

Package ‘blindreview’

February 18, 2023

Title Blind Review Using Forward Search Procedures

Version 1.1.0

Description Randomly assigns identification to one of the variables of the dataset, say Treatment, and assigns random numbers to all the observations of the dataset. Reorders the database according to the random numbers, and then runs the appropriate forward search function on the blinded dataset.

A file is created from which the user can identify any outliers using the graphics function in this package. An unmasking function is provided so that the user can identify the potential outliers in terms of their original values when blinding is no longer needed. Details of the forward search functions may be found in <https://CRAN.R-project.org/package=forsearch>.

Depends R (>= 4.2)

License GPL (>= 3)

SystemRequirements gmp (>= 4.1)

Encoding UTF-8

RoxygenNote 7.2.3

Imports forsearch(>= 3.1.0), Hmisc(>= 4.7.2)

Suggests knitr, rmarkdown

NeedsCompilation no

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Description

Assigns identification randomly to one of the variables of the dataset as chosen by the user, say Treatment, and assigns random number to the observations of the dataset. Then runs the appropriate forward search function on the blinded dataset. A file is created so that the user can identify any outliers identified by the forward search procedure in terms of their original, unchanged values. Output is primarily for plotting by the `plotdiag.blind.all` function.

Usage

```
brMask(data, blinded, analysis=c("lme", "lm", "glm"),
       initial.sample=1000, n.obs.per.level=1, skip.step1=NULL, fixed=NULL,
       lme.random=NULL, lme.formula=NULL,
       glm.estimate.phi=TRUE, glm.cobs=1, glm.response.cols=NULL,
       glm.indep.cols=NULL, glm.formula=NULL, glm.binomialrhs=NULL,
       glm.family=NULL, arguments=FALSE, verbose=TRUE)
```

Arguments

<code>data</code>	Dataset to be evaluated
<code>blinded</code>	Character, name of variable to be blinded
<code>analysis</code>	Character, one of "lme", "lm", or "glm"
<code>initial.sample</code>	Number of observations in Step 1 of forward search
<code>n.obs.per.level</code>	Number of observations per level of (possibly crossed) factor levels
<code>skip.step1</code>	NULL or a vector of integers for observations to be included in Step 1
<code>fixed</code>	Fixed effects formula as described in <code>stats::lm</code>
<code>lme.random</code>	Random effects formula as described in <code>nlme::lme</code>
<code>lme.formula</code>	a simplified formula of the form <code>resp ~ cov group</code> where <code>resp</code> is the response, <code>cov</code> is the primary covariate, and <code>group</code> is the grouping factor, as in <code>nlme::groupedData</code>
<code>glm.estimate.phi</code>	TRUE causes phi to be estimated; FALSE causes phi to be set = 1
<code>glm.cobs</code>	Number of observations to include in each inner subgroup of Step 1
<code>glm.response.cols</code>	Vector of column numbers (2) of responses and nonresponses
<code>glm.indep.cols</code>	Column number(s) of independent variables
<code>glm.formula</code>	Formula relating response to independent variables. Required except for <code>family=binomial</code>
<code>glm.binomialrhs</code>	Right-hand side of formula, as text object. Required for <code>family=binomial</code>

glm.family	Error distribution and link
arguments	Logical. TRUE causes display of arguments of forsearch_XXX function
verbose	TRUE causes function identifier to display before and after run

Value

LIST, unnecessary elements for current analysis are NULL

Analysis	"lme", "lm", or "glm"
Unmask	Data frame of original and masked values
Rows in stage	List of (masked) observation numbers in each stage
Standardized residuals	Matrix of errors at each stage
Number of model parameters	Rank of model
Sigma	Estimate of random error at final stage; used to standardize all residuals
Fixed parameter estimates	Matrix of parameter estimates at each stage
s ²	Estimate of random error at each stage
Leverage	Matrix of leverage of each observation at each stage
Modified Cook distance	Estimate of sum of squared changes in parameter estimates at each stage
t statistics	t statistics for each fixed parameter
Family	Family and link
Residual deviance	Vector of deviances
Null deviance	Vector of null deviances
PhiHat	Vector of values of phi parameter
Deviance residuals and augments	Deviance residuals with indication of whether each is included in fit
AIC	Vector of AIC values
Number of rows included in Step 1	Number of observations included in Step 1
Rows by subgroup	List of row numbers, by subgroup
Random parameter estimates	Matrix of parameter estimates at each stage
Dims	Dims from fit of lme function
Fit statistics	AIC, BIC, and log likelihood
forsearch Call	Call to forsearch function
Call	Call to this function

Author(s)

William R. Fairweather

References

Atkinson, A and M Riani. Robust Diagnostic Regression Analysis, Springer, New York, 2000.
 Pinheiro, JC and DM Bates. Mixed-Effects Models in S and S-Plus, Springer, New York, 2000.
<https://CRAN.R-project.org/package=nlme> <https://CRAN.R-project.org/package=forssearch>

plotdiag.blind.all *Plot Results of Blind Review*

Description

Plots results from running brMask on a dataset using plotting functions found in forssearch package.

Usage

```
plotdiag.blind.all(object, treatnum, mt=" ", st=" ", cc=NULL, ccrand=NULL,
  objnames=FALSE, verbose=TRUE)
```

Arguments

object	A brMask object
treatnum	Identifying number of plot, for use in graphs and as part of file name
mt	Main title of graph
st	Subtitle of graph
cc	Vector of integers of fixed parameters to include in plot or NULL to include all fixed parameters
ccrand	Vector of integers of random parameters to include in plot or NULL to include all random parameters
objnames	Logical. TRUE causes names of object to be printed
verbose	If TRUE, indicates beginning and end of function

Value

None returned, creates graphs only

Author(s)

William R. Fairweather

unmask	<i>Print Tables of Encoded and Original Variable IDs and Observation Numbers</i>
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Description

Prints tables resulting from masking performed by brMask function to permit user to identify potential outliers in their original identities

Usage

```
unmask(object, obsrange=NULL, verbose=TRUE)
```

Arguments

object	name of brMask object
obsrange	NULL or vector of integers, NULL causes entire data frame of observation numbers to be printed
verbose	TRUE causes function identifier to display before and after run

Value

None returned, printout only

Author(s)

William R. Fairweather

Examples

```
info4 <- system.file("extdata", "micebrM.R", package="blindreview");  
brMaskOut <- source(info4);  
print(brMaskOut);  
brMaskOut <- brMaskOut[[1]];  
unmask(brMaskOut)
```

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