Package 'userfriendlyscience'

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Title Quantitative Analysis Made Accessible

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License GPL (>= 2)

Description Contains a number of functions that serve two goals. First, to make R more accessible to people migrating from SPSS by adding a number of functions that behave roughly like their SPSS equivalents. Second, to make a number of slightly more advanced functions more user friendly to relatively novice users. The package also conveniently houses a number of additional functions that are intended to increase the quality of methodology and statistics in psychology, not by offering technical solutions, but by shifting perspectives, for example towards reasoning based on sampling distributions as opposed to on point estimates.

URL http://userfriendlyscience.com

Imports grDevices, stats, utils, grid, scales, rio, pwr, SuppDists, plyr, psych, fBasics, MBESS, GPArotation, lavaan, MASS, mosaic, diptest, car, SCRT, XML, knitr, xtable, pander, data.tree, DiagrammeR, ggplot2, GGally, gtable, gridExtra, ggrepel, RColorBrewer

NeedsCompilation no

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R topics documented:

`userfriendlyscience-package` *Userfriendlyscience*

Description

This package contains a number of functions that serve two goals: first, make R more accessible to people migrating from SPSS by adding a number of functions that behave roughly like their SPSS equivalents; and second, make a number of slightly more advanced functions more user friendly to relatively novice users.

Details

Package:	userfriendlyscience
Type:	Package
Version:	0.6-0
Date:	2017-04-01
License:	GPL (>= 2)

The package contains a variety of functions designed to make life easier. These functions are geared towards researchers in psychology.

The package implements many solutions provided by people all over the world, most from Stack Exchange (both from Cross Validated and Stack Overflow). I credit these authors in the help pages of those functions and in the Author(s) section of this page. If you wrote a function included here, and you want me to take it out, feel free to contact me of course (also, see http://meta.stackoverflow.com/questions/319171/i-would-like-to-use-a-function-written-by-a-stack-overflow-memb

Author(s)

Author: Gjalt-Jorn Peters (Open University of the Netherlands, Greater Good, and Maastricht University).

Contributors: Peter Verboon (`convert.omegasq.to.cohensf`, Open University of the Netherlands), Amy Chan (`ggPie`), Jeff Baggett (`posthocTGH`, University of Wisconsin - La Crosse), Daniel McNeish (`scaleStructure`, University of North Carolina), Nick Sabbe (`curfnfinder`, Artevelde-hogeschool), Douglas Bonett (`confIntR`, `pwr.confIntR`, UC Santa Cruz, United States), Murray Moinester (`confIntR`, `pwr.confIntR`, Tel Aviv University, Israel), Stefan Gruijters (`nnc`, `ggNNC`, `convert.d.to.eer`, `convert.d.to.nnc`, `erDataSeq`, Maastricht University).

A number of functions in this package use code fragments that were used without explicit communicating with the author (because I've been unable to find contact details of the authors, or because I haven't gotten around to contacting them yet). The authors of these fragments are John Fox (`car` code in `ggqq`), Floo0 (`ggqq`), Jason Aizkalns (`ggBoxplot`), Luke Tierney (in `pwr.cohensdCI`, its alias `pwr.confIntd`, and `cohensdCI`).

In addition, the function `escapeRegEx` from package `Hmisc` is included and used internally to avoid importing that entire package just for that function. This function was written by Charles Dupont

(Department of Biostatistics, Vanderbilt University). The help page was also taken from that package.

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Peters, G.-J. Y. (2014). The alpha and the omega of scale reliability and validity: why and how to abandon Cronbach's alpha and the route towards more comprehensive assessment of scale quality. *European Health Psychologist*, 16(2), 56-69.

See Also

psych and MBESS contain many useful functions for researchers in psychology.

Examples

```
### Create simple dataset
dat <- PlantGrowth[1:20,];
### Remove third level from group factor
dat$group <- factor(dat$group);

### Examine normality
normalityAssessment(dat$weight);

### Compute mean difference and show it
meanDiff(dat$weight ~ dat$group, plot=TRUE);

### Show the t-test
didacticPlot(meanDiff(dat$weight ~ dat$group)$t,
             statistic='t',
             df1=meanDiff(dat$weight ~ dat$group)$df);

### Load data from simulated dataset testRetestSimData (which
### satisfies essential tau-equivalence).
data(testRetestSimData);

### Select some items in the first measurement
exampleData <- testRetestSimData[2:6];

## Not run:
### Show reliabilities
scaleStructure(dat=exampleData, ci=FALSE,
               omega.psych=FALSE, poly=FALSE);

## End(Not run)

### Create a dichotomous variable
exampleData$group <- cut(exampleData$t0_item2, 2);

### Show item distributions and means
meansDiamondPlot(exampleData);
```

```
### Show a dlvPlot
dlvPlot(exampleData, x="group", y="t0_item1");

### show a dlvPlot with less participants, showing the confidence
### interval and standard error bars better
dlvPlot(exampleData[1:30, ], x="group", y="t0_item1");
```

---

areColors *Check whether elements of a vector are valid colors*

Description

This function by Josh O'Brien checks whether elements of a vector are valid colors. It has been copied from a Stack Exchange answer (see http://stackoverflow.com/questions/13289009/check-if-character-string-is-a-valid-color-representation).

Usage

```
areColors(x)
```

Arguments

x	The vector.

Value

A logical vector.

Author(s)

Josh O'Brien

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
areColors(c(NA, "black", "blackk", "1", "#00", "#000000"));
```

associationMatrix *associationMatrix*

Description

associationMatrix produces a matrix with confidence intervals for effect sizes, point estimates for those effect sizes, and the p-values for the test of the hypothesis that the effect size is zero, corrected for multiple testing.

Usage

```
associationMatrix(dat=NULL, x=NULL, y=NULL, conf.level = .95,
                  correction = "fdr", bootstrapV=FALSE,
                  info=c("full", "ci", "es"),
                  includeSampleSize = "depends",
                  bootstrapV.samples = 5000, digits = 2,
                  pValueDigits = digits + 1, colNames = FALSE,
                  type=c("R", "html", "latex"), file="",
                  statistic = associationMatrixStatDefaults,
                  effectSize = associationMatrixESDefaults,
                  var.equal = 'test')
```

Arguments

dat	A dataframe with the variables of interest. All variables in this dataframe will be used if both x and y are NULL. If dat is NULL, the user will be presented with a dialog to select a datafile.
x	If not NULL, this should be a character vector with the names of the variables to include in the rows of the association table. If x is NULL, all variables in the dataframe will be used.
y	If not NULL, this should be a character vector with the names of the variables to include in the columns of the association table. If y is NULL, the variables in x will be used for the columns as well (which produces a symmetric matrix, similar to most correlation matrices).
conf.level	Level of confidence of the confidence intervals.
correction	Correction for multiple testing: an element out of the vector c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"). NOTE: the p-values are corrected for multiple testing; The confidence intervals are not!
bootstrapV	Whether to use bootstrapping to compue the confidence interval for Cramer's V or whether to use the Fisher's Z conversion.
info	Information to print: either both the confidence interval and the point estimate for the effect size (and the p-value, corrected for multiple testing), or only the confidence intervals, or only the point estimate (and the corrected p-value). Must be on element of the vector c("full", "ci", "es").

`includeSampleSize`
: Whether to include the sample size when the effect size point estimate and p-value are shown. If this is "depends", it will depend on whether all associations have the same sample size (and the sample size will only be printed when they don't). If "always", the sample size will always be added. If anything else, it will never be printed.

`bootstrapV.samples`
: If using boostrapping for Cramer's V, the number of samples to generate.

`digits`
: Number of digits to round to when printing the results.

`pValueDigits`
: How many digits to use for formatting the p values.

`colNames`
: If true, the column heading will use the variables names instead of numbers.

`type`
: Type of output to generate: must be an element of the vector c("R", "html", "latex").

`file`
: If a file is specified, the output will be written to that file instead of shown on the screen.

`statistic`
: This is the complicated bit; this is where associationMatrix allows customization of the used statistics to perform null hypothesis significance testing. For everyday use, leaving this at the default value, associationMatrixStatDefaults, works fine. In case you want to customize, read the 'Notes' section below.

`effectSize`
: Like the 'statistics' argument, 'effectSize also allows customization, in this case of the used effect sizes. Again, the default value, associationMatrixESDefaults, works for everyday use. Again, see the 'Notes' section below if you want to customize.

`var.equal`
: Whether to test for equal variances ('test'), assume equality ('yes'), or assume unequality ('no'). See `meanDiff` for more information.

Value

An object with the input and several output variables, one of which is a dataframe with the association matrix in it. When this object is printed, the association matrix is printed to the screen. If the 'file' parameter is specified, a file with this matrix will also be written to disk.

Note

The 'statistic' and 'effectSize' parameter make it possible to use different functions to conduct null hypothesis significance testing and compute effect sizes. In both cases, the parameter needs to be a list containing four lists, named 'dichotomous', 'nominal', 'ordinal', and 'interval'. Each of these lists has to contain four elements, character vectors of length one (i.e. just one string value), again named 'dichotomous', 'nominal', 'ordinal', and 'interval'.

The combination of each of these names (e.g. 'dichotomous' and 'nominal', or 'ordinal' and 'interval', etc) determine which test should be done when computing the p-value to test the association between two variables of those types, or which effect sizes to compute. When called, associationMatrix determines the measurement levels of the relevant variables. It then uses these two levels (their string representation, e.g. 'dichotomous' etc) to find a string in the 'statistic' and 'effectSize' objects. Two functions with these names are then called from two lists, 'computeStatistic' and computeEffectSize. These lists list contain functions that have the same names as the strings in the 'statistic' list.

For example, when the default settings are used, the string (function name) found for two dichotomous variables when searching in associationMatrixStatDefaults is 'chisq', and the string found in associationMatrixESDefaults is 'v'. associationMatrix then calls computeStatistic[['chisq']] and computeEffectSize[['v']], providing the two variables as arguments, as well as passing the 'conf.level' argument. These two functions then each return an object that associationMatrix extracts the information from. Inspect the source code of these functions (by typing their names without parentheses in the R prompt) to learn how this object should look, if you want to write your own functions.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
### Generate a simple association matrix using all three variables in the
### Orange tree dataframe
associationMatrix(Orange);

### Or four variables from infert:
associationMatrix(infert, c("education", "parity",
                            "induced", "case"), colNames=TRUE);

### Use variable names in the columns and generate html
associationMatrix(Orange, colNames=TRUE, type='html');
```

`associationMatrix Helper Functions`

associationMatrix Helper Functions

Description

These objects contain a number of settings and functions for associationMatrix.

Usage

```
computeStatistic_t(var1, var2, conf.level=.95, var.equal='test', ...)
computeStatistic_r(var1, var2, conf.level=.95, ...)
computeStatistic_f(var1, var2, conf.level=.95, ...)
computeStatistic_chisq(var1, var2, conf.level=.95, ...)

computeEffectSize_d(var1, var2, conf.level=.95, var.equal='test', ...)
computeEffectSize_r(var1, var2, conf.level=.95, ...)
computeEffectSize_etasq(var1, var2, conf.level=.95, ...)
computeEffectSize_omegasq(var1, var2, conf.level=.95, ...)
```

```
computeEffectSize_v(var1, var2, conf.level=.95,
                          bootstrap=FALSE, samples=5000, ...)
```

Arguments

var1	One of the two variables for which to compute a statistic or effect size
var2	The other variable for which to compute the statistic or effect size
conf.level	The confidence for the confidence interval for the effect size
bootstrap	Whether to bootstrap to estimate the confidence interval for Cramer's V. If FALSE, the Fisher's Z conversion is used.
samples	If bootstrapping, the number of samples to generate (of course, more samples means more accuracy and longer processing time).
var.equal	Whether to test for equal variances ('test'), assume equality ('yes'), or assume unequality ('no'). See meanDiff for more information.
...	Any additonal arguments are sometimes used to specify exactly how statistics and effect sizes should be computed.

Value

associationMatrixStatDefaults and associationMatrixESDefaults contain the default functions from computeStatistic and computeEffectSize that are called (see the help file for associationMatrix for more details).

The other functions return an object with the relevant statistic or effect size, with a confidence interval for the effect size.

For computeStatistic, this object always contains:

statistic	The relevant statistic
statistic.type	The type of statistic
parameter	The degrees of freedom for this statistic
p.raw	The p-value of this statistic for NHST

And in addition, it often contains (among other things, sometimes):

object	The object from which the statistics are extracted

For computeEffectSize, this object always contains:

es	The point estimate for the effect size
esc.type	The type of effect size
ci	The confidence interval for the effect size

And in addition, it often contains (among other things, sometimes):

object	The object from which the effect size is extracted

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

meanDiff, associationMatrix

Examples

```
computeStatistic_f(Orange$Tree, Orange$circumference)
computeEffectSize_etasq(Orange$Tree, Orange$circumference)
```

---

associationsDiamondPlot

A diamondplot with confidence intervals for associations

Description

This function produces is a diamondplot that plots the confidence intervals for associations between a number of covariates and a criterion. It currently only supports the Pearson's r effect size metric; other effect sizes are converted to Pearson's r.

associationsToDiamondPlotDf is a helper function that produces the required dataframe.

Usage

```
associationsDiamondPlot(dat, covariates, criteria,
                        labels = NULL,
                        criteriaLabels = NULL,
                        decreasing=NULL,
                        sortBy=NULL,
                        conf.level=.95,
                        criteriaColors = brewer.pal(8, 'Set1'),
                        criterionColor = 'black',
                        returnLayerOnly = FALSE,
                        esMetric = 'r',
                        multiAlpha=.33,
                        singleAlpha = 1,
                        showLegend=TRUE,
                        xlab="Effect size estimates",
                        ylab="",
                        theme=theme_bw(),
                        lineSize = 1,
                        outputFile = NULL,
```

```
                        outputWidth = 10,
                        outputHeight = 10,
                        ggsaveParams = list(units='cm',
                                            dpi=300,
                                            type="cairo"),
                        ...)

associationsToDiamondPlotDf(dat, covariates, criterion, labels = NULL,
                            decreasing = NULL, conf.level = 0.95,
                            esMetric = "r")
```

Arguments

`dat`	The dataframe containing the relevant variables.
`covariates`	The covariates: the list of variables to associate to the criterion or criteria, usually the predictors.
`criteria, criterion`	The criteria, usually the dependent variables; one criterion (one dependent variable) can also be specified of course. The helper function `associationsToDiamondPlotDf` always accepts only one criterion.
`labels`	The labels for the covariates, for example the questions that were used (as a character vector).
`criteriaLabels`	The labels for the criteria (in the legend).
`decreasing`	Whether to sort the covariates by the point estimate of the effect size of their association with the criterion. Use `NULL` to not sort at all, `TRUE` to sort in descending order, and `FALSE` to sort in ascending order.
`sortBy`	When specifying multiple criteria, this can be used to indicate by which criterion the items should be sorted (if they should be sorted).
`conf.level`	The confidence of the confidence intervals.
`criteriaColors, criterionColor`	The colors to use for the different associations can be specified in `criteriaColors`. This should be a vector of valid colors with at least as many elements as criteria are specified in `criteria`. If only one criterion is specified, the color in `criterionColor` is used.
`returnLayerOnly`	Whether to return the entire object that is generated, or just the resulting ggplot2 layer.
`esMetric`	The effect size metric to plot - currently, only 'r' is supported, and other values will return an error.
`multiAlpha, singleAlpha`	The transparency (alpha channel) value of the diamonds for each association can be specified in `multiAlpha`, and if only one criterion is specified, the alpha level of the diamonds can be specified in `singleAlpha`.
`showLegend`	Whether to show the legend.
`xlab, ylab`	The label to use for the x and y axes (for `duoComparisonDiamondPlot`, must be vectors of two elements). Use `NULL` to not use a label.

theme	The ggplot theme to use.
lineSize	The thickness of the lines (the diamonds' strokes).
outputFile	A file to which to save the plot.
outputWidth, outputHeight	Width and height of saved plot (specified in centimeters by default, see ggsaveParams).
ggsaveParams	Parameters to pass to ggsave when saving the plot.
...	Any additional arguments are passed to diamondPlot and eventually to ggDiamondLayer.

Details

This function can be used to quickly plot multiple confidence intervals.

Value

A plot.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

diamondPlot, ggDiamondLayer, CIBER

Examples

```
### Simple diamond plot with correlations
### and their confidence intervals

associationsDiamondPlot(mtcars,
                        covariates=c('cyl', 'hp', 'drat', 'wt',
                                     'am', 'gear', 'vs', 'carb', 'qsec'),
                        criteria='mpg');

### Same diamond plot, but now with two criteria,
### and colouring the diamonds based on the
### correlation point estimates: a gradient
### is created where red is used for -1,
### green for 1 and blue for 0.

associationsDiamondPlot(mtcars,
                        covariates=c('cyl', 'hp', 'drat', 'wt',
                                     'am', 'gear', 'vs', 'carb', 'qsec'),
                        criteria=c('mpg', 'disp'),
                        generateColors=c("red", "blue", "green"),
                        fullColorRange=c(-1, 1));
```

asymmetricalScatterMatrix

asymmetricalScatterMatrix

Description

This function generates an asymmetrical scatterMatrix with histograms showing the distribution of each variable.

Usage

```
asymmetricalScatterMatrix(dat, cols, rows, theme = dlvTheme(),
                          autoSize = TRUE,
                          txtHeight = 1, histHeight = 3,
                          scatterWidth = 6, scatterHeight = 6, unit = "cm",
                          dpi = 200, showCorrelations=c('top-left',
                          'top-right', 'bottom-left', 'bottom-right'),
                          correlationSize = 15,
                          correlationColor = "#cadded",
                          pointSize = 1.5)
```

Arguments

dat	The dataframe containing the items to show in the scatterMatrix.
cols	The variable names of the variables to place on the columns.
rows	The variable names of the variables to place on the rows.
theme	Which ggplot theme to use.
autoSize	Whether to resize the plot depending on the viewport (i.e. device that is being drawn to) or whether to use the four measurements specified below (txtHeight, histHeight, scatterWidth, and scatterHeight) to size the plot.
txtHeight, histHeight, scatterWidth, scatterHeight	These numbers are used to determine the space used for displaying the scatterplots, histograms, and labels in the final scatterMatrix.
unit	The unit in which txtHeight, histHeight, scatterWidth, and scatterheight are provided.
dpi	The DPI of the final plot.
showCorrelations	Where to display correlation coefficients; set to NULL to display no correlation coefficients.
correlationSize	The size(s) of the correlation coefficient(s).
correlationColor	The color of the correlation coefficient(s).
pointSize	The size of the points in the scatterplots.

Value

A scatterMatrix, just not symmetrical.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
asymmetricalScatterMatrix(infert, cols=c("parity", "age"),
                          rows=c("induced", "case", "spontaneous"),
                          showCorrelations="top-right");
```

---

averageFishersZs *averageFishersZs*

Description

Takes pairs of Fisher's z's and the accompanying n's (sample sizes) and returns their average.

Usage

```
averageFishersZs(zs, ns)
```

Arguments

zs	The values of Fisher's z.
ns	The sample sizes (ns).

Value

The average of the Fisher's z values.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

averagePearsonRs

Examples

```
averageFishersZs(c(1.1, 5.4), c(10, 30));
```

averagePearsonRs *averagePearsonRs*

Description

Takes pairs of Pearson r's (correlation coefficients) and the accompanying n's (sample sizes) and returns their average.

Usage

```
averagePearsonRs(rs, ns, FishersZ = TRUE)
```

Arguments

rs	The correlation coefficients.
ns	The sample sizes.
FishersZ	Whether to compute the average through Fisher's z (only method implemented as of the writing of this document).

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

averageFishersZs, convert.r.to.fisherz

Examples

```
averagePearsonRs(c(.3, .4, .6), c(70, 80, 50));
```

basicSPSStranslationFunctions *Basic SPSS translation functions*

Description

Basic functons to make working with R easier for SPSS users: getData and getDat provide an easy way to load SPSS datafiles, and exportToSPSS to write to a datafile and syntax file that SPSS can import; filterBy and useAll allow easy temporary filtering of rows from the dataframe; mediaan and modus compute the median and mode of ordinal or numeric data.

Usage

```
getData(filename = NULL, file = NULL, errorMessage =
        "[defaultErrorMessage]", applyRioLabels = TRUE,
        use.value.labels = FALSE, to.data.frame = TRUE,
        stringsAsFactors = FALSE, silent=FALSE, ...)

getDat(..., dfName = "dat", backup = TRUE)

exportToSPSS(dat, savfile = NULL, datafile = NULL, codefile = NULL,
             fileEncoding = "UTF-8", newLinesInString = " |n| ")

filterBy(dat, expression, replaceOriginalDataframe = TRUE,
         envir = parent.frame())

useAll(dat, replaceFilteredDataframe = TRUE)

mediaan(vector)

modus(vector)
```

Arguments

filename, file	It is possible to specify a path and filename to load here. If not specified, the default R file selection dialogue is shown. file is still available for backward compatibility but will eventually be phased out.
errorMessage	The error message that is shown if the file does not exist or does not have the right extension; "[defaultErrorMessage]" is replaced with a default error message (and can be included in longer messages).
applyRioLabels	Whether to apply the labels supplied by Rio. This will make variables that has value labels into factors.
use.value.labels	Only useful when reading from SPSS files: whether to read variables with value labels as factors (TRUE) or numeric vectors (FALSE).
to.data.frame	Only useful when reading from SPSS files: whether to return a dataframe or not.
stringsAsFactors	Whether to read strings as strings (FALSE) or factors (TRUE).
silent	Whether to suppress potentially useful information.
...	Additional options, passed on to the function used to import the data (which depends on the extension of the file).
dfName	The name of the dataframe to create in the parent environment.
backup	Whether to backup an object with name dfName, if one already exists in the parent environment.
dat	Dataframe to process: for filterBy, dataframe to filter rows from; for useAll, dataframe to restore ('unfilter').
datafile	The name of the data file, a comma separated values file that can be read into SPSS by using the code file.

`codefile` The name of the code file, the SPSS syntax file that can be used to import the data file.

`savfile` The name of the SPSS format .sav file (alternative for writing a datafile and a codefile).

`fileEncoding` The encoding to use to write the files.

`newLinesInString`
A string to replace newlines with (SPSS has problems reading newlines).

`expression` Logical expression determining which rows to keep and which to drop. Can be either a logical vector or a string which is then evaluated. If it's a string, it's evaluated using 'with' to evaluate the expression using the variable names.

`replaceOriginalDataframe`
Whether to also replace the original dataframe in the parent environment. Very messy, but for maximum compatibility with the 'SPSS way of doing things', by default, this is true. After all, people who care about the messiness/inappropriateness of this function wouldn't be using it in the first place :-)

`envir` The environment where to create the 'backup' of the unfiltered dataframe, for when useAll is called and the filter is deactivated again.

`replaceFilteredDataframe`
Whether to replace the filtered dataframe passed in the 'dat' argument (see replaceOriginalDataframe).

`vector` For mediaan and modus, the vector for which to find the median or mode.

Value

getData returns the imported dataframe, with the filename from which it was read stored in the 'filename' attribute.

getDat is a simple wrapper for `getData()` which creates a dataframe in the parent environment, by default with the name 'dat'. Therefore, calling `getDat()` in the console will allow the user to select a file, and the data from the file will then be read and be available as 'dat'. If an object with `dfName` (i.e. 'dat' by default) already exists, it will be backed up with a warning. `getDat()` therefore returns nothing.

mediaan returns the median, or, in the case of a factor where the median is in between two categories, both categories.

modus returns the mode.

Note

getData() currently can't read from LibreOffice or OpenOffice files. There doesn't seem to be a platform-independent package that allows this. Non-CRAN package ROpenOffice from OmegaHat should be able to do the trick, but fails to install (manual download and installation using http://www.omegahat.org produces "ERROR: dependency 'Rcompression' is not available for package 'ROpenOffice'" - and manual download and installation of RCompression produces "Please define LIB_ZLIB; ERROR: configuration failed for package 'Rcompression'"). If you have any suggestions, please let me know!

Examples

```
## Not run:
### Open a dialogue to read an SPSS file
getData();

## End(Not run)

### Get a median and a mode
mediaan(c(1,2,2,3,4,4,5,6,6,6,7));
modus(c(1,2,2,3,4,4,5,6,6,6,7));

### Create an example dataframe
(exampleDat <- data.frame(x=rep(8, 8), y=rep(c(0,1), each=4)));
### Filter it, replacing the original dataframe
(filterBy(exampleDat, "y=0"));
### Restore the old dataframe
(useAll(exampleDat));
```

`biAxisDiamondPlot` *Diamondplot with two Y axes*

Description

This is basically a `meansDiamondPlot`, but extended to allow specifying subquestions and anchors at the left and right side. This is convenient for psychological questionnaires when the anchors or dimensions were different from item to item. This function is used to function the left panel of the `CIBER` plot.

Usage

```
biAxisDiamondPlot(dat, items = NULL,
                  leftAnchors = NULL, rightAnchors = NULL,
                  subQuestions = NULL,
                  decreasing = NULL, conf.level = 0.95,
                  showData = TRUE, dataAlpha = 0.1,
                  dataColor = "#444444", diamondColors = NULL,
                  jitterWidth = 0.45, jitterHeight = 0.45,
                  xbreaks = NULL, xLabels = NA,
                  xAxisLab = paste0("Scores and ",
                                    round(100 * conf.level, 2),
                                    "% CIs"),
                  drawPlot = TRUE, returnPlotOnly = TRUE,
                  baseSize = 1, dotSize = baseSize,
                  baseFontSize = 10 * baseSize,
                  theme = theme_bw(base_size = baseFontSize),
                  outputFile = NULL,
```

```
outputWidth = 10,
outputHeight = 10,
ggsaveParams = list(units='cm',
                    dpi=300,
                    type="cairo"),
...)
```

Arguments

dat	The dataframe containing the variables.
items	The variables to include.
leftAnchors	The anchors to display on the left side of the left hand panel. If the items were measured with one variable each, this can be used to show the anchors that were used for the respective scales. Must have the same length as items.
rightAnchors	The anchors to display on the left side of the left hand panel. If the items were measured with one variable each, this can be used to show the anchors that were used for the respective scales. Must have the same length as items.
subQuestions	The subquestions used to measure each item. This can also be used to provide pretty names for the variables if the items were not measured by one question each. Must have the same length as items.
decreasing	Whether to sort the items. Specify NULL to not sort at all, TRUE to sort in descending order, and FALSE to sort in ascending order.
conf.level	The confidence levels for the confidence intervals.
showData	Whether to show the individual datapoints.
dataAlpha	The alpha level (transparency) of the individual datapoints. Value between 0 and 1, where 0 signifies complete transparency (i.e. invisibility) and 1 signifies complete 'opaqueness'.
dataColor	The color to use for the individual datapoints.
diamondColors	The colours to use for the diamonds. If NULL, the generateColors argument can be used which will then be passed to diamondPlot.
jitterWidth	How much to jitter the individual datapoints horizontally.
jitterHeight	How much to jitter the individual datapoints vertically.
xbreaks	Which breaks to use on the X axis (can be useful to override ggplot's defaults).
xLabels	Which labels to use for those breaks (can be useful to override ggplot's defaults; especially useful in combination with xBreaks of course).
xAxisLab	Axis label for the X axis.
drawPlot	Whether to draw the plot, or only return it.
returnPlotOnly	Whether to return the entire object that is generated (including all intermediate objects) or only the plot.
baseSize	This can be used to efficiently change the size of most plot elements.
dotSize	This is the size of the points used to show the individual data points in the left hand plot.
baseFontSize	This can be used to set the font size separately from the baseSize.

theme	This is the theme that is used for the plots.
outputFile	A file to which to save the plot.
outputWidth, outputHeight	Width and height of saved plot (specified in centimeters by default, see ggsaveParams).
ggsaveParams	Parameters to pass to ggsave when saving the plot.
...	These arguments are passed on to diamondPlot.

Details

This is a diamondplot that can be used for items/questions where the anchors of the response scales could be different for every item. For the rest, it is very similar to meansDiamondPlot.

Value

Either just a plot (a gtable object) or an object with all produced objects and that plot.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

CIBER, associationsDiamondPlot

Examples

```
biAxisDiamondPlot(dat=mtcars,
                  items=c('cyl', 'wt'),
                  subQuestions=c('cylinders', 'weight'),
                  leftAnchors=c('few', 'light'),
                  rightAnchors=c('many', 'heavy'),
                  xBreaks=0:8);
```

CIBER *Confidence Interval-Based Estimation of Relevance (CIBER)*

Description

This function generates a high-level plot consisting of several diamond plots. This function is useful for estimating the relative relevance of a set of determinants of, for example, behavior. The plot in the left hand panel shows each determinant's distribution with a diamond representing the confidence interval. The right hand plot shows the determinants' associations to one or more 'target' variables, such as behavior or determinants of behavior.

Usage

```
CIBER(data, determinants, targets,
      conf.level = list(means = 0.9999,
                        associations = 0.95),
      subQuestions = NULL,
      leftAnchors = rep("Lo", length(determinants)),
      rightAnchors = rep("Hi", length(determinants)),
      orderBy = NULL, decreasing = NULL,
      generateColors = list(means = c("red", "blue", "green"),
                            associations = c("red", "grey", "green")),
      strokeColors = brewer.pal(9, "Set1"),
      titlePrefix = "Means and associations with",
      titleVarLabels = NULL, titleSuffix = "",
      fullColorRange = NULL, associationsAlpha = 0.5,
      returnPlotOnly = TRUE, drawPlot = TRUE,
      baseSize = 0.8, dotSize = 2.5 * baseSize,
      baseFontSize = 10 * baseSize,
      theme = theme_bw(base_size = baseFontSize), ...)

detStructCIBER(determinantStructure, dat,
               conf.level = list(means = 0.9999,
                                 associations = 0.95),
               subQuestions = NULL,
               leftAnchors = rep("Lo", length(determinants)),
               rightAnchors = rep("Hi", length(determinants)),
               orderBy = 1, decreasing = NULL,
               generateColors = list(means = c("red", "blue", "green"),
                                     associations = c("red", "grey", "green")),
               strokeColors = brewer.pal(9, "Set1"),
               titlePrefix = "Means and associations with",
               titleVarLabels = NULL, titleSuffix = "",
               fullColorRange = NULL, associationsAlpha = 0.5,
               baseSize = 0.8, dotSize = 2.5 * baseSize,
               baseFontSize = 10 * baseSize,
               theme = theme_bw(base_size = baseFontSize), ...)
```

Arguments

`data, dat`	The dataframe containing the variables.
`determinants`	The 'determinants': the predictors (or 'covariates') of the target variables(s) (or 'criteria').
`targets`	The 'targets' or 'criteria' variables: the variables predicted by the determinants.
`determinantStructure`	When using `detStructCIBER`, the determinant structure as generated by `determinantStructure` is included here. `determinants`, `targets`, `subQuestions`, `leftAnchors`, and `rightAnchors` are then read from the `determinantStructure` object. In other words: once a `determinantStructure` has been generated, only `dat` and `determinantStructure` have to be provided as argument to generate a CIBER diamond plot.

`conf.level` The confidence levels for the confidence intervals: has to be a named list with two elements: `means` and `associations`, specifying the desired confidence levels for the means and associations, respectively. The confidence level for the associations is also used for the intervals for the proportions of explained variance.

`subQuestions` The subquestions used to measure each determinants. This can also be used to provide pretty names for the variables if the determinants were not measured by one question each. Must have the same length as `determinants`.

`leftAnchors` The anchors to display on the left side of the left hand panel. If the determinants were measured with one variable each, this can be used to show the anchors that were used for the respective scales. Must have the same length as `determinants`.

`rightAnchors` The anchors to display on the left side of the left hand panel. If the determinants were measured with one variable each, this can be used to show the anchors that were used for the respective scales. Must have the same length as `determinants`.

`orderBy` Whether to sort the determinants. Set to `NULL` to not sort at all; specify the name or index of one of the `targets` to sort by the point estimates of the associations with that target variable. Use `decreasing` to determine whether to sort in ascending or descending order. For convenience, if `orderBy` is not `NULL`, but `decreasing` is, the determinants are sorted in descending (decreasing) order.

`decreasing` Whether to sort the determinants. Specify `NULL` to not sort at all, `TRUE` to sort in descending order, and `FALSE` to sort in ascending order. If `decreasing` is nor `NULL`, but `orderBy` is `NULL`, the determinants are sorted by their means. For convenience, if `orderBy` is not `NULL`, but `decreasing` is, the determinants are sorted in descending (decreasing) order.

`generateColors` The colors to use to generate the gradients for coloring the diamonds representing the confidence intervals. Has to be a named list with two elements: `means` and `associations`, specifying the desired colors for the means and associations, respectively.

`strokeColors` The palette to use to color the stroke of the confidence intervals for the associations between the determinants and the targets. Successive colors from this palette are used for the targets.

`titlePrefix` Text to add before the list of target names and the proportions of explained variance for each target. This plot title also serves as legend to indicate which target 'gets' which each color.

`titleVarLabels` Optionally, variable labels to use in the plot title. Has to be the exact same length as `targets`.

`titleSuffix` Text to add after the list of target names and the proportions of explained variance for each target.

`fullColorRange` If colors are specified, this can be used to specify which values, for the determinant confidence intervals in the left hand panel, are the minimum and maximum. This is useful if those scores are not actually in the data (e.g. for extremely skewed distributions). If `NULL`, the range of all individual scores on the determinants is used. For the associations, `c(-1, 1)` is always used as `fullColorRange`.

`associationsAlpha`
: The alpha level (transparency) of the confidence interval diamonds in the right hand plot. Value between 0 and 1, where 0 signifies complete transparency (i.e. invisibility) and 1 signifies complete 'opaqueness'.

`returnPlotOnly`
: Whether to return the entire object that is generated (including all intermediate objects) or only the plot.

`drawPlot`
: Whether the draw the plot, or only return it.

`baseSize`
: This can be used to efficiently change the size of most plot elements.

`dotSize`
: This is the size of the points used to show the individual data points in the left hand plot.

`baseFontSize`
: This can be used to set the font size separately from the `baseSize`.

`theme`
: This is the theme that is used for the plots.

`...`
: These arguments are passed on to `biAxisDiamondPlot` (for the left panel) and `diamondPlot` (for the right panel). Note that all argument are passed to both those functions.

Details

Details are explained in Crutzen & Peters (2017).

Value

Depending on the value of `returnPlotOnly`, either the plot only (a `gtable` object) or an object containing most objects created along the way (in which case the plot is stored in `$output$bla`).

The plot has `width` and `height` attributes which can be used when saving the plot.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Crutzen, R., Peters, G.-J. Y., & Noijen, J. (2017). How to Select Relevant Social-Cognitive Determinants and Use them in the Development of Behaviour Change Interventions? Confidence Interval-Based Estimation of Relevance. http://dx.doi.org/

See Also

`biAxisDiamondPlot`, `associationsDiamondPlot`, `determinantStructure`

Examples

```
CIBER(data=mtcars,
      determinants=c('drat', 'wt', 'am',
                     'gear', 'vs', 'carb'),
      targets=c('mpg', 'cyl'));
```

confIntOmegaSq *Confidence intervals for Omega Squared*

Description

This function used the MBESS function `conf.limits.ncf` and `convert.ncf.to.omegasq` to compute the point estimate and confidence interval for Omega Squared.

Usage

```
confIntOmegaSq(var1, var2, conf.level = 0.95)
```

Arguments

`var1, var2`	The two variables: one should be a factor (or will be made a factor), the other should have at least interval level of measurement. If none of the variables is a factor, the function will look for the variable with the least unique values and change it into a factor.
`conf.level`	Level of confidence for the confidence interval.

Value

A `confIntOmegaSq` object is returned, with as elements:

`input`	The input arguments
`intermediate`	Objects generated while computing the output
`output`	The output of the function, consisting of:
`output$es`	The point estimate
`output$ci`	The confidence interval

Note

Formula 16 in Steiger (2004) is used for the conversion in `convert.ncf.to.omegasq`.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Steiger, J. H. (2004). Beyond the F test: Effect size confidence intervals and tests of close fit in the analysis of variance and contrast analysis. Psychological Methods, 9(2), 164-82. https://doi.org/10.1037/1082-989X.9.2.164

Examples

```
confIntOmegaSq(mtcars$mpg, mtcars$cyl);
```

`confIntR` *A function to compute a correlation's confidence interval*

Description

This function computes the confidence interval for a given correlation and its sample size. This is useful to obtain confidence intervals for correlations reported in papers when informing power analyses.

Usage

```
confIntR(r, N, conf.level = 0.95)
```

Arguments

`r`	The observed correlation coefficient.
`N`	The sample size of the sample where the correlation was computed.
`conf.level`	The desired confidence level of the confidence interval.

Value

The confidence interval(s) in a matrix with two columns. The left column contains the lower bound, the right column the upper bound. The `rownames` are the observed correlations, and the `colnames` are 'lo' and 'hi'. The confidence level and sample size are stored as attributes. The results are returned like this to make it easy to access single correlation coefficients from the resulting object (see the examples).

Author(s)

Douglas Bonett (UC Santa Cruz, United States), with minor edits by Murray Moinester (Tel Aviv University, Israel) and Gjalt-Jorn Peters (Open University of the Netherlands, the Netherlands).

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Bonett, D. G., Wright, T. A. (2000). Sample size requirements for estimating Pearson, Kendall and Spearman correlations. *Psychometrika, 65*, 23-28.

Bonett, D. G. (2014). CIcorr.R and sizeCIcorr.R http://people.ucsc.edu/~dgbonett/psyc181.html

Moinester, M., & Gottfried, R. (2014). Sample size estimation for correlations with pre-specified confidence interval. *The Quantitative Methods of Psychology, 10*(2), 124-130. http://www.tqmp.org/RegularArticles/vol10-2/p124/p124.pdf

Peters, G. J. Y. & Crutzen, R. (forthcoming) An easy and foolproof method for establishing how effective an intervention or behavior change method is: required sample size for accurate parameter estimation in health psychology.

See Also

confIntR

Examples

```
### To request confidence intervals for one correlation
confIntR(.3, 100);

### The lower bound of a single correlation
confIntR(.3, 100)[1];

### To request confidence intervals for multiple correlations:
confIntR(c(.1, .3, .5), 250);

### The upper bound of the correlation of .5:
confIntR(c(.1, .3, .5), 250)['0.5', 'hi'];
```

---

confIntV *crossTab, confIntV and cramersV*

Description

These functions compute the point estimate and confidence interval for Cramer's V. The crossTab function also shows a crosstable.

Usage

```
crossTab(x, y=NULL, conf.level=.95,
         digits=2, pValueDigits=3, ...)
cramersV(x, y = NULL, digits=2)
confIntV(x, y = NULL, conf.level=.95,
         samples = 500, digits=2,
         method=c('bootstrap', 'fisher'),
         storeBootstrappingData = FALSE)
```

Arguments

x	Either a crosstable to analyse, or one of two vectors to use to generate that crosstable. The vector should be a factor, i.e. a categorical variable identified as such by the 'factor' class).
y	If x is a crosstable, y can (and should) be empty. If x is a vector, y must also be a vector.

digits	Minimum number of digits after the decimal point to show in the result.
pValueDigits	Minimum number of digits after the decimal point to show in the Chi Square p value in the result.
conf.level	Level of confidence for the confidence interval.
samples	Number of samples to generate when bootstrapping.
method	Whether to use Fisher's Z or bootstrapping to compute the confidence interval.
storeBootstrappingData	Whether to store (or discard) the data generating during the bootstrapping procedure.
...	Extra arguments to crossTab are passed on to confIntV.

Value

The cramersV and confIntV functions return either a point estimate or a confidence interval for Cramer's V, an effect size to describe the association between two categorical variables. The crossTab function is just a wrapper around confIntV.

Examples

```
### Get confidence interval for Cramer's V
### Note that removing the 'table', and so providing raw data, would enable
### bootstrapping, which can take a while.
confIntV(table(infert$education, infert$induced));
```

---

convert *conversion functions*

Description

These are a number of functions to convert statistics and effect size measures from/to each other.

Usage

```
convert.b.to.t(b, se)

convert.chisq.to.p(chisq, df, lower.tail=FALSE)
convert.chisq.to.V(chisq, n, minDim)

convert.cohensf.to.omegasq(cohensf)

convert.cohensfsq.to.omegasq(cohensfsq)

convert.d.to.logodds(d)
convert.d.to.r(d, n1 = NULL, n2 = NULL, akfEq8='if (n1 + n2) < 50')
```

```
convert.d.to.t(d, df = NULL, n1 = NULL, n2 = NULL, proportion = 0.5)
convert.d.to.variance(d, n1, n2)

convert.etasq.to.cohensf(etasq)

convert.f.to.etasq(f, df1, df2)
convert.f.to.omegasq(f, df1, df2)
convert.f.to.p(f, df1, df2, lower.tail=FALSE)
convert.f.to.d(f, df1, df2 = NULL, n1=NULL, n2=NULL, proportion=.5)

convert.fisherz.to.r(z)

convert.logodds.to.d(logodds)
convert.logodds.to.r(logodds)

convert.means.to.d(means, sds, ns = NULL, var.equal = NULL)

convert.ncf.to.omegasq(ncf, N)

convert.omegasq.to.cohensf(omegasq)
convert.omegasq.to.cohensfsq(omegasq)
convert.omegasq.to.f(omegasq, df1, df2)

convert.or.to.d(or)
convert.or.to.r(or)

convert.percentage.to.se(p, n)

convert.r.to.t(r, n)
convert.r.to.d(r)
convert.r.to.p(r, n)
convert.r.to.fisherz(r)

convert.t.to.r(t, n)
convert.t.to.d(t, df=NULL, n1=NULL, n2=NULL, proportion=.5)
convert.t.to.p(t, df)
```

Arguments

chisq, cohensf, cohensfsq, d, etasq, f, logodds, means, omegasq, or, p, r, t, z	The value of the relevant statistic or effect size.
ncf	The value of a noncentrality parameter of the F distribution.
n, n1, n2, N, ns	The number of observations that the r or t value is based on, or the number of observations in each of the two groups for an anova, or the total number of participants when specifying a noncentrality parameter.
df, df1, df2	The degrees of freedrom for that statistic (for F, the first one is the numerator

(i.e. the effect), and the second one the denominator (i.e. the error term).

`proportion` The proportion of participants in each of the two groups in a t-test or anova. This is used to compute the sample size in each group if the group sizes are unknown. Thus, if you only provide df1 and df2 when converting an F value to a Cohen's d value, equal group sizes are assumed.

`b` The value of a regression coefficient.

`se, sds` The standard error of standard errors of the relevant statistic (e.g. of a regression coefficient) or variables.

`minDim` The smallest of the number of columns and the number of rows of the crosstable for which the chisquare is translated to a Cramer's V value.

`lower.tail` For the F and chisquare distributions, whether to get the probability of the lower or upper tail.

`akfEq8` When converting Cohen's *d* to *r*, for small sample sizes, bias is introduced when the commonly suggested formula is used (Aaron, Kromrey & Ferron, 1998). Therefore, by default, this function uses different equations depending on the sample size (for n < 50 and for n > 50). When `akfEq8` is set to TRUE or FALSE, the corresponding action is taken; when `akfEq8` is not logical (i.e. TRUE or FALSE), the function depends on the sample size.

`var.equal` Whether to compute the value of *t* or Cohen's *d* assuming equal variances ('yes'), unequal variances ('no'), or whether to test for the difference ('test').

Details

Note that by default, the behavior of `convert.d.to.r` depends on the sample size (see Bruce, Kromrey & Ferron, 1998).

Value

The converted value as a numeric value.

Author(s)

Gjalt-Jorn Peters and Peter Verboon

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Aaron, B. Kromrey J. D. & Ferron, J. (1998) *Equating "r"-based and "d"-based Effect Size Indices: Problems with a Commonly Recommended Formula.* Paper presented at the Annual Meeting of the Florida Educational Research Association (43rd, Orlando, FL, November 2-4, 1998).

Examples

```
convert.t.to.r(t=-6.46, n=200);
convert.r.to.t(r=-.41, n=200);

### Compute some p-values
```

```
convert.t.to.p(4.2, 197);
convert.chisq.to.p(5.2, 3);
convert.f.to.p(8.93, 3, 644);

### Convert d to r using both equations
convert.d.to.r(d=.2, n1=5, n2=5, akfEq8 = FALSE);
convert.d.to.r(d=.2, n1=5, n2=5, akfEq8 = TRUE);
```

`convert.d.to.nnc` *Helper functions for Numbers Needed for Change*

Description

These two functions are used by nnc to compute the Numbers Needed for Change.

Usage

```
convert.d.to.nnc(d, cer, r = 1,
                 eventDesirable = TRUE,
                 eventIfHigher = TRUE)
convert.d.to.eer(d, cer,
                 eventDesirable = TRUE,
                 eventIfHigher = TRUE)
```

Arguments

`d`	The value of Cohen's *d*.
`cer`	The Control Event Rate.
`r`	The correlation between the determinant and behavior (for mediated Numbers Needed for Change).
`eventDesirable`	Whether an event is desirable or undesirable.
`eventIfHigher`	Whether scores above or below the threshold are considered 'an event'.

Details

These two functions are used by nnc to compute the Numbers Needed for Change.

Value

The converted value.

Author(s)

Gjalt-Jorn Peters & Stefan Gruijters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Gruijters, S. L. K., & Peters, G.-J. Y. (2017). Introducing the Numbers Needed for Change (NNC): A practical measure of effect size for intervention research.

See Also

nnc

Examples

```
convert.d.to.eer(d=.5, cer=.25);
convert.d.to.nnc(d=.5, cer=.25);
```

`createSigma` *createSigma: convenience function for mvrnorm*

Description

This function is made to quickly generate a Sigma matrix of the type required by mvrnorm. By specifying the number of variables, the mean correlation, and how much variation there should be in the correlations, it's easy to quickly generate a correlation matrix.

Usage

```
createSigma(nVar, meanR = 0.3, sdR = 0, diagonal = 1)
```

Arguments

nVar	The number of variables in the correlation matrix.
meanR	The average correlation, provided to rnorm together with sdR to generate the correlations.
sdR	The variation in the correlations, provided to rnorm together with meanR to generate the correlations.
diagonal	The value on the diagonal of the returned matrix: will normally be 1.

Value

A matrix of nVar x nVar.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

mvrnorm, rnorm, matrix

Examples

```
createSigma(3, .5, .1);
```

---

curfnfinder *Function to find the name of the calling function*

Description

This function finds and returns the name of the function calling it. This can be useful, for example, when generating functions algorithmically.

Usage

```
curfnfinder(skipframes = 0, skipnames = "(FUN)|(.+apply)|(replicate)",
            retIfNone = "Not in function", retStack = FALSE,
            extraPrefPerLevel = "\t")
```

Arguments

skipframes	Number of frames to skip; useful when called from an anonymous function.
skipnames	A regular expression specifying which substrings to delete.
retIfNone	What to return when called from outside a function.
retStack	Whether to return the entire stack or just one function.
extraPrefPerLevel	Extra prefixes to return for each level of the function.

Details

This function was written by Nick Sabbe for his package addendum. He posted it on Stack Exchange at http://stackoverflow.com/questions/7307987/logging-current-function-name and I included this here with this permission.

Value

The current function.

Author(s)

Nick Sabbe (Arteveldehogeschool)

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
functionA <- functionB <- function() {
  curFn <- curfnfinder();
  if (curFn == 'functionA') {
    cat('Doing something\n');
  } else {
    cat('Doing something else\n');
  }
  cat('Doing something generic.');
}
functionA();
functionB();
```

---

dCohensd *The distribution of Cohen's* d

Description

These functions use some conversion to and from the *t* distribution to provide the Cohen's *d* distribution. There are four versions that act similar to the standard distribution functions (the `d.`, `p.`, `q.`, and `r.` functions, and their longer aliases `.Cohensd`), three convenience functions (`pdExtreme`, `pdMild`, and `pdInterval`), a function to compute the confidence interval for a Cohen's *d* estimate `cohensdCI`, and a function to compute the sample size required to obtain a confidence interval around a Cohen's *d* estimate with a specified accuracy (`pwr.cohensdCI` and its alias `pwr.confIntd`).

Usage

```
dd(x, df, populationD = 0)
pd(q, df, populationD = 0, lower.tail = TRUE)
qd(p, df, populationD = 0, lower.tail = TRUE)
rd(n, df, populationD = 0)

dCohensd(x, df, populationD = 0)
pCohensd(q, df, populationD = 0, lower.tail = TRUE)
qCohensd(p, df, populationD = 0, lower.tail = TRUE)
rCohensd(n, df, populationD = 0)

pdExtreme(d, n, populationD=0)
pdMild(d, n, populationD=0)
pdInterval(ds, n, populationD=0)

cohensdCI(d, n, conf.level = .95, plot=FALSE, silent=TRUE)
pwr.cohensdCI(d, w = 0.1, conf.level = 0.95,
              extensive = FALSE, silent = TRUE)
pwr.confIntd(d, w = 0.1, conf.level = 0.95,
             extensive = FALSE, silent = TRUE)
```

Arguments

x, q, d	Vector of quantiles, or, in other words, the value(s) of Cohen's *d*.
ds	A vector with two Cohen's *d* values.
p	Vector of probabilites (*p*-values).
df	Degrees of freedom.
n	Desired number of Cohen's *d* values for rCohensd and rd, and the number of participants/datapoints for pdExtreme, pdMild, pdInterval, and cohensdCI.
populationD	The value of Cohen's *d* in the population; this determines the center of the Cohen's *d* distribution. I suppose this is the noncentrality parameter.
lower.tail	logical; if TRUE (default), probabilities are the likelihood of finding a Cohen's *d* smaller than the specified value; otherwise, the likelihood of finding a Cohen's *d* larger than the specified value.
conf.level	The level of confidence of the confidence interval.
plot	Whether to show a plot of the sampling distribution of Cohen's *d* and the confidence interval. This can only be used if specifying one value for d, n, and conf.level.
w	The desired 'half-width' or margin of error of the confidence interval.
extensive	Whether to only return the required sample size, or more extensive results.
silent	Whether to provide FALSE or suppress (TRUE) warnings. This is useful because function 'qt', which is used under the hood (see qt for more information), warns that 'full precision may not have been achieved' when the density of the distribution is very close to zero. This is normally no cause for concern, because with sample sizes this big, small deviations have little impact.

Details

The functions use convert.d.to.t and convert.t.to.d to provide the Cohen's *d* distribution.

More details about cohensdCI and pwr.cohensdCI are provided in Peters & Crutzen (2017).

Value

dCohensd (or dd) gives the density, pCohensd (or pd) gives the distribution function, qCohensd (or qd) gives the quantile function, and rCohensd (or rd) generates random deviates.

pdExtreme returns the probability (or probabilities) of finding a Cohen's *d* equal to or more extreme than the specified value(s).

pdMild returns the probability (or probabilities) of finding a Cohen's *d* equal to or *less* extreme than the specified value(s).

pdInterval returns the probability of finding a Cohen's *d* that lies in between the two specified values of Cohen's *d*.

cohensdCI provides the confidence interval(s) for a given Cohen's *d* value.

pwr.cohensdCI provides the sample size required to obtain a confidence interval for Cohen's *d* with a desired width.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Peters, G. J. Y. & Crutzen, R. (2017) Knowing exactly how effective an intervention, treatment, or manipulation is and ensuring that a study replicates: accuracy in parameter estimation as a partial solution to the replication crisis. http://dx.doi.org/

Maxwell, S. E., Kelley, K., & Rausch, J. R. (2008). Sample size planning for statistical power and accuracy in parameter estimation. Annual Review of Psychology, 59, 537-63. https://doi.org/10.1146/annurev.psych.59.1030

Cumming, G. (2013). The New Statistics: Why and How. Psychological Science, (November). https://doi.org/10.1177/0956797613504966

See Also

convert.d.to.t, convert.t.to.d, dt, pt, qt, rt

Examples

```
### Confidence interval for Cohen's d of .5
### from a sample of 200 participants, also
### showing this visually: this clearly shows
### how wildly our Cohen's d value can vary
### from sample to sample.
cohensdCI(.5, n=200, plot=TRUE);

### How many participants would we need if we
### would want a more accurate estimate, say
### with a maximum confidence interval width
### of .2?
pwr.cohensdCI(.5, w=.1);

### Show that 'sampling distribution':
cohensdCI(.5,
          n=pwr.cohensdCI(.5, w=.1),
          plot=TRUE);

### Generate 10 random Cohen's d values
rCohensd(10, 20, populationD = .5);

### Probability of findings a Cohen's d smaller than
### .5 if it's 0 in the population (i.e. under the
### null hypothesis)
pCohensd(.5, 64);

### Probability of findings a Cohen's d larger than
### .5 if it's 0 in the population (i.e. under the
### null hypothesis)
1 - pCohensd(.5, 64);
```

```
### Probability of findings a Cohen's d more extreme
### than .5 if it's 0 in the population (i.e. under
### the null hypothesis)
pdExtreme(.5, 64);

### Probability of findings a Cohen's d more extreme
### than .5 if it's 0.2 in the population.
pdExtreme(.5, 64, populationD = .2);
```

`descr` *descr (or descriptives)*

Description

This function provides a number of descriptives about your data, similar to what SPSS's DESCRIPTIVES (often called with DESCR) does.

Usage

```
descr(x, digits = 4, errorOnFactor = FALSE,
      include = c("central tendency", "spread", "range",
                  "distribution shape", "sample size"),
      maxModes = 1,
      t = FALSE, conf.level=.95,
      quantileType = 2);
```

Arguments

`x`	The vector for which to return descriptives.
`digits`	The number of digits to round the results to when showing them.
`errorOnFactor`	Whether to show an error when the vector is a factor, or just show the frequencies instead.
`include`	Which elements to include when showing the results.
`maxModes`	Maximum number of modes to display: displays "multi" if more than this number of modes if found.
`t`	Whether to transpose the dataframes when printing them to the screen (this is easier for users relying on screen readers).
`conf.level`	Confidence of confidence interval around the mean in the central tendency measures.
`quantileType`	The type of quantiles to be used to compute the interquartile range (IQR). See `quantile` for more information.

Details

Note that R (of course) has many similar functions, such as summary, describe in the excellent psych package.

The Hartigans' Dip Test may be unfamiliar to users; it is a measure of uni- vs. multidimensionality, computed by dip.test from the dip.test package. Depending on the sample size, values over .025 can be seen as mildly indicative of multimodality, while values over .05 probably warrant closer inspection (the p-value can be obtained using dip.test; also see Table 1 of Hartigan & Hartigan (1985) for an indication as to critical values).

Value

A list of dataframes with the requested values.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Hartigan, J. A.; Hartigan, P. M. The Dip Test of Unimodality. Ann. Statist. 13 (1985), no. 1, 70–84. doi:10.1214/aos/1176346577. http://projecteuclid.org/euclid.aos/1176346577.

See Also

summary, describe

Examples

```
descr(mtcars$mpg);
```

---

detectRareWords *Looking up word frequencies*

Description

This function checks, for each word in a text, how frequently it occurs in a given language. This is useful for eliminating rare words to make a text more accessible to an audience with limited vocabulary. htmlParse and xpathSApply from the XML package are used to process HTML files, if necessary. textToWords is a helper function that simply breaks down a character vector to a vector of words.

Usage

```
detectRareWords(textFile = NULL,
                wordFrequencyFile = "Dutch",
                output = c("file", "show", "return"),
                outputFile = NULL,
                wordCol = "Word", freqCol = "FREQlemma",
                textToWordsFunction = "textToWords",
                encoding = "ASCII",
                xPathSelector = "/text()",
                silent = FALSE)
textToWords(characterVector)
```

Arguments

`textFile`	If NULL, a dialog will be shown that enables users to select a file. If not NULL, this has to be either a filename or a character vector. An HTML file can be provided; this will be parsed using
`wordFrequencyFile`	The file with word frequencies to use. If 'Dutch' or 'Polish', files from the Center for Reading Research (`http://crr.ugent.be/`) are downloaded.
`output`	How to provide the output, as a character vector. If `file`, the filename to write to should be provided in `outputFile`. If `show`, the output is shown; and if `return`, the output is returned invisibly.
`outputFile`	The name of the file to store the output in.
`wordCol`	The name of the column in the `wordFrequencyFile` that contains the words.
`freqCol`	The name of the column in the `wordFrequencyFile` that contains the frequency with which each word occurs.
`textToWordsFunction`	The function to use to split a character vector, where each element contains one or more words, into a vector where each element is a word.
`encoding`	The encoding used to read and write files.
`xPathSelector`	If the file provided is an HTML file, `xpathSApply` is used to extract the content. `xPathSelector` specifies which content to extract (the default value extracts all text content).
`silent`	Whether to suppress detailed feedback about the process.
`characterVector`	A character vector, the elements of which are to be broken down into words.

Value

`detectRareWords` return a dataframe (invisibly) if `output` contains `return`. Otherwise, NULL is returned (invisibly), but the output is printed and/or written to a file depending on the value of `output`.

`textToWords` returns a vector of words.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
## Not run:
detectRareWords(paste('Dit is een tekst om de',
                      'werking van de detectRareWords',
                      'functie te demonstreren.'),
                output='show');

## End(Not run)
```

---

determinantStructure *Determinant Structure specification*

Description

These functions can be used to specify a determinant structure: a hierarchical structure of determinants that can then be conveniently plotted and analysed, for example using detStructCIBER.

These functions are made to be used together; see the example and the forthcoming article for more information.

Usage

```
determinantStructure(name, selection = NULL, ...)

determinantVar(name, selection = NULL, ...)

subdeterminants(name, selection = NULL, ...)

subdeterminantProducts(name, selection = NULL, ...)

## S3 method for class 'determinantStructure'
print(x, ...)
## S3 method for class 'determinantStructure'
plot(x, ...)
```

Arguments

name	The name of the variable that is specified.
selection	A regular expression to use to select the variables in a dataframe that are considered items that together form this variable. For determinantStructure, a list can be provided that also contains a named regular expression with the name 'behaviorRegEx', which specifies the name of the behavior to which this determinant structure pertains.

x	The `determinantStructure` object to print or plot.
...	Any additional arguments are other determinant structure building functions. These are used to construct the determinant structure 'tree'.

Details

This family of functions will be explained more in detail in a forthcoming paper.

`plot` and `print` methods plot and print a determinantStructure object.

Value

A determinantStructure object, which is a `data.tree` object.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

(Forthcoming)

See Also

`detStructAddVarLabels`, `detStructAddVarNames`, `detStructComputeProducts`, `detStructComputeScales`, `detStructCIBER`

Examples

```
determinantStructure('using R',
                     list('using R',
                          behaviorRegEx = 'some RegEx'),
                     determinantVar("Intention",
                                    "another RegEx",
                                    determinantVar("Attitude",
                                                   "third RegEX",
                                                   subdeterminants("Likelihood",
                                                                   "4th RegEx"),
                                                  subdeterminants("Evaluation",
                                                                  "5th RegEx"),
                                                  subdeterminantProducts("attProduct",
                                                                         c("4th RegEx",
                                                                         "5th RegEx"))),
                                    determinantVar("perceivedNorm",
                                                   "6th RegEx",
                                                   subdeterminants("Approval",
                                                                   "7th RegEx"),
                                                 subdeterminants("Motivation to comply",
                                                                   "8th RegEx"),
                                                  subdeterminantProducts("normProduct",
                                                                         c("7th RegEx",
```

```
                                                    "8th RegEx"))),
                                    determinantVar("pbc",
                                                   "9th RegEx",
                                           subdeterminants("Control beliefs",
                                                           "10th RegEx"))));
```

`determinantStructure Preprocessing`
Functions to preprocess determinant structures

Description

These functions are used in conjunction with the `determinantStructure` family of funtions to conveniently work with determinant structures.

Usage

```
detStructAddVarLabels(determinantStructure,
                      varLabelDf,
                      varNameCol = "varNames.cln",
                      leftAnchorCol = "leftAnchors",
                      rightAnchorCol = "rightAnchors",
                      subQuestionCol = "subQuestions",
                      questionTextCol = "questionText")

detStructAddVarNames(determinantStructure, names)

detStructComputeProducts(determinantStructure, dat, append = TRUE)

detStructComputeScales(determinantStructure, dat, append = TRUE, separator = "_")
```

Arguments

`determinantStructure`	The `determinantStructure` object.
`varLabelDf`	The variable label dataframe as generated by `processLSvarLabels`. It is also possible to specify 'homemade' dataframe, in which case the column names have to specified (see the next arguments).
`varNameCol`	The name of the column of the `varLabelDf` that contains the variable name. Only needs to be changed from the default value if `varLabelDf` is not a dataframe as produced by `processLSvarLabels`.
`leftAnchorCol`	The name of the column of the `varLabelDf` that contains the left anchor. Only needs to be changed from the default value if `varLabelDf` is not a dataframe as produced by `processLSvarLabels`.

`rightAnchorCol` The name of the column of the `varLabelDf` that contains the right anchor. Only needs to be changed from the default value if `varLabelDf` is not a dataframe as produced by `processLSvarLabels`.

`subQuestionCol` The name of the column of the `varLabelDf` that contains the subquestion. Only needs to be changed from the default value if `varLabelDf` is not a dataframe as produced by `processLSvarLabels`.

`questionTextCol` The name of the column of the `varLabelDf` that contains the question text. Only needs to be changed from the default value if `varLabelDf` is not a dataframe as produced by `processLSvarLabels`.

`names` A character vector with the variable names. These are matched against the regular expressions as specified in the `determinantStructure` object, and any matches will be stored in the `determinantStructure` object.

`dat` The dataframe containing the data; the variables names specified in `names` (when calling `detStructAddVarNames`) must be present in this dataframe.

`append` Whether to only return the products or scales, or whether to append these to the dataframe and return the entire dataframe.

`separator` The separator to use when constructing the scale variables names.

Details

This family of functions will be explained more in detail in a forthcoming paper.

Value

`detStructAddVarLabels` and `detStructAddVarNames` just change the `determinantStructure` object; `detStructComputeProducts` and `detStructComputeScales` return either the dataframe with the new variables appended (if `append = TRUE`) or just a dataframe with the new variables (if `append = FALSE`).

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

(Forthcoming)

See Also

`determinantStructure`, `determinantVar`, `subdeterminants`, `subdeterminantProducts`, `detStructCIBER`

Examples

```
### Generate a silly determinant structure
detStruct <- determinantStructure('This makes no sense',
                                  list('mpg',
                                       behaviorRegEx = 'mpg'),
                                  determinantVar("Proximal determinant",
                                                 "t",
                                                 determinantVar("Determinant",
                                                                "p",
                                                      subdeterminants("Subdeterminants",
                                                                      "a"))));

### Add the variable names
detStructAddVarNames(detStruct, names(mtcars));

### Add the determinant scale variable to the dataframe
mtcarsPlus <- detStructComputeScales(detStruct, mtcars);

### Show its presence
names(mtcarsPlus);
mean(mtcarsPlus$mpg_Determinant);
```

---

diamondPlot *Basic diamond plot construction function*

Description

This function constructs a diamond plot using ggDiamondLayer. It's normally not necessary to call this function directly: instead, use meansDiamondPlot, meanSDtoDiamondPlot, and factorLoadingDiamondCIplot.

Usage

```
diamondPlot(data, ciCols = 1:3,
            colorCol = NULL, otherAxisCol = NULL,
            yValues = NULL, yLabels = NULL,
            ylab = NULL, autoSize = NULL,
            fixedSize = 0.15,
            xlab = "Effect Size Estimate",
            theme = theme_bw(),
            color = "black",
            returnLayerOnly = FALSE,
            outputFile = NULL,
            outputWidth = 10,
            outputHeight = 10,
            ggsaveParams = list(units='cm',
                                dpi=300,
                                type="cairo"),
            ...)
```

Arguments

`data`	A dataframe (or matrix) containing lower bounds, centers (e.g. means), and upper bounds of intervals (e.g. confidence intervals).
`ciCols`	The columns in the dataframe with the lower bounds, centers (e.g. means), and upper bounds (in that order).
`colorCol`	The column in the dataframe containing the colors for each diamond, or a vector with colors (with as many elements as the dataframe has rows).
`otherAxisCol`	The column in the dataframe containing the values that determine where on the Y axis the diamond should be placed. If this is not available in the dataframe, specify it manually using `yValues`.
`yValues`	The values that determine where on the Y axis the diamond should be placed (can also be a column in the dataframe; in that case, use `otherAxisCol`.
`yLabels`	The labels to use for for each diamond (placed on the Y axis).
`xlab, ylab`	The labels of the X and Y axes.
`autoSize`	Whether to make the height of each diamond conditional upon its length (the width of the confidence interval).
`fixedSize`	If not using relative heights, `fixedSize` determines the height to use.
`theme`	The theme to use.
`color`	Color to use if colors are specified for each diamond.
`returnLayerOnly`	Set this to TRUE to only return the `ggplot` layer of the diamondplot, which can be useful to include it in other plots.
`outputFile`	A file to which to save the plot.
`outputWidth, outputHeight`	Width and height of saved plot (specified in centimeters by default, see `ggsaveParams`).
`ggsaveParams`	Parameters to pass to ggsave when saving the plot.
`...`	Additional arguments will be passed to `ggDiamondLayer`.

Value

A `ggplot` plot with a `ggDiamondLayer` is returned.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

`meansDiamondPlot`, `meanSDtoDiamondPlot`, `factorLoadingDiamondCIplot`, `ggDiamondLayer`

Examples

```
tmpDf <- data.frame(lo = c(1, 2, 3),
                    mean = c(1.5, 3, 5),
                    hi = c(2, 4, 10),
                    color = c('green', 'red', 'blue'));

### A simple diamond plot
diamondPlot(tmpDf);

### A diamond plot using the specified colours
diamondPlot(tmpDf, colorCol = 4);

### A diamond plot using automatically generated colours
### using a gradient
diamondPlot(tmpDf, generateColors=c('green', 'red'));

### A diamond plot using automatically generated colours
### using a gradient, specifying the minimum and maximum
### possible values that can be attained
diamondPlot(tmpDf, generateColors=c('green', 'red'),
            fullColorRange=c(1, 10));
```

`didacticPlot` *didacticPlot*

Description

didacticPlot is useful for making ggplot2 plots of distributions of t, F, Chi^2, and Pearson r, showing a given value, and shading the arie covering the more extreme values. didacticPlotTheme is the basic theme.

Usage

```
didacticPlot(foundValue, statistic, df1, df2 = NULL,
             granularity = 1000, xLim = NULL, yLab = NULL,
             lineCol = "red", lineSize=1,
             surfaceCol = "red", textMarginFactor = 20,
             sided="two")
didacticPlotTheme(base_size = 14, base_family = "")
```

Arguments

`foundValue`	The value to indicate (the 'found' value).
`statistic`	One of "r", "t", "f" or "chisq".
`df1, df2`	The degrees of freedom; only use df1 for the r, t and chi^2 test; for the F-test, use df1 for the degrees of freedom of the denominator and df2 for the degrees of freedom of the numerator.

granularity Steps to use for x-axis.

xLim Vector; minimum and maximum values on x axis.

yLab Label on y axis.

lineCol Colour of density line.

lineSize Size of density line.

surfaceCol Colour of coloured surface area.

textMarginFactor
Used to calculate how close to the vertical line text labels should appear.

sided Whether to make a plot for a 2-sided or 1-sided test.

base_size, base_family
Passed on to the grey ggplot theme.

Value

didacticPlot returns an object that contains the plot in the $plot element.

Examples

```
didacticPlot(1, statistic='chisq', df1=2);

didacticPlot(1, statistic='t', df1=40);

didacticPlot(2.02, statistic='t', df1=40, textMarginFactor=25);

### Two sample t-test for n1 = n2 = 250, showing
### p-value of 5%
# a<-didacticPlot(1.96, statistic='t', df1=498);
```

---

dlvPlot *dlvPlot*

Description

The dlvPlot function produces a dot-violin-line plot, and dlvTheme is the default theme.

Usage

```
dlvPlot(dat, x = NULL, y, z = NULL, conf.level = .95,
        jitter = "FALSE", binnedDots = TRUE, binwidth=NULL,
        error="lines", dotsize="density", densityDotBaseSize=3,
        normalDotBaseSize=1, violinAlpha = .2, dotAlpha = .4,
        lineAlpha = 1, connectingLineAlpha = 1,
        meanDotSize=5, posDodge=0.2, errorType = "both")
dlvTheme(base_size = 11, base_family = "", ...)
```

Arguments

`dat`	The dataframe containing x, y and z.
`x`	Character value with the name of the predictor ('independent') variable, must refer to a categorical variable (i.e. a factor).
`y`	Character value with the name of the critetion ('dependent') variable, must refer to a continuous variable (i.e. a numeric vector).
`z`	Character value with the name of the moderator variable, must refer to a categorical variable (i.e. a factor).
`conf.level`	Confidence of confidence intervals.
`jitter`	Logical value (i.e. TRUE or FALSE) whether or not to jitter individual datapoints. Note that jitter cannot be combined with posDodge (see below).
`binnedDots`	Logical value indicating whether to use binning to display the dots. Overrides jitter and dotsize.
`binwidth`	Numeric value indicating how broadly to bin (larger values is more binning, i.e. combining more dots into one big dot).
`error`	Character value: "none", "lines" or "whiskers"; indicates whether to show the confidence interval as lines with (whiskers) or without (lines) horizontal whiskers or not at all (none)
`dotsize`	Character value: "density" or "normal"; when "density", the size of each dot corresponds to the density of the distribution at that point.
`densityDotBaseSize`	Numeric value indicating base size of dots when their size corresponds to the density (bigger = larger dots).
`normalDotBaseSize`	Numeric value indicating base size of dots when their size is fixed (bigger = larger dots).
`violinAlpha`	Numeric value indicating alpha value of violin layer (0 = completely transparent, 1 = completely opaque).
`dotAlpha`	Numeric value indicating alpha value of dot layer (0 = completely transparent, 1 = completely opaque).
`lineAlpha`	Numeric value indicating alpha value of the confidence interval line layer (0 = completely transparent, 1 = completely opaque).
`connectingLineAlpha`	Numeric value indicating alpha value of the layer with the lines connecting the means (0 = completely transparent, 1 = completely opaque).
`meanDotSize`	Numeric value indicating the size of the dot used to indicate the mean in the line layer.
`posDodge`	Numeric value indicating the distance to dodge positions (0 for complete overlap).
`errorType`	If the error is shown using lines, this argument indicates Whether the errorbars should show the confidence interval (`errorType='ci'`), the standard errors (`errorType='se'`), or both (`errorType='both'`). In this last case, the standard error will be wider than the confidence interval.
`base_size, base_family, ...`	Passed on to the ggplot theme_grey() function.

Details

This function creates Dot Violin Line plots. One image says more than a thousand words; I suggest you run the example :-)

Value

The behavior of this function depends on the arguments.

If no x and z are provided and y is a character value, dlvPlot produces a univariate plot for the numerical y variable.

If no x and z are provided, and y is c character vector, dlvPlot produces multiple Univariate plots, with variable names determining categories on x-axis and with numerical y variables on y-axis

If both x and y are a character value, and no z is provided, dlvPlot produces a bivariate plot where factor x determines categories on x-axis with numerical variable y on the y-axis (roughly a line plot with a single line)

Finally, if x, y and z are each a character value, dlvPlot produces multivariate plot where factor x determines categories on x-axis, factor z determines the different lines, and with the numerical y variable on the y-axis

An object is returned with the following elements:

`dat.raw`	Raw datafile provided when calling dlvPlot
`dat`	Transformed (long) datafile dlvPlot uses
`descr`	Dataframe with extracted descriptives used to plot the mean and confidence intervals
`yRange`	The range of the Y variable used to construct the plot
`plot`	The plot itself

Examples

```
### Note: the 'not run' is simply because running takes a lot of time,
###       but these examples are all safe to run!
## Not run:
### Create simple dataset
dat <- data.frame(x1 = factor(rep(c(0,1), 20)),
                  x2 = factor(c(rep(0, 20), rep(1, 20))),
                  y=rep(c(4,5), 20) + rnorm(40));
### Generate a simple dlvPlot of y
dlvPlot(dat, y='y');
### Now add a predictor
dlvPlot(dat, x='x1', y='y');
### And finally also a moderator:
dlvPlot(dat, x='x1', y='y', z='x2');
### The number of datapoints might be a bit clearer if we jitter
dlvPlot(dat, x='x1', y='y', z='x2', jitter=TRUE);
### Although just dodging the density-sized dots might work better
dlvPlot(dat, x='x1', y='y', z='x2', posDodge=.3);

## End(Not run)
```

`escapeRegex` *Escapes any characters that would have special meaning in a regular expression.*

Description

Escapes any characters that would have special meaning in a requlr expression.

Usage

```
escapeRegex(string)
```

Arguments

`string`	string being operated on.

Details

`escapeRegex` will escape any characters that would have special meaning in a requlr expression. For any string `grep(regexpEscape(string), string)` will always be true.

Value

The value of the string with any characters that would have special meaning in a requlr expression escaped.

Note

Note that this function was copied literally from the `Hmisc` package (to prevent importing the entire package for one line of code).

Author(s)

Charles Dupont
Department of Biostatistics
Vanderbilt University

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

`grep`, `Hmisc`, http://biostat.mc.vanderbilt.edu/wiki/Main/Hmisc, https://github.com/harrelfe/Hmisc

Examples

```
string <- "this\\(system) {is} [full]."
escapeRegex(string)
```

`examine` *Examine one or more variables*

Description

These functions are one of many R functions enabling users to assess variable descriptives. They have been developed to mimic SPSS' 'EXAMINE' syntax command ('Explore' in the menu) as closely as possible to ease the transition for new R users and facilitate teaching courses where both programs are taught alongside each other.

Usage

```
examine(..., stem = TRUE, plots = TRUE,
        extremeValues = 5, descr.include = NULL,
        qqCI = TRUE, conf.level = 0.95)
examineBy(..., by=NULL, stem = TRUE, plots = TRUE,
          extremeValues = 5, descr.include=NULL,
          qqCI = TRUE, conf.level=.95)
```

Arguments

`...`	The first argument is a list of variables to provide descriptives for. Because these are the first arguments, the other arguments must be named explicitly so R does not confuse them for something that should be part of the dots.
`by`	A variable by which to split the dataset before calling `examine`. This can be used to show the descriptives separate by levels of a factor.
`stem`	Whether to display a stem and leaf plot.
`plots`	Whether to display the plots generated by the `dataShape` function.
`extremeValues`	How many extreme values to show at either end (the highest and lowest values). When set to FALSE (or 0), no extreme values are shown.
`qqCI`	Whether to display confidence intervals in the QQ-plot.
`descr.include`	Which descriptives to include; see `descr` for more information.
`conf.level`	The level of confidence of the confidence interval.

Details

This function basically just calls the `descr` function, optionally supplemented with calls to `stem`, `dataShape`.

Value

A list that is displayed when printed.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

descr, dataShape, stem

Examples

```
### Look at the miles per gallon descriptives:
examine(mtcars$mpg, stem=FALSE, plots=FALSE);

### Separate for the different number of cylinders:
examineBy(mtcars$mpg, by=mtcars$cyl,
          stem=FALSE, plots=FALSE,
          extremeValues=FALSE,
          descr.include=c('central tendency', 'spread'));
```

`exceptionalScore` *exceptionalScore*

Description

This function can be used to detect exceptionally high or low scores in a vector.

Usage

```
exceptionalScore(x, prob = 0.025, both = TRUE, silent = FALSE,
                 quantileCorrection = 1e-04, quantileType = 8)
```

Arguments

`x`	Vector in which to detect exceptional scores.
`prob`	Probability that a score is exceptionally positive or negative; i.e. scores with a quartile lower than `prob` or higher than 1-`prob` are considered exceptional (if both is TRUE, at least). So, note that a `prob` of .025 means that if both=TRUE, the most exceptional 5% of the values is marked as such.
`both`	Whether to consider values exceptional if they're below `prob` as well as above 1-`prob`, or whether to only consider values exceptional if they're below `prob` is `prob` is < .5, or above `prob` if `prob` > .5.
`silent`	Can be used to suppress messages.
`quantileCorrection`	By how much to correct the computed quantiles; this is used because when a distribution is very right-skewed, the lowest quantile is the lowest value, which is then also the mode; without subtracting a correction, almost all values would be marked as 'exceptional'.

quantileType The algorithm used to compute the quantiles; see quantile.

Details

Note that of course, by definition, prob of 2*prob percent of the values is exceptional, so it is usually not a wise idea to remove scores based on their 'exceptionalness'. Instead, use exceptionalScores, which calls this function, to see how often participants answered exceptionally, and remove them based on that.

Value

A logical vector, indicating for each value in the supplied vector whether it is exceptional.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

quantile, exceptionalScores

Examples

```
exceptionalScore(c(1,1,2,2,2,3,3,3,4,4,4,5,5,5,5,6,6,7,8,20), prob=.05);
```

---

exceptionalScores *exceptionalScores*

Description

A function to detect participants that consistently respond exceptionally.

Usage

```
exceptionalScores(dat, items = NULL, exception = 0.025, totalOnly = TRUE,
                  append = TRUE, both = TRUE, silent = FALSE,
                 suffix = "_isExceptional", totalVarName = "exceptionalScores")
```

Arguments

dat	The dataframe containing the variables to inspect, or the vector to inspect (but for vectors, exceptionalScore might be more useful).
items	The names of the variables to inspect.
exception	When an item will be considered exceptional, passed on as prob to exceptionalScore.
totalOnly	Whether to return only the number of exceptional scores for each row in the dataframe, or for each inspected item, which values are exceptional.

append	Whether to return the supplied dataframe with the new variable(s) appended (if TRUE), or whether to only return the new variable(s) (if FALSE).
both	Whether to look for both low and high exceptional scores (TRUE) or not (FALSE; see exceptionalScore).
silent	Can be used to suppress messages.
suffix	If not returning the total number of exceptional values, for each inspected variable, a new variable is returned indicating which values are exceptional. The text string is appended to each original variable name to create the new variable names.
totalVarName	If returning only the total number of exceptional values, and appending these to the provided dataset, this text string is used as variable name.

Value

Either a vector containing the number of exceptional values, a dataset containing, for each inspected variable, which values are exceptional, or the provided dataset where either the total or the exceptional values for each variable are appended.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

exceptionalScore

Examples

```
exceptionalScores(mtcars)
```

---

extractVarName *Extract variable names*

Description

Functions often get passed variables from within dataframes or other lists. However, printing these names with all their dollar signs isn't very userfriendly. This function simply uses a regular expression to extract the actual name.

Usage

```
extractVarName(x)
```

Arguments

x	A character vector of one or more variable names.

Value

The actual variables name, with all containing objectes stripped off.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
extractVarName('mtcars$mpg');
```

`faConfInt` *Extract confidence bounds from psych's factor analysis object*

Description

This function contains some code from a function in psych that's not exported `print.psych.fa.ci` but useful nonetheless. It basically takes the outcomes of a factor analysis and extracted the confidence intervals.

Usage

```
faConfInt(fa)
```

Arguments

`fa`	The object produced by the `fa` function from the psych package. It is important that the `n.iter` argument of `fa` was set to a realistic number, because otherwise, no confidence intervals will be available.

Details

THis function extract confidence interval bounds and combines them with factor loadings using the code from the `print.psych.fa.ci` in psych.

Value

A list of dataframes, one for each extracted factor, with in each dataframe three variables:

`lo`	lower bound of the confidence interval
`est`	point estimate of the factor loading
`hi`	upper bound of the confidence interval

Author(s)

William Revelle (extracted by Gjalt-Jorn Peters)

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
## Not run:
### Not run because it takes too long to run to test it,
### and may produce warnings, both because of the bootstrapping
### required to generate the confidence intervals in fa
faConfInt(fa(Thurstone.33, 2, n.iter=100, n.obs=100));

## End(Not run)
```

`factorLoadingDiamondCIplot`

Two-dimensional visualisation of factor analyses

Description

This function uses the `diamondPlot` to visualise the results of a factor analyses. Because the factor loadings computed in factor analysis are point estimates, they may vary from sample to sample. The factor loadings for any given sample are usually not relevant; samples are but means to study populations, and so, researchers are usually interested in population values for the factor loadings. However, tables with lots of loadings can quickly become confusing and intimidating. This function aims to facilitate working with and interpreting factor analysis based on confidence intervals by visualising the factor loadings and their confidence intervals.

Usage

```
factorLoadingDiamondCIplot(fa,
                           xlab="Factor Loading",
                           colors =
                             brewer.pal(max(3,
                                            fa$factors),
                                        "Set1"),
                           ...)
```

Arguments

`fa`	The object produced by the `fa` function from the `psych` package. It is important that the `n.iter` argument of `fa` was set to a realistic number, because otherwise, no confidence intervals will be available.
`xlab`	The label for the x axis.
`colors`	The colors used for the factors. The default uses the 'Set1' palette from colorbrewer using the `RColorBrewer` package. A vector can also be supplied; the colors must be valid arguments to `colorRamp` (and therefore, to `col2rgb`).
`...`	Additional arguments will be passed to `ggDiamondLayer`. This can be used to set, for example, the transparency (alpha value) of the diamonds to a lower value using e.g. `alpha=.5`.

Value

A ggplot plot with several ggDiamondLayers is returned.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

fa, meansDiamondPlot, meanSDtoDiamondPlot, diamondPlot, ggDiamondLayer

Examples

```
## Not run:
### Not run because it takes too long and may generate
### warnings because of the bootstrapping of the confidence
### intervals
factorLoadingDiamondCIplot(fa(Thurstone.33, 2,
                              n.iter=100, n.obs=100));

### And using a lower alpha value for the diamonds to
### make them more transparent
factorLoadingDiamondCIplot(fa(Thurstone.33, 2,
                              n.iter=100, n.obs=100),
                           alpha = .5);

## End(Not run)
```

---

formatCI *Pretty formatting of confidence intervals*

Description

Pretty much does what the title says.

Usage

```
formatCI(ci, sep = "; ",
         prefix = "[", suffix = "]",
         digits = 2, noZero = FALSE)
```

Arguments

ci	A confidence interval (a vector of 2 elements; longer vectors work, but I guess that wouldn't make sense).
sep	The separator of the values, usually "; " or ", ".
prefix	The prefix, usually a type of opening parenthesis/bracket.
suffix	The suffix, usually a type of closing parenthesis/bracket.
digits	The number of digits to which to round the values.
noZero	Whether to strip the leading zero (before the decimal point), as is typically done when following APA style and displaying correlations, *p* values, and other numbers that cannot reach 1 or more.

Value

A character vector of one element.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

noZero, formatR, formatPvalue

Examples

```
### With leading zero ...
formatCI(c(0.55, 0.021));

### ... and without
formatCI(c(0.55, 0.021), noZero=TRUE);
```

---

freq *Frequency tables*

Description

Function to show frequencies in a manner similar to what SPSS' "FREQUENCIES" command does. Note that `frequency` is an alias for `freq`.

Usage

```
freq(vector, digits = 1, nsmall=1, transposed=FALSE,
     round=1, plot=FALSE, plotTheme = theme_bw())
frequencies(..., digits = 1, nsmall = 1,
            transposed = FALSE, round = 1,
            plot = FALSE, plotTheme = theme_bw())
```

Arguments

vector	A vector of values to compute frequencies for.
digits	Minimum number of significant digits to show in result.
nsmall	Minimum number of digits after the decimal point to show in the result.
transposed	Whether to transpose the results when printing them (this can be useful for blind users).
round	Number of digits to round the results to (can be used in conjunction with digits to determine format of results).
plot	If true, a histogram is shown of the variable.
plotTheme	The ggplot2 theme to use.
...	The variables of which to provide frequencies

Value

An object with several elements, the most notable of which is:

dat	A dataframe with the frequencies

For `frequencies`, these objects are in a list of their own.

Examples

```
### Create factor vector
ourFactor <- factor(mtcars$gear, levels=c(3,4,5),
                    labels=c("three", "four", "five"));
### Add some missing values
factorWithMissings <- ourFactor;
factorWithMissings[10] <- factorWithMissings[20] <- NA;

### Show frequencies
freq(ourFactor);
freq(factorWithMissings);

### ... Or for all of them at one
frequencies(ourFactor, factorWithMissings);
```

---

fullFact *fullFact*

Description

This function provides a userfriendly interface to a number of advanced factor analysis functions in the psych package.

Usage

```
fullFact(dat = NULL, items = NULL, rotate = "oblimin")
```

Arguments

dat	Datafile to analyse; if NULL, a pop-up is provided to select a file.
items	Which variables (items) to factor-analyse. If NULL, all are selected.
rotate	Which rotation to use (see psych package).

Value

The outcomes, which are printed to the screen unless assigned.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

fa.parallel, vss

Examples

```
## Not run:
  ### Not run to save processing during package testing
  fullFact(attitude);

## End(Not run)
```

---

ggBarChart *Bar chart using ggplot*

Description

This function provides a simple interface to create a ggplot bar chart.

Usage

```
ggBarChart(vector, plotTheme = theme_bw(), ...)
```

Arguments

vector	The vector to display in the bar chart.
plotTheme	The theme to apply.
...	And additional arguments are passed to geom_bar.

Value

A ggplot plot is returned.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

geom_bar

Examples

```
ggBarChart(mtcars$cyl);
```

---

ggBoxplot *Box plot using ggplot*

Description

This function provides a simple interface to create a ggplot box plot, organising different boxplots by levels of a factor is desired, and showing row numbers of outliers.

Usage

```
ggBoxplot(dat, y = NULL, x = NULL,
          labelOutliers = TRUE,
          outlierColor = "red",
          theme = theme_bw(), ...)
```

Arguments

dat	Either a vector of values (to display in the box plot) or a dataframe containing variables to display in the box plot.
y	If dat is a dataframe, this is the name of the variable to make the box plot of.
x	If dat is a dataframe, this is the name of the variable (normally a factor) to place on the X axis. Separate box plots will be generate for each level of this variable.
labelOutliers	Whether or not to label outliers.
outlierColor	If labeling outliers, this is the color to use.
theme	The theme to use for the box plot.
...	Any additional arguments will be passed to geom_boxplot.

Details

This function is based on JasonAizkalns' answer to a question on Stack Exchange (Cross Validated; see http://stackoverflow.com/questions/33524669/labeling-outliers-of-boxplots-in-r).

Value

A ggplot plot is returned.

Author(s)

Jason Aizkalns; implemented in this package (and tweaked a bit) by Gjalt-Jorn Peters.

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

geom_boxplot

Examples

```
### A box plot for miles per gallon in the mtcars dataset:
ggBoxplot(mtcars$mpg);

### And separate for each level of 'cyl' (number of cylinder):
ggBoxplot(mtcars, y='mpg', x='cyl');
```

---

ggConfidenceCurve *Confidence Curves*

Description

Confidence curves are a way to show the confidence in an estimate computed from sample data. They are useful because they show all confidence levels simultaneously, thereby giving a good sense of the accuracy of the estimate, without forcing the researchers to make a more or less arbitrary choice for one confidence level.

Usage

```
ggConfidenceCurve(metric = "d",
                  value = NULL,
                  n = NULL,
                  conf.level = NULL,
                  wRange = c(0.05, 0.8),
                  curveSize = 1,
                  curveColor = "black",
                  confRange = c(1e-04, 0.9999),
                  confLines = c(0.5, 0.8, 0.95, 0.99),
                  confLineColor = "grey",
```

```
                confLineSize = 1,
                xlab = metric,
                steps = 1000,
                theme = theme_bw())
```

Arguments

metric	The metric, currently only 'd' (Cohen's *d*) and 'r' (Pearson's *r*) are implemented.
value	The value for which to create the confidence curve plot.
n	The sample size for which to create the confidence curve plot. If n is specified, the y axis shows confidence levels (i.e. a conventional confidence curve is generated). If n is set to NULL, the y axis shows sample sizes. Either n or conf.level must be NULL.
conf.level	The confidence level for which to create the confidence curve plot. If conf.level is specified, the y axis shows sample sizes. If conf.level is set to NULL, the y axis shows confidence levels (i.e. a conventional confidence curve is generated). Either n or conf.level must be NULL.
wRange	The range of 'half-widths', or margins of error, to plot in the confidence curve plot if no sample size is specified (if n=NULL).
curveSize	The line size of the confidence curve line.
curveColor	The color of the confidence curve line.
confRange	The range of confidence levels to plot.
confLines	If a traditional confidence curve is generated, lines can be added to indicate the metric values corresponding to the lower and upper confidence interval bounds.
confLineColor	If confidence lines are added (see confLines), this is the color in which they are drawn.
confLineSize	If confidence lines are added (see confLines), this is the size in which they are drawn.
xlab	The label on the x axis.
steps	The number of steps to use when generating the data for the confidence curves' more steps yield prettier, smoother curves, but take more time.
theme	The ggplot theme to use.

Value

A ggplot2 plot.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Bender, R., Berg, G., & Zeeb, H. (2005). Tutorial: Using confidence curves in medical research. *Biometrical Journal*, 47(2), 237-247. http://doi.org/10.1002/bimj.200410104

Birnbaum, A. (1961). Confidence curves: An omnibus technique for estimation and testing statistical hypotheses. *Journal of the American Statistical Association*, 56(294), 246-249. http://doi.org/10.1080/01621459.1961.10

See Also

cohensdCI, pwr.cohensdCI, confIntR, pwr.confIntR

Examples

```
ggConfidenceCurve(metric='d', value = .5, n = 128);
ggConfidenceCurve(metric='d', value = .5, conf.level = .95);
```

---

ggDiamondLayer *Basic ggplot2 diamond plot layer construction functions*

Description

These functions are used by diamondPlot to construct a diamond plot. It's normally not necessary to call this function directly: instead, use meansDiamondPlot, meanSDtoDiamondPlot, and factorLoadingDiamondCIplot.

Usage

```
ggDiamondLayer(data, ciCols = 1:3,
               colorCol = NULL,
               generateColors = NULL,
               fullColorRange = NULL,
               color = "black",
               lineColor=NA,
               otherAxisCol = 1:nrow(data),
               autoSize = NULL,
               fixedSize = 0.15,
               ...)
diamondCoordinates(values,
                   otherAxisValue = 1,
                   direction = "horizontal",
                   autoSize = NULL,
                   fixedSize = 0.15)
varsToDiamondPlotDf(dat, items = NULL,
                    labels = NULL, decreasing = NULL,
                    conf.level = 0.95)
rawDataDiamondLayer(dat, items = NULL,
                    itemOrder = 1:length(items),
                    dataAlpha = 0.1, dataColor = "#444444",
```

```
jitterWidth = 0.5, jitterHeight = 0.4,
size = 3, ...)
```

Arguments

data, dat	A dataframe (or matrix) containing lower bounds, centers (e.g. means), and upper bounds of intervals (e.g. confidence intervals) for ggDiamondLayer or items and raw data for varsToDiamondPlotDf and rawDataDiamondLayer.
ciCols	The columns in the dataframe with the lower bounds, centers (e.g. means), and upper bounds (in that order).
colorCol	The column in the dataframe containing the colors for each diamond, or a vector with colors (with as many elements as the dataframe has rows).
generateColors	A vector with colors to use to generate a gradient. These colors must be valid arguments to colorRamp (and therefore, to col2rgb).
fullColorRange	When specifying a gradient using generateColors, it is usually desirable to specify the minimum and maximum possible value corresponding to the outer anchors of that gradient. For example, when plotting numbers from 0 to 100 using a gradient from 'red' through 'orange' to 'green', none of the means may actually be 0 or 100; the lowest mean may be, for example, 50. If no fullColorRange is specified, the diamond representing that lowest mean of 50 wil be red, not orange. When specifying the fullColorRange, the lowest and highest 'colors' in generateColors are anchored to the minimum and maximum values of fullColorRange.
color	When no colors are automatically generated, all diamonds will have this color.
lineColor	If NA, lines will have the same colors as the diamonds' fill. If not NA, must be a valid color, which is then used as line color. Note that e.g. linetype and color can be used as well, which will be passed on to geom_polygon.
otherAxisCol	A vector of values, or the index of the column in the dataframe, that specifies the values for the Y axis of the diamonds. This should normally just be a vector of consecutive integers.
autoSize	Whether to make the height of each diamond conditional upon its length (the width of the confidence interval).
fixedSize	If not using relative heights, fixedSize determines the height to use.
...	Any additional arguments are passed to geom_polygon. This can be used to set, for example, the alpha value of the diamonds. Additional arguments for rawDataDiamondLayer are passed on to geom_jitter.
values	A vector of 2 or more values that are used to construct the diamond coordinates. If three values are provided, the middle one becomes the diamond's center. If two, four, or more values are provided, the median becomes the diamond's center.
otherAxisValue	The value on the other axis to use to compute the coordinates; this will be the Y axis value of the points of the diamond (if direction is 'horizontal') or the X axis value (if direction is 'vertical').
direction	Whether the diamonds should be constructed horizontally or vertically.
items	The items from the dataframe to include in the diamondplot or dataframe.

labels	The item labels to add to the dataframe.
decreasing	Whether to sort the items (rows) in the dataframe decreasing (TRUE), increasing (FALSE), or not at all (NULL).
conf.level	The confidence of the confidence intervals.
itemOrder	Order of the items to use (if not sorting).
dataAlpha	This determines the alpha (transparency) of the data points.
dataColor	The color of the data points.
jitterWidth	How much to jitter the individual datapoints horizontally.
jitterHeight	How much to jitter the individual datapoints vertically.
size	The size of the data points.

Value

ggDiamondLayer returns a ggplot geom_polygon object, which can then be used in ggplot plots (as diamondPlot does).

diamondCoordinates returns a set of four coordinates that together specify a diamond.

varsToDiamondPlotDf returns a dataframe of diamondCoordinates.

rawDataDiamondLayer returns a geom_jitter object.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

meansDiamondPlot, meanSDtoDiamondPlot, factorLoadingDiamondCIplot, diamondPlot

Examples

```
## Not run:
### (Don't run this example as a test, because we
###  need the ggplot function which isn't part of
###  this package.)

### The coordinates for a simple diamond
diamondCoordinates(values = c(1,2,3));

### Plot this diamond
ggplot() + ggDiamondLayer(data.frame(1,2,3));

## End(Not run)
```

ggNNC *Visualising Numbers Needed for Change*

Description

These functions can be used to visualise Numbers Needed for Change. `erDataSeq` is a helper function to generate an Event Rate Data Sequence, and it uses `convert.threshold.to.er` and `convert.er.to.threshold` to convert thresholds to event rates and vice versa.

Usage

```
erDataSeq(er = NULL, threshold = NULL,
          mean = NULL, sd = NULL,
          eventIfHigher = TRUE,
          pRange = c(1e-06, 0.99999),
          xStep = 0.01)

ggNNC(cerDataSeq, d = NULL, eventDesirable = TRUE,
      r = 1, xlab = "Continuous outcome",
      plotTitle = c("Numbers Needed for Change = ", ""),
      theme = theme_bw(), lineSize = 1,
      cerColor = "#EBF2F8", eerColor = "#172F47",
      cerLineColor = "#888888", eerLineColor = "#000000",
      dArrowColor = "#000000", cerAlpha = 0.66,
      eerAlpha = 0.66, xLim = NULL,
      xLimAutoDensityTolerance = 0.001,
      showLegend = TRUE, verticalLineColor = "#172F47",
      desirableColor = "#00FF00", desirableAlpha = 0.2,
      undesirableColor = "#FF0000", undesirableAlpha = 0.2,
      desirableTextColor = "#009900",
      undesirableTextColor = "#990000",
      dArrowDistance = 0.04 * max(cerDataSeq$density),
      dLabelDistance = 0.08 * max(cerDataSeq$density))

convert.threshold.to.er(threshold, mean, sd,
                        eventIfHigher = TRUE,
                        pdist = pnorm)

convert.er.to.threshold(er, mean, sd,
                        eventIfHigher = TRUE,
                        qdist = qnorm)
```

Arguments

`er`	Event rate to visualise (or convert).

threshold	If the event rate is not available, a threshold value can be specified instead, which is then used in conjunction with the mean (mean) and standard deviation (sd) and assuming a normal distribution to compute the event rate.
mean	The mean of the control group distribution.
sd	The standard deviation (of the control distribution, but assumed to be the same for both distributions).
eventIfHigher	Whether scores above or below the threshold are considered 'an event'.
pRange	The range of probabilities for which to so the distribution.
xStep	Precision of the drawn distribution; higher values mean lower precision/granularity/resolution.
cerDataSeq	The cerDataSeq object.
d	The value of Cohen's *d*.
eventDesirable	Whether an event is desirable or undesirable.
r	The correlation between the determinant and behavior (for mediated NNC's).
xlab	The label to display for the X axis.
plotTitle	The title of the plot; either one character value, this value if used; if two, they are considered a prefix and suffix to be pre/appended to the NNC value.
theme	The theme to use for the plot.
lineSize	The thickness of the lines in the plot.
cerColor	The color to use for the event rate portion of the control group distribution.
eerColor	The color to use for the event rate portion of the experimental group distribution.
cerLineColor	The line color to use for the control group distribution.
eerLineColor	The line color to use for the experimental group distribution.
dArrowColor	The color of the arrow to show the effect size.
cerAlpha	The alpha value (transparency) to use for the control group distribution.
eerAlpha	The alpha value (transparency) to use for the control group distribution.
xLim	This can be used to manually specify the limits for the X axis; if NULL, sensible limits will be derived using xLimAutoDensityTolerance.
xLimAutoDensityTolerance	If xLim is NULL, the limits will be set where the density falls below this proportion of its maximum value.
showLegend	Whether to show the legend (only if showing two distributions).
verticalLineColor	The color of the vertical line used to indicate the threshold.
desirableColor	The color for the desirable portion of the X axis.
desirableAlpha	The alpha for the desirable portion of the X axis.
undesirableColor	The color for the undesirable portion of the X axis.
undesirableAlpha	The color for the undesirable portion of the X axis.

`desirableTextColor`
: The color for the text to indicate the desirable portion of the X axis.

`undesirableTextColor`
: The color for the text to indicate the undesirable portion of the X axis.

`dArrowDistance`
: The distance of the effect size arrow from the top of the distributions.

`dLabelDistance`
: The distance of the effect size label from the top of the distributions.

`pdist, qdist`
: Distributions to use when converting thresholds to event rates and vice versa; defaults to the normal distribution.

Details

These functions are used by `nnc` to show the distributions, and event rates. They probably won't be used much on their own.

Value

`erDataSeq` returns a data sequence; `ggNNC` a `ggplot`.

Author(s)

Gjalt-Jorn Peters & Stefan Gruijters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Gruijters, S. L. K., & Peters, G.-J. Y. (2017). Introducing the Numbers Needed for Change (NNC): A practical measure of effect size for intervention research.

See Also

`nnc`

Examples

```
### Show distribution for an event rate value of 125
ggNNC(erDataSeq(threshold=125, mean=90, sd=30));

### If the event occurs under the threshold instead of
### above it
ggNNC(erDataSeq(threshold=125, mean=90, sd=30,
      eventIfHigher = FALSE));

### ... And for undesirable events (note how
### desirability is an argument for ggNNC, whereas
### whether an event occurs 'above' or 'below' the
### threshold is an argument for erDataSeq):
ggNNC(erDataSeq(threshold=125, mean=90, sd=30,
                eventIfHigher = FALSE),
      eventDesirable = FALSE);
```

```
### Show event rate for both experimental and
### control conditions, and show the numbers
### needed for change
ggNNC(erDataSeq(threshold=125, mean=90, sd=30), d=.5);

### Illustration of how even with very large effect
### sizes, if the control event rate is very high,
### you'll still need a high number of NNC
ggNNC(erDataSeq(er=.9), d=1);
```

---

ggPie *A ggplot pie chart*

Description

THis function creates a pie chart. Note that these are generally quite strongly advised against, as people are not good at interpreting relative frequencies on the basis of pie charts.

Usage

```
ggPie(vector)
```

Arguments

vector	The vector (best to pass a factor).

Value

A ggplot pie chart.

Note

This function is very strongly based on the Mathematical Coffee post at http://mathematicalcoffee.blogspot.com/2014/06/ggpi
pie-graphs-in-ggplot2.html.

Author(s)

Amy Chan; implemented in this package (and tweaked a bit) by Gjalt-Jorn Peters.

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
ggPie(mtcars$cyl);
```

ggqq *Easy ggplot Q-Q plot*

Description

This function creates a qq-plot with a confidence interval.

Usage

```
ggqq(x, distribution = "norm", ...,
     ci = TRUE, line.estimate = NULL,
     conf.level = 0.95,
     sampleSizeOverride = NULL,
     observedOnX = TRUE,
     scaleExpected = TRUE,
     theoryLab = "Theoretical quantiles",
     observeLab = "Observed quantiles",
     theme = theme_bw())
```

Arguments

x	A vector containing the values to plot.
distribution	The distribution to (a 'd' and 'q' are prepended, and the resulting functions are used, e.g. dnorm and qnorm for the normal curve).
...	Any additional arguments are passed to the quantile function (e.g. qnorm). Because of these dots, any following arguments must be named explicitly.
ci	Whether to show the confidence interval.
line.estimate	Whether to show the line showing the match with the specified distribution (e.g. the normal distribution).
conf.level	THe confidence of the confidence leven arround the estimate for the specified distribtion.
sampleSizeOverride	It can be desirable to get the confidence intervals for a different sample size (when the sample size is very large, for example, such as when this plot is generated by the function normalityAssessment). That different sample size can be specified here.
observedOnX	Whether to plot the observed values (if TRUE) or the theoretically expected values (if FALSE) on the X axis. The other is plotted on the Y axis.
scaleExpected	Whether the scale the expected values to match the scale of the variable. This option is provided to be able to mimic SPSS' Q-Q plots.
theoryLab	The label for the theoretically expected values (on the Y axis by default).
observeLab	The label for the observed values (on the Y axis by default).
theme	The theme to use.

Details

This is strongly based on the answer by user Floo0 to a Stack Overflow question at Stack Exchange (see http://stackoverflow.com/questions/4357031/qqnorm-and-qqline-in-ggplot2/27191036#27191036), also posted at GitHub (see https://gist.github.com/rentrop/d39a8406ad8af2a1066c). That code is in turn based on the qqPlot function from the car package.

Value

A ggplot plot is returned.

Author(s)

John Fox and Floo0; implemented in this package (and tweaked a bit) by Gjalt-Jorn Peters.

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
ggqq(mtcars$mpg);
```

`importLimeSurveyData` *importLimeSurveyData*

Description

This function can be used to import files exported by LimeSurvey, a powerful Open Source online survey application that can be used for, for example, psychological experiments and other research.

Usage

```
importLimeSurveyData(datafile = NULL,
  dataPath = NULL,
  datafileRegEx = NULL,
  scriptfile = NULL,
  limeSurveyRegEx.varNames =
    "names\\(data\\)\\[\\d*\\] <- ",
  limeSurveyRegEx.toChar =
    "data\\[, \\d*\\] <- as.character\\(data\\[, \\d*\\]\\)",
  limeSurveyRegEx.varLabels =
    "attributes\\(data\\)\$variable.labels\\[\\d*\\] <- \".*\"",
  limeSurveyRegEx.toFactor =
    paste0("data\\[, \\d*\\] <- factor\\(data\\[, \\d*\\], ",
           "levels=c\\(.*\\),.*labels=c\\(.*\\)\\)"),
  limeSurveyRegEx.varNameSanitizing =
    list(list(pattern = "#", replacement = "."),
         list(pattern = "\$", replacement = ".")),
  setVarNames = TRUE,
  setLabels = TRUE,
```

```
  convertToCharacter = FALSE,
  convertToFactor = FALSE,
  categoricalQuestions = NULL,
  massConvertToNumeric = TRUE,
  dataHasVarNames = TRUE,
  encoding = "NULL",
  dataEncoding = "unknown",
  scriptEncoding = "ASCII")
```

Arguments

`datafile` The path and filename of the file containing the data (comma separated values).

`dataPath, datafileRegEx`
Path containing datafiles: this can be used to read multiple datafiles, if the data is split between those. This is useful when downloading the entire datafile isn't possible because of server restrictions, for example when the processing time for the script in LimeSurvey that generates the datafiles is limited. In that case, the data can be downloaded in portions, and specifying a path here enables reading all datafiles in one go. Use the regular expression to indicate which files in the path should be read.

`scriptfile` The path and filename of the file containing the R script to import the data.

`limeSurveyRegEx.varNames`
The regular expression used to extract the variable names from the script file. The first regex expression (i.e. the first expression between parentheses) will be extracted as variable name.

`limeSurveyRegEx.toChar`
The regular expression to detect the lines in the import script where variables are converted to the character type.

`limeSurveyRegEx.varLabels`
The regular expression used to detect the lines in the import script where variable labels are set.

`limeSurveyRegEx.toFactor`
The regular expression used to detect the lines in the import script where vectors are converted to factors.

`limeSurveyRegEx.varNameSanitizing`
A list of regular expression patterns and their replacements to sanitize the variable names (e.g. replace hashes/pound signs ('#') by something that is not considered the comment symbol by R).

`setVarNames, setLabels, convertToCharacter, convertToFactor`
Whether to set variable names or labels, or convert to character or factor, using the code isolated using the specified regular expression.

`categoricalQuestions`
Which variables (specified using LimeSurvey variable names) are considered categorical questions; for these, the script to convert the variables to factors, as extracted from the LimeSurvey import file, is applied.

`massConvertToNumeric`
Whether to convert all variables to numeric using `massConvertToNumeric`.

`dataHasVarNames`
: Whether the variable names are included as header (first line) in the comma separated values file (data file).

`encoding, dataEncoding, scriptEncoding`
: The encoding of the files; `encoding` overrides `dataEncoding` and `scriptEncoding`, and so can be used to specify the same encoding for both.

Details

This function was intended to make importing data from LimeSurvey a bit easier. The default settings used by LimeSurvey are not always convenient, and this function provides a bit more control.

Value

The dataframe.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

`getData`

Examples

```
## Not run:
### Of course, you need valid LimeSurvey files. This is an example of
### what you'd do if you have them, assuming you specified that path
### containing the data in 'dataPath', the name of the datafile in
### 'dataFileName', the name of the script file in 'dataLoadScriptName',
### and that you only want variables 'informedConsent', 'gender', 'hasJob',
### 'currentEducation', 'prevEducation', and 'country' to be converted to
### factors.
dat <- importLimeSurveyData(datafile = file.path(dataPath, dataFileName),
                            scriptfile = file.path(dataPath, dataLoadScriptName),
                            categoricalQuestions = c('informedConsent',
                                                     'gender',
                                                     'hasJob',
                                                     'currentEducation',
                                                     'prevEducation',
                                                     'country'));

## End(Not run)
```

`invertItems` *invertItems*

Description

Inverts items (as in, in a questionnaire), by calling `invertItem` on all relevant items.

Usage

```
invertItems(dat, items = NULL, ...)
```

Arguments

`dat`	The dataframe containing the variables to invert.
`items`	The names or indices of the variables to invert. If not supplied (i.e. NULL), all variables in the dataframe will be inverted.
`...`	Arguments (parameters) passed on to data.frame when recreating that after having used lapply.

Value

The dataframe with the specified items inverted.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

`invertItem`

Examples

```
invertItems(mtcars, c('cyl'));
```

iqrOutlier *Identify outliers according to the IQR criterion*

Description

The IQR criterion holds that any value lower than one-and-a-half times the interquartile range below the first quartile, or higher than one-and-a-half times the interquartile range above the third quartile, is an outlier. This function returns a logical vector that identifies those outliers.

Usage

```
iqrOutlier(x)
```

Arguments

x	The vector to scan for outliers.

Value

A logical vector where TRUE identifies outliers.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

IQR

Examples

```
### One outlier in the miles per gallon
iqrOutlier(mtcars$mpg);
```

is.nr *is.nr*

Description

Convenience function that returns TRUE if the argument is not null, not NA, and is.numeric.

Usage

```
is.nr(x)
```

Arguments

x	The value or vector to check.

Value

TRUE or FALSE.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
is.nr(8);    ### Returns TRUE
is.nr(NULL); ### Returns FALSE
is.nr(NA);   ### Returns FALSE
```

---

isTrue *isTrue*

Description

Returns TRUE for TRUE elements, FALSE for FALSE elements, and whatever is specified in na for NA items.

Usage

```
isTrue(x, na = FALSE)
```

Arguments

x	The vector to check for TRUE, FALSE, and NA values.
na	What to return for NA values.

Value

A logical vector.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
isTrue(c(TRUE, FALSE, NA));
isTrue(c(TRUE, FALSE, NA), na=TRUE);
```

itemInspection *itemInspection*

Description

Function to generate a PDF with four panels per page, showing some basic item characteristics.

Usage

```
itemInspection(dat, items,
               docTitle = "Scale inspection", docAuthor = "Author",
               pdfLaTexPath, rnwPath, filename="itemInspection",
               convertFactors = TRUE, digits=4)
```

Arguments

dat	Dataframe containing the items of the relevant scale
items	Either a character vector with the itemnames, or, if the items are organised in scales, a list of character vectors with the items in each scale.
docTitle	Title to use when generating the PDF.
docAuthor	Author(s) to include when generating the PDF.
pdfLaTexPath	The path to PdfLaTex. This file is part of a LaTeX installation that creates a pdf out of a .tex file. In Windows, you can download (portable) MikTex from http://miktex.org/portable. You then decide yourself where to install MikTex; pdflatex will end up in a subfolder 'miktex\bin', so if you installed MikTex in, for example, 'C:\Program Files\MikTex', the total path becomes 'C:\Program Files\MikTex\miktex\bin'. Note that R uses slashes instead of backslashes to separate folders, so in this example, pdfLaTexPath should be 'C:/Program Files/MikTex/miktex/bin' In MacOS, you can install MacTex from http://tug.org/mactex/ By default, pdflatex ends up in folder '/user/texbin', which is what pdfLaTexPath should be in that default case. In Ubuntu, you can install TexLive base by using your package manager to install texlive-latex-base, or using the terminal: 'sudo apt-get install texlive-latex-base' In ubuntu, by default pdflatex ends un in folder '/usr/bin', which is what pdfLaTexPath should be in that default case.
rnwPath	The path where the temporary files and the resulting PDF should be stored.
filename	The filename to use to save the pdf.
convertFactors	Whether to convert factors to numeric vectors for the analysis.
digits	The number of digits to use in the tables.

Value

This function returns nothing; it just generates a PDF.

Examples

```
## Not run:
itemInspection(mtcars, items=c('disp', 'hp', 'drat'), pdfLaTexPath="valid/path/here");

## End(Not run)
```

`meanDiff` *meanDiff*

Description

The meanDiff function compares the means between two groups. It computes Cohen's d, the unbiased estimate of Cohen's d (Hedges' g), and performs a t-test. It also shows the achieved power, and, more usefully, the power to detect small, medium, and large effects.

Usage

```
meanDiff(x, y=NULL, paired = FALSE, r.prepost = NULL, var.equal = "test",
         conf.level = .95, plot = FALSE, digits = 2, envir = parent.frame())
```

Arguments

`x`	Dichotomous factor: variable 1; can also be a formula of the form y ~ x, where x must be a factor with two levels (i.e. dichotomous).
`y`	Numeric vector: variable 2; can be empty if x is a formula.
`paired`	Boolean; are x & y independent or dependent? Note that if x & y are dependent, they need to have the same length.
`r.prepost`	Correlation between the pre- and post-test in the case of a paired samples t-test. This is required to compute Cohen's d using the formula on page 29 of Borenstein et al. (2009). If NULL, the correlation is simply computed from the provided scores (but of course it will then be lower if these is an effect - this will lead to an underestimate of the within-groups variance, and therefore, of the standard error of Cohen's d, and therefore, to confidence intervals that are too narrow (too liberal). Also, of course, when using this data to compute the within-groups correlation, random variations will also impact that correlation, which means that confidence intervals may in practice deviate from the null hypothesis significance testing p-value in either direction (i.e. the p-value may indicate a significant association while the confidence interval contains 0, or the other way around). Therefore, if the test-retest correlation of the relevant measure is known, please provide this here to enable computation of accurate confidence intervals.
`var.equal`	String; only relevant if x & y are independent; can be "test" (default; test whether x & y have different variances), "no" (assume x & y have different variances; see the Warning below!), or "yes" (assume x & y have the same variance)

conf.level	Confidence of confidence intervals you want.
plot	Whether to print a dlvPlot.
digits	With what precision you want the results to print.
envir	The environment where to search for the variables (useful when calling meanDiff from a function where the vectors are defined in that functions environment).

Details

This function uses the formulae from Borenstein, Hedges, Higgins & Rothstein (2009) (pages 25-32).

Value

An object is returned with the following elements:

variables	Input variables
groups	Levels of the x variable, the dichotomous factor
ci.confidence	Confidence of confidence intervals
digits	Number of digits for output
x	Values of dependent variable in first group
y	Values of dependent variable in second group
type	Type of t-test (independent or dependent, equal variances or not)
n	Sample sizes of the two groups
mean	Means of the two groups
sd	Standard deviations of the two groups
objects	Objects used; the t-test and optionally the test for equal variances
variance	Variance of the difference score
meanDiff	Difference between the means
meanDiff.d	Cohen's d
meanDiff.d.var	Variance of Cohen's d
meanDiff.d.se	Standard error of Cohen's d
meanDiff.J	Correction for Cohen's d to get to the unbiased Hedges g
power	Achieved power with current effect size and sample size
power.small	Power to detect small effects with current sample size
power.medium	Power to detect medium effects with current sample size
power.largel	Power to detect large effects with current sample size
meanDiff.g	Hedges' g
meanDiff.g.var	Variance of Hedges' g
meanDiff.g.se	Standard error of Hedges' g
ci.usedZ	Z value used to compute confidence intervals

`meanDiff.d.ci.lower`
: Lower bound of confidence interval around Cohen's d

`meanDiff.d.ci.upper`
: Upper bound of confidence interval around Cohen's d

`meanDiff.g.ci.lower`
: Lower bound of confidence interval around Hedges' g

`meanDiff.g.ci.upper`
: Upper bound of confidence interval around Hedges' g

`meanDiff.ci.lower`
: Lower bound of confidence interval around raw mean

`meanDiff.ci.upper`
: Upper bound of confidence interval around raw mean

`t`
: Student t value for Null Hypothesis Significance Testing

`df`
: Degrees of freedom for t value

`p`
: p-value corresponding to t value

Warning

Note that when different variances are assumed for the t-test (i.e. the null-hypothesis test), the values of Cohen's d are still based on the assumption that the variance is equal. In this case, the confidence interval might, for example, not contain zero even though the NHST has a non-significant p-value (the reverse can probably happen, too).

References

Borenstein, M., Hedges, L. V., Higgins, J. P., & Rothstein, H. R. (2011). Introduction to meta-analysis. John Wiley & Sons.

Examples

```
### Create simple dataset
dat <- PlantGrowth[1:20,];
### Remove third level from group factor
dat$group <- factor(dat$group);
### Compute mean difference and show it
meanDiff(dat$weight ~ dat$group);

### Look at second treatment
dat <- rbind(PlantGrowth[1:10,], PlantGrowth[21:30,]);
### Remove third level from group factor
dat$group <- factor(dat$group);
### Compute mean difference and show it
meanDiff(x=dat$group, y=dat$weight);
```

meanDiff.multi *meanDiff.multi*

Description

The meanDiff.multi function compares many means for many groups. It presents the results in a dataframe summarizing all relevant information, and produces plot showing the confidence intervals for the effect sizes for each predictor (i.e. dichotomous variable). Like meanDiff, it computes Cohen's d, the unbiased estimate of Cohen's d (Hedges' g), and performs a t-test. It also shows the achieved power, and, more usefully, the power to detect small, medium, and large effects.

Usage

```
meanDiff.multi(dat, y, x=NULL, var.equal = "yes", conf.level = .95,
               digits = 2, orientation = "vertical",
               zeroLineColor = "grey", zeroLineSize = 1.2,
               envir = parent.frame())
```

Arguments

dat	The dataframe containing the variables involved in the mean tests.
y	Character vector containing the list of interval variables to include in the tests.
x	Character vector containing the list of the dichotomous variables to include in the tests. If x is empty, paired samples t-tests will be conducted.
var.equal	String; only relevant if x & y are independent; can be "test" (default; test whether x & y have different variances), "no" (assume x & y have different variances; see the Warning below!), or "yes" (assume x & y have the same variance)
conf.level	Confidence of confidence intervals you want.
digits	With what precision you want the results to print.
orientation	Whether to plot the effect size confidence intervals vertically (like a forest plot, the default) or horizontally.
zeroLineColor	Color of the horizontal line at an effect size of 0 (set to 'white' to not display the line; also adjust the size to 0 then).
zeroLineSize	Size of the horizontal line at an effect size of 0 (set to 0 to not display the line; also adjust the color to 'white' then).
envir	The environment where to search for the variables (useful when calling meanDiff from a function where the vectors are defined in that functions environment).

Details

This function uses the meanDiff function, which uses the formulae from Borenstein, Hedges, Higgins & Rothstein (2009) (pages 25-32).

Value

An object is returned with the following elements:

`results.raw`	Objects returned by the calls to meanDiff.
`plots`	For every comparison, a plot with the datapoints, means, and confidence intervals in the two groups.
`results.compiled`	Dataframe with the most important results from each comparison.
`plots.compiled`	For every dichotomous (x) variable, a plot with the confidence interval for the effect size of each dependent (y) variable.
`input`	The arguments with which the function was called.

Warning

Note that when different variances are assumed for the t-test (i.e. the null-hypothesis test), the values of Cohen's d are still based on the assumption that the variance is equal. In this case, the confidence interval might, for example, not contain zero even though the NHST has a non-significant p-value (the reverse can probably happen, too).

References

Borenstein, M., Hedges, L. V., Higgins, J. P., & Rothstein, H. R. (2011). Introduction to meta-analysis. John Wiley & Sons.

Examples

```
### Create simple dataset
dat <- data.frame(x1 = factor(rep(c(0,1), 20)),
                  x2 = factor(c(rep(0, 20), rep(1, 20))),
                  y=rep(c(4,5), 20) + rnorm(40));
### Compute mean difference and show it
meanDiff.multi(dat, x=c('x1', 'x2'), y='y', var.equal="yes");
```

`meansComparisonDiamondPlot` *meansComparisonDiamondPlot and duoComparisonDiamondPlot*

Description

These are two diamond plot functions to conveniently make diamond plots to compare subgroups or different samples. They are both based on a univariate diamond plot where colors are used to distinguish the data points and diamonds of each subgroup or sample. The means comparison diamond plot produces only this plot, while the duo comparison diamond plot combines it with a diamond plot visualising the effect sizes of the associations. The latter currently only works for two subgroups or samples, while the simple meansComparisonDiamondPlot also works when comparing more than two sets of datapoints. These functions are explained more in detail in Peters (2017).

Usage

```
meansComparisonDiamondPlot(dat, items = NULL,
                           compareBy = NULL,
                           labels = NULL,
                           compareByLabels = NULL,
                           decreasing = NULL,
                           sortBy = NULL,
                           conf.level = 0.95,
                           showData = TRUE,
                           dataAlpha = 0.1, dataSize = 3,
                           comparisonColors = brewer.pal(8, "Set1"),
                           alpha = 0.33,
                           jitterWidth = 0.5, jitterHeight = 0.4,
                           xlab = "Scores and means",
                           ylab = NULL,
                           theme = theme_bw(),
                           showLegend = TRUE,
                           lineSize = 1,
                           xbreaks = "auto",
                           outputFile = NULL,
                           outputWidth = 10,
                           outputHeight = 10,
                           ggsaveParams = list(units='cm',
                                               dpi=300,
                                               type="cairo"),
                           ...)

duoComparisonDiamondPlot(dat, items = NULL,
                         compareBy = NULL,
                         labels = NULL,
                         compareByLabels = NULL,
                         decreasing = NULL,
                         conf.level = c(0.95, 0.95),
                         showData = TRUE,
                         dataAlpha = 0.1,
                         dataSize = 3,
                         comparisonColors = brewer.pal(8, "Set1"),
                         associationsColor = "grey",
                         alpha = 0.33,
                         jitterWidth = 0.5, jitterHeight = 0.4,
                         xlab = c("Scores and means", "Effect size estimates"),
                         ylab = c(NULL, NULL),
                         theme = theme_bw(),
                         showLegend = TRUE,
                         lineSize = 1,
                         drawPlot = TRUE,
                         xbreaks = "auto",
                         outputFile = NULL,
```

```
                        outputWidth = 10,
                        outputHeight = 10,
                        ggsaveParams = list(units='cm',
                                            dpi=300,
                                            type="cairo"),
                        ...)
```

Arguments

dat	The dataframe containing the relevant variables.
items	The variables to plot (on the y axis).
compareBy	The variable by which to compare (i.e. the variable indicating to which subgroup or sample a row in the dataframe belongs).
labels	The labels to use on the y axis; these values will replace the variable names in the dataframe (specified in items).
compareByLabels	The labels to use to replace the value labels of the compareBy variable.
decreasing	Whether to sort the variables by their mean values (NULL to not sort, TRUE to sort in descending order (i.e. items with lower means are plotted more to the bottom), and FALSE to sort in ascending order (i.e. items with lower means are plotted more to the top).
sortBy	If the variables should be sorted (see decreasing), this variable specified which subgroup should be sorted by. Therefore, the value specified here must be a value label ('level label') of the comparisonBy variable.
conf.level	The confidence level of the confidence intervals specified by the diamonds for the means (for meansComparisonDiamondPlot) and for both the means and effect sizes (for duoComparisonDiamondPlot).
showData	Whether to plot the data points.
dataAlpha	The transparency (alpha channel) value for the data points: a value between 0 and 1, where 0 denotes complete transparency and 1 denotes complete opacity.
dataSize	The size of the data points.
comparisonColors	The colors to use for the different subgroups or samples. This should be a vector of valid colors with at least as many elements as sets of data points that should be plotted.
associationsColor	For duoComparisonDiamondPlot, the color to use to plot the effect sizes in the right-hand plot.
alpha	The alpha channel (transparency) value for the diamonds: a value between 0 and 1, where 0 denotes complete transparency and 1 denotes complete opacity.
jitterWidth, jitterHeight	How much noise to add to the data points (to prevent overplotting) in the horizontal (x axis) and vertical (y axis) directions.
xlab, ylab	The label to use for the x and y axes (for duoComparisonDiamondPlot, must be vectors of two elements). Use NULL to not use a label.

theme	The theme to use for the plots.
showLegend	Whether to show the legend (which color represents which subgroup/sample).
lineSize	The thickness of the lines (the diamonds' strokes).
drawPlot	Whether to draw the plot, or only (invisibly) return it.
xbreaks	Where the breaks (major grid lines, ticks, and labels) on the x axis should be.
outputFile	A file to which to save the plot.
outputWidth, outputHeight	Width and height of saved plot (specified in centimeters by default, see ggsaveParams).
ggsaveParams	Parameters to pass to ggsave when saving the plot.
...	Any additional arguments are passed to diamondPlot by meansComparisonDiamondPlot and to both meansComparisonDiamondPlot and associationsDiamondPlot by duoComparisonDiamondPlot.

Details

These functions are explained in Peters (2017).

Value

Diamond plots: a ggplot by meansComparisonDiamondPlot, and a gtable by duoComparisonDiamondPlot.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Peters, G.-J. Y. (2017). Diamond Plots: a tutorial to introduce a visualisation tool that facilitates interpretation and comparison of multiple sample estimates while respecting their inaccuracy. *PsyArXiv*. http://doi.org/10.17605/OSF.IO/9W8YV

See Also

diamondPlot, meansDiamondPlot, CIBER

Examples

```
meansComparisonDiamondPlot(mtcars,
                           items=c('disp', 'hp'),
                           compareBy='vs',
                           xbreaks=c(100,200, 300, 400));
meansComparisonDiamondPlot(chickwts,
                           items='weight',
                           compareBy='feed',
                           xbreaks=c(100,200,300,400),
                           showData=FALSE);
duoComparisonDiamondPlot(mtcars,
```

```
                        items=c('disp', 'hp'),
                        compareBy='vs',
                        xbreaks=c(100,200, 300, 400));
```

`meansDiamondPlot` *Diamond plots*

Description

This function generates a so-called diamond plot: a plot based on the forest plots that are commonplace in meta-analyses. The underlying idea is that point estimates are uninformative, and it would be better to focus on confidence intervals. The problem of the points with errorbars that are commonly employed is that the focus the audience's attention on the upper and lower bounds, even though those are the least relevant values. Using diamonds remedies this.

Usage

```
meansDiamondPlot(dat, items = NULL,
                 labels = NULL,
                 decreasing = NULL,
                 conf.level = 0.95,
                 showData = TRUE,
                 dataAlpha = .1,
                 dataSize = 3,
                 dataColor = "#444444",
                 diamondColors = NULL,
                 jitterWidth = 0.5,
                 jitterHeight = 0.4,
                 returnLayerOnly = FALSE,
                 xlab = "Scores and means",
                 ylab = NULL,
                 theme = theme_bw(),
                 xbreaks="auto",
                 outputFile = NULL,
                 outputWidth = 10,
                 outputHeight = 10,
                 ggsaveParams = list(units='cm',
                                     dpi=300,
                                     type="cairo"),
                 ...)
```

Arguments

`dat`	The dataframe containing the variables (`items`) to show in the diamond plot.
`items`	Optionally, the names (or numeric indices) of the variables (items) to show in the diamond plot. If NULL, all columns (variables, items) will be used.
`labels`	A character vector of labels to use instead of column names from the dataframe.

decreasing	Whether to sort the variables (rows) in the diamond plot decreasing (TRUE), increasing (FALSE), or not at all (NULL).
conf.level	The confidence of the confidence intervals.
showData	Whether to show the raw data or not.
dataAlpha	This determines the alpha (transparency) of the data points. Note that argument alpha can be used to set the alpha of the diamonds; this is eventually passed on to ggDiamondLayer.
dataSize	The size of the data points.
dataColor	The color of the data points.
diamondColors	A vector of the same length as there are rows in the dataframe, to manually specify colors for the diamonds.
jitterWidth	How much to jitter the individual datapoints horizontally.
jitterHeight	How much to jitter the individual datapoints vertically.
returnLayerOnly	Set this to TRUE to only return the ggplot layer of the diamondplot, which can be useful to include it in other plots.
xlab, ylab	The labels of the X and Y axes.
theme	The theme to use.
xbreaks	Where the breaks (major grid lines, ticks, and labels) on the x axis should be.
outputFile	A file to which to save the plot.
outputWidth, outputHeight	Width and height of saved plot (specified in centimeters by default, see ggsaveParams).
ggsaveParams	Parameters to pass to ggsave when saving the plot.
...	Additional arguments are passed to diamondPlot and eventually to ggDiamondLayer. This can be used to, for example, specify two or more colors to use to generate a gradient (using generateColors and maybe fullColorRange).

Value

A ggplot plot with a ggDiamondLayer is returned.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

diamondPlot, meanSDtoDiamondPlot, factorLoadingDiamondCIplot, ggDiamondLayer

Examples

```
tmpDf <- data.frame(item1 = rnorm(50, 1.6, 1),
                    item2 = rnorm(50, 2.6, 2),
                    item3 = rnorm(50, 4.1, 3));

### A simple diamond plot
meansDiamondPlot(tmpDf);

### A diamond plot with manually
### specified labels and colors
meansDiamondPlot(tmpDf,
                 labels=c('First',
                          'Second',
                          'Third'),
                  diamondColors=c('blue', 'magenta', 'yellow'));

### Using a gradient for the colors
meansDiamondPlot(tmpDf,
                 labels=c('First',
                          'Second',
                          'Third'),
                 generateColors = c("magenta", "cyan"),
                 fullColorRange = c(1,5));
```

---

meanSDtoDiamondPlot *A diamond plot based on means, standard deviations, and sample sizes*

Description

This function generates a so-called diamond plot: a plot based on the forest plots that are commonplace in meta-analyses. The underlying idea is that point estimates are uninformative, and it would be better to focus on confidence intervals. The problem of the points with errorbars that are commonly employed is that the focus the audience's attention on the upper and lower bounds, even though those are the least relevant values. Using diamonds remedies this.

Usage

```
meanSDtoDiamondPlot(dat = NULL, means = 1,
                    sds = 2, ns = 3,
                    labels = NULL,
                    colorCol = NULL,
                    conf.level = 0.95,
                    xlab='Means',
                    outputFile = NULL,
                    outputWidth = 10,
                    outputHeight = 10,
                    ggsaveParams = list(units='cm',
                                        dpi=300,
```

```
                                        type="cairo"),
    ...)
```

Arguments

dat	The dataset containing the means, standard deviations, sample sizes, and possible labels and manually specified colors.
means	Either the column in the dataframe containing the means, as numeric or as character index, or a vector of means.
sds	Either the column in the dataframe containing the standard deviations, as numeric or as character index, or a vector of standard deviations.
ns	Either the column in the dataframe containing the sample sizes, as numeric or as character index, or a vector of sample sizes.
labels	Optionally, either the column in the dataframe containing labels, as numeric or as character index, or a vector of labels.
colorCol	Optionally, either the column in the dataframe containing manually specified colours, as numeric or as character index, or a vector of manually specified colours.
conf.level	The confidence of the confidence intervals.
xlab	The label for the x axis.
outputFile	A file to which to save the plot.
outputWidth, outputHeight	Width and height of saved plot (specified in centimeters by default, see ggsaveParams).
ggsaveParams	Parameters to pass to ggsave when saving the plot.
...	Additional arguments are passed to diamondPlot and eventually to ggDiamondLayer. This can be used to, for example, specify two or more colors to use to generate a gradient (using generateColors and maybe fullColorRange).

Value

A ggplot plot with a ggDiamondLayer is returned.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

meansDiamondPlot, diamondPlot, factorLoadingDiamondCIplot, ggDiamondLayer

Examples

```
tmpDf <- data.frame(means = c(1, 2, 3),
                    sds = c(1.5, 3, 5),
                    ns = c(2, 4, 10),
                    labels = c('first', 'second', 'third'),
                    color = c('purple', 'grey', 'orange'));

### A simple diamond plot
meanSDtoDiamondPlot(tmpDf);

### A simple diamond plot with labels
meanSDtoDiamondPlot(tmpDf, labels=4);

### When specifying column names, specify column
### names for all columns
meanSDtoDiamondPlot(tmpDf, means='means',
                    sds='sds', ns='ns',
                    labels='labels');

### A diamond plot using the specified colours
meanSDtoDiamondPlot(tmpDf, labels=4, colorCol=5);

### A diamond plot using automatically generated colours
### using a gradient
meanSDtoDiamondPlot(tmpDf,
                    generateColors=c('green', 'red'));

### A diamond plot using automatically generated colours
### using a gradient, specifying the minimum and maximum
### possible values that can be attained
meanSDtoDiamondPlot(tmpDf,
                    generateColors=c('red', 'yellow', 'blue'),
                    fullColorRange=c(0, 5));
```

---

nnc *Numbers Needed for Change*

Description

This function computes the Numbers Needed for Change, and shows a visualisation to illustrate them.

Usage

```
nnc(d = NULL, cer = NULL, r = 1,
    threshold = NULL, mean = 0, sd = 1,
    eventDesirable = TRUE, eventIfHigher = TRUE,
    d.ci = NULL, cer.ci = NULL, r.ci = NULL,
    d.n = NULL, cer.n = NULL, r.n = NULL,
    plot = TRUE, returnPlot = TRUE, silent = FALSE)
```

Arguments

d	The value of Cohen's *d*.
cer	The Control Event Rate.
r	The correlation between the determinant and behavior (for mediated Numbers Needed for Change).
threshold	If the event rate is not available, a threshold value can be specified instead, which is then used in conjunction with the mean (mean) and standard deviation (sd) and assuming a normal distribution to compute the event rate.
mean	The mean value, used to draw the plot, or, if no CER is provided but instead the threshold value, to compute the CER.
sd	The standard deviation, used to draw the plot (and to compute the CER if a threshold value is supplied instead of the CER).
eventDesirable	Whether an event is desirable or undesirable.
eventIfHigher	Whether scores above or below the threshold are considered 'an event'.
d.ci	Instead of providing a point estimate for Cohen's *d*, a confidence interval can be provided.
cer.ci	Instead of providing a point estimate for the Control Event Rate, a confidence interval can be provided.
r.ci	Instead of providing a point estimate for the correlation, a confidence interval can be provided.
d.n	In addition to providing a point estimate for Cohen's *d*, a sample size can be provided; if it is, the confidence interval is computed.
cer.n	In addition to providing a point estimate for the Control Event Rate, a sample size can be provided; if it is, the confidence interval is computed.
r.n	In addition to providing a point estimate for the correlation, a sample size can be provided; if it is, the confidence interval is computed.
plot	Whether to generate and show the plot.
returnPlot	Whether to return the plot (as an attribute), or to only display it.
silent	Whether to suppress notifications.

Details

This function computes the Numbers Needed for Change. See Gruijters & Peters (2017) for details.

Value

The Numbers Needed for Change (NNC), potentially with a plot visualising the NNC in an attribute.

Author(s)

Gjalt-Jorn Peters & Stefan Gruijters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Gruijters, S. L. K., & Peters, G.-J. Y. (2017). Introducing the Numbers Needed for Change (NNC): A practical measure of effect size for intervention research.

Examples

```
### Simple example
nnc(d=.4, cer=.3);

### Or for a scenario where events are undesirable, and the
### intervention effective (therefore having a negative value for d):
nnc(d=-.4, cer=.3, eventDesirable=FALSE);
```

---

normalityAssessment *normalityAssessment and samplingDistribution*

Description

normalityAssessment can be used to assess whether a variable and the sampling distribution of its mean have an approximately normal distribution.

samplingDistribution is a convenient wrapper for normalityAssessment that makes it easy to quickly generate a sample and sampling distribution from frequencies (or proportions).

dataShape computes the skewness and kurtosis.

Usage

```
normalityAssessment(sampleVector, samples = 10000, digits=2,
                    samplingDistColor = "#2222CC",
                    normalColor = "#00CC00",
                    samplingDistLineSize = 2,
                    normalLineSize = 1,
                    xLabel.sampleDist = NULL,
                    yLabel.sampleDist = NULL,
                    xLabel.samplingDist = NULL,
                    yLabel.samplingDist = NULL,
                    sampleSizeOverride = TRUE)
samplingDistribution(popValues = c(0, 1),
                     popFrequencies = c(50, 50),
                     sampleSize = NULL,
                     sampleFromPop = FALSE, ...)
dataShape(sampleVector, na.rm = TRUE, type = 2,
          digits = 2, conf.level = 0.95,
          plots = TRUE, xLabs = NA,
          yLabs = NA, qqCI = TRUE,
          labelOutliers = TRUE,
          sampleSizeOverride = NULL)
```

Arguments

sampleVector	Numeric vector containing the sample data.
samples	Number of samples to use when constructing sampling distribution.
digits	Number of digits to use when printing results.
samplingDistColor	Color to use when drawing the sampling distribution.
normalColor	Color to use when drawing the standard normal curve.
samplingDistLineSize	Size of the line used to draw the sampling distribution.
normalLineSize	Size of the line used to draw the standard normal distribution.
xLabel.sampleDist	Label of x axis of the distribution of the sample.
yLabel.sampleDist	Label of y axis of the distribution of the sample.
xLabel.samplingDist	Label of x axis of the sampling distribution.
yLabel.samplingDist	Label of y axis of the sampling distribution.
xLabs, yLabs	The axis labels for the three plots (should be vectors of three elements; the first specifies the X or Y axis label for the rightmost plot (the histogram), the second for the middle plot (the QQ plot), and the third for the rightmost plot (the box plot).
popValues	The possible values (levels) of the relevant variable. For example, for a dichotomous variable, this can be "c(1:2)" (or "c(1, 2)"). Note that samplingDistribution is for manually specifying the frequency distribution (or proportions); if you have a vector with 'raw' data, just call normalityAssessment directly.
popFrequencies	The frequencies corresponding to each value in popValues; must be in the same order! See the examples.
sampleSize	Size of the sample; the sum of the frequencies if not specified.
na.rm	Whether to remove missing data first.
type	Type of skewness and kurtosis to compute; either 1 (g1 and g2), 2 (G1 and G2), or 3 (b1 and b2). See Joanes & Gill (1998) for more information.
conf.level	Confidence of confidence intervals.
plots	Whether to display plots.
qqCI	Whether to show the confidence interval for the QQ plot.
labelOutliers	Whether to label outliers with their row number in the box plot.
sampleFromPop	If true, the sample vector is created by sampling from the population information specified; if false, rep() is used to generate the sample vector. Note that is proportions are supplied in popFrequencies, sampling from the population is necessary!

`sampleSizeOverride`
: Whether to use the sample size of the sample as sample size for the sampling distribution, instead of the sampling distribution size. This makes sense, because otherwise, the sample size and thus sensitivity of the null hypothesis significance tests is a function of the number of samples used to generate the sampling distribution.

`...`
: Anything else is passed on my sampingDistribution to normalityAssessment.

Details

normalityAssessment provides a number of normality tests and draws histograms of the sample data and the sampling distribution of the mean (most statistical tests assume the latter is normal, rather than the first; normality of the sample data guarantees normality of the sampling distribution of the mean, but if the sample size is sufficiently large, the sampling distribution of the mean is approximately normal even when the sample data are not normally distributed). Note that for the sampling distribution, the degrees of freedom are usually so huge that the normality tests, negligible deviations from normality will already result in very small p-values.

samplingDistribution makes it easy to quickly assess the distribution of a variables based on frequencies or proportions, and dataShape computes skewness and kurtosis.

Value

An object with several results, the most notably of which are:

`plot.sampleDist`
: Histogram of sample distribution

`sw.sampleDist`
: Shapiro-Wilk normality test of sample distribution

`ad.sampleDist`
: Anderson-Darling normality test of sample distribution

`ks.sampleDist`
: Kolmogorov-Smirnof normality test of sample distribution

`kurtosis.sampleDist`
: Kurtosis for sample distribution

`skewness.sampleDist`
: Skewness for sample distribution

`plot.samplingDist`
: Histogram of sampling distribution

`sw.samplingDist`
: Shapiro-Wilk normality test of sampling distribution

`ad.samplingDist`
: Anderson-Darling normality test of sampling distribution

`ks.samplingDist`
: Kolmogorov-Smirnof normality test of sampling distribution

`dataShape.samplingDist`
: Skewness and kurtosis for sampling distribution

Examples

```
### Note: the 'not run' is simply because running takes a lot of time,
###       but these examples are all safe to run!
## Not run:

normalityAssessment(rnorm(35));

### Create a distribution of three possible values and
### show the sampling distribution for the mean
popValues <- c(1, 2, 3);
popFrequencies <- c(20, 50, 30);
sampleSize <- 100;
samplingDistribution(popValues = popValues,
                     popFrequencies = popFrequencies,
                     sampleSize = sampleSize);

### Create a very skewed distribution of ten possible values
popValues <- c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10);
popFrequencies <- c(2, 4, 8, 6, 10, 15, 12, 200, 350, 400);
samplingDistribution(popValues = popValues,
                     popFrequencies = popFrequencies,
                     sampleSize = sampleSize, digits=5);

## End(Not run)
```

`oddsratio` *oddsratio*

Description

The oddsratio function simply computes a point estimate and confidence interval for an odds ratio.

Usage

```
oddsratio(x, y = NULL, conf.level = .95, digits=2)
```

Arguments

`x`	x can be either a table (then y can be NULL) or a factor.
`y`	If x is a factor, y also has to be a factor; x and y are then used to create the crosstable.
`conf.level`	The confidence level of the confidence interval.
`digits`	Number of digits to round output to

Value

The oddsratio function returns an object with the input and output.

input	List with input arguments
or	Point estimate for odds ratio
or.ci	Confidence interval for odds ratio

Examples

```
### Generate two factor vectors
treatment <- factor(c(rep(0, 33), rep(1, 45), rep(0, 63), rep(1, 21)),
                    levels=c(0,1), labels=c("no", "yes"));
survival <- factor(c(rep(0, 78), rep(1, 84)),
                   levels=c(0, 1), labels=c("no", "yes"));

### Compute and display odds ratio
oddsratio(treatment, survival);

### Or present a table
oddsratio(table(treatment, survival));
```

---

omegaSqDist *The distribution of Omega Squared*

Description

These functions use some conversion to and from the *F* distribution to provide the Omega Squared distribution.

Usage

```
domegaSq(x, df1, df2, populationOmegaSq = 0)
pomegaSq(q, df1, df2, populationOmegaSq = 0, lower.tail = TRUE)
qomegaSq(p, df1, df2, populationOmegaSq = 0, lower.tail = TRUE)
romegaSq(n, df1, df2, populationOmegaSq = 0)
```

Arguments

x, q	Vector of quantiles, or, in other words, the value(s) of Omega Squared.
p	Vector of probabilites (*p*-values).
df1, df2	Degrees of freedom for the numerator and the denominator, respectively.
n	Desired number of Omega Squared values.
populationOmegaSq	The value of Omega Squared in the population; this determines the center of the Omega Squared distribution. This has not been implemented yet in this version of userfriendlyscience. If anybody has the inverse of convert.ncf.to.omegasq for me, I'll happily integrate this.

lower.tail — logical; if TRUE (default), probabilities are the likelihood of finding an Omega Squared smaller than the specified value; otherwise, the likelihood of finding an Omega Squared larger than the specified value.

Details

The functions use convert.omegasq.to.f and convert.f.to.omegasq to provide the Omega Squared distribution.

Value

domegaSq gives the density, pomegaSq gives the distribution function, qomegaSq gives the quantile function, and romegaSq generates random deviates.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

convert.omegasq.to.f, convert.f.to.omegasq, df, pf, qf, rf

Examples

```
### Generate 10 random Omega Squared values
romegaSq(10, 66, 3);

### Probability of findings an Omega Squared
### value smaller than .06 if it's 0 in the population
pomegaSq(.06, 66, 3);
```

---

oneway *oneway*

Description

The oneway function wraps a number of analysis of variance functions into one convenient interface that is similar to the oneway anova command in SPSS.

Usage

```
oneway(y, x, posthoc=NULL, means=FALSE,
       fullDescribe=FALSE, levene=FALSE,
       plot=FALSE, digits=2, omegasq = TRUE,
       etasq = TRUE, corrections = FALSE,
       pvalueDigits=3, t=FALSE, conf.level=.95,
       silent=FALSE)
```

Arguments

y	y has to be a numeric vector.
x	x has to be vector that either is a factor or can be converted into one.
posthoc	Which post-hoc tests to conduct. Valid values are any correction methods in p.adjust.methods (at the time of writing of this document, "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"), as well as "tukey" and "games-howell".
means	Whether to show the means for the y variable in each of the groups determined by the x variable.
fullDescribe	If TRUE, not only the means are shown, but all statistics acquired through the 'describe' function in the 'psych' package are shown.
levene	Whether to show Levene's test for equality of variances.
plot	Whether to show a plot of the means of the y variable in each of the groups determined by the x variable.
digits	The number of digits to show in the output.
omegasq	Whether to show the omega squared effect size.
etasq	Whether to show the eta squared effect size (this is biased and generally advised against; omega squared is less biased).
corrections	Whether to show the corrections for unequal variances (Welch and Brown-Forsythe).
pvalueDigits	The number of digits to show for p-values; smaller p-values will be shown as <.001 or <.0001 etc.
t	Whether to transpose the dataframes with the means (if requested) and the anova results. This can be useful for blind people.
conf.level	Confidence level to use when computing the confidence interval for eta^2. Note that the function we use doubles the 'unconfidence' level to maintain consistency with the NHST value (see http://yatani.jp/HCIstats/ANOVA#RCodeOneWay, http://daniellakens.blogspot.nl/2014/06/calculating-confidence-intervals-for.html or Steiger, J. H. (2004). Beyond the F test: Effect size confidence intervals and tests of close fit in the analysis of variance and contrast analysis. Psychological methods, 9(2), 164-82. doi:10.1037/1082-989X.9.2.164
silent	Whether to show warnings and other diagnostic information or remain silent.

Value

A list of three elements:

input	List with input arguments
intermediate	List of intermediate objects, such as the aov and Anova (from the car package) objects.
output	List with etasq, the effect size, and dat, a dataframe with the Oneway Anova results.

Note

By my knowledge the Brown-Forsythe correction was not yet available in R. I took this from the original paper (directed there by Field, 2014). Note that this is the corrected *F* value, not the Brown-Forsythe test for normality!

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Brown, M., & Forsythe, A. (1974). *The small sample behavior of some statistics which test the equality of several means.* Technometrics, 16(1), 129-132. https://doi.org/10.2307/1267501

Field, A. (2014) *Discovering statistics using SPSS* (4th ed.). London: Sage.

Steiger, J. H. (2004). *Beyond the F test: Effect size confidence intervals and tests of close fit in the analysis of variance and contrast analysis*. Psychological methods, 9(2), 164-82. doi:10.1037/1082-989X.9.2.164

Examples

```
### Do a oneway Anova
oneway(y=ChickWeight$weight, x=ChickWeight$Diet);

### Also order means and transpose the results
oneway(y=ChickWeight$weight, x=ChickWeight$Diet, means=TRUE, t=TRUE);
```

`paginatedAsymmetricalScatterMatrix`

paginatedAsymmetricalScatterMatrix

Description

A function that generates a series of asymmetricalScatterMatrices, so that they can be printed or included in PDFs.

Usage

```
paginatedAsymmetricalScatterMatrix(dat, cols, rows, maxRows = 5, ...)
```

Arguments

`dat`	The dataframe containing the variables specified in `cols` and `rows`.
`cols`	The names of the variables to use for the columns.
`rows`	The names of the variables to use for the rows.
`maxRows`	The maximum number of rows on one 'page' (i.e. in one `asymmetricalScatterMatrix`).
`...`	Extra arguments to pass on to each `asymmetricalScatterMatrix` call.

Value

An object containing the asymmetricalScatterMatrices in a list:

input	Input values.
intermediate	Some values/objects generated in the process.
output	A list containing the object 'scatterMatrices', which is a list of the generated scatterMatrices.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

asymmetricalScatterMatrix

Examples

```
## Not run:
### (Not run by default because it's quite timeconsuming.)
tmp <- paginatedAsymmetricalScatterMatrix(infert, cols=c("parity"),
                                          rows=c("induced", "case",
                                                 "spontaneous", "age",
                                                 "pooled.stratum"),
                                          maxRows = 3,
                                          showCorrelations="top-right");
tmp$output$scatterMatrices[[1]];

## End(Not run)
```

---

posthocTGH *posthocTGH*

Description

This function is used by the 'oneway' function for oneway analysis of variance in case a user requests post-hoc tests using the Tukey or Games-Howell methods.

Usage

```
posthocTGH(y, x, method=c("games-howell", "tukey"),
           conf.level = 0.95, digits=2, p.adjust="holm",
           formatPvalue = TRUE)
```

Arguments

y	y has to be a numeric vector.
x	x has to be vector that either is a factor or can be converted into one.
method	Which post-hoc tests to conduct. Valid values are "tukey" and "games-howell".
conf.level	Confidence level of the confidence intervals.
digits	The number of digits to show in the output.
p.adjust	Any valid p.adjust method.
formatPvalue	Whether to format the p values according to APA standards (i.e. replace all values lower than .001 with '<.001'). This only applies to the printing of the object, not to the way the p values are stored in the object.

Value

A list of three elements:

input	List with input arguments
intermediate	List of intermediate objects.
output	List with two objects 'tukey' and 'games.howell', containing the outcomes for the respective post-hoc tests.

Note

This function is based on a file that was once hosted at http://www.psych.yorku.ca/cribbie/6130/games_howell.R, but has been removed since. It was then adjusted for implementation in the userfriendlyscience package. Jeffrey Baggett needed the confidence intervals, and so emailed them, after which his updated functions was used. In the meantime, it appears Aaron Schlegel (https://rpubs.com/aaronsc32) independently developed a version with confidence intervals and posted it on RPubs at https://rpubs.com/aaronsc32/games-howell-test.

Author(s)

Gjalt-Jorn Peters (Open University of the Netherlands) & Jeff Bagget (University of Wisconsin - La Crosse)

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
### Compute post-hoc statistics using the tukey method
posthocTGH(y=ChickWeight$weight, x=ChickWeight$Diet, method="tukey");
### Compute post-hoc statistics using the games-howell method
posthocTGH(y=ChickWeight$weight, x=ChickWeight$Diet);
```

powerHist *powerHist*

Description

powerHist generates a histogram with a density curve and a normal density curve.

Usage

```
powerHist(vector, histColor = "#0000CC",
          distributionColor = "#0000CC",
          normalColor = "#00CC00", distributionLineSize = 1,
          normalLineSize = 1, histAlpha = 0.25, xLabel = NULL,
          yLabel = NULL, normalCurve = TRUE, distCurve = TRUE,
          breaks = 30, theme = dlvTheme(),
          rug = NULL, jitteredRug = TRUE, rugSides = "b",
          rugAlpha = .2, returnPlotOnly = FALSE)
```

Arguments

vector	A numeric vector.
histColor	The colour to use for the histogram.
distributionColor	The colour to use for the density curve.
normalColor	The colour to use for the normal curve.
distributionLineSize	The line size to use for the distribution density curve.
normalLineSize	The line size to use for the normal curve.
histAlpha	Alpha value ('opaqueness', as in, versus transparency) of the histogram.
xLabel	Label to use on x axis.
yLabel	Label to use on y axis.
normalCurve	Whether to display the normal curve.
distCurve	Whether to display the curve showing the distribution of the observed data.
breaks	The number of breaks to use (this is equal to the number of bins minus one, or in other words, to the number of bars minus one).
theme	The theme to use.
rug	Whether to add a rug (i.e. lines at the bottom that correspond to individual datapoints.
jitteredRug	Whether to jitter the rug (useful for variables with several datapoints sharing the same value.
rugSides	This is useful when the histogram will be rotated; for example, this can be set to 'r' if the histogram is rotated 270 degrees.

rugAlpha	Alpha value to use for the rug. When there is a lot of overlap, this can help get an idea of the number of datapoints at 'popular' values.
returnPlotOnly	Whether to return the usual powerHist object that also contains all settings and intermediate objects, or whether to only return the ggplot plot.

Value

An object, with the following elements:

input	The input when the function was called.
intermediate	The intermediate numbers and distributions.
dat	The dataframe used to generate the plot.
plot	The histogram.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
powerHist(mtcars$mpg)
```

---

prevalencePower *Power analysis for establishing a prevalence*

Description

This function can be used to establish how many participants are required to establish a prevalence rate with a given margin of error.

Usage

```
prevalencePower(expectedPrevalence,
                marginOfError = 0.05,
                conf.level = 0.95)
```

Arguments

expectedPrevalence	The expected prevalence.
marginOfError	The desired precision.
conf.level	The confidence of the confidence interval.

Details

Note that when uncertain as to the expected prevalence, it's better to assume a prevalence closer to 50%. Prevalences closer to 0% or 100% are easier to detect and therefore have more power.

Value

The required number of participants.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

convert.percentage.to.se

Examples

```
### Required participants for detecting a prevalence of 10%
### with a 95% confidence interval of 10% wide:
prevalencePower(.1);

### Required participants for detecting a prevalence of 10%
### with a 95% confidence interval of 4% wide:
prevalencePower(.1, .02);

### Required participants for detecting a prevalence of 60%
### with a 95% confidence interval of 10% wide:
prevalencePower(.6);
```

---

processLimeSurveyDropouts

processLimeSurveyDropouts

Description

This function makes it easy to parse the dropouts from a LimeSurvey questionnaire.

Usage

```
processLimeSurveyDropouts(lastpage,
                          pagenames = NULL,
                          relevantPagenames = NULL)
```

Arguments

`lastpage`	A vector with the 'lastpage' variable as LimeSurvey stores it (an integer denoting the last page a participant visited, in other words, where they dropped out).
`pagenames`	Optional: names for each page.
`relevantPagenames`	Optional: the names of those pages that should be included.

Details

This will be described more in detail in a forthcoming publications.

Value

A list with information about the dropout, including ggplots.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
processLimeSurveyDropouts(c(1,2,1,1,2,3,2,2,3,2,1));
```

---

processLSvarLabels *A function to conveniently process LimeSurvey labels*

Description

This function is meant to quickly parse the variable labels set by LimeSurvey. It works particularly well with dual anchor array questions, where the left and right anchors as well as the subquestions are extracted automatically.

Usage

```
processLSvarLabels(dat,
                   varnameRegExPairs = NULL,
                   labelExtractionRegExPair = c("\\[(.*)\\].*", "\\1"),
                   lengthToWrap = 50,
                   lengthToWrapAnchors = 20,
                 leftAnchorRegExPairs = list(c(".*[[:graph:]]([A-Z][a-z][^|]*)\\|(.+)",
                                               "\\1")),
                 rightAnchorRegExPairs = list(c(".*[[:graph:]]([A-Z][a-z][^|]*)\\|(.+)",
                                                "\\2")))
```

Arguments

dat	The dataframe as produced by importLimeSurveyData.
varnameRegExPairs	Pairs of regular expressions to replace in the variable names. This is useful when some pattern can be applied to the variable names to, for example, add underscores te denote different parts of the variable name. This has to be a list of character vectors that each have length 2.
labelExtractionRegExPair	The regular expression pair used to extract the labels.
lengthToWrap	At how many characters to wrap the subquestions.
lengthToWrapAnchors	At how many characters to wrap the anchors.
leftAnchorRegExPairs	The regular expression pairs to use to extract the left anchors.
rightAnchorRegExPairs	The regular expression pairs to use to extract the right anchors.

Details

This function processes LimeSurvey variable labels and applies regular expressions to automatically extract subquestions and left and right anchors.

Value

A dataframe that can conveniently be used with detStructAddVarLabels.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

(Forthcoming)

See Also

determinantStructure, determinantVar, subdeterminants, subdeterminantProducts, detStructAddVarLabels, detStructAddVarNames, detStructComputeProducts, detStructComputeScales, detStructCIBER

Examples

```
### No examples provided yet; this would require data to be included,
### and that's not available yet.
```

processOpenSesameIAT *processOpenSesameIAT*

Description

This function reads IAT files as generated by the OpenSesame script available at [INSERT URL].

Usage

```
processOpenSesameIAT(dataPath,
                     blocks.sizes = c(18, 36, 48, 36, 48),
                     blocks.congruent = c(2, 3),
                     blocks.incongruent = c(4, 5),
                     blocks.realTrials = c(3, 5),
                     blocks.practiceTrials = c(2, 4),
                     congruentLarger = TRUE,
                     responseTime.min = 400,
                     responseTime.max = 2500,
                     responseTime.penalty = 600,
                     outputFile = NULL,
                     wideOutputFile = NULL,
                     showLog = TRUE,
                     filenameRegEx = "subject-(\\d+)(\\w+)\\.csv",
                     regExValues = c("subject","session"),
                     participantVarName = "subject",
                     taskVarName = "session",
                     openSesameVarNames = list(correct = "correct",
                                               response_time = "response_time"),
                     stimulusSelectionVarName = NULL,
                     stimulusSelectionValues = NULL,
                     roundOutput = 6,
                     decimalSeparator = ".",
                     inputDecimalSeparator = ".",
                     inputfileSelectionColumns = NULL,
                     inputfileSelectionValues = NULL)
```

Arguments

dataPath	A directory containing the .csv files that OpenSesame provides.
blocks.sizes	A vector containing the number of trials of each block.
blocks.congruent	A vector containing the numbers of the congruent blocks.
blocks.incongruent	A vector containing the numbers of the incongruent blocks.
blocks.realTrials	A vector containing the numbers of the real trials.

`blocks.practiceTrials`
: A vector containing the numbers of the practice trials.

`congruentLarger`
: Whether the response latencies for the congruent trials (TRUE) or the incongruent trials (FALSE) are expected to be larger. This simply multiplies the final D600 measures with -1.

`responseTime.min`
: Minimum number of milliseconds of response time (all shorter times will be removed).

`responseTime.max`
: Maximum number of milliseconds of response time (all longer times will be replaced with this number).

`responseTime.penalty`
: Penalty in milliseconds to add to the response times for incorrect responses.

`outputFile`
: If specified, the aggregated datafile is stored in this file.

`wideOutputFile`
: If specified, the wide version of the datafile will be stored in this file.

`showLog`
: Boolean; if TRUE, shows the log (is stored in the resulting object anyway).

`filenameRegEx`
: Regular expression describing the filenames. This has two purposes. First, only files matching this regular expression will be processed (note that you can set it to `NULL` to process all files). Second, by using `"\1"`, `"\2"`, etc, matched patterns can be extracted from the filenames and stored as variables in the final datafile (see `sub` for more information on regular expression matching). The default pattern, `"subject-(\d+)(\w+)\.csv"`, which is read by R as `"subject-(\d+)(\w+)\.csv"` (because the backslash is the escape symbol, double backspaces are needed to specify one backspace, see `Quotes`), assumes that all filenames start with `'subject-'`, followed by the subject number (`"\d+"` matches one or more digits), immediately followed by one or more letters and digits (`"\w+"` matches one or more letters or digits) indicating the session that the datafile pertains to. If you only have subject numbers, you'd use `"subject-(\d+)\.csv"` or perhaps `"subject-(\w+)\.csv"` if the subjects could also have letters in their identifiers. Note that you have to include the variable names of each of these extractable patterns in `regExValues`!

`regExValues`
: Here, the names of the variables extracted using the regular expression specified in `filenameRegEx` are provided. Must of course have the same length as the number of patterns specified in `filenameRegEx`, and in the same order.

`participantVarName, taskVarName`
: Variable name of the variable identifying participants and tasks (usually extracted from the filename, so should be a value in regExValues). Tasks are usually different within-subject conditions.

`openSesameVarNames`
: A list with the two elements 'correct' and 'response_time', which should be the variable names that OpenSesame used to write, for each trial, whether the response was correct or not ('correct') and what the response time was ('response_time');

`stimulusSelectionVarName, stimulusSelectionValues`
: These arguments can be used to specify a subset of stimuli to process. Specify which column contains the values to select in `stimulusSelectionVarName`, and specify the value(s) to select in `stimulusSelectionValues`.

`roundOutput` Number of digits to round the output to. This is useful for importing into a program that doesn't quite get how storing numbers works, such as SPSS or Excel; they sometimes don't manage to import numbers with many decimals.

`decimalSeparator`
When working with e.g. Excel, it can be easier to just specify the decimal separator rather than switch Excel's (and therefore Windows') locale.

`inputDecimalSeparator`
The decimal separator to specify to `read.csv` when reading the data files.

`inputfileSelectionColumns, inputfileSelectionValues`
This functionality still has to be implemented. Once implemented, these arguments can be used to specify a column, and a (set of) value(s) in that column to use to select which rows to process (also see `stimulusSelectionVarName` and `stimulusSelectionValues`).

Details

Note that this function was developed to read the OpenSesame IAT datafiles created by the OpenSesame script developed by Kenny Wolfs, Jacques van Lankveld, and Frederik van Acker at the Open University of the Netherlands. If you use a different version (for example, the one contributed to the OpenSesame paradigm repository by Hansika Kapoor, see http://osdoc.cogsci.nl/3.0/standard-tasks/#implicit-association-test-iat), you will have to specify the variable names you specified to OpenSesame for the response time and for whether the response was correct in `openSesameVarNames`. For example, if you use Hansika's IAT task, you'll have to specify `openSesameVarNames = list(correct = "correct",response_time = "avg_rt")`

Similarly, of course you will probably have to specify the number of trials per block etc. Also, you may want to set showLog to FALSE, as the logging is quite detailed.

Value

An object with the raw files, the processed files, and the file converted to wide format. But most users will probably specify `outputFile` and/or `wideOutputFile` to just export the output files directly.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Mathot, S., Schreij, D., & Theeuwes, J. (2012). OpenSesame: An open-source, graphical experiment builder for the social sciences. *Behavior Research Methods*, 44(2), 314-324. doi:10.3758/s13428-011-0168-7

Kapoor, H. (2015). The creative side of the Dark Triad. *Creativity Research Journal*, 27(1), 58-67. doi:10.1080/10400419.2014.961775.

Examples

```
## Not run:
### This will process all files in the specified directory, but not
### export anything
processed <- processOpenSesameIAT("C:/directory/with/datafiles");

### This will export both the aggregated datafile and the wide datafile
processed <- processOpenSesameIAT("C:/directory/with/datafiles",
                                  outputFile="C:/directory/aggregated.csv",
                                  wideOutputFile="C:/directory/wide.csv");


## End(Not run)
```

---

pwr.confIntR *Determine required sample size for a given confidence interval width for Pearson's r*

Description

This function computes how many participants you need if you want to achieve a confidence interval of a given width. This is useful when you do a study and you are interested in how strongly two variables are associated.

Usage

```
pwr.confIntR(r, w = 0.1, conf.level = 0.95)
```

Arguments

r	The correlation you expect to find (confidence intervals for a given level of confidence get narrower as the correlation coefficient increases).
w	The required half-width (or margin of error) of the confidence interval.
conf.level	The level of confidence.

Value

The required sample size, or a vector or matrix of sample sizes if multiple correlation coefficients or required (half-)widths were supplied. The row and column names specify the r and w values to which the sample size in each cell corresponds. The confidence level is set as attribute to the resulting vector or matrix.

Author(s)

Douglas Bonett (UC Santa Cruz, United States), with minor edits by Murray Moinester (Tel Aviv University, Israel) and Gjalt-Jorn Peters (Open University of the Netherlands, the Netherlands).

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Bonett, D. G., Wright, T. A. (2000). Sample size requirements for estimating Pearson, Kendall and Spearman correlations. *Psychometrika, 65*, 23-28.

Bonett, D. G. (2014). CIcorr.R and sizeCIcorr.R http://people.ucsc.edu/~dgbonett/psyc181.html

Moinester, M., & Gottfried, R. (2014). Sample size estimation for correlations with pre-specified confidence interval. *The Quantitative Methods of Psychology, 10*(2), 124-130. http://www.tqmp.org/RegularArticles/vol10-2/p124/p124.pdf

Peters, G. J. Y. & Crutzen, R. (forthcoming) An easy and foolproof method for establishing how effective an intervention or behavior change method is: required sample size for accurate parameter estimation in health psychology.

See Also

`pwr.confIntR`

Examples

```
pwr.confIntR(c(.4, .6, .8), w=c(.1, .2));
```

`pwr.omegasq` *Power calculations for Omega Squared.*

Description

This function uses `pwr.anova.test` from the `pwr` package in combination with `convert.cohensf.to.omegasq` and `convert.omegasq.to.cohensf` to provide power analyses for Omega Squared.

Usage

```
pwr.omegasq(k = NULL, n = NULL, omegasq = NULL,
            sig.level = 0.05, power = NULL, digits = 4)
```

Arguments

`k`	The number of groups.
`n`	The sample size.
`omegasq`	The Omega Squared value.
`sig.level`	The significance level (alpha).
`power`	The power.
`digits`	The number of digits desired in the output (4, the default, is quite high; but omega squared value tend to be quite low).

Details

This function was written to work similarly to the power functions in the `pwr` package.

Value

An power.htest.ufs object that contains a number of input and output values, most notably:

power	The (specified or computed) power
n	The (specified or computed) sample size in each group
sig.level	The (specified or computed) significance level (alpha)
sig.level	The (specified or computed) Omega Squared value
cohensf	The computed value for the Cohen's f effect size measure

Author(s)

Gjalt-Jorn Peters & Peter Verboon

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

pwr.anova.test, convert.cohensf.to.omegasq, convert.omegasq.to.cohensf

Examples

```
pwr.omegasq(omegasq=.06, k=3, power=.8)
```

---

randomizationSuccess *Computations for successful randomization*

Description

prob.randomizationSuccess computes the probability that two groups are equivalent given a specific sample size, number of nuisance variables, and definition of 'equivalence' (in terms of the Cohen's d expressing the maximum acceptable difference between the groups on any of the nuisance variables).

pwr.randomizationSuccess computes the sample size required to make randomization succeed in a specified proportion of the studies with a two-cell design. 'Success' is defined as the two groups differing at most with a specified effect size on any of a given number or nuisance variables.

Usage

```
prob.randomizationSuccess(n = 1000,
                          dNonequivalence = .2,
                          nNuisanceVars = 100)
pwr.randomizationSuccess(dNonequivalence = 0.2,
                         pRandomizationSuccess = 0.95,
                         nNuisanceVars = 100)
```

Arguments

n	The sample size.
dNonequivalence	The maximum difference between the two groups that is deemed acceptable.
pRandomizationSuccess	The desired probability that the randomization procedure succeeded in generating two equivalent groups (i.e. differing at most with dNonequivalence).
nNuisanceVars	The number of nuisance variables that the researchers assumes exists.

Details

For more details, see Peters & Gruijters (2017).

Value

For prob.randomizationSuccess, the probability that the two groups are equivalent. The function is vectorized, so returns either a vector of length one, a vector of length > 1, a matrix, or an array.

For pwr.randomizationSuccess, the required sample size. The function is vectorized, so returns either a vector of length one, a vector of length > 1, a matrix, or an array.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Peters, G. J.-Y. & Gruijters, S. Why your experiments fail: sample sizes required for randomization to generate equivalent groups as a partial solution to the replication crisis (2017). http://dx.doi.org/

See Also

dCohensd

Examples

```
### To be on the safe side: sample size required to
### obtain 95% likelihood of success when assuming
### 100 nuisance variables exist.
pwr.randomizationSuccess(dNonequivalence = 0.2,
                         pRandomizationSuccess = 0.95,
                         nNuisanceVars = 100);

### Living on the edge:
pwr.randomizationSuccess(dNonequivalence = 0.2,
                         pRandomizationSuccess = 0.60,
                         nNuisanceVars = 10);

### For those with quite liberal ideas of 'equivalence':
```

```
pwr.randomizationSuccess(dNonequivalence = 0.5,
                         pRandomizationSuccess = 0.95,
                         nNuisanceVars = 100);

### And these results can be checked with
### prob.randomizationSuccess:
prob.randomizationSuccess(1212, .2, 100);
prob.randomizationSuccess(386, .2, 10);
prob.randomizationSuccess(198, .5, 100);

### Or in one go:
prob.randomizationSuccess(n=c(198, 386, 1212), c(.2, .5), c(10, 100));
```

`regr` *regr: a simple regression analysis wrapper*

Description

The `regr` function wraps a number of linear regression functions into one convenient interface that provides similar output to the regression function in SPSS. It automatically provides confidence intervals and standardized coefficients. Note that this function is meant for teaching purposes, and therefore it's only for very basic regression analyses.

Usage

```
regr(formula, dat = NULL, conf.level = .95,
     digits = 2, pvalueDigits = 3,
     coefficients = c("raw", "scaled"), plot = FALSE,
     ci.method = c("widest", "r.con", "olkinfinn"),
     ci.method.note = FALSE, env = parent.frame())
```

Arguments

`formula`	The formula of the regression analysis, of the form `y ~ x1 + x2`, where y is the dependent variable and x1 and x2 are the predictors.
`dat`	If the terms in the formula aren't vectors but variable names, this should be the dataframe where those variables are stored.
`conf.level`	The confidence of the confidence interval around the regression coefficients.
`digits`	Number of digits to round the output to.
`pvalueDigits`	The number of digits to show for p-values; smaller p-values will be shown as <.001 or <.0001 etc.
`coefficients`	Which coefficients to show; can be "raw" to only show the raw (unstandardized) coefficients; "scaled" to only show the scaled (standardized) coefficients), or c("raw", "scaled') to show both.

plot	For regression analyses with only one predictor (also sometimes confusingly referred to as 'univariate' regression analyses), scatterplots with regression lines and their standard errors can be produced.
ci.method, ci.method.note	Which method to use for the confidence interval around R squared, and whether to display a note about this choice.
env	The enviroment where to evaluate the formula.

Value

A list of three elements:

input	List with input arguments
intermediate	List of intermediate objects, such as the lm and confint objects.
output	List with two dataframes, one with the raw coefficients, and one with the scaled coefficients.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
### Do a simple regression analysis
regr(age ~ circumference, dat=Orange);

### Show more digits for the p-value
regr(Orange$age ~ Orange$circumference, pvalueDigits=18);
```

---

regrInfluential *Detecting influential cases in regression analyses*

Description

This function combines a number of criteria for determining whether a datapoint is an influential case in a regression analysis. It then sum the criteria to compute an index of influentiality. A list of cases with an index of influentiality of 1 or more is then displayed, after which the regression analysis is repeated without those influantial cases. A scattermatrix is also displayed, showing the density curves of each variable, and in the scattermatrix, points that are colored depending on how influential each case is.

Usage

```
regrInfluential(formula, data)
```

Arguments

formula	The formule of the regression analysis.
data	The data to use for the analysis.

Value

A regrInfluential object, which, if printed, shows the influential cases, the regression analyses repeated without those cases, and the scatter matrix.

Author(s)

Gjalt-Jorn Peters & Marwin Snippe

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
regrInfluential(mpg ~ hp, mtcars);
```

---

removeExceptionalValues
removeExceptionalValues

Description

A function to replace exceptional values with NA. This can be used to quickly remove impossible values, for example, when participants entered their age as 344.

Usage

```
removeExceptionalValues(dat, items = NULL, exception = 0.005,
                        silent = FALSE, stringsAsFactors = FALSE)
```

Arguments

dat	The dataframe containing the items to inspect.
items	The items to inspect.
exception	How rare a value must be to be considered exceptional (and replaced by NA).
silent	Can be used to suppress messages.
stringsAsFactors	Whether to convert strings to factors when creating a dataframe from lapply output.

Details

Note that exceptional values may be errors (e.g. participants accidently pressed a key twice, or during data entry, something went wrong), but they may also be indicative of participants who did not seriously participate in the study. Therefore, it is advised to first use `exceptionalScores` to look for patterns where participants enter many exceptional scores.

Value

The dataframe, with exceptional values replaced by NA.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

`exceptionalScores`

Examples

```
removeExceptionalValues(mtcars, exception=.1);
```

`rMatrix` *rMatrix*

Description

rMatrix provides a correlation matrix with confidence intervals and a p-value adjusted for multiple testing.

Usage

```
rMatrix(dat, x, y=NULL, conf.level = .95, correction = "fdr",
        digits = 2, pValueDigits=3, colspace=2, rowspace=0,
        colNames ="numbers",
        output="R",
        env.LaTeX = 'tabular',
        pboxWidthMultiplier = 1)
```

Arguments

`dat`	A dataframe containing the relevant variables.
`x`	Vector of 1+ variable names.
`y`	Vector of 1+ variable names; if this is left empty, a symmetric matrix is created; if this is filled, the matrix will have the x variables defining the rows and the y variables defining the columns.

conf.level	The confidence of the confidence intervals.
correction	Correction for multiple testing: an element out of the vector c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"). NOTE: the p-values are corrected for multiple testing; The confidence intervals are not (yet :-)).
digits	With what precision do you want the results to print.
pValueDigits	Determines the number of digits to use when displaying p values. P-values that are too small will be shown as p<.001 or p<.00001 etc.
colspace	Number of spaces between columns (only for R output, ignored for LaTeX output)
rowspace	Number of rows between table rows (note: one table row is 2 rows; only for R output, ignored for LaTeX output).
colNames	colNames can be "numbers" or "names". "Names" cause variables names to be printed in the heading; "numbers" causes the rows to become numbered and the numbers to be printed in the heading.
output	Can be "R" or "LaTeX"; if output is set to "LaTeX", the result is a LaTeX table (e.g. for use in knitr).
env.LaTeX	For LaTeX output, the environment can be set with env.LaTeX.
pboxWidthMultiplier	When using LaTeX, pboxWidthMultiplier can be used to make the cells narrower or wider (1 works for anything up until 4 or 5 digits).

Details

rMatrix provides a symmetric or asymmetric matrix of correlations their confidence intervals, and p-values. The p-values can be corrected for multiple testing.

Value

An object with the input and several output variables. Most notably a number of matrices:

r	Pearson r values.
parameter	Degrees of freedom.
ci.lo	Lower bound of Pearson r confidence interval.
ci.hi	Upper bound of Pearson r confidence interval.
p.raw	Original p-values.
p.adj	p-values adjusted for multiple testing.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
rMatrix(mtcars, x=c('disp', 'hp', 'drat'))
```

rnwString *rnwString functions*

Description

The rnwString functions make knitting PFDs a bit more userfriendly.

The sanitizeLatexString function sanitizes a LaTeX string by escaping special characters. It is strongly based on the function described on http://stackoverflow.com/questions/5406071/r-sweave-latex-escape-variables-to-be-printed-in-latex by Aaron Rendahl.

Usage

```
rnwString.initiate(studyName, authorName,
                   docClassArgs = 'a4paper,portrait,11pt',
                   newPage = TRUE, pageMargins=15)
rnwString.terminate(rnwString)
rnwString.generate(rnwString, rnwPath, fileName, pdfLatexPath,
                   envir = parent.frame())
sanitizeLatexString(str)
hasLaTeX(pdfLatexPath)
```

Arguments

studyName	The name of the study - used as the title of the PDF.
authorName	The name of the author(s) - also inserted on title page of the PDF.
docClassArgs	Default arguments for the document class in LaTeX. For example, to use landscape pages, this should be 'a4paper,landscape,11pt'.
newPage	Whether to end the initiation string with a newpage command. This can be set to false if you want to add more information on the first page(s).
pageMargins	Margin of the pages in millimeters.
rnwString	The rnwString to terminate or (after termination) generate.
rnwPath	The path where the temporary files (.rnw, .tex, etc) should be created. Use forward slashes. Note: the last character should not be a slash!
fileName	The filename to use for the temporary files. Omit the extension!
pdfLatexPath	The path to PdfLaTex. This file is part of a LaTeX installation that creates a pdf out of a .tex file. In Windows, you can download (portable) MikTex from http://miktex.org/portable. You then decide yourself where to install MikTex; pdflatex will end up in a subfolder 'miktex\bin', so if you installed MikTex in, for example, 'C:\Program Files\MikTex', the total path becomes 'C:\Program Files\MikTex\miktex\bin'. Note that R uses slashes instead of backslashes to separate folders, so in this example, pdfLatexPath should be 'C:/Program Files/MikTex/miktex/bin' In MacOS, you can install MacTex from http://tug.org/mactex/ By default, pdflatex ends up in folder '/user/texbin', which is what pdfLatexPath should be in that default case.

	In Ubuntu, you can install TexLive base by using your package manager to install texlive-latex-base, or using the terminal: 'sudo apt-get install texlive-latex-base' In ubuntu, by default pdflatex ends un in folder '/usr/bin', which is what pdfLatexPath should be in that default case.
envir	The environment where to evaluate the expressions (normally the environment where the function is called).
str	The character string to sanitize.

Value

rnwString.initiate starts an rnwString; rnwString.terminate closes it; and rnwString.generate takes an rnwString and creates a pdf.

sanitizeLatexString returns the sanitized string.

hasLaTeX checks pdfLatexPath to make sure pdflatex or pdflatex.exe exists.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
### sanitize a string
newString <- sanitizeLatexString('this is a tilde: ~.');
newString;
### newString is now: "this is a tilde: ~."
```

RsqDist *The distribution of R squared (as obtained in a regression analysis)*

Description

These functions use the beta distribution to provide the R Squared distribution.

Usage

```
dRsq(x, nPredictors, sampleSize, populationRsq = 0)
pRsq(q, nPredictors, sampleSize, populationRsq = 0, lower.tail = TRUE)
qRsq(p, nPredictors, sampleSize, populationRsq = 0, lower.tail = TRUE)
rRsq(n, nPredictors, sampleSize, populationRsq = 0)
```

Arguments

x, q	Vector of quantiles, or, in other words, the value(s) of R Squared.
p	Vector of probabilites (*p*-values).
nPredictors	The number of predictors.
sampleSize	The sample size.
n	The number of R Squared values to generate.
populationRsq	The value of R Squared in the population; this determines the center of the R Squared distribution. This has not been implemented yet in this version of userfriendlyscience. If anybody knows how to do this and lets me know, I'll happily integrate this of course.
lower.tail	logical; if TRUE (default), probabilities are the likelihood of finding an R Squared smaller than the specified value; otherwise, the likelihood of finding an R Squared larger than the specified value.

Details

The functions use convert.omegasq.to.f and convert.f.to.omegasq to provide the Omega Squared distribution.

Value

dRsq gives the density, pRsq gives the distribution function, qRsq gives the quantile function, and rRsq generates random deviates.

Note

These functions are based on the Stack Exchange (Cross Validated) post at http://stats.stackexchange.com/questions/130069/what-is-the-distribution-of-r2-in-linear-regression-under-the-null-hypothesis Thus, the credits go to Alecos Papadopoulos, who provided the answer that was used to write these functions.

Author(s)

Gjalt-Jorn Peters (based on a CrossValidated answer by Alecos Papadopoulos)

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

dbeta, pbeta, qbeta, rbeta

Examples

```
### Generate 10 random R Squared values
### with 2 predictors and 100 participants
rRsq(10, 2, 100);

### Probability of finding an R Squared of
### .15 with 4 predictors and 100 participants
```

```
pRsq(.15, 4, 100, lower.tail = FALSE);

### Probability of finding an R Squared of
### .15 with 15 predictors and 100 participants
pRsq(.15, 15, 100, lower.tail=FALSE);
```

`scaleDiagnosis` *scaleDiagnosis*

Description

scaleDiagnosis provides a number of diagnostics for a scale (an aggregative measure consisting of several items).

Usage

```
scaleDiagnosis(dat=NULL, items=NULL, plotSize=180, sizeMultiplier = 1,
               axisLabels = "none", scaleReliability.ci=FALSE, conf.level=.95,
               powerHist=TRUE, ...)
```

Arguments

`dat`	A dataframe containing the items in the scale. All variables in this dataframe will be used if items is NULL.
`items`	If not NULL, this should be a character vector with the names of the variables in the dataframe that represent items in the scale.
`plotSize`	Size of the final plot in millimeters.
`sizeMultiplier`	Allows more flexible control over the size of the plot elements
`axisLabels`	Passed to ggpairs function to set axisLabels.
`scaleReliability.ci`	TRUE or FALSE: whether to compute confidence intervals for Cronbach's Alpha and Omega (uses bootstrapping function in MBESS, takes a while).
`conf.level`	Confidence of confidence intervals for reliability estimates (if requested with scaleReliability.ci).
`powerHist`	Whether to use the default ggpairs histogram on the diagonal of the scattermatrix, or whether to use the powerHist version.
`...`	Additional arguments are passed on to powerHist.

Details

Function to generate an object with several useful statistics and a plot to assess how the elements (usually items) in a scale relate to each other, such as Cronbach's Alpha, omega, the Greatest Lower Bound, a factor analysis, and a correlation matrix.

Value

An object with the input and several output variables. Most notably:

`scaleReliability`	The results of scaleReliability.
`pca`	A Principal Components Analysis
`fa`	A Factor Analysis
`describe`	Decriptive statistics about the items
`scatterMatrix`	A scattermatrix with histograms on the diagonal and correlation coefficients in the upper right half.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
### Note: the 'not run' is simply because running takes a lot of time,
###       but these examples are all safe to run!
## Not run:
### This will prompt the user to select an SPSS file
scaleDiagnosis();

### Generate a datafile to use
exampleData <- data.frame(item1=rnorm(100));
exampleData$item2 <- exampleData$item1+rnorm(100);
exampleData$item3 <- exampleData$item1+rnorm(100);
exampleData$item4 <- exampleData$item2+rnorm(100);
exampleData$item5 <- exampleData$item2+rnorm(100);

### Use a selection of two variables
scaleDiagnosis(dat=exampleData, items=c('item2', 'item4'));

### Use all items
scaleDiagnosis(dat=exampleData);

## End(Not run)
```

---

scaleDiagnosisToPDF *scaleDiagnosisToPDF*

Description

scaleDiagnosis provides a number of diagnostics for a scale (an aggregative measure consisting of several items), and scaleDiagnosisToPDF takes the resulting object and generates a PDF file, which is then saved to disk.

Usage

```
scaleDiagnosisToPDF(scaleDiagnosisObject,
                    docTitle = "Scale diagnosis", docAuthor = "Author",
                    pdfLatexPath, rnwPath=getwd(),
                    filename = "scaleDiagnosis",
                    digits=2,
                    rMatrixColsLandscape = 6,
                    pboxWidthMultiplier = 1,
                    scatterPlotBaseSize = 4,
                    maxScatterPlotSize = NULL,
                    pageMargins=15,
                    pval=TRUE)
```

Arguments

scaleDiagnosisObject	An object generated by scaleDiagnosis.
docTitle	The title of the PDF file (printed on the first page).
docAuthor	The author to show in the PDF file (printed on the first page).
pdfLatexPath	The path to PdfLaTex. This file is part of a LaTeX installation that creates a pdf out of a .tex file. See rnwString for more information.
rnwPath	The path where the temporary files will be stored.
filename	Filename of the PDF (".pdf" is appended).
digits	Number of digits to show.
rMatrixColsLandscape	This number determines when the page(s) in the PDF is/are rotated; pages with matrices that have this number of columns or more are rotated.
pboxWidthMultiplier	Passed on to (unexported method) print.rMatrix.
scatterPlotBaseSize	Basic size of scatterplots in centimeters. If this number, multiplied by the number of items (i.e. columns/rows in scattermatrix) is larger than maxScatterPlotSize, it is ignored.
maxScatterPlotSize	Maximum size of scatterplots; automatically calculated if NULL.
pageMargins	Margins of landscape pages in millimeters.
pval	Whether to print p-values using the p-value formatting. Passed on to (unexported method) print.rMatrix.

Details

This functon generates a PDF file from a scaleDiagnosis object. scaleDiagnosis generates an object with several useful statistics and a plot to assess how the elements (usually items) in a scale relate to each other, such as Cronbach's Alpha, omega, the Greatest Lower Bound, a factor analysis, and a correlation matrix.

Value

Nothing is returned; the file is printed to disk.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
## Not run:

### Generate a datafile to use
exampleData <- data.frame(item1=rnorm(100));
exampleData$item2 <- exampleData$item1+rnorm(100);
exampleData$item3 <- exampleData$item1+rnorm(100);
exampleData$item4 <- exampleData$item2+rnorm(100);
exampleData$item5 <- exampleData$item2+rnorm(100);

### Use all items and create object
scaleDiagnosisObject <- scaleDiagnosis(dat=exampleData);

### Generate a PDF
scaleDiagnosisToPDF(scaleDiagnosisObject);


## End(Not run)
```

---

scaleInspection *scaleInspection and a number of useful helper functions*

Description

scaleInspection is a function to generate a PDF with information to diagnose and inspect scales (aggregate measures); makeScales actually generates the scales; and meanConfInt and sdConfInt provide confidence intervals for means and standard deviations.

Usage

```
scaleInspection(dat, items = NULL,
                docTitle = "Scale inspection", docAuthor = "Author",
                pdfLaTexPath, rnwPath=getwd(),
                filename = "scaleInspection", convertFactors=TRUE,
                scaleReliability.ci=FALSE, conf.level=.95, digits=2,
                rMatrixColsLandscape = 6,
                pboxWidthMultiplier = 1,
                scatterPlotBaseSize = 4,
```

```
                pageMargins=15, show=FALSE,
                pval=TRUE)
makeScales(dat, scales, append=TRUE)
meanConfInt(vector=NULL, mean=NULL, sd=NULL, n=NULL, se=NULL, conf.level=.95)
sdConfInt(vector=NULL, sd=NULL, n=NULL, conf.level=.95)
```

Arguments

dat	Dataframe containing the items of the relevant scale
items	Either a character vector with the itemnames, or, if the items are organised in scales, a list of character vectors with the items in each scale.
scales	A list of character vectors with the items in each scale, where each vectors' name is the name of the scale.
docTitle	Title to use when generating the PDF.
docAuthor	Author(s) to include when generating the PDF.
pdfLaTexPath	The path to PdfLaTex. This file is part of a LaTeX installation that creates a pdf out of a .tex file. In Windows, you can download (portable) MikTex from http://miktex.org/portable. You then decide yourself where to install MikTex; pdflatex will end up in a subfolder 'miktex\bin', so if you installed MikTex in, for example, 'C:\Program Files\MikTex', the total path becomes 'C:\Program Files\MikTex\miktex\bin'. Note that R uses slashes instead of backslashes to separate folders, so in this example, pdfLaTexPath should be 'C:/Program Files/MikTex/miktex/bin' In MacOS, you can install MacTex from http://tug.org/mactex/ By default, pdflatex ends up in folder '/user/texbin', which is what pdfLaTexPath should be in that default case. In Ubuntu, you can install TexLive base by using your package manager to install texlive-latex-base, or using the terminal: 'sudo apt-get install texlive-latex-base' In ubuntu, by default pdflatex ends un in folder '/usr/bin', which is what pdfLaTexPath should be in that default case.
rnwPath	The path where the temporary files and the resulting PDF should be stored.
filename	The filename to use to save the pdf.
convertFactors	Whether to convert factors to numeric vectors for the analysis.
scaleReliability.ci	TRUE or FALSE: whether to compute confidence intervals for Cronbach's Alpha and Omega (uses bootstrapping function in MBESS, takes a while).
conf.level	Confidence of confidence intervals (for reliability estimates (if requested with scaleReliability.ci), meand, and sd, for respectively scaleInspection, meanConfInt and sdConfInt).
digits	The number of digits to use in the tables.
rMatrixColsLandscape	At how many columns (or rather, variables) or more should rMatrices be printed landscape?
pboxWidthMultiplier	Used for print.rMatrix; used to tweak the width of columns in the correlation matrix.

scatterPlotBaseSize	Size of one scatterplot in the scattermatrix in centimeters. If the total scattermatrix becomes larger than 18 cm, it's scaled down to 18 cm.
pageMargins	Margins of the page in millimeters.
show	Whether to show the results (or only write them to the PDF).
pval	Whether to print p-values as p-values in correlation matrix.
append	Whether to return the dataframe including the new variables (TRUE), or a dataframe with only those new variables (FALSE).
vector	Numeric vector to use when computing confidence intervals.
mean	Mean to use when computing confidence intervals (when no vector is provided).
sd	Standard deviaton to use when computing confidence intervals (when no vector is provided).
n	Number of datapoints to base confidence intervals on.
se	Standard errorto use when computing confidence intervals (when no standard deviation or vector is provided).

Details

scaleInspection generates a PDF with useful diagnostics to assess a scale; those from scaleDiagnosis and an rMatrix.

makeScales generates the scales and stores them in the dataframe.

meanConfInt and sdConfInt just compute and return a confidence interval for a mean or standard deviation.

Value

scaleInspection returns nothing; it just generates a PDF.

makeScales returns the provided dataframe, now including the new scale variables.

meanConfInt and sdConfInt return an object, with in its 'output' list, the confidence interval for a mean or standard deviation.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
## Not run:
scaleInspection(mtcars, items=c('disp', 'hp', 'drat'), pdfLaTexPath="valid/path/here");

## End(Not run)

newDataframe <- makeScales(mtcars, list(senselessScale = c('disp', 'hp', 'drat')));
```

```
sdConfInt(sd=4, n=30);

meanConfInt(mean=5, sd=4, n=30)
```

---

scaleStructure *scaleStructure*

Description

The scaleStructure function (which was originally called scaleReliability) computes a number of measures to assess scale reliability and internal consistency.

If you use this function in an academic paper, please cite Peters (2014), where the function is introduced, and/or Crutzen & Peters (2015), where the function is discussed from a broader perspective.

Usage

```
scaleStructure(dat=NULL, items = 'all', digits = 2, ci = TRUE,
               interval.type="normal-theory", conf.level=.95,
               silent=FALSE, samples=1000, bootstrapSeed = NULL,
               omega.psych = TRUE, poly = TRUE)
scaleReliability(dat=NULL, items = 'all', digits = 2, ci = TRUE,
                 interval.type="normal-theory", conf.level=.95,
                 silent=FALSE, samples=1000, bootstrapSeed = NULL,
                 omega.psych = TRUE, poly = TRUE)
```

Arguments

dat	A dataframe containing the items in the scale. All variables in this dataframe will be used if items = 'all'. If dat is NULL, a the getData function will be called to show the user a dialog to open a file.
items	If not 'all', this should be a character vector with the names of the variables in the dataframe that represent items in the scale.
digits	Number of digits to use in the presentation of the results.
ci	Whether to compute confidence intervals as well. If true, the method specified in interval.type is used. When specifying a bootstrapping method, this can take quite a while!
interval.type	Method to use when computing confidence intervals. The list of methods is explained in ci.reliability. Note that when specifying a bootstrapping method, the method will be set to normal-theory for computing the confidence intervals for the ordinal estimates, because these are based on the polychoric correlation matrix, and raw data is required for bootstrapping.
conf.level	The confidence of the confidence intervals.
silent	If computing confidence intervals, the user is warned that it may take a while, unless silent=TRUE.

samples	The number of samples to compute for the bootstrapping of the confidence intervals.
bootstrapSeed	The seed to use for the bootstrapping - setting this seed makes it possible to replicate the exact same intervals, which is useful for publications.
omega.psych	Whether to also compute the interval estimate for omega using the omega function in the psych package. The default point estimate and confidence interval for omega are based on the procedure suggested by Dunn, Baguley & Brunsden (2013) using the MBESS function ci.reliability (because it has more options for computing confidence intervals, not always requiring bootstrapping), whereas the psych package point estimate was suggested in Revelle & Zinbarg (2008). The psych estimate usually (perhaps always) results in higher estimates for omega.
poly	Whether to compute ordinal measures (if the items have sufficiently few categories).

Details

This function is basically a wrapper for functions from the psych and MBESS packages that compute measures of reliability and internal consistency. For backwards compatibility, in addition to scaleStructure, scaleReliability can also be used to call this function.

Value

An object with the input and several output variables. Most notably:

input	Input specified when calling the function
intermediate	Intermediate values and objects computed to get to the final results
output	Values of reliability / internal consistency measures, with as most notable elements:
output$dat	A dataframe with the most important outcomes
output$omega	Point estimate for omega
output$glb	Point estimate for the Greatest Lower Bound
output$alpha	Point estimate for Cronbach's alpha
output$coefficientH	Coefficient H
output$omega.ci	Confidence interval for omega
output$alpha.ci	Confidence interval for Cronbach's alpha

Author(s)

Gjalt-Jorn Peters and Daniel McNeish (University of North Carolina, Chapel Hill, US).

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

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Sijtsma, K. (2009). On the Use, the Misuse, and the Very Limited Usefulness of Cronbach's Alpha. *Psychometrika*, 74(1), 107-120. doi:10.1007/s11336-008-9101-0

Zinbarg, R. E., Revelle, W., Yovel, I., & Li, W. (2005). Cronbach's alpha, Revelle's beta and McDonald's omega H: Their relations with each other and two alternative conceptualizations of reliability. *Psychometrika*, 70(1), 123-133. doi:10.1007/s11336-003-0974-7

See Also

omega, alpha, and ci.reliability.

Examples

```
## Not run:
### (These examples take a lot of time, so they are not run
###  during testing.)

### This will prompt the user to select an SPSS file
scaleStructure();

### Load data from simulated dataset testRetestSimData (which
### satisfies essential tau-equivalence).
data(testRetestSimData);

### Select some items in the first measurement
exampleData <- testRetestSimData[2:6];

### Use all items (don't order confidence intervals to save time
### during automated testing of the example)
scaleStructure(dat=exampleData, ci=FALSE);
```

```
### Use a selection of three variables (without confidence
### intervals to save time
scaleStructure(dat=exampleData, items=c('t0_item2', 't0_item3', 't0_item4'),
               ci=FALSE);

### Make the items resemble an ordered categorical (ordinal) scale
ordinalExampleData <- data.frame(apply(exampleData, 2, cut,
                                       breaks=5, ordered_result=TRUE,
                                       labels=as.character(1:5)));

### Now we also get estimates assuming the ordinal measurement level
scaleStructure(ordinalExampleData, ci=FALSE);

## End(Not run)
```

---

scatterMatrix *scatterMatrix*

Description

scatterMatrix produced a matrix with jittered scatterplots, histograms, and correlation coefficients.

Usage

```
scatterMatrix(dat, items=NULL, plotSize=180, sizeMultiplier = 1,
              axisLabels = "none", powerHist=TRUE, ...)
```

Arguments

dat	A dataframe containing the items in the scale. All variables in this dataframe will be used if items is NULL.
items	If not NULL, this should be a character vector with the names of the variables in the dataframe that represent items in the scale.
plotSize	Size of the final plot in millimeters.
sizeMultiplier	Allows more flexible control over the size of the plot elements
axisLabels	Passed to ggpairs function to set axisLabels.
powerHist	Whether to use the default ggpairs histogram on the diagonal of the scattermatrix, or whether to use the powerHist version.
...	Additional arguments are passed on to powerHist.

Value

An object with the input and several output variables. Most notably:

output$scatterMatrix
: A scattermatrix with histograms on the diagonal and correlation coefficients in the upper right half.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
### Note: the 'not run' is simply because running takes a lot of time,
###       but these examples are all safe to run!
## Not run:

### Generate a datafile to use
exampleData <- data.frame(item1=rnorm(100));
exampleData$item2 <- exampleData$item1+rnorm(100);
exampleData$item3 <- exampleData$item1+rnorm(100);
exampleData$item4 <- exampleData$item2+rnorm(100);
exampleData$item5 <- exampleData$item2+rnorm(100);

### Use all items
scatterMatrix(dat=exampleData);

## End(Not run)
```

---

scatterPlot *Easy ggplot2 scatter plots*

Description

This function is intended to provide a very easy interface to generating pretty (and pretty versatile) ggplot scatter plots.

Usage

```
scatterPlot(x, y, pointsize = 3,
            theme = theme_bw(),
            regrLine = FALSE, regrCI = FALSE,
            regrLineCol = "blue",
            regrCIcol = regrLineCol,
            regrCIalpha = 0.25,
            width = 0, height = 0,
            position = "identity",
            ...)
```

Arguments

x	The variable to plot on the X axis.
y	The variable to plot on the Y axis.
pointsize	The size of the points in the scatterplot.

theme	The theme to use.
regrLine	Whether to show the regression line.
regrCI	Whether to display the confidence interval around the regression line.
regrLineCol	The color of the regression line.
regrCIcol	The color of the confidence interval around the regression line.
regrCIalpha	The alpha value (transparency) of the confidence interval around the regression line.
width	If position is 'jitter', the points are 'jittered': some random noise is added to change their location slightly. In that case 'width' can be set to determine how much the location should be allowed to vary on the X axis.
height	If position is 'jitter', the points are 'jittered': some random noise is added to change their location slightly. In that case 'height' can be set to determine how much the location should be allowed to vary on the Y axis.
position	Whether to 'jitter' the points (adding some random noise to change their location slightly, used to prevent overplotting). Set to 'jitter' to jitter the points.
...	And additional arguments are passed to geom_point or geom_jitter (if jitter is set to 'jitter').

Details

Note that if position is set to 'jitter', unless width and/or height is set to a non-zero value, there will still not be any jittering.

Value

A ggplot plot is returned.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

geom_point, geom_jitter, geom_smooth

Examples

```
### A simple scatter plot
scatterPlot(mtcars$mpg, mtcars$hp);

### The same scatter plot, now with a regression line
### and its confidence interval added.
scatterPlot(mtcars$mpg, mtcars$hp, regrLine=TRUE, regrCI=TRUE);
```

`setCaptionNumbering` *Convenience function for numbered captions in knitr (and so, RMarkdown)*

Description

This function makes it easy to tell knitr (and so RMarkdown) to use numbered captions of any type.

Usage

```
setCaptionNumbering(captionName = "tab.cap",
                    prefix = ":Table %s: ",
                    suffix = "",
                    captionBefore = FALSE,
                    romanNumeralSetting = "counter_roman",
                    resetCounterTo = 1)
```

Arguments

`captionName`	The name of the caption; this is used both as unique identifier for the counter, and to set the caption text (included between the prefix and suffix) in the chunk options.
`prefix`	The text to add as prefix before the action caption; this will typically include '%s%' which will be replaced by the number of this caption.
`suffix`	The text to add as suffix after the action caption; this can also include '%s%' which will be replaced by the number of this caption. Together with the `prefix`, this can also be used to enclose the caption in html.
`captionBefore`	Whether the caption should appear before or after the relevant chunk output.
`romanNumeralSetting`	The name of the option (should be retrievable with `getOption`) where it's configured whether to use Roman (TRUE) or Latin (FALSE) numerals. FALSE is assumed if this option isn't set.
`resetCounterTo`	If not `NULL` and numeric, the counter will start at this number.

Value

This function returns nothing, but instead sets the appropriate `knit_hooks`. Or rather, just one hook.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
## Not run:
  setCaptionNumbering(captionName='tab.cap',
                      prefix = ":Table %s: ");

## End(Not run)
```

`setFigCapNumbering` *Automatic caption numbering knitr hooks for figures and tables*

Description

These function implement ideas by Max Gordon and DeanK (see Details) to add `knitr` hooks to automate the numbering of figures and tables when generating R Markdown documents.

Usage

```
setFigCapNumbering(figure_counter_str = "Figure %s: ",
                   figureClass = "", imgClass = "",
                   figureInlineStyle = c("display:block"),
                   imgInlineStyle = NULL,
                   resetCounterTo = 1)
setTabCapNumbering(table_counter_str = ":Table %s: ",
                   resetCounterTo = 1)
```

Arguments

`figure_counter_str, table_counter_str`
: The string in which to add the number of the figure or table. The text '%s' will be replaced by the number.

`figureClass`
: Optionally, a css class to pass to the <fig> HTML element that surrounds the <img>.

`imgClass`
: Optionall, a css class to pass to the <img> HTML element.

`figureInlineStyle`
: Any css style to pass to the figure element directly ('inline').

`imgInlineStyle`
: Any css style to pass to the image element directly ('inline').

`resetCounterTo`
: If not `NULL` and numeric, the counter will start at this number.

Details

The figure caption function is basically the one designed by Max Gordon (see http://gforge.se/2014/01/fast-track-publishing-using-knitr-part-iii/.

The table caption function is an implementation of the ideas of DeanK (see http://stackoverflow.com/questions/15258233/using-table-caption-on-r-markdown-file-using-knitr-to-use-in-pandoc-to-conv combined with Max Gordon's function.

Value

Nothing is returned; the correct hooks are configured for knitr.

Author(s)

Max Gordon (setFigCapNumbering) and DeanK (setTabCapNumbering); implemented by Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

knitr

Examples

```
## Not run:
  setFigCapNumbering("This is figure number %s, with caption text: ");

## End(Not run)
```

---

showPearsonPower *Visualisation of the power of a Pearson correlation test*

Description

This fuction is useful when conducting power analyses for a Pearson correlation. It draws the sampling distribution of Pearson's *r* assuming a null hypothesis value of *r* and assuming a the hypothetical population value. The probability of making a Type 1 error is also illustrated.

Usage

```
showPearsonPower(n = 100, rho = 0.3, rNull = 0,
                 distLabels = c("Null Hypothesis", "Population"),
                 rhoColor = "green", rhoFill = "green",
                 rhoAlpha = 0.1, rhoLineSize = 1,
                 rNullColor = "blue", rNullFill = "blue",
                 rNullAlpha = 0.1, rNullLineSize = 1,
                 type2Color = "red", type2Fill = "red",
                 type2Alpha = 0.1, type2LineSize = 0,
                 theme = dlvTheme(), alpha = 0.05, digits = 3)
```

Arguments

n	The number of participants.
rho	The value of the correlation coefficient in the population.
rNull	The value of the correlation coefficient according to the null hypothesis.

`distLabels` Labels for the two distributions; the first one is the null hypothesis distribution, the second one the alternative distribution.

`rhoColor, rNullColor, type2Color`
The border colors of the distributions and the region used to illustrate the Type 2 error probability.

`rhoFill, rNullFill, type2Fill`
The fill colors of the distributions and the region used to illustrate the Type 2 error probability.

`rhoAlpha, rNullAlpha, type2Alpha`
The alpha (transparency) of the distributions and the region used to illustrate the Type 2 error probability.

`rhoLineSize, rNullLineSize, type2LineSize`
The line thicknesses of the distributions and the region used to illustrate the Type 2 error probability.

`theme` The theme to use.

`alpha` The significance level (alpha) of the null hypothesis test.

`digits` The number of digits to round to.

Value

A `ggplot` plot is returned.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

`didacticPlot`

Examples

```
## Not run:
showPearsonPower();

## End(Not run)
```

`simDataSet` *simDataSet*

Description

simDataSet can be used to conveniently and quickly simulate a dataset that satisfies certain constraints, such as a specific correlation structure, means, ranges of the items, and measurement levels of the variables. Note that the results are approximate; mvrnorm is used to generate the correlation matrix, but the factor are only created after that, so cutting the variable into factors may change the correlations a bit.

Usage

```
simDataSet(n,
           varNames,
           correlations = c(0.1, 0.4),
           specifiedCorrelations = NULL,
           means = 0,
           sds = 1,
           ranges = c(1, 7),
           factors = NULL,
           cuts = NULL,
           labels = NULL,
           seed = 20160503,
           empirical = TRUE,
           silent = FALSE)
```

Arguments

n	Number of requires cases (records, entries, participants, rows) in the final dataset.
varNames	Names of the variables in a vector; note that the length of this vector will determine the number of variables simulated.
correlations	The correlations between the variables are randomly sampled from this range using the uniform distribution; this way, it's easy to have a relatively 'messy' correlation matrix without the need to specify every correlation manually.
specifiedCorrelations	The correlations that have to have a specific value can be specified here, as a list of vectors, where each vector's first two elements specify variables names, and the last one the correlation between those two variables. Note that tweaking the correlations may take some time; the mvrnorm function will complain that "'Sigma' is not positive definite", or in other words, you supplied a combination of correlations that can't exist simultaneously, if you get it wrong.
means, sds	The means and standard deviations of the variables. Note that is you set ranges for one or more variables (see below), those ranges are used to rescale those variables, overriding any specified means and standard deviations. If only one mean or standard deviation is supplied, it's recycled along the variables.
ranges	The desired ranges of the variables, supplied as a named list where the name of each element corresponds to a variable. The rescale function will be used to rescale those variables for which a desired scale is specified here. Note that for those variables, the means and standard deviations will be determined by these new ranges.
factors	A vector of variable names that should be converted into factors (using cut). Make sure to specify lists for cuts and labels as well (of the same length).
cuts	A list of vectors that specify, for each factor, where to 'cut' the numeric vector into factor levels.
labels	A list of vectors that specify, for each factor, and for each level, the labels that should be assigned to the factor levels. Each vector in this list has to have one more element than each vector in the cuts list.

seed	The seed to use when generating the dataset (to make sure the exact same dataset can be generated repeatedly).
empirical	Whether to generate the data using the exact (empirical = TRUE) or approximate (empirical = FALSE) correlation matrix; this is passed on to mvrnorm.
silent	Whether to show intermediate and final descriptive information (correlation and covariance matrices as well as summaries).

Details

This function was intended to allow relatively quick generation of datasets that satisfy specific constraints, e.g. including a number of factors, variables with a specified minimum and maximum value or specified means and standard deviations, and of course specific correlations. Because all correlations except those specified are randomly generated from a uniform distribution, it's quite convenient to generate messy kind of real looking datasets quickly. Note that it's mostly a convenience function, and datasets will still require tweaking; for example, factors are simply numeric vectors that are cut *after* mvrnorm generated the data, so the associations will change slightly.

Value

The generated dataframe is returned invisibly.

Author(s)

Gjalt-Jorn Peters

See Also

mvrnorm

Examples

```
dat <- simDataSet(500, varNames=c('age',
                                  'sex',
                                  'educationLevel',
                                  'negativeLifeEventsInPast10Years',
                                  'problemCoping',
                                  'emotionCoping',
                                  'resilience',
                                  'depression'),
                  means = c(40,
                            0,
                            0,
                            5,
                            3.5,
                            3.5,
                            3.5,
                            3.5),
                  sds = c(10,
                          1,
                          1,
                          1.5,
```

```
        1.5,
        1.5,
        1.5,
        1.5),
specifiedCorrelations =
  list(c('problemCoping', 'emotionCoping', -.5),
       c('problemCoping', 'resilience', .5),
       c('problemCoping', 'depression', -.4),
       c('depression', 'emotionCoping', .6),
       c('depression', 'resilience', -.3)),
ranges = list(age = c(18, 54),
              negativeLifeEventsInPast10Years = c(0,8),
              problemCoping = c(1, 7),
              emotionCoping = c(1, 7)),
factors=c("sex", "educationLevel"),
cuts=list(c(0),
          c(-.5, .5)),
labels=list(c('female', 'male'),
            c('lower', 'middle', 'higher')),
silent=FALSE);
```

`sort.associationMatrix` *sort.associationMatrix*

Description

This function sorts an `associationMatrix` ascendingly or descendingly by one of its columns.

Usage

```
## S3 method for class 'associationMatrix'
sort(x, decreasing = TRUE, byColumn = 1, ...)
```

Arguments

`x`	The `associationMatrix` object to sort.
`decreasing`	Whether to sort ascendingly (FALSE) or descending (TRUE).
`byColumn`	Which column to sort the matrix by, as an index.
`...`	Passed on to `sort`.

Details

Note that if the `associationMatrix` contains values of different effectsizes, the sorting may be misleading. For example, a value of Cohen's d of .45 is higher than a value of Pearson's r of .35, and so will end up higher in a 'decreasing' sort - even though the association represented by an r of .35 is stronger than that represented by a d of .45.

Furthermore, only asymmetrical associationMatrices can be sorted; sorting a symmetrical association matrix would also change the order of the columns, after all.

Value

The associationMatrix, but sorted.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

See Also

associationMatrix

Examples

```
sort(associationMatrix(infert, y=c("parity", "age"),
                       x=c("induced", "case", "spontaneous"), colNames=TRUE));
```

---

testRetestAlpha *testRetestAlpha*

Description

The testRetestAlpha function computes the test-retest alpha coefficient (Green, 2003).

Usage

```
testRetestAlpha(dat = NULL, moments = NULL,
                testDat = NULL, retestDat = NULL,
                sortItems = FALSE, convertToNumeric = TRUE)
```

Arguments

dat	A dataframe containing the items in the scale at both measurement moments. If no dataframe is specified, a dialogue will be launched to allow the user to select an SPSS datafile. If only one dataframe is specified, either the items have to be ordered chronologically (i.e. first all items for the first measurement, then all items for the second measurement), or the vector 'moments' has to be used to indicate, for each item, to which measurement moment it belongs.
moments	Used to indicate to which measurement moment each item in 'dat' belongs; should be a vector with the same length as dat has columns, and with two possible values (e.g. 1 and 2).
testDat, retestDat	Dataframes with the items for each measurement moment: note that the items have to be in the same order (unless sortItems is TRUE).
sortItems	If true, the columns (items) in each dataframe are ordered alphabetically before starting. This can be convenient to ensure that the order of the items at each measurement moment is the same.

convertToNumeric
: When TRUE, the function will attempt to convert all vectors in the dataframes to numeric.

Details

This function computes the test-retest alpha coefficient as described in Green (2003).

Value

An object with the input and several output variables. Most notably:

input
: Input specified when calling the function

intermediate
: Intermediate values and objects computed to get to the final results

output$testRetestAlpha
: The value of the test-retest alpha coefficient.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Green, S. N. (2003). A Coefficient Alpha for Test-Retest Data. Psychological Methods, 8(1), 88-101. doi:10.1037/1082-989X.8.1.88

Examples

```
## Not run:
### This will prompt the user to select an SPSS file
testRetestAlpha();

## End(Not run)

### Load data from simulated dataset testRetestSimData (which
### satisfies essential tau-equivalence).
data(testRetestSimData);

### The first column is the true score, so it's excluded in this example.
exampleData <- testRetestSimData[, 2:ncol(testRetestSimData)];

### Compute test-retest alpha coefficient
testRetestAlpha(exampleData);
```

testRetestCES *testRetestCES*

Description

The testRetestCES function computes the test-retest Coefficient of Equivalence and Stability (Schmidt, Le & Ilies, 2003).

Usage

```
testRetestCES(dat = NULL, moments = NULL,
              testDat = NULL, retestDat = NULL,
              parallelTests = 'means',
              sortItems = FALSE, convertToNumeric = TRUE,
              digits=4)
parallelSubscales(dat, convertToNumeric = TRUE)
```

Arguments

dat	A dataframe. For testRetestCES, this dataframe must contain the items in the scale at both measurement moments. If no dataframe is specified, a dialogue will be launched to allow the user to select an SPSS datafile. If only one dataframe is specified, either the items have to be ordered chronologically (i.e. first all items for the first measurement, then all items for the second measurement), or the vector 'moments' has to be used to indicate, for each item, to which measurement moment it belongs. The number of columns in this dataframe MUST be even! Note that instead of providing this dataframe, the items of each measurement moment can be provided separately in testDat and retestDat as well.
moments	Used to indicate to which measurement moment each item in 'dat' belongs; should be a vector with the same length as dat has columns, and with two possible values (e.g. 1 and 2).
testDat, retestDat	Dataframes with the items for each measurement moment: note that the items have to be in the same order (unless sortItems is TRUE).
parallelTests	A vector indicating which items belong to which parallel test; like the moments vector, this should have two possible values (e.g. 1 and 2). Alternatively, it can be character value with 'means' or 'variances'; in this case, parallelSubscales will be used to create roughly parallel halves.
sortItems	If true, the columns (items) in each dataframe are ordered alphabetically before starting. This can be convenient to ensure that the order of the items at each measurement moment is the same.
convertToNumeric	When TRUE, the function will attempt to convert all vectors in the dataframes to numeric.
digits	Number of digits to print.

Details

This function computes the test-retest Coefficient of Equivalence and Stability (CES) as described in Schmidt, Le & Ilies (2003). Note that this function only computes the test-retest CES for a scale that is administered twice and split into two parallel halves post-hoc (this procedure is explained on page 210, and the equations that are used, 16 and 17a are explained on page 212).

Value

An object with the input and several output variables. Most notably:

`input`	Input specified when calling the function
`intermediate`	Intermediate values and objects computed to get to the final results
`output$testRetestCES`	The value of the test-retest Coefficient of Equivalence and Stability.

Note

This function uses equations 16 and 17 on page 212 of Schmidt, Le & Ilies (2003): in other words, this function assumes that one scale is administered twice. If you'd like the computation for two different but parellel scales/measures to be implemented, please contact me.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

References

Schmidt, F. L., Le, H., & Ilies, R. (2003) Beyong Alpha: An Empirical Examination of the Effects of Different Sources of Measurement Error on Reliability Estimates for Measures of Individual-differences Constructs. Psychological Methods, 8(2), 206-224. doi:10.1037/1082-989X.8.x.206

Examples

```
## Not run:
### This will prompt the user to select an SPSS file
testRetestCES();

## End(Not run)

### Load data from simulated dataset testRetestSimData (which
### satisfies essential tau-equivalence).
data(testRetestSimData);

### The first column is the true score, so it's excluded in this example.
exampleData <- testRetestSimData[, 2:ncol(testRetestSimData)];

### Compute test-retest alpha coefficient
testRetestCES(exampleData);
```

testRetestReliability *testRetestReliability*

Description

The testRetestReliability function is a convenient interface to testRetestAlpha and testRetestCES.

Usage

```
testRetestReliability(dat = NULL, moments = NULL,
                      testDat = NULL, retestDat = NULL,
                      parallelTests = 'means',
                      sortItems = FALSE, convertToNumeric = TRUE,
                      digits=2)
```

Arguments

dat	A dataframe. This dataframe must contain the items in the scale at both measurement moments. If no dataframe is specified, a dialogue will be launched to allow the user to select an SPSS datafile. If only one dataframe is specified, either the items have to be ordered chronologically (i.e. first all items for the first measurement, then all items for the second measurement), or the vector 'moments' has to be used to indicate, for each item, to which measurement moment it belongs. The number of columns in this dataframe MUST be even! Note that instead of providing this dataframe, the items of each measurement moment can be provided separately in testDat and retestDat as well.
moments	Used to indicate to which measurement moment each item in 'dat' belongs; should be a vector with the same length as dat has columns, and with two possible values (e.g. 1 and 2).
testDat, retestDat	Dataframes with the items for each measurement moment: note that the items have to be in the same order (unless sortItems is TRUE).
parallelTests	A vector indicating which items belong to which parallel test; like the moments vector, this should have two possible values (e.g. 1 and 2). Alternatively, it can be character value with 'means' or 'variances'; in this case, parallelSubscales will be used to create roughly parallel halves.
sortItems	If true, the columns (items) in each dataframe are ordered alphabetically before starting. This can be convenient to ensure that the order of the items at each measurement moment is the same.
convertToNumeric	When TRUE, the function will attempt to convert all vectors in the dataframes to numeric.
digits	Number of digits to show when printing the output

Details

This function calls both testRetestAlpha and testRetestCES to compute and print measures of the test-retest reliability.

Value

An object with the input and several output variables. Most notably:

`input` Input specified when calling the function

`intermediate` Intermediate values and objects computed to get to the final results

`output$testRetestAlpha`
The value of the test-retest alpha coefficient.

`output$testRetestCES`
The value of the test-retest Coefficient of Equivalence and Stability.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
## Not run:
### This will prompt the user to select an SPSS file
testRetestReliability();

## End(Not run)

### Load data from simulated dataset testRetestSimData (which
### satisfies essential tau-equivalence).
data(testRetestSimData);

### The first column is the true score, so it's excluded in this example.
exampleData <- testRetestSimData[, 2:ncol(testRetestSimData)];

### Compute test-retest alpha coefficient
testRetestReliability(exampleData);
```

---

testRetestSimData *testRetestSimData is a simulated dataframe used to demonstrate the testRetestAlpha coefficient function.*

Description

This dataset contains the true scores of 250 participants on some variable, and 10 items of a scale administered twice (at t0 and at t1).

Usage

```
data(testRetestSimData)
```

Format

A data frame with 250 observations on the following 21 variables.

`trueScore` The true scores

`t0_item1` Score on item 1 at test

`t0_item2` Score on item 2 at test

`t0_item3` Score on item 3 at test

`t0_item4` Score on item 4 at test

`t0_item5` Score on item 5 at test

`t0_item6` Score on item 6 at test

`t0_item7` Score on item 7 at test

`t0_item8` Score on item 8 at test

`t0_item9` Score on item 9 at test

`t0_item10` Score on item 10 at test

`t1_item1` Score on item 1 at retest

`t1_item2` Score on item 2 at retest

`t1_item3` Score on item 3 at retest

`t1_item4` Score on item 4 at retest

`t1_item5` Score on item 5 at retest

`t1_item6` Score on item 6 at retest

`t1_item7` Score on item 7 at retest

`t1_item8` Score on item 8 at retest

`t1_item9` Score on item 9 at retest

`t1_item10` Score on item 10 at retest

Details

This dataset was generated with the code in the reliabilityTest.r test script.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
data(testRetestSimData);
head(testRetestSimData);
hist(testRetestSimData$t0_item1);
cor(testRetestSimData);
```

therapyMonitor *therapyMonitor & therapyMonitor.multi*

Description

therapyMonitor & therapyMonitor.multi are useful for simple n-of-1 designs, and were written to make it easy for therapists or other practitioners to get some insight into the effects of their treatments.

Usage

```
therapyMonitor(dat = NULL, design="AB", statistic="|A-B|",
               conditionColumn = NULL, variableColumn = NULL,
               timeColumn = NULL, conditionMoment = NULL,
               limit=NULL, lines=NULL, ylab=NULL, xlab=NULL,
               outputFile = NULL, outputFormats = c('svg', 'png'),
               plotTitle = "therapyMonitor results",
               plotWidth=25, plotHeight=15)
therapyMonitor.multi(dat = NULL,
                     variableColumn = NULL, conditionColumn = NULL,
                     conditionMoment = NULL, minLevels = 5,
                     outputFiles = FALSE, outputFilePath = getwd(),
                     outputFormats = c('svg', 'png'), silent=FALSE,
                     ...)
```

Arguments

dat	A dataframe containing the variables to analyse. If not dataframe is specified, get getData function is used to present a dialog to the user.
design	The design to use; see pvalue.systematic in the SCRT-package for more information. Note that currently, this function always assumes an "AB" design; changing this only changes the way pvalue.systematic is called.
statistic	The statistic to use; see pvalue.systematic in the SCRT-package for more information. Note that currently, this function always assumes the "|A-B|" statistic; changing this only changes the way pvalue.systematic is called.
conditionColumn	The name of the variable containing, for each measurement, the condition, or the phase of the treatment. This variable should normally only have two levels (e.g. 'A' and 'B'), indicating when the treatment changed from condition 'A' to condition 'B'.
variableColumn	For therapyMonitor, this must be a single value: the name of the variable to analyse as dependent variable. For therapyMonitor.multi, this can be a vector, in which case all the specified variables are analysed sequentially. In any case, the variable(s) specified here must have the 'interval' measurement level (i.e. be roughly continuous). For therapyMonitor.multi, if this argument is empty, all variables are used, provided they have at least minLevels levels.

timeColumn	The variable containing the time (datetime) of each measurement moment. If not specified in R's POSIXct format, the function tries to guess whether SPSS, SAS, or Stata timestamps were specified, and tries to convert. If the timeColumn isn't specified, the function will assume that all measurements were equidistant, and they'll simply be assigned consecutive numbers als measurement moments.
conditionMoment	The conditionMoment argument provides an alternative method of specifying when the condition changed; this can be the number of the first measurement in the new (second) condition/phase. For example, if the treatment started after the 6th measurement, this can be specified by passing 'conditionMoment=7'.
limit	The minimum number of consecutive measurements that has to be available within one condition/phase to enable the analysis (see pvalue.systematic).
lines	Which lines in the dat dataframe to use.
ylab, xlab	Labels to use when creating the plots.
outputFile	If not NULL, the filename to write the plot to. Note that this filename should not include the extension - this is appended based on the outputFormats argument.
outputFormats	Which format to use for the plot or plots to export.
plotTitle	The title for the plot.
plotWidth, plotHeight	The size of the plot (in centimeters).
minLevels	The minimum number of levels that a variable in the datafile has to have before it's included in the analyses.
outputFiles	Whether to export the plots and regular output to files.
outputFilePath	If outputFiles is TRUE, the path where to store the output files.
silent	Whether to suppress messages about progress etc.
...	Additional arguments to therapyMonitor.multi are passed on to therapyMonitor.

Details

This function started as a wrapper to the pvalue.systematic function in the SCRT-package, but it now also does some extra stuff.

Value

For therapyMonitor, an object with the input and several output variables, as well as a plot. For therapyMonitor.multi, an object containing several therapyMonitor objects, as well as collated output.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
### Explore and plot the weight of a chick in the ChickWeight dataset
therapyMonitor(ChickWeight, variableColumn='weight',
               conditionMoment=6, lines=1:12);
```

`userfriendlyscienceBasics` *userfriendlyscience basics*

Description

The userfriendlyscience basics functions are some very basic functions to make life that little bit easier.

Usage

```
safeRequire(packageName, mirrorIndex=NULL)
trim(str)
noZero(str)
formatPvalue(values, digits = 3, spaces=TRUE, includeP = TRUE)
formatR(r, digits)
repStr(n = 1, str = " ")
repeatStr(n = 1, str = " ")
ifelseObj(condition, ifTrue, ifFalse)
invertItem(item, fullRange=NULL, ignorePreviousInversion = FALSE)
is.odd(vector)
is.even(vector)
convertToNumeric(vector, byFactorLabel = FALSE)
massConvertToNumeric(dat, byFactorLabel = FALSE,
                     ignoreCharacter = TRUE,
                     stringsAsFactors = FALSE)
vecTxt(vector, delimiter = ", ", useQuote = "",
      firstDelimiter = NULL, lastDelimiter = " & ",
      firstElements = 0, lastElements = 1, lastHasPrecedence = TRUE)
vecTxtQ(vector, useQuote = "'", ...)
find %IN% table
cat0(..., sep="")
addToLog(fullLog, ..., showLog = FALSE);
```

Arguments

`packageName`	The name of the package, as character string.
`mirrorIndex`	The index of the mirror to use, in case you want to specify the mirror in the call (see e.g. /code/linkgetCRANmirrors()[, 1:4] for an overview of these mirrors. For example, at the time of writing, Antwerp is 7, Amsterdam is 60, and Auckland is 62).

`str` The character string to process.

`values` The p-values to format.

`digits` For formatPvalue, number of digits to round to. Numbers smaller than this number will be shown as <.001 or <.0001 etc.

For formatR, the number of digits to use when formatting the Pearson correlation.

`spaces` Whether to include spaces between symbols, operators, and digits.

`includeP` Whether to include the 'p' and '='-symbol in the results (the '<' symbol is always included).

`r` The Pearson correlation to format.

`n` The number of times to repeat the string.

`condition` Condition to evaluate.

`ifTrue` Object to return if the condition is true.

`ifFalse` Object to return if the condition is false.

`item` Item to invert

`fullRange` If provided it must be a numeric vector with the minimum and the maximum of the scale. If not provided, the range function is used (so, use this range argument if the scale minimum and/or maximum do not occur in the data).

`ignorePreviousInversion`
If this item has already been inverted, the function will halt with an error unless it's told to ignore previous inversions with this boolean.

`dat, vector` The dataframe of vector to process.

`byFactorLabel` If TRUE, convertToNumeric and massConvertToNumeric use the factor labels, interpreted as character vectors, to determine the numeric value, instead of the level's indices (which is what as.numeric() does).

`ignoreCharacter`
If TRUE, character vectors are ignored. If FALSE, character vectors are converted (or, an attempt is made :-)).

`stringsAsFactors`
If TRUE, strings (character vectors) in the dataframe will be converted to factors (by as.data.frame, after the function called lapply).

`find` The element(s) to look up in the vector or matrix.

`table` The vector or matrix in which to look up the element.

`delimiter, firstDelimiter, lastDelimiter`
The delimiters to use for respectively the middle, first `firstElements`, and last `lastElements` elements.

`useQuote` This character string is pre- and appended to all elements; so use this to quote all elements (`useQuote="'"`), doublequote all elements (`useQuote='"'`), or anything else (e.g. `useQuote='|'`). The only difference between `vecTxt` and `vecTxtQ` is that the latter by default quotes the elements.

`firstElements, lastElements`
The number of elements for which to use the first respective last delimiters

`lastHasPrecedence`
: If the vector is very short, it's possible that the sum of firstElements and lastElements is larger than the vector length. In that case, downwardly adjust the number of elements to separate with the first delimiter (`TRUE`) or the number of elements to separate with the last delimiter (`FALSE`)?

`sep`
: The separator to pass to `cat`, of course, "" by default.

`fullLog`
: The full log - the character vector(s) provided are appended to this character vector.

`showLog`
: Whether to `cat` the log.

`...`
: Extra arguments are passed to whatever function is wrapped (e.g. `cat` for `cat0`). For addToLog, the dots are used to provide character vectors that are concatenated using `paste0` and (potentially shown and) added to the log.

Details

The safeRequire function checks whether a package is already installed. If so, it loads the package (using require/library). If not, it first installs it, and then loads it.

The trim function removes whitespaces from the start and end of a text string.

The noZero function removes the first zero from a string that was originally a number.

The formatPvalue function formats a P value, roughly according to APA style guidelines. This means that the noZero is used to remove the zero preceding the decimal point, and p values that would round to zero given the requested number of digits are shown as e.g. p<.001.

The formatR function format a Pearson correlation for pretty printing (using noZero).

The repeatStr (or repStr) function repeats a string a given number of times.

The ifelseObj function just evaluates a condition, returning one object if it's true, and another if it's false.

The invertItem function 'unmirrors' an inverted item (i.e. for a 1-3 item, 1 becomes 3, 2 stays 2, and 3 becomes 1).

is.odd and is.even check whether a number is, or numbers in a vector are, odd or even.

The infix function %IN% is a case-insensitive version of `%in%`.

The cat0 function is to cat what paste0 is to paste; it simply makes concatenating many strings without a separator easier.

The addToLog function adds a character vector to a log.

Value

safeRequire returns nothing.

trim, formatPvalue, noZero, formatR, and repeatStr return a string.

ifelseObj return an object.

The invertItem function returns the inverted item vector, with an attribute "inverted" set to TRUE.

is.odd and is.even return a logical vector.

%IN% returns a logical vector of the same length as its first argument.

cat0 returns a string.

addToLog returns a string.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
### load a package
safeRequire('ggplot2');

### trim a string
trim(' this is a string with whitespace in front and at the end              ');
### Returns "this is a string with whitespace in front and at the end"

repeatStr("-", 8);
### Returns "--------" (incredibly useful, no? :-))

tempVector <- c(1,2,3,3,2,4,3,2,1,1,3,4,5,4,3,2,2,1,1,2);
invertedTempVector <- invertItem(tempVector);

### We can also invert it back, but then we have to override the security
### that prevents accidently inverting items back.
invertItem(tempVector, ignorePreviousInversion=TRUE);
```

---

userfriendlysciencePanderMethods

userfriendlyscience methods to pander objects

Description

These methods try to provide output that's ready for R Markdown. Note that they are not all documented; most of them are quite straightforward.

Usage

```
## S3 method for class 'freq'
pander(x, ...)
## S3 method for class 'meanDiff'
pander(x, digits=x$digits, powerDigits=x$digits + 2, ...)
## S3 method for class 'normalityAssessment'
pander(x, headerPrefix = "#####", suppressPlot = FALSE, ...)
## S3 method for class 'dataShape'
pander(x, digits=x$input$digits, extraNotification=TRUE, ...)
## S3 method for class 'associationMatrix'
pander(x, info = x$input$info, file = x$input$file, ...)
## S3 method for class 'crossTab'
pander(x, digits = x$input$digits,
```

```
                          pValueDigits=x$input$pValueDigits, ...)
## S3 method for class 'oneway'
pander(x, digits = x$input$digits,
                       pvalueDigits=x$input$pvalueDigits,
                       headerStyle = "**",
                       na.print="", ...)
## S3 method for class 'regr'
pander(x, digits=x$input$digits,
                     pvalueDigits=x$input$pvalueDigits, ...)
## S3 method for class 'descr'
pander(x, headerPrefix = "", headerStyle = "**", ...)
## S3 method for class 'examine'
pander(x, headerPrefix = "", headerStyle = "**",
                        secondaryHeaderPrefix = "", secondaryHeaderStyle =
                        "*", ...)
## S3 method for class 'examineBy'
pander(x, headerPrefix = "", headerStyle = "**",
                          secondaryHeaderPrefix = "", secondaryHeaderStyle =
                          "*", tertairyHeaderPrefix = "--> ",
                          tertairyHeaderStyle = "", separator = paste0("\n\n",
                          repStr("-", 10), "\n\n"), ...)
## S3 method for class 'frequencies'
pander(x, prefix = "###", ...)
```

Arguments

x	The object to print.
digits	The number of significant digits to print.
powerDigits	Number of digits to use when printing the power.
headerPrefix, secondaryHeaderPrefix, tertairyHeaderPrefix, prefix	Prefix for headers, can be used to output headers for pandoc using R Markdown by specifying e.g. '####' for a level 4 header.
headerStyle, secondaryHeaderStyle, tertairyHeaderStyle	A character value to pre- and append to the header. This can be used to make the header appear bold ('**') or italic ('*') when not using an actual header (see headerPrefix).
separator	Separator to show between sections of output.
suppressPlot	Whether to suppress printing plots.
pValueDigits	Output to produce; see /code/linkrMatrix for details.
info, file	Output to produce and file to write to; see /code/linkassociationMatrix for details.
extraNotification	Whether an extra notification about the type of skewness and kurtosis returned by dataShape is shown.
pvalueDigits	The number of digits to show for p-values; smaller p-values will be shown as <.001 or <.0001 etc.

na.print	What to print for missing values, for example for a oneway anova table.
...	Additional arguments that are passed on to the print functions when it is called.

Value

These printing methods use cat, cat0, and grid.draw to print stuff.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
userfriendlyscience:::pander.oneway(oneway(y=ChickWeight$weight, x=ChickWeight$Diet));
```

---

userfriendlysciencePrintMethods

userfriendlyscience print methods

Description

These methods print the userfriendlyscience objects. Note that they are not all documented; most of them are quite straightforward.

Usage

```
## S3 method for class 'dlvPlot'
print(x, ...)
## S3 method for class 'freq'
print(x, digits=x$input$digits, nsmall=x$input$nsmall,
transposed=x$input$transposed, ...)
## S3 method for class 'meanConfInt'
print(x, digits=2, ...)
## S3 method for class 'meanDiff'
print(x, digits=x$digits,powerDigits=x$digits + 2, ...)
## S3 method for class 'meanDiff.multi'
print(x, digits=x$digits,
powerDigits=x$digits + 2, ...)
## S3 method for class 'normalityAssessment'
print(x, ...)
## S3 method for class 'oddsratio'
print(x, digits=x$input$digits, ...)
## S3 method for class 'powerHist'
print(x, ...)
```

```
## S3 method for class 'rMatrix'
print(x, digits=x$digits, output=x$output,
pValueDigits = x$pValueDigits, env.LaTeX = x$env.LaTeX,
pboxWidthMultiplier = x$pboxWidthMultiplier,
colNames = x$colNames, ...)
## S3 method for class 'scaleDiagnosis'
print(x, ...)
## S3 method for class 'scaleStructure'
print(x, digits=x$input$digits, ...)
## S3 method for class 'sdConfInt'
print(x, digits=2, ...)
## S3 method for class 'testRetestAlpha'
print(x, ...)
## S3 method for class 'testRetestCES'
print(x, digits=x$input$digits, ...)
## S3 method for class 'testRetestReliability'
print(x, digits=x$input$digits, ...)
## S3 method for class 'parallelSubscales'
print(x, nsmall=2, ...)
## S3 method for class 'dataShape'
print(x, digits=x$input$digits, extraNotification=TRUE, ...)
## S3 method for class 'didacticPlot'
print(x, ...)
## S3 method for class 'scatterMatrix'
print(x, ...)
## S3 method for class 'CramersV'
print(x, digits = x$input$digits, ...)
## S3 method for class 'associationMatrix'
print(x, type = x$input$type,
                                info = x$input$info,
                                file = x$input$file, ...)
## S3 method for class 'confIntV'
print(x, digits = x$input$digits, ...)
## S3 method for class 'cohensdCI'
print(x, ...)
## S3 method for class 'crossTab'
print(x, digits = x$input$digits,
                        pValueDigits=x$input$pValueDigits, ...)
## S3 method for class 'oneway'
print(x, digits = x$input$digits,
                      pvalueDigits=x$input$pvalueDigits,
                      na.print="", ...)
## S3 method for class 'posthocTGH'
print(x, digits = x$input$digits, ...)
## S3 method for class 'scaleInspection'
print(x, show=x$show, ...)
## S3 method for class 'regr'
print(x, digits=x$input$digits,
```

```
                    pvalueDigits=x$input$pvalueDigits, ...)
## S3 method for class 'processOpenSesameIAT'
print(x, ...)
## S3 method for class 'processOpenSesameIAT.log'
print(x, ...)
## S3 method for class 'descr'
print(x, digits = attr(x, 'digits'),
                     t = attr(x, "transpose"),
                     row.names = FALSE, ...)
## S3 method for class 'therapyMonitor'
print(x, digits=2, printPlot = TRUE, ...)
## S3 method for class 'therapyMonitor.multi'
print(x, ...)
## S3 method for class 'asymmetricalScatterMatrix'
print(x, ...)
## S3 method for class 'fullFact'
print(x, ...)
## S3 method for class 'confIntOmegaSq'
print(x, ..., digits = 2)
## S3 method for class 'examine'
print(x, ...)
## S3 method for class 'examineBy'
print(x, ...)
## S3 method for class 'frequencies'
print(x, ...)
## S3 method for class 'power.htest.ufs'
print(x, digits = x$digits, ...)
## S3 method for class 'regrInfluential'
print(x, ...)
## S3 method for class 'nnc'
print(x, ...)
```

Arguments

x	The object to print.
digits	The number of significant digits to print.
nsmall	The minimum number of digits to the right of the decimal point in formatting real/complex numbers in non-scientific formats. Allowed values are 0 <= nsmall <= 20.
transposed, t	Whether the frequency object should be printed transposed (this can be useful for blind users).
powerDigits	Number of digits to use when printing the power.
output, env.LaTeX, pboxWidthMultiplier, colNames, pValueDigits	Output to produce; see /code/linkrMatrix for details.
type, info, file	Output to produce and file to write to; see /code/linkassociationMatrix for details.

extraNotification	Whether an extra notification about the type of skewness and kurtosis returned by dataShape is shown.
pvalueDigits	The number of digits to show for p-values; smaller p-values will be shown as <.001 or <.0001 etc.
printPlot	Whether to also print the plot.
na.print	What to print for missing values, for example for a oneway anova table.
show	To override the 'show' argument, which is sometimes used to inhibit printing of extensive information with e.g. many plots, which is useful for some functions that, for example, primarily generate a PDF.
row.names	Whether to print rownames.
...	Addition arguments that are passed on to the print functions when it's called.

Value

These printing methods return nothing, but print stuff.

Author(s)

Gjalt-Jorn Peters

Maintainer: Gjalt-Jorn Peters <gjalt-jorn@userfriendlyscience.com>

Examples

```
print.sdConfInt(sdConfInt(sd=4, n=20));

print(oneway(y=ChickWeight$weight, x=ChickWeight$Diet), na.print="[NO VALUE]");
```

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