

Package ‘skMisc’

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Title Sercan Kahveci's Miscellaneous Functions

Version 0.01

Description Contains a wide range of functions.

Depends R (\geq 3.6.1), magrittr, dplyr, doParallel, lmerTest, knitr

Imports tidyrr

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BugReports <https://github.com/Spiritspeak/skMisc/issues>

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aat_bootstrap	<i>Compute bootstrapped approach-bias scores</i>
---------------	--

Description

Compute bootstrapped approach-bias scores with confidence intervals.

Usage

```
aat_bootstrap(ds, subjvar, pullvar, targetvar, rtvar, iters, plot = T,
  algorithm = c("aat_doublemeandiff", "aat_doublemediandiff",
    "aat_dscore", "aat_dscore_multiblock", "aat_multilevelscore"),
  trialdropfunc = c("prune_nothing", "trial_prune_3SD"),
  errortrialfunc = c("prune_nothing", "error_replace_blockmeanplus"),
  ...)
```

Arguments

<code>ds</code>	a longformat data.frame
<code>subjvar</code>	Quoted name of the participant identifier column
<code>pullvar</code>	Quoted name of the column indicating pull trials. Pull trials should either be represented by 1, or by the second level of a factor.
<code>targetvar</code>	Name of the column indicating trials featuring the target stimulus. Target stimuli should either be represented by 1, or by the second level of a factor.
<code>rtvar</code>	Name of the reaction time column.
<code>iters</code>	Total number of desired iterations. At least 200 are required to get confidence intervals that make sense.
<code>plot</code>	Plot the bias scores and their confidence intervals after computation is complete. This gives a good overview of the data.
<code>algorithm</code>	Function (without brackets or quotes) to be used to compute AAT scores. See aat_doublemeandiff for a list of usable algorithms.
<code>trialdropfunc</code>	Function (without brackets or quotes) to be used to exclude outlying trials in each half. <code>prune_nothing</code> excludes no trials, while <code>trial_prune_3SD</code> excludes trials deviating more than 3SD from the mean per participant.
<code>errortrialfunc</code>	Function (without brackets or quotes) to apply to an error trial. <code>error_replace_blockmeanplus</code> replaces error trial reaction times with the block mean plus an arbitrary extra amount of time. If used, the following additional arguments are required: <ul style="list-style-type: none"> • <code>blockvar</code> - Quoted name of the block variable • <code>errorvar</code> - Quoted name of the error variable, where errors are 1 or TRUE and correct trials are 0 or FALSE • <code>errorbonus</code> - Amount to add to the reaction time of error trials. Default is 0.6 (recommended by Greenwald, Nosek, & Banaji, 2003)
<code>...</code>	Other arguments, to be passed on to the algorithm functions (see <code>algorithm</code> above)

Value

A list, containing bootstrapped bias scores, a data frame with bootstrapped 95 the number of iterations, and a matrix of bias scores for each iteration.

Author(s)

Sercan Kahveci

aat_doublemeandiff	<i>AAT score computation algorithms</i>
--------------------	---

Description

- `aat_doublemeandiff` computes a mean-based double-difference score:

$$(\text{mean}(\text{push_target}) - \text{mean}(\text{pull_target})) - (\text{mean}(\text{push_control}) - \text{mean}(\text{pull_control}))$$
- `aat_doublemediandiff` computes a median-based double-difference score:

$$(\text{median}(\text{push_target}) - \text{median}(\text{pull_target})) - (\text{median}(\text{push_control}) - \text{median}(\text{pull_control}))$$
- `aat_dscores` computes D-scores for a 2-block design (see Greenwald, Nosek, and Banaji, 2003):

$$((\text{mean}(\text{push_target}) - \text{mean}(\text{pull_target})) - (\text{mean}(\text{push_control}) - \text{mean}(\text{pull_control}))) / \text{sd}(\text{participant_reaction_times})$$
- `aat_dscores_multiblock` computes D-scores for pairs of sequential blocks and averages the resulting score (see Greenwald, Nosek, and Banaji, 2003). Requires extra `blockvar` argument, indicating the name of the block variable.
- `aat_multilevelscore` fits a multilevel model using `lme4` and extracts a random effect serving as AAT score. When using this function, additional arguments must be provided:
 - `formula` - a quoted formula to fit to the data;
 - `aatterm` the quoted random effect within the subject variable that indicates the approach bias; this is usually the interaction of the pull and target terms.

Usage

```
aat_doublemeandiff(ds, subjvar, pullvar, targetvar, rtvar, ...)

aat_doublemediandiff(ds, subjvar, pullvar, targetvar, rtvar, ...)

aat_dscores(ds, subjvar, pullvar, targetvar, rtvar, ...)

aat_dscores_multiblock(ds, subjvar, pullvar, targetvar, rtvar, blockvar,
  ...)

aat_multilevelscore(ds, subjvar, formula, aatterm, ...)
```

Arguments

<code>ds</code>	A long-format <code>data.frame</code>
<code>subjvar</code>	Column name of the participant identifier variable
<code>pullvar</code>	Column name of the movement variable (0: avoid; 1: approach)
<code>targetvar</code>	Column name of the stimulus category variable (0: control stimulus; 1: target stimulus)
<code>rtvar</code>	Column name of the reaction time variable
<code>...</code>	Other arguments passed on by functions (ignored)
<code>formula</code>	A character string containing a formula to fit to the data and derive multilevel scores from
<code>aatterm</code>	The random term, grouped under the subject variable, which represents the approach bias. Usually this is the interaction of the pull and target terms.

Value

A `data.frame` containing participant number and computed AAT score.

<code>aat_splithalf</code>	<i>Compute bootstrapped split-half reliability for approach-avoidance task data</i>
----------------------------	---

Description

Compute bootstrapped split-half reliability for approach-avoidance task data. `aat_splithalf()` uses multicore computation, which is fast, but provides no clear output when there are errors. `aat_splithalf_singlecore()` is much slower, but more easily debugged.

Usage

```
aat_splithalf(ds, subjvar, pullvar, targetvar, rtvar, iters, plot = T,
  algorithm = c("aat_doublemeandiff", "aat_doublemediandiff",
    "aat_dscore", "aat_dscore_multiblock", "aat_multilevelscore"),
  trialdropfunc = c("prune_nothing", "trial_prune_3SD"),
  errortrialfunc = c("prune_nothing", "error_replace_blockmeanplus"),
  casedropfunc = c("prune_nothing", "case_prune_3SD"), ...)

aat_splithalf_singlecore(ds, subjvar, pullvar, targetvar, rtvar, iters,
  plot = T, algorithm = c("aat_doublemeandiff", "aat_doublemediandiff",
    "aat_dscore", "aat_dscore_multiblock", "aat_multilevelscore"),
  trialdropfunc = c("prune_nothing", "trial_prune_3SD"),
  errortrialfunc = c("prune_nothing", "error_replace_blockmeanplus"),
  casedropfunc = c("prune_nothing", "case_prune_3SD"), ...)
```

Arguments

<code>ds</code>	a longformat data.frame
<code>subjvar</code>	Quoted name of the participant identifier column
<code>pullvar</code>	Quoted name of the column indicating pull trials. Pull trials should either be represented by 1, or by the second level of a factor.
<code>targetvar</code>	Name of the column indicating trials featuring the target stimulus. Target stimuli should either be represented by 1, or by the second level of a factor.
<code>rtvar</code>	Name of the reaction time column.
<code>iters</code>	Total number of desired iterations. At least 200 are recommended for reasonable confidence intervals; If you want to see plots of your data, 1 iteration is enough.
<code>plot</code>	Create a scatterplot of the AAT scores computed from each half of the data from the last iteration. This is highly recommended, as it helps to identify outliers that can inflate or diminish the reliability.
<code>algorithm</code>	Function (without brackets or quotes) to be used to compute AAT scores. See aat_doublemeandiff for a list of usable algorithms.
<code>trialdropfunc</code>	Function (without brackets or quotes) to be used to exclude outlying trials in each half. The way you handle outliers for the reliability computation should mimic the way you do it in your regular analyses. It is recommended to exclude outlying trials when computing AAT scores using the mean double-difference scores and multilevel scoring approaches, but not when using d-scores or median double-difference scores. <code>prune_nothing</code> excludes no trials, while <code>trial_prune_3SD</code> excludes trials deviating more than 3SD from the mean per participant.
<code>errortrialfunc</code>	Function (without brackets or quotes) to apply to an error trial. <code>error_replace_blockmeanplus</code> replaces error trial reaction times with the block mean plus an arbitrary extra amount of time. If used, the following additional arguments are required: <ul style="list-style-type: none"> • <code>blockvar</code> - Quoted name of the block variable • <code>errorvar</code> - Quoted name of the error variable, where errors are 1 or TRUE and correct trials are 0 or FALSE • <code>errorbonus</code> - Amount to add to the reaction time of error trials. Default is 0.6 (recommended by Greenwald, Nosek, & Banaji, 2003)
<code>casedropfunc</code>	Function (without brackets or quotes) to be used to exclude outlying participant scores in each half. The way you handle outliers here should mimic the way you do it in your regular analyses. <code>prune_nothing</code> excludes no participants, while <code>case_prune_3SD</code> excludes participants deviating more than 3SD from the sample mean.
<code>...</code>	Other arguments, to be passed on to the algorithm functions (see <code>algorithm</code> above)

Value

A list, containing the mean bootstrapped split-half reliability, bootstrapped 95 a list of data.frames used over each iteration, and a vector containing the split-half reliability of each iteration.

Author(s)

Sercan Kahveci

Examples

```
#Not Run
aat_splithalf(ds=ds2,subjvar="subjectid",pullvar="is_pull",targetvar="is_food",
              rtvar="rt",iters=1000,trialdropfunc=trial_prune_3SD,
              casedropfunc=case_prune_3SD,plot=T,algorithm=aat_dscore)

#Mean reliability: 0.521959
#Spearman-Brown-corrected r: 0.6859041
#95%CI: [0.4167018, 0.6172474]

#Multilevel Splithalf
aat_splithalf(ds=ds2,subjvar="subjectid",pullvar="is_pull",targetvar="is_food",
              rtvar="rt",iters=100,trialdropfunc=trial_prune_3SD,
              casedropfunc=case_prune_3SD,plot=T,algorithm=aat_multilevelscore,
              formula = "rt ~ is_pull * is_food + (is_pull * is_food | subjectid)",
              aatterm = "is_pull:is_food")

#Mean reliability: 0.5313939
#Spearman-Brown-corrected r: 0.6940003
#95%CI: [0.2687186, 0.6749176]
```

AnovaTable	<i>Compare multilevel models</i>
------------	----------------------------------

Description

Compare multilevel models

Usage

```
AnovaTable(..., fullmodel, models, serial = F, suppress = c("AIC",
  "deviance", "logLik"))
```

Arguments

<code>...</code>	Model objects to be compared
<code>fullmodel</code>	A model to which all other models are to be compared; only use if <code>...</code> is not specified.
<code>models</code>	Models to compare to <code>fullmodel</code> . Only use if <code>...</code> is not specified.
<code>serial</code>	If TRUE, models are compared serially; if false, all models will be compared to the first.
<code>suppress</code>	Character vector of column names to suppress in printed output.

Value

A data.frame containing model fit metrics such as AIC, BIC, marginal R-squared (the effect size of fixed effects only), conditional R-squared (the effect size of all model terms), loglikelihood, deviance, and a likelihood ratio test.

clamp	<i>clamp</i>
-------	--------------

Description

clamp

Usage

```
clamp(val, minval, maxval)
```

Arguments

val	The vector/matrix to clamp
minval	Minimum value; all lower values are clamped to this value
maxval	Maximum value; all higher values are clamped to this value

Value

Clamped vector.

Examples

```
clamp(0:10,2,8)
```

coerce	<i>coerce a vector to contain only TRUE and FALSE</i>
--------	---

Description

coerce a vector to contain only TRUE and FALSE

Usage

```
coerce(x, default = FALSE)
```

Arguments

x	Numeric/logical vector/matrix to coerce into TRUE/FALSE
default	default returned value if NULL or NA is encountered

Value

logical vector or matrix with only T and F

Examples

```
coerce(NULL)
# FALSE

coerce(c(T,F,NA,NA,T))
# T F F F T

coerce(matrix(c(T,T,F,F,NA,NA),nrow=2))
#      [,1] [,2] [,3]
#[1,] TRUE FALSE FALSE
#[2,] TRUE FALSE FALSE
```

combobulate	<i>Get all possible combinations of strings</i>
-------------	---

Description

combobulate() returns all possible combinations of the provided character strings, each combination merged into a single string.

Usage

```
combobulate(...)
```

Arguments

... Character vectors to combobulate.

Value

A character vector.

Examples

```
combobulate("Hello ",c("Sir","Madam"),",",",c("may I take your order?","what shall it be?"))
# [1] "Hello Sir, may I take your order?"
# [2] "Hello Madam, may I take your order?"
# [3] "Hello Sir, what shall it be?"
# [4] "Hello Madam, what shall it be?"
```

compcorr	<i>Test if two correlation coefficients significantly differ</i>
----------	--

Description

Uses Fisher's r to z transformation, then performs a z-test on the resulting z-scores

Usage

```
compcorr(cor1, cor2, n1, n2)
```


Arguments

cor1, cor2	Correlation values being compared
n1, n2	Sample sizes of the correlation coefficients

Value

List containing the z-score and p-value

References

<http://vassarstats.net/rdiff.html>

CorrCrunch

Analyse the robustness of a correlation

Description

CorrCrunch() computes the minimum number of cases that need to be removed from a dataset to flip the sign of a correlation coefficient. This can be useful in distinguishing genuine correlations from spurious findings that hinge on one or two outliers. Cases are removed iteratively; in each iteration the case that maximally shrinks the correlation coefficient is removed.

Usage

```
CorrCrunch(x, y, verbose = F)
```

Arguments

x, y	Numeric vectors to correlate.
verbose	if TRUE, prints verbose output.

Value

A list containing the number of cases that need to be removed to flip the sign of the correlation coefficient; the proportion removed cases in the data; and a data.frame without these cases.

Examples

```
CorrCrunch(mtcars$mpg,mtcars$wt)
#Holdout needed to flip the sign: 19 (63.33%)
#Final r: 0.01181141
```

CorTable	<i>Create a Correlation Table</i>
----------	-----------------------------------

Description

Create a Correlation Table

Usage

```
CorTable(df, rowids, columnids, rowdf, columndf)
```

Arguments

`df` A data.frame.
`rowids, columnids` character vectors containing column names from `df` that need to be correlated.
`rowdf, columndf` data.frames whose columns need to be correlated. Either `df, rowids, & columnids` or `rowdf & columndf` are required.

Value

A formatted markdown table containing correlation coefficients, p-values, and the number and percentage of cases that need to be removed to flip the sign of each correlation coefficient.

Examples

```
CorTable(mtcars, rowids=c("mpg", "disp", "hp"), columnids=c("drat", "wt", "qsec"))

CorTable(rowdf=mtcars[, c(1, 3, 4)], columndf=mtcars[, 5:7])
```

df.init	<i>Initiate an empty data frame</i>
---------	-------------------------------------

Description

Initiate an empty data frame

Usage

```
df.init(namelist)
```

Arguments

`namelist` A character vector of column names.

Value

A data.frame with 0 rows.

ExpandFormula	<i>Parse a lme4 formula and return all main effects and interactions as separate terms</i>
---------------	--

Description

Parse a lme4 formula and return all main effects and interactions as separate terms

Usage

```
ExpandFormula(form)
```

Arguments

form

Value

The same formula, but with all interactions and main effects as separate terms

Examples

```
ExpandFormula(rt ~ pull * target + (pull * target | subjectid))
#rt ~ pull + target + pull:target + (pull + target + pull:target | subjectid)
```

ExtractRandomTerms	<i>Extract random terms from a lme4 formula</i>
--------------------	---

Description

Extract random terms from a lme4 formula

Usage

```
ExtractRandomTerms(form)
```

Arguments

form A formula

Value

A named list containing character vectors with random terms; names are group variables.

Examples

```
ExtractRandomTerms(grade ~ ChildIQ * TeacherSkill * SchoolType +
                    (ChildIQ * TeacherSkill | School))
#$School
#[1] "ChildIQ"                      "TeacherSkill"                      "ChildIQ:TeacherSkill"
```

FindTopTerms	<i>Find all model terms that are not moderated by a higher-order interaction</i>
--------------	--

Description

Find all model terms that are not moderated by a higher-order interaction

Usage

```
FindTopTerms(form)
```

Arguments

form	a formula
------	-----------

Value

A character vector containing all model terms that are not moderated by a higher-order interaction.

Examples

```
FindTopTerms(speed ~ skill + weight * friction)
#[1] "skill"          "weight:friction"
```

logit.weightfun	<i>Downweight outliers</i>
-----------------	----------------------------

Description

Computes weights; trials within certain bounds of the mean receive the maximum weight while trials outside these bounds are downweighted to 0 or an optional minimum.

Usage

```
logit.weightfun(x, mean = mean(x), s = sd(x), sdist = 3,
  taper = 10, scale = c("max", "norm"), min = 0)
```

Arguments

x	A numeric vector
mean	An optional mean of the vector
s	An optional standard deviation of the vector
sdist	The number of standard deviations beyond which values should be down-weighted
taper	A number indicating how strongly values exceeding the standard deviation should taper off
scale	How the weight vector should be scaled: "norm" sets the sum to 1, "max" sets the maximum to 1.
min	A minimum weight.

Value

A numeric vector of weights

OLcrunch	<i>Crunch Outliers</i>
----------	------------------------

Description

Crunch Outliers

Usage

```
OLcrunch(x, DS = 3, hardlimit = NULL)
```

Arguments

<code>x</code>	Numeric vector to remove outliers from
<code>DS</code>	A positive numeric value. If value exceeds this many standard deviations, it is counted as an outlier
<code>hardlimit</code>	A numeric vector with two values. If set, values below the first value and above the second will be counted as outliers, and means/standard deviations will be computed from values within these bounds only.

Value

Vector with outlying values set to NA

<code>read.csv.folder</code>	<i>Read and merge all .csv files in a folder</i>
------------------------------	--

Description

Read and merge all .csv files in a folder

Usage

```
read.csv.folder(folder = "./", readfunc = list(read.csv, read.csv2,
  read.table))
```

Arguments

<code>folder</code>	path to a folder
<code>readfunc</code>	list of functions that will be used to read the files; if the first function fails, the second function will be used, etc.

Value

A data.frame containing all merged .csv files

RemoveTopTerms	<i>Remove all possible models with one unmoderated term removed</i>
----------------	---

Description

Remove all possible models with one unmoderated term removed

Usage

```
RemoveTopTerms(form, randeff = "")
```

Arguments

form	A formula
randeff	The name of the group from which unmoderated terms should be removed. To remove from fixed effects, use "" (the default).

Value

A list of formulas which have one unmoderated term removed each. The name of each list item is the term which was removed.

Examples

```
RemoveTopTerms(a ~ b * c + d + (1|e))
#$d
#a ~ b + c + b:c + (1 | e)
#$`b:c`
#a ~ b + c + d + (1 | e)
```

retype	<i>Change classes of columns in a data.frame</i>
--------	--

Description

retype() changes the class of specific columns; retype_all() changes the class of all columns of a given class.

Usage

```
retype(df, ...)
```

```
retype_all(df, from, to)
```

Arguments

<code>df</code>	a data frame
<code>...</code>	Unquoted column names, paired with the desired class, e.g. <code>age = numeric(), language = character()</code>
<code>from</code>	An empty vector of the class to convert from, or a string. Columns sharing the class of argument <code>from</code> will be converted to the class of argument <code>to</code> .
<code>to</code>	An empty vector of the class to convert to, or a string. Columns sharing the class of argument <code>from</code> will be converted to the class of argument <code>to</code> .
<code>df</code>	A data.frame

Examples

```
sapply(ToothGrowth, class)
#   len      supp    dose
# "numeric" "factor" "numeric"
NewToothGrowth <- retype(ToothGrowth, supp = character(), dose = factor())
sapply(NewToothGrowth, class)
#   len      supp    dose
# "numeric" "character" "factor"

sapply(mtcars, class)
#   mpg      cyl    disp      hp      drat      wt
# "numeric" "numeric" "numeric" "numeric" "numeric" "numeric"
#   qsec      vs      am      gear      carb
# "numeric" "numeric" "numeric" "numeric" "numeric"

newmtcars <- retype_all(mtcars, "numeric", "character")
sapply(newmtcars, class)
#   mpg      cyl    disp      hp      drat
# "character" "character" "character" "character" "character"
#   wt      qsec      vs      am      gear      carb
# "character" "character" "character" "character" "character" "character"
```

smoothvect

*Smooth a numeric vector using a moving window algorithm***Description**

Smooth a numeric vector using a moving window algorithm

Usage

```
smoothvect(vect, width = 2, both.sides = T, alg = c("mean", "gauss"))
```

Arguments

<code>vect</code>	
<code>width</code>	Over how many values should the vector be averaged?
<code>both.sides</code>	If TRUE (default), takes the mean of <code>width</code> values before and after the current index. If FALSE, only takes values ahead of the current index.

Value

Smoothed numeric vector

Examples

```
temp<- smoothvect(beaver1$temp)
plot(temp,type="l")
```

SpearmanBrown	<i>Correct a correlation coefficient for being based on only a subset of the data.</i>
---------------	--

Description

Perform a Spearman-Brown correction on the provided correlation score.

Usage

```
SpearmanBrown(corr, ntests = 2)
```

Arguments

corr	To-be-corrected correlation coefficient
ntests	An integer indicating how many times larger the full test is, for which the corrected correlation coefficient is being computed. When <code>ntests=2</code> , the formula will compute what the correlation coefficient would be if the test were twice as long.

Value

Spearman-Brown-corrected correlation coefficient. Values are bounded at zero.

TransformPlots	<i>Title</i>
----------------	--------------

Description

Visualize how different transformations of the data will fit to a normal distribution.

Usage

```
TransformPlots(x)
```

Arguments

x	A numeric vector.
---	-------------------

trypackages	<i>Install packages if neccesary, then load them.</i>
-------------	---

Description

Install packages if neccesary, then load them.

Usage

```
trypackages(...)
```

Arguments

...	Unquoted names of packages to try loading, and if unable, install and load.
-----	---

Examples

```
trypackages(stats,utils,compiler)
```

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