

Package ‘fsdaR’

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Title Robust Data Analysis Through Monitoring and Dynamic Visualization

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Description Provides interface to the 'MATLAB' toolbox 'Flexible Statistical Data Analysis (FSDA)' which is a comprehensive and computationally efficient software package for robust statistics in regression, multivariate and categorical data analysis. The current R version implements tools for regression: (forward search, S- and MM-estimation, least trimmed squares (LTS) and least median of squares (LMS)), for multivariate analysis (forward search, S- and MM-estimation), for cluster analysis and cluster-wise regression. The distinctive feature of our package is the possibility of monitoring the statistics of interest as function of breakdown point, efficiency or subset size, depending on the estimator. This is accompanied by a rich set of graphical features, such as dynamic brushing, linking, particularly useful for exploratory data analysis.

Depends R (>= 3.5.0), rrcov

Imports rJava, methods, stats4, ggplot2

Suggests MASS

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LazyLoad yes

LazyData yes

License GPL (>= 2)

Author Valentin Todorov [aut, cre] (<<https://orcid.org/0000-0003-4215-0245>>),
Emmanuele Sordini [aut],
Aldo Corbellini [ctb],
Francesca Torti [ctb],
Marco Riani [ctb],
Domenico Perrotta [ctb],
Andrea Cerioli [ctb]

Maintainer Valentin Todorov <valentin.todorov@chello.at>

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carbikplot	<i>Produces the carbike plot to find best relevant clustering solutions obtained by <code>tclustICsol</code></i>
------------	--

Description

Takes as input the output of function `tclustICsol` (that is a structure containing the best relevant solutions) and produces the car-bike plot. This plot provides a concise summary of the best relevant solutions. This plot shows on the horizontal axis the value of c and on the vertical axis the value of k . For each solution we draw a rectangle for the interval of values for which the solution is best and stable and a horizontal line which departs from the rectangle for the values of c in which the solution is only stable. Finally, for the best value of c associated to the solution, we show a circle with two numbers, the first number indicates the ranked solution among those which are not spurious and the second one the ranked number including the spurious solutions. This plot has been baptized 'car-bike', because the first best solutions (in general 2 or 3) are generally best and stable for a large number of values of c and therefore will have large rectangles. In addition, these solutions are likely to be stable for additional values of c and therefore are likely to have horizontal lines departing from the rectangles (from here the name 'cars'). Finally, local minor solutions (which are associated with particular values of c and k) do not generally present rectangles or lines and are shown with circles (from here the name 'bikes').

Usage

```
carbikplot(out, SpuriousSolutions = FALSE, trace = FALSE, ...)
```

Arguments

out	An S3 object of class <code>tclusticsol.object</code> , (output of <code>tclustICsol</code>) containing the relevant solutions.
SpuriousSolutions	Whether to include or not spurious solutions. By default spurious solutions are not included into the plot.
trace	Whether to print intermediate results. Default is <code>trace=FALSE</code> .
...	potential further arguments passed to lower level functions.

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Ceroli, A., Garcia-Escudero, L.A., Mayo-Iscar, A. and Riani M. (2017). Finding the Number of Groups in Model-Based Clustering via Constrained Likelihoods, *Journal of Computational and Graphical Statistics*, pp. 404-416, <https://doi.org/10.1080/10618600.2017.1390469>.

Examples

```
## Not run:
data(geyser2)
out <- tclustIC(geyser2, whichIC="MIXMIX", plot=FALSE, alpha=0.1)

## Plot first two best solutions using as Information criterion MIXMIX
print("Best solutions using MIXMIX")
outMIXMIX <- tclustICsol(out, whichIC="MIXMIX", plot=TRUE, NumberOfBestSolutions=2)

print(outMIXMIX$MIXMIXbs)

carbikeplot(outMIXMIX)

## End(Not run)
```

corfwdplot

Monitoring the correlations between consecutive distances or residuals

Description

Provides a method for obtaining the maximum empirical efficiency (in case of MM estimates) or maximum empirical breakdownplot (in case of S estimates) or maximum subset size (in case of forward search), using various measures of correlation between the n Mahalanobis distances or residuals at adjacent values of efficiency, breakdown point or subset size.

Usage

```
corfwdplot(out, trace = FALSE, ...)
```

Arguments

out An object of S3 class returned by one of the estimation functions with the monitoring option selected (`monitoring=TRUE`): `fsreda.object`, `sregeda.object`, `mmregeda.object`, `fsmeda.object`, `smulteda.object` or `mmmulteda.object`. This is a list containing the monitoring of minimum Mahalanobis distance in case of multivariate analysis or the monitoring of residuals in case of regression. The needed elements of `out` are

1. MAL: matrix containing the squared Mahalanobis distances monitored in each step of the forward search. Every row is associated with a unit (row of data matrix Y). This matrix can be created using one of the functions `fsmult`, `smult` or `mmmult` with the monitoring option selected, i.e. `monitoring=TRUE`.
2. RES: matrix containing the residuals monitored in each step of the forward search. Every row is associated with a unit (row of data matrix Y). This matrix can be created using the function `fsreg` with the monitoring option selected, i.e. `monitoring=TRUE`.
3. bdp: a vector containing breakdown point values that have been used, in case of S estimates.
4. eff: a vector containing efficiency values that have been used, in case of MM estimates.

trace Whether to print intermediate results. Default is `trace=FALSE`.

... potential further arguments passed to lower level functions.

Value

A ggplot plot object which can be printed on screen or to a file.

Author(s)

FSDA team, <valentin.todorov@chello.at>

Examples

```
## Not run:

data(hbk)
(out <- fsmult(hbk[,1:3], monitoring=TRUE))
corfwdplot(out)

(out <- fsmult(hbk[,1:3], monitoring=TRUE))
corfwdplot(out)

(out1 <- smult(hbk, monitoring=TRUE, trace=TRUE))
corfwdplot(out1)
```

```
(out2 <- mmmult(hbk[,1:3], monitoring=TRUE, trace=TRUE))
corfwdplot(out2)

(out3 <- fsreg(hbk[,1:3], hbk[,4], monitoring=TRUE, trace=TRUE, method="FS"))
corfwdplot(out3)

(out4 <- fsreg(hbk[,1:3], hbk[,4], monitoring=TRUE, trace=TRUE, method="S"))
corfwdplot(out4)

(out5 <- fsreg(hbk[,1:3], hbk[,4], monitoring=TRUE, trace=TRUE, method="MM"))
corfwdplot(out5)

## End(Not run)
```

diabetes

Diabetes data

Description

The diabetes dataset, introduced by Reaven and Miller (1979), consists of 145 observations (patients). For each patient three measurements are reported: plasma glucose response to oral glucose, plasma insulin response to oral glucose, degree of insulin resistance.

Usage

```
data("diabetes")
```

Format

A data frame with the following variables:

glucose Area under plasma glucose curve after a three hour oral glucose tolerance test (OGTT).

insulin Area under plasma insulin curve after a three hour oral glucose tolerance test (OGTT).

sspg Steady state plasma glucose.

class The type of diabete: Normal, Overt, and Chemical.

Source

Reaven, G. M. and Miller, R. G. (1979). An attempt to define the nature of chemical diabetes using a multidimensional analysis. *Diabetologia* 16:17-24.

Examples

```
data(diabetes)
head(diabetes)
plot(CovMcd(diabetes[, 1:3]), which="pairs", col=diabetes$class)
```

emilia2001	<i>Demographic data from the 341 municipalities in Emilia Romagna (an Italian region).</i>
------------	--

Description

A data set containing 28 demographic variables for 341 municipalities in Emilia Romagna (an Italian region).

Usage

```
data(emilia2001)
```

Format

A data frame with 341 rows and 28 variables. The variables are as follows:

- less10: population aged less than 10
- more75: population aged more than 75
- single: single-member families
- divorced": divorced
- widows: widows and widowers
- graduates: population aged more than 25 who are graduates
- no_education: of those aged over 6 having no education
- employed: activity rate
- unemployed: unemployment rate
- increase_popul: standardised natural increase in population
- migration: standardised change in population due to migration
- birth_92_94: average birth rate over 1992-94
- fecundity: three-year average birth rate amongst women of child-bearing age
- houses: occupied houses built since 1982
- houses_2WCs: occupied houses with 2 or more WCs
- houses_heating: occupied houses with fixed heating system
- TV: TV licence holders
- cars: number of cars for 100 inhabitants
- luxury_cars: luxury cars
- hotels: working in hotels and restaurants
- banking: working in banking and finance
- income: average declared income amongst those filing income tax returns
- income_tax_returns: inhabitants filing income tax returns

- factories: residents employed in factories and public services
- factories_more10: employees employed in factories withy more tha 10 employees
- factories_more50: employees employed in factories withy more tha 50 employees
- artisanal: artisanal enterprises
- entrepreneurs: enterpreneous and skilled self-employed among those of working age

@references Atkinson, A. C., Riani, M., and Cerioli, A. (2004). *Exploring Multivariate Data with the Forward Search*. Springer-Verlag, New York.

fsdalms.object

Description of fsdalms Objects

Description

An object of class `fsdalms.object` holds information about the result of a call to `fsreg`.

Value

The object itself is basically a `list` with the following components:

<code>rew</code>	If <code>rew=TRUE</code> all subsequent output refers to reweighted else no reweighting is done.
<code>beta</code>	p-by-1 vector containing the estimated regression parameters.
<code>bs</code>	p x 1 vector containing the units forming subset associated with bLMS (bLTS).
<code>residuals</code>	residuals.
<code>scale</code>	scale estimate of the residuals.
<code>weights</code>	Vector like <code>y</code> containing weights. The elements of this vector are 0 or 1. These weights identify the <code>h</code> observations which are used to compute the final LTS (LMS) estimate. <code>sum(weights)=h</code> if there is not a perfect fit otherwise <code>sum(weights)</code> can be greater than <code>h</code>
<code>h</code>	The number of observations that have determined the LTS (LMS) estimator, i.e. the value of <code>h</code> .
<code>outliers</code>	vector containing the list of the units declared as outliers using confidence level specified in input scalar <code>conflev</code> .
<code>conflev</code>	confidence level which is used to declare outliers. Remark: <code>conflev</code> will be used to draw the horizontal lines (confidence bands) in the plots. Default value is 0.975
<code>singsub</code>	Number of subsets wihtout full rank. Notice that if this number is greater than $0.1 * (\text{number of subsamples})$ a warning is produced
<code>X</code>	the data matrix <code>X</code>
<code>y</code>	the response vector <code>y</code>

The object has class "`fsdalms`".

Examples

```
## Not run:
  (out <- fsreg(Y~., data=hbk, method="LMS"))
  class(out)
  summary(out)

## End(Not run)
```

fsdalts.object	<i>Description of fsdalts Objects</i>
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Description

An object of class `fsdalts.object` holds information about the result of a call to `fsreg`.

Value

The object itself is basically a `list` with the following components:

rew	If rew=TRUE all subsequent output refers to reweighted else no reweighting is done.
beta	p-by-1 vector containing the estimated regression parameters.
bs	p x 1 vector containing the units forming subset associated with bLMS (bLTS).
residuals	residuals.
scale	scale estimate of the residuals.
weights	Vector like y containing weights. The elements of this vector are 0 or 1. These weights identify the h observations which are used to compute the final LTS (LMS) estimate. $\text{sum}(\text{weights})=h$ if there is not a perfect fit otherwise $\text{sum}(\text{weights})$ can be greater than h
h	The number of observations that have determined the LTS (LMS) estimator, i.e. the value of h.
outliers	vector containing the list of the units declared as outliers using confidence level specified in input scalar conflev.
conflev	confidence level which is used to declare outliers. Remark: conflev will be used to draw the horizontal lines (confidence bands) in the plots. Default value is 0.975
singsub	Number of subsets without full rank. Notice that if this number is greater than $0.1 * (\text{number of subsamples})$ a warning is produced
X	the data matrix X
y	the response vector y

The object has class "fsdalts".

Examples

```
## Not run:
  (out <- fsreg(Y~., data=hbk, method="LTS"))
  class(out)
  summary(out)

## End(Not run)
```

fsmeda.object	<i>Description of fsmeda.object Objects</i>
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Description

An object of class `fsmeda.object` holds information about the result of a call to `fsmult` when called with parameter `monitoring=TRUE`.

Value

The object itself is basically a `list` with the following components:

MAL	n x (n-init+1) matrix containing the monitoring of Each row represents the distance Mahalanobis distance for the corresponding unit.
BB	n x (n-init+1) matrix containing the information about the units belonging to the subset at each step of the forward search. The first column contains the indexes of the units forming subset in the initial step and each further column - the indexes of the units forming the corresponding step. The last column contains the units forming subset in the final step (all units).
md	n-by-1 vector containing the estimates of the robust Mahalanobis distances (in squared units). This vector contains the distances of each observation from the location of the data, relative to the scatter matrix cov.
mmd	(n-init) x 3 matrix. which contains the monitoring of minimum MD or (m+1)th ordered MD at each step of the forward search. <ul style="list-style-type: none"> • 1st column = fwd search index (from init to n-1) • 2nd column = minimum MD • 3rd column = (m+1)th-ordered MD
msr	(n-init+1) x 3 matrix which contains the monitoring of maximum MD or m-th ordered MD at each step of the forward search. <ul style="list-style-type: none"> • 1st column = fwd search index (from init to n) • 2nd column = maximum MD • 3rd column = mth-ordered MD
gap	(n-init+1) x 3 matrix which contains the monitoring of the gap (difference between minMD outside subset and max inside). <ul style="list-style-type: none"> • 1st column = fwd search index (from init to n) • 2nd column = min MD - max MD

	<ul style="list-style-type: none"> • 3rd column = (m+1)th-ordered MD - mth ordered distance
Loc	(n-init+1) x (p+1) matrix which contains the monitoring of the estimated means at each step of the fwd search.
S2cov	(n-init+1) x (p*(p+1)/2+1) matrix which contains the monitoring of the elements of the covariance matrix in each step of the forward search. <ul style="list-style-type: none"> • 1st column = fwd search index (from init to n) • 2nd column = monitoring of S[1,1] • 3rd column = monitoring of S[1,2] • ... • last column = monitoring of S[p,p]
detS	(n-init+1) x 2 matrix which contains the monitoring of the determinant of the covariance matrix in each step of the forward search.
Un	(n-init)-by-11 matrix which contains the unit(s) included in the subset at each step of the fwd search. REMARK: in every step the new subset is compared with the old subset. Un contains the unit(s) present in the new subset but not in the old one. Un[1 ,2] for example contains the unit included in step init+1. Un[end, 2] contains the units included in the final step of the search.
X	the data matrix X

The object has class "fsmmeda".

Examples

```
## Not run:
  (out <- fsmult(hbk[,1:3], monitoring=TRUE))
  class(out)
  summary(out)

## End(Not run)
```

fsmmdrs

Performs random start monitoring of minimum Mahalanobis distance

Description

The trajectories originate from many different random initial subsets and provide information on the presence of groups in the data. Groups are investigated by monitoring the minimum Mahalanobis distance outside the forward search subset.

Usage

```
fsmmdrs(x, plot = FALSE, init, bsbsteps, nsimul = 200,
  nocheck = FALSE, numpool, cleanpool = FALSE, msg = FALSE,
  trace = FALSE, ...)
```

Arguments

x	<p>An $n \times p$ data matrix (n observations and p variables). Rows of x represent observations, and columns represent variables.</p> <p>Missing values (NA's) and infinite values (Inf's) are allowed, since observations (rows) with missing or infinite values will automatically be excluded from the computations.</p>
plot	<p>Plots the random starts minimum Mahalanobis distance with 1. If <code>plot=FALSE</code> (default) or <code>plot=0</code> no plot is produced. The scale (<code>ylim</code>) for the y axis is defined as follows:</p> <ul style="list-style-type: none"> • <code>ylim[2]</code> is the maximum between the values of <code>mmd</code> in steps $[n \cdot 0.2 \ n]$ and the final value of the 99 per cent envelope multiplied by 1.1. • <code>ylim[1]</code> is the minimum between the values of <code>mmd</code> in steps $[n \cdot 0.2 \ n]$ and the 1 per cent envelope multiplied by 0.9. <p>Remark: the plot which is produced is very simple. In order to control a series of options in this plot (including the y scale) and in order to connect it dynamically to the other forward plots it is necessary to use function <code>mmdrsplot</code>.</p>
init	<p>Point where to start monitoring required diagnostics. If <code>init</code> is not specified it will be set equal to $(p+1)$.</p>
bsbsteps	<p>A vector which specifies for which steps of the forward search it is necessary to save the units forming subset for each random start. if <code>bsbsteps = 0</code> for each random start we store the units forming subset in all steps. The default is store the units forming subset in all steps if $n \leq 500$ else to store the units forming subset at step <code>init</code> and steps which are multiple of 100. For example, if $n = 753$ and <code>init = 6</code>, units forming subset are stored for $m = \text{init}, 100, 200, 300, 400, 500$ and 600.</p> <p>REMARK: The vector <code>bsbsteps</code> must contain numbers from <code>init</code> to n. if $\min(\text{bsbsteps}) < \text{init}$ a warning message will be issued.</p>
nsimul	<p>Number of random starts. Default value is <code>nsimul=200</code>.</p>
nocheck	<p>It controls whether to perform checks on matrix Y. If <code>nocheck=TRUE</code>, no check is performed.</p>
numpool	<p>If <code>numpool > 1</code>, the routine automatically checks if the Parallel Computing Toolbox is installed and distributes the random starts over <code>numpool</code> parallel processes. If <code>numpool <= 1</code>, the random starts are run sequentially. By default, <code>numpool</code> is set equal to the number of physical cores available in the CPU (this choice may be inconvenient if other applications are running concurrently). The same happens if the <code>numpool</code> value chosen by the user exceeds the available number of cores.</p> <p>REMARK: up to R2013b, there was a limitation on the maximum number of cores that could be addressed by the parallel processing toolbox (8 and, more recently, 12). From R2014a, it is possible to run a local cluster of more than 12 workers.</p> <p>REMARK: Unless you adjust the cluster profile, the default maximum number of workers is the same as the number of computational (physical) cores on the machine.</p>

REMARK: In modern computers the number of logical cores is larger than the number of physical cores. By default, MATLAB is not using all logical cores because, normally, hyper-threading is enabled and some cores are reserved to this feature.

REMARK: It is because of Remarks 3 that we have chosen as default value for `numpool` the number of physical cores rather than the number of logical ones. The user can increase the number of parallel pool workers allocated to the multiple start monitoring by:

- setting the `NumWorkers` option in the local cluster profile settings to the number of logical cores (Remark 2). To do so go on the menu *Home\Parallel\Manage Cluster Profile* and set the desired "Number of workers to start on your local machine".
- setting `numpool` to the desired number of workers

Therefore, *if a parallel pool is not already open*, `UserOption numpool` (if set) overwrites the number of workers set in the local/current profile. Similarly, the number of workers in the local/current profile overwrites default value of `numpool` obtained as `feature('numCores')` (i.e. the number of physical cores).

<code>cleanpool</code>	Set <code>cleanpool cleanpool=TRUE</code> if the parallel pool has to be cleaned after the execution of the random starts. Otherwise (default) <code>cleanpool=FALSE</code> . Clearly this option has an effect just if previous option <code>numpool > 1</code> .
<code>msg</code>	Level of output to <code>sidplay</code> . It controls whether to display or not messages about random start progress. More precisely, if previous option <code>numpool > 1</code> , then a progress bar is displayed, on the other hand a message will be displayed on the screen when 10 REMARK: in order to create the progress bar when <code>nparpool > 1</code> the program writes on a temporary <code>.txt</code> file in the folder where the user is working. Therefore it is necessary to work in a folder where the user has write permission. If this is not the case and the user (say) is working without write permission in folder <code>C:/Program Files/MATLAB</code> the following message will appear on the screen: <i>Error using ProgressBar (line 57) Do you have write permissions for C:/Program Files/MATLAB?"</i>
<code>trace</code>	Whether to print intermediate results. Default is <code>trace=FALSE</code> .
<code>...</code>	potential further arguments passed to lower level functions.

Value

Returns an object of class `fsmmdrs.object`.

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Atkinson, A.C., Riani, M., and Cerioli, A. (2006), Random Start Forward Searches with Envelopes for Detecting Clusters in Multivariate Data, in: Zani S., Cerioli A., Riani M., Vichi M., Eds., *Data Analysis, Classification and the Forward Search*, pp. 163-172, Springer Verlag.

Atkinson, A.C. and Riani, M., (2007), Exploratory Tools for Clustering Multivariate Data, *Computational Statistics and Data Analysis*, Vol. 52, pp. 272-285, doi:10.1016/j.csda.2006.12.034

Riani, M., Cerioli, A., Atkinson, A.C., Perrotta, D. and Torti, F. (2008), Fitting Mixtures of Regression Lines with the Forward Search, in: *Mining Massive Data Sets for Security*, F. Fogelman-Soulie et al. Eds., pp. 271-286, IOS Press.

Examples

```
## Not run:
data(hbk)
out <- fsmmdrs(hbk[,1:3])
class(out)
summary(out)

## End(Not run)
```

fsmmdrs.object	<i>Description of fsmmdrs.object Objects</i>
----------------	--

Description

An object of class `fsmmdrs.object` holds information about the result of a call to `fsmmdrs`.

Value

The object itself is basically a `list` with the following components:

mmdrs	<p>Minimum Mahalanobis distance, (n-init) by (nsimul+1) matrix which contains the monitoring of minimum Mahalanobis distance at each step of the forward search.</p> <ul style="list-style-type: none"> • 1st column = fwd search index (from init to n-1) • 2nd column = minimum Mahalanobis distance for random start 1 • 3rd column... • nsimul+1 column minimum Mahalanobis distance for random start nsimul
BBrs	<p>Units belonging to the subset at the steps specified by input option bsbsteps. If bsbsteps=0 BBrS has size n-by-(n-init+1)-by-nsimul. In this case BBrS[, , j] with j=1, 2, ..., nsimul has the following structure:</p> <ul style="list-style-type: none"> • 1st row = has number 1 in correspondence of the steps in which unit 1 is included inside subset and a missing value for the other steps • ... • (n-1)-th row= has number n-1 in correspondence of the steps in which unit n-1 is included inside subset and a missing value for the other steps • n-th row= has the number n in correspondence of the steps in which unit n is included inside subset and a missing value for the other steps

If, on the other hand, `bsbsteps` is a vector which specifies the steps of the search in which it is necessary to store subset, `BBr`s has size `n-by-length(bsbsteps)-by-nsimul`. In other words, `BBr`s[, , j] with `j=1, 2, ..., nsimul` has the same structure as before, but now contains just `length(bsbsteps)` columns.

`X` the data matrix `X`

The object has class "fsmmdrs".

Examples

```
## Not run:

out <- fsmmdrs(hbk[,1:3])
class(out)
summary(out)

## End(Not run)
```

fsmult	<i>Gives an automatic outlier detection procedure in multivariate analysis</i>
--------	--

Description

Gives an automatic outlier detection procedure in multivariate analysis and performs forward search in multivariate analysis with exploratory data

Usage

```
fsmult(x, bsb, monitoring = FALSE, crit = c("md", "biv", "uni"),
       rf = 0.95, init, plot = FALSE, bonflev, msg = TRUE,
       nocheck = FALSE, scaled = FALSE, trace = FALSE, ...)
```

Arguments

<code>x</code>	An <code>n x p</code> data matrix (<code>n</code> observations and <code>p</code> variables). Rows of <code>x</code> represent observations, and columns represent variables. Missing values (NA's) and infinite values (Inf's) are allowed, since observations (rows) with missing or infinite values will automatically be excluded from the computations.
<code>bsb</code>	List of units forming the initial subset or size of the initial subset. If <code>monitoring=FALSE</code> the default is to start the search with <code>p+1</code> units, containing those observations which are not outlying on any scatterplot, found as the intersection of all points lying within a robust contour containing a specified portion of the data (Riani and Zani 1997) and inside the univariate boxplot. Remark: if <code>bsb</code> is a vector, the option <code>crit</code> is ignored.

monitoring	Whether to perform monitoring of Mahalanobis distances and other specific quantities
crit	<p>If specified, the criterion to be used to initialize the search.</p> <ul style="list-style-type: none"> • If <code>crit="md"</code> the units which form initial subset are those which have the smallest m_0 pseudo Mahalanobis distances computed using procedure <code>unibiv()</code> (bivariate robust ellipses). • If <code>crit="biv"</code> sorting is done first in terms of times units fell outside robust bivariate ellipses and then in terms of <code>pseudoMD</code>. In other words, the units forming initial subset are chosen first among the set of those which never fell outside robust bivariate ellipses then among those which fell only once outside bivariate ellipses ... up to reach m_0. • If <code>crit="uni"</code> sorting is done first in terms of times units fell outside univariate boxplots and then in terms of <code>pseudoMD</code>. In other words, the units forming initial subset are chosen first among the set of those which never fell outside univariate boxplots then among those which fell only once outside univariate boxplots... up to reach m_0. <p>Remark: as the user can see the starting point of the search is not going to affect at all the results of the analysis. The user can explore this point with his own datasets.</p> <p>Remark: if <code>crit="biv"</code> the user can also supply in scalar <code>rf</code> (see below) the confidence level of the bivariate ellipses.</p>
rf	Confidence level for bivariate ellipses. The default is 0.95. This option is useful only if <code>crit='biv'</code> .
init	Point where to start monitoring required diagnostics. Note that if a vector m_0 is supplied, <code>init >= length(m0)</code> . If <code>init</code> is not specified it will be set equal to <code>floor(n*0.6)</code> .
plot	<p>Plots the minimum Mahalanobis distance. If <code>plot=FALSE</code> (default) or <code>plot=0</code> no plot is produced. If <code>plot=TRUE</code> the plot of minimum MD with envelopes based on <code>n</code> observations and the scatterplot matrix with the outliers highlighted is produced. If <code>plot=2</code> the additional plots of envelope resuperimposition are produced. If <code>plot</code> is a list it may contain the following fields:</p> <ul style="list-style-type: none"> • <code>yylim</code> vector with two elements controlling minimum and maximum on the y axis. Default value is "" (automatic scale) • <code>xylim</code> vector with two elements controlling minimum and maximum on the x axis. Default value is "" (automatic scale) • <code>resuper</code> vector which specifies for which steps it is necessary to show the plots of resuperimposed envelopes if <code>resuper</code> is not supplied a plot of each step in which the envelope is resuperimposed is shown. Example: if <code>resuper = c(85 87)</code> plots of resuperimposedenvelopes are shown at steps <code>m=85</code> and <code>m=87</code> • <code>ncoord</code> If <code>ncoord=1</code> plots are shown in normal coordinates else (default) plots are shown in traditional <code>mmd</code> coordinates • <code>labeladd</code> If <code>labeladd=1</code>, the outliers in the <code>spm</code> are labelled with the unit row index. The default value is <code>labeladd=""</code>, i.e. no label is added • <code>nameY</code> character vector containing the labels of the variables. As default value, the labels which are added are <code>Y1, ... Yp</code>.

- `lwd` controls line width of the curve which contains the monitoring of minimum Mahalanobis distance. Default is `lwd=2`.
- `lwdenv` Controls linewidth of the envelopes. Default is `lwdenv=2`.

`bonflev` Option that might be used to identify extreme outliers when the distribution of the data is strongly non normal. In these circumstances, the general signal detection rule based on consecutive exceedances cannot be used. In this case `bonflev` can be:

1. a scalar smaller than 1, which specifies the confidence level for a signal and a stopping rule based on the comparison of the minimum deletion residual with a Bonferroni bound. For example if `bonflev=0.99` the procedure stops when the trajectory exceeds for the first time the 99 per cent bonferroni bound.
2. a scalar value greater than 1. In this case the procedure stops when the residual trajectory exceeds for the first time this value.

Default value is empty, which means to rely on general rules based on consecutive exceedances.

`msg` It controls whether to display or not messages on the screen. If `msg=TRUE` (default) messages about the progression of the search are displayed on the screen otherwise only error messages will be displayed.

`nocheck` It controls whether to perform checks on matrix `Y`. If `nocheck=TRUE`, no check is performed.

`scaled` Controls whether to monitor scaled Mahalanobis distances (only if `monitoring=TRUE`). If `scaled=TRUE` Mahalanobis distances monitored during the search are scaled using ratio of determinant. If `scaled=2` Mahalanobis distances monitored during the search are scaled using asymptotic consistency factor. The default is `scaled=FALSE`, that is Mahalanobis distances are not scaled.

`trace` Whether to print intermediate results. Default is `trace=FALSE`.

... potential further arguments passed to lower level functions.

Value

Depending on the input parameter `monitoring`, one of the following objects will be returned:

1. `fsmult.object`
2. `fsmeda.object`

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

- Riani, M., Atkinson A.C., Cerioli A. (2009). Finding an unknown number of multivariate outliers. *Journal of the Royal Statistical Society Series B*, Vol. 71, pp. 201-221.
- Cerioli A., Farcomeni A., Riani M., (2014). Strong consistency and robustness of the Forward Search estimator of multivariate location and scatter, *Journal of Multivariate Analysis*, Vol. 126, pp. 167-183, <http://dx.doi.org/10.1016/j.jmva.2013.12.010>.

Atkinson Riani and Cerioli (2004), *Exploring multivariate data with the forward search* Springer Verlag, New York.

Examples

```
## Not run:

data(hbk)
(out <- fsmult(hbk[,1:3]))
class(out)
summary(out)

## Generate contaminated data (200,3)
n <- 200
p <- 3
set.seed(123456)
X <- matrix(rnorm(n*p), nrow=n)
Xcont <- X
Xcont[1:5, ] <- Xcont[1:5, ] + 3

out1 <- fsmult(Xcont, trace=TRUE)          # no plots (plot defaults to FALSE)
names(out1)

(out1 <- fsmult(Xcont, trace=TRUE, plot=TRUE))  # identical to plot=1

## plot=1 - minimum MD with envelopes based on n observations
## and the scatterplot matrix with the outliers highlighted
(out1 <- fsmult(Xcont, trace=TRUE, plot=1))

## plot=2 - additional plots of envelope resuperimposition
(out1 <- fsmult(Xcont, trace=TRUE, plot=2))

## plots is a list: plots showing envelope superimposition in normal coordinates.
(out1 <- fsmult(Xcont, trace=TRUE, plot=list(ncoord=1)))

## Choosing an initial subset formed by the three observations with
## the smallest Mahalanobis Distance.

(out1 <- fsmult(Xcont, m0=5, crit="md", trace=TRUE))

## fsmult() with monitoring
(out2 <- fsmult(Xcont, monitoring=TRUE, trace=TRUE))
names(out2)

## Monitor the exceedances from m=200 without showing plots.
n <- 1000
p <- 10
Y <- matrix(rnorm(10000), ncol=10)
(out <- fsmult(Y, init=200))

## Forgery Swiss banknotes examples.

data(swissbanknotes)
```

```

## Monitor the exceedances of Minimum Mahalanobis Distance
(out1 <- fsmult(swissbanknotes[101:200,], plot=1))

## Control minimum and maximum on the x axis
(out1 <- fsmult(swissbanknotes[101:200,], plot=list(xlim=c(60,90))))

## Monitor the exceedances of Minimum Mahalanobis Distance using
## normal coordinates for mmd.
(out1 <- fsmult(swissbanknotes[101:200,], plot=list(ncoord=1)))

## End(Not run)

```

fsmult.object	<i>Description of fsmult.object Objects</i>
---------------	---

Description

An object of class `fsmult.object` holds information about the result of a call to `fsmult`.

Value

The object itself is basically a `list` with the following components:

outliers	kx1 vector containing the list of the k units declared as outliers or NULL if the sample is homogeneous.
loc	p-by-1 vector containing location of the data.
cov	p-by-p robust estimate of covariance matrix.
md	n-by-1 vector containing the estimates of the robust Mahalanobis distances (in squared units). This vector contains the distances of each observation from the location of the data, relative to the scatter matrix cov.
mmd	(n-init)-by-2 matrix. 1st col is the forward search index; 2nd col is the value of minimum Mahalanobis Distance in each step of the fwd search.
Un	(n-init)-by-11 matrix which contains the unit(s) included in the subset at each step of the fwd search. REMARK: in every step the new subset is compared with the old subset. Un contains the unit(s) present in the new subset but not in the old one. Un[1 ,2] for example contains the unit included in step init+1. Un[end, 2] contains the units included in the final step of the search.
nout	2 x 5 matrix containing the number of times mdr went out of particular quantiles. First row contains quantiles 1 99 99.9 99.99 99.999. Second row contains the frequency distribution. It is NULL if bonflev threshold is used.
constr	This output is produced only if the search found at a certain step is a non singular matrix X. In this case the search run in a constrained mode, that is including the units which produced a singular matrix in the last n-constr steps. out.constr is a vector which contains the list of units which produced a singular X matrix.
X	the data matrix X

The object has class "fsmult".

Examples

```
## Not run:
  (out <- fsmult(hbk[,1:3]))
  class(out)
  summary(out)

## End(Not run)
```

 fsr.object

Description of fsr Objects

Description

An object of class `fsr.object` holds information about the result of a call to `fsreg`.

Value

The object itself is basically a `list` with the following components:

beta	p-by-1 vector containing the estimated regression parameters (in step n-k).
scale	scalar containing the estimate of the scale (sigma).
residuals	residuals.
fittedvalues	fitted values.
outliers	kx1 vector containing the list of the k units declared as outliers or NULL if the sample is homogeneous.
mdr	(n-init) x 2 matrix 1st col = fwd search index, 2nd col = value of minimum deletion residual in each step of the fwd search
Un	(n-init) x 11 matrix which contains the unit(s) included in the subset at each step of the fwd search. REMARK: in every step the new subset is compared with the old subset. Un contains the unit(s) present in the new subset but not in the old one. Un(1,2) for example contains the unit included in step init+1. Un(end,2) contains the units included in the final step of the search.
nout	2 x 5 matrix containing the number of times mdr went out of particular quantiles. First row contains quantiles 1 99 99.9 99.99 99.999. Second row contains the frequency distribution.
constr	This output is produced only if the search found at a certain step is a non singular matrix X. In this case the search run in a constrained mode, that is including the units which produced a singular matrix in the last n-constr steps. out.constr is a vector which contains the list of units which produced a singular X matrix.
X	the data matrix X
y	the response vector y

The object has class "fsr".

Examples

```
## Not run:
  (out <- fsreg(Y~., data=hbk, method="FS"))
  class(out)
  summary(out)

## End(Not run)
```

fsreda.object	<i>Description of fsreda Objects</i>
---------------	--------------------------------------

Description

An object of class `fsreda.object` holds information about the result of a call to `fsreg`.

Value

The object itself is basically a `list` with the following components:

RES	n x (n-init+1) matrix containing the monitoring of scaled residuals: the first row is the residual for the first unit, ..., n-th row is the residual for the n-th unit.
LEV	(n+1) x (n-init+1) matrix containing the monitoring of leverage: the first row is the leverage for the first unit, ..., n-th row is the leverage for the n-th unit.
BB	n x (n-init+1) matrix containing the information about the units belonging to the subset at each step of the forward search: first col contains indexes of the units forming subset in the initial step; ...; last column contains units forming subset in the final step (all units).
mdr	n-init x 3 matrix which contains the monitoring of minimum deletion residual or (m+1)-ordered residual at each step of the forward search: first col is the fwd search index (from init to n-1); 2nd col = minimum deletion residual; 3rd col = (m+1)-ordered residual. Remark: these quantities are stored with sign, that is the min deletion residual is stored with negative sign if it corresponds to a negative residual.
msr	n-init+1 x 3 matrix which contains the monitoring of maximum studentized residual or m-th ordered residual: first col is the fwd search index (from init to n); 2nd col = maximum studentized residual; 3rd col = (m)-ordered studentized residual.
nor	(n-init+1) x 4 matrix containing the monitoring of normality test in each step of the forward search: first col = fwd search index (from init to n); 2nd col = Asymmetry test; 3rd col = Kurtosis test; 4th col = Normality test.
Bo1s	(n-init+1) x (p+1) matrix containing the monitoring of estimated beta coefficients in each step of the forward search.
S2	(n-init+1) x 4 matrix containing the monitoring of S2 or R2 in each step of the forward search:

1. 1st col = fwd search index (from init to n);
2. 2nd col = monitoring of S2;
3. 3rd col = monitoring of R2;
4. 4th col = monitoring of rescaled S2.

In this case the estimated of s_2 at step m is divided by the consistency factor (to make the estimate asymptotically unbiased).

coo	(n-init+1) x 3 matrix containing the monitoring of Cook or modified Cook distance in each step of the forward search: <ol style="list-style-type: none"> 1. 1st col = fwd search index (from init to n); 2. 2nd col = monitoring of Cook distance; 3. 3rd col = monitoring of modified Cook distance.
Tols	(n-init+1) x (p+1) matrix containing the monitoring of estimated t-statistics (as specified in option input 'tstat') in each step of the forward search
Un	(n-init) x 11 matrix which contains the unit(s) included in the subset at each step of the fwd search. REMARK: in every step the new subset is compared with the old subset. Un contains the unit(s) present in the new subset but not in the old one Un(1,2) for example contains the unit included in step init+1 Un(end,2) contains the units included in the final step of the search.
betaINT	Confidence intervals for the elements of β . betaINT is a (n-init+1)-by-2*length(confint)-by-p 3D array. Each third dimension refers to an element of beta: <ol style="list-style-type: none"> 1. betaINT[, , 1] is associated with first element of beta; 2. ...; 3. betaINT[, , p] is associated with last element of beta. <p>The first two columns contain the lower and upper confidence limits associated with conflev(1). Columns three and four contain the lower and upper confidence limits associated with conflev(2); ...; The last two columns contain the lower and upper confidence limits associated with conflev(end). For example betaINT[, 3:4, 5] contain the lower and upper confidence limits for the fifth element of beta using confidence level specified in the second element of input option conflev.</p>
sigma2INT	confidence interval for s_2 . <ol style="list-style-type: none"> 1. 1st col = fwd search index; 2. 2nd col = lower confidence limit based on conflev(1); 3. 3rd col = upper confidence limit based on conflev(1); 4. 4th col = lower confidence limit based on conflev(2); 5. 5th col = upper confidence limit based on conflev(2); 6. ... 7. penultimate col = lower confidence limit based on conflev(end); 8. last col = upper confidence limit based on conflev(end).
X	the data matrix X
y	the response vector y

The object has class "fsreda".

Examples

```
## Not run:
(out <- fsreg(Y~., data=hbk, method="FS", monitoring=TRUE))
class(out)
summary(out)

## End(Not run)
```

FSReda_control	<i>Creates an FSReda_control object</i>
----------------	---

Description

Creates an object of class FSReda_control to be used with the fsreg() function, containing various control parameters.

Usage

```
FSReda_control(intercept = TRUE, init, nocheck = FALSE,
               tstat = c("trad", "scal"), conflev = c(0.95, 0.99))
```

Arguments

intercept	Indicator for constant term. Scalar. If intercept=TRUE, a model with constant term will be fitted (default), else, no constant term will be included.
init	Search initialization, scalar. It specifies the initial subset size to start monitoring exceedances of minimum deletion residual, if init is not specified it set equal to: $p+1$, if the sample size is smaller than 40 or $\min(3*p+1, \text{floor}(0.5*(n+p+1)))$, otherwise. For example, if $\text{init}=100$, the procedure starts monitoring from step $m=100$.
nocheck	Check input arguments, scalar. If nocheck=TRUE no check is performed on matrix y and matrix X . Notice that y and X are left unchanged. In other words the additional column of ones for the intercept is not added. As default nocheck=FALSE.
tstat	The kind of t-statistics which have to be monitored. $\text{tstat}=\text{"trad"}$ implies monitoring of traditional t statistics ($\text{out}\$Tols$). In this case the estimate of s^2 at step m is based on s^2_m (notice that $s^2_m \ll s^2$ when m/n is small) $\text{tstat}=\text{"scal"}$ (default) implies monitoring of rescaled t statistics. In this case the estimate of s^2 at step m is based on $s^2_m/\text{vartruncnorm}(m/n)$ where $\text{vartruncnorm}(m/n)$ is the variance of the truncated normal distribution.
conflev	Confidence level which is used to declare units as outliers. Usually $\text{conflev}=0.95, 0.975, 0.99$ (individual alpha) or $\text{conflev}=1-0.05/n, 1-0.025/n, 1-0.01/n$ (simultaneous alpha). Default value is 0.975.

Details

Creates an object of class FSReda_control to be used with the fsreg() function, containing various control parameters.

Value

An object of class "FSReda_control" which is basically a [list](#) with components the input arguments of the function mapped accordingly to the corresponding Matlab function.

Author(s)

FSDA team

See Also

See Also as [FSR_control](#), [MMreg_control](#) and [LXS_control](#)

Examples

```
## Not run:
(out <- fsreg(Y~., data=hbk, method="FS", monitoring=TRUE,
  control=FSReda_control(tstat="scal")))

## End(Not run)
```

 fsreg

fsreg: an automatic outlier detection procedure in linear regression

Description

An automatic outlier detection procedure in linear regression

Usage

```
fsreg(x, ...)

## S3 method for class 'formula'
fsreg(formula, data, subset, weights, na.action,
  model = TRUE, x.ret = FALSE, y.ret = FALSE,
  contrasts = NULL, offset, ...)

## Default S3 method:
fsreg(x, y, bsb, intercept = TRUE,
  family = c("homo", "hetero", "bayes"),
method = c("FS", "S", "MM", "LTS", "LMS"),
  monitoring = FALSE, control,
  ...)
```


Arguments

formula	a formula of the form $y \sim x_1 + x_2 + \dots$.
data	data frame from which variables specified in formula are to be taken.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of weights to be used in the fitting process. NOT USED YET.
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options , and is na.fail if that is unset. The “factory-fresh” default is na.omit . Another possible value is NULL, no action. Value na.exclude can be useful.
model, x.ret, y.ret	logicals indicating if the model frame, the model matrix and the response are to be returned, respectively.
contrasts	an optional list. See the contrasts.arg of model.matrix.default .
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. An offset term can be included in the formula instead or as well, and if both are specified their sum is used.
family	family of robust regression models, can be 'homo' for homoscedastic (same variance) regression model, 'hetero' for heteroskedastic regression model or 'bayes' Bayesian linear regression. The default is family='homo' for homoscedastic regression model.
method	robust regression estimation model, can be 'FS' for Forward search, 'S' for S regression, 'MM' for MM regression, 'LMS' or 'LTS'. The default is method='FS' for forward search estimation.
monitoring	whether to perform monitoring for several quantities in each step of the forward search or for series of values of the breakdown point in case of S estimates or for series of values of the efficiency in case of MM estimates. Deafault is monitoring=FALSE.
y	Response variable. Vector. Response variable, specified as a vector of length n, where n is the number of observations. Each entry in y is the response for the corresponding row of X. Missing values (NA's) and infinite values (Inf's) are allowed, since observations (rows) with missing or infinite values will automatically be excluded from the computations.
x	Predictor variables. Matrix. Matrix of explanatory variables (also called 'regressors') of dimension n x (p-1) where p denotes the number of explanatory variables including the intercept. Rows of X represent observations, and columns represent variables. By default, there is a constant term in the model, unless you explicitly remove it using input option intercept=FALSE, so do not include a column of 1s in X. Missing values (NA's) and infinite values (Inf's) are allowed, since observations (rows) with missing or infinite values will automatically be excluded from the computations.
bsb	Initial subset - vector of indices. If bsb=0 (default) then the procedure starts with p units randomly chosen. If bsb is not 0 the search will start with m0=length(bsb).

intercept	Indicator for constant term. Scalar. If intercept=TRUE, a model with constant term will be fitted (default), else, no constant term will be included.
control	A control object (SS) containing estimation options. If the control object is supplied, the parameters from it will be used. If parameters are passed also in the invocation statement, they will override the corresponding elements of the control object.
...	potential further arguments passed to lower level functions.

Value

Depending on the input parameters family and method, one of the following objects will be returned:

1. `fsr.object`
2. `sreg.object`
3. `mmreg.object`
4. `fsdalms.object`
5. `fsdalts.object`
6. `fsreda.object`
7. `sregeda.object`
8. `mmregeda.object`

Author(s)

FSDA team

References

Riani, M., Atkinson A.C., Cerioli A. (2009). Finding an unknown number of multivariate outliers. *Journal of the Royal Statistical Society Series B*, Vol. 71, pp. 201-221.

Examples

```
## Not run:

n <- 200
p <- 3

X <- matrix(data=rnorm(n*p), nrow=n, ncol=p)
y <- matrix(data=rnorm(n*1), nrow=n, ncol=1)
(out = fsreg(X, y))

## Now we use the formula interface:
(out1 = fsreg(y~X, control=FSR_control(plot=FALSE)))

## Or use the variables in a data frame
(out2 = fsreg(Y~., data=hbk, control=FSR_control(plot=FALSE)))
```

```

## let us compare to the LTS solution
(out3 = ltsReg(Y~., data=hbK))

## Now compute the model without intercept
(out4 = fsreg(Y~.-1, data=hbK, control=FSR_control(plot=FALSE)))

## And compare again with the LTS solution
(out5 = ltsReg(Y~.-1, data=hbK))

## using default (optional arguments)
(out6 = fsreg(Y~.-1, data=hbK, control=FSR_control(plot=FALSE, nsamp=1500, h=50)))

## End(Not run)

```

FSR_control	<i>Creates an FSR_control object</i>
-------------	--------------------------------------

Description

Creates an object of class `FSR_control` to be used with the `fsreg()` function, containing various control parameters.

Usage

```

FSR_control(intercept = TRUE, h, nsamp = 1000, lms = 1, init, nocheck = FALSE,
            bonflev = "", msg = TRUE, bsbmfullrank = 1,
            plot = FALSE, bivarfit = "", multivarfit = "",
            labeladd = "", nameX, namey, ylim, xlim)

```

Arguments

<code>intercept</code>	Indicator for constant term. Scalar. If <code>intercept=TRUE</code> , a model with constant term will be fitted (default), else, no constant term will be included.
<code>h</code>	The number of observations that have determined the least trimmed squares estimator, scalar. <code>h</code> is an integer greater or equal than <code>p</code> but smaller than <code>n</code> . Generally if the purpose is outlier detection <code>h=[0.5*(n+p+1)]</code> (default value). <code>h</code> can be smaller than this threshold if the purpose is to find subgroups of homogeneous observations. In this function the LTS/LMS estimator is used just to initialize the search.
<code>nsamp</code>	Number of subsamples which will be extracted to find the robust estimator, scalar. If <code>nsamp=0</code> all subsets will be extracted. They will be $\binom{n}{p}$. If the number of all possible subset is < 1000 the default is to extract all subsets otherwise just 1000.
<code>lms</code>	Criterion to use to find the initial subset to initialize the search (LMS, LTS with concentration steps, LTS without concentration steps or subset supplied directly by the user). The default value is 1 (Least Median of Squares is computed to initialize the search). On the other hand, if the user wants to initialize the search

with LTS with all the default options for concentration steps then `lms=2`. If the user wants to use LTS without concentration steps, `lms` can be a scalar different from 1 or 2. If `lms` is a list it is possible to control a series of options for concentration steps (for more details see option `lms` inside `LXS_control`). If, on the other hand, the user wants to initialize the search with a prespecified set of units there are two possibilities:

1. `lms` can be a vector with length greater than 1 which contains the list of units forming the initial subset. For example, if the user wants to initialize the search with units 4, 6 and 10 then `lms=c(4,6,10)`;
2. `lms` is a struct which contains a field named `bsb` which contains the list of units to initialize the search. For example, in the case of simple regression through the origin with just one explanatory variable, if the user wants to initialize the search with unit 3 then `lms=list(bsb=3)`.

<code>init</code>	Search initialization, scalar. It specifies the initial subset size to start monitoring exceedances of minimum deletion residual, if <code>init</code> is not specified it set equal to: $p+1$, if the sample size is smaller than 40 or $\min(3*p+1, \text{floor}(0.5*(n+p+1)))$, otherwise. For example, if <code>init=100</code> , the procedure starts monitoring from step $m=100$.
<code>nocheck</code>	Check input arguments, scalar. If <code>nocheck=TRUE</code> no check is performed on matrix <code>y</code> and matrix <code>X</code> . Notice that <code>y</code> and <code>X</code> are left unchanged. In other words the additional column of ones for the intercept is not added. As default <code>nocheck=FALSE</code> .
<code>bonflev</code>	Option to be used if the distribution of the data is strongly non normal and, thus, the general signal detection rule based on consecutive exceedances cannot be used. In this case <code>bonflev</code> can be: <ol style="list-style-type: none"> 1. a scalar smaller than 1 which specifies the confidence level for a signal and a stopping rule based on the comparison of the minimum MD with a Bonferroni bound. For example if <code>bonflev=0.99</code> the procedure stops when the trajectory exceeds for the first time the 99% bonferroni bound. 2. A scalar value greater than 1. In this case the procedure stops when the residual trajectory exceeds for the first time this value. Default value is <code>"</code> , which means to rely on general rules based on consecutive exceedances.
<code>msg</code>	Controls whether to display or not messages on the screen. If <code>msg==1</code> (default) messages are displayed on the screen about step in which signal took place else no message is displayed on the screen.
<code>bsbfullrank</code>	How to behave in case subset at step <code>m</code> (say <code>bsbm</code>) produces a singular <code>X</code> . In other words, this options controls what to do when $\text{rank}(X[\text{bsbm},])$ is smaller than number of explanatory variables. If <code>bsbfullrank=1</code> (default) these units (whose number is say <code>mnofullrank</code>) are constrained to enter the search in the final $n-\text{mnofullrank}$ steps else the search continues using as estimate of beta at step <code>m</code> the estimate of beta found in the previous step.
<code>plot</code>	Plot on the screen. Scalar. If <code>plots=TRUE</code> the plot of minimum deletion residual with envelopes based on <code>n</code> observations and the scatterplot matrix with the outliers highlighted is produced. If <code>plots=2</code> the user can also monitor the intermediate plots based on envelope superimposition. If <code>plots=FALSE</code> (default) no plot is produced.

bivarfit	Whether to superimpose bivariate least square lines on the plot (if plot=TRUE. This option adds one or more least squares lines, based on SIMPLE REGRESSION of y on Xi, to the plots of y Xi. The default is bivarfit=FALSE: no line is fitted. If bivarfit=1, a single OLS line is fitted to all points of each bivariate plot in the scatter matrix y X. If bivarfit=2, two OLS lines are fitted: one to all points and another to the group of the genuine observations. The group of the potential outliers is not fitted. If bivarfit=0 one OLS line is fitted to each group. This is useful for the purpose of fitting mixtures of regression lines. If bivarfit='i1' or bivarfit='i2', etc. an OLS line is fitted to a specific group, the one with index 'i' equal to 1, 2, 3 etc. Again, useful in case of mixtures.
multivarfit	Whether to superimpose multivariate least square lines. This option adds one or more least square lines, based on MULTIVARIATE REGRESSION of y on X, to the plots of y Xi. The default is multivarfit=FALSE: no line is fitted. If multivarfit=1, a single OLS line is fitted to all points of each bivariate plot in the scatter matrix y X. The line added to the scatter plot y Xi is $avconst + C_i * X_i$, where C_i is the coefficient of X_i in the multivariate regression and $avconst$ is the effect of all the other explanatory variables different from X_i evaluated at their centroid (that is $\overline{(y)'C}$). If multivarfit=2, same action as with multivarfit=1 but this time we also add the line based on the group of unselected observations (i.e. the normal units).
labeladd	Add outlier labels in plot. If labeladd=TRUE, we label the outliers with the unit row index in matrices X and y. The default value is labeladd=FALSE, i.e. no label is added.
nameX	Add variable labels in plot. A vector of strings of length p containing the labels of the variables of the regression dataset. If it is empty (default) the sequence X_1, \dots, X_p will be created automatically
namey	Add response label. A string containing the label of the response
ylim	Control y scale in plot. Vector with two elements controlling minimum and maximum on the y axis. Default is to use automatic scale.
xlim	Control x scale in plot. Vector with two elements controlling minimum and maximum on the x axis. Default is to use automatic scale.

Details

Creates an object of class FSR_control to be used with the fsreg() function, containing various control parameters.

Value

An object of class "FSR_control" which is basically a [list](#) with components the input arguments of the function mapped accordingly to the corresponding Matlab function.

Author(s)

FSDA team

See Also

See Also [Sreg_control](#), [MMreg_control](#), [LXS_control](#), [FSReda_control](#), [Sregeda_control](#) and [MMregeda_control](#).

Examples

```
## Not run:  
  
(out <- fsreg(Y~., data=hbk, method="FS", control=FSR_control(h=56, nsamp=500, lms=2)))  
summary(out)  
  
## End(Not run)
```

geyser2

Old Faithful Geyser Data.

Description

A bivariate data set obtained from the Old Faithful Geyser, containing the eruption length and the length of the previous eruption for 271 eruptions of this geyser in minutes.

Usage

```
data(geyser2)
```

Format

A data frame with 271 rows and 2 variables The variables are as follows:

- Eruption length: The eruption length in minutes.
- Previous eruption length: The length of the previous eruption in minutes.

References

Garcia-Escudero, L.A., Gordaliza, A. (1999). Robustness properties of k-means and trimmed k-means, *Journal of the American Statistical Assoc.*, Vol.94, No.447, 956-969.

Haerdle, W. (1991). *Smoothing Techniques with Implementation in S*, New York: Springer.

levfwdplot

*Plots the trajectories of the monitored scaled (squared) residuals***Description**

Plots the trajectories of the monitored scaled (squared) residuals

Usage

```
levfwdplot(out,
  xlim, ylim, xlab, ylab, main, lwd, lty, col, cex.lab, cex.axis,
  xvalues,
  fg.thresh, fg.unit, fg.labstep, fg.lwd, fg.lty, fg.col, fg.mark, fg.cex,
  bg.thresh, bg.style,
  xground=c("lev", "res"), tag, datatooltip, label, nameX, namey, msg, databrush,
  standard, fground, bground, ...)
```

Arguments

out	An object containing monitoring of leverage, fsreda.object . The needed elements of out are <ol style="list-style-type: none"> 1. LEV: matrix containing the leverage monitored in each step of the forward search. Every row is associated with a unit. This matrix can be created using function <code>fsreg()</code> with <code>method="FS", monitoring=TRUE</code>. 2. Un: (for FSR only) - matrix containing the order of entry in the subset of each unit (required only when <code>datatooltip</code> is true or <code>databrush</code> is not empty). 3. y: a vector containing the response (required only when option <code>databrush</code> is requested). 4. X: a matrix containing the explanatory variables (required only when option <code>databrush</code> is requested). 5. Bols: (n-init+1) x (p+1) matrix containing the estimated beta coefficients monitored in each step of the robust procedure (required only when option <code>databrush</code> is requested and suboption <code>multivarfit</code> is requested).
ylim	Control y scale in plot. Vector with two elements controlling minimum and maximum on the y axis. Default is to use automatic scale.
xlim	Control x scale in plot. Vector with two elements controlling minimum and maximum on the x axis. Default is to use automatic scale.
xlab	a title for the x axis
ylab	a title for the y axis
main	an overall title for the plot
lwd	The line width, a positive number, defaulting to 1
lty	The line type. Line types can either be specified as an integer (1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash". The latter two are not supported by Matlab.

<code>col</code>	colors to be used for the highlighted units
<code>cex.lab</code>	The magnification to be used for x and y labels relative to the current setting of <code>cex</code>
<code>cex.axis</code>	The magnification to be used for axis annotation relative to the current setting of <code>cex</code>
<code>xvalues</code>	values for the x axis. Numeric vector of <code>ncol(RES)</code> controlling the x axis coordinates. The default value of <code>xvalues</code> is $(nrow(RES) - ncol(RES) + 1) : nrow(RES)$
<code>fg.thresh</code>	(alternative to <code>fg.unit</code>) numeric vector of length 1 or 2 which specifies the highlighted trajectories. If $length(fthresh) == 1$ the highlighted trajectories are those of units that throughout the search had at least once a residual greater (in absolute value) than <code>thresh</code> . The default value is <code>fg.thresh=2.5</code> . If $length(fthresh) == 2$ the highlighted trajectories are those of units that throughout the search had a residual at least once bigger than <code>fg.thresh[2]</code> or smaller than <code>fg.thresh[1]</code> .
<code>fg.unit</code>	(alternative to <code>fg.thresh</code>), vector containing the list of the units to be highlighted. If <code>fg.unit</code> is supplied, <code>fg.thresh</code> is ignored.
<code>fg.labstep</code>	numeric vector which specifies the steps of the search where to put labels for the highlighted trajectories (units). The default is to put the labels at the initial and final steps of the search. <code>flabstep=''</code> means no label.
<code>fg.lwd</code>	The line width for the highlighted trajectories (units). Default is 1.
<code>fg.lty</code>	The line type for the highlighted trajectories (units). Line types can either be specified as an integer (1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash". The latter two are not supported by Matlab.
<code>fg.col</code>	colors to be used for the highlighted units.
<code>fg.mark</code>	Controls whether to plot highlighted trajectories as symbols. if <code>fg.mark==TRUE</code> each line is plotted using a different symbol else no marker is used (default).
<code>fg.cex</code>	controls the font size of the labels of the trajectories in foreground.
<code>bg.thresh</code>	numeric vector of length 1 or 2 which specifies how to define the unimportant trajectories. Unimportant trajectories will be plotted using a colormap, in greysh or will be hidden. If $length(bthresh) == 1$ the irrelevant units are those which always had a residual smaller (in absolute value) than <code>thresh</code> . If $length(bthresh) == 2$ the irrelevant units are those which always had a residual greater than <code>bthresh(1)</code> and smaller than <code>bthresh(2)</code> . The default is: <code>bg.thresh=2.5</code> if $n > 100$ and <code>bg.thresh=-Inf</code> if $n \leq 100$ i.e. to treat all trajectories as important if $n \leq 100$ and, if $n > 100$, to reduce emphasis only to trajectories having in all steps of the search a value of scaled residual smaller than 2.5.
<code>bg.style</code>	specifies how to plot the unimportant trajectories as defined in option <code>bthresh</code> . <ol style="list-style-type: none"> <code>bg.style="faint"</code>: unimportant trajectories are plotted using a colormap. <code>bg.style="hide"</code>: unimportant trajectories are hidden. <code>bg.style="greyish"</code>: unimportant trajectories are displayed in a faint grey. <p>When $n > 100$ the default option is <code>bg.style='faint'</code>. When $n \leq 100$ and <code>bg.thresh == -Inf</code> option <code>bstyle</code> is ignored. Remark: <code>bground=""</code> is equivalent to <code>-Inf</code> that is all trajectories are considered relevant.</p>

tag	Plot handle. String which identifies the handle of the plot which is about to be created. The default is to use tag 'pl_resfd'. Notice that if the program finds a plot which has a tag equal to the one specified by the user, then the output of the new plot overwrites the existing one in the same window else a new window is created.
xground	trajectories to highlight in connection with resfdplot. If xground="lev" (default), the levfwdplot trajectories are put in foreground or in background depending on the leverage values. If xground="res", the levfwdplot trajectories are put in foreground or in background depending on the residual values. See options <code>bg.thresh</code> and <code>fg.thresh</code> .
datatooltip	<p>Interactive clicking. It is inactive if this parameter is missing or empty. The default is <code>datatooltip=TRUE</code>, i.e. the user can select with the mouse an individual residual trajectory in order to have information about the corresponding unit. The information displayed depends on the estimator in use.</p> <p>For example for class <code>fsreda.object</code> the information concerns the label and the step of the search in which the unit enters the subset. If <code>datatooltip</code> is a list it may contain the following fields:</p> <ol style="list-style-type: none"> 1. <code>DisplayStyle</code> determines how the data cursor displays. Possible values are 'datatip' and 'window' (default). 'datatip' displays data cursor information in a small yellow text box attached to a black square marker at a data point you interactively select. 'window' displays data cursor information for the data point you interactively select in a floating window within the figure. 2. <code>SnapToDataVertex</code>: specifies whether the data cursor snaps to the nearest data value or is located at the actual pointer position. Possible values are <code>SnapToDataVertex='on'</code> (default) and <code>SnapToDataVertex='off'</code>. 3. <code>LineColor</code>: controls the color of the trajectory selected with the mouse. It can be an RGB triplet of values between 0 and 1, or character vector indicating a color name. Note that a RGB vector can be conveniently chosen with our MATLAB class <code>FSColor</code>, see documentation. 4. <code>SubsetLinesColor</code>: enables to control the color of the trajectories of the units that are in the subset at a given step of the search (if <code>levfwdplot()</code> is applied to an object of class <code>fsreda.object</code>) or have a weight greater than 0.9 (if <code>levfwdplot()</code> is applied to an object of class <code>sregeda.object</code> or <code>mmregeda.object</code>). This can be done (repeatedly) with a left mouse click in proximity of the step of interest. A right mouse click will terminate the selection by marking with a up-arrow the step corresponding to the highlighted lines. The highlighted lines by default are in red, but a different color can be specified as RGB triplet or character of color name. Note that a RGB vector can be conveniently chosen with our MATLAB class <code>FSColor</code>, see documentation. By default <code>SubsetLinesColor=""</code>, i.e. the modality is not active. Any initialization for <code>SubsetLinesColor</code> which cannot be interpreted as RGB vector will be converted to blue, i.e. <code>SubsetLinesColor</code> will be forced to be <code>[0 0 1]</code>. If <code>SubsetLinesColor</code> is not empty the previous option <code>LineColor</code> is ignored.
label	Character vector containing the labels of the units (optional argument used when <code>datatooltip=TRUE</code> . If this field is not present labels <code>row1, ..., rown</code> will be

	automatically created and included in the pop up datatooltip window).
nameX	Add variable labels in plot. A vector of strings of length p containing the labels of the variables of the regression dataset. If it is empty (default) the sequence X_1, \dots, X_p will be created automatically
namey	Add response label. A string containing the label of the response
msg	Controls whether to display or not messages on the screen. If <code>msg==1</code> (default) messages are displayed on the screen about step in which signal took place else no message is displayed on the screen.
databrush	interactive mouse brushing. If <code>databrush</code> is missing or empty (default), no brushing is done. The activation of this option (<code>databrush</code> is a scalar or a list) enables the user to select a set of trajectories in the current plot and to see them highlighted in the $y X$ plot, i.e. a matrix of scatter plots of y against each column of X , grouped according to the selection(s) done by brushing. If the plot $y X$ does not exist it is automatically created. In addition, brushed units are automatically highlighted in the minimum deletion residual plot if it is already open. The extension to the following plots will be available in future versions of the toolbox: <ol style="list-style-type: none"> 1. monitoring leverage plot; 2. maximum studentized residual; 3. s^2 and R^2; 4. Cook distance and modified Cook distance; 5. deletion t statistics.

Note that the window style of the other figures is set equal to that which contains the monitoring residual plot. In other words, if the monitoring residual plot is docked all the other figures will be docked too

If `databrush=TRUE` the default selection tool is a rectangular brush and it is possible to brush only once (that is `persist=""`).

If `databrush=list(...)`, it is possible to use all optional arguments of function `selectdataFS()` and the following optional argument:

1. `persist`. `Persist` is an empty value or a character containing 'on' or 'off'. The default value is `persist=""`, that is brushing is allowed only once. If `persist="on"` or `persist="off"` brushing can be done as many times as the user requires. If `persist='on'` then the unit(s) currently brushed are added to those previously brushed. It is possible, every time a new brushing is done, to use a different color for the brushed units. If `persist='off'` every time a new brush is performed units previously brushed are removed.
2. `bivarfit`. This option adds one or more least square lines based on SIMPLE REGRESSION to the plots of $y|X$, depending on the selected groups.
3. `bivarfitWheather` to superimpose bivariate least square lines on the plot (if `plot=TRUE`). This option adds one or more least squares lines, based on SIMPLE REGRESSION of y on X_i , to the plots of $y|X_i$. The default is `bivarfit=FALSE`: no line is fitted. If `bivarfit=1`, a single OLS line is fitted to all points of each bivariate plot in the scatter matrix $y|X$. If `bivarfit=2`, two OLS lines are fitted: one to all points and another to the group of the genuine observations. The group of the potential outliers is not

fitted. If `bivarfit=0` one OLS line is fitted to each group. This is useful for the purpose of fitting mixtures of regression lines. If `bivarfit='i1'` or `bivarfit='i2'`, etc. an OLS line is fitted to a specific group, the one with index 'i' equal to 1, 2, 3 etc. Again, useful in case of mixtures.

4. `multivarfit` Whether to superimpose multivariate least square lines. This option adds one or more least square lines, based on MULTIVARIATE REGRESSION of y on X , to the plots of $y|X_i$. The default is `multivarfit=FALSE`: no line is fitted. If `bivarfit=1`, a single OLS line is fitted to all points of each bivariate plot in the scatter matrix $y|X$. The line added to the scatter plot $y|X_i$ is $avconst + C_i * X_i$, where C_i is the coefficient of X_i in the multivariate regression and $avconst$ is the effect of all the other explanatory variables different from X_i evaluated at their centroid (that is $\overline{(y)'C}$). If `multivarfit=2`, same action as with `multivarfit=1` but this time we also add the line based on the group of unselected observations (i.e. the normal units).
5. `labeladd` Add outlier labels in plot. If `labeladd=TRUE`, we label the outliers with the unit row index in matrices X and y . The default value is `labeladd=FALSE`, i.e. no label is added.

<code>standard</code>	(MATLAB-style arguments) appearance of the plot in terms of <code>xlim</code> , <code>ylim</code> , axes labels and their font size style, color of the lines, etc.
<code>fground</code>	MATLAB-style arguments for the <code>fground</code> trajectories in foreground.
<code>bground</code>	MATLAB-style arguments for the <code>bground</code> trajectories in background.
<code>...</code>	potential further arguments passed to lower level functions.

Details

No details

Value

No value returned

Author(s)

FSDA team

Examples

```
## Not run:

n <- 100
y <- rnorm(n)
X <- matrix(rnorm(n*4), nrow=n)

out <- fsreg(y~X, method="LTS")
out <- fsreg(y~X, method="FS", bsb=out$bs, monitoring=TRUE)
levfwdplot(out)
```

```
## End(Not run)
```

loyalty

Loyalty data

Description

The loyalty data consist of 509 observations on the behaviour of customers with loyalty cards from a supermarket chain in Northern Italy. The response y is the amount in euros spent at the shop over six months and the explanatory variables are: X1, the number of visits to the supermarket in the six month period; X2, the age of the customer; X3, the number of members of the customers' family. To find out more about this data set please see Atkinson and Riani (2006), JCGS

Usage

```
data("loyalty")
```

Format

A data frame with 509 observations on the following 4 variables.

visits the number of visits to the supermarket in the six month period

age the age of the customer

family the number of members of the customers' family

amount_spent the amount in euros spent at the shop over six months

Details

To find out more about this data set please see Atkinson and Riani (2006), JCGS

Source

The data are themselves a random sample from a larger database. The sample of 509 observations is available at <http://www.riani.it/trimmed>.

References

Atkinson, A. and Riani, M (2006) Distribution Theory and Simulations for Tests of Outliers in Regression, *Journal of Computational and Graphical Statistics*, **15** 2, pp 460–476.

Examples

```
data(loyalty)
```

LXS_control	<i>Creates an LXS_control object</i>
-------------	--------------------------------------

Description

Creates an object of class LXS_control to be used with the fsreg() function, containing various control parameters.

Usage

```
LXS_control(intercept = TRUE, lms, h, bdp, nsamp, rew = FALSE, conflev = 0,
            msg = TRUE, nocheck = FALSE, nomes = FALSE, plot = FALSE)
```

Arguments

- | | |
|-----------|---|
| intercept | Indicator for constant term. Scalar. If intercept=TRUE, a model with constant term will be fitted (default), else, no constant term will be included. |
| lms | <p>Criterion to use to find the initial subset to initialize the search (LMS, LTS with concentration steps, LTS without concentration steps or subset supplied directly by the user). The default value is 1 (Least Median of Squares is computed to initialize the search). On the other hand, if the user wants to initialize the search with LTS with all the default options for concentration steps then lms=2. If the user wants to use LTS without concentration steps, lms can be a scalar different from 1 or 2. If lms is a list it is possible to control a series of options for concentration steps (for more details see option lms inside LXS_control). If, on the other hand, the user wants to initialize the search with a prespecified set of units there are two possibilities:</p> <ol style="list-style-type: none"> 1. lms can be a vector with length greater than 1 which contains the list of units forming the initial subset. For example, if the user wants to initialize the search with units 4, 6 and 10 then <code>lms=c(4, 6, 10)</code>; 2. lms is a struct which contains a field named bsb which contains the list of units to initialize the search. For example, in the case of simple regression through the origin with just one explanatory variable, if the user wants to initialize the search with unit 3 then <code>lms=list(bsb=3)</code>. |
| h | The number of observations that have determined the least trimmed squares estimator, scalar. h is an integer greater or equal than p but smaller than n. Generally if the purpose is outlier detection $h = \lceil 0.5 \cdot (n+p+1) \rceil$ (default value). h can be smaller than this threshold if the purpose is to find subgroups of homogeneous observations. In this function the LTS/LMS estimator is used just to initialize the search. |
| bdp | Breakdown point. It measures the fraction of outliers the algorithm should resist. In this case any value greater than 0 but smaller or equal than 0.5 will do fine. If on the other hand the purpose is subgroups detection then bdp can be greater than 0.5. In any case however $n \cdot (1 - \text{bdp})$ must be greater than p. If this condition is not fulfilled an error will be given. Please specify h or bdp not both. |

nsamp	Number of subsamples which will be extracted to find the robust estimator, scalar. If nsamp=0 all subsets will be extracted. They will be $(n \text{ choose } p)$. If the number of all possible subset is <1000 the default is to extract all subsets otherwise just 1000.
rew	LXS reweighted - if rew=1 the reweighted version of LTS (LMS) is used and the output quantities refer to the reweighted version else no reweighting is performed (default).
conflev	Confidence level which is used to declare units as outliers, usually conflev=0.95, 0.975, 0.99 (individual alpha) or 1-0.05/n, 1-0.025/n, 1-0.01/n (simultaneous alpha). Default value is 0.975.
msg	Controls whether to display or not messages on the screen If msg==1 (default) messages are displayed on the screen about step in which signal took place else no message is displayed on the screen.
nocheck	Check input arguments, scalar. If nocheck=TRUE no check is performed on matrix y and matrix X. Notice that y and X are left unchanged. In other words the additional column of ones for the intercept is not added. As default nocheck=FALSE.
nomes	It controls whether to display or not on the screen messages about estimated time to compute LMS (LTS). If nomes is equal to 1 no message about estimated time to compute LMS (LTS) is displayed, else if nomes is equal to 0 (default), a message about estimated time is displayed.
plot	Plot on the screen. Scalar. If plots=TRUE the plot of minimum deletion residual with envelopes based on n observations and the scatterplot matrix with the outliers highlighted is produced. If plots=2 the user can also monitor the intermediate plots based on envelope superimposition. If plots=FALSE (default) no plot is produced.

Details

Creates an object of class FSR_control to be used with the fsreg() function, containing various control parameters.

Value

An object of class "LXS_control" which is basically a `list` with components the input arguments of the function mapped accordingly to the corresponding Matlab function.

Author(s)

FSDA team

See Also

See Also as [Sreg_control](#), [MMreg_control](#) and [FSR_control](#)

Examples

```
## Not run:
(out <- fsreg(Y~., data=hbk, method="LMS", control=LXS_control(h=56, nsamp=500, lms=2)))

## End(Not run)
```

M5data

*Mixture M5 Data.***Description**

A bivariate data set obtained from three normal bivariate distributions with different scales and proportions 1:2:2. One of the components is strongly overlapping with another one. A 10 noise is added uniformly distributed in a rectangle containing the three normal components and not strongly overlapping with the three mixture components. A precise description of the M5 data set can be found in Garcia-Escudero et al. (2008).

Usage

```
data(M5data)
```

Format

A data frame with 2000 rows and 3 variables The first two columns are the two variables. The last column is the true classification vector where symbol "0" stands for the contaminating data points.

Source

Garcia-Escudero, L.A., Gordaliza, A., Matran, C. and Mayo-Iscar, A. (2008). A General Trimming Approach to Robust Cluster Analysis, *Annals of Statistics*, Vol.36, 1324-1345. Technical report available at <http://www.eio.uva.es/inves/grupos/representaciones/trTCLUST.pdf>

mal fwdplot

*Plots the trajectories of scaled Mahalanobis distances along the search***Description**

Plots the trajectories of scaled Mahalanobis distances along the forward search

Usage

```
mal fwdplot(out, xlim, ylim, xlab, ylab, main, lwd, lty, col, cex.lab,
  cex.axis, subsize, fg.thresh, fg.unit, fg.labstep, fg.lwd, fg.lty,
  fg.col, fg.mark, fg.cex, bg.thresh, bg.style, standard, fground, bground,
  tag, datatooltip, label, nameX, databrush, conflev, trace = FALSE, ...)
```

Arguments

out	An object of S3 class <code>fsmeda.object</code> returned by <code>fsmult</code> with <code>monitoring=TRUE</code> - a list containing the monitoring of minimum Mahalanobis distance. The needed elements of out are <ol style="list-style-type: none"> 1. MAL: matrix containing the squared Mahalanobis distances monitored in each step of the forward search. Every row is associated with a unit (row of data matrix Y). This matrix can be created using function <code>FSMeda</code> (mandatory argument) 2. Un: matrix containing the order of entry of each unit (necessary if <code>data-tooltip</code> or <code>databrush</code> is selected). 3. X: The data matrix.
xlim	Controls the x scale in the plot. <code>xlim</code> is a vector with two elements controlling minimum and maximum on the x-axis. Default is to use automatic scale.
ylim	Controls the y scale in the plot. <code>ylim</code> is a vector with two elements controlling minimum and maximum on the y-axis. Default is to use automatic scale.
xlab	A title for the x axis
ylab	A title for the y axis
main	An overall title for the plot
lwd	The line width, a positive number, defaulting to 1
lty	The line type. Line types can either be specified as an integer (1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash". The latter two are not supported by Matlab.
col	Colors to be used for the highlighted units
cex.lab	The magnification to be used for x and y labels relative to the current setting of <code>cex</code>
cex.axis	The magnification to be used for axis annotation relative to the current setting of <code>cex</code>
subsize	Numeric vector containing the subset size with length equal to the number of columns of matrix of mahalanobis distances. The default value of <code>subsize</code> is $(nrow(MAL) - ncol(MAL) + 1) : nrow(MAL)$
fg.thresh	(alternative to <code>fg.unit</code>) numeric vector of length 1 or 2 which specifies the highlighted trajectories. If $length(fg.thresh) == 1$ the highlighted trajectories are those of units that throughout the search had at least once a mahalanobis distance greater than <code>fg.thresh</code> . The default value is <code>fg.thresh=2.5</code> . If $length(fg.thresh) == 2$ the highlighted trajectories are those of units that throughout the search had a mahalanobis distance at least once bigger than <code>fg.thresh[2]</code> or smaller than <code>fg.thresh[1]</code> .
fg.unit	(alternative to <code>fg.thresh</code>), vector containing the list of the units to be highlighted. If <code>fg.unit</code> is supplied, <code>fg.thresh</code> is ignored.
fg.labstep	numeric vector which specifies the steps of the search where to put labels for the highlighted trajectories (units). The default is to put the labels at the initial and final steps of the search. <code>fg.labstep=''</code> means no label.

fg.lwd	The line width for the highlighted trajectories (units). Default is 1.
fg.lty	The line type for the highlighted trajectories (units). Line types can either be specified as an integer (1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash". The latter two are not supported by Matlab.
fg.col	colors to be used for the highlighted units.
fg.mark	Controls whether to plot highlighted trajectories as symbols. if fg.mark==TRUE each line is plotted using a different symbol else no marker is used (default).
fg.cex	Controls the font size of the labels of the trajectories in foreground. If fg.cex=0 no labels will be shown - equivalent to fg.labstop="".
bg.thresh	Numeric vector of length 1 or 2 which specifies how to define the <i>unimportant trajectories</i> . Unimportant trajectories will be plotted using a colormap, in greysh or will be hidden. If length(bg.thresh) == 1 the irrelevant units are those which always had a mahalanobis distance smaller than bg.thresh. If length(bg.thresh) == 2 the irrelevant units are those which always had a mahalanobis distance greater than bg.thresh[1] and smaller than bg.thresh[2]. The default is bg.thresh=2.5 if n > 100 and bg.thresh=-Inf if n <= 100 i.e. to treat all trajectories as important if n <= 100 and, if n > 100, to reduce emphasis only to trajectories having in all steps of the search a value of mahalanobis distance smaller than 2.5.
bg.style	Specifies how to plot the unimportant trajectories as defined in option bg.thresh. <ol style="list-style-type: none"> 1. bg.style="faint": unimportant trajectories are plotted using a colormap. 2. bg.style="hide": unimportant trajectories are hidden. 3. bg.style="greyish": unimportant trajectories are displayed in a faint grey. <p>When n > 100 the default option is bg.style='faint'. When n <= 100 and bg.thresh == -Inf option bg.style is ignored. Remark: bground="" is equivalent to -Inf that is all trajectories are considered relevant.</p>
standard	MATLAB-style arguments - appearance of the plot in terms of xlim, ylim, axes labels and their font size style, color of the lines, etc.
fground	MATLAB-style arguments - for the trajectories in foreground.
bground	MATLAB-style arguments - for the trajectories in background.
tag	Plot handle. String which identifies the handle of the plot which is about to be created. The default is to use tag 'pl_resfwd'. Notice that if the program finds a plot which has a tag equal to the one specified by the user, then the output of the new plot overwrites the existing one in the same window else a new window is created.
datatooltip	Interactive clicking. It is inactive if this parameter is set to FALSE. The default is datatooltip=TRUE, the user can select with the mouse an individual mahalanobis distance trajectory in order to have information about the corresponding unit, the associated label and the step of the search in which the unit enters the subset. If datatooltip is a list it may contain the following fields:

1. `DisplayStyle` determines how the data cursor displays. Possible values are 'datatip' and 'window' (default). 'datatip' displays data cursor information in a small yellow text box attached to a black square marker at a data point you interactively select. 'window' displays data cursor information for the data point you interactively select in a floating window within the figure.
2. `SnapToDataVertex`: specifies whether the data cursor snaps to the nearest data value or is located at the actual pointer position. Possible values are `SnapToDataVertex='on'` (default) and `SnapToDataVertex='off'`.
3. `LineColor`: controls the color of the trajectory selected with the mouse. It can be an RGB triplet of values between 0 and 1, or character vector indicating a color name. Note that a RGB vector can be conveniently chosen with our MATLAB class `FSColor`, see documentation.
4. `SubsetLinesColor`: enables to control the color of the trajectories of the units that are in the subset at a given step of the search (if `resfwdplot()` is applied to an object of class `fsreda.object`) or have a weight greater than 0.9 (if `resfwdplot()` is applied to an object of class `sregeda.object` or `mmregeda.object`). This can be done (repeatedly) with a left mouse click in proximity of the step of interest. A right mouse click will terminate the selection by marking with a up-arrow the step corresponding to the highlighted lines. The highlighted lines by default are in red, but a different color can be specified as RGB triplet or character of color name. Note that a RGB vector can be conveniently chosen with our MATLAB class `FSColor`, see documentation. By default `SubsetLinesColor=""`, i.e. the modality is not active. Any initialization for `SubsetLinesColor` which cannot be interpreted as RGB vector will be converted to blue, i.e. `SubsetLinesColor` will be forced to be `[0 0 1]`. If `SubsetLinesColor` is not empty the previous option `LineColor` is ignored.

<code>label</code>	Character vector containing the labels of the units (optional argument used when <code>datatooltip=TRUE</code> . If this field is not present labels <code>row1, ..., rown</code> will be automatically created and included in the pop up <code>datatooltip</code> window).
<code>nameX</code>	Add variable labels in plot. A vector of strings of length <code>p</code> containing the labels of the variables in the dataset. If it is empty (default) the sequence <code>X1, ..., Xp</code> will be created automatically
<code>databrush</code>	<p>Interactive mouse brushing. If <code>databrush</code> is missing or empty (default), no brushing is done. The activation of this option (<code>databrush</code> is <code>TRUE</code> or a list) enables the user to select a set of trajectories in the current plot and to see them highlighted in the scatterplot matrix. If the scatterplot matrix does not exist it is automatically created. In addition, brushed units can be highlighted in the monitoring mahalanobis distance plot. Note that the window style of the other figures is set equal to that which contains the monitoring mahalanobis distance plot. In other words, if the monitoring mahalanobis distance plot is docked all the other figures will be docked too.</p> <p>If <code>databrush=TRUE</code> the default selection tool is a rectangular brush and it is possible to brush only once (that is <code>persist=""</code>).</p> <p>If <code>databrush=list(...)</code>, it is possible to use all optional arguments of the MATLAB function <code>selectdataFS()</code> and the following optional arguments:</p>

- `persist`. Persist is an empty value or a character containing 'on' or 'off'. The default value is `persist=""`, that is brushing is allowed only once. If `persist="on"` or `persist="off"` brushing can be done as many time as the user requires. If `persist='on'` then the unit(s) currently brushed are added to those previously brushed. It is possible, every time a new brushing is done, to use a different color for the brushed units. If `persist='off'` every time a new brush is performed units previously brushed are removed.
 - `label`: add labels of brushed units in the monitoring plot.
 - `labeladd`: add labels of brushed units in the scatterplot matrix. If this option is '1', we label the units of the last selected group with the unit row index in the matrix X. The default value is `labeladd=""`, i.e. no label is added.
- `conflev` confidence interval for the horizontal bands. It can be a vector of different confidence level values, e.g. `c(0.95, 0.99, 0.999)`. The confidence interval is based on the χ^2 distribution.
- `trace` Whether to print intermediate results. Default is `trace=FALSE`.
- ... potential further arguments passed to lower level functions.

Value

none

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Atkinson A.C., Riani M. and Cerioli A. (2004), Exploring Multivariate Data with the Forward Search, Springer Verlag, New York.

Examples

```
## Not run:
## Produce monitoring MD plot with all the default options.
## Generate input structure for mal fwdplot
n <- 100
p <- 4
Y <- matrix(rnorm(n*p), ncol=p)
Y[1:10,] <- Y[1:10,] + 4

out <- fsmult(Y, monitoring=TRUE, init=30)

## Produce monitoring MD plot with all the default options
mal fwdplot(out)

## End(Not run)
```

malindexplot

Plots the trajectory of minimum Mahalanobis distance (mmd)

Description

Plots the trajectory of minimum Mahalanobis distance (mmd)

Usage

```
malindexplot(out, p, xlab, ylab, main, nameX, conflev, trace = FALSE,
  ...)
```

Arguments

out	a numeric vector or an object of S3 class (one of <code>fsmult.object</code> , <code>smult.object</code> or <code>mmmult.object</code>) returned by one of the functions <code>fsmult</code> or <code>smult</code> or <code>mmmult</code> - a list containing the monitoring of minimum Mahalanobis distance
p	If out is a vector, p is its length (i.e. number of variables).
xlab	A title for the x axis
ylab	A title for the y axis
main	An overall title for the plot
nameX	Add variable labels in the plot. A vector of strings of length p containing the labels of the variables of the original data matrix X. If it is empty (default) the sequence X_1, \dots, X_p will be created automatically
conflev	confidence interval for the horizontal bands. It can be a vector of different confidence level values, e.g. <code>c(0.95, 0.99, 0.999)</code> . The confidence interval is based on the χ^2 distribution.
trace	Whether to print intermediate results. Default is <code>trace=FALSE</code> .
...	potential further arguments passed to lower level functions.

Value

none

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Atkinson and Riani (2000), Robust Diagnostic Regression Analysis, Springer Verlag, New York.

Examples

```
## Not run:
## Mahalanobis distance plot of 100 random numbers.
## Numbers are from from the chisq with 5 degrees of freedom

malindexplot(rchisq(100, 5), 5)

## End(Not run)
```

 mdrplot

Plots the trajectory of minimum deletion residual (mdr)

Description

Plots the trajectory of minimum deletion residual (mdr).

Usage

```
mdrplot(out, quant = c(0.01, 0.5, 0.99), sign = TRUE,
        mplus1 = FALSE, envm,
        xlim, ylim, xlab, ylab, main,
        lwdenv, lwd, cex.lab, cex.axis,
        tag, datatooltip, label, nameX, namey, databrush,
        ...)
```

Arguments

out	An object returned by <code>FSReda()</code> (see FSReda_control). The needed elements of out are <ol style="list-style-type: none"> 1. mdr: Minimum deletion residual. A matrix containing the monitoring of minimum deletion residual in each step of the forward search. The first column of mdr must contain the fwd search index. 2. Un: (for FSR only) - matrix containing the order of entry in the subset of each unit (required only when <code>datatooltip</code> is true or <code>databrush</code> is not empty). 3. y: a vector containing the response (required only when option <code>databrush</code> is requested). 4. X: a matrix containing the explanatory variables (required only when option <code>databrush</code> is requested). 5. Bols: (n-init+1) x (p+1) matrix containing the estimated beta coefficients monitored in each step of the robust procedure (required only when option <code>databrush</code> is requested and suboption <code>multivarfit</code> is requested).
quant	Quantiles for which envelopes have to be computed. The default is to produce 1%, 50% and 99% envelopes. In other words the default is <code>quant=c(0.01, 0.5, 0.99)</code> .

sign	Whether to use MDR with sign: if sign=TRUE (default) we distinguish steps for which minimum deletion residual was associated with positive or negative value of the residual. Steps associated with positive values of mdr are plotted in black, while other steps are plotted in red.
mplus1	Whether to plot the (m+1)-th order statistic. Specifies if it is necessary to plot the curve associated with (m+1)-th order statistic.
envm	Sample size for drawing envelopes. Specifies the size of the sample which is used to superimpose the envelope. The default is to add an envelope based on all the observations (size n envelope).
ylim	Control y scale in plot. Vector with two elements controlling minimum and maximum on the y axis. Default is to use automatic scale.
xlim	Control x scale in plot. Vector with two elements controlling minimum and maximum on the x axis. Default is to use automatic scale.
xlab	a title for the x axis
ylab	a title for the y axis
main	an overall title for the plot
lwdenv	Controls the width of the lines associated with the envelopes, default is lwdenv=1.
lwd	Controls the linewidth of the curve which contains the monitoring of minimum deletion residual.
cex.lab	The magnification to be used for x and y labels relative to the current setting of cex
cex.axis	The magnification to be used for axis annotation relative to the current setting of cex
tag	Plot handle. String which identifies the handle of the plot which is about to be created. The default is to use tag 'pl_mdr'. Notice that if the program finds a plot which has a tag equal to the one specified by the user, then the output of the new plot overwrites the existing one in the same window else a new window is created.
datatooltip	If datatooltip is not empty the user can use the mouse in order to have information about the unit selected, the step in which the unit enters the search and the associated label. If datatooltip is a list, it is possible to control the aspect of the data cursor (see MATLAB function datacursor mode() for more details or see the examples below). The default options are DisplayStyle="Window" and SnapToDataVertex="on".
label	Character vector containing the labels of the units (optional argument used when datatooltip=TRUE. If this field is not present labels row1, ..., rown will be automatically created and included in the pop up datatooltip window).
nameX	Add variable labels in plot. A vector of strings of length p containing the labels of the variables of the regression dataset. If it is empty (default) the sequence X1, ..., Xp will be created automatically
namey	Add response label. A string containing the label of the response
databrush	interactive mouse brushing. If databrush is missing or empty (default), no brushing is done. The activation of this option (databrush is a scalar or a list) enables

the user to select a set of trajectories in the current plot and to see them highlighted in the $y|X$ plot, i.e. a matrix of scatter plots of y against each column of X , grouped according to the selection(s) done by brushing. If the plot $y|X$ does not exist it is automatically created. In addition, brushed units are automatically highlighted in the minimum deletion residual plot if it is already open. The extension to the following plots will be available in future versions of the toolbox:

1. monitoring leverage plot;
2. maximum studentized residual;
3. s^2 and R^2 ;
4. Cook distance and modified Cook distance;
5. deletion t statistics.

Note that the window style of the other figures is set equal to that which contains the monitoring residual plot. In other words, if the monitoring residual plot is docked all the other figures will be docked too

If `databrush=TRUE` the default selection tool is a rectangular brush and it is possible to brush only once (that is `persist=""`).

If `databrush=list(...)`, it is possible to use all optional arguments of function `selectdataFS()` and the following optional argument:

1. `persist`. `Persist` is an empty value or a character containing 'on' or 'off'. The default value is `persist=""`, that is brushing is allowed only once. If `persist="on"` or `persist="off"` brushing can be done as many time as the user requires. If `persist='on'` then the unit(s) currently brushed are added to those previously brushed. It is possible, every time a new brushing is done, to use a different color for the brushed units. If `persist='off'` every time a new brush is performed units previously brushed are removed.
2. `bivarfitWheather` to superimpose bivariate least square lines on the plot (if `plot=TRUE`). This option adds one or more least squares lines, based on SIMPLE REGRESSION of y on X_i , to the plots of $y|X_i$. The default is `bivarfit=FALSE`: no line is fitted. If `bivarfit=1`, a single OLS line is fitted to all points of each bivariate plot in the scatter matrix $y|X$. If `bivarfit=2`, two OLS lines are fitted: one to all points and another to the group of the genuine observations. The group of the potential outliers is not fitted. If `bivarfit=0` one OLS line is fitted to each group. This is useful for the purpose of fitting mixtures of regression lines. If `bivarfit='i1'` or `bivarfit='i2'`, etc. an OLS line is fitted to a specific group, the one with index 'i' equal to 1, 2, 3 etc. Again, useful in case of mixtures.
3. `multivarfitWheather` to superimpose multivariate least square lines. This option adds one or more least square lines, based on MULTIVARIATE REGRESSION of y on X , to the plots of $y|X_i$. The default is `multivarfit=FALSE`: no line is fitted. If `bivarfit=1`, a single OLS line is fitted to all points of each bivariate plot in the scatter matrix $y|X$. The line added to the scatter plot $y|X_i$ is $avconst + C_i * X_i$, where C_i is the coefficient of X_i in the multivariate regression and $avconst$ is the effect of all the other explanatory variables different from X_i evaluated at their centroid (that is $\overline{(y)'C}$). If `multivarfit=2`, same action as with `multivarfit=1` but this time we also

add the line based on the group of unselected observations (i.e. the normal units).

4. `labeladd` Add outlier labels in plot. If `labeladd=TRUE`, we label the outliers with the unit row index in matrices `X` and `y`. The default value is `labeladd=FALSE`, i.e. no label is added.

... potential further arguments passed to lower level functions.

Details

No details

Value

No value returned

Author(s)

FSDA team

Examples

```
## Not run:

n <- 100
y <- rnorm(n)
X <- matrix(rnorm(n*4), nrow=n)

out <- fsreg(y~X, method="LTS")
out <- fsreg(y~X, method="FS", bsb=out$bs, monitoring=TRUE)
mdrplot(out)

## End(Not run)
```

mmdplot

Plots the trajectory of minimum Mahalanobis distance (mmd)

Description

Plots the trajectory of minimum Mahalanobis distance (mmd)

Usage

```
mmdplot(out, quant = c(0.01, 0.5, 0.99), mplus1 = FALSE, envm, lwd,
  lwdenv, xlim, ylim, tag, datatooltip, label, xlab, ylab, main, nameX,
  cex.lab, cex.axis, databrush, trace = FALSE, ...)
```


Arguments

out	An object of S3 class <code>fsmeda.object</code> returned by <code>fsmult</code> with <code>monitoring=TRUE</code> - a list containing the monitoring of minimum Mahalanobis distance
quant	Quantiles for which envelopes have to be computed. The default is to produce 1%, 50% and 99% envelopes. In other words the default is <code>quant=c(0.01,0.5,0.99)</code> .
mplus1	Whether to plot the (m+1)-th order statistic.
envm	Sample size for drawing envelopes. Specifies the size of the sample which is used to superimpose the envelope. The default is to add an envelope based on all the observations (size n envelope).
lwd	Controls the line width of the curve which contains the monitoring of minimum deletion residual.
lwdenv	Controls the width of the lines associated with the envelopes. Default is <code>lwdenv=1</code>
xlim	Control the x scale in plot. Vector with two elements controlling minimum and maximum on the x axis. Default is to use automatic scale.
ylim	Control the y scale in plot. Vector with two elements controlling minimum and maximum on the y axis. Default is to use automatic scale.
tag	Plot handle. String which identifies the handle of the plot which is about to be created. The default is <code>tag='p1_mmd'</code> . Notice that if the program finds a plot which has a tag equal to the one specified by the user, then the output of the new plot overwrites the existing one in the same window else a new window is created.
datatooltip	If <code>datatooltip</code> is not empty the user can use the mouse in order to have information about the unit selected, the step in which the unit enters the search and the associated label. If <code>datatooltip</code> is a list, it is possible to control the aspect of the data cursor (see MATLAB function <code>datacursormode()</code> for more details or see the examples below). The default options are <code>DisplayStyle="Window"</code> and <code>SnapToDataVertex="on"</code> .
label	Row labels. Character vector containing the labels of the units (optional argument used when <code>datatooltip=TRUE</code> . If this field is not present labels row1, ..., rown will be automatically created and included in the pop up <code>datatooltip</code> window).
xlab	A title for the x axis
ylab	A title for the y axis
main	An overall title for the plot
nameX	Add variable labels in the plot. A vector of strings of length p containing the labels of the variables of the original data matrix X. If it is empty (default) the sequence <code>X1, . . . , Xp</code> will be created automatically
cex.lab	The magnification to be used for x and y labels relative to the current setting of <code>cex</code>
cex.axis	The magnification to be used for axis annotation relative to the current setting of <code>cex</code>

databrush	<p>Interactive mouse brushing. If databrush is missing or empty (default), no brushing is done. The activation of this option (databrush is TRUE or a list) enables the user to select a set of trajectories in the current plot and to see them highlighted in the scatterplot matrix. If the scatterplot matrix does not exist it is automatically created. In addition, brushed units can be highlighted in the monitoring MD plot. Note that the window style of the other figures is set equal to that which contains the monitoring residual plot. In other words, if the monitoring residual plot is docked all the other figures will be docked too.</p> <p>If databrush=TRUE the default selection tool is a rectangular brush and it is possible to brush only once (that is persist="").</p> <p>Note that the window style of the other figures is set equal to that which contains the monitoring residual plot. In other words, if the monitoring residual plot is docked all the other figures will be docked too</p> <p>If databrush=TRUE the default selection tool is a rectangular brush and it is possible to brush only once (that is persist="").</p> <p>If databrush=list(...), it is possible to use all optional arguments of the MATLAB function selectdataFS() and the following optional arguments:</p> <ul style="list-style-type: none"> • persist: This option can be an empty value or a character containing 'on' or 'off'. The default value is persist="", that is brushing is allowed only once. If persist="on" or persist="off" brushing can be done as many time as the user requires. If persist='on' then the unit(s) currently brushed are added to those previously brushed. It is possible, every time a new brushing is done, to use a different color for the brushed units. If persist='off' every time a new brush is performed units previously brushed are removed. • labeladd: add labels of brushed units in the scatterplot matrix. If this option is '1', we label the units of the last selected group with the unit row index in the matrix X. The default value is labeladd="", i.e. no label is added.
trace	Whether to print intermediate results. Default is trace=FALSE.
...	potential further arguments passed to lower level functions.

Value

none

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Atkinson and Riani (2000), Robust Diagnostic Regression Analysis, Springer Verlag, New York.

Examples

```
## Not run:
data(hbk)
```

```
(out <- fsmult(hbk[,1:3], monitoring=TRUE))
mmdplot(out)

## End(Not run)
```

mmdrplot	<i>Plots the trajectories of minimum Mahalanobis distances from different starting points</i>
----------	---

Description

Plots the trajectories of minimum Mahalanobis distances from different starting points

Usage

```
mmdrplot(out, quant = c(0.01, 0.5, 0.99), envm, lwd, lwdenv, xlim, ylim,
  tag, datatooltip, label, xlab, ylab, envlab = TRUE, main, nameX,
  cex.lab, cex.axis, databrush, scaled = FALSE, trace = FALSE, ...)
```

Arguments

out	An object of S3 class <code>fsmmdrs.object</code> returned by <code>fsmmdrs</code> - a list containing the following elements: <ul style="list-style-type: none"> • <code>mmdrs</code> = a matrix of size (n-ninit)-by-(nsimul+1) containing the monitoring of minimum Mahalanobis distance in each step of the forward search for each of the nsimul random starts. The first column of <code>mmdrs</code> must contain the forward search index. This matrix can be created using function <code>fsmmdrs</code>. • <code>BBr</code>s = 3D array of size n-by-n-(init)-by-nsimul containing units forming subset for each random start. This field is necessary if <code>datatooltip</code> is true or <code>databrush</code> is not empty. • <code>X</code> = n-by-v matrix containing the original data matrix. This field is necessary if <code>datatooltip</code> is true or <code>databrush</code> is not empty.
quant	Quantiles for which envelopes have to be computed. The default is to produce 1%, 50% and 99% envelopes. In other words the default is <code>quant=c(0.01, 0.5, 0.99)</code> .
envm	Sample size for drawing envelopes. Specifies the size of the sample which is used to superimpose the envelope. The default is to add an envelope based on all the observations (size n envelope).
lwd	Controls the linewidth of the curve which contains the monitoring of minimum deletion residual.
lwdenv	line width: a scalar which controls the width of the lines associated with the envelopes. Default is <code>lwdenv=1</code>
xlim	Control the x scale in plot. Vector with two elements controlling minimum and maximum on the x axis. Default is to use automatic scale.

<code>ylim</code>	Control the y scale in plot. Vector with two elements controlling minimum and maximum on the y axis. Default is to use automatic scale.
<code>tag</code>	Plot handle. String which identifies the handle of the plot which is about to be created. The default is <code>tag='p1_mmd'</code> . Notice that if the program finds a plot which has a tag equal to the one specified by the user, then the output of the new plot overwrites the existing one in the same window else a new window is created.
<code>datatooltip</code>	If <code>datatooltip</code> is not empty the user can use the mouse in order to have information about the unit selected, the step in which the unit enters the search and the associated label. If <code>datatooltip</code> is a list, it is possible to control the aspect of the data cursor (see MATLAB function <code>datacursormode()</code> for more details or see the examples below). The default options are <code>DisplayStyle="Window"</code> and <code>SnapToDataVertex="on"</code> .
<code>label</code>	Row labels. Character vector containing the labels of the units (optional argument used when <code>datatooltip=TRUE</code> . If this field is not present <code>label1, ..., labeln</code> will be automatically created and included in the pop up <code>datatooltip</code> window).
<code>xlab</code>	A title for the x axis
<code>ylab</code>	A title for the y axis
<code>envlab</code>	whether to label the envelopes. If <code>envlab</code> is true (default) labels of the confidence envelopes which are used are added on the y axis.
<code>main</code>	An overall title for the plot
<code>nameX</code>	Add variable labels in the plot. A vector of strings of length <code>p</code> containing the labels of the variables of the original data matrix <code>X</code> . If it is empty (default) the sequence <code>X1, ..., Xp</code> will be created automatically
<code>cex.lab</code>	The magnification to be used for x and y labels relative to the current setting of <code>cex</code>
<code>cex.axis</code>	The magnification to be used for axis annotation relative to the current setting of <code>cex</code>
<code>databrush</code>	Interactive mouse brushing. If <code>databrush</code> is missing or empty (default), no brushing is done. The activation of this option (<code>databrush</code> is <code>TRUE</code> or a list) enables the user to select a set of trajectories in the current plot and to see them highlighted in the scatterplot matrix. If the scatterplot matrix does not exist it is automatically created. In addition, brushed units can be highlighted in the monitoring MD plot. Note that the window style of the other figures is set equal to that which contains the monitoring residual plot. In other words, if the monitoring residual plot is docked all the other figures will be docked too. If <code>databrush=TRUE</code> the default selection tool is a rectangular brush and it is possible to brush only once (that is <code>persist=""</code>). Note that the window style of the other figures is set equal to that which contains the monitoring residual plot. In other words, if the monitoring residual plot is docked all the other figures will be docked too If <code>databrush=TRUE</code> the default selection tool is a rectangular brush and it is possible to brush only once (that is <code>persist=""</code>). If <code>databrush=list(...)</code> , it is possible to use all optional arguments of the MATLAB function <code>selectdataFS()</code> and the following optional arguments:

1. `persist`. Persist is an empty value or a character containing 'on' or 'off'. The default value is `persist=""`, that is brushing is allowed only once. If `persist="on"` or `persist="off"` brushing can be done as many time as the user requires. If `persist='on'` then the unit(s) currently brushed are added to those previously brushed. It is possible, every time a new brushing is done, to use a different color for the brushed units. If `persist='off'` every time a new brush is performed units previously brushed are removed.
- `scaled` Whether to use scaled or unscaled envelopes. If `scaled=TRUE` the envelopes are produced for scaled Mahalanobis distances (no consistency factor is applied) else the traditional consistency factor is applied. Default is `scaled=FALSE`
- `trace` Whether to print intermediate results. Default is `trace=FALSE`.
- `...` potential further arguments passed to lower level functions.

Value

none

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Atkinson, A.C., Riani, M. and Cerioli, A. (2004), *'Exploring multivariate data with the forward search*, Springer Verlag, New York.

Examples

```
## Not run:
data(hbk)
out <- fsmmdrs(hbk[,1:3])
mmdrplot(out)

## End(Not run)
```

mmmult

Computes MM estimators in multivariate analysis with auxiliary S-scale

Description

Computes MM estimators in multivariate analysis with auxiliary S-scale

Usage

```
mmmult(x, monitoring = FALSE, plot = FALSE, eff, conflev = 0.975,
       nocheck = FALSE, trace = FALSE, ...)
```

Arguments

<code>x</code>	An $n \times p$ data matrix (n observations and p variables). Rows of x represent observations, and columns represent variables. Missing values (NA's) and infinite values (Inf's) are allowed, since observations (rows) with missing or infinite values will automatically be excluded from the computations.
<code>monitoring</code>	Whether to perform monitoring of Mahalanobis distances and other specific quantities
<code>plot</code>	Plots the Mahalanobis distances against index number. If <code>plot=FALSE</code> (default) or <code>plot=0</code> no plot is produced. The confidence level used to draw the confidence bands for the MD is given by the input option <code>conflev</code> . If <code>conflev</code> is not specified a nominal 0.975 confidence interval will be used. If <code>plot=2</code> a scatter plot matrix with the outliers highlighted is produced. If <code>plot</code> is a list it may contain the following fields: <ul style="list-style-type: none"> • <code>labeladd</code> If <code>labeladd=1</code>, the outliers in the <code>spm</code> are labelled with the unit row index. The default value is <code>labeladd=""</code>, i.e. no label is added • <code>nameY</code> character vector containing the labels of the variables. As default value, the labels which are added are <code>Y1, ...Yp</code>.
<code>eff</code>	Defining the nominal efficiency (i.e. a number between 0.5 and 0.99). The default value is <code>eff=0.95</code> .
<code>conflev</code>	confidence interval for the horizontal bands. It can be a vector of different confidence level values, e.g. <code>c(0.95, 0.99, 0.999)</code> . The confidence interval is based on the χ^2 distribution.
<code>nocheck</code>	It controls whether to perform checks on matrix Y . If <code>nocheck=TRUE</code> , no check is performed.
<code>trace</code>	Whether to print intermediate results. Default is <code>trace=FALSE</code> .
<code>...</code>	potential further arguments passed to lower level functions.

Details

This function follows the lines of MATLAB/R code developed during the years by many authors. For more details see <http://www.econ.kuleuven.be/public/NDBAE06/programs/> and the R package [CovMMest](#) The core of these routines, e.g. the resampling approach, however, has been completely redesigned, with considerable increase of the computational performance.

Value

Depending on the input parameter `monitoring`, one of the following objects will be returned:

1. `mmmult.object`
2. `mmmulteda.object`

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Maronna, R.A., Martin D. and Yohai V.J. (2006), *Robust Statistics, Theory and Methods*, Wiley, New York.

Examples

```
## Not run:
data(hbk)
(out <- mmmult(hbk[,1:3]))
class(out)
summary(out)

## Generate contaminated data (200,3)
n <- 200
p <- 3
set.seed(123456)
X <- matrix(rnorm(n*p), nrow=n)
Xcont <- X
Xcont[1:5, ] <- Xcont[1:5, ] + 3

out1 <- mmmult(Xcont, trace=TRUE)          # no plots (plot defaults to FALSE)
names(out1)

## plot=TRUE - generates: (1) a plot of Mahalanobis distances against
##   index number. The confidence level used to draw the confidence bands for
##   the MD is given by the input option conflev. If conflev is
##   not specified a nominal 0.975 confidence interval will be used and
##   (2) a scatter plot matrix with the outliers highlighted.

(out1 <- mmmult(Xcont, trace=TRUE, plot=TRUE))

## plots is a list: the spm shows the labels of the outliers.
(out1 <- mmmult(Xcont, trace=TRUE, plot=list(labeladd="1"))))

## plots is a list: the spm uses the variable names provided by 'nameY'.
(out1 <- mmmult(Xcont, trace=TRUE, plot=list(nameY=c("A", "B", "C"))))

## mmmult() with monitoring
(out2 <- mmmult(Xcont, monitoring=TRUE, trace=TRUE))
names(out2)

## Forgery Swiss banknotes examples.

data(swissbanknotes)

(out1 <- mmmult(swissbanknotes[101:200,], plot=TRUE))

(out1 <- mmmult(swissbanknotes[101:200,], plot=list(labeladd="1"))))

## End(Not run)
```

mmmult.object	<i>Description of mmmult.object Objects</i>
---------------	---

Description

An object of class `mmmult.object` holds information about the result of a call to `mmmult`.

Value

The object itself is basically a `list` with the following components:

<code>loc</code>	p-by-1 vector containing MM estimate of location.
<code>shape</code>	p-by-p matrix with MM estimate of the shape matrix.
<code>cov</code>	matrix with MM estimate of the covariance matrix. Remark: <code>covariance = auxscale^2 * shape</code> .
<code>weights</code>	A vector containing the estimates of the weights.
<code>outliers</code>	A vector containing the list of the units declared as outliers using confidence level specified in input scalar <code>conflev</code> .
<code>Sloc</code>	A vector with S estimate of location.
<code>Sshape</code>	A matrix with S estimate of the shape matrix.
<code>Scov</code>	A matrix with S estimate of the covariance matrix.
<code>auxscale</code>	S estimate of the scale.
<code>md</code>	n-by-1 vector containing the estimates of the robust Mahalanobis distances (in squared units).
<code>conflev</code>	Confidence level that was used to declare outliers.
<code>X</code>	the data matrix X

The object has class "mmmult".

Examples

```
## Not run:
data(hbk)
(out <- mmmult(hbk[,1:3]))
class(out)
summary(out)

## End(Not run)
```

mmmulteda.object	<i>Description of mmmulteda.object Objects</i>
------------------	--

Description

An object of class `mmmulteda.object` holds information about the result of a call to `mmmult` with `monitoring=TRUE`.

Value

The object itself is basically a `list` with the following components:

Loc	length(eff)-by-p matrix containing MM estimate of location for each value of eff.
Shape	p-by-p-by-length(eff) 3D array containing robust estimate of the shape for each value of eff. Remark: <code>detlshape=1</code> .
Scale	length(eff) vector containing robust estimate of the scale for each value of eff.
Cov	p-by-p-by-length(eff) 3D array containing robust estimate of covariance matrix for each value of eff. Note that <code>scale(i)^2 * shape[, , i]</code> = robust estimate of covariance matrix.
Bs	(p+1)-by-length(eff) matrix containing the units forming best subset for each value of eff.
MAL	n-by-length(eff) matrix containing the estimates of the robust Mahalanobis distances (in squared units) for each value of eff.
Outliers	n-by-length(eff) matrix containing flags for the outliers. Boolean matrix containing the list of the units declared as outliers for each value of eff using confidence level specified in input scalar <code>conflev</code>
Weights	n x length(eff) matrix containing the weights for each value of eff.
conflev	Confidence level that was used to declare outliers.
singsub	Number of subsets without full rank. Notice that <code>singsub > 0.1*(number of subsamples)</code> produces a warning.
eff	vector which contains the values of eff which have been used.
X	the data matrix X.

The object has class "mmmulteda".

Examples

```
## Not run:
  data(hbk)
  (out <- mmmult(hbk[,1:3], monitoring=TRUE))
  class(out)
  summary(out)

## End(Not run)
```

mmreg.object	<i>Description of mmreg Objects</i>
--------------	-------------------------------------

Description

An object of class `mmreg.object` holds information about the result of a call to `fsreg` with `method="MM"`.

Value

The object itself is basically a `list` with the following components:

<code>beta</code>	p-by-1 vector containing the MM estimate of regression coefficients.
<code>auxscale</code>	scalar, S estimate of the scale (or supplied external estimate of scale, if option <code>InitialEst</code> is not empty).
<code>residuals</code>	residuals.
<code>fittedvalues</code>	fitted values.
<code>weights</code>	n x 1 vector. Weights assigned to each observation.
<code>Sbeta</code>	p x 1 vector containing S estimate of regression coefficients (or supplied initial external estimate of regression coefficients, if option <code>InitialEst</code> is not empty)
<code>Ssingsub</code>	Number of subsets without full rank in the S preliminary part. Notice that <code>out.singsub > 0.1*(number of subsamples)</code> produces a warning.
<code>outliers</code>	kx1 vector containing the list of the k units declared as outliers or NULL if the sample is homogeneous.
<code>conflev</code>	Confidence level which is used to declare units as outliers. Usually <code>conflev=0.95, 0.975, 0.99</code> (individual alpha) or <code>conflev=1-0.05/n, 1-0.025/n, 1-0.01/n</code> (simultaneous alpha). Default value is 0.975
<code>rhofunc</code>	Specifies the rho function which has been used to weight the residuals. If a different rho function is specified for S and MM loop then insted of <code>rhofunc</code> we will have <code>rhofuncS</code> and <code>rhofuncMM</code> .
<code>rhofuncparam</code>	Vector which contains the additional parameters for the specified rho function which has been used. For hyperbolic rho function the value of <code>k =sup CVC</code> . For Hampel rho function the parameters a, b and c. If a different rho function is specified for S and MM loop then insted of <code>rhofuncparam</code> we will have <code>rhofuncparamS</code> and <code>rhofuncparamMM</code> .
<code>X</code>	the data matrix X
<code>y</code>	the response vector y

The object has class `"mmreg"`.

Examples

```
## Not run:
  (out <- fsreg(Y~., data=hbk, method="MM"))
  class(out)
  summary(out)

## End(Not run)
```

mmregeda.object	<i>Description of mmregeda Objects</i>
-----------------	--

Description

An object of class `mmregeda.object` holds information about the result of a call to `fsreg` when `method="MM"` and `monitoring=TRUE`.

Value

The object itself is basically a `list` with the following components:

<code>auxscale</code>	scalar, S estimate of the scale (or supplied external estimate of scale, if option <code>InitialEst</code> is not empty).
<code>Beta</code>	$p \times \text{length}(\text{eff})$ matrix containing MM estimate of regression coefficients for each value of <code>eff</code> .
<code>RES</code>	$n \times \text{length}(\text{eff})$ matrix containing the monitoring of scaled residuals for each value of <code>eff</code> .
<code>Weights</code>	$n \times \text{length}(\text{eff})$ matrix containing the estimates of the weights for each value of <code>eff</code>
<code>Outliers</code>	Boolean matrix containing the list of the units declared as outliers for each value of <code>eff</code> using confidence level specified in input scalar <code>conflev</code> .
<code>conflev</code>	Confidence level which is used to declare units as outliers. Remark: <code>conflev</code> will be used to draw the horizontal line (confidence band) in the plot.
<code>Ssingsub</code>	Number of subsets without full rank. Notice that <code>singsub > 0.1 * (number of subsamples)</code> produces a warning
<code>rhofunc</code>	string identifying the rho function which has been used.
<code>rhofuncparam</code>	vector which contains the additional parameters for the specified rho function which have been used. For hyperbolic rho function the value of <code>k = sup CVC</code> . For Hampel rho function the parameters <code>a</code> , <code>b</code> and <code>c</code> .
<code>eff</code>	vector containing the value of <code>eff</code> which have been used.
<code>X</code>	the data matrix <code>X</code>
<code>y</code>	the response vector <code>y</code>

The object has class `"mmregeda"`.

Examples

```
## Not run:
  (out <- fsreg(Y~., data=hbk, method="MM", monitoring=TRUE))
  class(out)
  summary(out)

## End(Not run)
```

<code>MMregeda_control</code>	<i>Creates an MMregeda_control object</i>
-------------------------------	---

Description

Creates an object of class `MMregeda_control` to be used with the `fsreg()` function, containing various control parameters.

Usage

```
MMregeda_control(intercept = TRUE, InitialEst, Soptions, eff, effshape,
  refsteps = 3, tol = 1e-07, conflev, nocheck = FALSE, plot = FALSE)
```

Arguments

<code>intercept</code>	Indicator for constant term. Scalar. If <code>intercept=TRUE</code> , a model with constant term will be fitted (default), else, no constant term will be included.
<code>InitialEst</code>	Starting values of the MM-estimator, a list with the following elements: <code>loc</code> , a $p \times 1$ vector, location vector estimate and <code>scale</code> , a scalar, estimate of the scale. If empty (default) the program will use S estimators. In this last case it is possible to specify the options given in function <code>Sreg</code> .
<code>Soptions</code>	Options to pass to <code>Sreg</code> , an <code>Sreg_control</code> object. The options are: <code>Srhofunc</code> , <code>Snsamp</code> , <code>Srefsteps</code> , <code>Sreftol</code> , <code>Srefstepsbest</code> , <code>Sreftolbest</code> , <code>Sminsctol</code> , <code>Sbest</code> . See function <code>Sreg_control</code> for more details on these options. It is necessary to add to the S options the letter S at the beginning. For example, if you want to use the optimal rho function the supplied option is <code>'Srhofunc','optimal'</code> . For example, if you want to use 3000 subsets, the supplied option is <code>'Snsamp',3000</code>
<code>eff</code>	Vector defining nominal efficiency (i.e. a series of numbers between 0.5 and 0.99). The default value is the sequence <code>seq(0.5, 0.99, 0.01)</code>
<code>effshape</code>	Location or scale efficiency. If <code>effshape=1</code> efficiency refers to shape efficiency else (default) efficiency refers to location efficiency.
<code>refsteps</code>	Number of refining iterations in each subsample (default is <code>refsteps=3</code>). <code>refsteps = 0</code> means "raw-subsampling" without iterations.
<code>tol</code>	Scalar controlling tolerance in the MM loop. The default value is <code>tol=1e-6</code> .

conflev	Confidence level which is used to declare units as outliers. Usually conflev=0.95, 0.975, 0.99 (individual alpha) or conflev=1-0.05/n, 1-0.025/n, 1-0.01/n (simultaneous alpha). Default value is 0.975
nocheck	Check input arguments, scalar. If nocheck=TRUE no check is performed on matrix y and matrix X. Notice that y and X are left unchanged. In other words the additional column of ones for the intercept is not added. As default nocheck=FALSE.
plot	Plot on the screen. Scalar. If plots=TRUE the plot of minimum deletion residual with envelopes based on n observations and the scatterplot matrix with the outliers highlighted is produced. If plots=2 the user can also monitor the intermediate plots based on envelope superimposition. If plots=FALSE (default) no plot is produced.

Details

Creates an object of class MMregeda_control to be used with the fsreg() function, containing various control parameters.

Value

An object of class "MMregeda_control" which is basically a [list](#) with components the input arguments of the function mapped accordingly to the corresponding Matlab function.

Author(s)

FSDA team

See Also

See Also as [FSR_control](#), [Sreg_control](#), [MMreg_control](#) and [LXS_control](#)

Examples

```
## Not run:
(out <- fsreg(Y~., data=hbk, method="MM", monitoring=TRUE,
  control=MMregeda_control(eff=seq(0.75, 0.99, 0.01))))

## End(Not run)
```

MMreg_control

Creates an MMreg_control object

Description

Creates an object of class MMreg_control to be used with the fsreg() function, containing various control parameters for calling the MATLAB function MMreg().

Usage

```
MMreg_control(intercept = TRUE, InitialEst, Soptions, eff, effshape,
  rhofunc = c("bisquare", "optimal", "hyperbolic", "hampel"), rhofuncparam,
  refsteps = 3, tol = 1e-07, conflev,
  msg = TRUE, nocheck = FALSE, plot = FALSE)
```

Arguments

intercept	Indicator for constant term. Scalar. If intercept=TRUE, a model with constant term will be fitted (default), else, no constant term will be included.
InitialEst	Starting values of the MM-estimator, a list with the following elements: loc, a $p \times 1$ vector, location vector estimate and scale, a scalar, estimate of the scale. If empty (default) the program will use S estimators. In this last case it is possible to specify the options given in function Sreg.
Soptions	Options to pass to Sreg, an Sreg_control object. The options are: Srhofunc, Snsamp, Srefsteps, Sreftol, Srefstepsbest, Sreftolbest, Sminstol, Sbest. See function Sreg_control for more details on these options. It is necessary to add to the S options the letter S at the beginning. For example, if you want to use the optimal rho function the supplied option is 'Srhofunc','optimal'. For example, if you want to use 3000 subsets, the supplied option is 'Snsamp',3000
eff	Scalar defining nominal efficiency (i.e. a number between 0.5 and 0.99). The default value is 0.95.
effshape	Location or scale efficiency. If effshape=1 efficiency refers to shape efficiency else (default) efficiency refers to location efficiency.
rhofunc	Specifies the rho function which must be used to weight the residuals. Possible values are 'bisquare' 'optimal' 'hyperbolic' 'hampel'. <ol style="list-style-type: none"> 'bisquare' uses Tukey's rho and psi functions. See TBrho and TBpsi. 'optimal' uses optimal rho and psi functions. See OPTrho and OPTpsi. 'hyperbolic' uses hyperbolic rho and psi functions. See HYPrho and HYPpsi. 'hampel' uses Hampel rho and psi functions. See HARho and HAPsi. The default is 'bisquare'.
rhofuncparam	Additional parameters for the specified rho function. For hyperbolic rho function it is possible to set up the value of $k = \sup CVC$ (the default value of k is 4.5). For Hampel rho function it is possible to define parameters a, b and c (the default values are a=2, b=4, c=8)
refsteps	Number of refining iterations in each subsample (default is refsteps=3). refsteps = 0 means "raw-sampling" without iterations.
tol	Scalar controlling tolerance in the MM loop. The default value is tol=1e-6
conflev	Confidence level which is used to declare units as outliers. Usually conflev=0.95, 0.975, 0.99 (individual alpha) or conflev=1-0.05/n, 1-0.025/n, 1-0.01/n (simultaneous alpha). Default value is 0.975

msg	Controls whether to display or not messages on the screen. If msg==1 (default) messages are displayed on the screen about step in which signal took place else no message is displayed on the screen.
nocheck	Check input arguments, scalar. If nocheck=TRUE no check is performed on matrix y and matrix X. Notice that y and X are left unchanged. In other words the additional column of ones for the intercept is not added. As default nocheck=FALSE.
plot	Plot on the screen. Scalar. If plots=TRUE the plot of minimum deletion residual with envelopes based on n observations and the scatterplot matrix with the outliers highlighted is produced. If plots=2 the user can also monitor the intermediate plots based on envelope superimposition. If plots=FALSE (default) no plot is produced.

Details

Creates an object of class `MMreg_control` to be used with the `fsreg()` function, containing various control parameters.

Value

An object of class "MMreg_control" which is basically a `list` with components the input arguments of the function mapped accordingly to the corresponding Matlab function.

Author(s)

FSDA team

See Also

See Also as [FSR_control](#), [MMreg_control](#) and [LXS_control](#)

Examples

```
## Not run:
## (out <- fsreg(Y~., data=hbk, method="MM", control=MMreg_control(eff=0.99, rhofunc="optimal")))
(out <- fsreg(Y~., data=hbk, method="MM", control=MMreg_control(eff=0.99)))

## End(Not run)
```

resfwdplot

Plots the trajectories of the monitored scaled (squared) residuals

Description

Plots the trajectories of the monitored scaled (squared) residuals

Usage

```
resfwdplot(out,
  xlim, ylim, xlab, ylab, main, lwd, lty, col, cex.lab, cex.axis,
  xvalues,
  fg.thresh, fg.unit, fg.labstep, fg.lwd, fg.lty, fg.col, fg.mark, fg.cex,
  bg.thresh, bg.style,
  tag, datatooltip, label, nameX, namey, msg, databrush,
  standard, fground, bground, ...)
```

Arguments

out	<p>An object returned by one of the monitoring functions (see FSReda_control, Sregeda_control and MMregeda_control). The object is one of fsreda.object, sregeda.object or mmregeda.object.</p> <p>The needed elements of out are</p> <ol style="list-style-type: none"> 1. RES: matrix containing the residuals monitored in each step of the forward search or any other robust procedure. Every row is associated with a residual (unit). This matrix can be created using function FSReda, Sregeda, MMregeda. 2. Un: (for FSR only) - matrix containing the order of entry in the subset of each unit (required only when <code>datatooltip</code> is true or <code>databrush</code> is not empty). 3. bdp: (for Sreg only) - vector containing a sequence of breakdown point values to monitor on. 4. eff: (for MMreg only) - vector containing a sequence of efficiency values to monitor on. 5. y: a vector containing the response (required only when option <code>databrush</code> is requested). 6. X: a matrix containing the explanatory variables (required only when option <code>databrush</code> is requested). 7. Bols: $(n\text{-init}+1) \times (p+1)$ matrix containing the estimated beta coefficients monitored in each step of the robust procedure (required only when option <code>databrush</code> is requested and suboption <code>multivarfit</code> is requested).
ylim	Control y scale in plot. Vector with two elements controlling minimum and maximum on the y axis. Default is to use automatic scale.
xlim	Control x scale in plot. Vector with two elements controlling minimum and maximum on the x axis. Default is to use automatic scale.
xlab	a title for the x axis
ylab	a title for the y axis
main	an overall title for the plot
lwd	The line width, a positive number, defaulting to 1
lty	The line type. Line types can either be specified as an integer (1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash". The latter two are not supported by Matlab.

<code>col</code>	colors to be used for the highlighted units
<code>cex.lab</code>	The magnification to be used for x and y labels relative to the current setting of <code>cex</code>
<code>cex.axis</code>	The magnification to be used for axis annotation relative to the current setting of <code>cex</code>
<code>xvalues</code>	values for the x axis. Numeric vector of <code>ncol(RES)</code> controlling the x axis coordinates. The default value of <code>xvalues</code> is <code>(nrow(RES) - ncol(RES) + 1) : nrow(RES)</code>
<code>fg.thresh</code>	(alternative to <code>fg.unit</code>) numeric vector of length 1 or 2 which specifies the highlighted trajectories. If <code>length(fthresh) == 1</code> the highlighted trajectories are those of units that throughout the search had at least once a residual greater (in absolute value) than <code>thresh</code> . The default value is <code>fg.thresh=2.5</code> . If <code>length(fthresh) == 2</code> the highlighted trajectories are those of units that throughout the search had a residual at least once bigger than <code>fg.thresh[2]</code> or smaller than <code>fg.thresh[1]</code> .
<code>fg.unit</code>	(alternative to <code>fg.thresh</code>), vector containing the list of the units to be highlighted. If <code>fg.unit</code> is supplied, <code>fg.thresh</code> is ignored.
<code>fg.labstep</code>	numeric vector which specifies the steps of the search where to put labels for the highlighted trajectories (units). The default is to put the labels at the initial and final steps of the search. <code>fg.labstep=''</code> means no label.
<code>fg.lwd</code>	The line width for the highlighted trajectories (units). Default is 1.
<code>fg.lty</code>	The line type for the highlighted trajectories (units). Line types can either be specified as an integer (1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash". The latter two are not supported by Matlab.
<code>fg.col</code>	colors to be used for the highlighted units.
<code>fg.mark</code>	Controls whether to plot highlighted trajectories as symbols. if <code>fg.mark==TRUE</code> each line is plotted using a different symbol else no marker is used (default).
<code>fg.cex</code>	controls the font size of the labels of the trajectories in foreground.
<code>bg.thresh</code>	numeric vector of length 1 or 2 which specifies how to define the unimportant trajectories. Unimportant trajectories will be plotted using a colormap, in greyish or will be hidden. If <code>length(thresh) == 1</code> the irrelevant units are those which always had a residual smaller (in absolute value) than <code>thresh</code> . If <code>length(bthresh) == 2</code> the irrelevant units are those which always had a residual greater than <code>bthresh(1)</code> and smaller than <code>bthresh(2)</code> . The default is: <code>bg.thresh=2.5</code> if <code>n > 100</code> and <code>bg.thresh=-Inf</code> if <code>n <= 100</code> i.e. to treat all trajectories as important if <code>n <= 100</code> and, if <code>n > 100</code> , to reduce emphasis only to trajectories having in all steps of the search a value of scaled residual smaller than 2.5.
<code>bg.style</code>	specifies how to plot the unimportant trajectories as defined in option <code>bthresh</code> . <ol style="list-style-type: none"> <code>bg.style="faint"</code>: unimportant trajectories are plotted using a colormap. <code>bg.style="hide"</code>: unimportant trajectories are hidden. <code>bg.style="greyish"</code>: unimportant trajectories are displayed in a faint grey. <p>When <code>n>100</code> the default option is <code>bg.style='faint'</code>. When <code>n <= 100</code> and <code>bg.thresh == -Inf</code> option <code>bstyle</code> is ignored. Remark: <code>bground=""</code> is equivalent to <code>-Inf</code> that is all trajectories are considered relevant.</p>

tag	Plot handle. String which identifies the handle of the plot which is about to be created. The default is to use tag 'pl_resfwd'. Notice that if the program finds a plot which has a tag equal to the one specified by the user, then the output of the new plot overwrites the existing one in the same window else a new window is created.
datatooltip	<p>Interactive clicking. It is inactive if this parameter is missing or empty. The default is datatooltip=TRUE, i.e. the user can select with the mouse an individual residual trajectory in order to have information about the corresponding unit. The information displayed depends on the estimator in use.</p> <p>For example for class <code>fsreda.object</code> the information concerns the label and the step of the search in which the unit enters the subset. If datatooltip is a list it may contain the following fields:</p> <ol style="list-style-type: none"> 1. DisplayStyle determines how the data cursor displays. Possible values are 'datatip' and 'window' (default). 'datatip' displays data cursor information in a small yellow text box attached to a black square marker at a data point you interactively select. 'window' displays data cursor information for the data point you interactively select in a floating window within the figure. 2. SnapToDataVertex: specifies whether the data cursor snaps to the nearest data value or is located at the actual pointer position. Possible values are SnapToDataVertex='on' (default) and SnapToDataVertex='off'. 3. LineColor: controls the color of the trajectory selected with the mouse. It can be an RGB triplet of values between 0 and 1, or character vector indicating a color name. Note that a RGB vector can be conveniently chosen with our MATLAB class FSColor, see documentation. 4. SubsetLinesColor: enables to control the color of the trajectories of the units that are in the subset at a given step of the search (if resfwdplot() is applied to an object of class <code>fsreda.object</code>) or have a weight greater than 0.9 (if resfwdplot() is applied to an object of class <code>sregeda.object</code> or <code>mmregeda.object</code>). This can be done (repeatedly) with a left mouse click in proximity of the step of interest. A right mouse click will terminate the selection by marking with a up-arrow the step corresponding to the highlighted lines. The highlighted lines by default are in red, but a different color can be specified as RGB triplet or character of color name. Note that a RGB vector can be conveniently chosen with our MATLAB class FSColor, see documentation. By default SubsetLinesColor="", i.e. the modality is not active. Any initialization for SubsetLinesColor which cannot be interpreted as RGB vector will be converted to blue, i.e. SubsetLinesColor will be forced to be [0 0 1]. If SubsetLinesColor is not empty the previous option LineColor is ignored.
label	Character vector containing the labels of the units (optional argument used when datatooltip=TRUE. If this field is not present labels row1, ..., rown will be automatically created and included in the pop up datatooltip window).
nameX	Add variable labels in plot. A vector of strings of length p containing the labels of the variables of the regression dataset. If it is empty (default) the sequence X1, ..., Xp will be created automatically
namey	Add response label. A string containing the label of the response

`msg` Controls whether to display or not messages on the screen. If `msg==1` (default) messages are displayed on the screen about step in which signal took place else no message is displayed on the screen.

`databrush` interactive mouse brushing. If `databrush` is missing or empty (default), no brushing is done. The activation of this option (`databrush` is a scalar or a list) enables the user to select a set of trajectories in the current plot and to see them highlighted in the `y|X` plot, i.e. a matrix of scatter plots of `y` against each column of `X`, grouped according to the selection(s) done by brushing. If the plot `y|X` does not exist it is automatically created. In addition, brushed units are automatically highlighted in the minimum deletion residual plot if it is already open. The extension to the following plots will be available in future versions of the toolbox:

1. monitoring leverage plot;
2. maximum studentized residual;
3. s^2 and R^2 ;
4. Cook distance and modified Cook distance;
5. deletion t statistics.

Note that the window style of the other figures is set equal to that which contains the monitoring residual plot. In other words, if the monitoring residual plot is docked all the other figures will be docked too.

If `databrush=TRUE` the default selection tool is a rectangular brush and it is possible to brush only once (that is `persist=""`).

If `databrush=list(...)`, it is possible to use all optional arguments of function `selectdataFS()` and the following optional argument:

1. `persist`. `Persist` is an empty value or a character containing 'on' or 'off'. The default value is `persist=""`, that is brushing is allowed only once. If `persist="on"` or `persist="off"` brushing can be done as many times as the user requires. If `persist='on'` then the unit(s) currently brushed are added to those previously brushed. It is possible, every time a new brushing is done, to use a different color for the brushed units. If `persist='off'` every time a new brush is performed units previously brushed are removed.
2. `bivarfitWheather` to superimpose bivariate least square lines on the plot (if `plot=TRUE`). This option adds one or more least squares lines, based on SIMPLE REGRESSION of `y` on `Xi`, to the plots of `y|Xi`. The default is `bivarfit=FALSE`: no line is fitted. If `bivarfit=1`, a single OLS line is fitted to all points of each bivariate plot in the scatter matrix `y|X`. If `bivarfit=2`, two OLS lines are fitted: one to all points and another to the group of the genuine observations. The group of the potential outliers is not fitted. If `bivarfit=0` one OLS line is fitted to each group. This is useful for the purpose of fitting mixtures of regression lines. If `bivarfit='i1'` or `bivarfit='i2'`, etc. an OLS line is fitted to a specific group, the one with index 'i' equal to 1, 2, 3 etc. Again, useful in case of mixtures.
3. `multivarfitWheather` to superimpose multivariate least square lines. This option adds one or more least square lines, based on MULTIVARIATE REGRESSION of `y` on `X`, to the plots of `y|Xi`. The default is `multivarfit=FALSE`: no line is fitted. If `bivarfit=1`, a single OLS line is fitted to all points of

each bivariate plot in the scatter matrix $y|X$. The line added to the scatter plot $y|X_i$ is $avconst + C_i * X_i$, where C_i is the coefficient of X_i in the multivariate regression and $avconst$ is the effect of all the other explanatory variables different from X_i evaluated at their centroid (that is $\overline{(y)'C}$). If `multivarfit=2`, same action as with `multivarfit=1` but this time we also add the line based on the group of unselected observations (i.e. the normal units).

4. `labeladd` Add outlier labels in plot. If `labeladd=TRUE`, we label the outliers with the unit row index in matrices X and y . The default value is `labeladd=FALSE`, i.e. no label is added.

<code>standard</code>	(MATLAB-style arguments) appearance of the plot in terms of <code>xlim</code> , <code>ylim</code> , axes labels and their font size style, color of the lines, etc.
<code>fground</code>	MATLAB-style arguments for the <code>fground</code> trajectories in foreground.
<code>bground</code>	MATLAB-style arguments for the <code>fground</code> trajectories in background.
<code>...</code>	potential further arguments passed to lower level functions.

Details

No details

Value

No value returned

Author(s)

FSDA team

Examples

```
## Not run:

n <- 100
y <- rnorm(n)
X <- matrix(rnorm(n*4), nrow=n)

out <- fsreg(y~X, method="LTS")
out <- fsreg(y~X, method="FS", bsb=out$bs, monitoring=TRUE)
resfwdplot(out)

## End(Not run)
```

resindexplot	<i>Plots the residuals from a regression analysis versus index number or any other variable</i>
--------------	---

Description

The function `resindexplot()` plots the residuals from a regression analysis versus index number or any other variable. The residuals come from an output object of any of the regression functions or a simply a vector of values. In order to use the `databrush` option, the residuals must come from one of the `fsdaR` regression functions.

Usage

```
resindexplot(out, x, xlim, ylim, xlab, ylab, main, numlab, indlab, conflev, cex.axis,
             cex.lab, lwd, nameX, namey, tag, col, cex, databrush, ...)
```

Arguments

out	A vector containing the residuals from a regression analysis or an object returned by one of the regression functions (see FSR_control , LXS_control , Sreg_control and MMreg_control). The object is one of fsr.object , fsdalts.object , fsdalms.object , sreg.object or mmreg.object . The needed elements of out are at least residuals, but if the option <code>databrush</code> is used, also X and y will be needed.
x	The vector to be plotted on the x-axis. As default the sequence <code>1:length(residuals)</code> will be used
xlim	Control x scale in plot. Vector with two elements controlling minimum and maximum on the x axis. Default is to use automatic scale.
ylim	Control y scale in plot. Vector with two elements controlling minimum and maximum on the y axis. Default is to use automatic scale.
xlab	a title for the x axis
ylab	a title for the y axis
main	an overall title for the plot
numlab	Number of points to be identified in plots (see also <code>indlab</code>) . By default the five points with largest values will be identified. If <code>numlab</code> is a single number containing scalar k, the units with the k largest residuals are labelled in the plots. If <code>numlab</code> is a vector, the units inside vector <code>numlab</code> are labelled in the plots. The default value of <code>numlab=5</code> and the units with the 5 largest residuals will be labelled. If <code>numlab=0</code> or <code>numlab=NULL</code> no labelling will be done.
indlab	Which points to be identified in plots (see also <code>numlab</code>) - the units with indexes in the vector <code>indlab</code> are labelled in the plots.
conflev	Confidence interval for the horizontal bands (a numeric vector). It can be a vector of different confidence level values. Remark: confidence interval is based on the χ^2 distribution

<code>cex.axis</code>	The magnification to be used for axis annotation relative to the current setting of <code>cex</code>
<code>cex.lab</code>	The magnification to be used for x and y labels relative to the current setting of <code>cex</code>
<code>lwd</code>	The line width, a positive number, defaulting to 1
<code>tag</code>	Figure tag (character). Tag of the figure which will host the <code>resindexplot</code> . The default tag is <code>icodepl_resindex</code> .
<code>col</code>	Fill color for markers that are closed shapes (circle, square, diamond, pentagram, hexagram, and the four triangles). Can be 'none' or 'auto' or color name(string) or RGB triplet.
<code>cex</code>	Size of the point symbols. The magnification to be used relative to the current setting of <code>cex</code> .
<code>nameX</code>	Add variable labels in plot. A vector of strings of length <code>p</code> containing the labels of the variables of the regression dataset. If it is empty (default) the sequence <code>X1, . . . , Xp</code> will be created automatically
<code>namey</code>	Add response label. A string containing the label of the response
<code>databrush</code>	Interactive mouse brushing. If <code>databrush</code> is missing or empty (default) or <code>databrush=FALSE</code> , no brushing is done. The activation of this option (<code>databrush</code> is a scalar or a list) enables the user to select a set of trajectories in the current plot and to see them highlighted in the <code>y X</code> plot, i.e. a matrix of scatter plots of <code>y</code> against each column of <code>X</code> , grouped according to the selection(s) done by brushing. If the plot <code>y X</code> does not exist it is automatically created. In addition, brushed units are automatically highlighted in the minimum deletion residual plot if it is already open. The extension to the following plots will be available in future versions of the package: <ol style="list-style-type: none"> 1. monitoring leverage plot; 2. maximum studentized residual; 3. s^2 and R^2; 4. Cook distance and modified Cook distance; 5. deletion t statistics.

Note that the window style of the other figures is set equal to that which contains the monitoring residual plot. In other words, if the monitoring residual plot is docked all the other figures will be docked too

If `databrush=TRUE` the default selection tool is a rectangular brush and it is possible to brush only once (that is `persist=""`).

If `databrush=list(...)`, it is possible to use all optional arguments of function `selectdataFS()` and the following optional argument:

1. `persist`: Persist is an empty value or a character containing 'on' or 'off'. The default value is `persist=""`, that is brushing is allowed only once. If `persist="on"` or `persist="off"` brushing can be done as many time as the user requires. If `persist='on'` then the unit(s) currently brushed are added to those previously brushed. It is possible, every time a new brushing is done, to use a different color for the brushed units. If `persist='off'` every time a new brush is performed units previously brushed are removed.

2. `bivarfit`: This option adds one or more least square lines based on SIMPLE REGRESSION to the plots of $y|X$, depending on the selected groups. The default is `bivarfit=FALSE`: no line is fitted. If `bivarfit=1`, a single OLS line is fitted to all points of each bivariate plot in the scatter matrix $y|X$. If `bivarfit=2`, two OLS lines are fitted: one to all points and another to the group of the genuine observations. The group of the potential outliers is not fitted. If `bivarfit=0` one OLS line is fitted to each group. This is useful for the purpose of fitting mixtures of regression lines. If `bivarfit='i1'` or `bivarfit='i2'`, etc. an OLS line is fitted to a specific group, the one with index 'i' equal to 1, 2, 3 etc. Again, useful in case of mixtures.
3. `multivarfit`: Whether to superimpose multivariate least square lines. This option adds one or more least square lines, based on MULTIVARIATE REGRESSION of y on X , to the plots of $y|X_i$. The default is `multivarfit=FALSE`: no line is fitted. If `bivarfit=1`, a single OLS line is fitted to all points of each bivariate plot in the scatter matrix $y|X$. The line added to the scatter plot $y|X_i$ is $avconst + C_i * X_i$, where C_i is the coefficient of X_i in the multivariate regression and $avconst$ is the effect of all the other explanatory variables different from X_i evaluated at their centroid (that is $\overline{(y)'C}$). If `multivarfit=2`, same action as with `multivarfit=1` but this time we also add the line based on the group of unselected observations (i.e. the normal units).
4. `labeladd`: Add outlier labels in plot. If `labeladd=TRUE`, we label the outliers with the unit row index in matrices X and y . The default value is `labeladd=FALSE`, i.e. no label is added.

... potential further arguments passed to lower level functions.

Details

No details

Value

No value returned

Author(s)

FSDA team

Examples

```
## Not run:
out <- fsreg(stack.loss~., data=stackloss)
resindexplot(out, conflev=c(0.95,0.99), col="green")

## End(Not run)
```

smult

*Computes S estimators in multivariate analysis***Description**

Computes S estimators in multivariate analysis

Usage

```
smult(x, monitoring = FALSE, plot = FALSE, bdp, nsamp,
      conflev = 0.975, nocheck = FALSE, trace = FALSE, ...)
```

Arguments

x	An n x p data matrix (n observations and p variables). Rows of x represent observations, and columns represent variables. Missing values (NA's) and infinite values (Inf's) are allowed, since observations (rows) with missing or infinite values will automatically be excluded from the computations.
monitoring	Whether to perform monitoring of Mahalanobis distances and other specific quantities
plot	Plots the Mahalanobis distances against index number. If plot=FALSE (default) or plot=0 no plot is produced. The confidence level used to draw the confidence bands for the MD is given by the input option conflev. If conflev is not specified a nominal 0.975 confidence interval will be used. If plot=2 a scatter plot matrix with the outliers highlighted is produced. If plot is a list it may contain the following fields: <ul style="list-style-type: none"> • labeladd If labeladd=1, the outliers in the spm are labelled with the unit row index. The default value is labeladd="", i.e. no label is added • nameY character vector containing the labels of the variables. As default value, the labels which are added are Y1, ...Yp.
bdp	Measures the fraction of outliers the algorithm should resist. In this case any value greater than 0 but smaller or equal than 0.5 will do fine (default is bdp=0.5). Note that given bdp nominal efficiency is automatically determined.
nsamp	Number of subsamples which will be extracted to find the robust estimator. If nsamp=0 all subsets will be extracted. They will be (n choose p). If the number of all possible subset is <1000 the default is to extract all subsets otherwise just 1000.
conflev	confidence interval for the horizontal bands. It can be a vector of different confidence level values, e.g. c(0.95, 0.99, 0.999). The confidence interval is based on the chi ² distribution.
nocheck	It controls whether to perform checks on matrix Y. If nocheck=TRUE, no check is performed.
trace	Whether to print intermediate results. Default is trace=FALSE.
...	potential further arguments passed to lower level functions.

Details

This function follows the lines of MATLAB/R code developed during the years by many authors. For more details see <http://www.econ.kuleuven.be/public/NDBAE06/programs/> and the R package [CovSest](#). The core of these routines, e.g. the resampling approach, however, has been completely redesigned, with considerable increase of the computational performance.

Value

Depending on the input parameter `monitoring`, one of the following objects will be returned:

1. `smult.object`
2. `smulteda.object`

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Maronna, R.A., Martin D. and Yohai V.J. (2006), *Robust Statistics, Theory and Methods*, Wiley, New York.

Examples

```
## Not run:
data(hbk)
(out <- smult(hbk[,1:3]))
class(out)
summary(out)

## Generate contaminated data (200,3)
n <- 200
p <- 3
set.seed(123456)
X <- matrix(rnorm(n*p), nrow=n)
Xcont <- X
Xcont[1:5, ] <- Xcont[1:5, ] + 3

out1 <- smult(Xcont, trace=TRUE)           # no plots (plot defaults to FALSE)
names(out1)

## plot=TRUE - generates: (1) a plot of Mahalanobis distances against
##   index number. The confidence level used to draw the confidence bands for
##   the MD is given by the input option conflav. If conflav is
##   not specified a nominal 0.975 confidence interval will be used and
##   (2) a scatter plot matrix with the outliers highlighted.

(out1 <- smult(Xcont, trace=TRUE, plot=TRUE))

## plots is a list: the spm shows the labels of the outliers.
```

```
(out1 <- smult(Xcont, trace=TRUE, plot=list(labeladd="1")))

## plots is a list: the spm uses the variable names provided by 'nameY'.
(out1 <- smult(Xcont, trace=TRUE, plot=list(nameY=c("A", "B", "C"))))

## smult() with monitoring
(out2 <- smult(Xcont, monitoring=TRUE, trace=TRUE))
names(out2)

## Forgery Swiss banknotes examples.

data(swissbanknotes)

(out1 <- smult(swissbanknotes[101:200,], plot=TRUE))

(out1 <- smult(swissbanknotes[101:200,], plot=list(labeladd="1")))

## End(Not run)
```

smult.object	<i>Description of smult.object Objects</i>
--------------	--

Description

An object of class `smult.object` holds information about the result of a call to `smult`.

Value

The object itself is basically a `list` with the following components:

<code>loc</code>	p-by-1 vector containing S estimate of location.
<code>shape</code>	p-by-p matrix containing robust estimate of the shape matrix. Remark: <code>det(shape)=1</code> .
<code>scale</code>	robust estimate of the scale.
<code>cov</code>	$scale^2 * shape$: robust estimate of covariance matrix.
<code>bs</code>	a (p+1) vector containing the units forming best subset associated with S estimate of location.
<code>md</code>	n-by-1 vector containing the estimates of the robust Mahalanobis distances (in squared units). This vector contains the distances of each observation from the location of the data, relative to the scatter matrix <code>cov</code> .
<code>outliers</code>	A vector containing the list of the units declared as outliers using confidence level specified in input scalar <code>conflev</code> .
<code>conflev</code>	Confidence level that was used to declare outliers.
<code>singsub</code>	Number of subsets without full rank. Notice that <code>singsub > 0.1 * (number of subsamples)</code> produces a warning.
<code>weights</code>	n x 1 vector containing the estimates of the weights.
<code>X</code>	the data matrix X

The object has class "smult".

Examples

```
## Not run:
data(hbk)
(out <- smult(hbk[,1:3]))
class(out)
summary(out)

## End(Not run)
```

smulteda.object	<i>Description of smulteda.object Objects</i>
-----------------	---

Description

An object of class `smulteda.object` holds information about the result of a call to `smult` with `monitoring=TRUE`.

Value

The object itself is basically a `list` with the following components:

Loc	length(bdp)-by-p matrix containing S estimate of location for each value of bdp.
Shape	p-by-p-by-length(bdp) 3D array containing robust estimate of the shape for each value of bdp. Remark: $\text{det}(\text{shape})=1$.
Scale	length(bdp) vector containing robust estimate of the scale for each value of bdp.
Cov	p-by-p-by-length(bdp) 3D array containing robust estimate of covariance matrix for each value of bdp. Note that $\text{scale}(i)^2 * \text{shape}[, , i] = \text{robust estimate of covariance matrix}$.
Bs	(p+1)-by-length(bdp) matrix containing the units forming best subset for each value of bdp.
MAL	n-by-length(bdp) matrix containing the estimates of the robust Mahalanobis distances (in squared units) for each value of bdp.
Outliers	n-by-length(bdp) matrix containing flags for the outliers. Boolean matrix containing the list of the units declared as outliers for each value of bdp using confidence level specified in input scalar <code>conflev</code>
Weights	n x length(bdp) matrix containing the weights for each value of bdp.
conflev	Confidence level that was used to declare outliers.
singsub	Number of subsets without full rank. Notice that $\text{singsub} > 0.1 * (\text{number of subsamples})$ produces a warning.
bdp	vector which contains the values of bdp which have been used.
X	the data matrix X.

The object has class "smulteda".

Examples

```
## Not run:
  data(hbk)
  (out <- smult(hbk[,1:3], monitoring=TRUE))
  class(out)
  summary(out)

## End(Not run)
```

sreg.object

Description of sreg Objects

Description

An object of class `sreg.object` holds information about the result of a call to `fsreg`.

Value

The object itself is basically a `list` with the following components:

beta	p-by-1 vector containing the estimated regression parameters (in step n-k).
scale	scalar containing the estimate of the scale (sigma).
bs	p x 1 vector containing the units forming best subset associated with S estimate of regression coefficient.
residuals	residuals.
fittedvalues	fitted values.
outliers	kx1 vector containing the list of the k units declared as outliers or NULL if the sample is homogeneous.
conflev	Confidence level which is used to declare units as outliers. Usually <code>conflev=0.95, 0.975, 0.99</code> (individual alpha) or <code>conflev=1-0.05/n, 1-0.025/n, 1-0.01/n</code> (simultaneous alpha). Default value is 0.975
singsub	Number of subsets without full rank. Notice that <code>singsub > 0.1*(number of subsamples)</code> produces a warning
weights	n x 1 vector containing the estimates of the weights
rhofunc	Specifies the rho function which has been used to weight the residuals.
rhofuncparam	Vector which contains the additional parameters for the specified rho function which has been used. For hyperbolic rho function the value of k =sup CVC. For Hampel rho function the parameters a, b and c.
X	the data matrix X
y	the response vector y

The object has class "sreg".

Examples

```
## Not run:
  (out <- fsreg(Y~., data=hbk, method="S"))
  class(out)
  summary(out)

## End(Not run)
```

sregeda.object	<i>Description of sregeda Objects</i>
----------------	---------------------------------------

Description

An object of class `sregeda.object` holds information about the result of a call to `fsreg` when `method="S"` and `monitoring=TRUE`.

Value

The object itself is basically a `list` with the following components:

Beta	matrix containing the S estimator of regression coefficients for each value of bdp.
Scale	vector containing the estimate of the scale (sigma) for each value of bdp. This is the value of the objective function.
BS	p x 1 vector containing the units forming best subset associated with S estimate of regression coefficient.
RES	n x length(bdp) matrix containing the monitoring of scaled residuals for each value of bdp.
Weights	n x length(bdp) matrix containing the estimates of the weights for each value of bdp
Outliers	Boolean matrix containing the list of the units declared as outliers for each value of bdp using confidence level specified in input scalar conflev.
conflev	Confidence level which is used to declare units as outliers. Remark: conflev will be used to draw the horizontal line (confidence band) in the plot.
Singsub	Number of subsets without full rank. Notice that <code>singsub[bdp[jj]] > 0.1*(number of subsamples)</code> produces a warning
rhofunc	Specifies the rho function which has been used to weight the residuals.
rhofuncparam	Vector which contains the additional parameters for the specified rho function which has been used. For hyperbolic rho function the value of k =sup CVC. For Hampel rho function the parameters a, b and c.
X	the data matrix X
y	the response vector y

The object has class "sregeda".

Examples

```
## Not run:
  (out <- fsreg(Y~., data=hbk, method="S", monitoring=TRUE))
  class(out)
  summary(out)

## End(Not run)
```

Sregeda_control	<i>Creates an Sregeda_control object</i>
-----------------	--

Description

Creates an object of class `Sregeda_control` to be used with the `fsreg()` function, containing various control parameters.

Usage

```
Sregeda_control(intercept = TRUE, bdp = seq(0.5, 0.01, -0.01),
  rhofunc = c("bisquare", "optimal", "hyperbolic", "hampel"), rhofuncparam,
  nsamp = 1000, refsteps = 3, reftol = 1e-06, refstepsbest = 50, reftolbest = 1e-08,
  minsctol = 1e-07, best = 5,
  conflev, msg = TRUE, nocheck = FALSE, plot = FALSE)
```

Arguments

- | | |
|---------------------------|--|
| <code>intercept</code> | Indicator for constant term. Scalar. If <code>intercept=TRUE</code> , a model with constant term will be fitted (default), else, no constant term will be included. |
| <code>bdp</code> | Breakdown point. It measures the fraction of outliers the algorithm should resist. In this case any value greater than 0 but smaller or equal than 0.5 will do fine. The default value of <code>bdp</code> is a sequence from 0.5 to 0.01 with step 0.01 |
| <code>rhofunc</code> | Specifies the rho function which must be used to weight the residuals. Possible values are 'bisquare' 'optimal' 'hyperbolic' 'hampel'. <ol style="list-style-type: none"> 1. 'bisquare' uses Tukey's rho and psi functions. See <code>TBRho</code> and <code>TBpsi</code>. 2. 'optimal' uses optimal rho and psi functions. See <code>OPTrho</code> and <code>OPTpsi</code>. 3. 'hyperbolic' uses hyperbolic rho and psi functions. See <code>HYPrho</code> and <code>HYPpsi</code>. 4. 'hampel' uses Hampel rho and psi functions. See <code>HARho</code> and <code>HAPpsi</code>. The default is 'bisquare'. |
| <code>rhofuncparam</code> | Additional parameters for the specified rho function. For hyperbolic rho function it is possible to set up the value of $k = \sup CVC$ (the default value of k is 4.5).
For Hampel rho function it is possible to define parameters a , b and c (the default values are $a=2$, $b=4$, $c=8$) |

nsamp	Number of subsamples which will be extracted to find the robust estimator, scalar. If nsamp=0 all subsets will be extracted. They will be $(n \text{ choose } p)$. If the number of all possible subset is <1000 the default is to extract all subsets otherwise just 1000.
refsteps	Number of refining iterations in each subsample (default is refsteps=3). refsteps = 0 means "raw-subsampling" without iterations.
reftol	Tolerance for the refining steps. The default value is $1e-6$
refstepsbestr	Scalar defining number of refining iterations for each best subset (default = 50).
reftolbestr	Tolerance for the refining steps for each of the best subsets. The default value is reftolbestr= $1e-8$.
minsctol	Value of tolerance for the iterative procedure for finding the minimum value of the scale for each subset and each of the best subsets (It is used by subroutine minscale.m). The default value is minsctol= $1e-7$.
bestr	Defines the number of "best betas" to remember from the subsamples. These will be later iterated until convergence (default is bestr=5).
conflev	Confidence level which is used to declare units as outliers. Usually conflev=0.95, 0.975, 0.99 (individual alpha) or conflev= $1-0.05/n$, $1-0.025/n$, $1-0.01/n$ (simultaneous alpha). Default value is 0.975
msg	Controls whether to display or not messages on the screen If msg==1 (default) messages are displayed on the screen about step in which signal took place else no message is displayed on the screen.
nocheck	Check input arguments, scalar. If nocheck=TRUE no check is performed on matrix y and matrix X. Notice that y and X are left unchanged. In other words the additional column of ones for the intercept is not added. As default nocheck=FALSE.
plot	Plot on the screen. Scalar. If plots=TRUE the plot of minimum deletion residual with envelopes based on n observations and the scatterplot matrix with the outliers highlighted is produced. If plots=2 the user can also monitor the intermediate plots based on envelope superimposition. If plots=FALSE (default) no plot is produced.

Details

Creates an object of class Sregeda_control to be used with the fsreg() function, containing various control parameters.

Value

An object of class "Sregeda_control" which is basically a [list](#) with components the input arguments of the function mapped accordingly to the corresponding Matlab function.

Author(s)

FSDA team

See Also

See Also as [FSR_control](#), [MMreg_control](#) and [LXS_control](#)

Examples

```
## Not run:

(out <- fsreg(Y~., data=hbk, method="S", monitoring=TRUE,
  control=Sregeda_control(nsamp=500, rhofunc='hyperbolic'))))

## End(Not run)
```

<code>Sreg_control</code>	<i>Creates an Sreg_control object</i>
---------------------------	---------------------------------------

Description

Creates an object of class `Sreg_control` to be used with the `fsreg()` function, containing various control parameters for calling the MATLAB function `Sreg()`.

Usage

```
Sreg_control(intercept = TRUE, bdp = 0.5,
  rhofunc = c("bisquare", "optimal", "hyperbolic", "hampel"), rhofuncparam,
  nsamp = 1000, refsteps = 3, reftol = 1e-06, refstepsbestr = 50, reftolbestr = 1e-08,
  minsctol = 1e-07, bestr = 5,
  conflev, msg = TRUE, nocheck = FALSE, plot = FALSE)
```

Arguments

<code>intercept</code>	Indicator for constant term. Scalar. If <code>intercept=TRUE</code> , a model with constant term will be fitted (default), else, no constant term will be included.
<code>bdp</code>	Breakdown point. It measures the fraction of outliers the algorithm should resist. In this case any value greater than 0 but smaller or equal than 0.5 will do fine. Note that given <code>bdp</code> nominal efficiency is automatically determined.
<code>rhofunc</code>	Specifies the rho function which must be used to weight the residuals. Possible values are 'bisquare' 'optimal' 'hyperbolic' 'hampel'. <ol style="list-style-type: none"> 1. 'bisquare' uses Tukey's rho and psi functions. See <code>TBRho</code> and <code>TBpsi</code>. 2. 'optimal' uses optimal rho and psi functions. See <code>OPTrho</code> and <code>OPTpsi</code>. 3. 'hyperbolic' uses hyperbolic rho and psi functions. See <code>HYPrho</code> and <code>HYPpsi</code>. 4. 'hampel' uses Hampel rho and psi functions. See <code>HARho</code> and <code>HAPsi</code>. The default is 'bisquare'.
<code>rhofuncparam</code>	Additional parameters for the specified rho function. For hyperbolic rho function it is possible to set up the value of $k = \sup CVC$ (the default value of k is 4.5). For Hampel rho function it is possible to define parameters a , b and c (the default values are $a=2$, $b=4$, $c=8$)

nsamp	Number of subsamples which will be extracted to find the robust estimator, scalar. If nsamp=0 all subsets will be extracted. They will be $(n \text{ choose } p)$. If the number of all possible subset is <1000 the default is to extract all subsets otherwise just 1000.
refsteps	Number of refining iterations in each subsample (default is refsteps=3). refsteps = 0 means "raw-subsampling" without iterations.
reftol	Tolerance for the refining steps. The default value is $1e-6$
refstepsbestr	Scalar defining number of refining iterations for each best subset (default = 50).
reftolbestr	Tolerance for the refining steps for each of the best subsets. The default value is reftolbestr= $1e-8$.
minsctol	Value of tolerance for the iterative procedure for finding the minimum value of the scale for each subset and each of the best subsets (It is used by subroutine minscale.m). The default value is minsctol= $1e-7$.
bestr	Defines the number of "best betas" to remember from the subsamples. These will be later iterated until convergence (default is bestr=5).
conflev	Confidence level which is used to declare units as outliers. Usually conflev=0.95, 0.975, 0.99 (individual alpha) or conflev= $1-0.05/n$, $1-0.025/n$, $1-0.01/n$ (simultaneous alpha). Default value is 0.975
msg	Controls whether to display or not messages on the screen If msg==1 (default) messages are displayed on the screen about step in which signal took place else no message is displayed on the screen.
nocheck	Check input arguments, scalar. If nocheck=TRUE no check is performed on matrix y and matrix X. Notice that y and X are left unchanged. In other words the additional column of ones for the intercept is not added. As default nocheck=FALSE.
plot	Plot on the screen. Scalar. If plots=TRUE the plot of minimum deletion residual with envelopes based on n observations and the scatterplot matrix with the outliers highlighted is produced. If plots=2 the user can also monitor the intermediate plots based on envelope superimposition. If plots=FALSE (default) no plot is produced.

Details

Creates an object of class Sreg_control to be used with the fsreg() function, containing various control parameters.

Value

An object of class "Sreg_control" which is basically a [list](#) with components the input arguments of the function mapped accordingly to the corresponding Matlab function.

Author(s)

FSDA team

See Also

See Also as [FSR_control](#), [MMreg_control](#) and [LXS_control](#)

Examples

```
## Not run:
(out <- fsreg(Y~., data=hbk, method="S", control=Sreg_control(bdp=0.25, nsamp=500)))

## End(Not run)
```

summary.fsdalms	<i>Summary Method for fsdalms objects</i>
-----------------	---

Description

[summary](#) method for class "fsdalms".

Usage

```
## S3 method for class 'fsdalms'
summary(object, correlation = FALSE, ...)
## S3 method for class 'summary.fsdalms'
print(x, digits = max(3, getOption("digits") - 3),
      signif.stars = getOption("show.signif.stars"), ...)
```

Arguments

object, x	an object of class "fsdalms" (or "summary.fsdalms"); usually, a result of a call to fsreg .
correlation	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
digits	the number of significant digits to use when printing.
signif.stars	logical indicating if "significance stars" should be printed, see printCoefmat .
...	further arguments passed to or from other methods.

Details

`summary.fsdalms()`, the S3 method, simply returns an (S3) object of class "[summary.fsdalms](#)" for which there's a [print](#) method:

`print.summary.fsdalms` prints summary statistics for the forward search (FS) regression estimates. While the function [print.fsdalms](#) prints only the robust estimates of the coefficients, `print.summary.fsdalms` will print also the regression table.

Value

`summary.fsdalms` returns an `summary.fsdalms` object, whereas the print methods returns its first argument via [invisible](#), as all print methods do.

See Also

[fsreg](#), [summary](#)

Examples

```
## Not run:

data(Animals, package = "MASS")
brain <- Animals[c(1:24, 26:25, 27:28),]
lbrain <- log(brain)
(fs <- fsreg(brain~body, data=lbrain, method="LTS"))
summary(fs)

## compare to the result of ltsReg() from 'robustbase'
(lts <- ltsReg(brain~body, data=lbrain))
summary(lts)

## End(Not run)
```

summary.fsdalts

*Summary Method for fsdalts objects***Description**

[summary](#) method for class "fsdalts".

Usage

```
## S3 method for class 'fsdalts'
summary(object, correlation = FALSE, ...)
## S3 method for class 'summary.fsdalts'
print(x, digits = max(3, getOption("digits") - 3),
      signif.stars = getOption("show.signif.stars"), ...)
```

Arguments

object, x	an object of class "fsdalts" (or "summary.fsdalts"); usually, a result of a call to fsreg .
correlation	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
digits	the number of significant digits to use when printing.
signif.stars	logical indicating if "significance stars" should be printed, see printCoefmat .
...	further arguments passed to or from other methods.

Details

`summary.fsdalts()`, the S3 method, simply returns an (S3) object of class "[summary.fsdalts](#)" for which there's a [print](#) method:

`print.summary.fsdalts` prints summary statistics for the forward search (FS) regression estimates. While the function [print.fsdalts](#) prints only the robust estimates of the coefficients, `print.summary.fsdalts` will print also the regression table.

Value

summary.fsdalts returns an summary.fsdalts object, whereas the print methods returns its first argument via [invisible](#), as all print methods do.

See Also

[fsreg](#), [summary](#)

Examples

```
## Not run:

data(Animals, package = "MASS")
brain <- Animals[c(1:24, 26:25, 27:28),]
lbrain <- log(brain)
(fs <- fsreg(brain~body, data=lbrain, method="LTS"))
summary(fs)

## compare to the result of ltsReg() from 'robustbase'
(lts <- ltsReg(brain~body, data=lbrain))
summary(lts)

## End(Not run)
```

summary.fsr

Summary Method for FSR objects

Description

[summary](#) method for class "fsr".

Usage

```
## S3 method for class 'fsr'
summary(object, correlation = FALSE, ...)
## S3 method for class 'summary.fsr'
print(x, digits = max(3, getOption("digits") - 3),
      signif.stars = getOption("show.signif.stars"), ...)
```

Arguments

object, x	an object of class "fsr" (or "summary.fsr"); usually, a result of a call to fsreg .
correlation	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
digits	the number of significant digits to use when printing.
signif.stars	logical indicating if "significance stars" should be printer, see printCoefmat .
...	further arguments passed to or from other methods.

Details

`summary.fsr()`, the S3 method, simply returns an (S3) object of class "`summary.fsr`" for which there's a `print` method:

`print.summary.fsr` prints summary statistics for the forward search (FS) regression estimates. While the function `print.fsr` prints only the robust estimates of the coefficients, `print.summary.fsr` will print also the regression table.

Value

`summary.fsr` returns an `summary.fsr` object, whereas the `print` methods returns its first argument via `invisible`, as all `print` methods do.

See Also

[fsreg](#), [summary](#)

Examples

```
## Not run:

data(Animals, package = "MASS")
brain <- Animals[c(1:24, 26:25, 27:28),]
lbrain <- log(brain)
(fs <- fsreg(brain~body, data=lbrain, method="FS"))
summary(fs)

## End(Not run)
```

swissbanknotes

Swiss banknote data

Description

Six variables measured on 100 genuine and 100 counterfeit old (printed before the second world war) Swiss 1000-franc bank notes (Flury and Riedwyl, 1988).

Usage

```
data(swissbanknotes)
```

Format

A data frame with 200 observations on the following 7 variables.

`length` Length of bill, mm

`left` Width of left edge, mm

`right` Width of right edge, mm

bottom Bottom margin width, mm
 top Top margin width, mm
 diagonal Length of image diagonal, mm
 class 1 = genuine, 2 = counterfeit

Source

Flury, B. and Riedwyl, H. (1988). *Multivariate Statistics: A practical approach*. London: Chapman & Hall.

References

Weisberg, S. (2005). *Applied Linear Regression*, 3rd edition. New York: Wiley, Problem 12.5.

Examples

```
data(swissbanknotes)
head(swissbanknotes)
plot(CovMcd(swissbanknotes[, 1:6]), which="pairs", col=swissbanknotes$class)
```

swissheads

Swiss banknote data

Description

Six dimensions in millimetres of the heads of 200 twenty year old Swiss soldiers (Flury and Riedwyl, 1988, p. 218 and also Flury, 1997, p. 6).

The data were collected to determine the variability in size and shape of heads of young men in order to help in the design of a new protection mask for the Swiss army.

Usage

```
data(swissheads)
```

Format

A data frame with 200 observations on the following 6 variables.

minimal_frontal_breadth Minimal frontal breadth, mm
 breadth_angulus_mandibulae Breadth of angulus mandibulae, mm
 true_facial_height True facial height, mm
 length_glabella_nasi Length from glabella to apex nasi, mm
 length_tragion_nasion Length from tragion to nasion, mm
 length_tragion_gnathion Length from tragion to gnathion, mm

Source

Flury, B. and Riedwyl, H. (1988). *Multivariate Statistics: A practical approach*. London: Chapman & Hall.

References

Atkinson, A. C., Riani, M. and Cerioli, A. (2004) *Exploring multivariate data with the forward search*, New York: Springer-Verlag.

Examples

```
data(swissheads)
head(swissheads)
plot(CovMcd(swissheads), which="pairs")
```

tclusteda.object	<i>Objects returned by the function <code>tclustfsda</code> with the option <code>monitoring=TRUE</code></i>
------------------	--

Description

An object of class `tclusteda.object` holds information about the result of a call to `tclustfsda` with the option `monitoring=TRUE`.

Value

The functions `print()` and `summary()` are used to obtain and print a summary of the results. An object of class `tclusteda` is a list containing at least the following components:

call	the matched call
k	number of groups
alpha	trimming level
restrfactor	restriction factor
IDX	an n-by-length(alpha) vector containing assignment of each unit to each of the k groups. Cluster names are integer numbers from 1 to k. 0 indicates trimmed observations. The first column refers to alpha[1], the second column refers to alpha[2], ..., the last column refers to alpha[length(alpha)].
MU	a 3 dimensional array of size k-by-p-by-length(alpha) containing the monitoring of the centroid for each value of alpha. MU[, , 1], refers to alpha[1] ..., MU(, , length(alpha)] refers to alpha[length(alpha)]. The first row in each slice refers to group 1, second row refers to group 2, etc.
SIGMA	A list of length length(alpha) containing in element j, with j=1, 2, ..., length(alpha), the 3D array of size p-by-p-by-k containing the k (constrained) estimated covariance matrices associated with alpha[j].

Amon stands for alpha monitoring. Matrix of size $(\text{length}(\alpha)-1)$ -by-4 which contains for two consecutive values of alpha the monitoring of three quantities (change in classification, change in centroid location, change in covariance location).

- 1st col = value of alpha.
- 2nd col = ARI index.
- 3rd col = squared Euclidean distance between centroids.
- 4th col = squared Euclidean distance between covariance matrices.

Examples

```
## Not run:
data(hbk)
(out <- tclustfsda(hbk[, 1:3], k=2, monitoring=TRUE))
class(out)
summary(out)

## End(Not run)
```

tclustfsda

Computes trimmed clustering with scatter restrictions

Description

Partitions the points in the n -by- v data matrix Y into k clusters. This partition minimizes the trimmed sum, over all clusters, of the within-cluster sums of point-to-cluster-centroid distances. Rows of Y correspond to points, columns correspond to variables. Returns in the output object of class `tclustfsda.object` an n -by-1 vector `idx` containing the cluster indices of each point. By default, `tclustfsda()` uses (squared), possibly constrained, Mahalanobis distances.

Usage

```
tclustfsda(x, k, alpha, restrfactor = 12, monitoring = FALSE,
  plot = FALSE, nsamp, refsteps = 15, reftol = 1e-13,
  equalweights = FALSE, mixt = 0, msg = TRUE, nocheck = FALSE,
  startv1 = 1, restrtype = c("eigen", "deter"), UnitsSameGroup,
  numpool, cleanpool, trace = FALSE, ...)
```

Arguments

`x` An $n \times p$ data matrix (n observations and p variables). Rows of x represent observations, and columns represent variables.
Missing values (NA's) and infinite values (Inf's) are allowed, since observations (rows) with missing or infinite values will automatically be excluded from the computations.

`k` Number of groups.

- alpha** A scalar between 0 and 0.5 or an integer specifying the number of observations which have to be trimmed. If $\alpha=0$, tclust reduces to traditional model based or mixture clustering (mclust): see for example the Matlab function `gmdistribution`.
More in detail, if $0 < \alpha < 1$ clustering is based on $h = \text{fix}(n * (1-\alpha))$ observations, else if α is an integer greater than 1 clustering is based on $h = n - \text{floor}(\alpha)$. If `monitoring=TRUE`, α is a vector which specifies the values of trimming levels which have to be considered - contains decreasing elements which lie in the interval 0 and 0.5. For example if $\alpha=c(0.1, 0.05, 0)$, `tclust()` considers these 3 values of trimming level. The default for α is vector $\alpha=c(0.1, 0.05, 0)$. The sequence is forced to be monotonically decreasing.
- restrfactor** Positive scalar which constrains the allowed differences among group scatters. Larger values imply larger differences of group scatters. On the other hand a value of 1 specifies the strongest restriction forcing all eigenvalues/determinants to be equal and so the method looks for similarly scattered (respectively spherical) clusters. The default is to apply `restrfactor` to eigenvalues. In order to apply `restrfactor` to determinants it is necessary to use optional input argument `restrtype`.
- monitoring** If `monitoring=TRUE` TCLUS is performed for a series of values of the trimming factor α given k (number of groups) and given c (restriction factor). In order to increase the speed of the computations, `parfor` is used.
- plot** If `plot=FALSE` (default) or `plot=0` no plot is produced. If `plot=TRUE` and `monitoring=FALSE` a plot with the classification is shown (using the `spmplot` function). The plot can be:
- for $p = 1$, a histogram of the univariate data,
 - for $p = 2$, a bivariate scatterplot,
 - for $p > 2$, a scatterplot matrix generated by the MATLAB function `spmplot()`.
- When $p \geq 2$ the following additional features are offered (for $p = 1$ the behaviour is forced to be as for `plots=TRUE`):
- `plot = 'contourf'` adds in the background of the bivariate scatterplots a filled contour plot. The colormap of the filled contour is based on grey levels as default. This argument may also be inserted in a field named 'type' of a list. In the latter case it is possible to specify the additional field 'cmap', which changes the default colors of the color map used. The field 'cmap' may be a three-column matrix of values in the range [0,1] where each row is an RGB triplet that defines one color. Check the `colormap` function for additional informations.
 - `plot = 'contour'` adds in the background of the bivariate scatterplots a contour plot. The colormap of the contour is based on grey levels as default. This argument may also be inserted in a field named `type` of a list. In the latter case it is possible to specify the additional field `cmap`, which changes the default colors of the color map used. The field `cmap` may be a three-column matrix of values in the range [0,1] where each row is an RGB triplet that defines one color. Check the `colormap()` (MATLAB) function for additional information.

- `plot = 'ellipse'` superimposes confidence ellipses to each group in the bivariate scatterplots. The size of the ellipse is `qchisq(0.95,2)`, i.e. the confidence level used by default is 95 percent. This argument may also be inserted in a field named `type` of a list. In the latter case it is possible to specify the additional field `conflav`, which specifies the confidence level to use and it is a value between 0 and 1.
- `plot = 'boxplotb'` superimposes on the bivariate scatterplots the bivariate boxplots for each group, using the `boxplotb` function. This argument may also be inserted in a field named `type` of a list.

The parameter `plot` can be also a list and in this case its elements are:

- `type` - specifies the type of plot as when `plot` option is a character. Therefore, `plots$type` can be one of `'contourf'`, `'contour'`, `'ellipse'` or `'boxplotb'`.
- `cmap` - used to set a colormap for the plot type (MATLAB style). For example, `plot$cmap = 'autumn'`. See the MATLAB help of `colormap` for a list of colormap possibilities.
- `conflav` - this is the confidence level for the confidence ellipses. It must be a scalar between 0 and 1.

If `plot=TRUE` and `monitoring=TRUE` two plots are shown. The first plot (*monitor plot*) shows three panels with the monitoring between two consecutive values of `alpha`: (i) the change in classification using ARI index (top panel), (ii) the change in centroids using squared euclidean distances (central panel) and (iii) the change in covariance matrices using squared euclidean distance (bottom panel).

The second plot (*gscatter plot*) shows a series of subplots which monitor the classification for each value of `alpha`. In order to make sure that consistent labels are used for the groups, between two consecutive values of `alpha`, we assign label `r` to a group if this group shows the smallest distance with group `r` for the previous value of `alpha`. The type of plot which is used to monitor the stability of the classification depends on the data dimensionality `p`.

- for `p = 1`, a histogram of the univariate data (the MATLAB function `histFS()` is called),
- for `p = 2`, a bivariate scatterplot (the MATLAB function `gscatter()` is called),
- for `p > 2`, a scatterplot of the first two principal components (function `gscatter()` is called and we show on the axes titles the percentage of variance explained by the first two principal components).

Also in the case of `monitoring=TRUE` the parameter `plot` can be a list and its elements are:

- `name`: character vector which enables to specify which plot to display. `name = "gscatter"` produces a figure with a series of subplots which show the classification for each value of `alpha`. `name = "monitor"` shows a figure with three panels which monitor between two consecutive values of `alpha` the change in classification using ARI index (top panel), the change in centroids using squared euclidean distances (central panel), the change in covariance matrices using squared euclidean distance (bottom panel). If this field is not specified, by default `name=c("gscatter", "monitor")` and both figures will be shown.

- `alphasel`: a numeric vector which specifies for which values of `alpha` it is possible to see the classification. For example if `alphasel = c(0.05, 0.02)`, the classification will be shown just for `alpha=0.05` and `alpha=0.02`. If this field is not specified `alphasel=alpha` and therefore the classification is shown for each value of `alpha`.
- `nsamp` If a scalar, it contains the number of subsamples which will be extracted. If `nsamp = 0` all subsets will be extracted. Remark - if the number of all possible subset is greater than 300 the default is to extract all subsets, otherwise just 300. If `nsamp` is a matrix it contains in the rows the indexes of the subsets which have to be extracted. `nsamp` in this case can be conveniently generated by function `subsets()`. `nsamp` can have `k` columns or `k * (p + 1)` columns. If `nsamp` has `k` columns the `k` initial centroids each iteration `i` are given by `X[nsamp[i,],]` and the covariance matrices are equal to the identity.
- If `nsamp` has `k * (p + 1)` columns, the initial centroids and covariance matrices in iteration `i` are computed as follows:
- `X1 <- X[nsamp[i,],]`
 - `mean(X1[1:p + 1,])` contains the initial centroid for group 1
 - `cov(X1[1:p + 1,])` contains the initial cov matrix for group 1
 - `mean(X1[(p + 2):(2*p + 2),])` contains the initial centroid for group 2
 - `cov(X1[(p + 2):(2*p + 2),])` contains the initial cov matrix for group 2
 - ...
 - `mean(X1[(k-1)*p+1):(k*(p+1),])` contains the initial centroids for group `k`
 - `cov(X1[(k-1)*p+1):(k*(p+1),])` contains the initial cov matrix for group `k`.
- REMARK: If `nsamp` is not a scalar, the option `startv1` given below is ignored. More precisely, if `nsamp` has `k` columns `startv1 = 0` else if `nsamp` has `k*(p+1)` columns option `startv1=1`.
- `refsteps` Number of refining iterations in each subsample. Default is `refsteps=15`. `refsteps = 0` means "raw-subsampling" without iterations.
- `reftol` Tolerance of the refining steps. The default value is `1e-14`
- `equalweights` A logical specifying wheather cluster weights in the concentration and assignment steps shall be considered. If `equalweights=TRUE` we are (ideally) assuming equally sized groups, else if `equalweights = false` (default) we allow for different group weights. Please, check in the given references which functions are maximized in both cases.
- `mixt` Specifies whether mixture modelling or crisp assignment approach to model based clustering must be used. In the case of mixture modelling parameter `mixt` also controls which is the criterion to find the untrimmed units in each step of the maximization. If `mixt >=1` mixture modelling is assumed else crisp assignment. The default value is `mixt=0`, i.e. crisp assignment. Please see for details the provided references. The parameter `mixt` also controls the criterion to select the units to trim. If `mixt = 2` the `h` units are those which give the largest contribution to the likelihood, else if `mixt=1` the criterion to select the `h` units is exactly the same as the one which is used in crisp assignment.
- `msg` Controls whether to display or not messages on the screen If `msg==TRUE` (default) messages are displayed on the screen. If `msg=2`, detailed messages are displayed, for example the information at iteration level.

nocheck	Check input arguments. If nocheck=TRUE no check is performed on matrix X. The default nocheck=FALSE.
startv1	How to initialize centroids and covariance matrices. Scalar. If startv1=1 then initial centroids and covariance matrices are based on (p+1) observations randomly chosen, else each centroid is initialized taking a random row of input data matrix and covariance matrices are initialized with identity matrices. The default value is startv1=1. Remark 1: in order to start with a routine which is in the required parameter space, eigenvalue restrictions are immediately applied. Remark 2 - option startv1 is used just if nsamp is a scalar (see for more details the help associated with nsamp).
restrtype	Type of restriction to be applied on the cluster scatter matrices. Valid values are 'eigen' (default), or 'deter'. "eigen" implies restriction on the eigenvalues while "deter" implies restriction on the determinants.
UnitsSameGroup	List of the units which must (whenever possible) have a particular label. For example UnitsSameGroup=c(20,26), means that group which contains unit 20 is always labelled with number 1. Similarly, the group which contains unit 26 is always labelled with number 2, (unless it is found that unit 26 already belongs to group 1). In general, group which contains unit UnitsSameGroup(r) where r=2, ...length(kk)-1 is labelled with number r (unless it is found that unit UnitsSameGroup(r) has already been assigned to groups 1,2, ..., r-1).
numpool	The number of parallel sessions to open. If numpool is not defined, then it is set equal to the number of physical cores in the computer.
cleanpool	Logical, indicating if the open pool must be closed or not. It is useful to leave it open if there are subsequent parallel sessions to execute, so that to save the time required to open a new pool.
trace	Whether to print intermediate results. Default is trace=FALSE.
...	potential further arguments passed to lower level functions.

Details

This iterative algorithm initializes k clusters randomly and performs concentration steps in order to improve the current cluster assignment. The number of maximum concentration steps to be performed is given by input parameter refsteps. For approximately obtaining the global optimum, the system is initialized nsamp times and concentration steps are performed until convergence or refsteps is reached. When processing more complex data sets higher values of nsamp and refsteps have to be specified (obviously implying extra computation time). However, if more than 10 per cent of the iterations do not converge, a warning message is issued, indicating that nsamp has to be increased.

Value

Depending on the input parameter monitoring, one of the following objects will be returned:

1. `tclustfsda.object`
2. `tclusteda.object`

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Garcia-Escudero, L.A., Gordaliza, A., Matran, C. and Mayo-Isacar, A. (2008). A General Trimming Approach to Robust Cluster Analysis. *Annals of Statistics*, Vol. 36, 1324-1345. [Technical Report available at: <http://www.eio.uva.es/inves/grupos/representaciones/trTCLUST.pdf>]

Examples

```
## Not run:

data(hbk)
(out <- tclustfsda(hbk[, 1:3], k=2))
class(out)
summary(out)

## TCLUS of Gayser data with three groups (k=3), 10% trimming (alpha=0.1)
## and restriction factor (c=10000)
data(geyser2)
(out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=10000))

## Use the plot options to produce more complex plots -----

## Plot with all default options
out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=10000, plot=TRUE)

## Default confidence ellipses.
out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=10000, plot="ellipse")

## Confidence ellipses specified by the user: confidence ellipses set to 0.5
plots <- list(type="ellipse", conflev=0.5)
out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=10000, plot=plots)

## Confidence ellipses set to 0.9
plots <- list(type="ellipse", conflev=0.9)
out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=10000, plot=plots)

## Contour plots
out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=10000, plot="contour")

## Filled contour plots with additional options: contourf plot with autumn colormap
plots <- list(type="contourf", cmap="autumn")
out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=10000, plot=plots)

## We compare the output using three different values of restriction factor
## nsamp is the number of subsamples which will be extracted
data(geyser2)
out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=10000, nsamp=500, plot="ellipse")
out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=10, nsamp=500, refsteps=10, plot="ellipse")
out <- tclustfsda(geyser2, k=3, alpha=0.1, restrfactor=1, nsamp=500, refsteps=10, plot="ellipse")
```

```

## TCLUS applied to M5 data: A bivariate data set obtained from three normal
## bivariate distributions with different scales and proportions 1:2:2. One of the
## components is very overlapped with another one. A 10 per cent background noise is
## added uniformly distributed in a rectangle containing the three normal components
## and not very overlapped with the three mixture components. A precise description
## of the M5 data set can be found in Garcia-Escudero et al. (2008).
##

data(M5data)
plot(M5data[, 1:2])

## Scatter plot matrix
plot(CovClassic(M5data[,1:2]), which="pairs")

out <- tclustfsda(M5data[,1:2], k=3, alpha=0, restrfactor=1000, nsamp=100, plot=TRUE)
out <- tclustfsda(M5data[,1:2], k=3, alpha=0, restrfactor=10, nsamp=100, plot=TRUE)
out <- tclustfsda(M5data[,1:2], k=3, alpha=0.1, restrfactor=1, nsamp=1000,
  plot=TRUE, equalweights=TRUE)
out <- tclustfsda(M5data[,1:2], k=3, alpha=0.1, restrfactor=1000, nsamp=100, plot=TRUE)

## TCLUS with simulated data: 5 groups and 5 variables
##
n1 <- 100
n2 <- 80
n3 <- 50
n4 <- 80
n5 <- 70
p <- 5
Y1 <- matrix(rnorm(n1 * p) + 5, ncol=p)
Y2 <- matrix(rnorm(n2 * p) + 3, ncol=p)
Y3 <- matrix(rnorm(n3 * p) - 2, ncol=p)
Y4 <- matrix(rnorm(n4 * p) + 2, ncol=p)
Y5 <- matrix(rnorm(n5 * p), ncol=p)

group <- c(rep(1, n1), rep(2, n2), rep(3, n3), rep(4, n4), rep(5, n5))
Y <- Y1
Y <- rbind(Y, Y2)
Y <- rbind(Y, Y3)
Y <- rbind(Y, Y4)
Y <- rbind(Y, Y5)
dim(Y)
table(group)
out <- tclustfsda(Y, k=5, alpha=0.05, restrfactor=1.3, refsteps=20, plot=TRUE)

## Automatic choice of best number of groups for Geyser data -----
##
data(geyser2)
maxk <- 6
CLACLA <- matrix(0, nrow=maxk, ncol=2)
CLACLA[,1] <- 1:maxk
MIXCLA <- MIXMIX <- CLACLA

```

```

for(j in 1:maxk) {
  out <- tclustfsda(geyser2, k=j, alpha=0.1, restrfactor=5, msg=FALSE)
  CLACLA[j, 2] <- out$CLACLA
}

for(j in 1:maxk) {
  out <- tclustfsda(geyser2, k=j, alpha=0.1, restrfactor=5, mixt=2, msg=FALSE)
  MIXMIX[j, 2] <- out$MIXMIX
  MIXCLA[j, 2] <- out$MIXCLA
}

oldpar <- par(mfrow=c(1,3))
plot(CLACLA[,1:2], type="l", xlim=c(1, maxk), xlab="Number of groups", ylab="CLACLA")
plot(MIXMIX[,1:2], type="l", xlim=c(1, maxk), xlab="Number of groups", ylab="MIXMIX")
plot(MIXCLA[,1:2], type="l", xlim=c(1, maxk), xlab="Number of groups", ylab="MIXCLA")
par(oldpar)

## Monitoring examples -----

## Monitoring using Geysler data

## Monitoring using Geysler data (all default options)
## alpha and restriction factor are not specified therefore alpha=c(0.10, 0.05, 0)
## is used while the restriction factor is set to c=12
out <- tclustfsda(geyser2, k=3, monitoring=TRUE)

## Monitoring using Geysler data with alpha and c specified.
out <- tclustfsda(geyser2, k=3, restrfac=100, alpha=seq(0.10, 0, by=-0.01), monitoring=TRUE)

## Monitoring using Geysler data with plot argument specified as a list.
## The trimming levels to consider in this case are 31 values of alpha
##
out <- tclustfsda(geyser2, k=3, restrfac=100, alpha=seq(0.30, 0, by=-0.01), monitoring=TRUE,
  plot=list(alphasel=c(0.2, 0.10, 0.05, 0.01)), trace=TRUE)

## Monitoring using Geysler data with argument UnitsSameGroup
##
## Make sure that group containing unit 10 is in a group which is labelled "group 1"
## and group containing unit 12 is in group which is labelled "group 2"
##
## Mixture model is used (mixt=2)
##
out <- tclustfsda(geyser2, k=3, restrfac=100, alpha=seq(0.30, 0, by=-0.01), monitoring=TRUE,
  mixt=2, UnitsSameGroup=c(10, 12), trace=TRUE)

## Monitoring using M5 data
data(M5data)

## alphavec=vector which contains the trimming levels to consider
## in this case 31 values of alpha are considered
alphavec <- seq(0.10, 0, by=-0.02)
out <- tclustfsda(M5data[, 1:2], 3, alpha=alphavec, restrfac=1000, monitoring=TRUE,

```

```

nsamp=1000, plots=TRUE)

## End(Not run)

```

tclustfsda.object *Objects returned by the function tclustfsda*

Description

An object of class `tclustfsda.object` holds information about the result of a call to `tclustfsda`.

Value

The functions `print()` and `summary()` are used to obtain and print a summary of the results. An object of class `tclustfsda` is a list containing at least the following components:

<code>call</code>	the matched call
<code>muopt</code>	a k-by-p matrix containing cluster centroid locations. Robust estimate of final centroids of the groups
<code>sigmaopt</code>	a p-by-p-by-k array rray containing estimated constrained covariance for the k groups
<code>idx</code>	a vector of length n containing assignment of each unit to each of the k groups. Cluster names are integer numbers from 1 to k. 0 indicates trimmed observations.
<code>size</code>	a matrix of size (k+1)-by-3. The 1st col is sequence from 0 to k (cluster name); the 2nd col is the number of observations in each cluster; the 3rd col is the percentage of observations in each cluster. Remark: 0 denotes unassigned units.
<code>postprob</code>	n-by-k matrix containing posterior probabilities. <code>postprob[i, j]</code> contains posterior probability of unit i from component (cluster) j. For the trimmed units posterior probabilities are 0.
<code>emp</code>	"Empirical" statistics computed on final classification. When convergence is reached, <code>emp=0</code> . When convergence is not obtained, this field is a list which contains the statistics of interest: <code>idxemp</code> (ordered from 0 to k*, k* being the number of groups with at least one observation and 0 representing the possible group of outliers), <code>muemp</code> , <code>sigmaemp</code> and <code>sizeemp</code> , which are the empirical counterparts of <code>idx</code> , <code>muopt</code> , <code>sigmaopt</code> and <code>\codesize</code> .
<code>MIXMIX</code>	BIC which uses parameters estimated using the mixture loglikelihood and the maximized mixture likelihood as goodness of fit measure. Remark: this output is present just if <code>mixt > 0</code> .
<code>MIXCLA</code>	BIC which uses parameters estimated using the mixture loglikelihood and the maximized mixture likelihood as goodness of fit measure. Remark: this output is present just if <code>mixt > 0</code> .

CLACLA	BIC which uses the classification likelihood based on parameters estimated using the classification likelihood. Remark: this output is present just if <code>mixt > 0</code> .
notconver	number of subsets without convergence
bs	a vector of length <code>k</code> containing the units forming initial subset associated with <code>muopt</code> .
obj	value of the objective function which is minimized (value of the best returned solution).
equalweights	if <code>equalweights=TRUE</code> means that in the clustering procedure we (ideally) assumed equal cluster weights else (<code>codeequalweights=FALSE</code> means that we allowed for different cluster sizes.
h	number of observations that have determined the centroids (number of untrimmed units).
fullsol	a vector of size <code>nsamp</code> which contains the value of the objective function at the end of the iterative process for each extracted subsample.
X	the original data matrix <code>X</code> .

Examples

```
## Not run:
data(hbk)
(out <- tclustfsda(hbk[, 1:3], k=2))
class(out)
summary(out)

## End(Not run)
```

tclustIC	<i>Performs cluster analysis by calling <code>tclustfsda</code> for different number of groups <code>k</code> and restriction factors <code>c</code></i>
----------	--

Description

Computes the values of BIC (MIXMIX), ICL (MIXCLA) or CLA (CLACLA), for different values of `k` (number of groups) and different values of `c` (restriction factor), for a prespecified level of trimming (the last two letters in the name stand for 'Information Criterion'). If Parallel Computing toolbox is installed, `parfor` is used to compute `tclust` for different values of `c`. In order to minimize randomness, given `k`, the same subsets are used for each value of `c`.

Usage

```
tclustIC(x, kk = 1:5, cc = c(1, 2, 4, 8, 16, 32, 64, 128), alpha = 0,
  whichIC = c("ALL", "MIXMIX", "MIXCLA", "CLACLA"), nsamp,
  refsteps = 15, reftol = 1e-14, equalweights = FALSE, msg = TRUE,
  nocheck = FALSE, plot = FALSE, startv1 = 1,
  restrtype = c("eigen", "deter"), UnitsSameGroup, numpool, cleanpool,
  trace = FALSE, ...)
```

Arguments

- x** An $n \times p$ data matrix (n observations and p variables). Rows of x represent observations, and columns represent variables.
Missing values (NA's) and infinite values (Inf's) are allowed, since observations (rows) with missing or infinite values will automatically be excluded from the computations.
- kk** an integer vector specifying the number of mixture components (clusters) for which the BIC is to be calculated. By default $kk=1:5$.
- cc** an vector specifying the values of the restriction factor which have to be considered. By default $cc=c(1, 2, 4, 8, 16, 32, 64, 128)$.
- alpha** Global trimming level. A scalar between 0 and 0.5 or an integer specifying the number of observations which have to be trimmed. If $alpha=0$ all observations are considered. By default $alpha=0$.
More in detail, if $0 < alpha < 1$ clustering is based on $h = \text{fix}(n * (1-alpha))$ observations, else if $alpha$ is an integer greater than 1 clustering is based on $h = n - \text{floor}(alpha)$.
- whichIC** A character value which specifies which information criteria must be computed for each k (number of groups) and each value of the restriction factor c . Possible values for **whichIC** are:
- "MIXMIX": a mixture model is fitted and for computing the information criterion the mixture likelihood is used. This option corresponds to the use of the Bayesian Information criterion (BIC). In output just the matrix MIXMIX is given.
 - "MIXCLA": a mixture model is fitted but to compute the information criterion the classification likelihood is used. This option corresponds to the use of the Integrated Complete Likelihood (ICL). In the output just the matrix MIXCLA is given.
 - "CLACLA": everything is based on the classification likelihood. This information criterion will be called CLA. In the output just the matrix CLACLA is given.
 - "ALL": both classification and mixture likelihood are used. In this case all three information criteria CLA, ICL and BIC are computed. In the output all three matrices MIXMIX, MIXCLA and CLACLA are given.
- nsamp** If a scalar, it contains the number of subsamples which will be extracted. If $nsamp = 0$ all subsets will be extracted. Remark - if the number of all possible subset is greater than 300 the default is to extract all subsets, otherwise just 300. If **nsamp** is a matrix it contains in the rows the indexes of the subsets which have to be extracted. **nsamp** in this case can be conveniently generated by function `subsets()`. **nsamp** can have k columns or $k * (p + 1)$ columns. If **nsamp** has k columns the k initial centroids each iteration i are given by $X[nsamp[i,],]$ and the covariance matrices are equal to the identity.
If **nsamp** has $k * (p + 1)$ columns, the initial centroids and covariance matrices in iteration i are computed as follows:
- $X1 \leftarrow X[nsamp[i,],]$
 - $\text{mean}(X1[1:p + 1,]) contains the initial centroid for group 1$

- $\text{cov}(X1[1:p + 1,])$ contains the initial cov matrix for group 1
- $\text{mean}(X1[(p + 2):(2*p + 2),])$ contains the initial centroid for group 2
- $\text{cov}(X1[(p + 2):(2*p + 2),])$ contains the initial cov matrix for group 2
- ...
- $\text{mean}(X1[(k-1)*p+1):(k*(p+1),])$ contains the initial centroids for group k
- $\text{cov}(X1[(k-1)*p+1):(k*(p+1),])$ contains the initial cov matrix for group k.

REMARK: If `nsamp` is not a scalar, the option `startv1` given below is ignored. More precisely, if `nsamp` has `k` columns `startv1 = 0` else if `nsamp` has `k*(p+1)` columns option `startv1=1`.

<code>refsteps</code>	Number of refining iterations in each subsample. Default is <code>refsteps=15</code> . <code>refsteps = 0</code> means "raw-subsampling" without iterations.
<code>reftol</code>	Tolerance of the refining steps. The default value is <code>1e-14</code>
<code>equalweights</code>	A logical specifying wheather cluster weights in the concentration and assignment steps shall be considered. If <code>equalweights=TRUE</code> we are (ideally) assuming equally sized groups, else if <code>equalweights = false</code> (default) we allow for different group weights. Please, check in the given references which functions are maximized in both cases.
<code>msg</code>	Controls whether to display or not messages on the screen If <code>msg==TRUE</code> (default) messages are displayed on the screen. If <code>msg=2</code> , detailed messages are displayed, for example the information at iteration level.
<code>nocheck</code>	Check input arguments. If <code>nocheck=TRUE</code> no check is performed on matrix <code>X</code> . The default <code>nocheck=FALSE</code> .
<code>plot</code>	If <code>plot=TRUE</code> , a plot of the BIC (MIXMIX), ICL (MIXCLA) curve and CLA-CLA is shown on the screen. The plots which are shown depend on the input option <code>whichIC</code> .
<code>startv1</code>	How to initialize centroids and covariance matrices. Scalar. If <code>startv1=1</code> then initial centroids and covariance matrices are based on <code>(p+1)</code> observations randomly chosen, else each centroid is initialized taking a random row of input data matrix and covariance matrices are initialized with identity matrices. The default value is <code>startv1=1</code> . Remark 1: in order to start with a routine which is in the required parameter space, eigenvalue restrictions are immediately applied. Remark 2 - option <code>startv1</code> is used just if <code>nsamp</code> is a scalar (see for more details the help associated with <code>nsamp</code>).
<code>restrtype</code>	Type of restriction to be applied on the cluster scatter matrices. Valid values are 'eigen' (default), or 'deter'. "eigen" implies restriction on the eigenvalues while "deter" implies restriction on the determinants.
<code>UnitsSameGroup</code>	List of the units which must (whenever possible) have a particular label. For example <code>UnitsSameGroup=c(20, 26)</code> , means that group which contains unit 20 is always labelled with number 1. Similarly, the group which contains unit 26 is always labelled with number 2, (unless it is found that unit 26 already belongs to group 1). In general, group which contains unit <code>UnitsSameGroup(r)</code> where <code>r=2, ... length(kk)-1</code> is labelled with number <code>r</code> (unless it is found that unit <code>UnitsSameGroup(r)</code> has already been assigned to groups <code>1, 2, ..., r-1</code>).

numpool	The number of parallel sessions to open. If numpool is not defined, then it is set equal to the number of physical cores in the computer.
cleanpool	Logical, indicating if the open pool must be closed or not. It is useful to leave it open if there are subsequent parallel sessions to execute, so that to save the time required to open a new pool.
trace	Whether to print intermediate results. Default is trace=FALSE.
...	potential further arguments passed to lower level functions.

Value

An S3 object of class `tclustic.object`

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Cerioni, A., Garcia-Escudero, L.A., Mayo-Iscar, A. and Riani M. (2017). Finding the Number of Groups in Model-Based Clustering via Constrained Likelihoods, *emphJournal of Computational and Graphical Statistics*, pp. 404-416, <https://doi.org/10.1080/10618600.2017.1390469>.

See Also

`tclustfsda`, `tclustICplot`, `tclustICsol`, `carbikeplot`

Examples

```
## Not run:  
data(geyser2)  
out <- tclustIC(geyser2, whichIC="MIXMIX", plot=FALSE, alpha=0.1)  
out  
summary(out)  
  
## End(Not run)
```

tclustic.object

Objects returned by the function `tclustIC`

Description

An object of class `tclustic.object` holds information about the result of a call to `tclustIC`.

Value

The functions `print()` and `summary()` are used to obtain and print a summary of the results. An object of class `tclustic` is a list containing at least the following components:

<code>call</code>	the matched call
<code>kk</code>	a vector containing the values of <code>k</code> (number of components) which have been considered. This vector is identical to the optional argument <code>kk</code> (default is <code>kk=1:5</code>).
<code>cc</code>	a vector containing the values of <code>c</code> (values of the restriction factor) which have been considered. This vector is identical to the optional argument <code>cc</code> (default is <code>cc=c(1,2,4,8,16,32,64,128)</code>).
<code>alpha</code>	trimming level
<code>whichIC</code>	Information criteria used
<code>CLACLA</code>	a matrix of size <code>length(kk)-times-length(cc)</code> containing the value of the penalized classification likelihood. This output is present only if <code>whichIC="CLACLA"</code> or <code>whichIC="ALL"</code> .
<code>IDXCLA</code>	a matrix of lists of size <code>length(kk)-times-length(cc)</code> containing the assignment of each unit using the classification model. This output is present only if <code>whichIC="CLACLA"</code> or <code>whichIC="ALL"</code> .
<code>MIXMIX</code>	a matrix of size <code>length(kk)-times-length(cc)</code> containing the value of the penalized mixtrue likelihood. This output is present only if <code>whichIC="MIXMIX"</code> or <code>whichIC="ALL"</code> .
<code>IDXMIX</code>	a matrix of lists of size <code>length(kk)-times-length(cc)</code> containing the assignment of each unit using the classification model. This output is present only if <code>whichIC="MIXMIX"</code> or <code>whichIC="ALL"</code> .
<code>MIXCLA</code>	a matrix of size <code>length(kk)-times-length(cc)</code> containing the value of the ICL criterion. This output is present only if <code>whichIC="MIXCLA"</code> or <code>whichIC="ALL"</code> .

Examples

```
## Not run:
data(hbk)
(out <- tclustIC(hbk[, 1:3]))
class(out)
summary(out)

## End(Not run)
```

tclustICplot

Plots information criterion as a function of `c` and `k`, based on the solutions obtained by `tclustIC`

Description

The function `tclustICplot()` takes as input an object of class `tclustic.object`, the output of function `tclustIC` (that is a series of matrices which contain the values of the information criteria BIC/ICL/CLA for different values of k and c) and plots them as function of c or of k . The plot enables interaction in the sense that, if option `databrush` has been activated, it is possible to click on a point in the plot and to see the associated classification in the scatter plot matrix.

Usage

```
tclustICplot(out, whichIC = c("ALL", "MIXMIX", "MIXCLA", "CLACLA"), tag,
  datatooltip, databrush, nameY, trace = FALSE, ...)
```

Arguments

- | | |
|--------------------------|--|
| <code>out</code> | An S3 object of class <code>tclustic.object</code> (output of <code>tclustIC</code>) containing the values of the information criteria BIC (MIXMIX), ICL (MIXCLA) or CLA (CLACLA), for different values of k (number of groups) and different values of c (restriction factor), for a prespecified level of trimming. |
| <code>whichIC</code> | Specifies the information criterion to use for the plot. See <code>codetclustIC()</code> for the possible values of <code>whichIC</code> . |
| <code>tag</code> | plot handle. String which identifies the handle of the plot which is about to be created. The default is to use tag <code>'pl_IC'</code> . Notice that if the program finds a plot which has a tag equal to the one specified by the user, then the output of the new plot overwrites the existing one in the same window else a new window is created. |
| <code>datatooltip</code> | Interactive clicking. It is inactive if this parameter is set to <code>FALSE</code> . The default is <code>datatooltip=TRUE</code> , the user can select with the mouse a solution in order to have the following information: <ul style="list-style-type: none"> • 1) value of k which has been selected • 2) value of c which has been selected • 3) values of the information criterion • 4) frequency distribution of the associated classification. If <code>datatooltip</code> is a list it may contain the following fields: <ol style="list-style-type: none"> 1. <code>DisplayStyle</code> determines how the data cursor displays. Possible values are <code>'datatip'</code> and <code>'window'</code> (default). <code>'datatip'</code> displays data cursor information in a small yellow text box attached to a black square marker at a data point you interactively select. <code>'window'</code> displays data cursor information for the data point you interactively select in a floating window within the figure. 2. <code>SnapToDataVertex</code>: specifies whether the data cursor snaps to the nearest data value or is located at the actual pointer position. Possible values are <code>SnapToDataVertex='on'</code> (default) and <code>SnapToDataVertex='off'</code>. |
| <code>databrush</code> | Interactive mouse brushing. If <code>databrush</code> is missing or empty (default), no brushing is done. The activation of this option (<code>databrush</code> is <code>TRUE</code> or a list) enables the user to select a set of values of IC in the current plot and to see the corresponding classification highlighted in the scatterplot matrix. If the scatterplot matrix does |

not exist it is automatically created. Note that the window style of the other figures is set equal to that which contains the IC plot. In other words, if the IC plot is docked all the other figures will be docked too.

If `databrush=TRUE` the default selection tool is a rectangular brush and it is possible to brush only once (that is `persist=""`).

If `databrush=list(...)`, it is possible to use all optional arguments of the MATLAB function `selectdataFS()` and the following optional arguments:

- `persist`: Persist is an empty value or a character containing 'on' or 'off'. The default value is `persist=""`, that is brushing is allowed only once. If `persist="on"` or `persist="off"` brushing can be done as many time as the user requires. If `persist='on'` then the unit(s) currently brushed are added to those previously brushed. It is possible, every time a new brushing is done, to use a different color for the brushed units. If `persist='off'` every time a new brush is performed units previously brushed are removed.
- `label`: add labels of brushed units in the monitoring plot.
- `dispopt`: controls how to fill the diagonals in the scatterplot matrix of the brushed solutions. Set `dispopt="hist"` (default) to plot histograms, or `dispopt="box"` to plot boxplots.

<code>nameY</code>	Add variable labels in plot. A vector of strings of length <code>p</code> containing the labels of the variables in the dataset. If it is empty (default) the sequence X_1, \dots, X_p will be created automatically
<code>trace</code>	Whether to print intermediate results. Default is <code>trace=FALSE</code> .
<code>...</code>	potential further arguments passed to lower level functions.

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Cerioni, A., Garcia-Escudero, L.A., Mayo-Iscar, A. and Riani M. (2017). Finding the Number of Groups in Model-Based Clustering via Constrained Likelihoods, *emphJournal of Computational and Graphical Statistics*, pp. 404-416, <https://doi.org/10.1080/10618600.2017.1390469>.

Hubert L. and Arabie P. (1985), Comparing Partitions, *Journal of Classification*, Vol. 2, pp. 193-218.

See Also

[tclustIC](#), [tclustfsda](#)

Examples

```
## Not run:
data(geyser2)
out <- tclustIC(geyser2, whichIC="MIXMIX", plot=FALSE, alpha=0.1)

tclustICplot(out)
```

```
## End(Not run)
```

```
tclustICsol
```

```
Extracts a set of best relevant solutions obtained by tclustIC
```

Description

The function `tclustICsol()` takes as input an object of class `tclustic.object`, the output of function `tclustIC` (that is a series of matrices which contain the values of the information criteria BIC/ICL/CLA for different values of k and c) and extracts the first best solutions. Two solutions are considered equivalent if the value of the adjusted Rand index (or the adjusted Fowlkes and Mallows index) is above a certain threshold. For each tentative solution the program checks the adjacent values of c for which the solution is stable. A matrix with adjusted Rand indexes is given for the extracted solutions.

Usage

```
tclustICsol(out, NumberOfBestSolutions = 5, ThreshRandIndex = 0.7,
  whichIC = c("ALL", "CLACLA", "MIXMIX", "MIXCLA"), Rand = TRUE,
  msg = TRUE, plot = FALSE, trace = FALSE, ...)
```

Arguments

<code>out</code>	An S3 object of class <code>tclustic.object</code> (output of <code>tclustIC</code>) containing the values of the information criteria BIC (MIXMIX), ICL (MIXCLA) or CLA (CLACLA), for different values of k (number of groups) and different values of c (restriction factor), for a prespecified level of trimming.
<code>NumberOfBestSolutions</code>	Number of best solutions to extract from BIC/ICL matrix. The default value of <code>NumberOfBestSolutions</code> is 5
<code>ThreshRandIndex</code>	Threshold to identify spurious solutions - the threshold of the adjusted Rand index to use to consider two solutions as equivalent. The default value of <code>ThreshRandIndex</code> is 0.7
<code>whichIC</code>	Specifies the information criterion to use to extract best solutions. Possible values for <code>whichIC</code> are: <ul style="list-style-type: none"> • CLACLA = in this case best solutions are referred to the classification likelihood. • MIXMIX = in this case in this case best solutions are referred to the mixture likelihood (BIC). • MIXCLA = in this case in this case best solutions are referred to ICL. • ALL = in this case best solutions both three solutions using classification and mixture likelihood are produced. In the output class <code>out</code> all the three matrices <code>MIXMIXbs</code>, <code>CLACLABs</code> and <code>MIXCLABs</code> are given.

The default value is `whichIC="ALL"`.

Rand	Index to use to compare partitions. If Rand=TRUE (default) the adjusted Rand index is used, else the adjusted Fowlkes and Mallows index is used.
msg	It controls whether to display or not messages (from MATLAB) on the screen. If msg=TRUE (default) messages about the progression of the search are displayed on the screen otherwise only error messages will be displayed.
plot	If plot=TRUE, the best solutions which have been found are shown on the screen.
trace	Whether to print intermediate results. Default is trace=FALSE.
...	potential further arguments passed to lower level functions.

Value

An S3 object of class `tclusticsol.object`

Author(s)

FSDA team, <valentin.todorov@chello.at>

References

Cerioni, A., Garcia-Escudero, L.A., Mayo-Isacar, A. and Riani M. (2017). Finding the Number of Groups in Model-Based Clustering via Constrained Likelihoods, *emphJournal of Computational and Graphical Statistics*, pp. 404-416, <https://doi.org/10.1080/10618600.2017.1390469>.

Hubert L. and Arabie P. (1985), Comparing Partitions, *Journal of Classification*, Vol. 2, pp. 193-218.

See Also

`tclustIC`, `tclustfsda`, `carbikeplot`

Examples

```
## Not run:
data(geyser2)
out <- tclustIC(geyser2, whichIC="MIXMIX", plot=FALSE, alpha=0.1)

## Plot first two best solutions using as Information criterion MIXMIX
print("Best solutions using MIXMIX")
outMIXMIX <- tclustICsol(out, whichIC="MIXMIX", plot=TRUE, NumberOfBestSolutions=2)

print(outMIXMIX$MIXMIXbs)

## End(Not run)
```

tclusticsol.object *Objects returned by the function tclustICsol*

Description

An object of class `tclusticsol.object` holds information about the result of a call to `tclustICsol`.

Value

The functions `print()` and `summary()` are used to obtain and print a summary of the results. An object of class `tclusticsol` is a list containing at least the following components:

<code>call</code>	the matched call
<code>kk</code>	a vector containing the values of <code>k</code> (number of components) which have been considered. This vector is identical to the optional argument <code>kk</code> (default is <code>kk=1:5</code>).
<code>cc</code>	a vector containing the values of <code>c</code> (values of the restriction factor) which have been considered. This vector is identical to the optional argument <code>cc</code> (default is <code>cc=c(1,2,4,8,16,32,64,128)</code>).
<code>alpha</code>	trimming level
<code>whichIC</code>	Information criteria used
<code>MIXMIXbs</code>	<p>a matrix of lists of size <code>NumberOfBestSolutions-times-5</code> which contains the details of the best solutions for MIXMIX (BIC). Each row refers to a solution. The information which is stored in the columns is as follows.</p> <ul style="list-style-type: none"> • 1st col = value of <code>k</code> for which solution takes place • 2nd col = value of <code>c</code> for which solution takes place; • 3rd col = a vector of length <code>d</code> which contains the values of <code>c</code> for which the solution is uniformly better. • 4th col = a vector of length <code>d + r</code> which contains the values of <code>c</code> for which the solution is considered stable (i.e. for which the value of the adjusted Rand index (or the adjusted Fowlkes and Mallows index) does not go below the threshold defined in input option <code>ThreshRandIndex</code>). • 5th col = string which contains 'true' or 'spurious'. The solution is labelled spurious if the value of the adjusted Rand index with the previous solutions is greater than <code>ThreshRandIndex</code>.

Remark: the field `MIXMIXbs` is present only if `whichIC=ALL` or `whichIC="MIXMIX"`.

<code>MIXMIXbsari</code>	<p>a matrix of adjusted Rand indexes (or Fowlkes and Mallows indexes) associated with the best solutions for MIXMIX. A matrix of size <code>NumberOfBestSolutions-times-NumberOfBestSolutions</code> whose <code>i, j</code>-th entry contains the adjusted Rand index between classification produced by solution <code>i</code> and solution <code>j</code>, <code>i, j=1, 2, ..., NumberOfBestSolutions</code>.</p>
--------------------------	--

Remark: the field `MIXMIXbsari` is present only if `whichIC=ALL` or `whichIC="MIXMIX"`.

ARIMIX	<p>a matrix of adjusted Rand indexes between two consecutive value of c. Matrix of size k-by-length(cc)-1. The first column contains the ARI indexes between cc[2] and cc[1] given k. The second column contains the the ARI indexes between cc[3] and cc[2] given k.</p> <p>Remark: the field ARIMIX is present only if whichIC=ALL or whichIC="MIXMIX" or whichIC="MIXCLA".</p>
MIXCLAbs	<p>has the same structure as MIXMIXbs but referres to MIXCLA.</p> <p>Remark: the field MIXCLAbs is present only if whichIC=ALL or whichIC="MIXCLA".</p>
MIXCLAbsari	<p>has the same structure as MIXMIXbsari but referres to MIXCLA.</p> <p>Remark: the field MIXMIXbsari is present only if whichIC=ALL or whichIC="MIXCLA".</p>
CLACLABs	<p>has the same structure as MIXMIXbs but referres to CLACLA.</p> <p>Remark: the field CLACLABs is present only if whichIC=ALL or whichIC="CLACLA".</p>
CLACLABsari	<p>has the same structure as MIXMIXbsari but referres to CLACLA.</p> <p>Remark: the field CLACLABsari is present only if whichIC=ALL or whichIC="CLACLA".</p>
ARICLA	<p>a matrix of adjusted Rand indexes between two consecutive value of c. Matrix of size k-by-length(cc)-1. The first column contains the ARI indexes between cc[2] and cc[1] given k. The second column contains the the ARI indexes between cc[3] and cc[2] given k.</p> <p>Remark: the field ARICLA is present only if whichIC=ALL or whichIC="CLACLA".</p>

See Also

[tclustICsol](#), [carbikeplot](#)

Examples

```
## Not run:
data(hbk)
(out <- tclustIC(hbk[, 1:3]))
class(out)
summary(out)

## End(Not run)
```

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