Package ‘sdcMicro’

October 1, 2015

Type Package

Title Statistical Disclosure Control Methods for Anonymization of Microdata and Risk Estimation

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Date 2015-10-01

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Description Data from statistical agencies and other institutions are mostly confidential. This package can be used for the generation of anonymized (micro)data, i.e. for the creation of public- and scientific-use files. In addition, various risk estimation methods are included. Note that the package ‘sdcMicroGUI’ includes a graphical user interface for various methods in this package.

LazyData TRUE

ByteCompile TRUE

LinkingTo Rcpp

Depends R (>= 2.10), rmarkdown, knitr, data.table, xtable

Suggests laeken, testthat

Imports utils, stats, graphics, car, robustbase, cluster, MASS, e1071, tools, Rcpp, methods, sets, ggplot2

License GPL-2

URL https://github.com/alexkowa/sdcMicro

### NeedsCompilation
yes

### Repository
CRAN

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Statistical Disclosure Control (SDC) for the generation of protected microdata for researchers and for public use.

Description

This package includes all methods of the popular software mu-Argus plus several new methods. In comparison with mu-Argus the advantages of this package are that the results are fully reproducible even with the included GUI, that the package can be used in batch-mode from other software, that the functions can be used in a very flexible way, that everybody could look at the source code and that there are no time-consuming meta-data management is necessary. However, the user should have a detailed knowledge about SDC when applying the methods on data.

Details

The package is programmed using S4-classes and it comes with a well-defined class structure.

The implemented graphical user interface (GUI) for microdata protection serves as an easy-to-handle tool for users who want to use the sdcMicro package for statistical disclosure control but are not used to the native R command line interface. In addition to that, interactions between objects which results from the anonymization process are provided within the GUI. This allows an automated recalculation and displaying information of the frequency counts, individual risk, information loss and data utility after each anonymization step. In addition to that, the code for every anonymization step carried out within the GUI is saved in a script which can then be easily modified and reloaded.

Package: sdcMicro
Type: Package
Version: 2.5.9
Date: 2009-07-22
License: GPL 2.0
Author(s)
Mathias Templ, Alexander Kowarik, Bernhard Meindl
Maintainer: Matthias Templ <templ@statistik.tuwien.ac.at>

References

Examples

```r
## example from Capobianchi, Polettini and Lucarelli:
data(francdat)
f <- freqCalc(francdat, keyVars=c(2,4,5,6), w=8)
f f$ffk f$k
## with missings:
x <- francdat
x[3,5] <- NA
x[4,2] <- x[4,4] <- NA
x[5,6] <- NA
x[6,2] <- NA
f2 <- freqCalc(x, keyVars=c(2,4,5,6), w=8)
f2$f$k
## individual risk calculation:
indivf <- indivRisk(f)
indivf$frk
## Local Suppression
locals <- localSupp(f, keyVar=2, indivRisk=indivf$frk, threshold=0.25)
f2 <- freqCalc(locals$f.freqCalc, keyVars=c(2,4,5,6), w=8)
indivf2 <- indivRisk(f2)
indivf2$frk

## select another keyVar and run localSupp once again,
# if you think the table is not fully protected
data(free1)
f <- freqCalc(free1, keyVars=1:3, w=30)
```
```r
ind <- indivRisk(f)
## and now you can use the interactive plot for individual risk objects:
## plot(ind)

## example from Capobianchi, Polettini and Lucarelli:
data(francdat)
l1 <- localSuppression(francdat, keyVars=c(2,4,5,6), importance=c(1,3,2,4))
l1$x
l2 <- localSuppression(francdat, keyVars=c(2,4,5,6), k=2)
l3 <- localSuppression(francdat, keyVars=c(2,4,5,6), k=4)

## Data from mu-Argus:
## Global recoding:
data(free1)
free1[, "AGE"] <- globalRecode(free1[,"AGE"], c(1,9,19,29,39,49,59,69,100), labels=1:8)

## Top coding:
topBotCoding(free1[,"DEBTS"], value=9000, replacement=9100, kind="top")

## Numerical Rank Swapping:
## do not use the mu-Argus test data set (free1)
# since the numerical variables are (probably) faked.
data(Tarragona)
Tarragona <- rankSwap(Tarragona, P=10)

## Microaggregation:
m1 <- microaggregation(Tarragona, method="onedims", aggr=3)
m2 <- microaggregation(Tarragona, method="pca", aggr=3)
# summary(m1)
# approx. 1 minute computation time
# valTable(Tarragona, method=c("simple","onedims","pca"))

data(microData)
m1 <- microaggregation(microData, method="mdav")
x <- m1$x ### fix me
summary(m1)
plotMicro(m1, 0.1, which.plot=1) # too less observations...
data(free1)
plotMicro(microaggregation(free1[,31:34], method="onedims"), 0.1, which.plot=1)

## disclosure risk (interval) and data utility:
m1 <- microaggregation(Tarragona, method="onedims", aggr=3)
dRisk(obj=Tarragona, xm=m1$mx)
dRisk(obj=Tarragona, xm=m2$mx)
dUtility(obj=Tarragona, xm=m1$mx)
dUtility(obj=Tarragona, xm=m2$mx)

## S4 class code for Adding Noise methods will be included
# in the next version of sdcMicro.
```
## Fast generation of synthetic data with aprox.
# the same covariance matrix as the original one.

data(mtcars)
cov(mtcars[,4:6])
cov(dataGen(mtcars[,4:6],n=200))
pairs(mtcars[,4:6])
pairs(dataGen(mtcars[,4:6],n=200))

## PRAM

set.seed(123)
x <- factor(sample(1:4, 250, replace=TRUE))
pr1 <- pram(x)
length(which(pr1$xpramed == x))
x2 <- factor(sample(1:4, 250, replace=TRUE))
length(which(pram(x2)$xpramed == x2))

data(free1)
marstatPramed <- pram(free1[,"MARSTAT"])

## Not run:
# FOR OBJECTS OF CLASS sdcMicro
data(testdata)
sdc <- createSdcObj(testdata,
  keyVars=c('urbur','roof','walls','water','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight')
head(sdc@manipnumvars)

### Display Risks
sdc@risk$global
d <- dRisk(sdc)
sdc@risk$numeric

### use addNoise without Parameters
sdc <- addNoise(sdc,variables=c("expend","income"))
head(sdc@manipnumVars)
sdc@risk$numeric

### undolast
sdc <- undolast(sdc)
head(sdc@manipnumVars)
sdc@risk$numeric

### redo addNoise with Parameter
sdc <- addNoise(sdc, noise=0.2)
head(sdc@manipnumVars)
sdc@risk$numeric

### dataGen
#sdc <- undolast(sdc)
#head(sdc@risk$individual)
#sdc@risk$global
#sdc <- dataGen(sdc)
#head(sdc@risk$individual)
#sdc@risk$global

### LocalSuppression
sdc <- undolast(sdc)
head(sdc@risk$individual)
addNoise

```r
sdc$risk$global
sdc <- localSuppression(sdc)
head(sdc$risk$individual)

## microaggregation
sdc <- undolast(sdc)
head(get.sdcMicroObj(sdc, type="manipNumVars"))
sdc <- microaggregation(sdc)
head(get.sdcMicroObj(sdc, type="manipNumVars"))

## pram
sdc <- undolast(sdc)
head(sdc$risk$individual)

## rankSwap
sdc <- undolast(sdc)
head(sdc$risk$individual)

## suda2
sdc <- suda2(sdc)

## topBotCoding
head(get.sdcMicroObj(sdc, type="manipNumVars"))
sdc$risk$numeric
sdc <- topBotCoding(sdc, value=60000000, replacement=62000000, column="income")
head(get.sdcMicroObj(sdc, type="manipNumVars"))

## LocalRecProg
data(testdata2)
sdc <- createSdcObj(testdata2,
  keyVars=c("urbrur", "roof", "walls", "water", "sex", "relat"))
sdc$risk$global

## LlmogGlobalRisk
sdc <- llmodGlobalRisk(sdc, inclProb=0.001)
sdc$risk$model

## End(Not run)
```

---

**addNoise**

Adding noise to perturb data
Description

Various methods for adding noise to perturb continuous scaled variables.

Usage

addNoise(obj, variables = NULL, noise = 150, method = "additive", ...)

Arguments

obj either a data frame, matrix or a sdcMicroObj-class that should be perturbed
variables vector with names of variables that should be perturbed
noise amount of noise (in percentages)
method choose between 'additive', 'correlated', 'correlated2', 'restr', 'ROMM', 'outdect'
... see possible arguments below

Details

If ‘obj’ is of class sdcMicroObj-class all continuous key variables are selected per default. If ‘obj’ is of class “data.frame” or “matrix”, the continuous variables have to be specified.

Method ‘additive’ adds noise completely at random to each variable depending on there size and standard deviation. ‘correlated’ and method ‘correlated2’ adds noise and preserves the covariances as described in R. Brand (2001) or in the reference given below. Method ‘restr’ takes the sample size into account when adding noise. Method ‘ROMM’ is an implementation of the algorithm ROMM (Random Orthogonalized Matrix Masking) (Fienberg, 2004). Method ‘outdect’ adds noise only to outliers. The outliers are identified with univariate and robust multivariate procedures based on a robust mahalanobis distances calculated by the MCD estimator.

Value

If ‘obj’ was of class sdcMicroObj-class the corresponding slots are filled, like manipNumVars, risk and utility.

If ‘obj’ was of class “data.frame” or “matrix” an object of class “micro” with following entities is returned:

x the original data
xm the modified (perturbed) data
method method used for perturbation
noise amount of noise

Methods

list("signature(obj = "data.frame")")
list("signature(obj = "matrix")")
list("signature(obj = "sdcMicroObj")")
addNoise

Author(s)
Matthias Templ

References


See Also

sdcmicroObj-class, summary.micro

Examples

data(Tarragona)
 a1 <- addNoise(Tarragona)
 a1

data(testdata)
 testdata[, c('expend','income','savings')] <-
 addNoise(testdata[,c('expend','income','savings')])$xm

## for objects of class sdcmicroObj:
 data(testdata2)
 sdc <- createSdcObj(testdata2,
   keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
   numVars=c('expend','income','savings'), w='sampling_weight')
 sdc <- addNoise(sdc)
calcRisks

Recompute Risk and Frequencies for a sdcMicroObj

Description

Recomputation of Risk should be done after manual changing the content of an object of class sdcMicroObj-class.

Usage

calcRisks(obj, ...)

Arguments

obj an object of class sdcMicroObj-class

... no arguments at the moment

Details

By applying this function, the disclosure risk is re-estimated and the corresponding slots of an object of class sdcMicroObj-class are updated. This function mostly used internally to automatically update the risk after an sdc method is applied.

Methods

list("signature(obj = \"sdcMicroObj\")")

See Also

sdcMicroObj-class

Examples

data(testdata2)
sdc <- createSdcObj(testdata2,
keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- calcRisks(sdc)
casc1  

Small Artificial Data set

Description

Small Toy Example Data set which was used by Sanz-Mateo et.al.

Format

The format is: int [1:13, 1:7] 10 12 17 21 9 12 14 13 15 ... - attr(*, "dimnames")=List of 2 ..$ : 
  chr [1:13] "1" "2" "3" "4" ... ..$ : chr [1:7] "1" "2" "3" "4" ...

Examples

data(casc1)
casc1

CASCrefmicrodata  Census data set

Description

This test data set was obtained on July 27, 2000 using the public use Data Extraction System of the 
U.S. Bureau of the Census.

Format

A data frame sampled from year 1995 with 1080 observations on the following 13 variables.

AFNLWGT  Final weight (2 implied decimal places)
AGI  Adjusted gross income
EMCONTRB  Employer contribution for hlth insurance
FEDTAX  Federal income tax liability
PTOTVAL  Total person income
STATETAX  State income tax liability
TAXINC  Taxable income amount
POTHVAL  Total other persons income
INTVAL  Amt of interest income
PEARNVAL  Total person earnings
FICA  Soc. sec. retirement payroll deduction
WSALVAL  Amount: Total Wage and salary
ERNVAL  Business or Farm net earnings
Source
Public use file from the CASC project. More information on this test data can be found in the paper listed below.

References

Examples
data(CASCrefmicrodata)
str(CASCrefmicrodata)

datagen

Description
Fast generation of (primitive) synthetic multivariate normal data.

Usage
dataGen(obj, ...)

Arguments
obj data.frame or matix
... see possible arguments below
• namount of observations for the generated data

Details
Uses the cholesky decomposition to generate synthetic data with approx. the same means and covariances. For details see at the reference.

Value
the generated synthetic data.

Methods
list("signature(obj = "data.frame\")")
list("signature(obj = "matrix\")")
list("signature(obj = "sdcMicroObj\")")
Note

With this method only multivariate normal distributed data with approximately the same covariance as the original data can be generated without reflecting the distribution of real complex data, which are, in general, not follows a multivariate normal distribution.

Author(s)

Matthias Templ

References


See Also

sdcMicroObj-class, shuffle

Examples

data(mtcars)
cov(mtcars[,4:6])
cov(dataGen(mtcars[,4:6]))
pairs(mtcars[,4:6])
pairs(dataGen(mtcars[,4:6]))

# for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
  keyVars=c('urburur','roof','walls','water','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- dataGen(sdc)

---

dRisk

overall disclosure risk

Description

Distance-based disclosure risk estimation via standard deviation-based intervals around observations.

Usage

dRisk(obj, ...)

Arguments

obj original data or object of class sdcMicroObj-class
...
possible arguments are:

• xmperturbed data
• kpercentage of the standard deviation
Details

An interval (based on the standard deviation) is built around each value of the perturbed value. Then we look if the original values lay in these intervals or not. With parameter k one can enlarge or down scale the interval.

Value

The disclosure risk or/and the modified sdcmicroObj-class

Methods

list("signature(obj = \"data.frame\")")
list("signature(obj = \"matrix\")")
list("signature(obj = \"sdcmicroObj\")")

Author(s)

Matthias Templ

References


See Also
dUtility, dUtility

Examples

data(free1)
m1 <- microaggregation(free1[, 31:34], method="onedims", aggr=3)
m2 <- microaggregation(free1[, 31:34], method="pca", aggr=3)
dRisk(obj=free1[, 31:34], x=m1$mx)
dRisk(obj=free1[, 31:34], x=m2$mx)
dUtility(obj=free1[, 31:34], x=m1$mx)
dUtility(obj=free1[, 31:34], x=m2$mx)

## for objects of class sdcmicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
umVars=c('expend','income','savings'), w='sampling_weight')
## this is already made internally: sdc <- dRisk(sdc)
## and already stored in sdc
**Description**

Distance-based disclosure risk estimation via robust Mahalanobis Distances.

**Usage**

```r
dRiskRMD(obj, ...)```

**Arguments**

- `obj`: original data or object of class `sdcMicroObj-class`
- `...`: see possible arguments below

- `xM`: masked data
- `kweight`: for adjusting the influence of the robust Mahalanobis distances, i.e. to increase or decrease each of the disclosure risk intervals.
- `k2parameter`: for method RMDID2 to choose a small interval around each masked observation.

**Details**

This method is an extension of method SDID because it accounts for the “outlyingness” of each observation. This is a quite natural approach since outliers do have a higher risk of re-identification and therefore these outliers should have larger disclosure risk intervals as observations in the center of the data cloud.

The algorithm works as follows:

1. Robust Mahalanobis distances are estimated in order to get a robust multivariate distance for each observation.
2. Intervals are estimated for each observation around every data point of the original data points where the length of the interval is defined/weighted by the squared robust Mahalanobis distance and the parameter $k\$. The higher the RMD of an observation the larger the interval.
3. Check if the corresponding masked values fall into the intervals around the original values or not. If the value of the corresponding observation is within such an interval the whole observation is considered unsafe. So, we get a whole vector indicating which observation is save or not, and we are finished already when using method RMDID1).
4. For method RMDID1w: we return the weighted (via RMD) vector of disclosure risk.
5. For method RMDID2: whenever an observation is considered unsafe it is checked if $m\$ other observations from the masked data are very close (defined by a parameter $k2\$ for the length of the intervals as for SDID or RSDID) to such an unsafe observation from the masked data, using Euclidean distances. If more than $m\$ points are in such a small interval, we conclude that this observation is “save”.


Value

The disclosure risk or the modified sdcMicroObj-class

risk1 percentage of sensitive observations according to method RMDID1.

risk2 standardized version of risk1

wrisk1 amount of sensitive observations according to RMDID1 weighted by their corresponding robust Mahalanobis distances.

wrisk2 RMDID2 measure

indexRisk1 index of observations with high risk according to risk1 measure

indexRisk2 index of observations with high risk according to wrisk2 measure

Methods

list("signature(obj = "data.frame")")
list("signature(obj = "matrix")")
list("signature(obj = "sdcMicroObj")")

Author(s)

Matthias Templ

References


See Also

dRisk

Examples

data(Tarragona)
x <- Tarragona[, 5:7]
y <- addNoise(x)$xm
dRiskRMD(x, xm=y)
dRisk(x, xm=y)

data(testdata2)
sdc <- createSdcObj(testdata2,
keyVars=c('urbur','roof','walls','water','electcon','relat','sex'),
numVars=c('expend','income','savings'), w='sampling_weight')
## this is already made internally:
## sdc <- dRiskRMD(sdc)
## and already stored in sdc
**Description**

IL1s data utility.

**Usage**

dUtility(obj, ...)

**Arguments**

- **obj** original data or object of class `sdMicroObj-class`
- **...** see arguments below
  - `xmperturbed data`
  - `methodmethod IL1 or eigen. More methods are implemented in summary.micro()`

**Details**

The standardised distances of the perturbed data values to the original ones are measured. Measure IL1 measures the distances between the original values and the perturbed ones, scaled by the standard deviation. Method 'eigen' and 'robeigen' compares the eigenvalues and robust eigenvalues form the original data and the perturbed data.

**Value**

data utility or modified entry for data utility the `sdMicroObj-class`.

**Methods**

- `list("signature(obj = "data.frame")")`
- `list("signature(obj = "matrix")")`
- `list("signature(obj = "sdMicroObj")")`

**Author(s)**

Matthias Templ

**References**


See Also
dRisk, dRiskRMD

Examples

data(free1)
m1 <- microaggregation(free1[, 31:34], method="onedims", aggr=3)
m2 <- microaggregation(free1[, 31:34], method="pca", aggr=3)
dRisk(obj=free1[, 31:34], xM=m1$mx)
dRisk(obj=free1[, 31:34], xM=m2$mx)
dUtility(obj=free1[, 31:34], xM=m1$mx)
dUtility(obj=free1[, 31:34], xM=m2$mx)
data(Tarragona)
x <- Tarragona[, 5:7]
y <- addNoise(x)$xM
dRiskRMD(x, xM=y)
dRisk(x, xM=y)
dUtility(x, xM=y)
dUtility(x, xM=y, method="eigen")
dUtility(x, xM=y, method="robeigen")

## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
  keyvars=c('urbur','roof','walls','water','electcon','relat','sex'),
  numvars=c('expend','income','savings'), w='sampling_weight')
## this is already made internally:
## sdc <- dUtility(sdc)
## and already stored in sdc

---

EIA data set

Description

Data set obtained from the U.S. Energy Information Authority.

Format

A data frame with 4092 observations on the following 15 variables.

**UTILITYID**  UNIQUE UTILITY IDENTIFICATION NUMBER

<table>
<thead>
<tr>
<th>Company Name</th>
<th>City</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carroll Electric Coop</td>
<td>Musical Island</td>
</tr>
<tr>
<td>Cass County Electric Coop Inc</td>
<td></td>
</tr>
<tr>
<td>Central Illinois Pub Serv Co</td>
<td></td>
</tr>
<tr>
<td>Central Louisiana Elec Co Inc</td>
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<tr>
<td>Central Maine Power Co</td>
<td></td>
</tr>
<tr>
<td>Central Power &amp; Light Co</td>
<td></td>
</tr>
<tr>
<td>Central Vermont Pub Serv Corp</td>
<td></td>
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<tr>
<td>Chattanooga City</td>
<td></td>
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<tr>
<td>Cheyenne Light Fuel &amp; Power Co</td>
<td></td>
</tr>
<tr>
<td>Chugach Electric Assn Inc</td>
<td></td>
</tr>
<tr>
<td>Cincinnati Gas &amp; Electric Co</td>
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<tr>
<td>Citizens Utilities Company</td>
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<td>City of Groton Dept of Utilities</td>
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<td>City of Independence City</td>
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<td>Commonwealth Electric Co</td>
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<td>Connecticut Light &amp; Power Co</td>
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<td>Cumberland Electric Corp</td>
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<tr>
<td>Dakota Electric Assn Inc</td>
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Electric Portland General Electric Co Potomac Edison Co Potomac Electric Power Co
Poudre Valley R & E A, Inc Power Authority of State of NY Provo City Corporation
Public Service Co of Colorado Public Service Co of IN Inc Public Service Co of NH Public Service Co of NM Public Service Co of Oklahoma Public Service Electric & Gas Co
PUD No 1 of Clark County PUD No 1 of Snohomish County Puget Sound Power & Light Co
Rappahannock Electric Coop Rochester Public Utilities Rockland Electric Company
Rosebud Electric Coop Inc Rutherford Elec Member Corp Sacramento Municipal Util Dist
Salmon River Electric Coop Inc Salt River Proj Ag I & P Dist San Antonio City of
Sioux Valley Empire E A Inc South Carolina Electric & Gas Co South Carolina Pub Serv Auth
South Kentucky Rural E C C Southern California Edison Co Southern Nebraska Rural P P D
Southern Pine Elec Power Assn Southwest Tennessee E M C Southwestern Electric Power Co
Southwestern Public Service Co Springfield City of St Joseph Light & Power Co
State Level Adjustment Tacoma City of Tampa Electric Co Texas-New Mexico Power Co
Texas Utilities Electric Co Tri-County Electric Assn Inc Tucson Electric Power Co
Turner-Hutchinsin El Coop, Inc TVA U S Bureau of Indian Affairs Union Electric Co
Union Light & Power Co United Illuminating Co Upper Cumberland E M C
UtiliCorp United Inc Verdigris Valley Electric Coop Verendrye Electric Coop Inc
Virginia Electric & Power Co Volunteer Electric Coop Wallingford Town of
Warren Rural Elec Coop Corp Washington Water Power Co Watertown Municipal Utilis Dept
Wells Rural Electric Co West Penn Power Co West Plains Electric Coop Inc
West River Electric Assn, Inc Western Massachusetts Elec Co Western Resources Inc
Wheeling Power Company Wisconsin Electric Power Co Wisconsin Power & Light Co
Wisconsin Public Service Corp Wright-Henepin Coop Elec Assn Yellowstone Vlly Elec Coop Inc

STATE  STATE FOR WHICH THE UTILITY IS REPORTING. A factor with levels AK AL AR AZ CA CO CT DC DE FL GA HI IA ID IL IN KS KY LA MA MD ME MI MN MO MS MT NC ND NE NH NJ NM NV NY OH OK OR PA RI SC SD TN TX UT VA VT WA WI WV WY

YEAR  REPORTING YEAR FOR THE DATA

MONTH REPORTING MONTH FOR THE DATA

RESREVENUE  REVENUE FROM SALES TO RESIDENTIAL CONSUMERS
RESSALES  SALES TO RESIDENTIAL CONSUMERS
COMREVENUE  REVENUE FROM SALES TO COMMERCIAL CONSUMERS
COMSALES  SALES TO COMMERCIAL CONSUMERS
INDREVENUE  REVENUE FROM SALES TO INDUSTRIAL CONSUMERS
INDSALES  SALES TO INDUSTRIAL CONSUMERS
OTHEREVENUE  REVENUE FROM SALES TO OTHER CONSUMERS
OTHRSALES  SALES TO OTHER CONSUMERS
TOTREVENUE  REVENUE FROM SALES TO ALL CONSUMERS
TOTSALES  SALES TO ALL CONSUMERS

Source
Public use file from the CASC project.
References


Examples

data(EIA)
head(EIA)

extractManipData Remove certain variables from the data set inside a sdc object.

Description

Extract the manipulated data from an object of class sdcMicroObj-class

Usage

extractManipData(obj, ignoreKeyVars = FALSE, ignorePramVars = FALSE,
                 ignoreNumVars = FALSE, ignoreGhostVars = FALSE, ignoreStrataVar = FALSE)

Arguments

obj object of class sdcMicroObj-class
ignoreKeyVars If manipulated KeyVariables should be returned or the unchanged original variables
ignorePramVars If manipulated PramVariables should be returned or the unchanged original variables
ignoreNumVars If manipulated NumericVariables should be returned or the unchanged original variables
ignoreGhostVars If manipulated Ghost (linked) Variables should be returned or the unchanged original variables
ignoreStrataVar If manipulated StrataVariables should be returned or the unchanged original variables

Value

a data frame

Methods

list("signature(obj = "sdcMicroObj")")
Author(s)

Alexander Kowarik, Bernhard Meindl

Examples

```r
## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata, 
  keyVars=c('urbrur','roof'),
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- removeDirectID(sdc, var="age")
dataM <- extractManipData(sdc)
```

Description

Small synthetic data from Capobianchi, Polettini, Lucarelli

Format

A data frame with 8 observations on the following 8 variables.

- **Num1** a numeric vector
- **Key1** Key variable 1. A numeric vector
- **Num2** a numeric vector
- **Key2** Key variable 2. A numeric vector
- **Key3** Key variable 3. A numeric vector
- **Key4** Key variable 4. A numeric vector
- **Num3** a numeric vector
- **w** The weight vector. A numeric vector

Details

This data set is very similar to that one which are used by the authors of the paper given below. We need this data set only for demonstration effect, i.e. that the package provides the same results as their software.

Source


Examples

```r
data(francdat)
francdat```
Demo data set from mu-Argus

Description

The public use toy demo data set from the mu-Argus software for SDC.

Format

The format is: num[1:4000, 1:34] 36 36 36 36 36 36 36 36 36 36 ... - attr(*, "dimnames")=List of 2 ..$ : NULL ..$ : chr [1:34] "REGION" "SEX" "AGE" "MARSTAT" ...

Details

Please, see at the link given below. Please note, that the correlation structure of the data is not very realistic, especially concerning the continuous scaled variables which drawn independently from are a multivariate uniform distribution.

Source

Public use file from the CASC project.

Examples

data(free1)
head(free1)

freq

Print and Extractor Functions for objects of class sdcMicroObj-class

Description

Descriptive print function for Frequencies, local Supression, Recoding, categorical risk and numerical risk.

Usage

freq(obj, type = "fk")

## S4 method for signature 'sdcMicroObj'
print(x, type = "kAnon", ...)
Arguments

- **obj**: An object of class `sdcmicroObj-class`
- **type**: Selection of the content to be returned or printed
- **x**: An object of class `sdcmicroObj-class`

The type argument for the print method, currently supported are:

- **general**: basic information on the input obj such as the number of observations and variables.
- **kAnon**: displays information about 2- and 3-anonymity
- **ls**: displays various information if local suppression has been applied.
- **pram**: displays various information if post-randomization has been applied.
- **recode**: shows information about categorical key variables before and after recoding
- **risk**: displays information on re-identification risks
- **numrisk**: displays risk- and utility measures for numerical key variables

Details

Possible values for the type argument of the print function are: "freq": for Frequencies, "ls": for Local Suppression output, "pram": for results of post-randomization "recode":for Recodes, "risk": for Categorical risk and "numrisk": for Numerical risk.

Possible values for the type argument of the freq function are: "fk": Sample frequencies and "Fk": weighted frequencies.

Author(s)

Alexander Kowarik, Matthias Templ

Examples

data(testdata)
sdc <- createSdcObj(testdata,
    keyVars=c('urbrur','roof','walls','relat','sex'),
    pramVars=c('water','electcon'),
    numVars=c('expend','income','savings'), w='sampling_weight')
fk=freq(sdc)
Fk=freq(sdc,type="Fk")
print(sdc)
print(sdc,type="general")
print(sdc,type="ls")
print(sdc,type="recode")
print(sdc,type="risk")
print(sdc,type="numrisk")
print(sdc,type="pram")
print(sdc,type="kAnon")
freqCalc

Frequencies calculation for risk estimation

Description

Computation and estimation of the sample and population frequency counts.

Usage

freqCalc(x, keyVars, w = NULL, fast = TRUE)

Arguments

x data frame or matrix
keyVars key variables
w column index of the weight variable. Should be set to NULL if one deal with a population.
fast beta version of faster algorithm should not change the results in any way

Details

The function considers the case of missing values in the data. A missing value stands for any of the possible categories of the variable considered. It is possible to apply this function to large data sets with many (categorical) key variables, since the computation is done in C.

freqCalc() does not support sdcMicro S4 class objects.

Value

Object from class freqCalc.

data set
variables used for frequency calculation
index of weight vector. NULL if you do not have a sample.
the frequency of equal observations in the key variables subset sample given for each observation.
estimated frequency in the population
number of observations with fk=1
number of observations with fk=2

Author(s)

Bernhard Meindl and Matthias Templ
References


See Also

indivrisk, measure_risk

Examples

data(francdat)
f <- freqCalc(francdat, keyVars=c(2,4,5,6),w=8)
f$f$freqCalc
f$f$k
f$k
## with missings:
x <- francdat 
x[3,5] <- NA 
x[4,2] <- x[4,4] <- NA 
x[5,6] <- NA 
x[6,2] <- NA 
f2 <- freqCalc(x, keyVars=c(2,4,5,6),w=8)
f2$f$k
# time comparison freqCalc old version vs. new version
data(testdata)
system.time( f3 <- freqCalc(testdata,keyVars=c(1:4,7),w=14,fast=FALSE) )
system.time( f3f <- freqCalc(testdata,keyVars=c(1:4,7),w=14,fast=TRUE) )

---

generateStrata Generate one strata variable from multiple factors

Description

For strata defined by multiple variables (e.g. sex,age, country) one combined variable is generated.

Usage

generateStrata(df, stratavars, name)
**globalRecode**

**Arguments**

- `df` a data.frame
- `stratavars` character vector with variable name
- `name` name of the newly generated variable

**Value**

The original data set with one new column.

**Author(s)**

Alexander Kowarik

**Examples**

```r
x <- testdata
x <- generateStrata(x,c("sex","urbrur"),"strataIDvar")
head(x)
```

---

**Description**

Global recoding

**Usage**

`globalRecode(obj, ...)`

**Arguments**

- `obj` vector of class numeric or of class factor with integer labels for recoding or an object of class `sdcMicroObj-class`
- `...` see possible arguments below
  - `column` which keyVar should be changed
  - `breaks` either a numeric vector of cut points or number giving the number of intervals which `x` is to be cut into.
  - `labels` labels for the levels of the resulting category. By default, labels are constructed using "](a,b][ interval notation. If `labels` = `FALSE`, simple integer codes are returned instead of a factor.
  - `method` method “equidistant” for equal sized intervals; method “logEqui” for equal sized intervals for log-transformed data; method “equalAmount” for intervals with approximately the same amount of observations
Details

If a labels parameter is specified, its values are used to name the factor levels. If none is specified, the factor level labels are constructed.

Value

the modified `sdcmicroObj-class` or a factor, unless labels = FALSE which results in the mere integer level codes.

Methods

```r
list("signature(obj = "ANY")")
list("signature(obj = "sdcmicroObj")")
```

See Also

`cut`

Examples

```r
data(free1)
head(globalRecode(free1[, "AGE"], breaks=c(1, 9, 19, 29, 39, 49, 59, 69, 100), labels=1:8))
table(globalRecode(free1[, "AGE"], breaks=c(1, 9, 19, 29, 39, 49, 59, 69, 100), labels=1:8))
table(globalRecode(free1[, "AGE"], breaks=c(1, 9, 19, 29, 39, 49, 59, 69, 100)))
table(globalRecode(free1[, "AGE"], breaks=6))
table(globalRecode(free1[, "AGE"], breaks=6, method="logEqui"))
table(globalRecode(free1[, "AGE"], breaks=6, method="equalAmount"))
```

```r
## for objects of class sdcmicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
umVars=c('expend','income','savings'), w='sampling_weight')
sdc <- globalRecode(sdc, column="urbrur", breaks=5)
```

---

**groupVars**

Join levels of a keyVariable in an object of class `sdcmicroObj-class`

Description

Transforms the factor variable into a factors with less levels and recomputes risk.

Usage

```r
groupVars(obj, var, before, after)
```
### indivRisk

**Arguments**

- **obj**: object of class `sdcMicroObj-class`
- **var**: name of the keyVariable to change
- **before**: vector of levels before recoding
- **after**: vector of levels after recoding

**Value**

the modified `sdcMicroObj-class`

**Methods**

- `list("signature(obj = "sdcMicroObj\")")` This method transform a factor variable with some levels into a new factor variable with less levels. The user must make sure that all levels of the original variable are listed in argument ‘before’ and that the number of elements in argument ‘after’ (the new levels) have the same length. This means that there should be a one to one mapping from any level of the original factor to a level in the recoded variable.

**Examples**

```r
## for objects of class sdcMicro:
data(testdata2)
testdata2$urbrur <- as.factor(testdata2$urbrur)
sdc <- createSdcObj(testdata2,
   keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
   numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- groupVars(sdc, var="urbrur", before=c("1","2"), after=c("1","1"))
```

---

**Description**

Individual risk computation.

**Usage**

`indivRisk(x, method = "approx", qual = 1, survey = TRUE)`

**Arguments**

- **x**: object from class freqCalc
- **method**: approx (default) or exact
- **qual**: final correction factor
- **survey**: TRUE, if we have survey data and FALSE if we deal with a population.
Details

Estimation of the risk for each observation. After the risk is computed one can use e.g. the function localSuppr() for the protection of values of high risk. Further details can be found at the link given below.

S4 class sdcMicro objects are only supported by function measure_risk that also estimates the individual risk with the same method.

Value

- rk base individual risk
- method method
- qualfinal correction factor
- fkfrequency count
- knamescolnames of the key variables

Note

The base individual risk method was developed by Benedetti, Capobianchi and Franconi

Author(s)

Matthias Templ. Bug in method “exact” fixed since version 2.6.5. by Youri Baeyens.

References


additionally, have a look at the vignettes of sdcMicro for further reading.

See Also

measure_risk, freqCalc

Examples

```r
## example from Capobianchi, Polettini and Lucarelli:
data(francdat)
f <- freqCalc(francdat, keyVars=c(2,4,5,6),w=8)
f
f$fk
f$FK
## individual risk calculation:
indivf <- indivRisk(f)
indivf$rk
```
Global risk using log-linear models.

Description

The sample frequencies are assumed to be independent and following a Poisson distribution. The parameters of the corresponding parameters are estimated by a log-linear model including the main effects and possible interactions.

Usage

```r
LLmodGlobalRisk(obj, method = "IPF", inclProb = NULL, form = NULL, 
                   modOutput = FALSE)
```

Arguments

- `obj` An object of class sdcMicroObj or a numeric matrix or data frame containing the categorical key variables.
- `method` At this time, only iterative proportional fitting ("IPF") can be used.
- `inclProb` Inclusion probabilities (experimental)
- `form` A formula specifying the model.
- `modOutput` If TRUE, additional output is given.

Details

This measure aims to (1) calculate the number of sample uniques that are population uniques with a probabilistic Poisson model and (2) to estimate the expected number of correct matches for sample uniques.

ad 1) this risk measure is defined over all sample uniques (SU) as

$$
\tau_1 = \sum_{SU} P(F_k = 1|f_k = 1) \quad ,
$$

i.e. the expected number of sample uniques that are population uniques.

ad 2) this risk measure is defined over all sample uniques (SU) as

$$
\tau_2 = \sum_{SU} P(F_k = 1|f_k = 1) \quad , CORRECT!
$$

Since population frequencies $F_k$ are unknown, they has to be estimated.

The iterative proportional fitting method is used to fit the parameters of the Poisson distributed frequency counts related to the model specified to fit the frequency counts. The obtained parameters are used to estimate a global risk, defined in Skinner and Holmes (1998).

Value

Two global risk measures or the modified risk in the `sdcMicroObj-class` object.
**Note**

LL.modGlobalRisk is deprecated for `modRisk` and is only provided for compatibility with older versions of this package. It may be removed in future versions.

**Author(s)**

Matthias Templ

**References**


**See Also**

`loglm`, `measure_risk`, `modRisk`

**LocalRecProg**

`Local recoding via Edmond’s maximum weighted matching algorithm`

**Description**

To be used on both categorical and numeric input variables, although usage on categorical variables is the focus of the development of this software.

**Usage**

```r
LocalRecProg(obj, ancestors = NULL, ancestor_setting = NULL, k_level = 2, FindLowestK = TRUE, weight = NULL, lowMemory = FALSE, missingValue = NA, ...)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>obj</code></td>
<td>Input data or object of class sdcMicroObj</td>
</tr>
<tr>
<td><code>ancestors</code></td>
<td>Names of ancestors of the categorical variables</td>
</tr>
<tr>
<td><code>ancestor_setting</code></td>
<td>For each ancestor the corresponding categorical variable</td>
</tr>
<tr>
<td><code>k_level</code></td>
<td>Level for k-anonymity</td>
</tr>
<tr>
<td><code>FindLowestK</code></td>
<td>requests the program to look for the smallest k that results in complete matches of the data.</td>
</tr>
<tr>
<td><code>weight</code></td>
<td>A weight for each variable (Default=1)</td>
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</tbody>
</table>
localRecProg

lowMemory  Slower algorithm with less memory consumption
missingValue  The output value for a suppressed value.
...  see arguments below
  • categoricalNames of categorical variables
  • numericalNames of numerical variables

Details

Each record in the data represents a category of the original data, and hence all records in the input data should be unique by the N Input Variables. To achieve bigger category sizes (k-anonymity), one can form new categories based on the recoding result and repeatedly apply this algorithm.

Value

dataframe with original variables and the supressed variables (suffix _lr). / the modified sdcMicroObj-class

Methods

list("signature(obj = \"sdcMicroObj\")")

Author(s)

Alexander Kowarik, Bernd Prantner, IHSN C++ source, Akimichi Takemura

References


Examples

# LocalRecProg
data(testdata2)
r1=LocalRecProg(testdata2,
categorical=c("urbrur", "roof", "walls", "water", "sex", "relat"),
missingValue=-99)
r2=LocalRecProg(testdata2,
categorical=c("urbrur", "roof", "walls", "water", "sex", "relat"),
ancestor=c("water2", "water3", "relat2"),
ancestor_setting=c("water","water","relat"),missingValue=-99)
r3=LocalRecProg(testdata2,
categorical=c("urbrur", "roof", "walls", "water", "sex", "relat"),
ancestor=c("water2", "water3", "relat2"),
ancestor_setting=c("water","water","relat"),missingValue=-99,
FindLowestK=FALSE)

## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- LocalRecProg(sdc)
Description

A simple method to perform local suppression.

Usage

localSupp(obj, threshold = 0.15, keyVar, ...)

Arguments

obj object of class freqCalc or sdcMicroObj
threshold threshold for individual risk
keyVar Variable on which some values might be suppressed
... see arguments below

• indivRisk object from class indivRisk

Details

Values of high risk (above the threshold) of a certain variable (parameter keyVar) are suppressed.

Value

Manipulated data with suppressions or the sdcMicroObj-class object with manipulated data.

Methods

list("signature(obj = \"sdcMicroObj\")")
list("signature(obj = \"ANY\")")

Author(s)

Matthias Templ

References


See Also

freqCalc, indivRisk
localSuppression

Examples

## example from Capobianchi, Polettini and Lucarelli:
data(francdat)
f <- freqCalc(francdat, keyVars=c(2,4,5,6), w=8)
f
f$fk
f$fK

## individual risk calculation:
indivf <- indivRisk(f)
indivf$rk

## Local Suppression
localS <- localSupp(f, keyVar=2, indivRisk=indivf$rk, threshold=0.25)
f2 <- freqCalc(localS$freqCalc, keyVars=c(4,5,6), w=8)
indivf2 <- indivRisk(f2)
indivf2$rk

## select another keyVar and run localSupp once again,
# if you think the table is not fully protected

## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
  keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- localSupp(sdc, keyVar='urbrur')

localSuppression

Local Suppression to obtain k-anonymity

Description

Algorithm to achieve k-anonymity by performing local suppression.

Usage

localSuppression(obj, k = 2, importance = NULL, combs = NULL, ...)

Arguments

obj  an object of class sdcMicroObj or a data frame or matrix
k   threshold for k-anonymity
importance  numeric vector of numbers between 1 and n (n=length of vector keyVars). This vector represents the "importance" of variables that should be used for local suppression in order to obtain k-anonymity. key-variables with importance=1 will - if possible - not suppressed, key-variables with importance=n will be used whenever possible.
**combs** numeric vector. If specified, the algorithm will provide k-anonymity for each combination of n key variables (with n being the value of the ith element of this parameter. For example, if combs=c(4,3), the algorithm will provide k-anonymity to all combinations of 4 key variables and then k-anonymity to all combinations of 3 key variables. It is possible to apply different k to these subsets by specifying k as a vector. If k has only one element, the same value of k will be used for all subgroups.

see arguments below

• keyVars numeric vector specifying indices of (categorical) key-variables
• strataVars numeric vector specifying indices of variables that should be used for stratification within 'obj'

Details

The algorithm provides a k-anonymized data set by suppressing values in key variables. The algorithm tries to find an optimal solution to suppress as few values as possible and considers the specified importance vector. If not specified, the importance vector is constructed in a way such that key variables with a high number of characteristics are considered less important than key variables with a low number of characteristics.

The implementation provides k-anonymity per strata, if slot 'strataVar' has been set in *sdcmicroObj-class* or if parameter 'strataVar' is used when applying the data.frame- or matrix method. For details, have a look at the examples provided.

Value

Manipulated data set with suppressions that has k-anonymity with respect to specified key-variables or the manipulated data stored in the *sdcmicroObj-class*.

Methods

```
list("signature(obj = "data.frame")")
list("signature(obj = "matrix")")
list("signature(obj = "sdcmicroObj")")
```

Note

Deprecated methods 'localSupp2' and 'localSupp2Wrapper' are no longer available in sdcMicro > 4.5.0. kAnon is a more intuitive term for localSuppression because the aim is always to obtain k-anonymity for some parts of the data.

Author(s)

Bernhard Meindl, Matthias Templ
Examples

```r
data(franceDat)
## Local Suppression
localS <- localSuppression(franceDat, keyVar=c(4,5,6))
plot(localS)

## for objects of class sdcMicro, no stratification
data(testData2)
sdc <- createSdcObj(testData2,
keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- localSuppression(sdc)

## for objects of class sdcMicro, no with stratification
testData2$ageG <- cut(testData2$age, 5, labels=paste0("AG",1:5))
sdc <- createSdcObj(testData2,
keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
numVars=c('expend','income','savings'), w='sampling_weight',
strataVar='ageG')
sdc <- localSuppression(sdc)

## it is also possible to provide k-anonymity for subsets of key-variables
## with different parameter k!
## in this case we want to provide 10-anonymity for all combinations
## of 5 key variables, 20-anonymity for all combinations with 4 key variables
## and 30-anonymity for all combinations of 3 key variables.
## note: stratas are automatically considered!
combs <- 5:3
k <- c(10,20,30)
sdc <- localSuppression(sdc, k=k, combs=combs)

## data.frame method (no stratification)
keyVars <- c("urbrur","roof","walls","water","electcon","relat","sex")
strataVars <- c("ageG")
inp <- testData2[.,c(keyVars, strataVars)]
lS <- localSuppression(inp, keyVars=1:7)
print(lS)
plot(lS)

## data.frame method (with stratification)
lS <- kAnon(inp, keyVars=1:7, strataVars=8)
print(lS)
plot(lS, showTotalSupps=TRUE)
```

mafast

**Fast and Simple Microaggregation**

**Description**

Function to perform a fast and simple (primitive) method of microaggregation. (for large datasets)
Usage

`mafast(obj, variables = NULL, by = NULL, aggr = 3, measure = mean)`

Arguments

- **obj** either an object of class `sdcMicroObj` or a data frame or matrix
- **variables** variables to microaggregate. If `obj` is of class `sdcMicroObj` the numerical key variables are chosen per default.
- **by** grouping variable for microaggregation. If `obj` is of class `sdcMicroObj` the strata variables are chosen per default.
- **aggr** aggregation level (default=3)
- **measure** aggregation statistic, mean, median, trim, onestep (default = mean)

Value

If `obj` was of class `sdcMicroObj-class` the corresponding slots are filled, like `manipNumVars`, risk and utility. If `obj` was of class “data.frame” or “matrix” an object of the same class is returned.

Methods

```
list("signature(obj = "ANY")")
list("signature(obj = "data.frame")")
list("signature(obj = "matrix")")
list("signature(obj = "sdcMicroObj")")
```

Author(s)

Alexander Kowarik

See Also

`microaggregation`

Examples

data(Tarragona)
m1 <- mafast(Tarragona, variables=c("GROSS.PROFIT","OPERATING.PROFIT","SALES"),aggr=3)
data(testdata)
m2 <- mafast(testdata,variables=c("expend","income","savings"),aggr=50,by="sex")
summary(m2)

## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
keyVars=c("urbur","roof","walls","water","electcon","relat","sex"),
numVars=c("expend","income","savings"), w="sampling_weight")
sdc <- dRisk(sdc)
sdc@risk$numeric
measure_risk

Disclosure Risk for Categorical Variables

Description
The function measures the disclosure risk for weighted or unweighted data. It computes the individual risk (and household risk if reasonable) and the global risk. It also computes a risk threshold based on a global risk value.

Print method for objects from class lddiversity
Print method for objects from class lddiversity

Usage
measure_risk(obj, ...)

lddiversity(obj, lddiv_index = NULL, l_recurs_c = 2, missing = -999, ...)

## S3 method for class 'measure_risk'
print(x, ...)

## S3 method for class 'lddiversity'
print(x, ...)

Arguments

obj Object of class sdcMicroObj-class
... see arguments below
  - dataInput data, either a matrix or a data.frame.
  - keyVarsNames of categorical key variables
  - wname of variable containing sample weights
  - hidname of the clustering variable, e.g. the household ID

sdc1 <- mafast(sdc, aggr=4)
sdc1@risk$numeric

sdc2 <- mafast(sdc, aggr=10)
sdc2@risk$numeric

## Not run:
## Performance tests
x <- testdata
for(i in 1:20){
  x <- rbind(x,testdata)
}
system.time(xx <- mafast(x,variables=c("expend","income","savings"),aggr=50,by="sex"))

## End(Not run)
- max_global_risk: Maximal global risk for threshold computation.
- fast_hier: If TRUE a fast approximation is computed if household data are provided.

ldiv_index: indices (or names) of the variables used for l-diversity.

l_recurs_c: l-Diversity Constant.

missing: a integer value to be used as missing value in the C++ routine.

x: Output of measure_risk() or ldiversity().

Details

To be used when risk of disclosure for individuals within a family is considered to be statistical independent.

Internally, function freqCalc() and indivRisk are used for estimation.

Measuring individual risk: The individual risk approach based on so-called super-population models. In such models population frequency counts are modeled given a certain distribution. The estimation procedure of sample frequency counts given the population frequency counts is modeled by assuming a negative binomial distribution. This is used for the estimation of the individual risk. The extensive theory can be found in Skinner (1998), the approximation formulas for the individual risk used is described in Franconi and Polettini (2004).

Measuring hierarchical risk: If “hid” - the index of variable holding information on the hierarchical cluster structures (e.g., individuals that are clustered in households) - is provided, the hierarchical risk is additional estimated. Note that the risk of re-identifying an individual within a household may also affect the probability of disclosure of other members in the same household. Thus, the household or cluster-structure of the data must be taken into account when estimating disclosure risks. It is commonly assumed that the risk of re-identification of a household is the risk that at least one member of the household can be disclosed. Thus this probability can be simply estimated from individual risks as 1 minus the probability that no member of the household can be identified.

Global risk: The sum of the individual risks in the dataset gives the expected number of re-identifications that serves as measure of the global risk.

l-Diversity: If “ldiv_index” is unequal to NULL, i.e. if the indices of sensible variables are specified, various measures for l-diversity are calculated. l-diversity is an extension of the well-known k-anonymity approach where also the uniqueness in sensible variables for each pattern spanned by the key variables are evaluated.

Value

A modified sdcMicroObj-class object or a list with the following elements:

- global_risk_ER: Expected number of re-identification.
- global_risk: global risk (sum of individual risks).
- global_risk_pct: global risk in percent.
- Res: matrix with the risk, frequency in the sample and grossed-up frequency in the population (and the hierarchical risk) for each observation.
- global_threshold: for a given max_global_risk the threshold for the risk of observations.
- max_global_risk: the input max_global_risk of the function.
• hier_risk_ERexpected number of re-identification with household structure.
• hier_risk_global risk with household structure (sum of individual risks).
• hier_risk_pctglobal risk with household structure in percent.
• ldiversityMatrix with Distinct_Ldiversity, Entropy_Ldiversity and Recursive_Ldiversity for each sensitivity variable.

Prints risk-information into the console
Information on L-Diversity Measures in the console

Methods

list("signature(obj = "data.frame")") Method for object of class “data.frame”
list("signature(obj = "matrix")") Method for object of class “matrix”
list("signature(obj = "sdcMicroObj")") Method for object of S4 class sdcMicroObj-class

Note

internal function

Author(s)

Alexander Kowarik, Bernd Prantner, Matthias Templ, minor parts of IHSN C++ source
Bernhard Meindl <bernhard.meindl@statistik.gv.at>
Bernhard Meindl, Matthias Templ
Bernhard Meindl, Matthias Templ

References

additionally, have a look at the vignettes of sdcMicro for further reading.

See Also

freqCalc, indivRisk
measure_risk
measure_risk
Examples

```r
## measure risk with sdcMicro objects:
data(testdata)
sdc <- createSdcObj(testdata,
    keyVars=c('urbrur', 'roof', 'walls', 'water', 'electcon'),
    numVars=c('expend', 'income', 'savings'), w='sampling_weight')

## risk is already estimated and available in...
names(sdc@risk)

## measure risk on data frames or matrices:
res <- measure_risk(testdata,
    keyVars=c('urbrur', 'roof', 'walls', 'water', 'sex'))
print(res)
head(res$Res)
resw <- measure_risk(testdata,
    keyVars=c('urbrur', 'roof', 'walls', 'water', 'sex'), w='sampling_weight')
print(resw)
head(resw$Res)
res1 <- ldiversity(testdata,
    keyVars=c('urbrur', 'roof', 'walls', 'water', 'sex'), ldiv_index='electcon')
print(res1)
head(res1)
res2 <- ldiversity(testdata,
    keyVars=c('urbrur', 'roof', 'walls', 'water', 'sex'), ldiv_index=c('electcon', 'relat'))
print(res2)
head(res2)

# measure risk with household risk
resh <- measure_risk(testdata,
    keyVars=c('urbrur', 'roof', 'walls', 'water', 'sex'), w='sampling_weight', hid='ori_hid')
print(resh)

# change max_global_risk
rest <- measure_risk(testdata,
    keyVars=c('urbrur', 'roof', 'walls', 'water', 'sex'),
    w='sampling_weight', max_global_risk=0.0001)
print(rest)

## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
    keyVars=c('urbrur', 'roof', 'walls', 'water', 'electcon', 'relat', 'sex'),
    numVars=c('expend', 'income', 'savings'), w='sampling_weight')
## already interally applied and available in object sdc:
## sdc <- measure_risk(sdc)
```
**microaggregation**

**Description**

Function to perform various methods of microaggregation.

**Usage**

```r
microaggregation(obj, variables = NULL, aggr = 3, strata_variables = NULL,
    method = "mdav", weights = NULL, nc = 8, clustermethod = "clara",
    opt = FALSE, measure = "mean", trim = 0, varsort = 1,
    transf = "log")
```

**Arguments**

- **obj**: either an object of class sdcMicroObj or a data frame or matrix
- **variables**: variables to microaggregate. For NULL: If obj is of class sdcMicroObj the categorical key variables are chosen per default. For data.frames and matrices all columns are chosen per default.
- **aggr**: aggregation level (default=3)
- **strata_variables**: by-variables for applying microaggregation only within strata defined by the variables
- **method**: pca, rmd, onedims, single, simple, clustpca, pppca, clustpppca, mdav, clustmdpca, influence, mcdpca
- **weights**: sampling weights. If obj is of class sdcMicroObj the vector of sampling weights is chosen automatically. If determined, a weighted version of the aggregation measure is chosen automatically, e.g. weighted median or weighted mean.
- **nc**: number of cluster, if the chosen method performs cluster analysis
- **clustermethod**: clustermethod, if necessary
- **opt**: experimental
- **measure**: aggregation statistic, mean, median, trim, onestep (default=mean)
- **trim**: trimming percentage, if measure=trim
- **varsort**: variable for sorting, if method= single
- **transf**: transformation for data x

**Details**

On [http://neon.vb.cbs.nl/casc/Glossary.htm](http://neon.vb.cbs.nl/casc/Glossary.htm) one can found the “official” definition of microaggregation:

Records are grouped based on a proximity measure of variables of interest, and the same small groups of records are used in calculating aggregates for those variables. The aggregates are released instead of the individual record values.

The recommended method is “rmd” which forms the proximity using multivariate distances based on robust methods. It is an extension of the well-known method “mdav”. However, when computational speed is important, method “mdav” is the preferable choice.
While for the proximity measure very different concepts can be used, the aggregation itself is naturally done with the arithmetic mean. Nevertheless, other measures of location can be used for aggregation, especially when the group size for aggregation has been taken higher than 3. Since the median seems to be unsuitable for microaggregation because of being highly robust, other measures which are included can be chosen. If a complex sample survey is microaggregated, the corresponding sampling weights should be determined to either aggregate the values by the weighted arithmetic mean or the weighted median.

This function contains also a method with which the data can be clustered with a variety of different clustering algorithms. Clustering observations before applying microaggregation might be useful. Note, that the data are automatically standardised before clustering.

The usage of clustering method ‘Mclust’ requires package mclust02, which must be loaded first. The package is not loaded automatically, since the package is not under GPL but comes with a different licence.

The are also some projection methods for microaggregation included. The robust version ‘pppca’ or ‘clustpppca’ (clustering at first) are fast implementations and provide almost everytime the best results.

Univariate statistics are preserved best with the individual ranking method (we called them ‘onedims’, however, often this method is named ‘individual ranking’), but multivariate statistics are strongly affected.

With method ‘simple’ one can apply microaggregation directly on the (unsorted) data. It is useful for the comparison with other methods as a benchmark, i.e. replies the question how much better is a sorting of the data before aggregation.

Value

If ‘obj’ was of class sdcMicroObj-class the corresponding slots are filled, like manipNumVars, risk and utility. If ‘obj’ was of class “data.frame” or “matrix” an object of class “micro” with following entities is returned:

- \texttt{mx}\ the aggregated data
- \texttt{x}\ original data
- \texttt{method}\ method
- \texttt{aggr}\ aggregation level
- \texttt{measure}\ proximity measure for aggregation
- \texttt{fot}\ correction factor, necessary if totals calculated and n divided by aggr is not an integer.

Methods

\begin{verbatim}
list("signature(obj = "ANY")")
list("signature(obj = "data.frame")")
list("signature(obj = "matrix")")
list("signature(obj = "sdcMicroObj")")
\end{verbatim}
Author(s)

Matthias Templ

For method “mdav”: This work is being supported by the International Household Survey Network (IHSN) and funded by a DGF Grant provided by the World Bank to the PARIS21 Secretariat at the Organisation for Economic Co-operation and Development (OECD). This work builds on previous work which is elsewhere acknowledged.

Author for the integration of the code for mdav in R: Alexander Kowarik.

References

http://www.springerlink.com/content/v257655u88w2/?sortorder=asc&p_o=20


See Also

summary.micro, plotMicro, valTable

Examples

data(Tarragona)
m1 <- microaggregation(Tarragona, method="onedims", aggr=3)
  ## summary(m1)
data(testdata)
m2 <- microaggregation(testdata[1:100, ,c("expend","income","savings")],
  method="mdav", aggr=4)
summary(m2)

  ## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2, keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- microaggregation(sdc)
Description
Small artificial toy data set.

Format
The format is: num [1:13, 1:5] 5 7 2 1 7 8 12 3 15 4 ... - attr(*, "dimnames")=List of 2 ..$ : chr [1:13] "10000" "11000" "12000" "12100" ... ..$ : chr [1:5] "one" "two" "three" "four" ...

Examples
```r
data(microData)
m1 <- microaggregation(microData, method="mdav")
summary(m1)
```

Description
Global risk using log-linear models.

Usage
```r
modRisk(obj, method = "default", weights, formulaM, bound = Inf, ...)
```

Arguments
- **obj**: An `sdcmicroObj-class`-object or a numeric matrix or data.frame containing all variables required in the specified model.
- **method**: chose method for model-based risk-estimation. Currently, the following methods can be selected:
  - "default": the standard log-linear model.
  - "CE": the Clogg Eliason method, additionally, considers survey weights by using an offset term.
  - "PML": the pseudo maximum likelihood method.
  - "weightedLLM": the weighted maximum likelihood method, considers survey weights by including them as one of the predictors.
  - "IPF": iterative proportional fitting as used in deprecated method 'LLmodGlobalRisk'.
weights a variable name specifying sampling weights
formulaM A formula specifying the model.
bound a number specifying a threshold for 'risky' observations in the sample.
... additional parameters passed through, currently ignored.

Details

This measure aims to (1) calculate the number of sample uniques that are population uniques with a probabilistic Poisson model and (2) to estimate the expected number of correct matches for sample uniques.

ad 1) this risk measure is defined over all sample uniques as

\[ \tau_1 = \sum_{j: f_j = 1} P(F_j = 1 | f_j = 1), \]

i.e. the expected number of sample uniques that are population uniques.

ad 2) this risk measure is defined over all sample uniques as

\[ \tau_2 = \sum_{j: f_j = 1} P(1/F_j | f_j = 1). \]

Since population frequencies \( F_k \) are unknown, they need to be estimated.

The iterative proportional fitting method is used to fit the parameters of the Poisson distributed frequency counts related to the model specified to fit the frequency counts. The obtained parameters are used to estimate a global risk, defined in Skinner and Holmes (1998).

Value

Two global risk measures and some model output given the specified model. If this method is applied to an \texttt{sdcmicroObj-class}-object, the slot 'risk' in the object ist updated with the result of the model-based risk-calculation.

Author(s)

Matthias Templ, Marius Totter, Bernhard Meindl

References


See Also

`loglm`, `measure_risk`

Examples

```r
## data.frame method
data(testdata2)
form <- ~sex+water+roof
w <- "sampling_weight"
(modRisk(testdata2, method="default", formula=form, weights=w))
(modRisk(testdata2, method="CE", formula=form, weights=w))
(modRisk(testdata2, method="PML", formula=form, weights=w))
(modRisk(testdata2, method="weightedLLM", formula=form, weights=w))
(modRisk(testdata2, method="IPF", formula=form, weights=w))

## application to a sdcMicroObj
data(testdata2)
sdc <- createSdcObj(testdata2,
  keyVars=c('urbur','roof','walls','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- modRisk(sdc,form=~sex+water+roof)
slot(sdc, "risk")$model
```

Description

Barplot for objects from class `localSuppression`.

Usage

```r
## S3 method for class 'localSuppression'
plot(x, ...)
```

Arguments

- `x` object of class `localSuppression`
- `...` Additional arguments, currently available are:
  - `showDetails` logical, if set, a plot of suppressions by strata is shown (if possible)

Details

Just look at the resulting plot.

Author(s)

Bernhard Meindl, Matthias Templ
See Also

localSuppression

Examples

```r
## example from Capobianchi, Polettini and Lucarelli:
data(francdat)
l1 <- localSuppression(francdat, keyVars=c(2,4,5,6))
plot(l1)

## with details of suppression by strata
data(testdata2)
testdata2$ageG <- cut(testdata2$age, 5, labels=paste0("AG",1:5))
keyVars <- c("urbur", "roof", "walls", "water", "electcon", "relat", "sex")
strataVars <- c("ageG")
inp <- testdata2[,c(keyVars, strataVars)]
ls <- localSuppression(inp, keyVars=1:7, strataVars=8)
print(ls)
plot(ls)
plot(ls, showDetails=TRUE)
```

Author(s)

Bernhard Meindl

Examples

data(testdata)
sdc <- createSdcObj(testdata,  
  keyVars=c('urbur', 'roof', 'walls', 'relat', 'sex'),  
  pramVars=c('water', 'electcon'),  
  numVars=c('expend', 'income', 'savings'), w='sampling_weight')
sdc <- kAnon(sdc, k=5)
plot(sdc, type="ls")

plotMicro

Comparison plots

Description

Plots for the comparison of the original data and perturbed data.

Usage

plotMicro(x, p, which.plot = 1:3)

Arguments

x object from class micro
p necessary parameter for the box cox transformation (lambda)
which.plot which plot should be created?
  • 1: density traces
  • 2: parallel boxplots
  • 3: differences in totals

Details

Univariate and multivariate comparison plots are implemented to detect differences between the perturbed and the original data, but also to compare perturbed data which are produced by different methods.

Author(s)

Matthias Templ

References

pram

See Also

microaggregation

Examples

data(free1)
m1 <- microaggregation(free1[, 31:34], method="onedims", aggr=3)
m2 <- microaggregation(free1[, 31:34], method="pca", aggr=3)
plotMicro(m1, 0.1, which.plot=1)

---

pram

Post Randomization

Description

To be used on categorical data. It randomly change the values of variables on selected records (usually the risky ones) according to an invariant probability transition matrix.

Usage

pram(obj, variables = NULL, strata_variables = NULL, pd = 0.8, alpha = 0.5)

Arguments

obj

Input data. Allowed input data are objects of class 'matrix', 'data.frame', 'vector' or sdcMicroObj-class.

variables

Names of variables in 'obj' on which post-randomization should be applied. If obj is a vector, this argument is ignored.

strata_variables

Names of variables for stratification (will be set automatically for an object of class sdcMicroObj-class. One can also specify an integer vector or factor that specifies that desired groups. This vector must match the dimension of the input data set, however. For a possible use case, have a look at the examples.

pd

minimum diagonal entries for the generated transition matrix P. Either a vector of length 1 or a vector of length (number of categories).

alpha

amount of perturbation for the invariant Pram method

... further input, currently ignored.

Value

a modified sdcMicroObj-class object or a new object containing original and post-randomized variables (with suffix "_pram").
Methods

list("signature(obj = "sdcMicroObj")")  ...
list("signature(obj = "data.frame")")  ...
list("signature(obj = "matrix")")  ...
list("signature(obj = "vector")")  ...

Note

Deprecated method 'pram_strata' is no longer available in sdcMicro > 4.5.0

Author(s)

Alexander Kowarik, Matthias Templ, Bernhard Meindl

References

http://www.gnu.org/software/glpk

Examples

data(testdata)
res <- pram(testdata,
  variables="roof",
  strata_variables=c("urbrur","sex"))
print(res)

res1 <- pram(testdata,variables=c("roof","walls","water"),strata_variables=c("urbrur","sex"))
print(res1)

res2 <- pram(testdata,variables=c("roof","walls","water"),
  strata_variables=NULL)
print(res2)

## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
  keyVars=c('roof','walls','water','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- pram(sdc, variables=c("urbrur"))

# this is equal to the previous application:
sdc <- createSdcObj(testdata2,
  keyVars=c('roof','walls','water','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight',
  pramVars="urbrur")
sdc <- pram(sdc)

## using a custom strata variable
# we want to apply pram to variable 'urbrur' for each group of variable 'urbrur'


# however: values no value should be changed where roof==4
# thus, we are creating a new value for these observations
data(testdata)
sdc <- createSdcObj(testdata,
  keyVars=c('walls','water','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight')
sv <- testdata$urbur
# new category for those that observations that should not change:
sv[testdata$roof==4] <- max(sv)+1
sdc <- pram(sdc, variables=c("roof"), strata_variables=sv)
orig <- get.sdcMicroObj(sdc, "origData")$roof
pramed <- get.sdcMicroObj(sdc, "manipPramVars")$roof
all(pramed[orig==4]==4) # nothing has changed!

print.freqCalc

Print method for objects from class freqCalc

Description

Print method for objects from class freqCalc.

Usage

## S3 method for class 'freqCalc'
print(x, ...)

Arguments

x object from class freqCalc

... Additional arguments passed through.

Value

information about the frequency counts for key variables for object of class freqCalc.

Author(s)

Matthias Templ

See Also

freqCalc

Examples

## example from Capobianchi, Polettini and Lucarelli:
data(francdat)
f <- freqCalc(francdat, keyVars=c(2,4,5,6),w=8)
f
print.indivRisk  

Description

Print method for objects from class indivRisk

Usage

```r
## S3 method for class 'indivRisk'
print(x, ...)
```

Arguments

- `x` object from class indivRisk
- `...` Additional arguments passed through.

Value

few information about the method and the final correction factor for objects of class 'indivRisk'.

Author(s)

Matthias Templ

See Also

indivRisk

Examples

```r
## example from Capobianchi, Polettini and Lucarelli:
data(francdat)
f <- freqCalc(francdat, keyVars=c(2,4,5,6),w=8)
f
f$fk
f$Fk
## individual risk calculation:
indivRisk(f)
```
print.localSuppression

Print method for objects from class localSuppression

Description

Print method for objects from class localSuppression.

Usage

```r
## S3 method for class 'localSuppression'
print(x, ...)
```

Arguments

- `x`: object from class localSuppression
- `...`: Additional arguments passed through.

Value

Information about the frequency counts for key variables for object of class `localSuppression`.

Author(s)

Matthias Templ

See Also

`localSuppression`

Examples

```r
## example from Capobianchi, Polettini and Lucarelli:
data(frcndat)
l1 <- localSuppression(frcndat, keyVars=c(2,4,5,6))
l1
```
print.micro  

Print method for objects from class micro

Description

Print method for objects from class micro.

Usage

## S3 method for class 'micro'
print(x, ...)

Arguments

x  object from class micro
...

Additional arguments passed through.

Value

information about method and aggregation level from objects of class micro.

Author(s)

Matthias Templ

See Also

microaggregation

Examples

data(free1)
m1 <- microaggregation(free1[, 31:34], method="onedims", aggr=3)
m1

print.modrisk  

Print method for objects from class modrisk

Description

Print method for objects from class modrisk

Usage

## S3 method for class 'modrisk'
print(x, ...)


Arguments

x an object of class `modrisk`

... Additional arguments passed through.

Value

Output of model-based risk estimation

Author(s)

Bernhard Meindl

See Also

`modrisk`

---

`pram`

**Print method for objects from class pram**

Description

Print method for objects from class pram

Usage

```r
## S3 method for class 'pram'
print(x, ...)
```

Arguments

x an object of class `pram`

... Additional arguments passed through.

Value

absolute and relative frequencies of changed observations in each modified variable

Author(s)

Bernhard Meindl, Matthias Templ

See Also

`pram`
print.suda2  Print method for objects from class suda2

Description

Print method for objects from class suda2.

Usage

```r
## S3 method for class 'suda2'
print(x, ...)
```

Arguments

- `x` an object of class suda2
- `...` additional arguments passed through.

Value

Table of dis suda scores.

Author(s)

Matthias Templ

See Also

suda2

Examples

```r
## Not run:
data(testdata)
data_suda2 <- suda2(testdata, variables=c("urbrur","roof","walls","water","sex"))
data_suda2

## End(Not run)
```
rankSwap

Rank Swapping

Description

Swapping values within a range so that, first, the correlation structure of original variables are preserved, and second, the values in each record are disturbed. To be used on numeric or ordinal variables where the rank can be determined and the correlation coefficient makes sense.

Usage

rankSwap(obj, variables = NULL, TopPercent = 5, BottomPercent = 5, K0 = -1, R0 = 0.95, P = 0, missing = NA, seed = NULL)

Arguments

obj object of class sdcMicroObj or matrix or data frame
variables names or index of variables for that rank swapping is applied. For an object of class sdcMicroObj-class, all numeric key variables are selected if variables=NULL.
TopPercent Percentage of largest values that are grouped together before rank swapping is applied.
BottomPercent Percentage of lowest values that are grouped together before rank swapping is applied.
K0 Subset-mean preservation factor. Preserves the means before and after rank swapping within a range based on K0. K0 is the subset-mean preservation factor such that $|X_1 - X_2| \leq 2K_0X_1/\sqrt{N_S}$, where $X_1$ and $X_2$ are the subset means of the field before and after swapping, and $N_S$ is the sample size of the subset.
R0 Multivariate preservation factor. Preserves the correlation between variables within a certain range based on the given constant R0. We can specify the preservation factor as $R_0 = \frac{R_1}{R_2}$ where $R_1$ is the correlation coefficient of the two fields after swapping, and $R_2$ is the correlation coefficient of the two fields before swapping.
P Rank range as percentage of total sample size. We can specify the rank range itself directly, noted as $P$, which is the percentage of the records. So two records are eligible for swapping if their ranks, $i$ and $j$ respectively, satisfy $|i - j| \leq \frac{PN}{100}$, where $N$ is the total sample size.
missing missing - the value to be used as missing value in the C++ routine instead of NA. If NA, a suitable value is calculated internally. Note that in the returned dataset, all NA-values (if any) will be replaced with this value.
seed Seed.
Rank swapping sorts the values of one numeric variable by their numerical values (ranking). The restricted range is determined by the rank of two swapped values, which cannot differ, by definition, by more than \( P \) percent of the total number of observations. \( R_0 \) and \( K_0 \) are only used if positive. Only one of the two are used (\( R_0 \) is prefered if both are positive).

Value

The rank-swapped data set or a modified `sdcmicroObj-class` object.

Methods

- `list("signature(obj = "data.frame")")`
- `list("signature(obj = "matrix")")`
- `list("signature(obj = "sdcmicroObj")")`

Author(s)

Alexander Kowarik for the interface, Bernhard Meindl for improvements.

For the underlying C++ code: This work is being supported by the International Household Survey Network (IHSN) and funded by a DGF Grant provided by the World Bank to the PARIS21 Secretariat at the Organisation for Economic Co-operation and Development (OECD). This work builds on previous work which is elsewhere acknowledged.

References


Examples

data(testdata2)
data_swap <- rankSwap(testdata2,variables=c("age","income","expend","savings"))

## for objects of class sdcmicro:
data(testdata2)
sdc <- createSdcObj(testdata2,  
  keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),  
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- rankSwap(sdc)
Remove certain variables from the data set inside a sdc object.

**Description**
Delete variables without changing anything else in the sdcObject (writing NAs).

**Usage**
```r
removedirectID(obj, var)
```

**Arguments**
- **obj**: object of class `sdcmicroObj-class`
- **var**: name of the variable(s) to be remove

**Value**
the modified `sdcmicroObj-class`

**Methods**
```
list("signature(obj = \"sdcmicroObj\")")
```

**Author(s)**
Alexander Kowarik

**Examples**
```r
## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata, keyVars=c('urbrur','roof'),
numVars=c('expend','income','savings'), we='sampling_weight')
sdc <- removedirectID(sdc, var="age")
```

---

Change the name of levels of a keyVariable in an object of class `sdcmicroObj-class`

**Description**
Change the labels of levels.

**Usage**
```r
renameVars(obj, var, before, after)
```
Arguments

<table>
<thead>
<tr>
<th>obj</th>
<th>object of class sdcMicroObj-class</th>
</tr>
</thead>
<tbody>
<tr>
<td>var</td>
<td>name of the keyVariable to change</td>
</tr>
<tr>
<td>before</td>
<td>vector of levels before</td>
</tr>
<tr>
<td>after</td>
<td>vector of levels after</td>
</tr>
</tbody>
</table>

Value

the modified sdcMicroObj-class

Methods

```
list("signature(obj = \"sdcMicroObj\")")
```

Examples

```r
## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
  keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- renameVars(sdc, var="urbrur", before=2, after=78)
```

---

Generate a HTML/LATEX output from an sdcMicroObj

Description

Summary statistics of the original and the perturbed data set

Usage

```
report(obj, outdir = getwd(), filename = "SDC-Report", format = "HTML",
  title = "SDC-Report", internal = FALSE)
```

Arguments

<table>
<thead>
<tr>
<th>obj</th>
<th>an object of class sdcMicroObj-class or 'reportObj'</th>
</tr>
</thead>
<tbody>
<tr>
<td>outdir</td>
<td>output folder</td>
</tr>
<tr>
<td>filename</td>
<td>output filename</td>
</tr>
<tr>
<td>format</td>
<td>HTML, TEXT or LATEX</td>
</tr>
<tr>
<td>title</td>
<td>Title for the report</td>
</tr>
<tr>
<td>internal</td>
<td>TRUE/FALSE, if TRUE a detailed internal report is produced, else a non-disclosive overview</td>
</tr>
</tbody>
</table>
Details

The application of this function provides you with a html, text or pdf-report for your sdcMicro object that contains useful summaries about the anonymization process.

Author(s)

Matthias Templ, Bernhard Meindl

Examples

```r
## Not run:
data(testdata2)
sdc <- createSdcObj(testdata2, 
    keyvars=c('urbrur','roof','walls','water','electcon','relat','sex'), 
    numvars=c('expend','income','savings'), w='sampling_weight')
report(sdc)
## End(Not run)
```

---

**sampleCat**

Microaggregation for numerical and categorical key variables based on a distance similar to the GOWER DISTANCE

**Description**

The microaggregation is based on the distances computed similar to the Gower distance. The distance function makes distinction between the variable types factor, ordered, numerical and mixed (semi-continuous variables with a fixed probability mass at a constant value e.g. 0)

**Usage**

```r
sampleCat(x)
maxCat(x)
```

```r
microaggrGower(obj, variables = NULL, aggr = 3, dist_var = NULL, 
    by = NULL, mixed = NULL, mixed.constant = NULL, trace = FALSE, 
    weights = NULL, numFun = mean, catFun = sampleCat, addrandom = FALSE)
```

**Arguments**

- `x` a factor vector
- `obj` an object of class sdcMicroObj or a data frame
- `variables` character vector with names of variables to be aggregated (Default for sdcMicroObj is all keyVariables and all numeric key variables)
- `aggr` aggregation level (default=3)
- `dist_var` character vector with variable names for distance computation
by character vector with variable names to split the dataset before performing microaggregation (Default for sdcMicroObj is strataVar)
mixed character vector with names of mixed variables
mixed.constant numeric vector with length equal to mixed, where the mixed variables have the probability mass
trace TRUE/FALSE for some console output
weights numerical vector with length equal the number of variables for distance computation
numFun function: to be used to aggregated numerical variables
catFun function: to be used to aggregated categorical variables
addRandom TRUE/FALS if a random value should be added for the distance computation.

Details
The function sampleCat samples with probabilities corresponding to the occurrence of the level in the NNs. The function maxCat chooses the level with the most occurrences and random if the maximum is not unique.

Value
The function returns the updated sdcMicroObj or simply an altered data frame.

Note
In each by group all distance are computed, therefore introducing more by-groups significantly decreases the computation time and memory consumption.

Author(s)
Alexander Kowarik

Examples
```r
data(testdata, package="sdcMicro")
testdata <- testdata[1:200,]
for(i in c(1:7,9)) testdata[,i] <- as.factor(testdata[,i])
test <- microaggrGower(testdata, variables=c("relat","age","expend"),
    dist_var=c("age","sex","income","savings"), by=c("urbrur","roof"))
sdc <- createSdcObj(testdata,
    keyVars=c("urbrur","roof","walls","water","electcon","relat","sex"),
    numVars=c("expend","income","savings"), w="sampling_weight")
sdc <- microaggrGower(sdc)
```
sdcMicroObj-class
Class "sdcMicroObj"

Description
Class to save all information about the SDC process
modify sdcMicroObj-objects depending on argument type
undo last changes to sdcMicroObj-objects if possible note that this will only work if the user makes
use of the prev slot or uses the sdcMicroObj functions

Usage
createSdcObj(dat, keyVars, numVars = NULL, pramVars = NULL,
  ghostVars = NULL, weightVar = NULL, hhId = NULL, strataVar = NULL,
  sensibleVar = NULL, options = NULL)

get.sdcMicroObj(object, type)

set.sdcMicroObj(object, type, input)

undolast(object)

## S4 method for signature 'sdcMicroObj,character'
get.sdcMicroObj(object, type)

## S4 method for signature 'sdcMicroObj,character,listOrNULL'
set.sdcMicroObj(object, type, 
  input)

## S4 method for signature 'sdcMicroObj'
undolast(object)

Arguments
dat The microdata set. A numeric matrix or data frame containing the data.
keyVars Indices or names of categorical key variables. They must, of course, match with
  the columns of ‘dat’.
numVars Index or names of continuous key variables.
pramVars Indices or names of categorical variables considered to be pramed.
ghostVars if specified a list which each element being a list of exactly two elements. The
  first element must be a character vector specifying exactly one variable name
that was also specified as a categorical key variable (keyVars), while the second
  element is a character vector of valid variable names (that must not be listed as
keyVars). If `localSuppression` or `kAnon` was applied, the resulting suppres-
  sion pattern for each key-variable is transferred to the depending variables.
weightVar  Indices or name determining the vector of sampling weights.

hid   Index or name of the cluster ID (if available).

strataVar  Indices or names of stratification variables.

sensibleVar  Indices or names of sensible variables (for l-diversity)

options  additional options.

object  an object of class sdcMicroObj

type  a character vector of length 1 defining what to calculate|return|modify. Allowed
types are:

  • origData: set slot 'origData' of argument object

input  a list depending on argument type.

  • type==dataOrig: a list containing original microdata

Value

an object of class sdcMicroObj

an object of class sdcMicroObj

Objects from the Class

Objects can be created by calls of the form new("sdcMicroObj", ...).

Note

internal function

internal function

internal function

Author(s)

Bernhard Meindl, Alexander Kowarik, Matthias Templ, Elias Rut

Bernhard Meindl <bernhard.meindl@statistik.gv.at>

Bernhard Meindl <bernhard.meindl@statistik.gv.at>

Elias Rut

Examples

showClass("sdcMicroObj")
## Not run:
data(testdata)
sdc <- createSdcObj(testdata,
   keyVars=c('urbur','roof','walls','water','electcon','relat','sex'),
   numVars=c('expend','income','savings'), w='sampling_weight')
head(sdc@manipNumVars)
### Display Risks
sdc@risk$global
sdc <- dRisk(sdc)
```r
sdcrisk$numeric
### use addNoise without Parameters
sdcrisk$numeric
sdcrisk$numeric
### undolast
sdcrisk$numeric
### redo addNoise with Parameter
sdcrisk$numeric
### dataGen
sdcrisk$numeric
### LocalSuppression
sdcrisk$numeric
### microaggregation
sdcrisk$numeric
### pram
sdcrisk$numeric
### rankSwap
sdcrisk$numeric
### suda2
sdcrisk$numeric
```
sdcmicroobj-class

sdcrec$numeric
sd <- topBotCoding(sdc, value=60000000, replacement=6200000, column="income")
head(get.sdcmicroobj(sdc, type=\"manipNumVars\")
sdcrec$numeric
### LocalRecProg
data(testdata2)
sdc <- createSdcObj(testdata2,
  keyVars=c("urbrur", "roof", "walls", "water", "sex", "relat"))
sdcrec$global
sdcrec$global
### llmodGlobalRisk
sdcrec$undolast(sdc)
sdcrec$llmodGlobalRisk(sdc, inclProb=0.001)
sdcrec$model

## End (Not run)
## we can also specify ghost (linked) variables
## these variables are linked to some categorical key variables
## and have the same suppression pattern as the variable that they
## are linked to after \code{\link{localsuppression}} has been applied
data(testdata)
testdata$electcon2 <- testdata$selectcon
testdata$electcon3 <- testdata$selectcon
testdata$water2 <- testdata$water
keyVars <- c("urbrur", "roof", "walls", "water", "electcon", "relat", "sex")
numVars <- c("expend", "income", "savings")
w <- \"sampling_weight\"
## we want to make sure that some variables not used as key-variables
## have the same suppression pattern as variables that have been
## selected as key variables. Thus, we are using 'ghost'-variables.
ghostVars <- list()

## we want variables 'electcon2' and 'electcon3' to be linked
## to key-variable 'electcon'
ghostVars[[1]] <- list()
ghostVars[[1]][[1]] <- "electcon"
ghostVars[[1]][[2]] <- c("electcon2", "electcon3")

## we want variable 'water2' to be linked to key-variable 'water'
ghostVars[[2]] <- list()
ghostVars[[2]][[1]] <- "water"
ghostVars[[2]][[2]] <- "water2"

## create the sdcmicroobj
obj <- createSdcObj(testdata, keyVars=keyVars,
  numVars=numVars, w=w, ghostVars=ghostVars)

## apply 3-anonymity to selected key variables
obj <- kAnon(obj, k=3); obj

## check, if the suppression patterns are identical
manipGhostVars <- get.sdcmicroobj(obj, \"manipGhostVars\")
manipKeyVars <- get.sdcMicroObj(obj, "manipKeyVars")
all(is.na(manipKeyVars$electron) == is.na(manipGhostVars$electron2))
all(is.na(manipKeyVars$electron) == is.na(manipGhostVars$electron3))
all(is.na(manipKeyVars$water) == is.na(manipGhostVars$water2))

shuffle (Shuffling and EGADP)

Description
Data shuffling and General Additive Data Perturbation.

Usage
shuffle(obj, form, method = "ds", weights = NULL, covmethod = "spearman",
regmethod = "lm", gadp = TRUE)

Arguments
obj An object of class sdcMicroObj or a data.frame including the data.
form An object of class “formula” (or one that can be coerced to that class): a symbolic description of the model to be fitted. The responses have to consists of at least two variables of any class and the response variables have to be of class numeric. The response variables belongs to numeric key variables (quasi-identifiers of numeric scale). The predictors are can be distributed in any way (numeric, factor, ordered factor).
method currently either the original form of data shuffling (“ds” - default), “mvn” or “mlm”, see the details section. The last method is in experimental mode and almost untested.
weights Survey sampling weights. Automatically chosen when obj is of class sdcMicroObj-class.
covmethod Method for covariance estimation. “spearman”, “pearson” and \dQuote{mcd} are possible. For the latter one, the implementation in package robustbase is used.
regmethod Method for multivariate regression. “lm” and “MM” are possible. For method “MM”, the function “rlm” from package MASS is applied.
gadp TRUE, if the egadp results from a fit on the origianl data is returned.

Details
Perturbed values for the sensitive variables are generated. The sensitive variables have to be stored as responses in the argument ‘form’, which is the usual formula interface for regression models in R.

For method “ds” the EGADP method is applied on the norm inverse percentiles. Shuffling then ranks the original values according to the GADP output. For further details, please see the references.
Method “mvn” uses a simplification and draws from the normal Copulas directly before these draws are shuffled.

Method “mlm” is also a simplification. A linear model is applied the expected values are used as the perturbed values before shuffling is applied.

Value

If ‘obj’ is of class sdcMicroObj-class the corresponding slots are filled, like manipNumVars, risk and utility. If ‘obj’ is of class “data.frame” an object of class “micro” with following entities is returned:

shConf the shuffled numeric key variables
egadp the perturbed (using gadp method) numeric key variables

Methods

list("signature(obj = "data.frame")")
list("signature(obj = "matrix")")
list("signature(obj = "sdcMicroObj")")

Note

In this version, the covariance method chosen is used for any covariance and correlation estimations in the whole gadp and shuffling function.

Author(s)

Matthias Templ, Alexander Kowarik

References


See Also

rankSwap, lm
Examples

data(Prestige, package="car")
form <- formula(income + education + women + prestige + type, data=Prestige)
sh <- shuffle(obj=Prestige, form)
plot(Prestige[,c("income", "education")])
plot(sh$sh)
colMeans(Prestige[,c("income", "education")])
colMeans(sh$sh)
cor(Prestige[,c("income", "education")], method="spearman")
cor(sh$sh, method="spearman")

## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2, 
  keyVars=c('urbrur', 'roof', 'walls', 'water', 'electcon', 'relat', 'sex'),
  numVars=c('expend', 'income', 'savings'), w='sampling_weight')
sdc <- shuffle(sdc, method="ds", regmethod= "lm", covmethod= "spearman", form=savings+expend ~ urbrur+walls)

suda2

Suda2: Detecting Special Uniques

Description

SUDA risk measure for data from (stratified) simple random sampling.

Usage

sudaR(obj, ...)

Arguments

obj object of class “data.frame” or object of class sdcMicroObj-class
... see arguments below
  • variablesCategorical (key) variables. Either the column names or and index
    of the variables to be used for risk measurement.
  • missingMissing value coding in the given data set.
  • DisFractionIt is the sampling fraction for the simple random sampling, and
    the common sampling fraction for stratified sampling. By default, it’s set
    to 0.01.

Details

Suda 2 is a recursive algorithm for finding Minimal Sample Uniques. The algorithm generates all
possible variable subsets of defined categorical key variables and scans them for unique patterns in
the subsets of variables. The lower the amount of variables needed to receive uniqueness, the higher
the risk of the corresponding observation.
Value

A modified `sdcmicroobj-class` object or the following list

- ContributionPercent: The contribution of each key variable to the SUDA score, calculated for each row.
- score: The suda score.
- disscore: The dis suda score

Methods

```r
#`
list("signature(obj = \"data.frame\")")
list("signature(obj = \"matrix\")")
list("signature(obj = \"sdcmicroObj\")")
```

Author(s)

Alexander Kowarik based on the C++ code from the Organisation For Economic Co-Operation And Development.

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References


M. J. Elliot, A. Manning, K. Mayes, J. Gurd and M. Bane (20xx) SUDA: A Program for Detecting Special Uniques, Using DIS to Modify the Classification of Special Uniques


Examples

```r
## Not run:
data(testdata2)
data_suda2 <- suda2(testdata2, variables=c("urbrur","roof","walls","water","sex"))
data_suda2
summary(data_suda2)

## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2, 
  keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'), 
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- suda2(sdc)
```

## End(Not run)
**summary.freqCalc**

Summary method for objects of class `freqCalc` to provide information about local suppressions.

**Usage**

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

**Arguments**

- `object` object from class `freqCalc`
- `...` Additional arguments passed through.

**Details**

Shows the amount of local suppressions on each variable in which local suppression was applied.

**Value**

Information about local suppression in each variable (only if a local suppression is already done).

**Author(s)**

Matthias Templ

**See Also**

`freqCalc`

**Examples**

```r
## example from Capobianchi, Polettini and Lucarelli:  
data(francdat)  
f <- freqCalc(francdat, keyVars=c(2,4,5,6),w=8)  
f  
f$fk  
f$FK  
## individual risk calculation:  
indivf <- indivRisk(f)  
indivf$rk  
## Local Suppression  
locals <- localSupp(f, keyVar=2, indivRisk=indivf$rk, threshold=0.25)  
f2 <- freqCalc(locals$freqCalc, keyVars=c(4,5,6), w=8)  
summary(f2)
```
Summary method for objects from class ‘micro’.

Usage

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

Arguments

- `object`: objects from class micro
- `...`: Additional arguments passed through.

Details

This function computes several measures of information loss, such as

Value

- `meanx`: A conventional summary of the original data
- `meanxm`: A conventional summary of the microaggregated data
- `amean`: average relative absolute deviation of means
- `amedian`: average relative absolute deviation of medians
- `aonestep`: average relative absolute deviation of one step from median
- `devvar`: average relative absolute deviation of variances
- `amad`: average relative absolute deviation of the mad
- `acov`: average relative absolute deviation of covariances
- `arcov`: average relative absolute deviation of robust (with mcd) covariances
- `acor`: average relative absolute deviation of correlations
- `arcor`: average relative absolute deviation of robust (with mcd) correlations
- `acors`: average relative absolute deviation of rank-correlations
- `adlm`: average absolute deviation of lm regression coefficients (without intercept)
- `adits`: average absolute deviation of its regression coefficients (without intercept)
- `apcaload`: average absolute deviation of pca loadings
- `apppacaloid`: average absolute deviation of robust (with projection pursuit approach) pca loadings
- `atotals`: average relative absolute deviation of totals
- `pmtotals`: average relative deviation of totals
**summary.pram**

**Author(s)**
Matthias Templ

**References**

**See Also**
`microaggregation`, `valTable`

**Examples**
```r
data(Tarragona)
m1 <- microaggregation(Tarragona, method="onedims", aggr=3)
## summary(m1)
```

---

**Description**
Summary method for objects from class ‘pram’ to provide information about transitions.

**Usage**
```r
## S3 method for class 'pram'
summary(object, ...)
```

**Arguments**
- `object` object from class ‘pram’
- `...` Additional arguments passed through.

**Details**
Shows various information about the transitions.

**Value**
The summary of object from class ‘pram’.

**Author(s)**
Matthias Templ
References


See Also

pram

Examples

data(free1)
x <- free1[,"MARSTAT"]
x2 <- pram(x)
x
summary(x2)

Tarragona

Tarragona data set

Description

A real data set comprising figures of 834 companies in the Tarragona area. Data correspond to year 1995.

Format

A data frame with 834 observations on the following 13 variables.

FIXED.ASSETS  a numeric vector
CURRENT.ASSETS  a numeric vector
TREASURY  a numeric vector
UNCOMMITTED.FUNDS  a numeric vector
PAID.UP.CAPITAL  a numeric vector
SHORT.TERM.DEBT  a numeric vector
SALES  a numeric vector
LABOR.COSTS  a numeric vector
DEPRECIATION  a numeric vector
OPERATING.PROFIT  a numeric vector
FINANCIAL.OUTCOME  a numeric vector
GROSS.PROFIT  a numeric vector
NET.PROFIT  a numeric vector
Source

Public use data from the CASC project.

References


Examples

data(Tarragona)
head(Tarragona)
dim(Tarragona)

testdata

A real-world data set on household income and expenditures

Description

A concise (1-5 lines) description of the dataset.

Format

A data frame with 4580 observations on the following 14 variables.

urbrur  a numeric vector
roof    a numeric vector
walls   a numeric vector
water   a numeric vector
electcon a numeric vector
relat   a numeric vector
sex     a numeric vector
age     a numeric vector
hhcivil  a numeric vector
expend  a numeric vector
income  a numeric vector
savings a numeric vector
ori_hid a numeric vector
sampling_weight  a numeric vector

A data frame with 93 observations on the following 19 variables.

urbrur  a numeric vector
topBotCoding

roof a numeric vector
columns a numeric vector
water a numeric vector
electcon a numeric vector
relat a numeric vector
sex a numeric vector
age a numeric vector
hhcivil a numeric vector
expend a numeric vector
income a numeric vector
savings a numeric vector
ori_hid a numeric vector
sampling_weight a numeric vector
represent a numeric vector
category_count a numeric vector
relat2 a numeric vector
water2 a numeric vector
water3 a numeric vector

References

The International Household Survey Network, www.ihsn.org

Examples

data(testdata)
## maybe str(testdata) ; plot(testdata) ...

tagBotCoding Top and Bottom Coding

description

Function for Top and Bottom Coding.

Usage

tagBotCoding(obj, value, replacement, kind = "top", column = NULL)
Arguments

- **obj**: vector or one-dimensional matrix or data.frame or object of class `sdcmicroObj-class`
- **value**: limit, from where it should be top- or bottom-coded
- **replacement**: replacement value.
- **kind**: top or bottom
- **column**: xxx

Details

Extreme values are replaced by one value to reduce the disclosure risk.

Value

Top or bottom coded data or modified `sdcmicroObj-class`.

Methods

- `list("signature(obj = \"ANY\")")`
- `list("signature(obj = \"sdcmicroObj\")")`

Author(s)

Matthias Templ

See Also

`indivrisk`

Examples

data(free1)
topBotCoding(free1[, "DEBTS"], value=9000, replacement=9100, kind="top")

## for objects of class `sdcmicro`

data(testdata2)
sdc <- createSdcObj(testdata2, keyVars=c('urbrur', 'roof', 'walls', 'water', 'electcon', 'relat', 'sex'),
                    numVars=c('expend', 'income', 'savings'), w='sampling_weight')
sdc <- topBotCoding(sdc, value=500000, replacement=1000, column="income")
testdataout <- extractManipData(sdc)
valTable

Comparison of different microaggregation methods

Description

A Function for the comparison of different perturbation methods.

Usage

valTable(x, method = c("simple", "onedims", "clustppca", "addNoise: additive", "swappNum"), measure = "mean", clustermethod = "clara", aggr = 3, nc = 8, transf = "log", p = 15, noise = 15, w = 1:dim(x)[2], delta = 0.1)

Arguments

x
  data frame or matrix

method
  microaggregation methods or adding noise methods or rank swapping.

measure
  FUN for aggregation. Possible values are mean (default), median, trim, onestep.

clustermethod
  clustermethod, if a method will need a clustering procedure

aggr
  aggregation level (default=3)

nc
  number of clusters. Necessary, if a method will need a clustering procedure

transf
  Transformation of variables before clustering.

p
  Swapping range, if method swappNum has been chosen

noise
  noise addition, if an addNoise method has been chosen

w
  variables for swapping, if method swappNum has been chosen

delta
  parameter for adding noise method ‘correlated2’

Details

Tabelarise the output from summary.micro. Will be enhanced to all perturbation methods in future versions.

Value

Measures of information loss splitted for the comparison of different methods.

Methods for adding noise should be named via “addNoise: method”, e.g. “addNoise: correlated”, i.e. the term ‘at first’ then followed by a ':' and a blank and then followed by the name of the method as described in function ‘addNoise’.

Author(s)

Matthias Templ
References

See Also
microaggregation, summary.micro

Examples
```r
data(Tarragona)
## Not run:
valTable(Tarragona[100:200,],
method=c("simple","onedims","pca","addNoise: additive"))
valTable(Tarragona,
method=c("simple","onedims","pca","clustpppca",
"mdav", "addNoise: additive", "swappNum"))
## clustpppca in combination with Mclust outperforms
## the other algorithms for this data set...

## End(Not run)
```

---

**varToFactor**

*Change the a keyVariable of an object of class sdcMicroObj-class from Numeric to Factor or from Factor to Numeric*

### Description
Change the scale of a variable

### Usage
```
varToFactor(obj, var)
```

### Arguments
- **obj**: object of class sdcMicroObj-class
- **var**: name of the keyVariable to change

### Value
the modified sdcMicroObj-class

### Methods
```
list("signature(obj = \"sdcMicroObj\")")
```
Examples

```r
## for objects of class sdcMicro:
data(testdata2)
sdc <- createSdcObj(testdata2,
  keyVars=c('urbrur','roof','walls','water','electcon','relat','sex'),
  numVars=c('expend','income','savings'), w='sampling_weight')
sdc <- varToFactor(sdc, var="urbrur")
```
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