

Package ‘MCPAN’

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Type Package

Title Multiple comparisons using normal approximation

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Description Multiple contrast tests and simultaneous confidence intervals based on normal approximation. With implementations for binomial proportions in a 2xk setting (risk difference and odds ratio), poly-3-adjusted tumour rates, and multiple comparisons of biodiversity indices. Approximative power calculation for multiple contrast tests of binomial proportions.

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Description

Multiple contrast tests and simultaneous confidence intervals using normal approximation, if individuals are randomly assigned to treatments in a oneway layout. For dichotomous variables, approximate confidence intervals for the risk difference, risk ratio and odds ratio are available. If the variable of interest is the rate of tumours in long-term rodent carcinogenicity trials (without cause of death information), confidence intervals for poly-k-adjusted tumour rates are available. For abundance data of multiple species, approximate simultaneous confidence intervals for differences of Simpson and Shannon-indices are implemented.

Please note, that the methods implemented in this package are NOT validated yet and NOT published so far.

Details

Package: MCPAN
Type: Package
Version: 1.1-9
Date: 2009-10-12
License: GPL

Author(s)

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References

Reference for multiple differences of proportions:

Schaarschmidt, F., Sill, M., and Hothorn, L.A. (2008): Approximate Simultaneous Confidence Intervals for Multiple Contrasts of Binomial Proportions. *Biometrical Journal* 50, 782-792.

See [binomRDci](#) for the code that reproduces the examples in this reference.

Reference for multiple differences of poly-k-rates:

Schaarschmidt, F., Sill, M., and Hothorn, L.A. (2008): Poly-k-trend tests for survival adjusted analysis of tumor rates formulated as approximate multiple contrast test. *Journal of Biopharmaceutical Statistics* 18, 934-948.

See [poly3ci](#) for the code that reproduces the example in this reference.

Simultaneous confidence intervals for Dunnett-type comparisons to control using odds ratios:

Holford, T.R., Walter, S.D. and Dunnett, C.W. (1989): Simultaneous interval estimates of the odds ratio in studies with two or more comparisons. *Journal of Clinical Epidemiology* 42, 427-434.

Background references:

The Add-2 Confidence interval for the difference of two binomial proportions:

Agresti, A. and Caffo, B.(2000): Simple and effective confidence intervals for proportions and differences of proportions result from adding two successes and two failures. *American Statistician* 54, p. 280-288.

and its generalization to a single contrast of several proportions in:

Price, R.M. and Bonett, D.G. (2004): An improved confidence interval for a linear function of binomial proportions. *Computational Statistics and Data Analysis* 45, 449-456.

For long-term rodent carcinogenicity data: The assumptions of poly-3-adjustment are outlined in:

Bailer, J.A. and Portier, C.J. (1988): Effects of treatment-induced mortality and tumor-induced mortality on tests for carcinogenicity in small samples. *Biometrics* 44, 417-431.

Peddada, S.D., Dinse, G.E., and Haseman, J.K. (2005): A survival-adjusted quantal response test for comparing tumor incidence rates. *Applied Statistics* 54, 51-61.

For correlation of multiple contrasts of binomial proportions, see: *Bretz F, Hothorn L.:* Detecting dose-response using contrasts: asymptotic power and sample size determination for binomial data. *Statistics in Medicine* 2002; 21: 3325-3335.

Examples

```
# # # 1)
# Adjusted p-values and simultaneous confidence intervals
# for 2xk tables of binomial data:
# binomRDtest, binomRDci

# Difference of proportions

binomRDtest(x=c(2,6,4,13), n=c(34,33,36,34),
  names=c("Placebo", "50", "75", "150"),
  type="Dunnett", method="ADD1")

binomRDci(x=c(2,6,4,13), n=c(34,33,36,34),
  names=c("Placebo", "50", "75", "150"),
  type="Dunnett", method="ADD1")

# Odds ratios:

binomORci(x=c(2,6,4,13), n=c(34,33,36,34),
  names=c("Placebo", "50", "75", "150"),
  type="Dunnett")

# For more details on evaluation,
# see:
# ?liarozole

data(liarozole)

# # # 2)
# Adjusted p-values and simultaneous confidence intervals
```

```

# for poly-3-adjusted tumour rates:
# poly3test, poly3ci

data(methyl)
methyl

# poly-3-adjusted sample estimates:

poly3estf(time=methyl$death,
  status=methyl$tumour,
  f=methyl$group)

# Simultaneous Add-1-confidence intervals
# for difference to the control group:

poly3ci(time=methyl$death, status=methyl$tumour,
  f=methyl$group, method="ADD1",
  type="Dunnett", alternative="greater")

# Test for trend, based on Changepoint contrasts:

poly3test(time=methyl$death, status=methyl$tumour,
  f=methyl$group, method="ADD1",
  type="Changepoint", alternative="greater")

# # # 3) Plot of confidence intervals
# created by binomRDci and poly3ci:

MethylCI <- poly3ci(time=methyl$death, status=methyl$tumour,
  f=methyl$group, method="ADD1",
  type="Dunnett", alternative="greater")

plot(MethylCI)

```

binomest

Only for internal use.

Description

Groupwise point and variance estimates for binomials, if data are given as numeric vectors of successes x and trials n , with I the number of levels in the one-way layout

Usage

```

binomest(x, ...)

## Default S3 method:
binomest(x, n, names=NULL,
  method="Wald", success=NULL, ...)

```

```
## S3 method for class 'formula':
binomest(formula, data,
  method="Wald", success=NULL, ...)

## S3 method for class 'table':
binomest(x, method="Wald",
  success=NULL, ...)
```

Arguments

<code>x</code>	either a numeric vector of the number of successes, then n must be specified, or an object of class "table" as can be obtained by using table on a data.frame with to categorical variables
<code>n</code>	a numeric vector of the number of trials, only needed, if x is a numeric vector
<code>names</code>	optional character vector of group names (labels for later output), must have the same length as x and n
<code>formula</code>	a two-sided formula of the style 'response ~ treatment', where 'response' should be a categorical variable with two levels, while treatment should be a factor specifying the treatment levels
<code>data</code>	a data.frame, containing the variables specified in formula
<code>method</code>	a character string, specifying the method for variance estimator, with options "Wald", "ADD1", "ADD2"
<code>success</code>	an optional character string, to indicate the level considered as success if data are given as table, or data.frame, or, serving as label for the event considered as success in later functions
<code>...</code>	currently not used

Details

Only for internal use.

Value

<code>Y</code>	a numeric vector of the groupwise number of successes
<code>n</code>	a numeric vector of the groupwise number of trials (observations)
<code>estimate</code>	a numeric vector of groupwise point estimates for the probability of success, Y/n
<code>estp</code>	a numeric vector of groupwise interval midpoints
<code>varp</code>	a numeric vector of groupwise variance estimators, to be used for CI construction
<code>varcor</code>	a numeric vector of groupwise variance estimators, to be used for correlation structures and test these values are adjusted to be larger than zero also in cases where $Y=0$ or $Y=n$
<code>names</code>	a character vector of the level names of f
<code>success</code>	a character string naming the category which has been defined as success

Examples

```

# if data are available as counts:

nsuccess<-c(1,2,6,8)
ntrials<-c(20,20,20,20)
binomest(x=nsuccess, n=ntrials)

binomest(x=nsuccess, n=ntrials,
  names=c("Control", "A", "B", "C"))

# if data are available as data.frame
# with categorical response variable
# and factor as grouping variable

data(liarozole)
binomest(Improved ~ Treatment, data=liarozole)
binomest(Improved ~ Treatment, data=liarozole, success="y")

# if data are available as table
# and factor as grouping variable

data(liarozole)
tab<-table(liarozole)

binomest(tab)
binomest(tab, success="y")

```

binomORci

Simultaneous confidence intervals for odds ratios

Description

Approximate simultaneous confidence intervals for (weighted geometric means of) odds ratios are constructed. Estimates are derived from fitting a glm on the logit-link, approximate intervals are constructed on the log-link, and transformed to original scale.

Usage

```

binomORci(x, ...)

## Default S3 method:
binomORci(x, n, names = NULL,
  type = "Dunnett", method="GLM", cmat = NULL,
  alternative = "two.sided", conf.level = 0.95,
  dist="MVN", ...)

## S3 method for class 'formula':

```

```

binomORci(formula, data,
  type = "Dunnett", method="GLM", cmat = NULL,
  alternative = "two.sided", conf.level = 0.95,
  dist="MVN", ...)

## S3 method for class 'table':
binomORci(x,
  type = "Dunnett", method="GLM", cmat = NULL,
  alternative = "two.sided", conf.level = 0.95,
  dist="MVN", ...)

## S3 method for class 'matrix':
binomORci(x,
  type = "Dunnett", method="GLM", cmat = NULL,
  alternative = "two.sided", conf.level = 0.95,
  dist="MVN", ...)

```

Arguments

<code>x</code>	a numeric vector, giving the number of successes in I independent samples, or an object of class <i>"table"</i> , representing the 2xk-table, or an object of class <i>"matrix"</i> , representing the 2xk-table
<code>n</code>	numeric vector, giving the number of trials (i.e. the sample size) in each of the I groups (only required if <code>x</code> is a numeric vector, ignored otherwise)
<code>names</code>	an optional character string, giving the names of the groups/ sample in <code>x</code> , <code>n</code> ; if not specified the possible names of <code>x</code> are taken as group names (ignored if <code>x</code> is a table or matrix)
<code>formula</code>	a two-sided formula of the style 'response ~ treatment', where 'response' should be a categorical variable with two levels, while treatment should be a factor specifying the treatment levels
<code>data</code>	a data.frame, containing the variables specified in formula
<code>type</code>	a character string, giving the name of a contrast method, as defined in <i>contrMat (multcomp)</i> ; ignored if <code>cmat</code> is specified
<code>method</code>	a single character string, specifying the method for confidence interval computation; Options are <i>"GLM"</i> and <i>"Woolf"</i> . <i>"GLM"</i> takes the maximum likelihood estimates and the their standard errors; this yields a conservative confidence intervals with uninformative limits if $x=0$ and $x=n$ occurs. <i>"Woolf"</i> adds 0.5 to the cell counts, resulting in less conservative bounds. These can be liberal when extreme proportions are compared.
<code>cmat</code>	a optional contrast matrix
<code>alternative</code>	a single character string, one of "two.sided", "less", "greater"
<code>conf.level</code>	a single numeric value, simultaneous confidence level
<code>dist</code>	a character string, <i>"MVN"</i> invokes multiplicity adjustment via the multivariate normal distribution, <i>"N"</i> invokes use of quantiles of the univariate normal distribution
<code>...</code>	arguments to be passed to binomest , currently only <i>success</i> labelling the event which should be considered as success

Details

This function calls `glm` and fits a one-way-model with family binomial on the logit-link. Then, the point estimates and variances estimates from the fit are taken to construct simultaneous confidence intervals for differences (of weighted arithmetic means) of log-odds. Applying the exponential function to these intervals on the logit scale yields intervals for ratios (of weighted geometric) of odds. For simple groupwise comparisons, one yields intervals for oddsratios. For the case of Dunnett-type contrasts, the calculated simultaneous confidence intervals are those described in Holford et al. (1989).

Specifying `method="GLM"` takes maximum likelihood estimates for the log-odds and their standard errors evaluated at the estimate.

Specifying `method="Woolf"` takes adds 0.5 to each cell count and computes point estimates and standard errors for these continuity corrected values. For the two-sample comparison this method is referred to as "adjusted Woolf" (Lawson, 2005). In this implementation, the lower bounds yielded by this method are additionally expanded to 0, if all values in the denominator are $x=n$ or all values in the numerator are $x=0$, and the upper bounds are expanded to Inf , if all values in the denominator are $x=0$ or all values in the numerator are $x=n$.

Note, that for the case of general contrasts, the methods are not described explicitly so far.

Value

A object of class "binomORci", a list containing:

<code>conf.int</code>	a matrix with 2 columns: lower and upper confidence bounds, and M rows
<code>alternative</code>	character string, as input
<code>conf.level</code>	single numeric value, as input
<code>estimate</code>	a matrix with 1 column: containing the estimates of the contrasts
<code>x</code>	the observed number of successes
<code>n</code>	the number of trials
<code>p</code>	the estimated proportions
<code>success</code>	a character string labelling the event considered as success
<code>names</code>	the group names
<code>method</code>	a character string, specifying the method of interval construction
<code>cmat</code>	the contrast matrix used

Author(s)

Frank Schaarschmidt, Daniel Gerhard

References

Holford, TR, Walter, SD and Dunnett, CW (1989). Simultaneous interval estimates of the odds ratio in studies with two or more comparisons. *Journal of Clinical Epidemiology* 42, 427-434.

See Also

Intervals for the risk difference [binomRDci](#), summary for odds ratio confidence intervals [summary.binomORci](#) plot for confidence intervals [plot.sci](#)

Examples

```

data(liarozole)

table(liarozole)

# Comparison to the control group "Placebo",
# which is the fourth group in alpha-numeric
# order:

ORlia<-binomORci(Improved ~ Treatment,
  data=liarozole, success="y", type="Dunnett", base=4)
ORlia
summary(ORlia)
plot(ORlia)

# if data are available as table:

tab<-table(liarozole)
tab
ORlia2<-binomORci(tab, success="y", type="Dunnett", base=4)
ORlia2

plot(ORlia2, lines=1, lineslty=3)

#####

# Performance for extreme cases

# method="GLM" (the default)

test1<-binomORci(x=c(0,1,5,20), n=c(20,20,20,20), names=c("A","B","C","D"))
test1
plot(test1)

# adjusted Woolf interval

test2<-binomORci(x=c(0,1,5,20), n=c(20,20,20,20), names=c("A","B","C","D"), method="Woolf")
test2
plot(test2)

```

Description

Simultaneous asymptotic CI for contrasts of binomial proportions, assuming that standard normal approximation holds. The contrasts can be interpreted as differences of (weighted averages) of proportions (risk ratios).

Usage

```
binomRDci(x, ...)

## Default S3 method:
binomRDci(x, n, names=NULL,
  type="Dunnett", cmat=NULL, method="Wald",
  alternative="two.sided", conf.level=0.95,
  dist="MVN", ...)

## S3 method for class 'formula':
binomRDci(formula, data,
  type="Dunnett", cmat=NULL, method="Wald",
  alternative="two.sided", conf.level=0.95,
  dist="MVN", ...)

## S3 method for class 'table':
binomRDci(x, type="Dunnett",
  cmat=NULL, method="Wald", alternative="two.sided",
  conf.level=0.95, dist="MVN", ...)

## S3 method for class 'matrix':
binomRDci(x, type="Dunnett",
  cmat=NULL, method="Wald", alternative="two.sided",
  conf.level=0.95, dist="MVN", ...)
```

Arguments

<code>x</code>	a numeric vector, giving the number of successes in I independent samples, or an object of class <i>"table"</i> , representing the 2xk-table, or an object of class <i>"matrix"</i> , representing the 2xk-table
<code>n</code>	a numeric vector, giving the number of trials (i.e. the sample size) in each of the I groups (only required if <code>x</code> is a numeric vector, ignored otherwise)
<code>names</code>	an optional character string, giving the names of the groups/ sample in <code>x</code> , <code>n</code> ; if not specified the possible names of <code>x</code> are taken as group names (ignored if <code>x</code> is a table or matrix)
<code>formula</code>	a two-sided formula of the style 'response ~ treatment', where 'response' should be a categorical variable with two levels, while treatment should be a factor specifying the treatment levels
<code>data</code>	a data.frame, containing the variables specified in formula

type	a character string, giving the name of a contrast method, as defined in <i>contrMat</i> (<i>multcomp</i>); ignored if <i>cmat</i> is specified
cmat	a optional contrast matrix
method	a single character string, specifying the method for confidence interval construction; options are: "Wald", "ADD1", or "ADD2"
alternative	a single character string, one of "two.sided", "less", "greater"
conf.level	a single numeric value, simultaneous confidence level
dist	a character string, "MVN" invokes multiplicity adjustment via the multivariate normal distribution, "N" invokes use of quantiles of the univariate normal distribution
...	arguments to be passed to <i>binomest</i> , currently only <i>success</i> labelling the event which should be considered as success

Details

See the examples for different usages.

Value

A object of class "binomRDci", a list containing:

conf.int	a matrix with 2 columns: lower and upper confidence bounds, and M rows
alternative	character string, as input
conf.level	single numeric value, as input
quantile	the quantile used to construct the confidence intervals
estimate	a matrix with 1 column: containing the estimates of the contrasts
x	the observed number of successes in the treatment groups
n	the number of trials in the treatment groups
p	the estimated proportions in the treatment groups
success	a character string labelling the event considered as success
names	the group names
method	a character string, specifying the method of interval construction
cmat	the contrast matrix used

Note

Note, that all implemented methods are approximate only. The coverage probability of the intervals might seriously deviate from the nominal level for small sample sizes and extreme success probabilities. See the simulation results in Sill (2007) for details.

References

Schaarschmidt, F., Sill, M. and Hothorn, L.A. (2008): Approximate simultaneous confidence intervals for multiple contrasts of binomial proportions. *Biometrical Journal* 50, 782-792.

Background references:

The ideas underlying the "ADD1" and "ADD2" adjustment are described in:

Agresti, A. and Caffo, B.(2000): Simple and effective confidence intervals for proportions and differences of proportions result from adding two successes and two failures. *American Statistician* 54, p. 280-288.

And have been generalized for a single contrast of several proportions in:

Price, R.M. and Bonett, D.G. (2004): An improved confidence interval for a linear function of binomial proportions. *Computational Statistics and Data Analysis* 45, 449-456.

More detailed simulation results are available in:

Sill, M. (2007): Approximate simultaneous confidence intervals for multiple comparisons of binomial proportions. Master thesis, Institute of Biostatistics, Leibniz University Hannover.

See Also

[summary.binomRDci](#), [plot.sci](#)

Examples

```
#####
### Example 1 Tables 1,7,8 in Schaarschmidt et al. (2008): ###
#####

# Number of patients under observation:
n <- c(29, 24, 25, 24, 46)

# Number of patients with complete response:
cr <- c(7, 11, 10, 12, 21)

# (Optional) names for the treatments
dn <- c("0.3_1.0", "3", "10", "30", "90")

# Assume we aim to infer an increasing trend with increasing dosage,
# Using the changepoint contrasts (Table 7, Schaarschmidt et al., 2008)

contrMat(n=n, type="Changepoint")

# The results in Table 8 can be reproduced by calling:

binomRDci(n=n, x=cr, names=dn, alternative="greater",
  method="ADD2", type="Changepoint")

binomRDci(n=n, x=cr, names=dn, alternative="greater",
```

```

method="ADD1", type="Changepoint")

binomRDci(n=n, x=cr, names=dn, alternative="greater",
method="Wald", type="Changepoint")

#####

### Example 2, Tables 2,9,10 in Schaarschmidt et al. 2008 ###

#####

# Data (Table 2)

# animals under risk
n<-c(30,30,30,30)

# animals showing cancer
cancer<-c(20,14,27,19)

# short names for the treatments
trtn<-c("HFaFi", "LFaFi", "HFaNFi", "LFaNFi")

# User-defined contrast matrix (Table 9),
# columns of the contrast matrix

cmat<-rbind(
"Fiber - No Fiber"=c( 0.5, 0.5,-0.5,-0.5),
"Low Fat - High Fat"=c(-0.5, 0.5,-0.5, 0.5),
"Interaction Fat:Fiber"=c( 1, -1, -1, 1))

cmat

# The results in Table 10 can be reproduced by calling:

# simultaneous CI using the add-2 adjustment

sci<-binomRDci(x=cancer, n=n, names=trtn, method="ADD2",
cmat=cmat, dist="MVN")

sci

# marginal CI using the basic Wald formula

ci<-binomRDci(x=cancer, n=n, names=trtn, method="Wald",
cmat=cmat, dist="N")

ci

# check, whether the intended contrasts have been defined:

summary(sci)

# plot the result:

```

```

plot(sci, lines=0, lineslty=3)

#####

# In simple cases, counts of successes
# and number of trials can be just typed:

ntrials <- c(40,20,20,20)
xsuccesses <- c(1,2,2,4)
names(xsuccesses) <- LETTERS[1:4]
ex1D<-binomRDci(x=xsuccesses, n=ntrials, method="ADD1",
  type="Dunnett")
ex1D

ex1W<-binomRDci(x=xsuccesses, n=ntrials, method="ADD1",
  type="Williams", alternative="greater")
ex1W

# results can be plotted:
plot(ex1D, main="Comparisons to control group A", lines=0, linescol="red", lineslwd=2)

# summary gives a more detailed print out:
summary(ex1W)

# if data are represented as dichotomous variable
# in a data.frame one can make use of table:

#####

data(liarozole)

head(liarozole)

binomRDci(Improved ~ Treatment, data=liarozole,
  type="Tukey")

# here, it might be important to define which level of the
# variable 'Improved' is to be considered as success

binomRDci(Improved ~ Treatment, data=liarozole,
  type="Dunnett", success="y", base=4)

# If data are available as a named kx2-contingency table:

tab<-table(liarozole)
tab

# Comparison to the control group "Placebo",
# which is the fourth group in alpha-numeric order:

CIs<-binomRDci(tab, type="Dunnett", success="y", base=4)

```

```
plot(CIs, lines=0)
```

binomRDtest	<i>Simultaneous test for contrasts of independent binomial proportions (in a oneway layout)</i>
-------------	---

Description

P-value of maximum test and adjusted p-values for M contrasts of I groups in a one-way layout. Tests are performed for contrasts of proportions, which can be interpreted as differences of (weighted averages of) proportions.

Usage

```
binomRDtest(x, ...)

## Default S3 method:
binomRDtest(x, n, names=NULL,
  type="Dunnett", cmat=NULL, method="Wald",
  alternative="two.sided", dist="MVN", ...)

## S3 method for class 'formula':
binomRDtest(formula, data,
  type="Dunnett", cmat=NULL, method="Wald",
  alternative="two.sided", dist="MVN", ...)

## S3 method for class 'table':
binomRDtest(x, type="Dunnett",
  cmat=NULL, method="Wald", alternative="two.sided",
  dist="MVN", ...)

## S3 method for class 'matrix':
binomRDtest(x, type="Dunnett",
  cmat=NULL, method="Wald", alternative="two.sided",
  dist="MVN", ...)
```

Arguments

x	a numeric vector, giving the number of successes in I independent samples, or an object of class <i>"table"</i> , representing the 2xk-table, or an object of class <i>"matrix"</i> , representing the 2xk-table
n	a numeric vector, giving the number of trials (i.e. the sample size) in each of the I groups
names	an optional character vector, giving the names of the groups in x, n; if not specified, possibly available names of x are taken as group names

formula	a two-sided formula of the style 'response ~ treatment', where 'response' should be a categorical variable with two levels, while treatment should be a factor specifying the treatment levels
data	a data.frame, containing the variables specified in formula
type	a character string specifying the contrast type
cmat	an optional user defined contrast matrix of dimension MxI
method	a single character string, specifying the method for adjustment, with options: "Wald" (Maximum likelihood estimators), "ADD1" (add1-adjustment on the raw proportion estimates) "ADD2" (add2-adjustment on proportion estimates following Agresti Caffo (2000))
alternative	a character string specifying the direction of the alternative hypothesis
dist	a character string, where "MVN" invokes the computation of p-values using the multivariate normal distribution, and "N" invokes use p-value computation using the univariate normal distribution
...	arguments to be passed to binomest , currently only <i>success</i> labelling the event which should be considered as success

Details

For usage, see the examples.

Value

An object of class "binomRDtest", a list containing:

teststat	a numeric vector of teststatistics of length M
pval	a single numeric p-value, the p-value of the maximum test (minimum p-value)
p.val.adj	a vector of length M, the adjusted p-values of the single contrasts
dist	character string indicating whether the multivariate normal or normal distribution was used for computation of p-values
alternative	a single character vector, as the input
x	the observed number of successes in the treatment groups
n	the number of trials in the treatment groups
p	the estimated proportions in the treatment groups
success	a character string labelling the event considered as success
method	as input, a character string
cmat	used contrast matrix

Note

Note, that all implemented methods are approximate only. The size of the test might seriously deviate from the nominal level for small sample sizes and extreme success probabilities. See the simulation results in Sill (2007) for details.

References

Statistical procedures and characterization of coverage probabilities are described in: Sill, M. (2007): Approximate simultaneous confidence intervals for multiple comparisons of binomial proportions. Master thesis, Institute of Biostatistics, Leibniz University Hannover.

See Also

[summary.binomRDtest](#)

Examples

```
ntrials <- c(40,20,20,20)
xsuccesses <- c(1,2,2,4)
names(xsuccesses) <- LETTERS[1:4]
binomRDtest(x=xsuccesses, n=ntrials, method="ADD1",
  type="Dunnett")

binomRDtest(x=xsuccesses, n=ntrials, method="ADD1",
  type="Williams", alternative="greater")

binomRDtest(x=xsuccesses, n=ntrials, method="ADD2",
  type="Williams", alternative="greater")
```

binomRRci

Simultaneous confidence intervals for ratios of independent binomial proportions

Description

Simultaneous asymptotic CI for contrasts of binomial proportions, assuming that standard normal approximation holds on the log scale. Confidence intervals for ratios of (weighted geometric means) of proportions are calculated based on differences of log-proportions, and normal approximation on the log-scale.

Usage

```
binomRRci(x, ...)

## Default S3 method:
binomRRci(x, n, names=NULL,
  type="Dunnett", cmat=NULL,
  alternative="two.sided", conf.level=0.95,
  dist="MVN", ...)

## S3 method for class 'formula':
binomRRci(formula, data,
```

```

type="Dunnett", cmat=NULL,
alternative="two.sided", conf.level=0.95,
dist="MVN",...)

## S3 method for class 'table':
binomRRci(x, type="Dunnett",
  cmat=NULL, alternative="two.sided",
  conf.level=0.95, dist="MVN",...)

## S3 method for class 'matrix':
binomRRci(x, type="Dunnett",
  cmat=NULL, alternative="two.sided",
  conf.level=0.95, dist="MVN",...)

```

Arguments

<code>x</code>	a numeric vector, giving the number of successes in I independent samples, or an object of class <i>"table"</i> , representing the $2 \times k$ -table, or an object of class <i>"matrix"</i> , representing the $2 \times k$ -table
<code>n</code>	a numeric vector, giving the number of trials (i.e. the sample size) in each of the I groups (only required if <code>x</code> is a numeric vector, ignored otherwise)
<code>names</code>	an optional character string, giving the names of the groups/ sample in <code>x</code> , <code>n</code> ; if not specified the possible names of <code>x</code> are taken as group names (ignored if <code>x</code> is a table or matrix)
<code>formula</code>	a two-sided formula of the style 'response ~ treatment', where 'response' should be a categorical variable with two levels, while treatment should be a factor specifying the treatment levels
<code>data</code>	a data.frame, containing the variables specified in formula
<code>type</code>	a character string, giving the name of a contrast method, as defined in <code>contrMat(multcomp)</code> ; ignored if <code>cmat</code> is specified
<code>cmat</code>	a optional contrast matrix
<code>alternative</code>	a single character string, one of "two.sided", "less", "greater"
<code>conf.level</code>	a single numeric value, simultaneous confidence level
<code>dist</code>	a character string, <i>"MVN"</i> invokes multiplicity adjustment via the multivariate normal distribution, <i>"N"</i> invokes use of quantiles of the univariate normal distribution
<code>...</code>	arguments to be passed to <code>binomest</code> , currently only <i>success</i> labelling the event which should be considered as success

Details

The interval for the ratio of two independent proportions, described in section "Crude Methods using first-order variance estimation" in Gart and Nam (1988) are extended to multiple contrasts. Confidence intervals are constructed based on contrasts for differences of $\log(x+0.5)/(n+0.5)$, using quantiles of the multivariate normal or normal approximation. Applying the exponential

functions to the bounds results in intervals for the risk ratio. In case that 0 occur in both, the numerator and denominator of the ratio, the interval is expanded to $[0, \text{Inf}]$, in case that only 0s numerator go to the numerator, the lower bound is expanded to 0, in case that only 0s go to the denominator, the upper bound is expanded to Inf .

See the examples for different usages.

Value

A object of class "binomRDci", a list containing:

<code>conf.int</code>	a matrix with 2 columns: lower and upper confidence bounds, and M rows
<code>alternative</code>	character string, as input
<code>conf.level</code>	single numeric value, as input
<code>quantile</code>	the quantile used to construct the confidence intervals
<code>estimate</code>	a matrix with 1 column: containing the estimates of the contrasts
<code>x</code>	the observed number of successes in the treatment groups
<code>n</code>	the number of trials in the treatment groups
<code>p</code>	the estimated proportions in the treatment groups
<code>success</code>	a character string labelling the event considered as success
<code>names</code>	the group names
<code>method</code>	a character string, specifying the method of interval construction
<code>cmat</code>	the contrast matrix used

Note

Note, that all implemented methods are approximate only. The coverage probability of the intervals might seriously deviate from the nominal level for small sample sizes and extreme success probabilities.

References

Gart, JJ and Nam, J-m (1988): Approximate interval estimation of the ratio of binomial parameters: a review and corrections for skewness. *Biometrics* 44, 323-338.

See Also

[summary.binomRDci](#) for the risk difference, [summary.binomORci](#) for the odds ratio, [plot.sci](#) for plotting

Examples

```
# In simple cases, counts of successes
# and number of trials can be just typed:

ntrials <- c(40, 20, 20, 20)
xsucceses <- c(1, 2, 2, 4)
```

```

names(xsuccesses) <- LETTERS[1:4]
ex1D<-binomRRci(x=xsuccesses, n=ntrials,
  type="Dunnett")
ex1D

ex1W<-binomRRci(x=xsuccesses, n=ntrials,
  type="Williams", alternative="greater")
ex1W

# results can be plotted:
plot(ex1D, main="Comparisons to control group A")

# summary gives a more detailed print out:
summary(ex1W)

# if data are represented as dichotomous variable
# in a data.frame one can make use of table:

data(liarozole)

head(liarozole)

# here, it might be important to define which level of the
# variable 'Improved' is to be considered as success

binomRRci(Improved ~ Treatment, data=liarozole,
  type="Dunnett", success="y", base=4, alternative="greater")

# If data are available as a named kx2-contingency table:

tab<-table(liarozole)
tab

binomRRci(tab, type="Dunnett", success="y", base=4, alternative="greater")

# Performance for extreme cases:

binomRRci(x=c(0,0,20,5), n=c(20,20,20,20), names=c("A", "B", "C", "D"),
  type="Dunnett", alternative="greater")

```

branch

Rodent bronchial carcinoma data

Description

In a long term rodent carcinogenicity study on female B6C3F1 mice, the effect of vinylcyclohexene diepoxide on the incidence of murine alveolar/bronchiolar tumors was assessed. The mice were exposed to 0 mg/ml, (group 0), 25 mg/ml (group 1), 50 mg/ml (group 2), and 100 (group 3) mg/ml, with 50 animals per group.

Usage

```
data(bronch)
```

Format

A data frame with 200 observations on the following 3 variables.

group a factor with levels 0, 1, 2, 3, labelling the control and the three dose groups

Y a logical vector, indicating whether a tumour was present at time of death (if TRUE), or not (if FALSE)

time a numeric vector, the time of death, counted in days? from begin of the study

Details

Not yet checked for consistency with the source!

Source

Piegorsch WW and Bailer AJ (1997): Statistics for environmental biology and toxicology. Chapman and Hall, London. Table 6.5, page 238.

References

Portier cJ and Bailer AJ (1989): Testing for increased carcinogenicity using survival-adjusted quantal response tests. Fundamental and Applied Toxicology 12, 731.

Examples

```
data(bronch)
# raw tumour counts:

table(bronch[c("group", "Y")])

# groupwise times of death:

boxplot(time ~ group, data=bronch, horizontal=TRUE)

# Using poly3estf, we can produce the
# summary statistics as presented in
# Table 6.6, page 239, of Piegorsch and Bailer (1997):

poly3estf(status=bronch$Y, time=bronch$time, f=bronch$group)
```

censsample	<i>Random data for Poly-k</i>
------------	-------------------------------

Description

Random numbers from two independent Weibull distributions for Mortality and tumour induction.

Usage

```
censsample(n, scale.m, shape.m,  
           scale.t, shape.t = 3, tmax)
```

Arguments

n	a single numeric value, the number of individuals
scale.m	a single numeric value, scale parameter of the Weibull distribution for mortality
shape.m	a single numeric value, shape parameter of the Weibull distribution for mortality
scale.t	a single numeric value, scale parameter of the Weibull distribution for tumour induction
shape.t	a single numeric value, shape parameter of the Weibull distribution for tumour induction
tmax	a single numeric value, maximum time in the trial

Value

A data.frame with columns

time	a numeric vector of length n , the time of death of an individual
status	a logical vector of length n , the tumour status at time of death (TRUE: tumour present, FALSE: no tumour present)
T.t	time of tumour induction (unobservable)
T.m	time of death
tmax	maximum time of death

censsamplef *Random data for Poly-k*

Description

Random data for Poly-k for a one-way layout, with I groups.

Usage

```
censsamplef(n, scale.m, shape.m, scale.t, shape.t = 3, tmax)
```

Arguments

n	a numeric vector, the numbers of individuals of length I
scale.m	a numeric vector, scale parameters of the Weibull distribution for mortality
shape.m	a numeric vector, shape parameters of the Weibull distribution for mortality
scale.t	a numeric vector, scale parameters of the Weibull distribution for tumour induction
shape.t	a numeric vector, shape parameters of the Weibull distribution for tumour induction
tmax	a single numeric value, maximum time in the trial

Value

A data.frame with columns

time	a numeric vector of length <i>n</i> , the time of death of an individual
status	a logical vector of length <i>n</i> , the tumour status at time of death (TRUE: tumour present, FALSE: no tumour present)
T.t	time of tumour induction (unobservable)
T.m	time of death
tmax	maximum time of death
f	a factor of containing an appropriate grouping variable

`corrMatgen`*A function to calculate the correlation matrix*

Description

Correlation matrix for test statistics and confidence intervals assuming multivariate standard normal distribution

Usage

```
corrMatgen(CM, varp)
```

Arguments

CM	a matrix of contrast coefficients, dimension $M \times I$, where M =number of contrasts, and I =number of groups in a oneway layout
varp	a numeric vector of groupwise variance estimates (length = I)

Value

A matrix of dimension $M \times M$.

References

For correlation of contrasts of binomial proportion, see: Bretz F, Hothorn L.: Detecting dose-response using contrasts: asymptotic power and sample size determination for binomial data. *Statistics in Medicine* 2002; 21: 3325-3335.

`estShannon`*Estimate the Shannon Index*

Description

Calculates estimates of the Shannon-Wiener from count data.

Usage

```
estShannon(x, Nspec = NULL)
```

Arguments

x	a integer(numeric) vector of species counts
Nspec	a single integer value, fixing the number of species to a certain value

Value

A list, containing the elements:

estimate	a single numeric value, the estimate with bias correction according to Fritsch and Hsu (1999)
estraw	a single numeric value, the raw estimate
varest	a single numeric value, the variance estimate according to Fritsch and Hsu (1999)

References

Fritsch, KS, and Hsu, JC (1999): Multiple Comparison of Entropies with Application to Dinosaur Biodiversity. *Biometrics* 55, 1300-1305.

See Also

[estSimpsonf](#) for estimating Shannon indices pooled over several samples, grouped by a factor

 estShannonf

Estimate the Shannon-Wiener index

Description

Calculate estimates of the Shannon-Wiener index after pooling over several samples, grouped by a factor variable.

Usage

```
estShannonf(X, f)
```

Arguments

<i>X</i>	a data.frame of dimension n times p with integer entries, where n is the number of samples and p is the number of species
<i>f</i>	a factor variable of length n, grouping the observations in <i>X</i>

Details

The function splits *X* according to the levels of the grouping variable *f*, builds the sum over each column and calculates the Shannon index over the resulting counts.

Value

A list, containing the elements:

estimae	a named numeric vector, the groupwise Shannon indices with bias correction according to Fritsch and Hsu (1999)
estraw	a named numeric vector, the groupwise Shannon indices, without bias correction
varest	a named numeric vector, the groupwise variance estimates of the Shannon indices
table	a matrix, giving the summarized counts of the groups in the rows

References

Fritsch, KS, and Hsu, JC (1999): Multiple Comparison of Entropies with Application to Dinosaur Biodiversity. *Biometrics* 55, 1300-1305.

Examples

```
data(HCD)
HCD

# Groupwise point estimates:
est<-estShannonf(X=HCD[, -1], f=HCD[, 1])

est
```

 estSimpson

Simpson index

Description

Calculates the estimate of the Simpson index from a vector of counts.

Usage

```
estSimpson(x)
```

Arguments

x a integer (numeric) vector, giving the counts of p species in a community

`estSimpsonf`*Estimate the Simpson index from several samples*

Description

Calculate estimates of the Simpson index after pooling over several samples, grouped by a factor variable.

Usage

```
estSimpsonf(X, f)
```

Arguments

`X` a data.frame of dimension n times p with integer entries, where n is the number of samples and p is the number of species

`f` a factor variable of length n , grouping the observations in X

Details

The function splits X according to the levels of the grouping variable f , builds the sum over each column and calculates the Shannon index over the resulting counts.

Value

A list containing the items:

`estimate` the groupwise point estimates of the Simpson index

`varest` the groupwise variance estimates of the Simpson index

`table` a matrix of counts, containing the summed observations for each level of f in its rows

References

Rogers, JA and Hsu, JC (2001): Multiple Comparisons of Biodiversity. *Biometrical Journal* 43, 617-625.

See Also

[estShannonf](#)

Examples

```

# Here, the estimates for the Hell Creek Dinosaur
# example are compared to the estimates in
# Tables 2 and 3 of Rogers and Hsu (2001).

data(HCD)
HCD

# Groupwise point estimates:

est<-estSimpsonf(X=HCD[,-1], f=HCD[,1])

est

# Table 2:

cmat<-rbind(
"lower-middle"=c(1,-1,0),
"lower-upper"=c(1, 0,-1),
"middle-upper"=c(0,1,-1))

# the point estimates:

# cmat
crossprod(t(cmat), est$estimate)

# the standard errors:
# sqrt(diag(cmat

sqrt(diag(crossprod(t(cmat), crossprod(diag(est$varest), t(cmat)) ) ) )

# Table 3:

cmat<-rbind(
"middle-lower"=c(-1,1,0),
"upper-lower"=c(-1,0,1))

# cmat
crossprod(t(cmat), est$estimate)

# sqrt(diag(cmat

sqrt(diag(crossprod(t(cmat), crossprod(diag(est$varest), t(cmat)) ) ) )

# Note, that the point estimates are exactly
# the same as in Rogers and Hsu (2001),
# but the variance estimates are not, whenever
# the Upper group is involved.

```

HCD

Hell Creek Dinosaur Data

Description

Counts of dinosaur families found in three stratigraphic levels of the Cretaceous period in the Hell Creek formation in North Dakota. The eight families are the Ceratopsidae (Ce), Hadrosauridae (Ha), Hypsilophodontidae (Hy), Pachycephalosauridae (Pa), Tyrannosauridae (Ty), Ornithomimidae (Or), Sauronithoididae (Sa) and Dromiaesauridae (Dr).

Usage

```
data(HCD)
```

Format

A data frame with 3 observations on the following 9 variables.

Level a factor with levels *Lower, Middle, Upper*, specifying the stratigraphic levels

Cr a numeric vector, counts of the Ceratopsidae

Ha a numeric vector, counts of the Hadrosauridae

Hy a numeric vector, counts of the Hypsilophodontidae

Pa a numeric vector, counts of the Pachycephalosauridae

Ty a numeric vector, counts of the Tyrannosauridae

Or a numeric vector, counts of the Ornithomimidae

Sa a numeric vector, counts of the Sauronithoididae

Dr a numeric vector, counts of the Dromiaesauridae

Source

Table 1 in: Rogers, JA and Hsu, JC (2001): Multiple Comparisons of Biodiversity. Biometrical Journal 43, 617-625.

References

Sheehan, P.M., et al. (1991): Sudden extinction of the Dinosaurs: Latest Cretaceous, Upper Great Plains, U.S.A. Science 254, 835-839.

Examples

```
data(HCD)
str(HCD)
HCD

mat<-as.matrix(HCD[,-c(1)])
```

```
rownames(mat) <- HCD$Level  
mosaicplot(mat, las=1)  
estSimpsonf(X=HCD[, -c(1)], f=HCD$Level)  
estShannonf(X=HCD[, -c(1)], f=HCD$Level)
```

liarozole

Marked improvement of psoriasis after application of liarozole

Description

In a placebo controlled clinical trial, patients with psoriasis were randomly assigned to a placebo group and three dose groups (50 mg, 75 mg, and 150 mg). Variable of primary interest was the proportion of patients with marked improvement of psoriasis. This data.frame mimics how raw data could have been represented in a larger data frame.

Usage

```
data(liarozole)
```

Format

A data frame with 137 observations on the following 2 variables.

Improved a factor with levels *n, y*, for "no" and "yes"

Treatment a factor with levels *Dose150, Dose50, Dose75, Placebo*

Details

For illustrative purpose only. Number of successes recalculated from proportions presented in the publication, while the number of patients in group *Dose50* was not exactly clear.

Source

Berth-Jones J, Todd G, Hutchinson PE, Thestrup-Pedersen K, Vanhoutte FP: Treatment of psoriasis with oral liarozole: a dose-ranging study. *British Journal of Dermatology* 2000; 143: 1170-1176.

Examples

```
data(liarozole)  
head(liarozole)  
# create a contingency table:  
  
table(liarozole)
```

```

# the order of the groups is alpha-numeric,
# and "y" for success is of higher order than
# to change the order:

liarozole$Treatment<-factor(liarozole$Treatment,
  levels=c("Placebo", "Dose50", "Dose75", "Dose150"))

liarozole$Improved<-factor(liarozole$Improved,
  levels=c("y", "n"))

tab<-table(liarozole)
tab

# Approximate simultaneous confidence intervals
# for the differences pDose-pPlacebo:

LCI<-binomRDci(tab, type="Dunnett",
  alternative="greater", method="ADD1")

LCI

plot(LCI, main="Proportion of patients
  with marked improvement")

# Perform a test on increasing trend
# vs. the placebo group:

Ltest<-binomRDtest(tab, type="Williams",
  alternative="greater", method="ADD1")

summary(Ltest)

```

methyl

NTP bioassay data: effect of methyleugenol on skin fibroma

Description

NTP bioassay of methyleugenol: 200 male rats were randomly assigned to 4 treatment groups with balanced sample size 50. Individuals in treatment group 0, 1, 2, and 3 received doses of 0, 37, 75, and 150 mg methyleugenol per kg body weight, respectively. The response variable *tumour* is the presence of skin fibroma at time of death. The variable *death* gives individual time of death, with a final sacrifice of surviving animals at 730 days after begin of the assay.

Usage

```
data(methyl)
```

Format

A data frame with 200 observations on the following 3 variables.

group a factor with levels 0, 1, 2, 3, specifying dose groups 0, 37, 75, and 150 mg/kg, respectively

tumour a numeric vector, specifying whether a tumour was present at time of death

death a numeric vector, specifying the time of death

Source

National toxicology program (2000).

References

SD Peddada, GE Dinse, JK Haseman (2005): A survival-adjusted quantal response test for comparing tumour incidence rates. *Applied Statistics* 54, 51-61.

Examples

```
data(methyl)
# raw tumour proportions:
table(methyl[c("group", "tumour")])

# time of death:
boxplot(death~group, data=methyl, horizontal=TRUE)
```

mosaicplot.Shannonci

Mosaicplot for Shannonci and Simpsonci

Description

Create a mosaicplot from objects of class Shannonci or Simpsonci

Usage

```
## S3 method for class 'Shannonci':
mosaicplot(x, decreasing = NULL, ...)
## S3 method for class 'Simpsonci':
mosaicplot(x, decreasing = NULL, ...)
```

Arguments

<code>x</code>	an object of class <code>"Simpsonci"</code> or <code>"Shannonci"</code> as can be obtained from calling <code>Simpsonci</code> or <code>Shannonci</code>
<code>decreasing</code>	a single logical value, indicating whether the species should be plotted in the current order (if <code>decreasing=NULL</code>), in decreasing order (if <code>decreasing=TRUE</code>), or in increasing order (if <code>decreasing=FALSE</code>)
<code>...</code>	further arguments to be passed to <code>mosaicplot</code> , see <code>?mosaicplot</code> and <code>?par</code> for details

Details

This function uses the counts in `[["sample.estimate"]][["table"]]` to produce a mosaicplot.

Value

A plot.

Examples

```
data(HCD)

HCDFam <- HCD[, -1]

SCI <- Simpsonci(X=HCDFam, f=HCD[, 1])

mosaicplot(SCI, decreasing=TRUE, col=rainbow(n=8))
```

plot.sci

Plot confidence intervals

Description

Function for convenient plotting of confidence intervals.

Usage

```
## S3 method for class 'sci':
plot(x, ...)
## S3 method for class 'binomRDci':
plot(x, ...)
## S3 method for class 'binomORci':
plot(x, ...)
## S3 method for class 'binomRRci':
plot(x, ...)
```

```
## S3 method for class 'poly3ci':
plot(x, ...)
## S3 method for class 'Shannonci':
plot(x, ...)
## S3 method for class 'Simpsonci':
plot(x, ...)
```

Arguments

`x` an object of class `"binomRDci"`, `"binomORci"`, `"binomRRci"`, `"poly3ci"`, `"sci"`

`...` further arguments as described in [plotCI](#)

Details

Extracts some values and calls [plotCI](#).

Value

A plot.

plotCI	<i>Plot confidence intervals</i>
--------	----------------------------------

Description

A function for convenient plotting of confidence intervals.

Usage

```
## Default S3 method:
plotCI(x, ...)
## S3 method for class 'sci':
plotCI(x, ...)
## S3 method for class 'sci.ratio':
plotCI(x, ...)
## S3 method for class 'confint.glht':
plotCI(x, ...)
```

Arguments

`x` An object of class `"sci"`, `"sci.ratio"` or `"conf.int.glht"` or a list with elements `estimate`, containing a numeric vector, `conf.int`, containing a matrix with two columns, giving the lower and upper bounds, and a string `alternative`, one of `"two.sided"`, `"less"`, `"greater"`

`...` additional arguments to be passed to [plotCI](#)

Details

Plots the estimates, upper and lower limits using *points* and *segments*. The names of *estimate* are passed as labels of the confidence intervals. If infinite bounds occur, the plot region is limited by the most extreme non infinite bound or estimate.

Value

A plot.

See Also

Internally, the function [plotCII](#) is used.

Examples

```
x=c(8,9,9,18,39,44)
n=c(2000,2000,2000,2000,2000,2000)

x<-binomORci(x=x, n=n, names=c("0","120","240","480","600","720"))

plotCI(x, lines=1)
```

plotCII

Plot confidence intervals

Description

A function for convenient plotting of confidence intervals.

Usage

```
plotCII(estimate, lower = NULL, upper = NULL,
        alternative = c("two.sided", "less", "greater"),
        lines = NULL, lineslty = 2, lineslwd = 1,
        linescol = "black", CIvert = FALSE, CIlty = 1,
        CIlwd = 1, CICex = 1, Cicol = "black", CIlength=NULL,
        HL = TRUE, ...)
```

Arguments

<code>estimate</code>	a (named) numeric vector, the names of the elements are taken as labels of the CI
<code>lower</code>	an optional numeric vector, of the same length as <code>estimate</code>
<code>upper</code>	an optional numeric vector, of the same length as <code>estimate</code>
<code>alternative</code>	a single character string, one of "two.sided", "less", "greater"

<code>lines</code>	a numeric (vector) giving the position(s) of line(s) to draw into the plots orthogonal to the confidence intervals
<code>lineslty</code>	possible a vector of line type of the <code>lines</code> , see the options for <code>lty</code> in par
<code>lineslwd</code>	possible a vector of line width of the <code>lines</code> , see the options for <code>lwd</code> in par
<code>linescol</code>	possible a vector of line colors of the <code>lines</code>
<code>CIvert</code>	logical indicating, whether confidence intervals shall be drawn horizontal (default), or vertical (if set to TRUE)
<code>CIlty</code>	single value, to specify the line type used for the CI, see options for <code>lty</code> in ?par
<code>CIlwd</code>	single value, to specify the width type used for the CI, see options for <code>lty</code> in ?par
<code>CIcex</code>	single value, to specify the extension of symbols in the plot, see options for <code>cex</code> in ?par
<code>CIcol</code>	single value, to specify the color used for the CI
<code>CIlength</code>	single numeric value, to be passed to the argument <code>length</code> in function arrows ; to specify the lengths of the CI bounds (in inches); defaults to 0.08 and 0.05 for less than 25 and more than 25 CIs, respectively
<code>HL</code>	a logical, if TRUE (default), plot margins of the are adjusted depending on the length of the names by appropriate calls to <code>par</code> ; this might be incompatible with combining the plot with others in the same device. If set to FALSE, its up to the user to choose appropriate plot margins by calling to <code>par</code> .
<code>...</code>	further arguments to be passed to <code>plot</code>

Details

Test version.

Value

A plot.

See Also

[plotCI](#), for more convenient methods

Examples

```
est<-c(1,2,3)
names(est)<-c("A", "B", "C")
lw=c(0,1,2)
up=c(2,3,4)

plotCII(estimate=est, lower=lw, upper=up)

plotCII(estimate=est, lower=lw, upper=up,
lines=c(-1,0,1),
```

```

lineslty=c(3,1,3),
lineslwd=c(1,2,1))

#####

names(est)<-c("very long names",
  "e v e n l o n g e r n a m e s", "C")

plotCII(estimate=est, lower=lw, upper=up,
  Cicol=c("black","green","red"),
  HL=TRUE
)

#####

names(est)<-c("very long names",
  "e v e n l o n g e r n a m e s", "C")

plotCII(estimate=est, lower=lw, upper=up,
  Cicol=c("black","green","red"),
  HL=TRUE
)

op<-par(no.readonly = TRUE)

layout(matrix(1:2, ncol=1))

par(mar=c(5,14,3,1))

plotCII(estimate=est, lower=lw, upper=up,
  main="Lala 1",
  Cicol=c("black","green","red"),
  lines=-1,
  HL=FALSE
)

plotCII(estimate=est, lower=lw, upper=up,
  main="Lala 2",
  Cicol=c("black","green","red"),
  lines=c(0,1),
  HL=FALSE
)

par(op)

```

Description

Function to calculate simultaneous confidence intervals for several contrasts of poly-3-adjusted tumour rates in a oneway layout. Assuming a data situation as in Peddada(2005) or Bailer and Portier (1988). Simultaneous asymptotic CI for contrasts of tumour rates, assuming that standard normal approximation holds.

Usage

```
poly3ci(time, status, f, type = "Dunnett",
        cmat = NULL, method = "BP", alternative = "two.sided",
        conf.level = 0.95, dist="MVN", k=3, ...)
```

Arguments

time	a numeric vector of times of death of the individuals
status	a logical (or numeric, consisting of 0,1 only) vector giving the tumour status at time of death of each individual, where TRUE (1) = tumour present, FALSE (0) = no tumour present
f	a factor, giving the classification variable
type	a character string, giving the name of a contrast method, as defined in <i>contrMat (multcomp)</i>
cmat	a optional contrast matrix
method	a single character string, specifying the method for adjustment, with options: "BP" (Bailer Portier: assuming poly-3-adjusted rates are binomial variables), "BW" (Bieler, Williams: delta method as in Bieler and Williams (1993)) "ADD1" (as Bailer Portier, including an add1-adjustment on the raw tumour rates) "ADD2" (as Bailer Portier, including an add2-adjustment on the raw tumour rates following Agresti and Caffo (2000) for binomials)
alternative	a single character string
conf.level	a single numeric value, simultaneous confidence level
dist	a character string, "MVN" invokes multiplicity adjustment via the multivariate normal distribution, "N" invokes use of quantiles of the univariate normal distribution
k	the exponent to calculate survival adjusted proportions, default is k=3
...	further arguments to be passed; currently only base, to be passed to <i>contrMat</i> to choose the control group with <i>type="Dunnett"</i>

Value

A object of class "poly3ci", a list containing:

conf.int	a matrix with 2 columns: lower and upper confidence bounds, and M rows
alternative	character string, as input
conf.level	single numeric value, as input
quantile	the quantile used to construct the CIs
estimate	a numeric vector with the point estimates of the contrasts

```

time          as input
status        as input
f             as input
method        as input
cmat          as input, with colnames= factor levels of f
sample.est    a list containing sample estimates

```

Note

Please note that all methods here described are only approximative, and might violate the nominal level in certain situations. Please note further that appropriateness of the point estimates, and consequently of tests and confidence intervals is based on the assumptions in Bailer and Portier (1988), which might be a matter of controversies.

Author(s)

Frank Schaarschmidt

References

The implemented methodology is described in:

Schaarschmidt, F., Sill, M., and Hothorn, L.A. (2008): Approximate Simultaneous confidence intervals for multiple contrasts of binomial proportions. *Biometrical Journal* 50, 782-792.

Background references are:

Assumption for poly-3-adjustment: Bailer, J.A. and Portier, C.J. (1988): Effects of treatment-induced mortality and tumor-induced mortality on tests for carcinogenicity in small samples. *Biometrics* 44, 417-431.

Peddada, S.D., Dinse, G.E., and Haseman, J.K. (2005): A survival-adjusted quantal response test for comparing tumor incidence rates. *Applied Statistics* 54, 51-61.

Bieler, G.S. and Williams, R.L. (1993): Ratio estimates, the Delta Method, and quantal response tests for increased carcinogenicity. *Biometrics* 49, 793-801.

Statistical procedures and characterization of the coverage probabilities are described in: Sill, M. (2007): Approximate simultaneous confidence intervals for multiple comparisons of binomial proportions. Master thesis, Institute of Biostatistics, Leibniz University Hannover.

Examples

```

#####
### Methyleugenol example in Schaarschmidt et al. (2008) ###
#####

# load the data:

data(methyl)

```

```

# The results in Table 5 (Schaarschmidt et al. 2008) can be
# reproduced by calling:

methylW<-poly3ci(time=methyl$death, status=methyl$tumour,
  f=methyl$group, type = "Williams", method = "ADD1", alternative="greater" )

methylW

methylWT<-poly3test(time=methyl$death, status=methyl$tumour,
  f=methyl$group, type = "Williams", method = "ADD1", alternative="greater" )

methylWT

plot(methylW, main="Simultaneous CI for Poly-3-adjusted tumour rates")

# The results in Table 6 can be reproduced by calling:

methylD<-poly3ci(time=methyl$death, status=methyl$tumour,
  f=methyl$group, type = "Dunnett", method = "ADD1", alternative="greater" )

methylD

methylDT<-poly3test(time=methyl$death, status=methyl$tumour,
  f=methyl$group, type = "Dunnett", method = "ADD1", alternative="greater" )

methylDT

plot(methylD, main="Simultaneous CI for Poly-3-adjusted tumour rates")

#####

# unadjusted CI

methylD1<-poly3ci(time=methyl$death, status=methyl$tumour,
  f=methyl$group, type = "Dunnett", method = "ADD1", dist="N" )

methylD1

plot(methylD1, main="Local CI for Poly-3-adjusted tumour rates")

```

poly3est

Only for internal use.

Description

Poly-3- adjusted point and variance estimates for long term carcinogenicity data

Usage

```
poly3est(time, status, tmax, method = "BP", k=NULL)
```

Arguments

time	a numeric vector of times of death of the individuals
status	a logical (or numeric, consisting of 0,1 only) vector giving the tumour status at time of death of each individual, where TRUE (1) = tumour present, FALSE (0) = no tumour present
tmax	a single numeric vector, the final time of the trial
method	a single character string, specifying the method for adjustment, with options: "BP" (Bailer Portier: assuming poly-3-adjusted rates are binomial variables), "BW" (Bieler, Williams: delta method as in Bieler-Williams (1993)) "ADD1" (as Bailer Portier, including an add1-adjustment on the raw tumour rates) "ADD2" (as Bailer Portier, including an add2-adjustment on the raw tumour rates following Agresti Caffo (2000) for binomials)
k	a single numeric value, the exponent to calculate survival adjusted proportions according to Bailer and Portier (1988), defaults to 3

Details

Only for internal use of [poly3test](#) and [poly3ci](#).

Value

A list containing:

Y	number of tumours
n	number of individuals
estimate	poly-3-adjusted rates according to Bailer, Portier (1988)
weight	a vector of poly-3-adjusted weights, of length n
estp	poly-3-adjusted rate (according to method)
nadj	adjusted n (sum of weights)
varp	variance estimate (according to method)
varcor	variance estimate, if necessary corrected such that estimates of 0 can not occur

Note

Please note, that appropriateness of the point estimates seriously depends on whether the assumptions in Bailer and Portier are met or not.

References

Bailer, J.A. and Portier, C.J. (1988): Effects of treatment-induced mortality and tumor-induced mortality on tests for carcinogenicity in small samples. *Biometrics* 44, 417-431.

poly3estf *Only for internal use.*

Description

Poly-3- adjusted point and variance estimates for long term carcinogenicity data if data are given as a numeric time vector, a logical status vector and a factor containing a grouping variable

Usage

```
poly3estf(time, status, tmax=NULL, f, method = "BP", k=NULL)
```

Arguments

time	a numeric vector of times of death of the individuals
status	a logical (or numeric, consisting of 0,1 only) vector giving the tumour status at time of death of each individual, where TRUE (1) = tumour present, FALSE (0) = no tumour present
tmax	a single numeric value, the time of sacrifice in the trial, or the last last time of death, defaults to the maximal value observed in <i>time</i>
f	a factor of the same length as <i>time</i> , <i>status</i> , giving the levels of a grouping variable in a one-way layout
method	a single character string, specifying the method for adjustment, with options: "BP" (Bailer Portier: assuming poly-3-adjusted rates are binomial variables), "BW" (Bieler, Williams: delta method as in Bieler-Williams (1993)) "ADD1" (as Bailer Portier, including an add1-adjustment on the raw tumour rates) "ADD2" (as Bailer Portier, including an add2-adjustment on the raw tumour rates following Agresti Caffo (2000) for binomials)
k	a single numeric value, the exponent to calculate survival adjusted proportions according to Bailer and Portier (1988), defaults to 3

Details

For internal use.

Value

A list containing:

Y	a numeric vector, groupwise number of tumours
n	a numeric vector, groupwise number of individuals
estimate	a numeric vector, groupwise poly-3-adjusted rates according to Bailer, Portier (1988)
weight	a numeric vector of poly-3-adjusted weights
estp	a numeric vector, groupwise poly-3-adjusted rate (according to method)

nadj	adjusted n (sum of weights)
varp	a numeric vector, groupwise variance estimate (according to method)
varcor	a numeric vector, groupwise variance estimate, if necessary corrected such that estimates of 0 can not occur
names	a character vector, the levels of the grouping variable f
k	a single numeric value, as input

Note

See [poly3est](#)

References

See [poly3est](#)

Examples

```
data(bronch)

poly3estf(status=bronch$Y, time=bronch$time, f=bronch$group, k=3)

poly3estf(status=bronch$Y, time=bronch$time, f=bronch$group, k=5)
```

poly3table

Summarize long term carcinogenicity data

Description

Function to summarize data of long term carcinogenicity trials in a text format. Data are assumed to consist of (1) a dichotomous variable, defining whether the tumour of interest was present in an individual animal at time of death, and (2) a numeric variable containing the time of death of an individual animal, and (3) a grouping factor.

Usage

```
poly3table(time, status, f, tumour = NULL, symbol = "*")
```

Arguments

time	a numeric vector, containing the time of death of an individual
status	a logical (or dichotomous categorical) vector
f	a factor, specifying treatment groups
tumour	the value which <i>status</i> obtains if a tumour is present in an individual at time of death
symbol	symbol to indicate presence of tumour in the text representation

Value

A named list, containing a character string for each group

Author(s)

Frank Schaarschmidt

Examples

```
data(methyl)
methyl
poly3table(time=methyl$death, status=methyl$tumour,
  f=methyl$group, tumour = 1, symbol = "*")
```

poly3test

Approximate simultaneous test for poly-3-adjusted tumour rates

Description

P-value of maximum test and adjusted p-values for M contrasts of I groups in a one-way layout. Based on approximation of the true distribution of the M test statistics by an M-variate normal distribution.

Usage

```
poly3test(time, status, f, type = "Dunnett",
  cmat = NULL, method = "BP", alternative = "two.sided",
  dist="MVN", k=3, ...)
```

Arguments

time	a numeric vector of times of death of the individuals
status	a logical (or numeric, consisting of 0,1 only) vector giving the tumour status at time of death of each individual, where TRUE (1) = tumour present, FALSE (0) = no tumour present
f	a factor of the same length as <i>time</i> , <i>status</i> , giving the levels of a grouping variable in a one-way layout
type	a character string specifying the contrast type
cmat	an optional user defined contrast matrix of dimension MxI
method	a single character string, specifying the method for adjustment, with options: "BP" (Bailer Portier: assuming poly-3-adjusted rates are binomial variables), "BW" (Bieler, Williams: delta method as in Bieler-Williams (1993)) "ADD1" (as Bailer Portier, including an add1-adjustment on the raw tumour rates) "ADD2" (as Bailer Portier, including an add2-adjustment on the raw tumour rates following Agresti Caffo (2000) for binomials)

alternative	a character string specifying the direction of the alternative hypothesis
dist	a character string, where "MVN" invokes the computation of p-values using the multivariate normal distribution, and "N" invokes use p-value computation using the univariate normal distribution
k	a single numeric value, the exponent to calculate survival adjusted proportions according to Bailer and Portier (1988), defaults to 3
...	further arguments to be passed; currently only <i>base</i> , to choose the control group with <i>type="Dunnett"</i>

Details

Testversion.

Value

An object of class "poly3test", a list containing:

teststat	a numeric vector of teststatistics of length M
pval	a single numeric p-value, the p-value of the maximum test (minimum p-value)
p.val.adj	a vector of length M, the adjusted p-values of the single contrasts
alternative	a single character vector, as the input
dist	a character string specifying which distribution
time	as input
status	as input
f	as input
method	as input
cmat	used contrast matrix
sample.est	a list containing sample estimates

Note

Please note that all methods here described are only approximative, and might violate the nominal level in certain situations. Please note further that appropriateness of the point estimates, and consequently of tests and confidence intervals is based on the assumptions in Bailer and Portier (1988), which might be a matter of controversies.

References

Assumptions corresponding to the poly-k-adjustment:

Bailer, J.A. and Portier, C.J. (1988): Effects of treatment-induced mortality and tumor-induced mortality on tests for carcinogenicity in small samples. *Biometrics* 44, 417-431.

Peddada, S.D., Dinse, G.E., and Haseman, J.K. (2005): A survival-adjusted quantal response test for comparing tumor incidence rates. *Applied Statistics* 54, 51-61.

Statistical procedures and characterization of coverage probabilities are described in: Sill, M. (2007): Approximate simultaneous confidence intervals for multiple comparisons of binomial proportions. Master thesis, Institute of Biostatistics, Leibniz University Hannover.

Examples

```

# poly-3-adjusted tumour rates with a potential
# down-turn effect for the highest dose group "4":

data(methyl)

# many-to-one:
methylD<-poly3test(time=methyl$death, status=methyl$tumour,
  f=methyl$group, type = "Dunnett", method = "ADD1")

methylD

# Williams-Contrast:
methylW<-poly3test(time=methyl$death, status=methyl$tumour,
  f=methyl$group, type = "Williams", method = "ADD1", alternative="greater" )

methylW

# Changepoint-Contrast:
methylCh<-poly3test(time=methyl$death, status=methyl$tumour,
  f=methyl$group, type = "Change", method = "ADD1", alternative="greater" )

methylCh

```

powerbinom

*Approximate power for multiple contrast tests of binomial proportions***Description**

Approximative power calculation for multiple contrast tests of binomial proportions, based on probabilities of the multivariate standard normal distribution.

Usage

```
powerbinom(p, n, alpha = 0.05, type = "Williams", cmat = NULL, method = "Wald", alt
```

Arguments

p	a numeric vector, the proportions assumed under the alternative
n	an integer vector, the number of observations, must be of same length as p
alpha	a single numeric value, the alpha-level of the test
type	if <i>cmat</i> is not specified, the type of multiple contrast test to be applied on the proportions <i>p</i> ; will be ignored if <i>cmat</i> is specified
cmat	a numeric contrast matrix, number of columns must be the same as length of <i>n</i> , and <i>p</i> ; if scified, <i>type</i> will be ignored

method	a character string, the method for variance estimation in test / confidence interval construction: one of "Wald", "ADD1", "ADD2"; see binomRDtest
alternative	a character string, specifying the alternative, options are "two.sided", "less", "greater"

Details

Calls [powermcp](#).

Power for an Union-Intersection-Test is calculated, i.e. the power that H_0 is rejected for at least one of the contrasts specified by *cmat* or *type*.

For the Wald-method, see the methods in Bretz and Hothorn (2002). The implementation in this function differs slightly from the methods described in Bretz and Hothorn. Here, we use an un-pooled variance estimator, while Bretz and Hothorn us a pooled variance estimator.

Note, that currently only power calculation for Union-Intersection-Tests of type $H_0: \text{ALL } L_m \leq 0$ vs. $H_A: \text{ANY } L_m > 0$ (alternative="greater"), $H_0: \text{ALL } L_m \geq 0$ vs. $H_A: \text{ANY } L_m < 0$ (alternative="less"), or $H_0: \text{ALL } L_m = 0$ vs. $H_A: \text{ANY } L_m < \text{or} > 0$ (alternative="two.sided") are implemented. Power for tests against $\delta > 0$ or $\delta < 0$ is not implemented.

Calculation is based on probabilities of the multivariate standard normal distribution, thus will be only appropriate if normal approximation for the test statistics holds. Therefore, results might be misleading for small sample sizes, such as $n < 40$, and a warning is posted. In this case, simulation is recommended.

Value

A single numeric value, the power.

References

Bretz F, Hothorn L.: Detecting dose-response using contrasts: asymptotic power and sample size determination for binomial data. *Statistics in Medicine* 2002; 21: 3325-3335.

See Also

[powermcp](#)

Examples

```
# Assume, one wants to perform a test for increasing trend
# using Williams type of contrasts among I=5 groups
# (e.g. 4 doses and one control).
# Proportions are assumed to have values
# pi=(0.1,0.12,0.14,0.14,0.2) under the alternative.

powerbinom(p=c(0.1, 0.12, 0.14, 0.14, 0.2),
n=c(20,20,20,20,20), type = "Williams",
method = "ADD1", alternative = "greater")
```

```

powerbinom(p=c(0.1, 0.12, 0.14, 0.14, 0.2),
  n=c(30,30,30,30,30), type = "Williams",
  method = "ADD1", alternative = "greater")

powerbinom(p=c(0.1, 0.12, 0.14, 0.14, 0.2),
  n=c(60,60,60,60,60), type = "Williams",
  method = "ADD1", alternative = "greater")

powerbinom(p=c(0.1, 0.12, 0.14, 0.14, 0.2),
  n=c(80,80,80,80,80), type = "Williams",
  method = "ADD1", alternative = "greater")

powerbinom(p=c(0.1, 0.12, 0.14, 0.14, 0.2),
  n=c(100,100,100,100,100), type = "Williams",
  method = "ADD1", alternative = "greater")

powerbinom(p=c(0.1, 0.12, 0.14, 0.14, 0.2),
  n=c(150,150,150,150,150), type = "Williams",
  method = "ADD1", alternative = "greater")

powerbinom(p=c(0.1, 0.12, 0.14, 0.14, 0.2),
  n=c(190,140,140,140,140), type = "Williams",
  method = "ADD1", alternative = "greater")

```

powermcp

Approximative power calculation for multiple contrast tests

Description

Approximative power calculation for multiple contrast tests, based on normal approximation.

Usage

```
powermcp(TExpH1, alpha = 0.05, corrmath1, alternative = "two.sided")
```

Arguments

TExpH1	numeric vector: the expectation of the test statistics under the alternative
alpha	a single numeric value: alpha-level, defaults to 0.05
corrmath1	a numeric matrix, the correlation matrix of the teststatistics under the alternative, must have same dimensions as length of <i>TExpH1</i>
alternative	a single character string, specifying the alternative, one of "two.sided", "less", or "greater"

Details

Any-pair-power is calculated, the power of a Union-Intersection-Test.

The probability, that any teststatistic exceeds the critical value is calculated from a central multivariate standard normal distribution. The appropriateness of the result strongly depends on the assumptions, that teststatistics are truly following a standard normal distributions, which might not be the case for small sample sizes.

Note that differing definitions of power are possible, but not implemented here.

Value

A single numeric value, the approximative power.

```
print.binomORci    Print method for binomORci
```

Description

Print method for objects of class "binomORci" as can be created by calling binomORci.

Usage

```
## S3 method for class 'binomORci':
print(x, ...)
```

Arguments

```
x            an object of class "binomRDci"
...          ...
```

Value

A print out.

```
print.binomRDci    Print method for binomRDci
```

Description

Print method for objects of class "binomRDci" as can be created by calling binomRDci.

Usage

```
## S3 method for class 'binomRDci':
print(x, digits = 4, ...)
```

Arguments

x an object of class "binomRDci"
digits a single integer value specifying the number of digits for rounding
... further arguments to be passed to "print.default"

Value

A print out.

`print.binomRDtest` *Print method for binomRDtest*

Description

Print method for objects of class "binomRDtest" as can be created by calling `binomRDtest`.

Usage

```
## S3 method for class 'binomRDtest':  
print(x, digits = 4, ...)
```

Arguments

x an object of class "binomRDtest"
digits a single integer value specifying the number of digits for rounding
... further arguments to be passed to "print.default"

Value

A print out.

`print.binomRRci` *Print method for binomRRci*

Description

Print method for objects of class "binomRRci" as can be created by calling `binomRRci`.

Usage

```
## S3 method for class 'binomRRci':  
print(x, digits = 4, ...)
```

Arguments

`x` an object of class "binomRRci"
`digits` a single integer value specifying the number of digits for rounding
`...` further arguments to be passed to "print.default"

Value

A print out.

`print.poly3ci` *Print method for poly3ci*

Description

Print method for objects of class "poly3ci" as can be created by calling `poly3ci`

Usage

```
## S3 method for class 'poly3ci':
print(x, digits = 4, ...)
```

Arguments

`x` an object of class "poly3ci"
`digits` a single integer value specifying the number of digits for rounding
`...` further arguments to be passed to "print.default"

Value

A print out.

`print.poly3est` *Print function for poly3est*

Description

Print function for objects of class "poly3est", as can be created by calling "poly3estf"

Usage

```
## S3 method for class 'poly3est':
print(x, digits = 4, ...)
```

Arguments

x	An object of class "poly3test", as can be created by calling poly3testf
digits	a single integer, the number of digits for rounding of the results
...	currently not used...

```
print.poly3test
```

Print method for poly3test

Description

Print method for objects of class "poly3test" as can be created by calling poly3test.

Usage

```
## S3 method for class 'poly3test':
print(x, digits = 4, ...)
```

Arguments

x	an object of class "poly3test"
digits	a single integer value specifying the number of digits for rounding
...	further arguments to be passed to "print.default"

Value

A print out.

```
print.Shannonci
```

Print function for Shannonci

Description

Print out the confidence intervals calculated by Shannonci.

Usage

```
## S3 method for class 'Shannonci':
print(x, ...)
```

Arguments

x	An object of class " <i>Shannonci</i> ", as produced by calling Shannonci
...	currently only <i>digits</i> is passed to <i>print</i>

Value

A print out.

See Also

For a more detailed print out, use [summary.Simpsonci](#)

```
print.Simpsonci
```

Print function for Simpsonci

Description

Print out the confidence intervals calculated by Simpsonci.

Usage

```
## S3 method for class 'Simpsonci':
print(x, ...)
```

Arguments

`x` An object of class "*Simpsonci*", as produced by calling [Simpsonci](#)
`...` currently only *digits* is passed to *print*

Value

A print out.

```
scalechoice
```

Only for internal use.

Description

How to define scale parameters of the Weibull distribution in the poly-k-setting

Usage

```
scalechoice(shape = 3, pm = 0.2, t = 1)
```

Arguments

`shape` shape parameter (usually shape=3)
`pm` a numeric value ($0 < p < 1$), probability that an individual dies before time `t`
`t` a numeric value, time `t`

Value

a single numeric value, giving the scale parameter needed to fulfill $pm(t)$ for the current definition of the Weibull distribution.

Note

Scale parameter is defined differently than that in Peddada (2005)

See Also

`?pweibull`

Shannon

Shannon index

Description

Calculates the Shannon-Wiener index.

Usage

Shannon(p)

Arguments

p A numeric vector of proportions.

Shannonci

Confidence intervals for multiple contrasts of Shannon indices

Description

Calculates simultaneous and local confidence intervals for differences of Shannon indices.

Usage

```
Shannonci(X, f, cmat = NULL, type = "Dunnett", alternative = "two.sided",
  conf.level = 0.95, dist = "MVN", ...)
```

Arguments

<code>X</code>	a data.frame of dimensions n times p with integer entries, where n is the number of samples and p is the number of species
<code>f</code>	a factor variable of length n, grouping the observations in <i>X</i>
<code>cmat</code>	an contrast matrix; the number of columns should match the number of levels in <i>f</i>
<code>type</code>	a single character string, currently one of "Dunnett", "Tukey", "Sequen"
<code>alternative</code>	a single character string, one of "two.sided", "less" (upper bounds), "greater" (lower bounds)
<code>conf.level</code>	the confidence level of the simultaneous (or local) confidence intervals
<code>dist</code>	a single character string, defining the type of quantiles to be used for interval calculation; "MVN" invokes simultaneous intervals, "N" invokes unadjusted confidence intervals with coverage probability <code>conf.level</code> for each of them
<code>...</code>	further arguments to be passed; currently only <i>base</i> is used, a single integer value, specifying which group to be taken as the control in case that <code>type="Dunnett"</code> , ignored otherwise

Details

This function implements confidence intervals described by Fritsch and Hsu (1999) for the difference of Shannon indices between several groups. Deviating from Fritsch and Hsu, quantiles of the multivariate normal distribution are used which take the sample variance into account.

Note, that this approach ignores the variability of the individual samples.

Value

A list containing the elements:

<code>conf.int</code>	a matrix, containing the lower and upper confidence limits in the columns
<code>quantile</code>	a single numeric value, the quantile used for interval calculation
<code>estimate</code>	a matrix, containing the point estimates of the contrasts in its column
<code>cmat</code>	the contrast matrix used
<code>methodname</code>	a character string, for printing
<code>sample.estimate</code>	A list of sample estimates as returned by estShannonf

and some of the input arguments

Author(s)

Frank Schaarschmidt

References

Fritsch, KS, and Hsu, JC (1999): Multiple Comparison of Entropies with Application to Dinosaur Biodiversity. *Biometrics* 55, 1300-1305.

See Also

[Simpsonci](#) for simultaneous and local intervals of differences of the Simpson index

Examples

```

data(HCD)

HCDcounts<-HCD[, -1]
HCDf<-HCD[, 1]

# Comparison to the confidence bounds shown in
# Fritsch and Hsu (1999), Table 5, "Standard normal".

cmat<-rbind(
  "HM-HU"=c(0, 1, -1),
  "HL-HM"=c(1, -1, 0),
  "HL-HU"=c(1, 0, -1)
)

Shannonci(X=HCDcounts, f=HCDf, cmat=cmat,
  alternative = "two.sided", conf.level = 0.9, dist = "N")

# Note, that the calculated confidence intervals
# differ from those published by Fritsch and Hsu (1999),
# whenever Lower is involved.

# Comparison to the lower cretaceous,
# unadjusted confidence intervals:

Shannonci(X=HCDcounts, f=HCDf, type = "Dunnett",
  alternative = "greater", conf.level = 0.9, dist = "N")

# Stepwise comparison between the strata,
# unadjusted confidence intervals:

ShannonS<-Shannonci(X=HCDcounts, f=HCDf, type = "Sequen",
  alternative = "greater", conf.level = 0.9, dist = "N")

ShannonS

summary(ShannonS)

plot(ShannonS)

# A trend test based on multiple contrasts:

cmatTREND<-rbind(
  "U-LM"=c(-0.5, -0.5, 1),
  "MU-L"=c(-1, 0.5, 0.5),
  "U-L"=c(-1, 0, 1)
)

```

```
)
TrendCI<-Shannonci(X=HCDcounts, f=HCDf, cmat=cmatTREND,
  alternative = "greater", conf.level = 0.95, dist = "MVN")
TrendCI

plot(TrendCI)
```

Simpson

Calculate the Simpson index

Description

Calculate the Simpson index from a vector of proportions.

Usage

```
Simpson(p)
```

Arguments

`p` a numeric vector of proportions

Simpsonci

Confidence intervals for differences of Simpson indices

Description

Calculates simultaneous and local confidence intervals for differences of Simpson indices.

Usage

```
Simpsonci(X, f, cmat = NULL, type = "Dunnett", alternative = "two.sided", conf.level)
```

Arguments

`X` a data.frame of dimensions n times p with integer entries, where n is the number of samples and p is the number of species

`f` a factor variable of length n , grouping the observations in X

`cmat` an contrast matrix; the number of columns should match the number of levels in f

`type` a single character string, currently one of "Dunnett", "Tukey", "Sequen"

<code>alternative</code>	a single character string, one of "two.sided", "less" (upper bounds), "greater" (lower bounds)
<code>conf.level</code>	the confidence level of the simultaneous (or local) confidence intervals
<code>dist</code>	a single character string, defining the type of quantiles to be used for interval calculation; "MVN" invokes simultaneous intervals, "N" invokes unadjusted confidence intervals with coverage probability <code>conf.level</code> for each of them
<code>...</code>	further arguments to be passed; currently only <code>base</code> is used, a single integer value, specifying which group to be taken as the control in case that <code>type="Dunnnett"</code> , ignored otherwise

Details

This function implements confidence intervals described by Rogers and Hsu (1999) for the difference of Shannon indices between several groups. Deviating from Fritsch and Hsu, quantiles of the multivariate normal distribution are used which take the sample variance into account.

Note, that this approach ignores the variability of the individual samples.

Value

A list containing the elements:

<code>conf.int</code>	a matrix, containing the lower and upper confidence limits in the columns
<code>quantile</code>	a single numeric value, the quantile used for interval calculation
<code>estimate</code>	a matrix, containing the point estimates of the contrasts in its column
<code>cmat</code>	the contrast matrix used
<code>methodname</code>	a character string, for printing
<code>sample.estimate</code>	A list of sample estimates as returned by estShannonf

and some of the input arguments.

Author(s)

Frank Schaarschmidt

References

Rogers, JA and Hsu, JC (2001): Multiple Comparisons of Biodiversity. *Biometrical Journal* 43, 617-625.

See Also

[Shannonci](#)

Examples

```

data(HCD)

HCDcounts<-HCD[,-1]
HCDf<-HCD[,1]

# Rogers and Hsu (2001), Table 2:
# All pair wise comparisons:

Simpsonci(X=HCDcounts, f=HCDf, type = "Tukey",
  conf.level = 0.95, dist = "MVN")

# Rogers and Hsu (2001), Table 3:
# Comparison to the lower cretaceous:

Simpsonci(X=HCDcounts, f=HCDf, type = "Dunnett",
  alternative = "less", conf.level = 0.95, dist = "MVN")

# Note, that the confidence bounds here differ
# from the bounds in Rogers and Hsu (2001)
# in the second digit, whenever the group Upper
# is involved in the comparison.

# Stepwise comparison between the strata:

SimpsonS<-Simpsonci(X=HCDcounts, f=HCDf, type = "Sequen",
  alternative = "greater", conf.level = 0.95, dist = "MVN")

SimpsonS
summary(SimpsonS)

plot(SimpsonS)

# # # Hell Creek Dinosaur data:
# Is there a downward trend in biodiversity during the
# Cretaceous period?

# A trend test based on multiple contrasts:

cmatTREND<-rbind(
  "U-LM"=c(-0.5,-0.5,1),
  "MU-L"=c(-1,0.5,0.5),
  "U-L"=c(-1,0,1)
)

TrendCI<-Simpsonci(X=HCDcounts, f=HCDf, cmat=cmatTREND, alternative = "greater", conf.level
TrendCI

plot(TrendCI)

```

summary.binomORci *Detailed print out for binomORci*

Description

Produces a more detailed print out of objects of class "binomORci", including summary statistics, the used contrast matrix and the confidence intervals.

Usage

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

Arguments

object an object of class "binomORci" as created by function [binomORci](#)
... ...

Value

A print out.

Examples

```
x<-c(1, 3, 6, 7, 5)  
n<-c(30, 30, 30, 30, 30)  
names<-LETTERS[1:5]  
  
ORD<-binomORci(x=x, n=n, names=names,  
  type="Dunnett", alternative="greater")  
summary(ORD)  
  
ORW<-binomORci(x=x, n=n, names=names,  
  type="Williams", alternative="greater")  
summary(ORW)
```

summary.binomRDci *Detailed print out for binomRDci*

Description

Produces a more detailed print out of objects of class "binomRDci", including summary statistics, the used contrast matrix and the confidence intervals.

Usage

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

Arguments

object	an object of class "binomRDci" as created by function binomRDci
...	further arguments to be passed to summary, currently only <i>digits</i> for rounding is supported

Value

A print out.

Examples

```
data(liarozole)

head(liarozole)

LiWi<-binomRDci(Improved ~ Treatment, data=liarozole,
  type="Williams")

LiWi

summary(LiWi)
```

```
summary.binomRDtest
```

Detailed print out for binomRDtest

Description

Produces a more detailed print out of objects of class "binomRDtest", including summary statistics, the used contrast matrix and the p-values.

Usage

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

Arguments

object an object of class "binomRDtest" as created by function [binomRDtest](#)
 ... further arguments to be passed to summary, currently only *digits* for rounding is supported

Value

A print out.

Examples

```
ntrials <- c(40,20,20,20)
xsuccesses <- c(1,2,2,4)
names(xsuccesses) <- LETTERS[1:4]
test<-binomRDtest(x=xsuccesses, n=ntrials, method="ADD1",
  type="Changepoint", alternative="greater")

test

summary(test)
```

summary.binomRRci *Detailed print out for binomRRci*

Description

Produces a more detailed print out of objects of class "binomRRci", including summary statistics, the used contrast matrix and the confidence intervals.

Usage

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

Arguments

object an object of class "binomRRci" as created by function [binomRRci](#)
 ... further arguments to be passed to summary, currently only *digits* for rounding is supported

Value

A print out.

Examples

```
data(liarozole)

head(liarozole)

LiDu<-binomRRci(Improved ~ Treatment, data=liarozole,
  type="Dunnett", alternative="greater")

LiDu

summary(LiDu)
```

summary.poly3est *Detailed print out for poly3est*

Description

Summary statistics for long-term carcinogenicity data, including poly-3-estimates. For internal use.

Usage

```
## S3 method for class 'poly3est':
summary(object, ...)
```

Arguments

object	An object of class "poly3est", as can be obtained by poly3est
...	further argument for the print out, as e.g. <code>digits</code> for rounding

Details

For internal use.

Value

A print out.

Author(s)

Frank Schaarschmidt

Examples

```

data(methyl)
head(methyl)

estk3<-poly3estf(time=methyl$death, status=methyl$tumour, f=methyl$group)
summary(estk3)

estk5<-poly3estf(time=methyl$death, status=methyl$tumour, f=methyl$group, k=5)
summary(estk5)

```

```
summary.Shannonci Summary for Shannonci
```

Description

Produces a detailed print out of the results of the function Shannonci.

Usage

```

## S3 method for class 'Shannonci':
summary(object, ...)

```

Arguments

object	An object of class "Shannonci", see Shannonci
...	further arguments to be passed to print, currently only digits

Value

A print out, comprising a table of the (possibly aggregated) data used for estimation, the sample estimates for the Shannon index with bias corrected and raw values, its variance estimates, the used contrast matrix, and the confidence intervals.

Examples

```

data(HCD)

HCDcounts<-HCD[, -1]
HCDf<-HCD[, 1]

# Comparison to the confidence bounds shown in
# Fritsch and Hsu (1999), Table 5, "Standard normal".

cmat<-rbind(
  "HM-HU"=c(0, 1, -1),
  "HL-HM"=c(1, -1, 0),

```

```
"HL-HU"=c(1,0,-1)
)

ShannonS<-Shannonci(X=HCDcounts, f=HCDf, type = "Sequen",
  alternative = "greater", conf.level = 0.9, dist = "N")

summary(ShannonS)
```

```
summary.Simpsonci Summary function for Simpsonci
```

Description

Produces a detailed print out of the results of function Simpsonci.

Usage

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

Arguments

object	an object of class "Simpsonci" as obtained by calling Simpsonci
...	further arguments to be passed to print and round: currently only digits

Value

A print out, comprising a table of the (possibly aggregated) data used for estimation, the sample estimates for the Simpsons index, and its variance estimates, the used contrast matrix, and the confidence intervals.

Examples

```
data(HCD)

HCDcounts<-HCD[, -1]
HCDf<-HCD[, 1]

SimpsonS<-Simpsonci(X=HCDcounts, f=HCDf, type = "Sequen",
  alternative = "greater", conf.level = 0.95, dist = "MVN")

summary(SimpsonS)
```

Waldci *Simultaneous Wald confidence intervals*

Description

General function for simultaneous CIs in a one-way layout using multivariate normal distribution.

Usage

```
Waldci(cmat, estp, varp, varcor, alternative = "two.sided", conf.level = 0.95, dist
```

Arguments

cmat	Contrast matrix of dimension $M \times I$, with M = the number of contrasts, I = the number of samples
estp	numeric vector of point estimates of length I , with I = the number of samples
varp	numeric vector of variance estimates of length I , to be used for interval construction
varcor	numeric vector of variance estimates of length I
alternative	character string
conf.level	single numeric vector
dist	a character string, "MVN" invokes multiplicity adjustment via the multivariate normal distribution, "N" invokes use of quantiles of the univariate normal distribution

Details

Mainly for internal use.

Value

A list containing:

conf.int	a matrix with 2 columns: lower and upper confidence bounds, and M rows
alternative	character string, as input
conf.level	single numeric value, as input
quantile	the quantile used to construct the CIs

Author(s)

Frank Schaarschmidt

See Also

For user level implementations see: [binomRDci](#), [binomORci](#), [poly3ci](#)

Waldtest

Simultaneous Wald tests

Description

General function for adjusted p-values for an UIT in a one-way layout using multivariate normal distribution.

Usage

```
Waldtest(estp, varp, cmat, alternative = "greater", dist="MVN")
```

Arguments

estp	numeric vector of point estimates of length I, with I = the number of samples
varp	numeric vector of variance estimates of length I, to be used for interval construction
cmat	Contrast matrix of dimension MxI, with M = the number of contrasts, I= the number of samples
alternative	character string
dist	a character string, where "MVN" invokes the computation of p-values using the multivariate normal distribution, and "N" invokes use p-value computation using the univariate normal distribution

Value

A list containing:

teststat	a numeric vector of teststatistics of length M
pval	a single numeric p-value, the p-value of the maximum test (minimum p-value)
p.val.adj	a vector of length M, the adjusted p-values of the single contrasts
alternative	a single character vector, as the input
dist	a character string specifying which distribution

Author(s)

Frank Schaarschmidt

See Also

For user level implementations see:

[binomRDtest](#), [poly3test](#)

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