

Package ‘twowaytests’

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Type Package

Title Two-Way Tests in Independent Groups Designs

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Description Performs two-way tests in independent groups designs; Parametric Bootstrap based Generalized Test and Generalized Pivotal Quantity based Generalized Test (Weerahandi and Krishnamoorthy, 2019) <doi:10.1080/03610926.2017.1419264>. The package performs descriptive statistics and graphical approaches. Moreover, it assesses variance homogeneity and normality of data in each group via tests and plots. All 'twowaytests' functions are designed for two-way layout.

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twowaytests-package *Two-Way Tests in Independent Groups Designs*

Description

Performs two-way tests in independent groups designs; Parametric Bootstrap based Generalized Test and Generalized Pivotal Quantity based Generalized Test (Weerahandi and Krishnamoorthy, 2019) <doi:10.1080/03610926.2017.1419264>. The package performs descriptive statistics and graphical approaches. Moreover, it assesses variance homogeneity and normality of data in each group via tests and plots. All 'twowaytests' functions are designed for two-way layout.

Details

Package: twowaytests
 Type: Package
 License: GPL (>=2)

alveolar *Alveolar Cell Count Data*

Description

Alveolar cell count data were collected by Lacroix et al. (2002).

Usage

```
data(alveolar)
```

Format

A data frame with 36 observations on the following 3 variables.

ovalbumin a factor with levels: no (ovalbumin-nonsensitized); yes (ovalbumin-sensitized)

treatment a factor with levels: acetaldehyde; air; benzaldehyde

count Alveolar count x 10⁶

References

Lacroix, G., Tissot, S., Rogerieux, F., Beaulieu, R., Cornu, L., Gillet, C., ..., Bois, F. Y. (2002). Decrease in ovalbumin-induced pulmonary allergic response by benzaldehyde but not acetaldehyde exposure in a guinea pig model. *Journal of Toxicology and Environmental Health, Part A*, **65:14**, 995-1012.

Examples

```
library(twowaytests)
data(alveolar)
```

descTwoWay

Descriptive Statistics for Two-Way Layout

Description

descTwoWay produces basic descriptive statistics including sample size, mean, standard deviation, median, minimum value, maximum value, 25th quantile, 75th quantile, skewness, kurtosis, the number of missing value for two-way layout.

Usage

```
descTwoWay(formula, data)
```

Arguments

formula	a formula of the form lhs ~ rhs where lhs gives the sample values and rhs gives two factors.
data	a data frame containing the variables in the formula formula

Value

Returns a data.frame of output.

Author(s)

Osman Dag, Sam Weerahandi, Malwane Ananda

Examples

```
library(twowaytests)
data(alveolar)
descTwoWay(count ~ ovalbumin*treatment, data = alveolar)
```

gplotTwoWay

*Box-and-Whisker Plots and Error Bars for Two-Way Layout***Description**

`gplotTwoWay` produce box-and-whisker plots and error bars for two-way layout.

Usage

```
gplotTwoWay(formula, data, type = c("errorbar", "boxplot"), xlab = NULL,
  ylab = NULL, title = NULL, legend.title = NULL, width = NULL,
  option = c("se", "sd"), na.rm = TRUE)
```

Arguments

<code>formula</code>	a formula of the form <code>lhs ~ rhs</code> where <code>lhs</code> gives the sample values and <code>rhs</code> gives the corresponding two factors.
<code>data</code>	a data frame containing the variables in the formula <code>formula</code>
<code>type</code>	a character string to select one of the plots. "errorbar": error bar, "boxplot": box-and-whisker plot.
<code>xlab</code>	a label for the x axis, defaults to a description of x.
<code>ylab</code>	a label for the y axis, defaults to a description of y.
<code>title</code>	a main title for the plot.
<code>legend.title</code>	a legend title for the plot.
<code>width</code>	a numeric giving the width of the little lines at the tops and bottoms of the error bars (defaults to 0.20) and the width of the boxes for box-and-whisker plots (defaults to 0.75).
<code>option</code>	a character string to select one of the options to draw error bars with standard error or standard deviation. "se": standard error, "sd": standard deviation. Defaults to "se".
<code>na.rm</code>	a logical indicating whether NA values should be stripped before the computation proceeds.

Details

The upper whisker of box-and-whisker plots extends from the hinge to the highest value that is within $1.5 * \text{IQR}$ of the hinge, where IQR is the inter-quartile range. The lower whisker extends from the hinge to the lowest value within $1.5 * \text{IQR}$ of the hinge. Data out of the ends of the whiskers are outliers and plotted as points.

Author(s)

Osman Dag, Malwane Ananda, Sam Weerahandi

Examples

```

library(twowaytests)
data(alveolar)

# to obtain error bar (mean +- standard deviation)
gplotTwoWay(count ~ ovalbumin*treatment, data = alveolar, type = "errorbar", option = "sd")

# to obtain error bar (mean +- standard error)
gplotTwoWay(count ~ ovalbumin*treatment, data = alveolar, type = "errorbar", option = "se")

# to obtain box-and-whisker plot
gplotTwoWay(count ~ ovalbumin*treatment, data = alveolar, type = "boxplot")

```

gpTwoWay

*Two-Way ANOVA under Heteroscedasticity***Description**

gpTwoWay The gpTwoWay function computes a two-way ANOVA for main effects and interaction effect under heteroscedasticity.

Usage

```
gpTwoWay(formula, data, method = c("gPB", "gPQ"), alpha = 0.05, na.rm = TRUE,
         verbose = TRUE)
```

Arguments

formula	a formula of the form lhs ~ rhs where lhs gives the sample values and rhs gives the two factors.
data	a data frame containing the variables in the formula formula
method	a character string to select the method. "gPB": Parametric Bootstrap based Generalized Test, "gPQ": Generalized Pivotal Quantity based Generalized Test.
alpha	the level of significance to assess the statistical difference. Default is set to alpha = 0.05.
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
verbose	a logical for printing output to R console.

Value

A list containing the following components:

output	a data frame of output.
alpha	the level of significance to assess the statistical difference.

method	the selected method used in generalized test.
data	a data frame containing the variables in which NA values (if exist) are removed.
formula	a formula of the form lhs ~ rhs where lhs gives the sample values and rhs gives the two factors.

Note

The tests available from this R library are based on two Generalized P-value approach, for Two-Way ANOVA under unequal variances and cell frequencies. The first test, the gPQ, is an extension Li et al. (2011), and the second test, gPB, is a generalized test that is numerically equivalent to the Parametric Bootstrap test derived by Xu et al. (2013). The gPQ test tends to assure the intended size of the test, but somewhat conservative, especially when the sample sizes are small.

The gPB test tends to exceed the intended size of the test. Hence, the gPB is recommended for situations of small sample sizes, and gPQ otherwise.

Author(s)

Sam Weerahandi, Osman Dag, Malwane Ananda

References

Li, X., Wang J., Liang H. (2011). Comparison of several means: a fiducial based approach. *Computational Statistics and Data Analysis*, **55:5**, 1993-2002.

Xu L., Yang F., Abula A., Qin, S. (2013). A parametric bootstrap approach for two-way ANOVA in presence of possible interactions with unequal variances. *Journal of Multivariate Analysis*, **115**, 172-180.

Examples

```
###Example 1

library(twowaytests)
data(alveolar)

# to use Parametric Bootstrap based Generalized Test
gpTwoWay(count ~ ovalbumin*treatment, data = alveolar, method = "gPB")

# to use Generalized Pivotal Quantity based Generalized Test
gpTwoWay(count ~ ovalbumin*treatment, data = alveolar, method = "gPQ")

gpTwoWay(count ~ as.factor(ovalbumin)*as.factor(treatment), data = alveolar, method = "gPQ")

result <- gpTwoWay(count ~ as.factor(ovalbumin)*as.factor(treatment), data = alveolar,
method = "gPQ", verbose = FALSE)

result$output
```

result\$method

homogtestTwoWay *Variance Homogeneity Tests for for Two-Way Layout*

Description

homogtestTwoWay performs variance homogeneity tests including Levene, Bartlett, Fligner-Killeen tests for two-way layout.

Usage

```
homogtestTwoWay(formula, data, method = c("Levene", "Bartlett", "Fligner"),
  alpha = 0.05, na.rm = TRUE, verbose = TRUE)
```

Arguments

formula	a formula of the form lhs ~ rhs where lhs gives the sample values and rhs the corresponding two factors.
data	a data frame containing the variables in the formula formula
method	a character string to select one of the variance homogeneity tests. "Levene": Levene's test, "Bartlett": Bartlett's test, "Fligner": Fligner-Killeen test.
alpha	the level of significance to assess variance homogeneity. Default is set to alpha = 0.05.
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
verbose	a logical for printing output to R console.

Value

A list containing the following components:

statistic	the corresponding test statistic.
parameter	the parameter(s) of the approximate corresponding distribution of the test statistic. The corresponding distribution is F distribution for Levene's test, Chi-square distribution for Bartlett's test and Fligner-Killeen test.
p.value	the p-value of the test.

Author(s)

Osman Dag, Malwane Ananda, Sam Weerahandi

See Also

[leveneTest](#) [bartlett.test](#) [fligner.test](#)

Examples

```
library(twowaytests)
data(alveolar)

homogtestTwoWay(count ~ ovalbumin*treatment, data = alveolar)
homogtestTwoWay(count ~ ovalbumin*treatment, data = alveolar, method = "Bartlett")
```

nortestTwoWay

Normality Tests for Two-Way Layout

Description

nortestTwoWay performs normality tests including Shapiro-Wilk, Shapiro-Francia, Kolmogorov-Smirnov, Anderson-Darling, Cramer-von Mises, Pearson Chi-square tests, and also assess the normality of each group through plots for two-way layout.

Usage

```
nortestTwoWay(formula, data, method = c("SW", "SF", "LT", "AD", "CVM", "PT"),
  alpha = 0.05, plot = c("qqplot", "histogram"), na.rm = TRUE, verbose = TRUE)
```

Arguments

formula	a formula of the form lhs ~ rhs where lhs gives the sample values and rhs the corresponding two factors.
data	a data frame containing the variables in the formula formula
method	a character string to select one of the normality tests. "SW": Shapiro-Wilk test, "SF": Shapiro-Francia test, "LT": Lilliefors (Kolmogorov-Smirnov) test, "AD": Anderson-Darling test, "CVM": Cramer-von Mises test, "PT": Pearson Chi-square test.
alpha	the level of significance to assess normality. Default is set to alpha = 0.05.
plot	a character string to select one of the plots including qqplot and histogram. The red line is the density line of normal distribution. If plot is set to NULL, the plot is not returned.
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
verbose	a logical for printing output to R console.

Value

A data frame gives the test results for the normality of each subset via corresponding normality.

Author(s)

Osman Dag, Sam Weerahandi, Malwane Ananda

See Also

[gplotTwoWay](#) [shapiro.test](#)

Examples

```
library(twowaytests)
data(alveolar)
nortestTwoWay(count ~ ovalbumin*treatment, data = alveolar)
```

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