is worth noting that λ , τ and U are asymmetric measures of the proportional reduction of the variance of the row column when passing from its marginal distribution to its conditional distribution given the column variable obtained starting from the general expression (cf. Agresti, 2002, p. 56):

$$\frac{V(R) - E[V(R|C)]}{V(R)}$$

They differ in the way of measuring variance, in fact it does not exist a general accepted definition of the variance of a categorical variable.

Value

A list object with for components.

V	A vector with the estimated Cramer's V for each couple response-predictor.
labda	A vector with the values of Goodman-Kruskal $\lambda(R C)$ for each couple response-predictor.
tau	A vector with the values of Goodman-Kruskal $\tau(R C)$ for each couple response-predictor.
U	A vector whit the values of Theil's uncertainty coefficient U(RIC) for each couple response-predictor.

Author(s)

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References

Agresti A (2002) *Categorical Data Analysis. Second Edition*. Wiley, new York.

Examples

```
data(quine, package="MASS") #loads quine from MASS
str(quine)

# how Lrn is response variable
pw.assoc(Lrn~Age+Sex+Eth, data=quine)

# usage of units' weights
quine$ww <- runif(nrow(quine), 1,4) #random gen 1<=weights<=4
pw.assoc(Lrn~Age+Sex+Eth, data=quine, weights="ww")
```

RANDwNND.hotdeck

Random Distance hot deck.

Description

This function implements a variant of the distance hot deck method. For each recipient record a subset of of the closest donors is retained and then a donor is selected.

Usage

```
RANDwNND.hotdeck(data.rec, data.don, match.vars=NULL,
                  don.class=NULL, dist.fun="Manhattan",
                  cut.don="rot", k=NULL, weight.don=NULL,
                  keep.t=FALSE, ...)
```

Arguments

<code>data.rec</code>	<p>A numeric matrix or data frame that plays the role of <i>recipient</i>. This data frame must contain the variables (columns), specified via <code>match.vars</code> and <code>don.class</code>, that should be used in the matching.</p> <p>Missing values (NA) are allowed.</p>
<code>data.don</code>	<p>A matrix or data frame that plays the role of <i>donor</i>. This data frame must contain the variables (columns), specified via <code>match.vars</code> and <code>don.class</code>, that should be used in the matching.</p>
<code>match.vars</code>	<p>A character vector with the names of the variables (the columns in both the data frames) that have to be used to compute distances among records (rows) in <code>data.rec</code> and those in <code>data.don</code>. When no matching variables are considered (<code>match.vars=NULL</code>) then all the units in the same donation class are considered as possible donors. Hence one of them is selected at random or with probability proportional to its weight (see argument <code>weight.don</code>). When <code>match.vars=NULL</code> and the donation classes are not created (<code>don.class=NULL</code>) then all the available records in the <code>data.don</code> are considered as potential donors.</p>
<code>don.class</code>	<p>A character vector with the names of the variables (columns in both the data frames) that have to be used to identify donation classes. In this case the computation of distances is limited to those units in <code>data.rec</code> and <code>data.doc</code> that belong to the same donation class. The case of empty donation classes should be avoided. It would be preferable that variables used to form donation classes are defined as factor.</p> <p>When not specified (default), no donation classes are used. This may result in a heavy computational effort.</p>
<code>dist.fun</code>	<p>A string with the name of the distance function that has to be used. The following distances can be used: “Manhattan” (aka “City block”; default), “Euclidean”, “Mahalanobis”, “exact” or “exact matching”, “Gower”, “minimax”, “difference”, or one of the distance functions available in the package proxy. Note that the distances are computed using the function <code>dist</code> of the package proxy with the exception of the “Gower” (see function <code>gower.dist</code> for details), “Mahalanobis” (function <code>mahalanobis.dist</code>), “minimax” (see <code>maximum.dist</code>) “difference” case. Note that <code>dist.fun="difference"</code> computes just the difference between the values of the unique numeric matching variable considered; in practice, it should be used when the subset of the donation classes should be formed by comparing the values of the unique matching variable (for further details see the argument <code>cut.don</code>).</p> <p>By setting <code>dist.fun="ANN"</code> or <code>dist.fun="RANN"</code> it is possible to search for the <i>k</i> nearest neighbours for each recipient record by using the Artificial Neural Network (ANN) implemented in the package ANN. The search is done via the function <code>nn2</code> provided by the package RANN.</p> <p>When <code>dist.fun="Manhattan"</code>, “Euclidean”, “Mahalanobis” or “minimax” all the non numeric variables in <code>data.rec</code> and <code>data.don</code> will be converted to numeric. On the contrary, when <code>dist.fun="exact"</code> or <code>dist.fun="exact matching"</code>, all the variables in <code>data.rec</code> and <code>data.don</code> will be converted to character and, as far as the distance computation is concerned,</p>

they will be treated as categorical nominal variables, i.e. distance is 0 if a couple of units shows the same response category and 1 otherwise.

cut.don	<p>A character string that, jointly with the argument k, identifies the rule to be used to form the subset of the closest donor records.</p> <ul style="list-style-type: none"> • cut.don="rot": (default) then the number of the closest donors to retain is given by $\lceil \sqrt{n_D} \rceil + 1$; being n_D the total number of available donors. In this case k must not to be specified. • cut.don="span": the number of closest donors is determined as the proportion k of all the available donors, i.e. $\lceil n_D \times k \rceil$. Note that, in this case, $0 < k \leq 1$. • cut.don="exact": the kth closest donors out of the n_D are retained. In this case, $0 < k \leq n_D$. • cut.don="min": the donors at the minimum distance from the recipient are retained. • cut.don="k.dist": only the donors whose distance from the recipient is less or equal to the value specified with the argument k. Note that in this case it is not possible to use dist.fun="ANN". • cut.don="lt" or cut.don="<": only the donors whose value of the matching variable is smaller than the value of the recipient Note that in this case it is has to be set dist.fun="difference". • cut.don="le" or cut.don="<=": only the donors whose value of the matching variable is smaller or equal to the value of the recipient Note that in this case it is has to be set dist.fun="difference". • cut.don="ge" or cut.don=">=": only the donors whose value of the matching variable is greater or equal to the value of the recipient Note that in this case it is has to be set dist.fun="difference". • cut.don="gt" or cut.don=">": only the donors whose value of the matching variable is greater than the value of the recipient Note that in this case it is has to be set dist.fun="difference".
k	Depends on the cut.don argument.
weight.don	A character string providing the name of the variable with the weights associated to the donor units in data.don. When this variable is specified, then the selection of a donor among those in the subset of the closest donors is done with probability proportional to its weight (units with larger weight will have a higher chance of being selected). When weight.don=NULL (default) all the units in the subset of the closest donors will have the same probability of being selected.
keep.t	Logical, when donation classes are used by setting keep.t=TRUE prints information on the donation classes being processed (by default keep.t=FALSE).
...	Additional arguments that may be required by <code>gower.dist</code> , by <code>maximum.dist</code> , by <code>dist</code> or by <code>nn2</code> .

Details

This function finds a donor record for each record in the recipient data set. The donor is chosen at random in the subset of available donors. This procedure is known as *random hot deck* (cf. Andridge and Little, 2010). In RANDwNND.hotdeck, the number of closest donors retained to form

the subset is determined according to criterion specified with the argument `cut.don`. The selection of the donor among those in the subset is carried out with equal probability (`weight.don=NULL`) or with probability proportional to a weight associated to the donors (specified via the `weight.don` argument). This procedure is known as *weighted random hot deck* (cf. Andridge and Little, 2010).

The search for the subset of the closest donors can be speed up by using the Artificial Neural Network as implemented in the package **ANN** that is called by the function `nn2` provided by the package **RANN**. Note that this search can be used in all the cases with the exception of `cut.don="k.dist"`. The search of the closest donors can be exact or approximate (for details see `nn2`).

Note that the same donor can be used more than once.

This function can also be used to impute missing values in a data set. In this case `data.rec` is the part of the initial data set that contains missing values; on the contrary, `data.don` is the part of the data set without missing values. See **R** code in the Examples for details.

Value

A **R** list with the following components:

<code>mtc.ids</code>	A matrix with the same number of rows of <code>data.rec</code> and two columns. The first column contains the row names of the <code>data.rec</code> and the second column contains the row names of the corresponding donors selected from the <code>data.don</code> . When the input matrices do not contain row names, then a numeric matrix with the indexes of the rows is provided.
<code>sum.dist</code>	A matrix with summary statistics concerning the subset of the closest donors. The first three columns report the minimum, the maximum and the standard deviation of the distances among the recipient record and the donors in the subset of the closest donors, respectively. The 4th column reports the cutting distance, i.e. the value of the distance such that donors at a higher distance are discarded. The 5th column reports the distance between the recipient and the donor chosen at random in the subset of the donors.
<code>noad</code>	For each recipient unit, reports the number of donor records in the subset of closest donors.
<code>call</code>	How the function has been called.

Author(s)

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References

- Andridge, R.R., and Little, R.J.A. (2010) "A Review of Hot Deck Imputation for Survey Non-response". *International Statistical Review*, **78**, 40–64.
- D'Orazio, M., Di Zio, M. and Scanu, M. (2006). *Statistical Matching: Theory and Practice*. Wiley, Chichester.
- Rodgers, W.L. (1984). "An evaluation of statistical matching". *Journal of Business and Economic Statistics*, **2**, 91–102.

Singh, A.C., Mantel, H., Kinack, M. and Rowe, G. (1993). "Statistical matching: use of auxiliary information as an alternative to the conditional independence assumption". *Survey Methodology*, **19**, 59–79.

See Also

[NND.hotdeck](#)

Examples

```
data(samp.A, samp.B, package="StatMatch") #loads data sets
?samp.A
?samp.B

# samp.A plays the role of recipient
# samp.B plays the role of donor
# find a donor in the in the same region ("area5") and with the same
# gender ("sex"), then only the closest k=20 donors in terms of
# "age" are considered and one of them is picked up at random

out.NND.1 <- RANDwNND.hotdeck(data.rec=samp.A, data.don=samp.B,
                             don.class=c("area5", "sex"), dist.fun="ANN",
                             match.vars="age", cut.don="exact", k=20)

# create the synthetic (or fused) data.frame:
# fill in "labour5" in A
fused.1 <- create.fused(data.rec=samp.A, data.don=samp.B,
                       mtc.ids=out.NND.1$mtc.ids, z.vars="labour5")
head(fused.1)

# weights ("ww") are used in selecting the donor in the final step

out.NND.2 <- RANDwNND.hotdeck(data.rec=samp.A, data.don=samp.B,
                             don.class=c("area5", "sex"), dist.fun="ANN",
                             match.vars="age", cut.don="exact",
                             k=20, weight.don="ww")
fused.2 <- create.fused(data.rec=samp.A, data.don=samp.B,
                       mtc.ids=out.NND.2$mtc.ids, z.vars="labour5")
head(fused.2)

# find a donor in the in the same region ("area5") and with the same
# gender ("sex"), then only the donors with "age" <= to the age of the
# recipient are considered,
# then one of them is picked up at random

out.NND.3 <- RANDwNND.hotdeck(data.rec=samp.A, data.don=samp.B,
                             don.class=c("area5", "sex"), dist.fun="diff",
                             match.vars="age", cut.don="<=")

# create the synthetic (or fused) data.frame:
```

```

# fill in "labour5" in A
fused.3 <- create.fused(data.rec=samp.A, data.don=samp.B,
                       mtc.ids=out.NND.3$mtc.ids, z.vars="labour5")
head(fused.3)

# Example of Imputation of missing values
# introducing missing vales in iris
ir.mat <- iris
miss <- rbinom(nrow(iris), 1, 0.3)
ir.mat[miss==1,"Sepal.Length"] <- NA
iris.rec <- ir.mat[miss==1,-1]
iris.don <- ir.mat[miss==0,]

#search for NND donors
imp.NND <- RANDwNND.hotdeck(data.rec=iris.rec, data.don=iris.don,
                            match.vars=c("Sepal.Width", "Petal.Length", "Petal.Width"),
                            don.class="Species")

# imputing missing values
iris.rec.imp <- create.fused(data.rec=iris.rec, data.don=iris.don,
                             mtc.ids=imp.NND$mtc.ids, z.vars="Sepal.Length")

# rebuild the imputed data.frame
final <- rbind(iris.rec.imp, iris.don)

```

rankNND.hotdeck

Rank distance hot deck method.

Description

This function implements rank hot deck distance method. For each recipient record the closest donors is chosen by considering the distance among the percentage points of the empirical cumulative distribution function.

Usage

```

rankNND.hotdeck(data.rec, data.don, var.rec, var.don=var.rec,
                don.class=NULL, weight.rec=NULL, weight.don=NULL,
                constrained=FALSE, constr.alg="Hungarian",
                keep.t=FALSE)

```

Arguments

`data.rec` A numeric matrix or data frame that plays the role of *recipient*. This data frame must contain the variable `var.rec` to be used in computing the percentage points of the empirical cumulative distribution function and eventually the variables that should be used to identify the donation classes (see argument `don.class`) and the case weights (see argument `weight.rec`).

	Missing values (NA) are not allowed.
data.don	A matrix or data frame that plays the role of <i>donor</i> . This data frame must contain the variable <code>var.rec</code> to be used in computing percentage points of the the empirical cumulative distribution function and eventually the variables that should be used to identify the donation classes (see argument <code>don.class</code>) and the case weights (see argument <code>weight.don</code>).
var.rec	A character vector with the name of the variable in <code>data.rec</code> that should be ranked.
var.don	A character vector with the name of the variable <code>data.don</code> that should be ranked. If not specified, by default <code>var.don=var.rec</code> .
don.class	A character vector with the names of the variables (columns in both the data frames) that have to be used to identify donation classes. In each donation class the computation of percentage points is carried out independently. Then only distances among percentage points of the units in the same donation class are computed. The case of empty donation classes should be avoided. It would be preferable the variables used to form donation classes are defined as factor. When not specified (default), no donation classes are used.
weight.rec	Eventual name of the variable in <code>data.rec</code> that provides the weights that should be used in computing the the empirical cumulative distribution function for <code>var.rec</code> (see Details).
weight.don	Eventual name of the variable in <code>data.don</code> that provides the weights that should be used in computing the the empirical cumulative distribution function for <code>var.don</code> (see Details).
constrained	Logical. When <code>constrained=FALSE</code> (default) each record in <code>data.don</code> can be used as a donor more than once. On the contrary, when <code>constrained=TRUE</code> each record in <code>data.don</code> can be used as a donor only once. In this case, the set of donors is selected by solving a transportation problem, in order to minimize the overall matching distance. See description of the argument <code>constr.alg</code> for details.
constr.alg	A string that has to be specified when <code>constrained=TRUE</code> . Two choices are available: "lpSolve" and "Hungarian". In the first case, <code>constr.alg="lpSolve"</code> , the transportation problem is solved by means of the function <code>lp.transport</code> available in the package lpSolve . When <code>constr.alg="Hungarian"</code> (default) the transportation problem is solved using the Hungarian method, implemented in function <code>solve_LSAP</code> available in the package clue . Note that <code>constr.alg="Hungarian"</code> is faster and more efficient.
keep.t	Logical, when donation classes are used by setting <code>keep.t=TRUE</code> prints information on the donation classes being processed (by default <code>keep.t=FALSE</code>).

Details

This function finds a donor record for each record in the recipient data set. The chosen donor is the one at the closest distance in terms of empirical cumulative distribution (Singh et al., 1990). In practice the distance is computed by considering the estimated empirical cumulative distribution for the reference variable (`var.rec` and `var.don`) in `data.rec` and `data.don`. The empirical cumulative distribution function is estimated by:

$$\hat{F}(y) = \frac{1}{n} \sum_{i=1}^n I(y_i \leq y)$$

being $I() = 1$ if $y_i \leq y$ and 0 otherwise.

In the presence of weights the empirical cumulative distribution function is estimated by:

$$\hat{F}(y) = \frac{\sum_{i=1}^n w_i I(y_i \leq y)}{\sum_{i=1}^n w_i}$$

In the unconstrained case, when there are more donors at the same distance, one of them is chosen at random.

Note that when the donation classes are introduced then empirical cumulative distribution function is estimated independently in each donation classes and the search of a recipient is restricted to donors in the same donation class.

A donor can be chosen more than once. To avoid this set `constrained=TRUE`. In such a case a donor can be chosen just once and the selection of the donors is carried out by solving a transportation problem with the objective of minimizing the overall matching distance (sum of the distances recipient-donor).

Value

A R list with the following components:

<code>mtc.ids</code>	A matrix with the same number of rows of <code>data.rec</code> and two columns. The first column contains the row names of the <code>data.rec</code> and the second column contains the row names of the corresponding donors selected from the <code>data.don</code> . When the input matrices do not contain row names, then a numeric matrix with the indexes of the rows is provided.
<code>dist.rd</code>	A vector with the distances among each recipient unit and the corresponding donor.
<code>noad</code>	The number of available donors at the minimum distance for each recipient unit (only in unconstrained case)
<code>call</code>	How the function has been called.

Author(s)

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References

- D'Orazio, M., Di Zio, M. and Scanu, M. (2006). *Statistical Matching: Theory and Practice*. Wiley, Chichester.
- Singh, A.C., Mantel, H., Kinack, M. and Rowe, G. (1993). "Statistical matching: use of auxiliary information as an alternative to the conditional independence assumption". *Survey Methodology*, **19**, 59–79.

See Also

[NND.hotdeck](#)

Examples

```
data(samp.A, samp.B, package="StatMatch") #loads data sets

# samp.A plays the role of recipient
?samp.A

# samp.B plays the role of donor
?samp.B

# rankNND.hotdeck()
# donation classes formed using "area5"
# ecdf computed on "age"
# UNCONSTRAINED case
out.1 <- rankNND.hotdeck(data.rec=samp.A, data.don=samp.B, var.rec="age",
                        don.class="area5")
fused.1 <- create.fused(data.rec=samp.A, data.don=samp.B,
                      mtc.ids=out.1$mtc.ids, z.vars="labour5")
head(fused.1)

# as before but ecdf estimated using weights
# UNCONSTRAINED case
out.2 <- rankNND.hotdeck(data.rec=samp.A, data.don=samp.B, var.rec="age",
                        don.class="area5",
                        weight.rec="ww", weight.don="ww")
fused.2 <- create.fused(data.rec=samp.A, data.don=samp.B,
                      mtc.ids=out.2$mtc.ids, z.vars="labour5")
head(fused.2)
```

samp.A

Artificial data set resembling EU-SILC survey

Description

This data set provides a limited number of variables observed at persons levels among those usually collected in the European Union Statistics on Income and Living Conditions Survey (EU-SILC). The data are artificially generated, just to show the application of the statistical matching techniques implemented in **StatMatch**.

Usage

```
data(samp.A)
```

Format

A data frame with 3009 observations and the following variables:

HH.P.id unique unit identifier of the type aa.bb where aa identifies the Household while bb identifies the household member

area5 large geographic area, factor with 5 levels: 'NE'=North-East, 'NO'=North-West, 'C'=center, 'S'=South, 'I'=islands

urb Degree of urbanization, factor with 3 levels: '1'=densely populated area, '2'=intermediate area, '3'=thinly populated area

hsize integer, size of the household in which the person lives

hsize5 factor with 5 levels derived from hsize, where the 5th level '>=5' denotes 5 and more people in the household

age integer, the person's age

c.age factor, age categorized in 5 classes

sex factor, the person's gender: '1'=male, '2'=female

marital factor, the person's marital status: '1'=never married, '2'=married, '3'=other (separated, widowed, divorced)

edu7 factor, the person's highest education level attained, follows the ISCED-97 categories: '0'=pre-primary education, '1'=primary education, '2'=lower secondary education, '3'=(upper) secondary education, '4'= post-secondary non tertiary education, '5'=first stage of tertiary education (not leading directly to an advanced research qualification), '6'=second stage of tertiary education (leading to an advanced research qualification)

n.income numeric, the person's net income in Euros

c.neti factor, the person's net income categorized in 7 classes of thousand of Euros

ww numeric, the unit's weight

Details

Please note that this data set is just for illustrative purposes. The unit's weight do not reflect the Italian population size. The variables included are derived starting from the those usually observed in the EU-SILC survey.

Source

This data set is artificially created starting from the EU-SILC survey structure.

References

http://epp.eurostat.ec.europa.eu/portal/page/portal/microdata/eu_silc

samp.B

*Artificial data set resembling EU–SILC survey***Description**

This data set provides a limited number of variables observed at persons levels among those usually collected in the European Union Statistics on Income and Living Conditions Survey (EU–SILC). The data are artificially generated, just to show the application of the statistical matching techniques implemented in **StatMatch**.

Usage

```
data(samp.B)
```

Format

A data frame with 6686 observations and the following variables:

HH.P.id unique unit identifier of the type aa.bb where aa identifies the Household while bb identifies the household member

area5 large geographic area, factor with 5 levels: ‘NE’=North–East, ‘NO’=North–West, ‘C’=center, ‘S’=South, ‘I’=islands

urb Degree of urbanization, factor with 3 levels: ‘1’=densely populated area, ‘2’=intermediate area, ‘3’=thinly populated area

hsize integer, size of the household in which the person lives

hsize5 factor with 5 levels derived from hsize, where the 5th level ‘>=5’ denotes 5 and more people in the household

age integer, the person’s age

c.age factor, age categorized in 5 classes

sex factor, the person’s gender: ‘1’=male, ‘2’=female

marital factor, the person’s marital status: ‘1’=never married, ‘2’=married, ‘3’=other (separated, widowed, divorced)

edu7 factor, the person’s highest education level attained, follows the ISCED-97 categories: ‘0’=pre–primary education, ‘1’=primary education, ‘2’=lower secondary education, ‘3’= (upper) secondary education, ‘4’= post–secondary non tertiary education, ‘5’=first stage of tertiary education (not leading directly to an advanced research qualification), ‘6’=second stage of tertiary education (leading to an advanced research qualification)

labour5 the person’s self–defined economic status, factor with 5 levels: ‘1’=employee working full–time or part–time, ‘2’=self–employed working full–time or part–time, ‘3’=unemployed, ‘4’=In retirement or in early retirement or has given up business, ‘5’=other status (student, permanent disabled, in compulsory military service, fulfilling domestic tasks, etc.)

ww numeric, the unit’s weight

Details

Please note that this data set is just for illustrative purposes. The unit's weight do not reflect the Italian population size. The variables included are derived starting from the those usually observed in the EU–SILC survey.

Source

This data set is artificially created starting from the EU–SILC survey structure.

References

http://epp.eurostat.ec.europa.eu/portal/page/portal/microdata/eu_silc

 samp.C

Artificial data set resembling EU–SILC survey

Description

This data set provides a limited number of variables observed at persons levels among those usually collected in the European Union Statistics on Income and Living Conditions Survey (EU–SILC). The data are artificially generated, just to show the application of the statistical matching techniques implemented in **StatMatch**.

Usage

```
data(samp.C)
```

Format

A data frame with 980 observations and the following variables:

- HH.P.id** unique unit identifier of the type aa.bb where aa identifies the Household while bb identifies the household member
- area5** large geographic area, factor with 5 levels: 'NE'=North–East, 'NO'=North–West, 'C'=center, 'S'=South, 'I'=islands
- urb** Degree of urbanization, factor with 3 levels: '1'=densely populated area, '2'=intermediate area, '3'=thinly populated area
- hsize** integer, size of the household in which the person lives
- hsize5** factor with 5 levels derived from hsize, where the 5th level '>=5' denotes 5 and more people in the household
- age** integer, the person's age
- c.age** factor, age categorized in 5 classes
- sex** factor, the person's gender: '1'=male, '2'=female
- marital** factor, the person's marital status: '1'=never married, '2'=married, '3'=other (separated, widowed, divorced)

edu7 factor, the person's highest education level attained, follows the ISCED-97 categories: '0'=pre-primary education, '1'=primary education, '2'=lower secondary education, '3'=(upper) secondary education, '4'= post-secondary non tertiary education, '5'=first stage of tertiary education (not leading directly to an advanced research qualification), '6'=second stage of tertiary education (leading to an advanced research qualification)

labour5 the person's self-defined economic status, factor with 5 levels: '1'=employee working full-time or part-time, '2'=self-employed working full-time or part-time, '3'=unemployed, '4'=In retirement or in early retirement or has given up business, '5'=other status (student, permanent disabled, in compulsory military service, fulfilling domestic tasks, etc.)

n.income numeric, the person's net income in Euros

c.neti factor, the person's net income categorized in 7 classes of thousand of Euros

ww numeric, the unit's weight

Details

Please note that this data set is just for illustrative purposes. The unit's weight do not reflect the Italian population size. The variables included are derived starting from the those usually observed in the EU-SILC survey.

Source

This data set is artificially created starting from the EU-SILC survey structure.

References

http://epp.eurostat.ec.europa.eu/portal/page/portal/microdata/eu_silc

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