Package ‘blindreview’

January 18, 2023

Title Blind Review Using Forward Search Procedures

Version 1.0.1

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(>= 3.0.1), Hmisc(>= 4.7.2)

Suggests rmarkdown, knitr

NeedsCompilation no

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R topics documented:

`brMask` *Blind Review of Database Using Forward Search Procedures*

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.family=NULL, arguments=FALSE, verbose=TRUE)
```

Arguments

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

Examples

```
Observation <- 1:14
Dose <- c(3.4,5.2,7,8.5,10.5,13,18,21,28,6.5,10,14,21.5,29)
Prep <- factor(c(rep(0,9),rep(1,5)))
Convulse <- c(0,5,11,14,18,21,23,30,27,2,10,18,21,27)
Total <- c(33,32,38,37,40,37,31,37,30,40,30,40,35,37)
NoConvulse <- Total-Convulse
mice <- data.frame(Observation,Dose,Prep,Convulse,Total,NoConvulse)

brMask(data=mice,blinded="Prep",analysis="glm",initial.sample=100,
fixed=Convulse~Prep:Dose,glm.response.cols=c(4,6),glm.indep.cols=2,
glm.family=binomial("log"))
```

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

Description

Plots results from running brMask on a dataset using plotting functions found in forsearch 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)

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`unmask` *Print Tables of Encoded and Original Variable IDs and Observation Numbers*

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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