# Package ‘PMCMR’

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**Type** Package  
**Title** Calculate Pairwise Multiple Comparisons of Mean Rank Sums  
**Version** 4.1  
**Date** 2016-01-06  
**Author** Thorsten Pohlert  
**Maintainer** Thorsten Pohlert <thorsten.pohlert@gmx.de>  

**Description**  
The Kruskal and Wallis one-way analysis of variance by ranks or van der Waerden's normal score test can be employed, if the data do not meet the assumptions for one-way ANOVA. Provided that significant differences were detected by the omnibus test, one may be interested in applying post-hoc tests for pairwise multiple comparisons (such as Nemenyi's test, Dunn's test, Conover's test, van der Waerden's test). Similarly, one-way ANOVA with repeated measures that is also referred to as ANOVA with unreplicated block design can also be conducted via the Friedman-Test or the Quade-test. The consequent post-hoc pairwise multiple comparison tests according to Nemenyi, Conover and Quade are also provided in this package. Finally Durbin's test for a two-way balanced incomplete block design (BIBD) is also given in this package.

**Depends** R (>= 3.0.0), stats, base  
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**License** GPL (>= 3)  
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## R topics documented:

PCMCR-package ................................. 2
Description

The Kruskal and Wallis one-way analysis of variance by ranks or van der Waerden’s normal score test can be employed, if the data do not meet the assumptions for one-way ANOVA. Provided that significant differences were detected by the omnibus test, one may be interested in applying post-hoc tests for pairwise multiple comparisons (such as Nemenyi’s test, Dunn’s test, Conover’s test, van der Waerden’s test). Similarly, one-way ANOVA with repeated measures that is also referred to as ANOVA with unreplicated block design can also be conducted via the Friedman-Test or the Quade-test. The consequent post-hoc pairwise multiple comparison tests according to Nemenyi, Conover and Quade are also provided in this package. Finally Durbin’s test for a two-way balanced incomplete block design (BIBD) is also given in this package.

Details

Package: PMCMR
Type: Package
Version: 4.1
Date: 2016-01-06
License: >= GPL-3

See the vignette for details.

Author(s)

Thorsten Pohlert
Maintainer: <thorsten.pohlert@gmx.de>

References


See Also

*posthoc.kruskal.nemenyi.test, posthoc.kruskal.dunn.test, posthoc.kruskal.conover.test,
posthoc.friedman.nemenyi.test, posthoc.friedman.conover.test, posthoc.quade.test,
dunn.test.control, jonckheere.test, durbin.test, posthoc.durbin.test, kruskal.test,
friedman.test, Tukey, TDist, Chisquare, Normal, p.adjust, print.PMCMR, summary.PMCMR,
get.pvalues, multcompletters*

dunn.test.control

Pairwise Test for Multiple Comparisons of Mean Rank Sums with one control (Dunn's-Test)

Description

Calculate pairwise multiple comparisons with one control according to Dunn.

Usage

dunn.test.control (x, g, p.adjust.method = p.adjust.methods, ...)

Arguments

x a numeric vector of data values, or a list of numeric data vectors.
g a vector or factor object giving the group for the corresponding elements of x. Ignored if x is a list.
p.adjust.method Method for adjusting p values (see p.adjust).

Details

For one-factorial designs with samples that do not meet the assumptions for one-way-ANOVA and subsequent post-hoc tests, the Kruskal-Wallis-Test \texttt{kruskal.test} can be employed that is also referred to as the Kruskal–Wallis one-way analysis of variance by ranks. Provided that significant differences were detected by this global test, one may be interested in applying post-hoc tests according to Dunn for pairwise multiple comparisons with one control.

See the vignette for details.

Value

A list with class "PMCMR"

method The applied method.
data.name The name of the data.
p.value The two-sided p-value of the standard normal distribution.
statistic The estimated quantile of the standard normal distribution.
p.adjust.method The applied method for p-value adjustment.

Note

A tie correction will be employed according to Glantz (2012). As it is the case for multiple testing with one control using \texttt{aov}, the user must make sure that the control appears as the first level in the group vector. There is no formula method enclosed.

Author(s)

Thorsten Pohlert

References

**durbin.test**

**See Also**

`kruskal.test`, `friedman.test`, `posthoc.friedman.nemenyi.test`, `pnorm`, `p.adjust`

**Examples**

```r
##
require(stats)
data(PlantGrowth)attach(PlantGrowth)kruskal.test(weight, group)dunn.test.control(weight, group, "bonferroni")
detach(PlantGrowth)rm(PlantGrowth)
```

**Description**

The omnibus test according to Durbin tests whether k groups (or treatments) in a two-way balanced incomplete block design (BIBD) have identical effects.

**Usage**

`durbin.test(y, ...)

### Default S3 method:
durbin.test(y, groups, blocks, ...)

### S3 method for class 'formula'
durbin.test(formula, data, subset, na.action, ...)

**Arguments**

- `y` either a numeric vector of data values, or a data matrix.
- `groups` a vector giving the group for the corresponding elements of `y` if this is a vector; ignored if `y` is a matrix. If not a factor object, it is coerced to one.
- `blocks` a vector giving the block for the corresponding elements of `y` if this is a vector; ignored if `y` is a matrix. If not a factor object, it is coerced to one.
- `formula` a formula of the form `a ~ b | c`, where `a`, `b` and `c` give the data values and corresponding groups and blocks, respectively.
- `data` an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
subset an optional vector specifying a subset of observations to be used.
na.action a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
... further arguments to be passed to or from methods.

Details
The friedman.test can be used to test k groups (treatments) for identical effects in a two-way balanced complete block design. In the case of an two-way balanced incomplete block design, the Durbin test can be employed. The H0 is rejected, if at least one group (treatment) is significantly different. The Durbin test is equivalent to the Friedman test in the case of a two-way balanced complete block design.

If y is a matrix, then the columns refer to the groups (treatment) and the rows indicate the block. See vignette("PMCMR") for details.

Value
A list with class "PMCMR":

method The applied method.
data.name The name of the data.
p.value The p-value according to the studentized range distribution.
statistic The estimated upper quantile of the studentized range distribution.
p.adjust.method

Note
The function does not test, whether it is a true BIBD.
This function does not test for ties.

Author(s)
Thorsten Pohlert

References

See Also
friedman.test, posthoc.durbin.test
Examples

```r
## Example for an incomplete block design:
## Data from Conover (1999, p. 391).
y <- matrix(c(2,NA,NA,NA,3, NA, 3, 3, NA, NA, NA, 3, NA, NA,
             1, 2, NA, NA, NA, 1, 1, NA, 1, 1,
             NA, NA, NA, NA, 2, NA, 2, 1, NA, NA, NA, NA,
             3, NA, 2, 1, NA, NA, NA, NA, 3, NA, 2, 2
             ), ncol=7, nrow=7, byrow=FALSE,
dimnames=list(1:7, LETTERS[1:7]))
y
durbin.test(y)

## Example for a complete block design:
## Sachs, 1997, p. 675
## Six persons (block) received six different diuretics (A to F, treatment).
## The responses are the Na-concentration (mval)
## in the urine measured 2 hours after each treatment.
##
y <- matrix(c(3.88, 5.64, 5.76, 4.25, 5.91, 4.33, 30.58, 30.14, 16.92,
             23.19, 26.74, 10.91, 25.24, 33.52, 25.45, 18.85, 20.45,
             26.67, 4.44, 7.94, 4.04, 4.4, 4.23, 4.36, 29.41, 30.72,
             32.92, 28.23, 23.35, 12, 38.87, 33.12, 39.15, 28.06, 38.23,
             26.65), nrow=6, ncol=6,
dimnames=list(1:6, LETTERS[1:6]))
print(y)
friedman.test(y)
durbin.test(y)
```

get.pvalues  

Prints PMCMR objects

Description

Returns a vector of p-values that includes the names of the pairwise groups (i.e. the null hypothesis). The output can be used by multcompLetters to find homogeneous groups.

Usage

get.pvalues(object, ...)

Arguments

object  
either an object of class "PMCMR", usually, a result of a call to any of the posthoc-tests included in the package PMCMR. Or an object of class "pairwise.htest", a result of a call to pairwise.prop.test, pairwise.t.test or pairwise.wilcox.test.

...  
further arguments, currently ignored.
Jonckheere-Terpstra test for testing $k$ independent samples against ordered alternatives

Applies the Jonckheere-Terpstra test.

Value

out a named vector with p-values

See Also

multcompLetters, xtable, pairwise.prop.test, pairwise.t.test, pairwise.wilcox.test

Examples

data(InsectSprays)
attach(InsectSprays)
out <- posthoc.kruskal.dunn.test(count ~ spray, p.adjust="bonf")
out.p <- get.pvalues(out)
out.p

### a barplot, significant level at $p < 0.05$
require(multcompView)
out.mcV <- multcompLetters(out.p, threshold=0.05)
Rij <- rank(count)
Rj.mean <- tapply(Rij, spray, mean)
ti <- paste(out$method, ",\n-p-adjustment method:" , out$p.adjust.method)
xx <- barplot(Rj.mean, ylim=c(0, 1.2* max(Rj.mean)),
xlab="Spray", ylab="Mean rank", main=ti)
yy <- Rj.mean + 3
text(xx, yy, lab=out.mcV$Letters)

### table format
dat <- data.frame(Group = names(Rj.mean),
                   meanRj = Rj.mean,
                   M = out.mcV$Letters)
dat

### LaTeX table
require(xtable)
xtable(dat, caption=ti, digits=1)

detach(InsectSprays)

---
jonckheere.test Jonckheere-Terpstra test for testing $k$ independent samples against ordered alternatives

Description

Applies the Jonckheere-Terpstra test.
Usage

jonckheere.test (x, ...)

## Default S3 method:
jonckheere.test(x, g, alternative = c("monotonic", "increasing", "decreasing"), ...)

Arguments

x a numeric vector of data values, or a list of numeric data vectors.

g a vector or factor object giving the group for the corresponding elements of x.
Ignored if x is a list.

alternative The alternative hypothesis. Defaults to monotonic.

... further arguments to be passed to or from methods.

Details

The global H0, the k medians (med) are equal, is tested against the HA: med_1 <= med_2 <= ... <= med_k (increasing trend; one-sided test). It can also be tested for decreasing trend (one-sided test) and monotonic trend (two sided test).

See the vignette for details.

Value

A list with class "PMCMR"

method The applied method.
data.name The name of the data.
p.value The p-value of the standard normal distribution.
statistic The estimated quantile of the standard normal distribution.
alternative The alternative hypothesis.

Author(s)

Thorsten Pohlert

References


See Also

kruskal.test
Examples

```r
## Example from Sachs (1997, p. 402)
x <- c(106, 114, 116, 127, 145, 110, 125,
      143, 148, 151, 136, 139, 149, 160,
      174)
g <- as.factor(c(rep(1L), rep(2.5L), rep(3.5L)))
levels(g) <- c("A", "B", "C")
jonckheere.test(x, g, "increasing")
```

---

**posthoc.durbin.test**  
*Posthoc Durbin test*

**Description**

Pairwise post-hoc test for multiple comparisons of rank sums according to Durbin and Conover for a two-way balanced incomplete block design (BIBD).

**Usage**

```r
posthoc.durbin.test(y, ...)
```

## Default S3 method:
```r
posthoc.durbin.test(y, groups, blocks,
p.adjust.method = p.adjust.methods, ...)
```

**Arguments**

- `y`  
either a numeric vector of data values, or a data matrix.
- `groups`  
a vector giving the group for the corresponding elements of `y` if this is a vector; ignored if `y` is a matrix. If not a factor object, it is coerced to one.
- `blocks`  
a vector giving the block for the corresponding elements of `y` if this is a vector; ignored if `y` is a matrix. If not a factor object, it is coerced to one.
- `p.adjust.method`  
Method for adjusting p values (see `p.adjust`).
- `...`  
further arguments to be passed to or from methods.

**Details**

In the case of an two-way balanced incomplete block design, the Durbin test, `durbin.test` can be employed. The H0 is rejected, if at least one group (treatment) is significantly different. The pairwise multiple comparisons are conducted with this function. The `posthoc.durbin.test` is equivalent to the `posthoc.friedman.conover.test` in the case of a two-way balanced complete block design.
If \( y \) is a matrix, than the columns refer to the groups (treatment) and the rows indicate the block. The statistics refer to the student-t-distribution (TDist).

See vignette("PMCMR") for details.

Value

A list with class "PMCMR"

- **method**: The applied method.
- **data.name**: The name of the data.
- **p.value**: The two-sided p-value according to the student-t-distribution.
- **statistic**: The estimated quantiles of the student-t-distribution.
- **p.adjust.method**: The applied method for p-value adjustment.

Note

The function does not test, whether it is a true BIBD.
This function does not test for ties.

Author(s)

Thorsten Pohlert

References


See Also

durbin.test, friedman.test, posthoc.friedman.nemenyi.test, posthoc.friedman.conover.test, TDist p.adjust

Examples

```r
## Example for an incomplete block design:
## Data from Conover (1999, p. 391).
y <- matrix(c(2,NA,NA,NA,3, NA, 3, 3, NA, NA, NA, NA, NA, 3, NA, NA, 1, 2, NA, NA, NA, 1, 1, NA, 1, 1, NA, NA, NA, 2, NA, 2, 1, NA, NA, NA, NA, 3, NA, 2, 1, NA, NA, NA, NA, 3, NA, 2, 2), ncol=7, nrow=7, byrow=FALSE, dimnames=list(1:7, LETTERS[1:7]))
y
durbin.test(y)
posthoc.durbin.test(y, p.adj="none")
```
## Example for a complete block design:

Sachs, 1997, p. 675

Six persons (block) received six different diuretics (A to F, treatment).
The responses are the Na-concentration (mval) in the urine measured 2 hours after each treatment.

```r
y <- matrix(c(
  3.88, 5.64, 5.76, 4.25, 5.91, 4.33, 30.58, 30.14, 16.92,
  23.19, 26.74, 10.91, 25.24, 33.52, 25.45, 18.85, 20.45,
  26.67, 4.44, 7.94, 4.04, 4.4, 4.23, 4.36, 29.41, 30.72,
  32.92, 28.23, 23.35, 12, 38.87, 33.12, 39.15, 28.06, 38.23,
  26.65), nrow=6, ncol=6,
dimnames = list(1:6, LETTERS[1:6])))
print(y)
friedman.test(y)
durbin.test(y)
posthoc.durbin.test(y, p.adj="none")
posthoc.friedman.conover.test(y, p.adj="none")
```

---

**posthoc.friedman.conover.test**

*Pairwise post-hoc Test for Multiple Comparisons of Rank Sums for Unreplicated Blocked Data (Conover-Test)*

### Description

Calculate pairwise comparisons using Conover post-hoc test for unreplicated blocked data. This test is usually conducted post-hoc after significant results of the `friedman.test`. The statistics refer to the student-t-distribution (`tdist`).

### Usage

```r
posthoc.friedman.conover.test(y, ...)
```

**## Default S3 method:**

```r
posthoc.friedman.conover.test(y, groups, blocks,
p.adjust.method = p.adjust.methods, ...)
```

### Arguments

- `y` either a numeric vector of data values, or a data matrix.
- `groups` a vector giving the group for the corresponding elements of `y` if this is a vector; ignored if `y` is a matrix. If not a factor object, it is coerced to one.
blocks: a vector giving the block for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.


... further arguments to be passed to or from methods.

Details

A one-way ANOVA with repeated measures that is also referred to as ANOVA with unreplicated block design can also be conducted via the friedman.test. The consequent post-hoc pairwise multiple comparison test according to Conover is conducted with this function.

If y is a matrix, than the columns refer to the treatment and the rows indicate the block.

See vignette("PMCMR") for details.

Value

A list with class "PMCMR"

  method: The applied method.
  data.name: The name of the data.
  p.value: The two-sided p-value according to the student-t-distribution.
  statistic: The estimated quantiles of the student-t-distribution.
  p.adjust.method: The applied method for p-value adjustment.

Note

This function does not test for ties.

Author(s)

Thorsten Pohlert

References


See Also

friedman.test, posthoc.friedman.nemenyi.test, TDist p.adjust
Examples

```r
##
## Sachs, 1997, p. 675
## Six persons (block) received six different diuretics
## (A to F, treatment).
## The responses are the Na-concentration (mval)
## in the urine measured 2 hours after each treatment.
##
## y <- matrix(c(
3.88, 5.64, 5.76, 4.25, 5.91, 4.33, 30.58, 30.14, 16.92,
23.19, 26.74, 10.91, 25.24, 33.52, 25.45, 18.85, 20.45,
26.67, 4.44, 7.94, 4.04, 4.4, 4.23, 4.36, 29.41, 30.72,
32.92, 28.23, 23.35, 12, 38.87, 33.12, 39.15, 28.86, 38.23,
26.65), nrow=6, ncol=6,
dimnames=list(1:6,c("A","B","C","D","E","F")))
print(y)
friedman.test(y)
posthoc.friedman.conover.test(y=y, p.adjust="none")
```

---

posthoc.friedman.nemenyi.test

*Pairwise post-hoc Test for Multiple Comparisons of Mean Rank Sums for Unreplicated Blocked Data (Nemenyi-Test)*

Description

Calculate pairwise comparisons using Nemenyi post-hoc test for unreplicated blocked data. This test is usually conducted post-hoc after significant results of the Friedman test. The statistics refer to upper quantiles of the studentized range distribution (Tukey).

Usage

```r
posthoc.friedman.nemenyi.test(y, ...)
```

## Default S3 method:
posthoc.friedman.nemenyi.test(y, groups, blocks, ...)

## S3 method for class 'formula'
posthoc.friedman.nemenyi.test(formula, data, subset, na.action, ...)

Arguments

- `y`: either a numeric vector of data values, or a data matrix.
- `groups`: a vector giving the group for the corresponding elements of `y` if this is a vector; ignored if `y` is a matrix. If not a factor object, it is coerced to one.
blocks  
a vector giving the block for the corresponding elements of y if this is a vector; 
ignored if y is a matrix. If not a factor object, it is coerced to one.

formula  
a formula of the form a ~ b | c, where a, b and c give the data values and 
corresponding groups and blocks, respectively.

data  
an optional matrix or data frame (or similar: see model.frame) containing 
the variables in the formula formula. By default the variables are taken from 
environment(formula).

subset  
an optional vector specifying a subset of observations to be used.

na.action  
a function which indicates what should happen when the data contain NAs. De-
defaults to getOption("na.action").

...  
further arguments to be passed to or from methods.

Details

A one-way ANOVA with repeated measures that is also referred to as ANOVA with unreplicated 
block design can also be conducted via the friedman.test. The consequent post-hoc pairwise 
multiple comparison test according to Nemenyi is conducted with this function.

If y is a matrix, than the columns refer to the treatment and the rows indicate the block.

See vignette("PMCMR") for details.

Let R_i and n_i denote the sum of Friedman-ranks and the sample size of the j-th group, respectively, 
then a difference between two groups is significant on the level of α, if the following inequality is 
met:

\[
\left| \frac{R_i}{n_i} - \frac{R_j}{n_j} \right| > q_{\infty;\alpha} \sqrt{\frac{k}{n}} \sqrt{\frac{k(k+1)}{6n}}
\]

with k the number of groups (or treatments) and n the total number of data.

Value

A list with class "PMCMR"

method  
The applied method.

data.name  
The name of the data.
p.value  
The p-value according to the studentized range distribution.

statistic  
The estimated upper quantile of the studentized range distribution.
p.adjust.method  
Defaults to "none"

Note

This function does not test for ties.

Author(s)

Thorsten Pohlert
References


See Also

`friedman.test, kruskal.test, posthoc.kruskal.nemenyi.test, Tukey`

Examples

```r
## Sachs, 1997, p. 675
## Six persons (block) received six different diuretics (A to F, treatment).
## The responses are the Na-concentration (mval)
## in the urine measured 2 hours after each treatment.
##
## y <- matrix(c(
3.88, 5.64, 5.76, 4.25, 5.91, 4.33, 30.58, 30.14, 16.92,
23.19, 26.74, 10.91, 25.24, 33.52, 25.45, 18.85, 20.45,
26.67, 4.44, 7.94, 4.04, 4.4, 4.23, 4.36, 29.41, 30.72,
32.92, 28.23, 23.35, 12, 38.87, 33.12, 39.15, 28.86, 38.23,
26.65), nrow=6, ncol=6,
dimnames=list(1:6,c("A","B","C","D","E","F")))
print(y)
friedman.test(y)
posthoc.friedman.nemenyi.test(y)
```

**posthoc.kruskal.conover.test**

*Pairwise Test for Multiple Comparisons of Mean Rank Sums (Conover's Test)*

Description

Calculate pairwise multiple comparisons between group levels according to Conover.

Usage

`posthoc.kruskal.conover.test(x, ...)`

## Default S3 method:
`posthoc.kruskal.conover.test( x, g, p.adjust.method =
p.adjust.methods, ...)

## S3 method for class 'formula'

```r
```
`posthoc.kruskal.conover.test` function in R is used for post-hoc tests after a Kruskal-Wallis test.

**Arguments**

- `x`: A numeric vector of data values, or a list of numeric data vectors.
- `g`: A vector or factor object giving the group for the corresponding elements of `x`. Ignored if `x` is a list.
- `formula`: A formula of the form `response ~ group` where `response` gives the data values and `group` a vector or factor of the corresponding groups.
- `data`: An optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
- `subset`: An optional vector specifying a subset of observations to be used.
- `na.action`: A function which indicates what should happen when the data contain `NA`s. Defaults to `getOption("na.action")`.
- `...`: Further arguments to be passed to or from methods.

**Details**

For one-factorial designs with samples that do not meet the assumptions for one-way-ANOVA and subsequent post-hoc tests, the Kruskal-Wallis-Test `kruskal.test` can be employed that is also referred to as the Kruskal–Wallis one-way analysis of variance by ranks. Provided that significant differences were detected by this global test, one may be interested in applying post-hoc tests according to Conover for pairwise multiple comparisons of the ranked data.

See vignette("PMCMR") for details.

**Value**

A list with class "PMCMR"

- `method`: The applied method.
- `data.name`: The name of the data.
- `p.value`: The two-sided p-value of the student-t-distribution.
- `statistic`: The estimated quantile of the student-t-distribution.

**Note**

A tie correction will be employed according to Conover (1979).
Author(s)

Thorsten Pohlert

References


See Also

`kruskal.test`, `posthoc.kruskal.nemenyi.test`, `posthoc.kruskal.dunn.test`, `TDist.p.adjust`

Examples

```r
##
require(stats)
data(InsectSprays)
attach(InsectSprays)
kruskal.test(count ~ spray)
posthoc.kruskal.conover.test(count, spray, "bonferroni")
detach(InsectSprays)
rm(InsectSprays)
## Formula Interface
posthoc.kruskal.conover.test(count ~ spray, data = InsectSprays, p.adjust="bonf")
```

---

**posthoc.kruskal.dunn.test**

*Pairwise Test for Multiple Comparisons of Mean Rank Sums (Dunn’s-Test)*

Description

Calculate pairwise multiple comparisons between group levels according to Dunn.

Usage

`posthoc.kruskal.dunn.test(x, ...)`

## Default S3 method:
`posthoc.kruskal.dunn.test( x, g, p.adjust.method = p.adjust.methods, ...)`

## S3 method for class 'formula'
`posthoc.kruskal.dunn.test(formula, data, subset, na.action, p.adjust.method = p.adjust.methods, ...)`
Arguments

x  a numeric vector of data values, or a list of numeric data vectors.
g  a vector or factor object giving the group for the corresponding elements of x. Ignored if x is a list.

formula  a formula of the form response ~ group where response gives the data values and group a vector or factor of the corresponding groups.

data  an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).

subset  an optional vector specifying a subset of observations to be used.

na.action  a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").

p.adjust.method  Method for adjusting p values (see p.adjust).

...  further arguments to be passed to or from methods.

Details

For one-factorial designs with samples that do not meet the assumptions for one-way-ANOVA and subsequent post-hoc tests, the Kruskal-Wallis-Test kruskal.test can be employed that is also referred to as the Kruskal–Wallis one-way analysis of variance by ranks. Provided that significant differences were detected by this global test, one may be interested in applying post-hoc tests according to Dunn for pairwise multiple comparisons of the ranked data.

See vignette("PMCMR") for details.

Value

A list with class "PMCMR"

method  The applied method.
data.name  The name of the data.
p.value  The two-sided p-value of the standard normal distribution.
statistic  The estimated quantile of the standard normal distribution.
p.adjust.method  The applied method for p-value adjustment.

Note

A tie correction will be employed according to Glantz (2012).

Author(s)

Thorsten Pohlert
References


See Also

kruskal.test, friedman.test, posthoc.friedman.nemenyi.test, pnorm, p.adjust

Examples

```r
##
require(stats)
data(InsectSprays)
attach(InsectSprays)
kruskal.test(count, spray)
posthoc.kruskal.nemenyi.test(count, spray, "bonferroni")
detach(InsectSprays)
rm(InsectSprays)
## Formula Interface
posthoc.kruskal.nemenyi.test(count ~ spray, data = InsectSprays, p.adjust="bonf")
```

---

posthoc.kruskal.nemenyi.test

**Pairwise Test for Multiple Comparisons of Mean Rank Sums**

*(Nemenyi-Tests)*

Description

Calculate pairwise multiple comparisons between group levels. These tests are sometimes referred to as Nemenyi-tests for multiple comparisons of (mean) rank sums of independent samples.

Usage

```r
posthoc.kruskal.nemenyi.test(x, ...)
```

## Default S3 method:
posthoc.kruskal.nemenyi.test( x, g, dist = c("Tukey", "Chisquare"), ...)

## S3 method for class 'formula'
posthoc.kruskal.nemenyi.test(formula, data, subset, na.action, dist = c("Tukey", "Chisquare"), ...)
"
Arguments

x          a numeric vector of data values, or a list of numeric data vectors.
g          a vector or factor object giving the group for the corresponding elements of x. Ignored if x is a list.
formula   a formula of the form response ~ group where response gives the data values and group a vector or factor of the corresponding groups.
data       an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset    an optional vector specifying a subset of observations to be used.
na.action a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
...        further arguments to be passed to or from methods.
dist       the method for determining the p-value. The default distribution is "Tukey", else "Chisq".

Details

For one-factorial designs with samples that do not meet the assumptions for one-way-ANOVA and subsequent post-hoc tests, the Kruskal-Wallis-Test kruskal.test can be employed that is also referred to as the Kruskal–Wallis one-way analysis of variance by ranks. Provided that significant differences were detected by this global test, one may be interested in applying post-hoc tests according to Nemenyi for pairwise multiple comparisons of the ranked data.

See vignette("PMCMR") for details.

Value

A list with class "PMCMR"

method      The applied method.
data.name   The name of the data.
p.value     The p-value according to the studentized range distribution.
statistic   The estimated upper quantile of the studentized range distribution. (or quantile of Chisq distribution)
p.adjust.method Defaults to "none"

Note

Only for method = "Chisq" a tie correction is employed.

Author(s)

Thorsten Pohlert
posthoc.quade.test

References

See Also

kruskal.test, friedman.test, posthoc.friedman.nemenyi.test, Tukey, Chisquare

Examples

```r
## require(stats)
data(InsectSprays)
attach(InsectSprays)
kruskal.test(count ~ spray)
posthoc.kruskal.nemenyi.test(count, spray)
posthoc.kruskal.nemenyi.test(count, spray, "Chisq")
detach(InsectSprays)
rm(InsectSprays)
## Formula Interface
posthoc.kruskal.nemenyi.test(count ~ spray, data = InsectSprays, dist="Tukey")
```

---

posthoc.quade.test  
Pairwise post-hoc Test for Multiple Comparisons of Rank Sums for Unreplicated Blocked Data (Quade multiple comparison test)

Description
Calculate pairwise comparisons using Quade’s post-hoc test for unreplicated blocked data. This test is usually conducted post-hoc after significant results of the omnibus test, quade.test.

Usage

```r
posthoc.quade.test(y, ...)  
```

## Default S3 method:

```r
posthoc.quade.test(y, groups, blocks, dist = c("TDist", "Normal"), p.adjust.method = p.adjust.methods, ...)  
```

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>y</td>
<td>either a numeric vector of data values, or a data matrix.</td>
</tr>
<tr>
<td>groups</td>
<td>a vector giving the group for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.</td>
</tr>
<tr>
<td>blocks</td>
<td>a vector giving the block for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.</td>
</tr>
<tr>
<td>dist</td>
<td>the method for determining the p-value. The default distribution is &quot;TDist&quot;, else &quot;Normal&quot;.</td>
</tr>
</tbody>
</table>
**posthoc.quade.test**

```r
p.adjust.method
  Method for adjusting p values (see `p.adjust`).

... further arguments to be passed to or from methods.
```

**Details**

A one-way ANOVA with repeated measures that is also referred to as ANOVA with unreplicated block design can also be conducted via the `quade.test`. The consequent post-hoc pairwise multiple comparison test according to Quade is conducted with this function.

If `y` is a matrix, then the columns refer to the treatment and the rows indicate the block.

See vignette("PMCMR") for details.

**Value**

A list with class "PMCMR"

- `method`: The applied method.
- `data.name`: The name of the data.
- `p.value`: The two-sided p-value according to the selected distribution.
- `statistic`: The estimated quantiles of the selected distribution.

**Author(s)**

Thorsten Pohlert

**References**


**See Also**

`quade.test`, `Normal`, `TDist`, `p.adjust`

**Examples**

```r
## Conover (1999, p. 375f):
## Numbers of five brands of a new hand lotion sold in seven stores
## during one week.
y <- matrix(c( 5, 4,  7, 10, 12,
            1, 3,  1,  8,  2,
            16, 12, 22, 22, 35,
            24, 14, 19, 13, 16),
           nrow = 7, ncol = 5)
```
posthoc.vanWaerden.test

Pairwise Test for Multiple Comparisons of normal scores (van der Waerden test)

Description

Calculate pairwise multiple comparisons between group levels according to van der Waerden.

Usage

posthoc.vanWaerden.test(x, ..., 

## Default S3 method:
posthoc.vanWaerden.test( x, g, p.adjust.method = p.adjust.methods, ...)

## S3 method for class 'formula'
posthoc.vanWaerden.test(formula, data, subset, na.action, p.adjust.method = p.adjust.methods, ...)

Arguments

x a numeric vector of data values, or a list of numeric data vectors.
g a vector or factor object giving the group for the corresponding elements of x. Ignored if x is a list.
formula a formula of the form response ~ group where response gives the data values and group a vector or factor of the corresponding groups.
data an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset an optional vector specifying a subset of observations to be used.
na.action a function which indicates what should happen when the data contain NAs. Defaults togetOption("na.action").
**Details**

For one-factorial designs with samples that do not meet the assumptions for one-way-ANOVA and subsequent post-hoc tests, the van der Waerden test `vanWaerden.test` using normal scores can be employed. Provided that significant differences were detected by this global test, one may be interested in applying post-hoc tests according to van der Waerden for pairwise multiple comparisons of the group levels.

First, the data are ranked according to Kruskal-Wallis. Second, the ranks are transformed to normal scores. The group means of normal scores and the total variance is used to calculate quantiles of the student-t-distribution and consequent p-values.

See vignette("PMCMR") for details.

**Value**

A list with class "PMCMR"

- **method**: The applied method.
- **data.name**: The name of the data.
- **p.value**: The two-sided p-value of the student-t-distribution.
- **statistic**: The estimated quantile of the student-t-distribution.
- **p.adjust.method**: The applied method for p-value adjustment.

**Note**

There is no tie correction applied in this function.

**Author(s)**

Thorsten Pohlert

**References**


**See Also**

`kruskal.test, vanWaerden.test, posthoc.kruskal.nemenyi.test, posthoc.kruskal.dunn.test, TDist, p.adjust`
Examples

```r
##
require(stats)
data(InsectSprays)
attach(InsectSprays)
vanaerden.test(count, spray)
posthoc.vanaerden.test(count, spray, "bonferroni")
detach(InsectSprays)
rm(InsectSprays)
```

---

print.PMCMR  

*Prints PMCMR objects*

Description

print method for class "PMCMR".

Usage

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

Arguments

- `x` an object of class "PMCMR", usually, a result of a call to any of the posthoc-tests included in the package PMCMR.
- `...` further arguments, currently ignored.

Value

The function `print.PMCMR` returns the lower triangle of the (adjusted) p-values from any of the posthoc tests included in the package PMCMR.

Examples

```r
out <- posthoc.kruskal.conover.test(count ~ spray,
data = InsectSprays, p.adjust="bonf")
print(out)
```
summary.PMCMR

Summarizing PMCMR objects

Description

summary method for class "PMCMR".

Usage

## S3 method for class 'PMCMR'
summary(object, ...

Arguments

- **object**: an object of class "PMCMR", usually, a result of a call to any of the posthoc-tests included in the package PMCMR.
- **...**: further arguments, currently ignored.

Value

The function `summary.PMCMR` computes and returns a list of the pairwise comparisons including the H0, the corresponding statistic and the (adjusted) p-value.

Examples

```r
out <- posthoc.kruskal.conover.test(count ~ spray,
data = InsectSprays, p.adjust="bonf")
summary(out)
```

vanWaerden.test

van der Waerden’s normal scores test

Description

Performs a van der Waerden’s normal scores test.

Usage

vanWaerden.test(x, ...)

## Default S3 method:
vanWaerden.test(x, g, ...)

## S3 method for class 'formula'
vanWaerden.test(formula, data, subset, na.action, ...)
vanWaerden.test

Arguments

- **x**: a numeric vector of data values, or a list of numeric data vectors.
- **g**: a vector or factor object giving the group for the corresponding elements of `x`. Ignored if `x` is a list.
- **formula**: a formula of the form `response ~ group` where `response` gives the data values and `group` a vector or factor of the corresponding groups.
- **data**: an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
- **subset**: an optional vector specifying a subset of observations to be used.
- **na.action**: a function which indicates what should happen when the data contain NAs. Defaults to `getOption("na.action")`.
- **...**: further arguments to be passed to or from methods.

Details

`vanWaerden.test` performs a van der Waerden test of the null that the location parameters of the distribution of `x` are the same in each group (sample). The alternative is that they differ in at least one.

See vignette("PMCMR") for details.

Value

A list with class "htest" that contains the following components:

- **statistic**: the van der Waerden chi-squared statistic.
- **parameter**: the degrees of freedom of the approximate chi-squared distribution of the test statistic.
- **p.value**: the p-value of the test.
- **method**: the character string "Van der Waerden normal scores test".
- **data.name**: a character string giving the names of the data.

Note

A tie correction is not applied in this function.

Author(s)

Thorsten Pohlert

References

See Also
   \texttt{kruskal.test}

Examples
   
   ```r
   ##
   require(stats)
   data(InsectSprays)
   attach(InsectSprays)
   vanWaerden.test(count, spray)
   posthoc.vanWaerden.test(count, spray, "bonferroni")
   detach(InsectSprays)
   rm(InsectSprays)
   ```
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