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 (Ananda et al., 2022) <doi:10.1080/03610926.2022.2059682>, two-way ANOVA for medians, trimmed means, M-estimators (Wilcox, 2011; ISBN:978-0-12-386983-8). 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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Contents

  twowaytests-package ......................................................... 2
  alveolar ........................................................................ 2
  aovTwoWay ................................................................. 3
  descTwoWay ................................................................. 4
  gplotTwoWay ............................................................... 5
  gpTwoWay ................................................................. 7
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 (Ananda et al., 2022) <doi:10.1080/03610926.2022.2059682>, two-way ANOVA for medians, trimmed means, M-estimators (Wilcox, 2011; ISBN:978-0-12-386983-8). 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
- **cell** Alveolar count x 10^6

**References**


**Examples**

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

---

**aovTwoWay**

**Two-Way ANOVA**

**Description**

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

**Usage**

```r
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

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**

```r
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.
gpTwoWay

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


Examples

###Example 1

```r
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**

```r
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 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

```r
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**

```r
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


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


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

```r
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

```r
## 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

```r
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 \( lhs \sim rhs \) where \( lhs \) gives the sample values and \( rhs \) gives the two factors.

Author(s)

Muhammed Ali Yilmaz, Osman Dag

References


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)
Index

* datasets
  alveolar, 2

* functions
  aovTwoWay, 3
descTwoWay, 4
gplotTwoWay, 5
gpTwoWay, 7
homogtestTwoWay, 9
medTwoWay, 10
MestTwoWay, 11
nortestTwoWay, 13
paircompTwoWay, 14
tmeanTwoWay, 15

alveolar, 2
aovTwoWay, 3
bartlett.test, 9
descTwoWay, 4
fligner.test, 9
gplotTwoWay, 5, 13
gpTwoWay, 7
homogtestTwoWay, 9
leveneTest, 9
med2way, 11
medTwoWay, 10
MestTwoWay, 11
mw.test, 14

nortestTwoWay, 13
p.adjust, 14
paircompTwoWay, 14
shapiro.test, 13
st.test, 14

t2way, 12, 16
tmeanTwoWay, 15
twowaytests-package, 2
wes_palette, 5
wt.test, 14