Package ‘rosetta’

March 5, 2023

Title Parallel Use of Statistical Packages in Teaching
Version 0.3.12
Description When teaching statistics, it can often be desirable to uncouple the content from specific software packages. To ease such efforts, the Rosetta Stats website (<https://rosettastats.com>) allows comparing analyses in different packages. This package is the companion to the Rosetta Stats website, aiming to provide functions that produce output that is similar to output from other statistical packages, thereby facilitating 'software-agnostic' teaching of statistics.
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buildModMedSemModel

Builds model for moderated mediation analysis using SEM

Usage

buildModMedSemModel(
  xvar,
  mvars,
  yvar,
  xmmod = NULL,
  mymod = NULL,
  cmvars = NULL,
  cyvars = NULL
)

Arguments

xvar      independent variable (predictor)
mvars     vector of names of mediators
yvar      dependent variable
xmmod     moderator of a path(s)
mymod     moderator of b path(s)
cmvars    covariates for predicting the mediators
cyvars    covariates for predicting the dependent variable

Value

lavaan model to be used in mediatedMediationSem

Examples

model <- buildModMedSemModel(xvar="procJustice", mvars= c("cynicism"),
yvar = "CPB", xmmod = "insecure",mymod = "gender", cmvars =c("age"))
**cat0**

*Concatenate to screen without spaces*

**Description**

The `cat0` function is to `cat` what `paste0` is to `paste`; it simply makes concatenating many strings without a separator easier.

**Usage**

```r
cat0(..., sep = "")
```

**Arguments**

- `...`: The character vector(s) to print; passed to `cat`.
- `sep`: The separator to pass to `cat`, of course, "" by default.

**Value**

Nothing (invisible NULL, like `cat`).

**Examples**

```r
cat0("The first variable is ", names(mtcars)[1], ".")
```

---

**confIntSD**

*Confidence interval for standard deviation*

**Description**

This function is vectorized.

**Usage**

```r
confIntSD(x, n = NULL, conf.level = 0.95)
```

**Arguments**

- `x`: Either a standard deviation, in which case `n` must also be provided, or a vector, in which case `n` must be NULL.
- `n`: The sample size is `x` is a standard deviation.
- `conf.level`: The confidence level

**Value**

A vector or matrix.
Examples

rosetta::confIntSD(mtcars$mpg);
rosetta::confIntSD(c(6, 7), c(32, 32));

Description

The data are about the attitudes of employees of an organisation that is in the middle of a reorganization. The model predicts that feelings of procedural injustice may lead to cynicism and less trust in the management. This relation may be stronger among employees who are insecure about their job continuation. Cynicism may lead to contra-productive behaviour (CPB). However, strong personal norms may prevent CPB. Cynicism is expected to increase with age, and men may be more inclined towards CPB than women.

Usage

cpbExample

Format

A data frame with 320 rows and 8 variables:

gender  gender participant
age  age participant
procJustice  procedural justice
trust  trust in management
cynicism  cynicism about the management
CPB  contra-productive behaviour
insecure  insecure about job continuation
norms  personal norms about CPB
Description

This function produces a cross table, computes Chi Square, and computes the point estimate and confidence interval for Cramer’s V.

Usage

```r
crossTab(x, y = NULL, conf.level = 0.95, digits = 2, pValueDigits = 3, ...)
```

```r
## S3 method for class 'crossTab'
print(x, digits = x$input$digits, pValueDigits = x$input$pValueDigits, ...)
```

```r
## S3 method for class 'crossTab'
pander(x, digits = x$input$digits, pValueDigits = x$input$pValueDigits, ...)
```

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.

- **conf.level**: Level of confidence for the confidence interval.

- **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.

- **...**: Extra arguments to `crossTab` are passed on to `ufs::confIntV()`.

Value

The results of `ufs::confIntV()`, but also prints the cross table and the chi square test results.

Examples

```r
crossTab(infert$education, infert$induced, samples=50);
```
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,
  items = names(x),
  varLabels = NULL,
  mean = TRUE,
  meanCI = TRUE,
  median = TRUE,
  mode = TRUE,
  var = TRUE,
  sd = TRUE,
  se = FALSE,
  min = TRUE,
  max = TRUE,
  q1 = FALSE,
  q3 = FALSE,
  IQR = FALSE,
  skewness = TRUE,
  kurtosis = TRUE,
  dip = TRUE,
  totalN = TRUE,
  missingN = TRUE,
  validN = TRUE,
  histogram = FALSE,
  boxplot = FALSE,
  digits = 2,
  errorOnFactor = FALSE,
  convertFactor = FALSE,
  maxModes = 1,
  maxPlotCols = 4,
  t = FALSE,
  headingLevel = 3,
  conf.level = 0.95,
  quantileType = 2
)

rosettaDescr_partial(
  x,
digits = attr(x, "digits"),
show = attr(x, "show"),
headingLevel = attr(x, "headingLevel"),
maxPlotCols = attr(x, "maxPlotCols"),
echoPartial = FALSE,
partialFile = NULL,
quiet = TRUE,
...)

## S3 method for class 'rosettaDescr'
knit_print(
x,
digits = attr(x, "digits"),
show = attr(x, "show"),
headingLevel = attr(x, "headingLevel"),
maxPlotCols = attr(x, "maxPlotCols"),
echoPartial = FALSE,
partialFile = NULL,
quiet = TRUE,
...)

## S3 method for class 'rosettaDescr'
print(
x,
digits = attr(x, "digits"),
show = attr(x, "show"),
maxPlotCols = attr(x, "maxPlotCols"),
headingLevel = attr(x, "headingLevel"),
forceKnitrOutput = FALSE,
...
)

Arguments

x The object to print (i.e. as produced by descr).

items Optionally, if x is a data frame, the variable names for which to produce the descriptives.

varLabels Optionally, a named vector with 'pretty labels' to show for the variables. This has to be a vector of the same length as items, and if it is not a named vector with the names corresponding to the items, it has to be in the same order.

mean, meanCI, median, mode

Whether to compute the mean, its confidence interval, the median, and/or the mode (all logical, so TRUE or FALSE).

var, sd, se

Whether to compute the variance, standard deviation, and standard error (all logical, so TRUE or FALSE).
min, max, q1, q3, IQR
   Whether to compute the minimum, maximum, first and third quartile, and interquartile range (all logical, so TRUE or FALSE).

skewness, kurtosis, dip
   Whether to compute the skewness, kurtosis and dip test (all logical, so TRUE or FALSE).

totalN, missingN, validN
   Whether to show the total sample size, the number of missing values, and the number of valid (i.e. non-missing) values (all logical, so TRUE or FALSE).

histogram, boxplot
   Whether to show a histogram and/or boxplot

digits
   The number of digits to round the results to when showing them.

errorOnFactor, convertFactor
   If errorOnFactor is TRUE, factors throw an error. If not, if convertFactor is TRUE, they will be converted to numeric values using as.numeric(as.character(x)), and then the same output will be generated as for numeric variables. If convertFactor is false, the frequency table will be produced.

maxModes
   Maximum number of modes to display: displays "multi" if more than this number of modes if found.

maxPlotCols
   The maximum number of columns when plotting multiple histograms and/or boxplots.

t
   Whether to transpose the dataframes when printing them to the screen (this is easier for users relying on screen readers). **Note: this functionality has not yet been implemented!**

headingLevel
   The number of hashes to print in front of the headings when printing while knitting

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.

show
   A vector of elements to show in the results, based on the arguments that activate/deactivate the descriptives (from mean to validN).

echoPartial
   Whether to show the executed code in the R Markdown partial (TRUE) or not (FALSE).

partialFile
   This can be used to specify a custom partial file. The file will have object x available.

quiet
   Passed on to knitr::knit() whether it should be chatty (FALSE) or quiet (TRUE).

... Any additional arguments are passed to the default print method by the print method, and to rmdpartials::partial() when knitting an RMarkdown partial.

forceKnitrOutput
   Force knitr output.
Details

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

The Hartigans’ Dip Test may be unfamiliar to users; it is a measure of uni- vs. multimodality, computed by the `dip.test()` function from the `{diptest}` package from the. 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 that `dip.test()` function from `{diptest}`; 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)

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References


See Also

`summary`, `[psych::describe()`

Examples

```r
### Simplest example with default settings
descr(mtcars$mpg);

### Also requesting a histogram and boxplot
descr(mtcars$mpg, histogram=TRUE, boxplot=TRUE);

### To show the output as Rmd Partial in the viewer
rosetta::rosettaDescr_partial(
  rosetta::descr(
    mtcars$mpg
  )
);

### Multiple variables, including one factor
rosetta::rosettaDescr_partial(
  rosetta::descr(
    iris
  )
);
```
### descriptiveCIs

**Descriptives with confidence intervals**

#### Description
Descriptives with confidence intervals

#### Usage

```r
descriptiveCIs(  
data,  
items = NULL,  
itemLabels = NULL,  
conf.level = 0.95,  
digits = 2  
)
```

```r
## S3 method for class 'rosettaDescriptiveCIs'
print(x, digits = attr(x, "digits"), forceKnitrOutput = FALSE, ...)
```

#### Arguments

- **data**
  The data frame holding the data, or a vector.
- **items**
  If supplying a data frame as `data`, the names of the columns to process.
- **itemLabels**
  Optionally, labels to use for the items (optionally, named, with the names corresponding to the items; otherwise, the order of the labels has to match the order of the items).
- **conf.level**
  The confidence level of the confidence intervals.
- **digits**
  The number of digits to round the output to.
- **x**
  The object to print (i.e. the object returned by `descriptiveCIs`).
- **forceKnitrOutput**
  Whether to force `knitr` output even when not knitting.
- **...**
  Any additional arguments are passed on to `knitr::kable()` or to `base::print()`.

#### Value
A data frame with class `rosettaDescriptiveCIs` prepended to allow printing neatly while knitting to Markdown.

#### Examples
```r
descriptiveCIs(mtcars);
```
### dlvPlot

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

#### Usage

```r
dlvTheme(base_size = 11, base_family = "", ...)  
dlvPlot(
  dat,
  x = NULL,
  y,
  z = NULL,
  conf.level = 0.95,
  jitter = "FALSE",
  binnedDots = TRUE,
  binwidth = NULL,
  error = "lines",
  dotsize = "density",
  singleColor = "black",
  comparisonColors = rosetta::opts$­get("dlvPlotCompCols"),
  densityDotBaseSize = 3,
  normalDotBaseSize = 1,
  violinAlpha = 0.2,
  dotAlpha = 0.4,
  lineAlpha = 1,
  connectingLineAlpha = 1,
  meanDotSize = 5,
  posDodge = 0.2,
  errorType = "both",
  outputFile = NULL,
  outputWidth = 10,
  outputHeight = 10,
  ggsaveParams = list(units = "cm", dpi = 300, type = "cairo")
)
```

#### Arguments

- `base_size`, `base_family`, ...
  - Passed on to the `ggplot theme_grey()` function.
- `dat`
  - The dataframe containing x, y and z.

---

### dlvTheme

The `dlvTheme` function sets the theme for the `dlvPlot` function.

#### Usage

```r
dlvTheme(base_size = 11, base_family = "", ...)  
```

#### Arguments

- `base_size`, `base_family`, ...
  - Passed on to the `theme_grey()` function.
Character value with the name of the predictor ('independent') variable, must refer to a categorical variable (i.e. a factor).

Character value with the name of the criterion ('dependent') variable, must refer to a continuous variable (i.e. a numeric vector).

Character value with the name of the moderator variable, must refer to a categorical variable (i.e. a factor).

Confidence of confidence intervals.

Logical value (i.e. TRUE or FALSE) whether or not to jitter individual data-points. Note that jitter cannot be combined with posDodge (see below).

Logical value indicating whether to use binning to display the dots. Overrides jitter and dotsize.

Numeric value indicating how broadly to bin (larger values is more binning, i.e. combining more dots into one big dot).

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)

Character value: "density" or "normal"; when "density", the size of each dot corresponds to the density of the distribution at that point.

The color to use when drawing one or more univariate distributions (i.e. when no z is specified).

The colors to use when a z is specified. This should be at least as many colors as z has levels. By default, palette Set1 from RColorBrewer is used.

Numeric value indicating base size of dots when their size corresponds to the density (bigger = larger dots).

Numeric value indicating base size of dots when their size is fixed (bigger = larger dots).

Numeric value indicating alpha value of violin layer (0 = completely transparent, 1 = completely opaque).

Numeric value indicating alpha value of dot layer (0 = completely transparent, 1 = completely opaque).

Numeric value indicating alpha value of the confidence interval line layer (0 = completely transparent, 1 = completely opaque).

Numeric value indicating alpha value of the layer with the lines connecting the means (0 = completely transparent, 1 = completely opaque).

Numeric value indicating the size of the dot used to indicate the mean in the line layer.

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 error-bars 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.

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.

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
### 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)

---

### 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, 
  qqCI = TRUE, 
  conf.level = 0.95 
)
```

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

```
# S3 method for class 'examine'
pander(
  x, 
  headerPrefix = "", 
  headerStyle = "**", 
  secondaryHeaderPrefix = "", 
  secondaryHeaderStyle = "*", 
  ...
)
```

examineBy(  

...,
  by = NULL,
  stem = TRUE,
  plots = TRUE,
  extremeValues = 5,
  qqCI = TRUE,
  conf.level = 0.95
)

## S3 method for class 'examineBy'
print(x, ...)

## S3 method for class 'examineBy'
pander(
  x,
  headerPrefix = "",
  headerStyle = "**",
  secondaryHeaderPrefix = "",
  secondaryHeaderStyle = "*",
  tertiaryHeaderPrefix = "-->",
  tertiaryHeaderStyle = "",
  separator = paste0("\n\n", repStr("--", 10), "\n\n"),
  ...
)

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.

stem Whether to display a stem and leaf plot.

plots Whether to display the plots generated by the ufs::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.

conf.level The level of confidence of the confidence interval.

x The object to print or pander.

headerPrefix, secondaryHeaderPrefix, tertiaryHeaderPrefix Prefixes for the primary, secondary header, and tertiary headers

headerStyle, secondaryHeaderStyle, tertiaryHeaderStyle Characteres to surround the primary, secondary, and tertiary headers with

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.

separator Separator for the result blocks.
exportToSPSS

Details

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

Value

A list that is displayed when printed.

Author(s)

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Examples

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

### Separate for the different number of cylinders:
rosetta::examineBy(mtcars$mpg, by=mtcars$cyl, stem=FALSE, plots=FALSE, extremeValues=FALSE);

---

**exportToSPSS**  
*Basic SPSS translation functions*

Description

Basic functions 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

```r
exportToSPSS(
  dat,  
savfile = NULL,  
datafile = NULL,  
codefile = NULL,  
fileEncoding = "UTF-8",  
newLinesInString = " |n| "
)
```
filterBy(
  dat,
  expression,
  replaceOriginalDataframe = TRUE,
  envir = parent.frame()
)

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)

mediaan(vector)

modus(vector)

useAll(dat, replaceFilteredDataframe = TRUE)

Arguments

dat          Dataframe to process: for filterBy, dataframe to filter rows from; for useAll, dataframe to restore ('unfilter').
savfile      The name of the SPSS format .sav file (alternative for writing a datafile and a codefile).
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.
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.

**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; "[defaultValueMessage]" 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.

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

**replaceFilteredDataFrame**
Whether to replace the filtered dataframe passed in the ’dat’ argument (see replaceOriginalDataFrame).

### Value

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

gDat is a simple wrapper for gData() which creates a dataframe in the parent environment, by default with the name ‘dat’. Therefore, calling gDat() 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. gDat() 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

gData() 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 Omega-Hat 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

```r
## Not run:
### Open a dialogue to read an SPSS file
gData();
### Get a median and a mode
median(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));
```
factorAnalysis

loadings = TRUE,
summary = FALSE,
correlations = FALSE,
modelFit = FALSE,
eigenValues = FALSE,
screenPlot = FALSE,
residuals = FALSE,
itemLabels = items,
colorLoadings = FALSE,
fm = "minres",
digits = 2,
headingLevel = 3,
...
)

principalComponentAnalysis(
data,
items,
nfactors,
rotate = "oblimin",
covar = FALSE,
na.rm = TRUE,
kaiser = 1,
loadings = TRUE,
summary = FALSE,
correlations = FALSE,
eigenValues = FALSE,
screenPlot = FALSE,
residuals = FALSE,
itemLabels = items,
colorLoadings = FALSE,
digits = 2,
headingLevel = 3,
...
)

rosettaDataReduction_partial(
x,
digits = x$input$digits,
headingLevel = x$input$headingLevel,
echoPartial = x$input$headingLevel,
partialFile = NULL,
quiet = TRUE,
...
)

## S3 method for class 'rosettaDataReduction'
knit_print(
x,
digits = x$input$digits,
headingLevel = x$input$headingLevel,
echoPartial = FALSE,
partialFile = NULL,
quiet = TRUE,
...
)

## S3 method for class 'rosettaDataReduction'
print(
  x,
  digits = x$input$digits,
  headingLevel = x$input$headingLevel,
  forceKnitrOutput = FALSE,
  ...
)

Arguments

data The data frame that contains the items.
nfactors The number of factors to extract, or 'eigen' to extract all factors with an eigen value higher than the number specified in kaiser. In the future, parallel can be specified here to extract the number of factors suggested by parallel analysis.
items The items to analyse; if not specified, all variables in data will be used.
rotate Which rotation to use; see psych::fa() for all options. The most common options are 'none' to not rotate at all; 'varimax' for an orthogonal rotation (assuming/imposing that the components or factors are not correlated); or 'oblimin' for an oblique rotation (allowing the components/factors to correlate).
covar Whether to analyse the correlation matrix (FALSE) or the covariance matrix (TRUE).
na.rm Whether to first remove all cases with missing values.
kaiser The minimum eigenvalue when applying the Kaiser criterion (see nfactors).
loadings Whether to display the component or factor loadings.
summary Whether to display the factor or component summary.
correlations Whether to display the correlations between factors of components.
modelFit Whether to display the model fit Only for EFA).
eigenValues Whether to display the eigen values.
screePlot Whether to display the scree plot.
residuals Whether to display the matrix with residuals.
itemLabels Optionally, labels to use for the items (optionally, named, with the names corresponding to the items; otherwise, the order of the labels has to match the order of the items)
colorLoadings Whether, when producing an Rmd partial (i.e. when calling the command while knitting) to colour the cells using kableExtra::kable_styling().
factorAnalysis

- **fm** The method to use for the factor analysis: 'fm' for Minimum Residuals; 'ml' for Maximum Likelihood; and 'pa' for Principal Factor.
- **digits** The number of digits to round to.
- **headingLevel** The number of hashes to print in front of the headings when printing while knitting...
- **x** The object to print.
- **echoPartial** Whether to show the executed code in the R Markdown partial (TRUE) or not (FALSE).
- **partialFile** This can be used to specify a custom partial file. The file will have object x available.
- **quiet** Passed on to knitr::knit() whether it should be chatty (FALSE) or quiet (TRUE).
- **forceKnitrOutput** Force knitr output.

**Details**

The code in these functions uses parts of the code in jamovi, written by Jonathon Love and Ravi Selker.

**Value**

An object with the object resulting from the call to the psych functions and some extracted information that will be printed.

**Examples**

```r
### Load example dataset
data("pp15", package="rosetta");

### Get variable names with expected ### effects of a high dose of MDMA
items <-
grep(
  "highDose_AttBeliefs_",
  names(pp15),
  value=TRUE
);

### Do a factor analysis
rosetta::factorAnalysis(
data = pp15,
items = items,
nfactors = "eigen",
scree = TRUE
);
```
if (FALSE) {
  ### To get more output, show the
  ### output as Rmd Partial in the viewer,
  ### and color/size the factor loadings
  rosetta::rosettaDataReduction_partial(
    rosetta::factorAnalysis(
      data = pp15,
      items = items,
      nfactors = "eigen",
      summary = TRUE,
      correlations = TRUE,
      colorLoadings = TRUE
    )
  );
}

---

factorAnalysisjmv  
Factor Analysis

### Description

Factor Analysis

### Usage

factorAnalysisjmv(
  data,
  items,
  nFactorMethod = "eigen",
  nFactors = 1,
  minEigen = 1,
  extraction = "minres",
  rotation = "oblimin",
  colorLoadings = TRUE,
  screePlot = FALSE,
  eigen = FALSE,
  factorCor = FALSE,
  factorSummary = FALSE,
  modelFit = FALSE
)

### Arguments

- **data**: the data as a data frame
- **items**: a vector of strings naming the variables of interest in data
- **nFactorMethod**:
fanova

fanova

Flexible anova

Description
This function is meant as a user friendly wrapper to approximate the way analysis of variance is done in SPSS.

Usage
fanova(
data,    
y,    
between = NULL,    
covar = NULL,    
withinReference = 1,    
betweenReference = NULL,    
withinNames = NULL,    
plot = FALSE,    
levene = FALSE,    
digits = 2,
contrast = NULL
)

## S3 method for class 'fanova'
print(x, digits = x$input$digits, ...)

### Arguments

data  The dataset containing the variables to analyse.
y    The dependent variable. For one-way anova, factorial anova, or ancova, this is the name of a variable in dataframe data. For repeated measures anova, this is a vector with the names of all variable names in dataframe data, e.g. c('t0_value', 't1_value','t2_value').
between A vector with the variables name(s) of the between subjects factor(s).
covar  A vector with the variables name(s) of the covariate(s).
withinReference Number of reference category (variable) for within subjects treatment contrast (dummy).
betweenReference Name of reference category for between subject factor in RM anova.
withinNames Names of within subjects categories (dependent variables).
plot    Whether to produce a plot. Note that a plot is only produced for one-way and twoway anova and one-way repeated measures designs: if covariates or more than two between-subjects factors are specified, no plot is produced. For twoway anova designs, the second predictor is plotted as moderator (and the first predictor is plotted on the x axis).
levene  Whether to show Levene's test for equality of variances (using car's leveneTest function but specifying mean as function to compute the center of each group).
digits Number of digits (actually: decimals) to use when printing results. The p-value is printed with one extra digit.
contrast This functionality has been implemented for repeated measures only.
x The object to print (i.e. as produced by regr).
... Any additional arguments are ignored.

### Details

This wrapper uses oneway and lm and lmer in combination with car's Anova function to conduct the analysis of variance.

### Value

Mainly, this function prints its results, but it also returns them in an object containing three lists:

input  The arguments specified when calling the function
intermediate Intermediat objects and values
output  The results such as the plot.
formatPvalue

Pretty formatting of p values

Description

Pretty formatting of p values

Usage

formatPvalue(values, digits = 3, spaces = TRUE, includeP = TRUE)
Arguments

values  The p-values to format.
digits  The number of digits to round to. Numbers smaller than this number will be shown as <.001 or <.0001 etc.
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).

Value

A formatted P value, roughly according to APA style guidelines. This means that the noZero function 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.

See Also

formatCI(), formatR(), noZero()

Examples

```r
formatPvalue(cor.test(mtcars$mpg, mtcars$disp)$p.value);
formatPvalue(cor.test(mtcars$drat, mtcars$qsec)$p.value);
```

---

formatR  

Pretty formatting of correlation coefficients

Description

Pretty formatting of correlation coefficients

Usage

```r
formatR(r, digits = 2)
```

Arguments

r  The Pearson correlation to format.
digits  The number of digits to round to.

Value

The formatted correlation.
freq

See Also

noZero(), formatCI(), formatPvalue()

Examples

formatR(cor(mtcars$mpg, mtcars$disp));

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 = ggplot2::theme_bw()
)

## S3 method for class 'freq'
print(
  x,
  digits = x$input$digits,
  nsmall = x$input$nsmall,
  transposed = x$input$transposed,
  ...
)

## S3 method for class 'freq'
pander(x, ...)

frequencies(
  ..., 
  digits = 1,
  nsmall = 1,
  transposed = FALSE,
  round = 1,
  plot = FALSE,
  plotTheme = ggplot2::theme_bw()
## S3 method for class 'frequencies'
print(x, ...)

## S3 method for class 'frequencies'
pander(x, prefix = "###", ...)

### 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.

- **x**
  The freq or frequencies object to print.

- **...**
  For frequencies, the variables of which to provide frequencies; for the print methods, additional arguments are passed on to the print function.

- **prefix**
  The prefix to use when printing frequencies, to easily prepend Markdown headers.

### 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

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

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

---

**freqjmv**

**Frequencies**

**Description**

Frequencies

**Usage**

`freqjmv(data, vector)`

**Arguments**

- `data`
- `vector`

**Value**

A results object containing:

```
results$table  a table
```

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$table$asDF
as.data.frame(results$table)
```

---

**gemm**

**Analyze moderated mediation model using SEM**

**Description**

Analyze moderated mediation model using SEM

**Usage**

```r
gemm(
    data = NULL,
    xvar,
    mvars,
```
ggBarChart

Bar chart using ggplot

Description

This function provides a simple interface to create a `ggplot2::ggplot()` bar chart.
**ggBoxplot**

**Usage**

```r
ggBoxplot(  
  dat,
  y = NULL,
  x = NULL,
  labelOutliers = TRUE,
  outlierColor = "red",
  theme = ggplot2::theme_bw(),
  ...
)
```

**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.
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 https://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');
Description

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

Usage

```r
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 = ggplot2::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 level around the estimate for the specified distribution.
- **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 `ufs::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.
ggScatterPlot

```
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 https://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);
```

---

### ggScatterPlot  

Bar chart using `ggplot`

Description

This function provides a simple interface to create a `ggplot2::ggplot()` bar chart.

Usage

```
ggScatterPlot(
  x, 
  y, 
  jitter = TRUE, 
  size = 3, 
  alpha = 0.66, 
  shape = 16, 
  color = "black", 
  fill = "black", 
  stroke = 1, 
  plotTheme = ggplot2::theme_bw(), 
  ...
)
```
histogram

Arguments

- **x, y**  The vectors to display in the scatter plot. Alternatively, x can be a data frame; then y has to be a vector with (numeric or character) indices, e.g. column names.
- **jitter**  Whether to jitter the points (TRUE by default).
- **size, alpha, shape, color, fill, stroke**  Quick way to set the aesthetics.
- **plotTheme**  The theme to apply.
- **...**  And additional arguments are passed to `ggplot2::geom_point()`.

Value

A `ggplot2::ggplot()` plot is returned.

See Also

`ggplot2::geom_point()`

Examples

```r
rosetta::ggScatterPlot(mtcars$hp, mtcars$mpg);
```

---

**histogram**  
*Simple function to create a histogram*

Description

Simple function to create a histogram

Usage

```r
histogram(
  vector,
  bins = NULL,
  theme = ggplot2::theme_bw(),
  xLabel = NULL,
  yLabel = "Count"
)
```

Arguments

- **vector**  A variable or vector.
- **bins**  The number of bins; when 0, either the number of unique values in vector or 20, whichever is lower.
- **theme**  The ggplot2 theme to use.
- **xLabel, yLabel**  Labels for x and y axes; variable name is used for x axis if no label is specified.
This function is meant as a user-friendly wrapper to approximate the way logistic regression is done in SPSS.

Usage

```r
def logRegr(
  formula,
  data = NULL,
  conf.level = 0.95,
  digits = 2,
  predictGroupValue = NULL,
  comparisonGroupValue = NULL,
  pvalueDigits = 3,
  crossTabs = TRUE,
  oddsRatios = TRUE,
  plot = FALSE,
  collinearity = FALSE,
  env = parent.frame(),
  predictionColor = rosetta::opts$get("viridis3")[3],
  predictionAlpha = 0.5,
  predictionSize = 2,
  dataColor = rosetta::opts$get("viridis3")[1],
  dataAlpha = 0.33,
  dataSize = 2,
  observedMeansColor = rosetta::opts$get("viridis3")[2],
  binObservedMeans = 7,
  observedMeansSize = 2,
  observedMeansWidth = NULL,
  observedMeansAlpha = 0.5,
  theme = ggplot2::theme_bw(),
  headingLevel = 3
)
```

```r
rosettaLogRegr_partial(
  x,
  
```
logRegr

digits = x$input$digits,
pvalueDigits = x$input$pvalueDigits,
headingLevel = x$input$headingLevel,
echoPartial = FALSE,
partialFile = NULL,
quiet = TRUE,
...
)

## S3 method for class 'rosettaLogRegr'
knit_print(
  x,
  digits = x$input$digits,
  headingLevel = x$input$headingLevel,
pvalueDigits = x$input$pvalueDigits,
  echoPartial = FALSE,
  partialFile = NULL,
  quiet = TRUE,
  ...
)

## S3 method for class 'rosettaLogRegr'
print(
  x,
  digits = x$input$digits,
pvalueDigits = x$input$pvalueDigits,
  headingLevel = x$input$headingLevel,
  forceKnitrOutput = FALSE,
  ...
)

Arguments

formula          The formula, specified in the same way as for stats::glm() (which is used for the actual analysis).
data             Optionally, a dataset containing the variables in the formula (if not specified, the variables must exist in the environment specified in env).
conf.level       The confidence level for the confidence intervals.
digits           The number of digits used when printing the results.
predictGroupValue, comparisonGroupValue Can optionally be used to set the value to predict and the value to compare with.
pvalueDigits     The number of digits used when printing the p-values.
crossTabs        Whether to show cross tabulations of the correct predictions for the null model and the tested model, as well as the percentage of correct predictions.
oddsRatios       Whether to also present the regression coefficients as odds ratios (i.e. simply after a call to base::exp()).
plot             Whether to display the plot.
collinearity  Whether to show collinearity diagnostics.

env  If no dataframe is specified in data, use this argument to specify the environment holding the variables in the formula.

predictionColor, dataColor, observedMeansColor
  The color of, respectively, the line and confidence interval showing the prediction; the points representing the observed data points; and the means based on the observed data.

predictionAlpha, dataAlpha, observedMeansAlpha
  The alpha of, respectively, the confidence interval of the prediction; the points representing the observed data points; and the means based on the observed data (set to 0 to hide an element).

predictionSize, dataSize, observedMeansSize
  The size of, respectively, the line of the prediction; the points representing the observed data points; and the means based on the observed data (set to 0 to hide an element).

binObservedMeans
  Whether to bin the observed means; either FALSE or a single numeric value specifying the number of bins.

observedMeansWidth
  The width of the lines of the observed means. If not specified (i.e. NULL), this is computed automatically and set to the length of the shortest interval between two successive points in the predictor data series (found using ufs::findShortestInterval()).

theme
  The theme used to display the plot.

headingLevel
  The number of hashes to print in front of the headings

x
  The object to print (i.e. as produced by rosetta::logRegr).

echoPartial
  Whether to show the executed code in the R Markdown partial (TRUE) or not (FALSE).

partialFile
  This can be used to specify a custom partial file. The file will have object x available.

quiet
  Passed on to knitr::knit() whether it should be chatty (FALSE) or quiet (TRUE).

...
  Any additional arguments are passed to the default print method by the print method, and to rmdpartials::partial() when knitting an RMarkdown partial.

forceKnitrOutput
  Force knitr output.

Value

Mainly, this function prints its results, but it also returns them in an object containing three lists:

input
  The arguments specified when calling the function

intermediate
  Intermediate objects and values

output
  The results, such as the plot, the cross tables, and the coefficients.
### Simplest way to call logRegr
rosetta::logRegr(data=mtcars, formula = vs ~ mpg);

### Also ordering a plot
rosetta::logRegr(
  data=mtcars,
  formula = vs ~ mpg,
  plot=TRUE
);

### Only use five bins
rosetta::logRegr(
  data=mtcars,
  formula = vs ~ mpg,
  plot=TRUE,
  binObservedMeans=5
);

## Not run:
### Mimic output that would be obtained
### when calling from an R Markdown file
rosetta::rosettaLogRegr_partial(
  rosetta::logRegr(
    data=mtcars,
    formula = vs ~ mpg,
    plot=TRUE
  )
);

## End(Not run)
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

```r
meanDiff(
  x,
  y = NULL,
  paired = FALSE,
  r.prepost = NULL,
  var.equal = "test",
  conf.level = 0.95,
  plot = FALSE,
  digits = 2,
  envir = parent.frame()
)
```

## S3 method for class 'meanDiff'
print(x, digits = x$digits, powerDigits = x$digits + 2, ...)

## S3 method for class 'meanDiff'
pander(x, digits = x$digits, powerDigits = x$digits + 2, ...)

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.
meanDiff

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 function’s environment).

powerDigits With what precision you want the power to print.

... Additional arguments are passed on to the ggplot2::ggplot() print method.

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

cl.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


Examples

```r
### 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

```r
meanDiff(x = dat$group, y = dat$weight);
```

---

**Description**

The `meanDiff.multi` function compares many means for many groups. It presents the results in a dataframe summarizing all relevant information, and produces a 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**

```r
meanDiff.multi(
  dat,
  y,
  x = NULL,
  var.equal = "yes",
  conf.level = 0.95,
  digits = 2,
  orientation = "vertical",
  zeroLineColor = "grey",
  zeroLineSize = 1.2,
  envir = parent.frame()
)
```

```r
## S3 method for class 'meanDiff.multi'
print(x, digits = x$ digits, powerDigits = x$ digits + 2, ...)
```

**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).
-powerDigits With what precision you want the power to print.
...
Additional arguments are passed on to the meanDiff() print methods.

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


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
means

\[
\text{meanDiff.multi}(\text{dat}, x=c(\text{'x1'}, \text{'x2'}), y=\text{'y'}, \text{var.equal}="\text{yes}");
\]

---

**means**

**Compute means and sums**

**Description**

These functions allow easily computing means and sums. Note that if you attach rosetta to the search path.

**Usage**

```r
means(
  ..., 
  data = NULL, 
  requiredValidValues = 0, 
  returnIfInvalid = NA, 
  silent = FALSE 
)

sums(
  ..., 
  data = NULL, 
  requiredValidValues = 0, 
  returnIfInvalid = NA, 
  silent = FALSE 
)
```

**Arguments**

- `...`: The dataframe or vectors for which to compute the means or sums. When passing a dataframe as an unnamed argument (i.e. in the "dots", 
  ...), the means or sums for all columns in the dataframe will be computed. If you want to select one or more columns, make sure to pass the dataframe as `data`. 
- `data`: If a dataframe is passed as `data`, the values passed in the "dots" (...) will be taken as column names or indices in that dataframe. This allows easy indexing. 
- `requiredValidValues`: The number (if larger than 1) or proportion (if between 0 and 1) of values that have to be valid (i.e. nonmissing) before the mean or sum is returned. 
- `returnIfInvalid`: Which value to return for rows not meeting the criterion specified in `requiredValidValues`. 
- `silent`: Whether to suppress messages.

**Value**

The means or sums.
Examples

rosetta::means(mtcars$mpg, mtcars$disp, mtcars$wt);
rosetta::means(data=mtcars, 'mpg', 'disp', 'wt');
rosetta::sums(mtcars$mpg, mtcars$disp, mtcars$wt);
rosetta::sums(data=mtcars, 'mpg', 'disp', 'wt');

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 = 0.95,
  posthocLetters = FALSE,
  posthocLetterAlpha = 0.05,
  overrideVarNames = NULL,
  silent = FALSE
)

## S3 method for class 'oneway'
print(
  x,
  digits = x$input$digits,
  pvalueDigits = x$input$pvalueDigits,
  na.print = "",
  ...
)

## S3 method for class 'oneway'
pander(
  x,
  digits = x$input$digits,
  pvalueDigits = x$input$pvalueDigits,
  headerStyle = "**",
  na.print = "",
  ...
)

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 (using car's `leveneTest` function but specifying `mean` as function to compute the center of each group).

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

posthocLetters Whether to also compute and show the letters signifying differences between groups when conducting post hoc tests. This requires package multcompView to be installed.
posthocLetterAlpha
  The alpha to use when determining whether groups have different means when using posthocLetters.

overrideVarNames
  Can be used to override the variable names (most useful in functions).

silent
  Whether to show warnings and other diagnostic information or remain silent.

na.print
  How to print missing values.

...  
  Any additional arguments are passed to the print or pander function.

headerStyle
  The header pre- and suffix to use when pandering the result (useful when working with Markdown).

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


Examples

```r
### Do a oneway Anova
oneway(y=ChickWeight$weight, x=ChickWeight$Diet);
```
### Also order means and transpose the results

```r
oneway(y=ChickWeight$weight, x=ChickWeight$Diet, means=TRUE, t=TRUE);
```

---

**Options for the rosetta package**

**Description**

The `rosetta::opts` object contains three functions to set, get, and reset options used by the rosetta package. Use `rosetta::opts$set` to set options, `rosetta::opts$get` to get options, or `rosetta::opts$reset` to reset specific or all options to their default values.

**Usage**

```r
opts
```

**Format**

An object of class `list` of length 4.

**Details**

It is normally not necessary to get or set `rosetta` options. The following arguments can be passed:

- `...` For `rosetta::opts$set`, the dots can be used to specify the options to set, in the format `option = value`, for example, `varViewCols = c("values", "level")`. For `rosetta::opts$reset`, a list of options to be reset can be passed.
  - `option` For `rosetta::opts$set`, the name of the option to set.
  - `default` For `rosetta::opts$get`, the default value to return if the option has not been manually specified.

The following options can be set:

- `varViewCols` The order and names of the columns to include in the variable view.
- `showLabellerWarning` Whether to show a warning if labeller labels are encountered.

**Examples**

```r
### Get the default columns in the variable view
rosetta::opts$get(varViewCols);

### Set it to a custom version
rosetta::opts$set(varViewCols = c("values","level"));

### Check that it worked
rosetta::opts$get(varViewCols);
```
partypanelData

### Reset this option to its default value
rosetta::opts$reset(varViewCols);

### Check that the reset worked, too
rosetta::opts$get(varViewCols);

---

**partypanelData**  
*Subsets of the Party Panel 2015 dataset*

**Description**

This is a subsets of the Party Panel 2015 dataset. Party Panel is an annual semi-panel determinant study among Dutch nightlife patrons, where every year, the determinants of another nightlife-related risk behavior are mapped. In 2015, determinants were measured of behaviors related to using highly dosed ecstasy pills.

**Usage**

```r
data(pp15)
```

**Format**

A `data.frame` with 128 columns and 829 rows. Note that many rows contain missing values; the columns and rows were taken directly from the original Party Panel dataset, and represent all participants that made it past a given behavior.

**Details**

The full dataset is publicly available through the Open Science Framework (https://osf.io/s4fmu/). Also see the GitLab repository (https://gitlab.com/partypanel) and the website at https://partypanel.eu.

**Examples**

```r
data('pp15', package='rosetta');
rosetta::freq(pp15$gender);
```
plotIMM

Makes plot of Index of Moderated Mediation of gemm object

Description

Makes plot of Index of Moderated Mediation of gemm object

Usage

plotIMM(x, ...)

Arguments

x  object moderatedMediationSem
...

...  optional

Value

simple slope plots for each mediator and simple slopes parameter estimates

plotIMM3d

Makes 3D plots of Index of Moderated Mediation of gemm object

Description

Makes 3D plots of Index of Moderated Mediation of gemm object

Usage

plotIMM3d(x, ...)

Arguments

x  results of gemm function
...

...  optional

Value

empty, directly plots all indices of mediation
plotSS

Makes simple slope plots of gemm object

Description

Makes simple slope plots of gemm object

Usage

plotSS(x, ...)

Arguments

x

object moderatedMediationSem

...

optional

Value

simple slope plots for each mediator and simple slopes parameter estimates

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 = "none",
    formatPvalue = TRUE
)

## S3 method for class 'posthocTGH'
print(x, digits = x$input$ digits, ...)
Arguments

- **y**: y has to be a numeric vector.
- **x**: x has to be a 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.
- ...: Any additional arguments are passed on to the `print` function.

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 function 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.

Also, for some reason, `p.adjust` can be used to specify additional correction of p values. I’m not sure why I implemented this, but I’m not entirely sure it was a mistake either. Therefore, in `userfriendlyscience` version 0.6-2, the default of this setting changed from "holm" to "none" (also see https://stats.stackexchange.com/questions/83941/games-howell-post-hoc-test-in-r).

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

```r
### 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);
```
prepIMM3d  
* Computes Index of moderated mediation of gemm object

**Description**
Computes Index of moderated mediation of gemm object

**Usage**
prepIMM3d(M1, M2, parEst = parEst, i = 1)

**Arguments**
- **M1**: moderator of x-m path
- **M2**: moderator of m-y path
- **parEst**: parameter estimates from lavaan results
- **i**: index of vector of mediators names

**Value**
vector of index of moderated mediation with CI limits for a given mediator

prepPlotIMM  
* Makes Index of Mediated Moderated plots

**Description**
Makes Index of Mediated Moderated plots

**Usage**
prepPlotIMM(
  data,
  xvar,
  yvar,
  mod,
  mvars,
  parEst,
  vdichotomous,
  modLevels,
  path = NULL
)
prepPlotSS

Arguments

- data: data frame containing the variables of the model
- xvar: predictor variable name
- yvar: dependent variable name
- mod: moderator name
- mvars: vector of mediators names
- parEst: parameter estimates from lavaan results
- vdichotomous: indicates whether moderator is dichotomous (TRUE)
- modLevels: levels of dichotomous moderator
- path: which path is used

Value

empty, directly plots all simple slopes and all indices of mediation

Description

Makes simple slope plots

Usage

prepPlotSS(
  data,
  xvar,
  yvar,
  mod,
  mvars,
  parEst,
  vdichotomous,
  modLevels,
  predLevels = NULL,
  xquant,
  yquant,
  path = NULL
)
Arguments

- `data`: data frame containing the variables of the model
- `xvar`: predictor variable name
- `yvar`: dependent variable name
- `mod`: moderator name
- `mvars`: vector of mediators names
- `parEst`: parameter estimates from lavaan results
- `vdichotomous`: indicates whether moderator is dichotomous (TRUE)
- `modLevels`: levels of dichotomous moderator
- `predLevels`: levels of dichotomous moderator
- `xquant`: quantiles of x
- `yquant`: quantiles of y
- `path`: which path is used

Value

empty, directly plots all simple slopes and all indices of mediation

Description

print method of object of class gemm

Usage

```r
## S3 method for class 'gemm'
print(x, ..., digits = 2, silence = FALSE)
```

Arguments

- `x`: object of class gemm
- `...`: additional pars
- `digits`: number of digits
- `silence`: boolean, if true out is not printed
randomSlug

Generate a random slug

Description
idSlug is a convenience function with swapped argument order.

Usage
randomSlug(x = 10, id = NULL, chars = c(letters, LETTERS, 0:9))
idSlug(id = NULL, x = 10, chars = c(letters, LETTERS, 0:9))

Arguments
x  Length of slug
id  If not NULL, prepended to slug (separated with a dash) as id; in that case, it’s also braces and a hash is added.
chars  Characters to sample from

Value
A character value.

Examples
randomSlug();
idSlug("identifier");

recode
Recode a Variable (car version)

Description
This function is from the car package. Please see that help page for details: car::recode().

Usage
recode(
  var,
  recodes,
  as.factor,
  as.numeric = TRUE,
  levels,
  to.value = "=",
  interval = "::",
  separator = ","
)
**Arguments**

- **var** numeric vector, character vector, or factor.
- **recodes** character string of recode specifications: see below.
- **as.factor** return a factor; default is TRUE if var is a factor, FALSE otherwise.
- **as.numeric** if TRUE (the default), and as.factor is FALSE, then the result will be coerced to numeric if all values in the result are numerals—i.e., represent numbers.
- **levels** an optional argument specifying the order of the levels in the returned factor; the default is to use the sort order of the level names.
- **to.value** The operator to separate old from new values, "=" by default; some other possibilities: "->", "~", "-->". Cannot include the interval operator (by default :) or the separator string (by default ,), so, e.g., by default ":=>" is not allowed. The discussion in Details assumes the default ":=". Use a non-default to.value if factor levels contain =.
- **interval** the operator used to denote numeric intervals, by default ":". The discussion in Details assumes the default ":". Use a non-default interval if factor levels contain :.
- **separator** the character string used to separate recode specifications, by default ";". The discussion in Details assumes the default ";". Use a non-default separator if factor levels contain ;.

**Author(s)**

John Fox <jfox@mcmaster.ca>

**References**


**Examples**

```r
x<-rep(1:3,3)
x
rosetta::recode(  
x,  
  "c(1,2)='A'; else='B'"
);  
rosetta::recode(  
x,  
  "1:2='A'; 3='B'"
);  
```
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; for more functionality, use the base R function `lm` or e.g. the `lme4` package.

Usage

```r
regr(
  formula,
  data = NULL,
  conf.level = 0.95,
  digits = 2,
  pvalueDigits = 3,
  coefficients = c("raw", "scaled"),
  plot = FALSE,
  pointAlpha = 0.5,
  collinearity = FALSE,
  influential = FALSE,
  ci.method = c("widest", "r.con", "olkinfinn"),
  ci.method.note = FALSE,
  headingLevel = 3,
  env = parent.frame()
)
```

```r
rosettaRegr_partial(
  x,
  digits = x$input$digits,
  pvalueDigits = x$input$pvalueDigits,
  headingLevel = x$input$headingLevel,
  echoPartial = FALSE,
  partialFile = NULL,
  quiet = TRUE,
  ...
)
```

```r
## S3 method for class 'rosettaRegr'
knit_print(
  x,
  digits = x$input$digits,
  headingLevel = x$input$headingLevel,
  pvalueDigits = x$input$pvalueDigits,
)
Arguments

formula | The formula of the regression analysis, of the form \( y \sim x_1 + x_2 \), where \( y \) is the dependent variable and \( x_1 \) and \( x_2 \) are the predictors.
data | 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.
pointAlpha | The alpha channel (transparency, or rather: ‘opaqueness’) of the points drawn in the plot.
collinearity | Whether to compute and show collinearity diagnostics (specifically, the tolerance \( (1 - R^2) \), where \( R^2 \) is the one obtained when regressing each predictor on all the other predictors) and the Variance Inflation Factor (VIF), which is the reciprocal of the tolerance, i.e. \( VIF = 1 / \text{tolerance} \).
influential | Whether to compute diagnostics for influential cases. These are stored in the returned object in the \texttt{lm.influence.raw} and \texttt{lm.influence.scaled} objects in the intermediate object. They are not printed.
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.
headingLevel  The number of hashes to print in front of the headings when printing while knitting

env  The environment where to evaluate the formula.

x  The object to print (i.e. as produced by regr).

echoPartial  Whether to show the executed code in the R Markdown partial (TRUE) or not (FALSE).

partialFile  This can be used to specify a custom partial file. The file will have object x available.

quiet  Passed on to knitr::knit() whether it should be chatty (FALSE) or quiet (TRUE).

...  Any additional arguments are passed to the default print method by the print method, and to rmdpartials::partial() when knitting an RMarkdown partial.

forceKnitrOutput  Force knitr output.

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
rosetta::regr(age ~ circumference, dat=Orange);

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

## Not run:
### An example with an interaction term, showing in the
### viewer
rosetta::rosettaRegr_partial(
  rosetta::regr(
    mpg ~ wt + hp + wt:hp,
    dat=mtcars,
    coefficients = "raw",
    plot=TRUE,
    collinearity=TRUE
  )
)
Conduct reliability analyses with output similar to jamovi and SPSS

Description

The `reliability()` analysis is the only one most users will need. It tries to apply best practices by, as much as possible, complementing point estimates with confidence intervals.

Usage

```r
reliability(
  data,
  items = NULL,
  scaleStructure = TRUE,
  descriptives = FALSE,
  itemLevel = FALSE,
  scatterMatrix = FALSE,
  scatterMatrixArgs = list(progress = FALSE),
  digits = 2,
  conf.level = 0.95,
  itemLabels = NULL,
  itemOmittedCorsWithRest = FALSE,
  itemOmittedCorsWithTotal = FALSE,
  alphaOmittedCIs = FALSE,
  omegaFromMBESS = FALSE,
  omegaFromPsych = TRUE,
  ordinal = FALSE,
  headingLevel = 3,
  ...)
```

```r
rosettaReliability_partial(
  x,
  digits = x$digits,
  headingLevel = x$headingLevel,
  printPlots = TRUE,
  echoPartial = FALSE,
  partialFile = NULL,
  quiet = TRUE,
  ...)
```
## S3 method for class 'rosettaReliability'

```r
knit_print(
  x,
  digits = x$digits,
  headingLevel = x$headingLevel,
  printPlots = TRUE,
  echoPartial = FALSE,
  partialFile = NULL,
  quiet = TRUE,
  ...
)
```

## S3 method for class 'rosettaReliability'

```r
print(
  x,
  digits = x$digits,
  headingLevel = x$headingLevel,
  forceKnitrOutput = FALSE,
  printPlots = TRUE,
  ...
)
```

### Arguments

- **data**
  - The data frame

- **items**
  - The items (if omitted, all columns are used)

- **scaleStructure**
  - Whether to include scale-level estimates using `ufs::scaleStructure()`

- **descriptives**
  - Whether to include mean and standard deviation estimates and their confidence intervals

- **itemLevel**
  - Whether to include item-level internal consistency estimates

- **scatterMatrix**, **scatterMatrixArgs**
  - Whether to produce a scatter matrix, and the arguments to pass to the `scatterMatrix()` function.

- **digits**
  - The number of digits to round the result to

- **conf.level**
  - The confidence level of confidence intervals

- **itemLabels**
  - Optionally, labels to use for the items (optionally, named, with the names corresponding to the items; otherwise, the order of the labels has to match the order of the items)

- **itemOmittedCorsWithRest**, **itemOmittedCorsWithTotal**
  - Whether to include each item’s correlations with, respectively, the scale with that item omitted, or the full scale.

- **alphaOmittedCIs**
  - Whether to include the confidence intervals for the Coefficient Alpha estimates with the item omitted.

- **omegaFromMBESS**, **omegaFromPsych**
  - Whether to include omega from MBESS and/or psych
Whether to set `poly=TRUE` when calling `ufs::scaleStructure()`, which will compute the polychoric correlation matrix to provide the scale estimates assuming ordinal-level items. Note that this may throw a variety of errors from within the psych package if the data are somehow not what psych expects.

The number of hashes to print in front of the headings when printing while knitting.

Any additional arguments are passed to `ufs::scaleStructure()` by reliability, to the default print method by `print.reliability`, and to `rmdpartials::partial()` when knitting an RMarkdown partial.

The object to print.

Whether to print plots (can be used to suppress plots, which can be useful sometimes).

Whether to show the executed code in the R Markdown partial (TRUE) or not (FALSE).

This can be used to specify a custom partial file. The file will have object `x` available.

Passed on to `knitr::knit()` whether it should be chatty (FALSE) or quiet (TRUE).

Force knitr output.

The rosettaReliability object that is returned has its own `print()` method, that, when using knitr, will use the rmdpartials package to insert an RMarkdown partial. That partial is created using rosettaReliability_partial(), which is also called by a specific `knit_print()` method.

An object with all results.

### These examples aren't run during tests
### because they can take quite long

```r
### Simple example with only main reliability results
data(pp15, package="rosetta");
rosetta::reliability(
  pp15,
  c(
    "highDose_AttGeneral_good",
    "highDose_AttGeneral_prettig",
    "highDose_AttGeneral_slim",
    "highDose_AttGeneral_gezond",
    "highDose_AttGeneral_spannend"
  )
);
```
### More extensive example with an RMarkdown partial that displays in the viewer

```r
rosetta::rosettaReliability_partial(
  rosetta::reliability(
    attitude,
    descriptives = TRUE,
    itemLevel = TRUE,
    scatterMatrix = TRUE
  )
);
```

## End(Not run)

---

**repeatStr**  

*Repeat a string a number of times*

---

**Description**

Repeat a string a number of times

**Usage**

```r
repeatStr(n = 1, str = " ")
```

**Arguments**

- `n`, `str`  
  Normally, respectively the frequency with which to repeat the string and the string to repeat; but the order of the inputs can be switched as well.

**Value**

A character vector of length 1.

**Examples**

```r
### 10 spaces:
repStr(10);

### Three euro symbols:
repStr("\u20ac", 3);
```
**rMatrix**

### Description

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

### Usage

```r
rMatrix(
  dat,
  x,
  y = NULL,
  conf.level = 0.95,
  correction = "fdr",
  digits = 2,
  pValueDigits = 3,
  colspace = 2,
  rowspace = 0,
  colNames = "numbers"
)
```

```r
## S3 method for class 'rMatrix'
print(
  x,
  digits = x$digits,
  pValueDigits = x$pValueDigits,
  colNames = x$colNames,
  ...
)
```

### 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.
rMatrix

colspace  Number of spaces between columns
rowspace  Number of rows between table rows (note: one table row is 2 rows).
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.
...  Additional arguments are ignored.

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 rMatrix object that when printed shows the correlation matrix
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'))
scatterMatrix  

Description

scatterMatrix produces a matrix with jittered scatterplots, histograms, and correlation coefficients.

Usage

scatterMatrix(
  dat,
  items = NULL,
  itemLabels = NULL,
  plotSize = 180,
  sizeMultiplier = 1,
  pointSize = 1,
  axisLabels = "none",
  normalHist = TRUE,
  progress = NULL,
  theme = ggplot2::theme_minimal(),
  hideGrid = TRUE,
  conf.level = 0.95,
  ...
)

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.
itemLabels Optionally, labels to use for the items (optionally, named, with the names corresponding to the items; otherwise, the order of the labels has to match the order of the items)
plotSize Size of the final plot in millimeters.
sizeMultiplier Allows more flexible control over the size of the plot elements
pointSize Size of the points in the scatterplots
axisLabels Passed to ggpairs function to set axisLabels.
normalHist Whether to use the default ggpairs histogram on the diagonal of the scattermatrix, or whether to use the ufs::normalHist() version.
progress Whether to show a progress bar; set to FALSE to disable. See GGally::ggpairs() help for more information.
theme The ggplot2 theme to use.
hideGrid Whether to hide the gridlines in the plot.
scatterPlot

conf.level The confidence level of confidence intervals
... Additional arguments for scatterMatrix() are passed on to ufs::normalHist(), and additional arguments for the print method are passed on to the default print method.

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.

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
exaipleData <- data.frame(item1=rnorm(100));
exaipleData$item2 <- exampleData$item1+rnorm(100);
exaipleData$item3 <- exampleData$item1+rnorm(100);
exaipleData$item4 <- exampleData$item2+rnorm(100);
exaipleData$item5 <- exampleData$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) `ggplot2::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",
xVarName = NULL,
yVarName = NULL,
...
}

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.
xVarName, yVarName Can be used to manually specify the names of the variables on the x and y axes.
...

And additional arguments are passed to ggplot2::geom_point() or ggplot2::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 ggplot2::ggplot() plot is returned.
### Examples

#### A simple scatter plot

```r
rosetta::scatterPlot(
    mtcars$mpg, mtcars$hp
);
```

#### The same scatter plot, now with a regression line and its confidence interval added.

```r
rosetta::scatterPlot(
    mtcars$mpg, mtcars$hp,
    regrLine=TRUE,
    regrCI=TRUE
);
```

---

### varView

<table>
<thead>
<tr>
<th>varView</th>
<th>Variable View</th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td></td>
</tr>
</tbody>
</table>

This function provides an overview of the variables in a dataframe, allowing efficient inspection of the factor levels, ranges for numeric variables, and numbers of missing values.

### Usage

```r
varView(
    data,  
    columns = names(data),  
    varViewCols = rosetta::opts$get(varViewCols),  
    varViewRownames = TRUE,  
    maxLevels = 10,  
    truncLevelsAt = 50,  
    showLabellerWarning = rosetta::opts$get(showLabellerWarning),  
    output = rosetta::opts$get("tableOutput")
)
```

```r
## S3 method for class 'rosettaVarView'
print(x, output = attr(x, "output"), ...)
```

### Arguments

- **data**: The dataframe containing the variables to view.
- **columns**: The columns to include.
- **varViewCols**: The columns of the variable view.
- **varViewRownames**: Whether to set the variable names as row names of the variable view dataframe that is returned.
maxLevels  For factors, the maximum number of levels to show.
truncLevelsAt For factors levels, the number of characters at which to truncate.
showLabellerWarning Whether to show a warning if labeller labels are encountered.
output A character vector containing one or more of "console", "viewer", and one or more filenames in existing directories. If output contains viewer and RStudio is used, the variable view is shown in the RStudio viewer.
x The varView data frame to print.
...
Any additional arguments are passed along to the print.data.frame() function.

Value
A dataframe with the variable view.

Author(s)
Gjalt-Jorn Peters & Melissa Gordon Wolf

Examples

### The default variable view
rosetta::varView(iris);

### Only for a few variables in the dataset
rosetta::varView(iris, columns=c("Sepal.Length", "Species"));

### Set some variable and value labels using the 'labelled' standard, which is also used by 'haven'
dat <- iris;
attr(dat$Sepal.Length, "label") <- "Sepal length";
attr(dat$Sepal.Length, "labels") <-
c('one' = 1,
   'two' = 2,
   'three' = 3);

### varView automatically recognizes and shows these, adding a 'label' column
rosetta::varView(dat);

### You can also specify that you only want to see some columns
### in the variable view
rosetta::varView(dat,
                varViewCols = c('label', 'values', 'level'));
vecTxt

**vecTxt**  
_Easily parse a vector into a character value_

**Description**

vecTxtQ, vecTxtB, and vecTxtM and are convenience functions with default quotes that can be useful when working in R Markdown documents.

**Usage**

vecTxt(
  vector,  
  delimiter = ", ",  
  useQuote = "",  
  firstDelimiter = NULL,  
  lastDelimiter = " & ",  
  firstElements = 0,  
  lastElements = 1,  
  lastHasPrecedence = TRUE
)

vecTxtQ(vector, useQuote = "'", ...)  
vecTxtB(vector, useQuote = "\"", ...)  
vecTxtM(vector, useQuote = "$", ...)

**Arguments**

- **vector** The vector to process.
- **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)?
- **...** Any addition arguments to vecTxtQ are passed on to vecTxt.
Value

A character vector of length 1.

Examples

```r
vecTxtQ(names(mtcars));
```
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