Package 'twowaytests'

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Description Performs two-way tests in independent groups designs. These are two-way ANOVA, two-way ANOVA under heteroscedasticity: parametric bootstrap based generalized test and generalized pivotal quantity based generalized test, two-way ANOVA for medians, trimmed means, M-estimators. 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 (Dag et al., 2024, <doi:10.1016/j.softx.2024.101862>).

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`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

`cell` Alveolar count x 10^6

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)
```

aovTwoWay *Two-Way ANOVA*

Description

aovTwoWay computes a two-way ANOVA for main effects and interaction effect.

Usage

```
aovTwoWay(formula, data, 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 formula.
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 method name.
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.

Author(s)

Muhammed Ali Yilmaz, Osman Dag

References

Dag, O., Kasikci, M., Yilmaz, M.A., Weerahandi, S., Ananda, M.M.A. (2024). twowaytests: An R Package for Two-Way Tests in Independent Groups Designs. *SoftwareX*, **27**, 1-8.

Toutenburg, H., Shalabh, S., Shalabh, H. (2002). Statistical analysis of designed experiments. Springer.

Examples

```
library(twowaytests)
data(alveolar)

aovTwoWay(cell ~ ovalbumin*treatment, data = alveolar)

out <- aovTwoWay(cell ~ ovalbumin*treatment, data = alveolar)
paircompTwoWay(out)

out <- aovTwoWay(cell ~ ovalbumin*treatment, data = alveolar, alpha = 0.10)
paircompTwoWay(out)

out <- aovTwoWay(cell ~ treatment*ovalbumin, data = alveolar, alpha = 0.10)
paircompTwoWay(out)
```

`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 `formula`.

Value

Returns a data.frame of output.

Author(s)

Osman Dag, Sam Weerahandi, Malwane Ananda

Examples

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

gplotTwoWay *Box-and-Whisker, Violin Plots and Error Bars for Two-Way Layout*

Description

gplotTwoWay produces box-and-whisker, violin plots, and error bars for two-way layout.

Usage

```
gplotTwoWay(formula, data, type = c("errorbar", "violin", "boxplot",
  "interaction"), color_manual = NULL, back_color = FALSE, xlab = NULL,
  ylab = NULL, title = NULL, legend.title = NULL, width = NULL,
  option = c("sd", "se"), metric = c("mean", "median"), na.rm = TRUE)
```

Arguments

formula	a formula of the form lhs ~ rhs where lhs gives the sample values and rhs gives the corresponding two factors.
data	a data frame containing the variables in formula.
type	a character string to select one of the plots. "errorbar": error bar, "violin": violin plot, "boxplot": box-and-whisker plot, and "interaction": interaction plot.
color_manual	a vector of colors. A palette can also be defined with wes_palette. Default is set to "FantasticFox1" available in wes_palette.
back_color	a logical to make background grey or white.
xlab	a label for the x axis, defaults to a description of x.
ylab	a label for the y axis, defaults to a description of y.
title	a main title for the plot.
legend.title	a legend title for the plot.
width	a numeric giving the width of the little lines at the tops and bottoms of the error bars (defaults to 0.35) and the width of the boxes for box-and-whisker plots (defaults to 0.75).
option	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".
metric	a character string to draw interaction plot with a desired metric. Defaults to "mean".
na.rm	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 * 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 * IQR of the hinge. Data out of the ends of the whiskers are outliers and plotted as points.

Author(s)

Osman Dag, Muhammed Ali Yilmaz, Merve Kasikci

Examples

```
library(twowaytests)
data(alveolar)

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

# to change factor places in graph
gplotTwoWay(cell ~ treatment*ovalbumin, data = alveolar, type = "errorbar", option = "sd")

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

# to draw interaction plot with mean
gplotTwoWay(cell ~ ovalbumin*treatment, data = alveolar, type = "interaction", metric = "mean")

# to draw interaction plot with median
gplotTwoWay(cell ~ ovalbumin*treatment, data = alveolar, type = "interaction", metric = "median")

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

# to obtain violin plot
gplotTwoWay(cell ~ ovalbumin*treatment, data = alveolar, type = "violin")

# to define specific colors
gplotTwoWay(cell ~ ovalbumin*treatment, data = alveolar, type = "errorbar", option = "sd",
color_manual = c("#999999", "#E69F00", "#56B4E9"))

# to change color palette
library(wesanderson)
gplotTwoWay(cell ~ ovalbumin*treatment, data = alveolar, type = "errorbar", option = "sd",
color_manual = wes_palette(name = "GrandBudapest1", n = 3))
```

---

gpTwoWay *Two-Way ANOVA under Heteroscedasticity*

Description

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

Usage

```
gpTwoWay(formula, data, method = c("gPB","gPQ"), seed = 123, 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 formula.
method	a character string to select the method. "gPB": Parametric Bootstrap based Generalized Test, "gPQ": Generalized Pivotal Quantity based Generalized Test.
seed	a seed number for the reproducibility of results. Default is set to 123.
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

These tests available from this R library are based on two Generalized P-value approaches, 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

Dag, O., Kasikci, M., Yilmaz, M.A., Weerahandi, S., Ananda, M.M.A. (2024). twowaytests: An R Package for Two-Way Tests in Independent Groups Designs. *SoftwareX*, **27**, 1-8.

Ananda, M.M., Dag, O., Weerahandi, S. (2023). Heteroscedastic two-way ANOVA under constraints. *Communications in Statistics-Theory and Methods*, **52:22**, 8207-8222.

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

```
library(twowaytests)
data(alveolar)



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

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

out <- gpTwoWay(cell ~ ovalbumin*treatment, data = alveolar, method = "gPB")
paircompTwoWay(out)

out <- gpTwoWay(cell ~ treatment*ovalbumin, data = alveolar, method = "gPB")
paircompTwoWay(out)
```

`homogtestTwoWay` *Variance Homogeneity Tests 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 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 homogenity. 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 disribution 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(cell ~ ovalbumin*treatment, data = alveolar)
homogtestTwoWay(cell ~ ovalbumin*treatment, data = alveolar, method = "Bartlett")
```

medTwoWay *Two-Way ANOVA for Medians*

Description

medTwoWay computes a two-way ANOVA for medians.

Usage

```
medTwoWay(formula, data, 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 formula.
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 method name.
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.

Author(s)

Muhammed Ali Yilmaz, Osman Dag

References

Dag, O., Kasikci, M., Yilmaz, M.A., Weerahandi, S., Ananda, M.M.A. (2024). twowaytests: An R Package for Two-Way Tests in Independent Groups Designs. *SoftwareX*, **27**, 1-8.

Wilcox, R.R. (2011). Introduction to robust estimation and hypothesis testing. Academic press.

See Also

med2way

Examples

```
library(twowaytests)
data(alveolar)

medTwoWay(cell ~ ovalbumin*treatment, data = alveolar)

out <- medTwoWay(cell ~ ovalbumin*treatment, data = alveolar, verbose = FALSE)
paircompTwoWay(out)

out <- medTwoWay(cell ~ treatment*ovalbumin, data = alveolar, verbose = FALSE)
paircompTwoWay(out)
```

`MestTwoWay` *Two-Way ANOVA for M-estimators*

Description

`MestTwoWay` computes a two-way ANOVA for M-estimators.

Usage

```
MestTwoWay(formula, data, estimator = c("mom_est", "onestep_est", "median",
  "bisquare", "hampel"), nboot = 500, distance = c("mahalanobis", "projected"),
  seed = 123, 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 `formula`.
`estimator`	a character string to select one of the estimators. "mom_est": the modified one-step estimator of location based on Huber's Psi, "onestep_est": one-step estimator of location using Huber's Psi, "median": median, "bisquare": Tukey's biweight (bisquare) estimator, "hampel": Hampel's estimator.
`nboot`	the number of bootstrap samples.
`distance`	the specified distance. Default is set to "mahalanobis".
`seed`	a seed number for the reproducibility of results. Default is set to 123.
`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 method name.
`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.

Author(s)

Muhammed Ali Yilmaz, Osman Dag

References

Dag, O., Kasikci, M., Yilmaz, M.A., Weerahandi, S., Ananda, M.M.A. (2024). twowaytests: An R Package for Two-Way Tests in Independent Groups Designs. *SoftwareX*, **27**, 1-8.

Wilcox, R.R. (2011). Introduction to robust estimation and hypothesis testing. Academic press.

See Also

`t2way`

Examples

```
library(twowaytests)
data(alveolar)

MestTwoWay(cell ~ ovalbumin*treatment, data = alveolar)

out <- MestTwoWay(cell ~ ovalbumin*treatment, data = alveolar, verbose = FALSE)
paircompTwoWay(out)

out <- MestTwoWay(cell ~ treatment*ovalbumin, data = alveolar, verbose = FALSE)
paircompTwoWay(out)
```

---

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 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(cell ~ ovalbumin*treatment, data = alveolar)
```

`paircompTwoWay` *Pairwise Comparisons for Two Way Layout*

Description

`paircompTwoWay` is a generic function for pairwise comparisons by adjusting p-values.

Usage

```
## S3 method for class 'twt'
paircompTwoWay(x, adjust.method = c("bonferroni", "holm", "hochberg", "hommel", "BH",
  "BY", "fdr", "none"), verbose = TRUE, ...)
```

Arguments

`x`	a `twt` object.
`adjust.method`	Method for adjusting p values (see `p.adjust`). Default is set to "bonferroni".
`verbose`	a logical for printing output to R console.
`...`	Additional arguments affecting multiple comparisons of groups in two-way independent designs.

Details

The paircompTwoWay function makes pairwise comparisons depending on significance of interaction term. It calculates p-values with corresponding same test if the interaction term is not statistically significant. Otherwise, it calculates p-values with `st.test` after two-way ANOVA, `wt.test` after two-way ANOVA under heteroscedasticity and `mw.test` after other tests. Then, it adjusts p-values with `p.adjust`.

Value

Returns a data.frame of output.

Author(s)

Muhammed Ali Yilmaz, Osman Dag

Examples

```
library(twowaytests)
data(alveolar)

out <- aovTwoWay(cell ~ ovalbumin*treatment, data = alveolar)
paircompTwoWay(out)

out <- aovTwoWay(cell ~ treatment*ovalbumin, data = alveolar)
paircompTwoWay(out)
```

```
out <- aovTwoWay(cell ~ ovalbumin*treatment, data = alveolar, alpha = 0.10)
pairCompTwoWay(out)

out <- aovTwoWay(cell ~ treatment*ovalbumin, data = alveolar, alpha = 0.10)
pairCompTwoWay(out)
pairCompTwoWay(out, adjust.method = "hochberg")
```

`tmeanTwoWay` *Two-Way ANOVA for Trimmed Means*

Description

`tmeanTwoWay` computes a two-way ANOVA for trimmed means.

Usage

```
tmeanTwoWay(formula, data, tr = 0.1, 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 `formula`.
`tr`	the rate of observations trimmed from each tail of the distribution. Default is set to 0.1.
`alpha`	the level of significance to assess the statistical difference. Default is set to 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 method name.
`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.

Author(s)

Muhammed Ali Yilmaz, Osman Dag

References

Dag, O., Kasikci, M., Yilmaz, M.A., Weerahandi, S., Ananda, M.M.A. (2024). twowaytests: An R Package for Two-Way Tests in Independent Groups Designs. *SoftwareX*, **27**, 1-8.

Wilcox, R.R. (2011). Introduction to robust estimation and hypothesis testing. Academic press.

See Also

t2way

Examples

```
library(twowaytests)
data(alveolar)

tmeanTwoWay(cell ~ ovalbumin*treatment, data = alveolar)

out <- tmeanTwoWay(cell ~ ovalbumin*treatment, data = alveolar, verbose = FALSE)
paircompTwoWay(out)

out <- tmeanTwoWay(cell ~ treatment*ovalbumin, data = alveolar, verbose = FALSE)
paircompTwoWay(out)
```

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