Package 'nparcomp'

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Type Package

Title Perform multiple comparisons and compute simultaneous confidence intervals for the nonparametric relative contrast effects.

Version 2.0

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Description With this package, it is possible to compute nonparametric simultaneous confidence intervals for relative contrast effects in the unbalanced one way layout. Moreover, it computes simultaneous p-values. The simultaneous confidence intervals can be computed using multivariate normal distribution,multivariate t-distribution with a Satterthwaite Approximation of the degree of freedom or using multivariate range preserving transformations with Logit or Probit as transformation function. 2 sample comparisons can be performed with the same methods described above. There is no assumption on the underlying distribution function, only that the data have to be at least ordinal numbers.

License GPL

LazyLoad yes

Depends multcomp, mvtnorm

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`nparcomp-package` *Nparcomp: Nonparametric relative contrast effects.*

Description

With this package, it is possible to compute nonparametric simultaneous confidence intervals for relative contrast effects in the unbalanced one way layout. Moreover, it computes simultaneous p-values. The simultaneous confidence intervals can be computed using multivariate normal distribution, multivariate t-distribution with a Satterthwaite Approximation of the degree of freedom or using multivariate range preserving transformations with Logit or Probit as transformation function. 2 sample comparisons can be performed with the same methods described above. There is no assumption on the underlying distribution function, only that the data have to be at least ordinal numbers.

Details

Package:	nparcomp
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Author(s)

Frank Konietschke

Maintainer: Frank Konietschke <fkoniet@gwdg.de>

References

Konietschke, F. (2009). Simultane Konfidenzintervalle fuer nichtparametrische relative Kontrasteffekte. PhD-thesis, University of Goettingen.

Konietschke, F., Brunner, E., Hothorn, L.A. (2008). Nonparametric Relative Contrast Effects: Asymptotic Theory and Small Sample Approximations, Research report.

Munzel. U., Hothorn, L.A. (2001). A unified Approach to Simultaneous Rank Tests Procedures in the Unbalanced One-way Layout. Biometric Journal, 43, 553-569.

Examples

```
# two sample comparisons: Nonparametric Behrens-Fisher Problem

data(impla)
a<-npar.t.test(impla~group, data = impla,
               method = "t.app",
               alternative = "two.sided")
summary(a)
plot(a)



#--Analysis of relative contrast effects in different contrast settings

data(liver)

 # Williams Contrast

a<-nparcomp(weight ~dosage, data=liver, asy.method = "probit",
 type = "Williams", alternative = "two.sided",
 plot.simci = TRUE, info = FALSE)
summary(a)


 # Dunnett dose 3 is baseline

c<-nparcomp(weight ~dosage, data=liver, asy.method = "probit",
 type = "Dunnett", control = "3",alternative = "two.sided",
 plot.simci = TRUE, info = FALSE)
summary(c)
```

```
data(colu)

  # Tukey comparison - one sided(lower)

a<-nparcomp(corpora~ dose, data=colu, asy.method = "mult.t",
 type = "Tukey",alternative = "less")
summary(a)
plot(a)

  # Tukey comparison- one sided(greater)

b<-nparcomp(corpora~ dose, data=colu, asy.method = "mult.t",
 type = "Tukey",alternative = "greater")
summary(b)
plot(b)
```

---

appetite *Appetite scores of colorectal cancer patients*

Description

Data from one of the quality of life measurements collected from colorectal cancer patients enrolled in the North Central Cancer Treatment Group phase III trials N9741. The patient received three treatment regimens: IFL (irinotecan, bolus fluorouracil, and leucovorin), FOLFOX (infused fluorouracil, leucovorin, and ocaliplatin), and IROX (irinotecan and oxaliplatin).

Usage

```
data(appetite)
```

Format

A data frame with 174 observations on the following 2 variables.

`Group` A factor with levels `FOLFOX` `IFL` `IROX`.

`Score` A numeric vector containing the appetite scores.

Details

The objective is to test whether there are differences between the treatment regimens in terms of different appetite scores.

Source

Ryu, E. (2009): Simultaneous confidence intervals using ordinal effect measures for ordered categorical outcomes. Statistics In Medicine, 28(25), 3179-3188.

Examples

```
library(nparcomp)
data(appetite)
```

---

colu *Numbers of corpora lutea*

Description

Data from a fertility trial with 92 female Wistar rats: numbers of the corpora lutea in a placebo group and in 4 dose groups with an increasing dose of an active treatment.

Usage

```
data(colu)
```

Format

A data frame with 92 observations on the following 2 variables.

`dose` A factor with levels `dose1`, `dose2`, `dose3`, `dose4`, `Placebo`, where Placebo is the placebo group and dose1-dose4 are the 4 dose groups with an increasing dose.

`corpora` A numeric vector containing the numbers of the corpora lutea.

Details

The objective is to test if the active treatment influences the fertiliy of the rats.

Source

Brunner, E., Munzel, U. (2002): Nichtparametrische Datenanalyse - Unverbundene Stichproben. Statistik und ihre Anwendungen, Springer-Verlag.

Examples

```
library(nparcomp)
data(colu)
boxplot(corpora~dose,data=colu)
```

gao *Nonparametric multiple test procedure for many-to-one comparisons*

Description

This function can be used to perform the nonparametric multiple tests for many-to-one comparisons by Gao et al. (2008). The multiple level is strongly controlled by the Hochberg-adjustment.

Usage

```
gao(formula, data, alpha = 0.05, control = NULL, silent = FALSE)
```

Arguments

formula	A two-sided 'formula' specifying a numeric response variable and a factor with more than two levels. If the factor contains less than 3 levels, an error message will be returned.
data	A dataframe containing the variables specified in formula.
alpha	The significance level (by default = 0.05).
control	Character string defining the control group in Dunnett comparisons. By default it is the first group by lexicographical ordering
silent	A logical indicating more informations should be print on screen.

Value

Info	Samples and sizes with estimated relative effects and variance estimators.
Analysis	Comparison: Distributions being compared, Estimator: Estimated effect, df: Degree of Freedom, Statistic: Teststatistic, P.Raw: Raw p-Value P.Hochberg: Adjusted p-Value by the Hochberg adjustment, Rejected: A logical indicating rejected hypotheses, P.Bonf: Bonferroni adjusted p-Values, P.Holm: Holm adjusted p-Value.

Note

The procedure can only be used to test hypotheses in terms of the distribution functions.

Author(s)

Frank Konietschke

References

Gao, X. et al. (2008). Nonparametric Multiple Comparison Procedures for Unbalanced One-Way Factorial Designs. JSPI 138, 2574 - 2591.

See Also

For nonparametric all-pairs comparison see gao_cs.

Examples

```
data(liver)

gao(weight ~dosage, data=liver,alpha=0.05)

 # Control= 3

gao(weight ~dosage, data=liver,alpha=0.05,control="3")
```

---

gao_cs *Nonparametric multiple test procedure for all-pairs comparisons*

Description

This function can be used to perform the nonparametric multiple tests for all-pairs comparisons by Gao et al. (2008). This procedure is a nonparametric equivalent of Campbell and Skillings (1981) sequential test procedure.

Usage

```
gao_cs(formula, data, alpha = 0.05, silent = FALSE)
```

Arguments

formula	A two-sided 'formula' specifying a numeric response variable and a factor with more than two levels. If the factor contains less than 3 levels, an error message will be returned.
data	A dataframe containing the variables specified in formula.
alpha	The significance level (by default = 0.05).
silent	A logical indicating more informations should be print on screen.

Value

Info	Samples and sizes with estimated relative effects and variance estimators.
Single.Analysis	Comp: Distributions being compared, Effect: Estimated effect, Statistic: Test-statistic, DF: Degree of Freedom, P.Raw: Raw p-Value, P.Bonf: Bonferroni adjusted p-Values, P.Holm: Holm adjusted p-Value.
CS.Analysis	Comp: Distributions being compared, Effect: Estimated effect, Statistic: Test-statistic, DF: Degree of Freedom, Quantiles: quantile, Adj. P: adjusted p-Value, Alpha: Significance level alpha, Rejected: A logical indicating rejected hypotheses, Layer: Layer of the stepwise analysis.

Note

The generalized Campbell and Skillings' analysis is performed in the CS.Analysis output. The adjusted quantiles and p-Values are reported. Due to the non-monotonicity of the adjusted quantiles, all results are checked for non-logical relations.

Author(s)

Frank Konietschke

References

Gao, X. et al. (2008). Nonparametric Multiple Comparison Procedures for Unbalanced One-Way Factorial Designs. JSPI 138, 2574 - 2591.

See Also

For nonparametric many-to-one comparison see gao.

Examples

```
data(reaction)

gao_cs(Time ~Group, data=reaction,alpha=0.05)
```

---

impla *Numbers of implantations*

Description

Data from a fertility trial with 29 female Wistar rats: numbers of the implantations in a placebo group and in an active treatment group.

Usage

```
data(impla)
```

Format

A data frame with 29 observations on the following 2 variables.

`group` A factor with levels `Placebo`, `Verum`, where Verum denotes the active treatment group.

`impla` A numeric vector.

Details

The objective is to test if the active treatment influences the fertiliy of the rats.

Source

Brunner, E., Munzel, U. (2002): Nichtparametrische Datenanalyse - Unverbundene Stichproben. Statistik und ihre Anwendungen, Springer-Verlag.

Examples

```
library(nparcomp)
data(impla)
boxplot(impla~group,data=impla)
```

---

liver *Relative liver weights*

Description

Data from a toxicity trial with male Wistar rats: Relative liver weights in a negative control group and in 4 dose groups with an increasing dose of an active treatment. After treatment the relative liver weights of the rats were computed.

Usage

```
data(liver)
```

Format

A data frame with 38 observations on the following 2 variables.

`dosage` A numeric vector indicating the dose/control group.

`weight` A numeric vector containing the relative liver weights.

Details

The objective is to test if the active treatment influences the liver weight of the rats.

Source

Brunner, E., Munzel, U. (2002): Nichtparametrische Datenanalyse - Unverbundene Stichproben. Statistik und ihre Anwendungen, Springer-Verlag.

Examples

```
data(liver)
boxplot(weight~dosage,data=liver)
```

mctp *Nonparam. multiple contrast tests and simult. confidence intervals*

Description

The function mctp computes the estimator of nonparametric relative effects based on global rankings, simultaneous confidence intervals for the effects and adjusted p-values based on special contrasts like "Tukey", "Dunnett", "Sequen", "Williams", "Changepoint", "AVE", "McDermott", "Marcus", "UmbrellaWilliams", "UserDefined". The statistics are computed using multivariate normal distribution, multivariate Satterthwaite t-Approximation and multivariate transformations (Fisher function). The function 'mctp' also computes one-sided and two-sided confidence intervals and p-values. The confidence intervals can be plotted.

Usage

```
mctp(formula, data, type = c("Tukey", "Dunnett", "Sequen",
     "Williams", "Changepoint", "AVE", "McDermott", "Marcus",
     "UmbrellaWilliams", "UserDefined"), conf.level = 0.95,
     alternative = c("two.sided", "less", "greater"),
     asy.method = c("fisher", "mult.t", "normal"),
     plot.simci = FALSE, control = NULL, info = TRUE, rounds = 3,
     contrast.matrix = NULL, correlation = FALSE,
     effect=c("unweighted","weighted"))
```

Arguments

formula	A two-sided 'formula' specifying a numeric response variable and a factor with more than two levels. If the factor contains less than 3 levels, an error message will be returned.
data	A dataframe containing the variables specified in formula.
type	Character string defining the type of contrast. It should be one of "Tukey", "Dunnett", "Sequen", "Williams", "Changepoint", "AVE", "McDermott", "Marcus", "UmbrellaWilliams", "UserDefined".
conf.level	The confidence level for conflevel-confidence intervals (default is 0.95).
alternative	Character string defining the alternative hypothesis, one of "two.sided", "less" or "greater".
asy.method	Character string defining the asymptotic approximation method, one of "mult.t" for using a multivariate t-distribution with a Satterthwaite Approximation, "fisher" for using the Fisher transformation function, "normal", for using the multivariate normal distribution.
plot.simci	A logical indicating whether you want a plot of the confidence intervals.
control	Character string defining the control group in Dunnett comparisons. By default it is the first group by definition of the factor variable.
info	A logical whether you want a brief overview with informations about the output.

rounds	Number of rounds for the numeric values of the output (default is 3).
contrast.matrix	User defined contrast matrix.
correlation	A logical whether the estimated correlation matrix and covariance matrix should be printed.
effect	Character string defining the type of effect, one of "unweighted" and "weighted".

Value

Data.Info	List of samples and sample sizes and estimated effect per group.
Contrast	Contrast matrix.
Analysis	Estimator: Estimated relative effect, Lower: Lower limit of the simultaneous confidence interval, Upper: Upper limit of the simultaneous confidence interval, Statistic: Teststatistic p.Value: Adjusted p-values for the hypothesis by the choosen approximation method.
input	List of input by user.

Note

If the samples are completely seperated the variance estimators are Zero by construction. In these cases the Null-estimators are replaced by 0.001. Estimated relative effects with 0 or 1 are replaced with 0.001, 0.999 respectively.

A summary and a graph can be created separately by using the functions summary.mctp and plot.mctp.

For the analysis, the R packages 'multcomp' and 'mvtnorm' are required.

Author(s)

Frank Konietschke

References

F. Konietschke, L.A. Hothorn, E. Brunner: Rank-Based Multiple Test Procedures and Simultaneous Confidence Intervals. Electronic Journal of Statistics, Vol.0 (2011) 1-8.

See Also

For simultaneous confidence intervals for relative contrast effects, see nparcomp.

Examples

```
data(liver)

  # Williams Contrast

a<-mctp(weight ~dosage, data=liver, asy.method = "fisher",
        type = "Williams", alternative = "two.sided",
```

```
        plot.simci = TRUE, info = FALSE)
summary(a)

 # Dunnett Contrast

b<-mctp(weight ~dosage, data=liver, asy.method = "fisher",
        type = "Dunnett", alternative = "two.sided",
        plot.simci = TRUE, info = FALSE)
summary(b)

 # Dunnett dose 3 is baseline

c<-mctp(weight ~dosage, data=liver, asy.method = "fisher",
        type = "Dunnett", control = "3",alternative = "two.sided",
        plot.simci = TRUE, info = FALSE)
summary(c)


data(colu)

  # Tukey comparison- one sided(less)

a<-mctp(corpora~ dose, data=colu, asy.method = "mult.t",
        type = "Tukey",alternative = "less",
        plot.simci = TRUE, info = FALSE)
summary(a)

 # Tukey comparison- one sided(greater)

b<-mctp(corpora~ dose, data=colu, asy.method = "mult.t",
        type = "Tukey",alternative = "greater",
        plot.simci = TRUE, info = FALSE)
summary(b)

  # Tukey comparison- one sided(less)

c<-mctp(corpora~ dose, data=colu, asy.method = "mult.t",
        type = "Tukey",alternative = "less",
        plot.simci = TRUE, info = FALSE)
summary(c)

 # Marcus comparison- one sided(greater)

d<-mctp(corpora~ dose, data=colu, asy.method = "fisher",
        type = "Marcus",alternative = "greater",
        plot.simci = TRUE, info = FALSE)
summary(d)
```

---

mctp.rm *MCTP and SCIs in a repeated measures design (one group)*

Description

In the setting of a repeated measures design with n independent individuals and d repeated measures the function mctp.rm computes the estimator of nonparametric relative effects based on global rankings. Simultaneous confidence intervals for the effects and adjusted p-values based on special contrasts like "UserDefined", "Tukey", "Dunnett", "Sequen", "Williams", "Changepoint", "AVE", "McDermott", "Marcus", "UmbrellaWilliams" are provided. The statistics are computed using multivariate normal distribution, multivariate Satterthwaite t-Approximation and multivariate transformations (Fisher function). The function 'mctp.rm' also computes one-sided and two-sided confidence intervals and p-values. The confidence intervals can be plotted.

Usage

```
mctp.rm(formula, data, type = c("UserDefined", "Tukey", "Dunnett",
        "Sequen", "Williams", "Changepoint", "AVE", "McDermott",
        "Marcus", "UmbrellaWilliams"), control = NULL, conf.level = 0.95,
        alternative = c("two.sided", "lower", "greater"), rounds = 3,
        correlation = FALSE,
        asy.method = c("fisher", "normal", "mult.t"),
        plot.simci = FALSE, info = TRUE, contrast.matrix = NULL)
```

Arguments

formula	A two-sided 'formula' specifying a numeric response variable and a repeated measures factor with more than two levels. If the factor contains less than 3 levels, an error message will be returned.
data	A dataframe containing the variables specified in formula.
type	Character string defining the type of contrast. It should be one of "UserDefined", "Tukey", "Dunnett", "Sequen", "Williams", "Changepoint", "AVE", "McDermott", "Marcus", "UmbrellaWilliams".
control	If type=Dunnett, specification of the factor code which should serve as control (first level is default).
conf.level	The confidence level for conflevel-confidence intervals (default is 0.95).
alternative	Character string defining the alternative hypothesis, one of "two.sided", "less" or "greater".
rounds	Number of rounds for the numeric values of the output (default is 3).
correlation	A logical whether the estimated correlation matrix and covariance matrix should be printed.
asy.method	Character string defining the asymptotic approximation method, one of "mult.t" for using a multivariate t-distribution with a Satterthwaite Approximation, "fisher" for using the Fisher transformation function, "normal", for using the multivariate normal distribution.
plot.simci	A logical indicating whether you want a plot of the confidence intervals.
info	A logical whether you want a brief overview with informations about the output.
contrast.matrix	User defined contrast matrix.

Value

`Data.Info`	List of samples and sample sizes and estimated effect per repeated measures level.
`Contrast`	Contrast matrix.
`Analysis`	Estimator: Estimated relative effect, Lower: Lower limit of the simultaneous confidence interval, Upper: Upper limit of the simultaneous confidence interval, Statistic: Teststatistic p.Value: Adjusted p-values for the hypothesis by the choosen approximation method.
`input`	List of input by user.

Note

Estimated relative effects with 0 or 1 are replaced with 0.001 and 0.999.

A summary and a graph can be created separately by using the functions `summary.mctp.rm` and `plot.mctp.rm`.

For the analysis, the R packages 'multcomp' and 'mvtnorm' are required.

Author(s)

Marius Placzek

References

F. Konietschke, A.C. Bathke, L.A. Hothorn, E. Brunner: Testing and estimation of purely nonparametric effects in repeated measures designs. Computational Statistics and Data Analysis 54 (2010) 1895-1905.

See Also

To analyse simple one-way layouts with independent samples use `mctp`.

Examples

```
data(panic)
a<-mctp.rm(CGI~week, data=panic, type = "Dunnett",
           alternative = "two.sided",
           asy.method = "mult.t", plot.simci = FALSE,
           info = FALSE, contrast.matrix = NULL)
summary(a)
plot(a)

mctp.rm(CGI~week, data=panic, type = "Tukey",
        alternative = "two.sided",
        asy.method = "mult.t", plot.simci = TRUE)
```

npar.t.test *The nonparametric Behrens-Fisher problem*

Description

The function npar.t.test performs two sample tests for the nonparametric Behrens-Fisher problem, that is testing the hypothesis

$$H_0 : p = 1/2$$

where p denotes the relative effect of 2 independent samples and computes confidence intervals for the relative effect p. The statistics are computed using standard normal distribution, Satterthwaite t-Approximation and variance stabilising transformations (Probit and Logit transformation function). For small samples there is also a studentized permutation test implemented. npar.t.test also computes one-sided and two-sided confidence intervals and p-values. The confidence interval can be plotted.

Usage

```
npar.t.test(formula, data, conf.level = 0.95, alternative = c("two.sided",
            "less", "greater"), rounds = 3, method = c("logit",
            "probit", "normal", "t.app", "permu"),
            plot.simci = FALSE, info = TRUE, nperm=10000)
```

Arguments

formula	A two-sided 'formula' specifying a numeric response variable and a factor with two levels. If the factor contains more than two levels, an error message will be returned.
data	A dataframe containing the variables specified in formula.
conf.level	The confidence level (default is 0.95).
alternative	Character string defining the alternative hypothesis, one of "two.sided", "less" or "greater".
rounds	Number of rounds for the numeric values of the output (default is 3).
method	Character string defining the (asymptotic approximation) method, one of "logit", for using the logit transformation function, "probit", for using the probit transformation function, "normal", for using the standard normal distribution or "t.app" for using a t-Distribution with a Satterthwaite Approximation. The studentized permutation test can be obtained by choosing "permu".
plot.simci	A logical indicating whether you want a plot of the confidence interval.
info	A logical whether you want a brief overview with informations about the output.
nperm	The number of permutations for the studentized permutation test. By default it is nperm=10,000.

Value

`Info`	List of samples and sample sizes.
`Analysis`	Effect: relative effect p(a,b) of the two samples 'a' and 'b', Estimator: estimated relative effect, Lower: Lower limit of the confidence interval, Upper: Upper limit of the confidence interval, T: teststatistic p.Value: p-value for the hypothesis by the choosen approximation method.
`input`	List of input by user.

Note

If the samples are completely seperated the variance estimators are Zero by construction. In these cases the Null-estimators are replaced by a replacing method as proposed in the paper from Neubert and Brunner (2006). Estimated relative effects with 0 or 1 are replaced with 0.001, 0.999 respectively.

A summary and a graph can be created separately by using the functions `summary.nparttest` and `plot.nparttest`.

Author(s)

Frank Konietschke

References

Brunner, E., Munzel, U. (2000). The Nonparametric Behrens-Fisher Problem: Asymptotic Theory and a Small Sample Approximation. Biometrical Journal 42, 17 -25.

Neubert, K., Brunner, E., (2006). A Studentized Permutation Test for the Nonparametric Behrens-Fisher Problem. Computational Statistics and Data Analysis.

See Also

For multiple comparison procedures based on relative effects, see `nparcomp`.

Examples

```
data(impla)
a<-npar.t.test(impla~group, data = impla, method = "t.app",
               alternative = "two.sided", info=FALSE)
summary(a)
plot(a)
b<-npar.t.test(impla~group, data = impla, method= "permu",
               alternative = "two.sided", info=FALSE)
summary(b)
plot(b)
```

nparcomp *Nonparametric relative contrast effects*

Description

The function nparcomp computes the estimator of nonparametric relative contrast effects, simultaneous confidence intervals for the effects and simultaneous p-values based on special contrasts like "Tukey", "Dunnett", "Sequen", "Williams", "Changepoint", "AVE", "McDermott", "Marcus", "UmbrellaWilliams", "UserDefined". The statistics are computed using multivariate normal distribution, multivariate Satterthwaite t-Approximation and multivariate transformations (Probit and Logit transformation function). The function 'nparcomp' also computes one-sided and two-sided confidence intervals and p-values. The confidence intervals can be plotted.

Usage

```
nparcomp(formula, data, type = c("Tukey", "Dunnett",
         "Sequen", "Williams", "Changepoint", "AVE", "McDermott",
         "Marcus", "UmbrellaWilliams", "UserDefined"), control = NULL,
         conf.level = 0.95, alternative = c("two.sided", "less",
         "greater"), rounds = 3, correlation = FALSE,
         asy.method = c("logit", "probit", "normal", "mult.t"),
         plot.simci = FALSE, info = TRUE, contrast.matrix=NULL,
         weight.matrix=FALSE)
```

Arguments

formula	A two-sided 'formula' specifying a numeric response variable and a factor with more than two levels. If the factor contains less than 3 levels, an error message will be returned.
data	A dataframe containing the variables specified in formula.
type	Character string defining the type of contrast. It should be one of "Tukey", "Dunnett", "Sequen", "Williams", "Changepoint", "AVE", "McDermott", "Marcus", "UmbrellaWilliams", "UserDefined".
control	Character string defining the control group in Dunnett comparisons. By default it is the first group by definition of the dataset.
conf.level	The confidence level for the conflevel confidence intervals (default is 0.95).
alternative	Character string defining the alternative hypothesis, one of "two.sided", "less" or "greater".
rounds	Number of rounds for the numeric values of the output. By default it is rounds=3.
correlation	A logical whether the estimated correlation matrix and covariance matrix should be printed.
asy.method	Character string defining the asymptotic approximation method, one of "logit", for using the logit transformation function, "probit", for using the probit transformation function, "normal", for using the multivariate normal distribution or "mult.t" for using a multivariate t-distribution with a Satterthwaite Approximation.

plot.simci	A logical indicating whether you want a plot of the confidence intervals.
info	A logical whether you want a brief overview with informations about the output.
contrast.matrix	User defined contrast matrix.
weight.matrix	A logical indicating whether the weight matrix should be printed.

Value

Data.Info	List of samples and sample sizes.
Contrast	Contrast matrix.
Analysis	Comparison: relative contrast effect , relative.effect: estimated relative contrast effect, Estimator: Estimated relative contrast effect, Lower: Lower limit of the simultaneous confidence interval, Upper: Upper limit of the simultaneous confidence interval, Statistic: Teststatistic p.Value: Adjusted p-values for the hypothesis by the choosen approximation method.
input	List of input by user.

Note

If the samples are completely seperated the variance estimators are Zero by construction. In these cases the Null-estimators are replaced by 0.001. Estimated relative effects with 0 or 1 are replaced with 0.001, 0.999 respectively.

A summary and a graph can be created separately by using the functions summary.nparcomp and plot.nparcomp.

For the analysis, the R packages 'multcomp' and 'mvtnorm' are required.

Author(s)

Frank Konietschke

References

Konietschke, F., Brunner, E., Hothorn, L.A. (2008). Nonparametric Relative Contrast Effects: Asymptotic Theory and Small Sample Approximations.

Munzel. U., Hothorn, L.A. (2001). A unified Approach to Simultaneous Rank Tests Procedures in the Unbalanced One-way Layout. Biometric Journal, 43, 553-569.

See Also

For two-sample comparisons based on relative effects, see npar.t.test.

Examples

```
data(liver)

  # Williams Contrast
```

```
a<-nparcomp(weight ~dosage, data=liver, asy.method = "probit",
            type = "Williams", alternative = "two.sided",
            plot.simci = TRUE, info = FALSE,correlation=TRUE)
summary(a)



 # Dunnett dose 3 is baseline

c<-nparcomp(weight ~dosage, data=liver, asy.method = "probit",
            type = "Dunnett", control = "3",
            alternative = "two.sided", info = FALSE)
summary(c)
plot(c)


data(colu)

  # Tukey comparison- one sided(lower)

a<-nparcomp(corpora~ dose, data=colu, asy.method = "mult.t",
            type = "Tukey",alternative = "less",
            plot.simci = TRUE, info = FALSE)
summary(a)


 # Tukey comparison- one sided(greater)

b<-nparcomp(corpora~ dose, data=colu, asy.method = "mult.t",
            type = "Tukey",alternative = "greater",
            plot.simci = TRUE, info = FALSE)
summary(b)
```

---

panic *Clinical Global Impression (CGI) Scores*

Description

Scores for the clinical global impression (CGI) measured on an ordinal scale (ranging from 2 to 8) during eight weeks for 16 patients with panic disorder attacks in a psychiatric clinical trial.

Usage

```
data(panic)
```

Format

A data frame with 80 observations on the following 2 variables.

`CGI` A numeric vector containing the CGI score.

`week` A numeric vector indicating the week (0,2,4,6,8) of measurement.

Details

Note that the first observation in each week corresponds to the first patient, the second one to the second patient, and so on. There are 5 repeated measures per patient.

Source

Brunner, E., Domhof, S., Langer, F. (2002): Nonparametric Analysis of Longitudinal Data in Factorial Experiments. Wiley, New York.

Examples

```
data(panic)
boxplot(CGI~week,data=panic)
```

`plot.mctp` *Visualizing the result of* `mctp`

Description

This function takes an object of class "mctp" and creates a plot of the confidence intervals for the estimated effects.

Usage

```
## S3 method for class 'mctp'
plot(x,...)
```

Arguments

`x`	An object of class "mctp", i.e. the result when applying `mctp` to a dataset. Otherwise an error will occur.
`...`	Arguments to be passed to methods.

Details

It is not possible to change any parameter set in the `mctp`-statement.

Since plot.mctp is a S3 method it suffices to use plot(x) as long as x is of class "mctp". It will be interpreted as plot.mctp(x).

Value

plot.mctp returns a graph that contains a confidence interval for the estimated effect of each contrast. It just visualizes the result of the mctp-statement.

Note

It is possible to create a graphical result of the multiple comparison test procedure directly by setting plot.simci=TRUE in the mctp-statement.

To get a complete result summary of mctp the function summary.mctp can be used.

Author(s)

Frank Konietschke

References

F. Konietschke, L.A. Hothorn, E. Brunner: Rank-Based Multiple Test Procedures and Simultaneous Confidence Intervals. Electronic Journal of Statistics, Vol.0 (2011) 1-8.

See Also

For further information on the usage of mctp, see mctp.

Examples

```
data(liver)
a<-mctp(weight ~dosage, data=liver, asy.method = "fisher",
        type = "Dunnett", alternative = "two.sided", plot.simci = FALSE,
        info = FALSE)
plot(a)
```

---

plot.mctp.rm *Visualizing the result of* mctp.rm

Description

This function takes an object of class "mctp.rm" and creates a plot of the confidence intervals for the estimated effects.

Usage

```
## S3 method for class 'mctp.rm'
plot(x,...)
```

Arguments

x	An object of class "mctp.rm", i.e. the result when applying mctp.rm to a dataset. Otherwise an error will occur.
...	Arguments to be passed to methods.

Details

It is not possible to change any parameter set in the mctp.rm-statement.

Since plot.mctp.rm is a S3 method it suffices to use plot(x) as long as x is of class "mctp.rm". It will be interpreted as plot.mctp.rm(x).

Value

plot.mctp.rm returns a graph that contains a confidence interval for the estimated effect of each contrast. It just visualizes the result of the mctp.rm-statement.

Note

It is possible to create a graphical result of the multiple comparison test procedure directly by setting plot.simci=TRUE in the mctp.rm-statement.

To get a complete result summary of mctp.rm the function summary.mctp.rm can be used.

Author(s)

Marius Placzek

References

F. Konietschke, A.C. Bathke, L.A. Hothorn, E. Brunner: Testing and estimation of purely nonparametric effects in repeated measures designs. Computational Statistics and Data Analysis 54 (2010) 1895-1905.

See Also

For further information on the usage of mctp.rm, see mctp.rm.

Examples

```
data(panic)
a<-mctp.rm(CGI~week, data=panic, type = "Dunnett",
           alternative = "two.sided",
           asy.method =  "fisher", contrast.matrix = NULL)
plot(a)
```

---

plot.nparcomp *Visualizing the result of* nparcomp

Description

This function takes an object of class "nparcomp" and creates a plot of the confidence intervals for the estimated nonparametric contrast effects.

Usage

```
## S3 method for class 'nparcomp'
plot(x,...)
```

Arguments

x	An object of class "nparcomp", i.e. the result when applying nparcomp to a dataset. Otherwise an error will occur.
...	Arguments to be passed to methods.

Details

It is not possible to change any parameter set in the nparcomp-statement.

Since plot.nparcomp is a S3 method it suffices to use plot(x) as long as x is of class "nparcomp". It will be interpreted as plot.nparcomp(x).

Value

plot.nparcomp returns a graph that contains a confidence interval for the estimated nonparametric contrast effect of each contrast. It just visualizes the result of the nparcomp-statement.

Note

It is possible to create a graphical result directly by setting plot.simci=TRUE in the nparcomp-statement.

Author(s)

Frank Konietschke

References

Konietschke, F., Brunner, E., Hothorn, L.A. (2008). Nonparametric Relative Contrast Effects: Asymptotic Theory and Small Sample Approximations.

Munzel. U., Hothorn, L.A. (2001). A unified Approach to Simultaneous Rank Tests Procedures in the Unbalanced One-way Layout. Biometric Journal, 43, 553-569.

See Also

For further information on the usage of nparcomp, see nparcomp.

Examples

```
data(liver)
a<-nparcomp(weight ~dosage, data=liver, asy.method = "probit",
            type = "Williams", alternative = "two.sided",
            plot.simci = FALSE, info = FALSE)
plot(a)
```

plot.nparttest *Visualizing the result of* npar.t.test

Description

This function takes an object of class "nparttest" and creates a plot of the confidence interval for the estimated effect.

Usage

```
## S3 method for class 'nparttest'
plot(x,...)
```

Arguments

x	x An object of class "nparttest", i.e. the result when applying npar.t.test to a dataset. Otherwise an error will occur.
...	... Arguments to be passed to methods.

Details

It is not possible to change any parameter set in the npar.t.test-statement.

Since plot.nparttest is a S3 method it suffices to use plot(x) as long as x is of class "nparttest". It will be interpreted as plot.nparttest(x).

Value

plot.npar.t.test returns a graph that contains a confidence interval for the estimated effect of the nonparametric t-test. It just visualizes the result of the npar.t.test-statement.

Note

It is possible to create a graphical result of the nonparametric t-test directly by setting plot.simci=TRUE in the npar.t.test-statement.

Author(s)

Frank Konietschke

References

Brunner, E., Munzel, U. (2000). The Nonparametric Behrens-Fisher Problem: Asymptotic Theory and a Small Sample Approximation. Biometrical Journal 42, 17 -25.

Neubert, K., Brunner, E., (2006). A Studentized Permutation Test for the Nonparametric Behrens-Fisher Problem. Computational Statistics and Data Analysis.

See Also

For further information on the usage of npar.t.test, see npar.t.test.

Examples

```
data(impla)
a<-npar.t.test(impla~group, data = impla, method = "t.app",
               alternative = "two.sided", plot.simci=FALSE)
plot(a)
```

`reaction` *Reaction times of mice [sec]*

Description

Data from a toxicity trial with 40 mice.

Usage

```
data(reaction)
```

Format

A data frame with 40 observations on the following 2 variables.

`Group` A numeric vector indicating the group.

`Time` A numeric vector containing the reaction times.

Details

The objective is to test if the active treatment influences the reaction time of the mice.

Source

Shirley, E. (1977). Nonparametric Equivalent of Williams Test for Contrasting Increasing Dose Levels of a Treatment. Biometrics 33, 386 - 389.

References

Shirley, E. (1977). Nonparametric Equivalent of Williams Test for Contrasting Increasing Dose Levels of a Treatment. Biometrics 33, 386 - 389.

Examples

```
library(nparcomp)
data(reaction)
boxplot(Time~Group,data=reaction)
```

summary.mctp *Summary of* mctp

Description

The function summary.mctp produces a result summary of mctp. It can only be applied to objects of class "mctp".

Usage

```
## S3 method for class 'mctp'
summary(object,...)
```

Arguments

object	An object of class "mctp", i.e. the result when applying mctp to a dataset. Otherwise an error will occur.
...	Arguments to be passed to methods.

Details

Since summary.mctp is a S3 method it suffices to use summary(x) as long as x is of class "mctp". It will be interpreted as summary.mctp(x).

Value

The function produces a summary of the result of mctp starting with some global information: alternative hypothesis, estimation method, type of contrast, confidence level. This is followed by:

Data.Info	List of samples and sample sizes and estimated effect per group.
Contrast	Contrast matrix.
Analysis	Estimator: Estimated relative effect, Lower: Lower limit of the simultaneous confidence interval, Upper: Upper limit of the simultaneous confidence interval, Statistic: Teststatistic p.Value: Adjusted p-values for the hypothesis by the choosen approximation method.

Note

It is possible to create a graphical result of the multiple comparison test procedure by using the function plot.mctp.

Author(s)

Frank Konietschke

References

F. Konietschke, L.A. Hothorn, E. Brunner: Rank-Based Multiple Test Procedures and Simultaneous Confidence Intervals. Electronic Journal of Statistics, Vol.0 (2011) 1-8.

See Also

For further information on the usage of mctp, see `mctp`.

Examples

```
data(liver)
a<-mctp(weight ~dosage, data=liver, asy.method = "fisher",
        type = "Dunnett", alternative = "two.sided", plot.simci = FALSE,
        info = FALSE)
summary(a)
```

---

summary.mctp.rm *Summary of* `mctp.rm`

Description

The function summary.mctp.rm produces a result summary of `mctp.rm`. It can only be applied to objects of class "mctp.rm".

Usage

```
## S3 method for class 'mctp.rm'
summary(object,...)
```

Arguments

`object`	An object of class "mctp.rm", i.e. the result when applying `mctp.rm` to a dataset. Otherwise an error will occur.
`...`	Arguments to be passed to methods.

Details

Since summary.mctp.rm is a S3 method it suffices to use summary(x) as long as x is of class "mctp.rm". It will be interpreted as summary.mctp.rm(x).

Value

The function produces a summary of the result of `mctp.rm` starting with some global information: alternative hypothesis, estimation method, type of contrast, confidence level. This is followed by:

`Data.Info`	List of samples and sample sizes and estimated effect per group.
`Contrast`	Contrast matrix.

`Analysis` Estimator: Estimated relative effect, Lower: Lower limit of the simultaneous confidence interval, Upper: Upper limit of the simultaneous confidence interval, Statistic: Teststatistic p.Value: Adjusted p-values for the hypothesis by the choosen approximation method.

Note

It is possible to create a graphical result of the multiple comparison test procedure by using the function `plot.mctp.rm`.

Author(s)

Marius Placzek

References

F. Konietschke, A.C. Bathke, L.A. Hothorn, E. Brunner: Testing and estimation of purely nonparametric effects in repeated measures designs. Computational Statistics and Data Analysis 54 (2010) 1895-1905.

See Also

For further information on the usage of mctp.rm, see `mctp.rm`.

Examples

```
data(panic)
a<-mctp.rm(CGI~week, data=panic, type = "Dunnett",
           alternative = "two.sided",
           asy.method =  "fisher", contrast.matrix = NULL)
summary(a)
```

---

summary.nparcomp *Summary of* `nparcomp`

Description

The function summary.nparcomp produces a result summary of `nparcomp`. It can only be applied to objects of class "nparcomp".

Usage

```
## S3 method for class 'nparcomp'
summary(object,...)
```

Arguments

`object`	An object of class "nparcomp", i.e. the result when applying `nparcomp` to a dataset. Otherwise an error will occur.
`...`	Arguments to be passed to methods.

Details

Since summary.nparcomp is a S3 method it suffices to use summary(x) as long as x is of class "nparcomp". It will be interpreted as summary.nparcomp(x).

Value

The function produces a summary of the result of `nparcomp` starting with some global information: alternative hypothesis, estimation method, type of contrast, confidence level, method, interpretation. This is followed by:

`Data.Info`	List of samples and sample sizes.
`Contrast`	Contrast matrix.
`Analysis`	Comparison: relative contrast effect , relative.effect: estimated relative contrast effect, Estimator: Estimated relative contrast effect, Lower: Lower limit of the simultaneous confidence interval, Upper: Upper limit of the simultaneous confidence interval, Statistic: Teststatistic p.Value: Adjusted p-values for the hypothesis by the choosen approximation method.
`Overall`	Overall p-value and critical value.

Note

It is possible to create a graphical result of the nonparametric test procedure nparcomp by using the function `plot.nparcomp`.

Author(s)

Frank Konietschke

References

Konietschke, F., Brunner, E., Hothorn, L.A. (2008). Nonparametric Relative Contrast Effects: Asymptotic Theory and Small Sample Approximations.

Munzel. U., Hothorn, L.A. (2001). A unified Approach to Simultaneous Rank Tests Procedures in the Unbalanced One-way Layout. Biometric Journal, 43, 553-569.

See Also

For further information on the usage of nparcomp, see `nparcomp`.

Examples

```
data(liver)
a<-nparcomp(weight ~dosage, data=liver, asy.method = "probit",
            type = "Williams", alternative = "two.sided",
            plot.simci = FALSE, info = FALSE)
summary(a)
```

---

summary.nparttest *Summary of* npar.t.test

Description

The function summary.npar.t.test produces a result summary of npar.t.test. It can only be applied to objects of class "nparttest".

Usage

```
## S3 method for class 'nparttest'
summary(object,...)
```

Arguments

object	An object of class "nparttest", i.e. the result when applying npar.t.test to a dataset. Otherwise an error will occur.
...	Arguments to be passed to methods.

Details

Since summary.nparttest is a S3 method it suffices to use summary(x) as long as x is of class "nparttest". It will be interpreted as summary.nparttest(x).

Value

The function produces a summary of the result of npar.t.test starting with some global information: alternative hypothesis, confidence level, interpretation. This is followed by:

Info	List of samples and sample sizes.
Analysis	Effect: relative effect p(a,b) of the two samples 'a' and 'b', Estimator: estimated relative effect, Lower: Lower limit of the confidence interval, Upper: Upper limit of the confidence interval, T: teststatistic p.Value: p-value for the hypothesis by the choosen approximation method.
Permutation_Test	Result of the studentized permutation test.

Note

You can create a graphical result of the nonparametric t-test by using the function plot.nparttest.

Author(s)

Frank Konietschke

References

Brunner, E., Munzel, U. (2000). The Nonparametric Behrens-Fisher Problem: Asymptotic Theory and a Small Sample Approximation. Biometrical Journal 42, 17-25.

Neubert, K., Brunner, E., (2006). A Studentized Permutation Test for the Nonparametric Behrens-Fisher Problem. Computational Statistics and Data Analysis.

See Also

For further information on the usage of npar.t.test, see `npar.t.test`.

Examples

```
data(impla)
a<-npar.t.test(impla~group, data = impla, method = "t.app",
               alternative = "two.sided",
               plot.simci=FALSE, info=FALSE)
summary(a)
```

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