

Package ‘scitb’

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Type Package

Title Provides Some Useful Functions for Making Statistical Tables

Version 0.1.8

Maintainer Qiang Liu <dege857@163.com>

Description You can use the functions provided by the package to make various statistical tables, such as baseline data tables. Creates 'Table 1', i.e., a description of the baseline patient characteristics, which is essential in every medical research.

Supports both continuous and categorical variables, as well as p-values and standardized mean differences.

This method was described by Mary L McHugh (2013) <[doi:10.11613/bm.2013.018](https://doi.org/10.11613/bm.2013.018)>.

License GPL-3

Encoding UTF-8

LazyData true

Depends R (>= 3.50)

RoxygenNote 7.2.1

Imports ggplot2, MASS, nortest, reshape2, stringi

NeedsCompilation no

Author Qiang Liu [aut, cre]

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 confinterval

confinterval

Description

P-values were inferred from confidence intervals.

Usage

```
confinterval(est = NULL, ratio = NULL, ul = NULL, ll = NULL)
```

Arguments

<code>est</code>	Enter the effect value.
<code>ratio</code>	Effect ratio values. Includes OR,HR,RR.
<code>ul</code>	The upper limit of the credible interval.
<code>ll</code>	Lower limit of the credible interval.

Details

Limitations of the method: The formula for P is unreliable for very small P values and if your P value is smaller than 0.0001, just report it as $P < 0.0001$. The methods described can be applied in a wide range of settings, including the results from meta-analysis and regression analyses. The main context where they are not correct is small samples where the outcome is continuous and the analysis has been done by a t test or analysis of variance, or the outcome is dichotomous and an exact method has been used for the confidence interval. However, even here the methods will be approximately correct in larger studies with, say, 60 patients or more.

Value

A list of results.

References

Altman DG, Bland JM. How to obtain the P value from a confidence interval. *BMJ*. 2011;343:d2304. doi: 10.1136/bmj.d2304. PMID: 22803193.

Examples

```
confinterval(est=0.05917381, ul=0.06756194, ll=0.05091284)
```

plotsmd	<i>plotsmd</i>
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Description

You can use it to draw a baseline table of data.

Usage

```
plotsmd(vars,unmatchdata,matchdata,refline=NULL,title=NULL,xlab='SMD',ylab='variable')
```

Arguments

vars	List the variables you need to compare.
unmatchdata	Data before conducting propensity matching.
matchdata	The data after propensity score matching.
refline	Set a reference line with a default value of 0.1.
title	The title of the image.
xlab	The name of the X-axis.
ylab	The name of the Y-axis.

Details

The differences between variables can be represented using SMD. This program can draw SMD graphs of variable differences.

Value

A picture.

prematurity	<i>A data on indicators for premature newborns.</i>
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Description

A data on indicators for premature newborns.

Usage

```
data(prematurity)
```

Format

An object of class `data.frame` with 189 rows and 11 columns.

Examples

```
data(prematurity)
```

```
scifreq
```

```
scifreq
```

Description

You can use it to draw a baseline table of data. Creates 'Table 1', i.e., description of baseline patient characteristics, which is essential in every medical research. Supports both continuous and categorical variables, as well as p-values and standardized mean differences.

Arguments

<code>mvars</code>	The full range of variables you don't want to compare.
<code>x</code>	Enter the variables to be layered. If you fill in consecutive variables, by default they will be split into 3 layers.
<code>data</code>	Enter your data.
<code>dec</code>	The precision of the data, which defaults to 2 decimal places.
<code>nonnormal</code>	When the data belongs to a non-normal distribution, this parameter is needed to indicate which variable is non-normally distributed.
<code>statistic</code>	Statistical effect values. Usually, it is the default F, and selecting T will return a statistical effect value.
<code>fisher</code>	Fisher's exact test. The default is FALSE.
<code>correct</code>	Chi square test for continuity correction. The default is FALSE.
<code>Overall</code>	Generate summary data. The default is FALSE.
<code>smd</code>	The default is FALSE. If it is true, return the SMD value.

Details

Table 1 represents the relationship between the baseline values of the data. This function can be easily done.

Value

A data frame.

scilmean

scilmean

Description

You can use it to draw a baseline table of data. Creates 'Table 1', i.e., description of baseline patient characteristics, which is essential in every medical research. Supports both continuous and categorical variables, as well as p-values and standardized mean differences.

Arguments

mvars	The full range of variables you don't want to compare.
x	Enter the variables to be layered. If you fill in consecutive variables, by default they will be split into 3 layers.
data	Enter your data.
dec	The precision of the data, which defaults to 2 decimal places.
nonnormal	When the data belongs to a non-normal distribution, this parameter is needed to indicate which variable is non-normally distributed.
type	The type of encoding generally does not require input.
statistic	Statistical effect values. Usually, it is the default F, and selecting T will return a statistical effect value.
atotest	Check if the data is normally distributed. The default is T.
NormalTest	A method for detecting whether data is normally distributed. The default values are Kolmogorov Smirnov test and Kolmogorov Smirnov test. Other options are: "ad", "cvm", "pearson".
Overall	Generate summary data. The default is FALSE.
smd	The default is FALSE. If it is true, return the SMD value.

Details

Table 1 represents the relationship between the baseline values of the data. This function can be easily done.

Value

A data frame.

scitb1 *scitb1*

Description

You can use it to draw a baseline table of data.

Usage

```
scitb1(vars, fvars=NULL, strata, data, dec, num, nonnormal=NULL, type=NULL,
        statistic=F, atotest=T, NormalTest=NULL, fisher=FALSE, correct=FALSE, Overall=FALSE, smd=FALSE)
```

Arguments

vars	The full range of variables you don't want to compare.
fvars	Define the categorical variables in your data.
strata	Enter the variables to be layered. If you fill in consecutive variables, by default they will be split into 3 layers.
data	Enter your data.
dec	The precision of the data, which defaults to 2 decimal places.
num	When continuous variables are layered, use it to control the number of layers, which defaults to 3.
nonnormal	When the data belongs to a non-normal distribution, this parameter is needed to indicate which variable is non-normally distributed.
type	The type of encoding generally does not require input. Contains three types: "A", "B", and "C".
statistic	Statistical effect values. Usually, it is the default F, and selecting T will return a statistical effect value.
atotest	Check if the data is normally distributed. The default is T.
NormalTest	A method for detecting whether data is normally distributed. The default values are Kolmogorov Smirnov test and Kolmogorov Smirnov test. Other options are: "ad", "cvm", "pearson".
fisher	Fisher's exact test. The default is FALSE.
correct	Chi square test for continuity correction. The default is FALSE.
Overall	Generate summary data. The default is FALSE.
smd	The default is FALSE. If it is true, return the SMD value.

Details

Table 1 represents the relationship between the baseline values of the data. This function can be easily done. Creates 'Table 1', i.e., description of baseline patient characteristics, which is essential in every medical research. Supports both continuous and categorical variables, as well as p-values and standardized mean differences.

Value

A data frame.

Examples

```
## Import data
bc<-prematernity
## Hierarchical variables converted to factors.
bc$race<-as.factor(bc$race)
###Define all variables, categorical and stratified.
allVars <-c("age", "lwt", "smoke", "ptl", "ht", "ui", "ftv", "bwt")
fvars<-c("smoke","ht","ui")
strata<-"race"
out<-scitb1(vars=allVars,fvars=fvars,strata=strata,data=bc)
out<-scitb1(vars=allVars,fvars=fvars,strata=strata,data=bc,statistic=TRUE)
out<-scitb1(vars=allVars,fvars=fvars,strata=strata,data=bc,statistic=TRUE,Overall=TRUE)
out<-scitb1(vars=allVars,fvars=fvars,strata=strata,data=bc,statistic=TRUE,Overall=TRUE,smd=TRUE)
print(out)

###Stratified variables are continuous variables.
allVars <-c("race", "lwt", "smoke", "ptl", "ht", "ui", "ftv", "bwt")
fvars<-c("smoke","ht","ui","race")
strata<-"age"
out<-scitb1(vars=allVars,fvars=fvars,strata=strata,data=bc)
out<-scitb1(vars=allVars,fvars=fvars,strata=strata,data=bc,statistic=TRUE)
out<-scitb1(vars=allVars,fvars=fvars,strata=strata,data=bc,statistic=TRUE,Overall=TRUE,smd=TRUE)
print(out)
```

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