

# Package ‘modi’

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**Type** Package

**Title** Multivariate Outlier Detection and Imputation for Incomplete Survey Data

**Version** 0.1.0

**Description** Algorithms for multivariate outlier detection when missing values occur. Algorithms are based on Mahalanobis distance or data depth. Imputation is based on the multivariate normal model or uses nearest neighbour donors. The algorithms take sample designs, in particular weighting, into account. The methods are described in Bill and Hulliger (2016) <doi:10.17713/ajs.v45i1.86>.

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**URL** <https://github.com/martinSter/modi>

**BugReports** <https://github.com/martinSter/modi/issues>

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**RoxygenNote** 6.0.1

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BEM	<i>BACON-EEM Algorithm for multivariate outlier detection in incomplete multivariate survey data</i>
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### Description

BEM starts from a set of uncontaminated data with possible missing values, applies a version of the EM-algorithm to estimate the center and scatter of the good data, then adds (or deletes) observations to the good data which have a Mahalanobis distance below a threshold. This process iterates until the good data remain stable. Observations not among the good data are outliers.

### Usage

```
BEM(data, weights, v = 2, c0 = 3, alpha = 0.01, md.type = "m",
     em.steps.start = 10, em.steps.loop = 5, better.estimation = FALSE,
     monitor = FALSE)
```

### Arguments

data	a matrix or data frame. As usual, rows are observations and columns are variables.
weights	a non-negative and non-zero vector of weights for each observation. Its length must equal the number of rows of the data. Default is <code>rep(1, nrow(data))</code> .
v	an integer indicating the distance for the definition of the starting good subset: $v = 1$ uses the Mahalanobis distance based on the weighted mean and covariance, $v = 2$ uses the Euclidean distance from the componentwise median.

<code>c0</code>	the size of initial subset is <code>c0 * ncol(data)</code> .
<code>alpha</code>	a small probability indicating the level $(1 - \alpha)$ of the cutoff quantile for good observations.
<code>md.type</code>	type of Mahalanobis distance: "m" marginal, "c" conditional.
<code>em.steps.start</code>	number of iterations of EM-algorithm for starting good subset.
<code>em.steps.loop</code>	number of iterations of EM-algorithm for good subset.
<code>better.estimation</code>	if <code>better.estimation = TRUE</code> , then the EM-algorithm for the final good subset iterates <code>em.steps.start</code> more.
<code>monitor</code>	if TRUE, verbose output.

### Details

The BACON algorithm with  $\nu = 1$  is not robust but affine equivariant while  $\nu = 1$  is robust but not affine equivariant. The threshold for the (squared) Mahalanobis distances, beyond which an observation is an outlier, is a standardised chisquare quantile at  $(1 - \alpha)$ . For large data sets it may be better to choose  $\alpha / n$  instead. The internal function `EM.normal` is usually called from BEM. `EM.normal` is implementing the EM-algorithm in such a way that part of the calculations can be saved to be reused in the BEM algorithm. `EM.normal` does not contain the computation of the observed sufficient statistics, they will be computed in the main program of BEM and passed as parameters as well as the statistics on the missingness patterns.

### Value

BEM returns a list whose first component output is a sublist with the following components:

`sample.size` Number of observations  
`discarded.observations` Number of discarded observations  
`number.of.variables` Number of variables  
`significance.level` The probability used for the cutpoint, i.e.  $\alpha$   
`initial.basic.subset.size` Size of initial good subset  
`final.basic.subset.size` Size of final good subset  
`number.of.iterations` Number of iterations of the BACON step  
`computation.time` Elapsed computation time  
`center` Final estimate of the center  
`scatter` Final estimate of the covariance matrix  
`cutpoint` The threshold MD-value for the cut-off of outliers

The further components returned by BEM are:

`outind` Indicator of outliers  
`dist` Final Mahalanobis distances

### Note

BEM uses an adapted version of the EM-algorithm in function `.EM.normal`.

**Author(s)**

Beat Hulliger

**References**

Béguin, C. and Hulliger, B. (2008) The BACON-EEM Algorithm for Multivariate Outlier Detection in Incomplete Survey Data, *Survey Methodology*, Vol. 34, No. 1, pp. 91-103.

Billor, N., Hadi, A.S. and Vellemann, P.F. (2000). BACON: Blocked Adaptative Computationally-efficient Outlier Nominators. *Computational Statistics and Data Analysis*, 34(3), 279-298.

Schafer J.L. (2000), *Analysis of Incomplete Multivariate Data*, Monographs on Statistics and Applied Probability 72, Chapman & Hall.

**Examples**

```
# Bushfire data set with 20% MCAR
data(bushfirem, bushfire.weights)
bem.res <- BEM(bushfirem, bushfire.weights, alpha = (1 - 0.01 / nrow(bushfirem)))
print(bem.res$output)
```

---

bushfire

*Bushfire scars.*

---

**Description**

The bushfire data set was used by Campbell (1984, 1989) to locate bushfire scars. The dataset contains satellite measurements on five frequency bands, corresponding to each of 38 pixels.

**Usage**

bushfire

**Format**

A data frame with 38 rows and 5 variables.

**Details**

The data contains an outlying cluster of observations 33 to 38 a second outlier cluster of observations 7 to 11 and a few more isolated outliers, namely observations 12, 13, 31 and 32.

For testing purposes weights are provided: `bushfire.weights <- rep(c(1,2,5), length = nrow(bushfire))`

**References**

Campbell, N. (1989) *Bushfire Mapping using NOAA AVHRR Data*. Technical Report. Commonwealth Scientific and Industrial Research Organisation, North Ryde.

**Examples**

```
data(bushfire)
```

---

bushfire.weights	<i>Weights for Bushfire scars.</i>
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---

**Description**

The bushfire data set was used by Campbell (1984, 1989) to locate bushfire scars. The dataset contains satellite measurements on five frequency bands, corresponding to each of 38 pixels.

**Usage**

```
bushfire.weights
```

**Format**

A vector of length 38.

**Details**

For testing purposes, `bushfire.weights` provides artificial weights created according to: `bushfire.weights <- rep(c(1, 2, 3, 4, 5), 8)`

**References**

Campbell, N. (1989) Bushfire Mapping using NOAA AVHRR Data. Technical Report. Commonwealth Scientific and Industrial Research Organisation, North Ryde.

**Examples**

```
data(bushfire.weights)
```

---

bushfirem	<i>Bushfire scars with missing data.</i>
-----------	--

---

**Description**

The bushfire data set was used by Campbell (1984, 1989) to locate bushfire scars. The dataset contains satellite measurements on five frequency bands, corresponding to each of 38 pixels. However, this dataset contains missing values.

**Usage**

```
bushfirem
```

**Format**

A data frame with 38 rows and 5 variables.

**Details**

The data contains an outlying cluster of observations 33 to 38 a second outlier cluster of observations 7 to 11 and a few more isolated outliers, namely observations 12, 13, 31 and 32.

bushfirem is created from bushfire by setting a proportion of 0.2 of the values to missing.

For testing purposes weights are provided: `bushfire.weights <- rep(c(1,2,5), length = nrow(bushfire))`

**References**

Campbell, N. (1989) Bushfire Mapping using NOAA AVHRR Data. Technical Report. Commonwealth Scientific and Industrial Research Organisation, North Ryde.

**Examples**

```
data(bushfirem)
```

---

EAdet	<i>Epidemic Algorithm for detection of multivariate outliers in incomplete survey data</i>
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---

**Description**

In EAdet an epidemic is started at a center of the data. The epidemic spreads out and infects neighbouring points (probabilistically or deterministically). The last points infected are outliers. After running EAdet an imputation with EAimp may be run.

**Usage**

```
EAdet(data, weights, reach = "max", transmission.function = "root",
       power = ncol(data), distance.type = "euclidean", max1 = 5,
       plotting = TRUE, monitor = FALSE, prob.quantile = 0.9,
       random.start = FALSE, fix.start, threshold = FALSE,
       deterministic = TRUE, rm.missobs = FALSE, verbose = FALSE)
```

**Arguments**

data	a data frame or matrix with data.
weights	a vector of positive sampling weights.
reach	if reach = "max" the maximal nearest neighbor distance is used as the basis for the transmission function, otherwise the weighted $(1 - (p + 1)/n)$ quantile of the nearest neighbor distances is used.

transmission.function	form of the transmission function of distance d: "step" is a heaviside function which jumps to 1 at d0, "linear" is linear between 0 and d0, "power" is $(\text{beta} \cdot d + 1)^{-p}$ for $p = \text{ncol}(\text{data})$ as default, "root" is the function $1 - (1 - d/d0)^{1/\text{maxl}}$ .
power	sets $p = \text{power}$ .
distance.type	distance type in function <code>dist()</code> .
maxl	maximum number of steps without infection.
plotting	if TRUE, the cdf of infection times is plotted.
monitor	if TRUE, verbose output on epidemic.
prob.quantile	if mads fail, take this quantile absolute deviation.
random.start	if TRUE, take a starting point at random instead of the spatial median.
fix.start	force epidemic to start at a specific observation.
threshold	infect all remaining points with infection probability above the threshold $1 - 0.5^{1/\text{maxl}}$ .
deterministic	if TRUE, the number of infections is the expected number and the infected observations are the ones with largest infection probabilities.
rm.missobs	set <code>rm.missobs=TRUE</code> if completely missing observations should be discarded. This has to be done actively as a safeguard to avoid mismatches when imputing.
verbose	more output with <code>verbose=TRUE</code> .

## Details

The form and parameters of the transmission function should be chosen such that the infection times have at least a range of 10. The default cutting point to decide on outliers is the median infection time plus three times the mad of infection times. A better cutpoint may be chosen by visual inspection of the cdf of infection times. EAdet calls the function `EA.dist`, which passes the counterprobabilities of infection (a  $n * (n - 1)/2$  size vector!) and three parameters (sample spatial median index, maximal distance to nearest neighbor and transmission distance = reach) as arguments to EAdet. The distances vector may be too large to be passed as arguments. Then either the memory size must be increased. Former versions of the code used a global variable to store the distances in order to save memory.

## Value

EAdet returns a list whose first component output is a sub-list with the following components:

<code>sample.size</code>	Number of observations
<code>discarded.observations</code>	Indices of discarded observations
<code>missing.observations</code>	Indices of completely missing observations
<code>number.of.variables</code>	Number of variables
<code>n.complete.records</code>	Number of records without missing values
<code>n.usable.records</code>	Number of records with less than half of values missing (unusable observations are discarded)
<code>medians</code>	Component wise medians

mads Component wise mads  
 prob.quantile Use this quantile if mads fail, i.e. if one of the mads is 0  
 quantile.deviations Quantile of absolute deviations  
 start Starting observation  
 transmission.function Input parameter  
 power Input parameter  
 maxl Maximum number of steps without infection  
 min.nn.dist Maximal nearest neighbor distance  
 transmission.distance  $d_0$   
 threshold Input parameter  
 distance.type Input parameter  
 deterministic Input parameter  
 number.infected Number of infected observations  
 cutpoint Cutpoint of infection times for outlier definition  
 number.outliers Number of outliers  
 outliers Indices of outliers  
 duration Duration of epidemic  
 computation.time Elapsed computation time  
 initialisation.computation.time Elapsed computation time for standardisation and calculation of distance matrix

The further components returned by EAdet are:

infected Indicator of infection  
 infection.time Time of infection  
 outind Indicator of outliers

### Author(s)

Beat Hulliger

### References

Béguin, C. and Hulliger, B. (2004) Multivariate outlier detection in incomplete survey data: the epidemic algorithm and transformed rank correlations, JRSS-A, 167, Part 2, pp. 275-294.

### See Also

[EAimp](#) for imputation with the Epidemic Algorithm.

### Examples

```

data(bushfirem, bushfire.weights)
det.res <- EAdet(bushfirem, bushfire.weights)
print(det.res$output)

```



---

EAimp	<i>Epidemic Algorithm for imputation of multivariate outliers in incomplete survey data.</i>
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---

## Description

After running EAdet an imputation of the detected outliers with EAimp may be run.

## Usage

```
EAimp(data, weights, outind, reach = "max", transmission.function = "root",
       power = ncol(data), distance.type = "euclidean", duration = 5,
       maxl = 5, kdon = 1, monitor = FALSE, threshold = FALSE,
       deterministic = TRUE, fixedprop = 0)
```

## Arguments

data	a data frame or matrix with the data.
weights	a vector of positive sampling weights.
outind	a logical vector with component TRUE for outliers.
reach	reach of the threshold function (usually set to the maximum distance to a nearest neighbour, see internal function EA.dist).
transmission.function	form of the transmission function of distance d: "step" is a heaviside function which jumps to 1 at d0, "linear" is linear between 0 and d0, "power" is $\beta \cdot d + 1^{-p}$ for $p = \text{ncol}(\text{data})$ as default, "root" is the function $1 - (1 - d/d0)^{1/\text{maxl}}$ .
power	sets $p = \text{power}$ , where p is the parameter in the above transmission function.
distance.type	distance type in function dist().
duration	the duration of the detection epidemic.
maxl	maximum number of steps without infection.
kdon	the number of donors that should be infected before imputation.
monitor	if TRUE verbose output on epidemic.
threshold	Infect all remaining points with infection probability above the threshold $1 - 0.5^{1/\text{maxl}}$ .
deterministic	if TRUE the number of infections is the expected number and the infected observations are the ones with largest infection probabilities.
fixedprop	if TRUE a fixed proportion of observations is infected at each step.

## Details

EAimp uses the distances calculated in EAdet (actually the counterprobabilities, which are stored in a global data set) and starts an epidemic at each observation to be imputed until donors for the missing values are infected. Then a donor is selected randomly.

**Value**

EAimp returns a list with two components: `parameters` and `imputed.data`. `parameters` contains the following elements:

`sample.size` Number of observations

`number.of.variables` Number of variables

`n.complete.records` Number of records without missing values

`n.usable.records` Number of records with less than half of values missing (unusable observations are discarded)

`duration` Duration of epidemic

`reach` Transmission distance ( $d_0$ )

`threshold` Input parameter

`deterministic` Input parameter

`computation.time` Elapsed computation time

`imputed.data` contains the imputed data.

**Author(s)**

Beat Hulliger

**References**

Béguin, C. and Hulliger, B. (2004) Multivariate outlier detection in incomplete survey data: the epidemic algorithm and transformed rank correlations, *JRSS-A*, 167, Part 2, pp. 275-294.

**See Also**

[EAdet](#) for outlier detection with the Epidemic Algorithm.

**Examples**

```
data(bushfirem, bushfire.weights)
det.res <- EAdet(bushfirem, bushfire.weights)
imp.res <- EAimp(bushfirem, bushfire.weights, outind = det.res$outind,
reach = det.res$output$max.min.di, kdon = 3)
print(imp.res$output)
```

---

ER *Robust EM-algorithm ER*

---

### Description

The ER function is an implementation of the ER-algorithm of Little and Smith (1987).

### Usage

```
ER(data, weights, alpha = 0.01, psi.par = c(2, 1.25), em.steps = 100,
  steps.output = FALSE, Estep.output = FALSE, tolerance = 1e-06)
```

### Arguments

data	a data frame or matrix with the data.
weights	sampling weights.
alpha	probability for the quantile of the cut-off.
psi.par	further parameters passed to the psi-function.
em.steps	number of iteration steps of the EM-algorithm.
steps.output	if TRUE, verbose output.
Estep.output	if TRUE, estimators are output at each iteration.
tolerance	convergence criterion (relative change).

### Details

The M-step of the EM-algorithm uses a one-step M-estimator.

### Value

sample.size	Number of observations
number.of.variables	Number of variables
significance.level	alpha
computation.time	Elapsed computation time
good.data	Indices of the data in the final good subset
outliers	Indices of the outliers
center	Final estimate of the center
scatter	Final estimate of the covariance matrix
dist	Final Mahalanobis distances
rob.weights	Robustness weights in the final EM step

### Author(s)

Beat Hulliger

## References

Little, R. and P. Smith (1987). Editing and imputation for quantitative survey data. *Journal of the American Statistical Association*, 82, 58-68.

## See Also

[BEM](#)

## Examples

```
data(bushfire, bushfire.weights)
det.res <- ER(bushfire, weights = bushfire.weights, alpha = 0.05,
steps.output = TRUE, em.steps = 100, tol = 2e-6)
PlotMD(det.res$dist, ncol(bushfire))
```

---

GIMCD

*Gaussian imputation followed by MCD*

---

## Description

Gaussian imputation uses the classical non-robust mean and covariance estimator and then imputes predictions under the multivariate normal model. Outliers may be created by this procedure. Then a high-breakdown robust estimate of the location and scatter with the Minimum Covariance Determinant algorithm is obtained and finally outliers are determined based on Mahalanobis distances based on the robust location and scatter.

## Usage

```
GIMCD(data, alpha = 0.05, seedem = 23456789, seedmcd)
```

## Arguments

data	a data frame or matrix with the data.
alpha	a threshold value for the cut-off for the outlier Mahalanobis distances.
seedem	random number generator seed for EM algorithm
seedmcd	random number generator seed for MCD algorithm, if seedmcd is missing, an internal seed will be used.

## Details

Normal imputation from package `norm` and MCD from package `MASS`. Note that currently MCD does not accept weights.

**Value**

Result is stored in a global list GIMCD.r:

center robust center

scatter robust covariance

alpha quantile for cut-off value

computation.time elapsed computation time

outind logical vector of outlier indicators

dist Mahalanobis distances

**Author(s)**

Beat Hulliger

**References**

Béguin, C. and Hulliger, B. (2008), The BACON-EEM Algorithm for Multivariate Outlier Detection, in Incomplete Survey Data, Survey Methodology, Vol. 34, No. 1, pp. 91-103.

**See Also**

[cov.rob](#)

**Examples**

```
data(bushfirem)
det.res <- GIMCD(bushfirem, alpha = 0.1)
print(det.res$center)
PlotMD(det.res$dist, ncol(bushfirem))
```

---

MDmiss

*Mahalanobis distance (MD) for data with missing values*

---

**Description**

For each observation the missing dimensions are omitted before calculating the MD. The MD contains a correction factor  $p/q$  to account for the number of observed values, where  $p$  is the number of variables and  $q$  is the number of observed dimensions for the particular observation.

**Usage**

```
MDmiss(data, center, cov)
```

### Arguments

data	the data as a dataframe or matrix.
center	the center to be used (may not contain missing values).
cov	the covariance to be used (may not contain missing values).

### Details

The function loops over the observations. This is not optimal if only a few missingness patterns occur. If no missing values occur the function returns the Mahalanobis distance.

### Value

The function returns a vector of the (squared) Mahalanobis distances.

### Author(s)

Beat Hulliger

### References

Béguin, C., and Hulliger, B. (2004). Multivariate outlier detection in incomplete survey data: The epidemic algorithm and transformed rank correlations. *Journal of the Royal Statistical Society, A167 (Part 2.)*, pp. 275-294.

### See Also

[mahalanobis](#)

### Examples

```
data(bushfirem, bushfire)
MDmiss(bushfirem, apply(bushfire, 2, mean), var(bushfire))
```

---

modi

*modi: Multivariate outlier detection for incomplete survey data.*

---

### Description

The package `modi` is a collection of functions for multivariate outlier detection and imputation. The aim is to provide a set of functions which cope with missing values and take sampling weights into account. The original functions were developed in the EUREDIT project. This work was partially supported by the EU FP5 ICT programme, the Swiss Federal Office of Education and Science and the Swiss Federal Statistical Office. Subsequent development was in the AMELI project of the EU FP7 SSH Programme and also supported by the University of Applied Sciences and Arts Northwestern Switzerland (FHNW).

**modi functions**

BACON-EEM algorithm in BEM(), Epidemic algorithm in EAdet() and EAimp(), Transformed Rank Correlations in TRC(), Gaussian imputation with MCD in GIMCD().

**References**

Béguin, C., and Hulliger, B. (2004). Multivariate outlier detection in incomplete survey data: The epidemic algorithm and transformed rank correlations. *Journal of the Royal Statistical Society, A167 (Part 2.)*, pp. 275-294.

Béguin, C., and Hulliger, B. (2008). The BACON-EEM Algorithm for Multivariate Outlier Detection in Incomplete Survey Data, *Survey Methodology*, Vol. 34, No. 1, pp. 91-103.

---

 PlotMD

---

*QQ-Plot of Mahalanobis distances*


---

**Description**

QQ-plot of (squared) Mahalanobis distances vs. scaled F-distribution (or a scaled chisquare distribution). In addition, two default cutpoints are proposed.

**Usage**

```
PlotMD(dist, p, alpha = 0.95, chisquare = FALSE)
```

**Arguments**

dist	a vector of Mahalanobis distances.
p	the number of variables involved in the Mahalanobis distances.
alpha	a probability for cut-off, usually close to 1.
chisquare	a logical indicating the the chisquare distribution should be used instead of the F-distribution.

**Details**

Scaling of the F-distribution as  $\text{median}(\text{dist}) * \text{qf}((1:n)/(n+1), p, n-p) / \text{qf}(0.5, p, n-p)$ . First default cutpoint is  $\text{median}(\text{dist}) * \text{qf}(\text{alpha}, p, n-p) / \text{qf}(0.5, p, n-p)$  and the second default cutpoint is the alpha quantile of the Mahalanobis distances.

**Value**

hmed	first proposed cutpoint based on F-distribution
halpha	second proposed cutpoint (alpha-quantile)
QQ-plot	

**Author(s)**

Beat Hulliger

**References**

Little, R. & Smith, P. (1987) Editing and imputation for quantitative survey data, *Journal of the American Statistical Association*, 82, 58-68

**Examples**

```
data(bushfirem, bushfire.weights)
det.res <- TRC(bushfirem, weights = bushfire.weights)
PlotMD(det.res$dist, ncol(bushfirem))
```

---

 POEM

---

*Nearest Neighbour Imputation with Mahalanobis distance*


---

**Description**

POEM takes into account missing values, outlier indicators, error indicators and sampling weights.

**Usage**

```
POEM(data, weights, outind, errors, missing.matrix, alpha = 0.5, beta = 0.5,
      reweight.out = FALSE, c = 5, preliminary.mean.imputation = FALSE,
      monitor = FALSE)
```

**Arguments**

data	a data frame or matrix with the data.
weights	sampling weights.
outind	an indicator vector for the outliers with 1 indicating an outlier.
errors	matrix of indicators for items which failed edits.
missing.matrix	the missingness matrix can be given as input. Otherwise, it will be recalculated.
alpha	scalar giving the weight attributed to an item that is failing.
beta	minimal overlap to accept a donor.
reweight.out	if TRUE, the outliers are redefined.
c	tuning constant when redefining the outliers (cutoff for Mahalanobis distance).
preliminary.mean.imputation	assume the problematic observation is at the mean of good observations.
monitor	if TRUE verbose output.



## Details

POEM assumes that an multivariate outlier detection has been carried out beforehand and assumes the result is summarized in the vector `out.ind`. In addition, further observations may have been flagged as failing edit-rules and this information is given in the vector `errors`. The mean and covariance estimate is calculated with the good observations (no outliers and downweighted errors). Preliminary mean imputation is sometimes needed to avoid a non-positive definite covariance estimate at this stage. Preliminary mean imputation assumes that the problematic values of an observation (with errors, outliers or missing) can be replaced by the mean of the rest of the non-problematic observations. Note that the algorithm imputes these problematic observations afterwards and therefore the final covariance matrix with imputed data is not the same as the working covariance matrix (which may be based on preliminary mean imputation).

## Value

POEM returns a list whose first component output is a sub-list with the following components:

`preliminary.mean.imputation` Logical. TRUE if preliminary mean imputation should be used  
`completely.missing` Number of observations with no observed values  
`good.values` Weighted number of good values (not missing, not outlying, not erroneous)  
`nonoutliers.before` Number of nonoutliers before reweighting  
`weighted.nonoutliers.before` Weighted number of nonoutliers before reweighting  
`nonoutliers.after` Number of nonoutliers after reweighting  
`weighted.nonoutliers.after` Weighted number of nonoutliers after reweighting  
`old.center` Coordinate means after weighting, before imputation  
`old.variances` Coordinate variances after weighting, before imputation  
`new.center` Coordinate means after weighting, after imputation  
`new.variances` Coordinate variances after weighting, after imputation  
`covariance` Covariance (of standardised observations) before imputation  
`imputed.observations` Indices of observations with imputed values  
`donors` Indices of donors for imputed observations  
`new.outind` Indices of new outliers

The further component returned by POEM is:

`imputed.data` Imputed data set

## Author(s)

Beat Hulliger

## References

Béguin, C. and Hulliger B., (2002), EUREDIT Workpackage x.2 D4-5.2.1-2.C Develop and evaluate new methods for statistical outlier detection and outlier robust multivariate imputation, Technical report, EUREDIT 2002.

**Examples**

```

data(bushfirem, bushfire.weights)
outliers <- rep(0, nrow(bushfirem))
outliers[31:38] <- 1
imp.res <- POEM(bushfirem, bushfire.weights, outliers,
preliminary.mean.imputation = TRUE)
print(imp.res$output)
var(imp.res$imputed.data)

```

---

sepe

*Sample Environment Protection Expenditure Survey.*


---

**Description**

The sepe data set is a sample of the pilot survey in 1993 of the Swiss Federal Statistical Office on environment protection expenditures of Swiss private economy in the previous accounting year. The units are enterprises, the monetary variables are in thousand Swiss Francs (CHF). From the original sample a random subsample was chosen of which certain enterprises were excluded for confidentiality reasons. In addition, noise has been added to certain variables, and certain categories have been collapsed. The data set has missing values. The data set has first been prepared for the EU FP5 project EUREDIT and later been data protected for educational purposes.

**Usage**

```
sepe
```

**Format**

A data frame with 675 rows and 23 variables:

**idnr** identifier (anonymous)

**exp** categorical variable where 1 = 'non-zero total expenditure' and 2 = 'zero total expenditure, and 3 = 'no answer'

**totinvwp** total investment for water protection

**totinvwm** total investment for waste management

**totinvap** total investment for air protection

**totinvnp** total investment for noise protection

**totinvot** total investment for other environmental protection

**totinvto** overall total investment in all environmental protection areas

**totexpwp** total current expenditure in environmental protection area water protection

**totexpwm** total current expenditure in environmental protection area waste management

**totexpap** total current expenditure in environmental protection area air protection

**totexpnp** total current expenditure in environmental protection area noise protection

**totexpot** total current expenditure in other environmental protection

**totexpto** overall total current expenditure in all environmental protection  
**subtot** total subsidies for environmental protection received  
**rectot** total receipts from environmental protection  
**employ** number of employees  
**sizeclass** size class (according to number of employees)  
**stratum** stratum number of sample design  
**activity** code of economic activity (aggregated)  
**popsize** number of enterprises in the population-stratum  
**popempl** number of employees in population activity group  
**weight** sampling weight (for extrapolation to the population)

### Details

The sample design is stratified random sampling with different sampling rates. Use package `survey` or `sampling` to obtain correct point and variance estimates. In addition a ratio estimator may be built using the variable `popemple` which gives the total employment per activity.

There are two balance rules: the subtotals of the investment variables should sum to `totinvto` and the expenditure subtotals should sum to `totexpto`.

The missing values stem from the survey itself. In the actual survey the missing values were declared as 'guessed' rather than copied from records.

The sampling weight `weight` is adjusted for non-response in the stratum, i.e.  $\text{weight} = \text{popsize} / \text{sampsize}$ .

### References

Swiss Federal Statistical Office (1996), *Umweltausgaben und -investitionen in der Schweiz 1992/1993, Ergebnisse einer Pilotstudie*.

Charlton, J. (ed.), *Towards Effective Statistical Editing and Imputation Strategies - Findings of the Euredit project*, unpublished manuscript available from Eurostat and <http://www.cs.york.ac.uk/euredit/>.

### Examples

```
data(sepe)
```

---

TRC

*Transformed rank correlations for multivariate outlier detection*

---

### Description

TRC starts from bivariate Spearman correlations and obtains a positive definite covariance matrix by back-transforming robust univariate medians and mads of the eigenspace. TRC can cope with missing values by a regression imputation using the a robust regression on the best predictor and it takes sampling weights into account.

**Usage**

```
TRC(data, weights, overlap = 3, mincor = 0, robust.regression = "rank",
     gamma = 0.5, prob.quantile = 0.75, alpha = 0.05, md.type = "m",
     monitor = FALSE)
```

**Arguments**

<code>data</code>	a data frame or matrix with the data.
<code>weights</code>	sampling weights.
<code>overlap</code>	minimum number of jointly observed values for calculating the rank correlation.
<code>mincor</code>	minimal absolute correlation to impute.
<code>robust.regression</code>	type of regression: "irls" is iteratively reweighted least squares M-estimator, "rank" is based on the rank correlations.
<code>gamma</code>	minimal number of jointly observed values to impute.
<code>prob.quantile</code>	if mads are 0, try this quantile of absolute deviations.
<code>alpha</code>	(1 - alpha) Quantile of F-distribution is used for cut-off.
<code>md.type</code>	type of Mahalanobis distance when missing values occur: "m" marginal (default), "c" conditional.
<code>monitor</code>	if TRUE, verbose output.

**Details**

TRC is similar to a one-step OGK estimator where the starting covariances are obtained from rank correlations and an ad hoc missing value imputation plus weighting is provided.

**Value**

TRC returns a list whose first component output is a sublist with the following components:

<code>sample.size</code>	Number of observations
<code>number.of.variables</code>	Number of variables
<code>number.of.missing.items</code>	Number of missing values
<code>significance.level</code>	1 - alpha
<code>computation.time</code>	Elapsed computation time
<code>medians</code>	Componentwise medians
<code>mads</code>	Componentwise mads
<code>center</code>	Location estimate
<code>scatter</code>	Covariance estimate
<code>robust.regression</code>	Input parameter
<code>md.type</code>	Input parameter
<code>cutpoint</code>	The default threshold MD-value for the cut-off of outliers

The further components returned by TRC are:

<code>outind</code>	Indicator of outliers
<code>dist</code>	Mahalanobis distances (with missing values)

**Author(s)**

Beat Hulliger

**References**

Béguin, C. and Hulliger, B. (2004) Multivariate outlier detection in incomplete survey data: the epidemic algorithm and transformed rank correlations, JRSS-A, 167, Part 2, pp. 275-294.

**Examples**

```
data(bushfirem, bushfire.weights)
det.res <- TRC(bushfirem, weights = bushfire.weights)
PlotMD(det.res$dist, ncol(bushfirem))
print(det.res)
```

---

weighted.quantile      *Quantiles of a weighted cdf*

---

**Description**

A weighted cdf is calculated and quantiles are evaluated. Missing values are discarded.

**Usage**

```
weighted.quantile(x, w, prob = 0.5, plot = FALSE)
```

**Arguments**

x	a vector of data.
w	a vector of (sampling) weights.
prob	the probability for the quantile.
plot	if TRUE, the weighted cdf is plotted.

**Details**

Weighted linear interpolation in case of non-unique inverse. Gives a warning when the contribution of the weight of the smallest observation to the total weight is larger than prob.

**Value**

The quantile according to prob (by default it returns the weighted median).

**Note**

No variance calculation.

**Author(s)**

Beat Hulliger

**See Also**[svyquantile](#)**Examples**

```
x <- rnorm(100)
x[sample(1:100, 20)] <- NA
w <- rchisq(100, 2)
weighted.quantile(x, w, 0.2, TRUE)
```

---

 weighted.var

*Weighted univariate variance coping with missing values*


---

**Description**

This function is analogous to `weighted.mean`.

**Usage**

```
weighted.var(x, w, na.rm = FALSE)
```

**Arguments**

`x` a vector of data.  
`w` a vector of positive weights (may not have missings where `x` is observed).  
`na.rm` if TRUE remove missing values.

**Details**

The weights are standardised such that  $\sum_{observed} w_i$  equals the number of observed values in  $x$ . The function calculates

$$\sum_{observed} w_i (x_i - \text{weighted.mean}(x, w, na.rm = TRUE))^2 / ((\sum_{observed} w_i) - 1)$$

**Value**

The weighted variance of `x` with weights `w` (with missing values removed when `na.rm = TRUE`).

**Author(s)**

Beat Hulliger

**See Also**[weighted.mean](#)**Examples**

```
x <- rnorm(100)
x[sample(1:100, 20)] <- NA
w <- rchisq(100, 2)
weighted.var(x, w, na.rm = TRUE)
```

Winsimp

*Winsorization followed by imputation***Description**

Winsorization of outliers according to the Mahalanobis distance followed by an imputation under the multivariate normal model. Only the outliers are winsorized. The Mahalanobis distance MD-miss allows for missing values.

**Usage**

```
Winsimp(data, center, scatter, outind, seed = 1000003)
```

**Arguments**

data	a data frame with the data.
center	(robust) estimate of the center (location) of the observations.
scatter	(robust) estimate of the scatter (covariance-matrix) of the observations.
outind	logical vector indicating outliers with 1 or TRUE for outliers.
seed	seed for random number generator.

**Details**

It is assumed that center, scatter and outind stem from a multivariate outlier detection algorithm which produces robust estimates and which declares outliers observations with a large Mahalanobis distance. The cutpoint is calculated as the least (unsquared) Mahalanobis distance among the outliers. The winsorization reduces the weight of the outliers:

$$\hat{y}_i = \mu_R + (y_i - \mu_R) \cdot c/d_i$$

where  $\mu_R$  is the robust center and  $d_i$  is the (unsquared) Mahalanobis distance of observation  $i$ .

**Value**

Winsimp returns a list whose first component output is a sublist with the following components:

cutpoint Cutpoint for outliers

proc.time Processing time

n.missing.before Number of missing values before imputation

n.missing.after Number of missing values after imputation

The further component returned by winsimp is:

imputed.data Imputed data set

**Author(s)**

Beat Hulliger

**References**

Hulliger, B. (2007), Multivariate Outlier Detection and Treatment in Business Surveys, Proceedings of the III International Conference on Establishment Surveys, Montréal.

**See Also**

[MDmiss](#). Uses [imp.norm](#).

**Examples**

```
data(bushfirem, bushfire.weights)
det.res <- TRC(bushfirem, weight = bushfire.weights)
imp.res <- Winsimp(bushfirem, det.res$output$center, det.res$output$scatter, det.res$outind)
print(imp.res$output)
```



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