Package ‘mratios’

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Type Package

Title Inferences for ratios of coefficients in the general linear model

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Suggests multcomp, nlme

Imports mvtnorm

Description With this package, it is possible to perform (simultaneous) inferences for ratios of linear combinations of coefficients in the general linear model. In particular, tests and confidence interval estimations for ratios of treatment means in the normal one-way layout and confidence interval estimations like in (multiple) slope ratio and parallel line assays can be carried out. Moreover, it is possible to calculate the sample sizes required in comparisons with a control based on relative margins. For the simple two-sample problem, functions for a t-test for ratio-formatted hypotheses and the corresponding Fieller-type confidence interval are provided assuming homogeneous or heterogeneous group variances.

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mratios-package .......................................................... 2
Description

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Author(s)

Gemechis Dilba Djira, Mario Hasler, Daniel Gerhard, Frank Schaarschmidt

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References


See Also

Multiple comparisons for differences of means: multcomp

Examples

library(mratios)

# 1) comparing whether the active control is more effective than vehicle control
net.test.ratio(MM-Treatment, data=subset(Mutagenicity, Treatment=="Cyclo25" | Treatment=="Vehicle"), alternative="greater", rho=1, var.equal=FALSE)

# 2) lowest dose vs. vehicle control
net.test.ratio(MM-Treatment, data=subset(Mutagenicity, Treatment=="Hydro30" | Treatment=="Vehicle"),
alternative="greater", rho=1, var.equal=FALSE)

# Calculation of simultaneous confidence intervals for ratios
# of linear combinations of treatment means in a one-way ANOVA model

data(BW)
boxplot(Weight~Dose, data=BW)

# Body weights of a 90-day chronic toxicology study on rats
# with a control (1) and three dose groups (2,3,4).
# Calculate upper confidence limits for the ratio of means
# of the three dose groups vs. the control group:
# Which of the doses lead to not more than 90 percent weight loss
# compared to the control group:

m21 <- sci.ratio(Weight~Dose, data=BW, type="Dunnett",
                  alternative="greater")

summary(m21)

plot(m21, rho=0.9)

# Simultaneous tests for ratios of means

data(AP)
boxplot(prepost~treatment, data=AP)

# Test whether the differences of doses 50, 100, 150 vs. Placebo
# are non-inferior to the difference Active Control vs. Placebo

NC <- rbind(
            "(D100-D0)" = c(0,-1,1,0,0),
            "(D150-D0)" = c(0,-1,0,1,0),
            "(D50-D0)" = c(0,-1,0,0,1))

DC <- rbind(
            "(AC-D0)" = c(1,-1,0,0,0),
            "(AC-D0)" = c(1,-1,0,0,0),
            "(AC-D0)" = c(1,-1,0,0,0))

NC
DC

simtest.ratio(prepost ~ treatment, data=AP,
Num.Contrast=NC, Den.Contrast=DC, Margin.vec=c(0.9,0.9,0.9))

summary(simtest.ratio(prepost ~ treatment, data=AP,
                         Num.Contrast=NC, Den.Contrast=DC, Margin.vec=c(0.9,0.9,0.9)))

# Comparisons vs. Control (default type of comparisons):
many21 <- simtest.ratio(prepost ~ treatment, data=AP,
                         type="Dunnett")
summary(many21)

# Simultaneous confidence intervals for ratios of coefficients
# in the general linear model:
# Slope-ratio assay, data from Jensen(1989), Biometrical Journal 31,
# 841-853.
data(SRAssay)
SRAssay

# In this problem, the interest is in simultaneous estimation
# of the ratios of slopes relative to the slope of the standard
# treatment.
# First it is needed to carefully define the vector of responses
# and the design matrix of the general linear model:
# The design matrix can be constructed using model.matrix,
# and the vector of the response variable can be extracted
# from the dataframe.
X <- model.matrix(Response~Treatment:Dose, data=SRAssay)
Response <- SRAssay[,"Response"]

# The response vector and the design matrix are:
X
Response

# The following coefficients result:
lm(Response~0+X)

# where the last four coefficients are the estimated slopes
# of the control treatment and the three new treatments
# Contrasts for the ratios of the slopes of the three new treatments
The angina data set

Description

Dose response study of a drug to treat Angina pectoris. Response variable was the duration of pain-free walking after treatment, relative to the values before treatment. Large values indicate positive effects on patients. Data set taken from Westfall et al. (1999), p. 164.

Usage

data(angiA)
Format

A data frame with 50 observations on the following 2 variables.

- **dose** a factor with levels 0, 1, 2, 3, 4
- **response** a numeric vector giving the change from pretreatment as measured in minutes of pain-free walking.

Details

See Westfall et al. (1999, p. 164)

Source


References

angina(multcomp)

Examples

```r
library(mratiost)
data(angina)
str(angina)
plot(response~dose, data=angina)
```

---

### Description

A data set is generated (from normal distribution) to imitate the summary statistics in Table II of Bauer et al. (1998). In the experiment, patients with chronic stable angina pectoris were randomized to five treatment arms (placebo, three doses of a new compound, and an active control). The primary endpoint is the difference in the duration of an exercise test before and after treatment.

Usage

data(AP)
Format

A data frame with 303 observations on the following 2 variables.

prepost a numeric vector, the difference post treatment measurement minus pre treatment measurement

treatment a factor with levels AC (the active control), D0 (the zero dose, placebo), and D50, D100, D150, the three dose groups of the new compound.

Source


Examples

```r
library(mratios)

data(AP)

str(AP)

boxplot(prepost ~ treatment, data=AP)

by(AP, AP$treatment, function(x)(mean(x$prepost)))

by(AP, AP$treatment, function(x)(sd(x$prepost)))
```

---

**ASAT**

**ASAT data**

Description

Data from a toxicity study: ASAT values of the serum of female Wistar rats six months after application

Usage

data(ASAT)

Format

A data frame with 34 observations on the following 2 variables.

group a factor with two levels KON, and TREAT, where KON is the control group consisting of 19 subjects and TREAT is the treatment group consisting of only 15 subjects due to mortality

ASAT a numeric vector containing values of the response variable
Details

The objective is to test that ASAT values of treatment group are not relevantly heightened compared to the control group, where average ASAT value which is more than 25 percent higher than the average of the control group is defined as relevant.

Source


Examples

```r
library(mratios)
data(ASAT)
str(ASAT)
boxplot(ASAT~group, data=ASAT)
```

**BW**

Body weights measured in a toxicological study

Description

Body weights of a 90-day chronic toxicological study on rats with a control and three dose groups.

Usage

data(BW)

Format

A data frame with 60 observations on the following 2 variables.

- **Weight** a numeric vector containing the bodyweights of rats
- **Dose** a factor with levels 1, 2, 3, 4, specifying the dose groups, where 1 is the control group

Source

contrMatRatio

Examples

library(mratios)
data(BW)
str(BW)

boxplot(Weight~Dose, data=BW)

contrMatRatio Creates numerator and denominator contrast matrices for ratio-based hypotheses for common multiple comparison and trend test problems

Description

Creates numerator and denominator contrast matrices for some common multiple comparison and trend test problems. These matrices are internally used by the sci.ratio and simtest.ratio functions. The contrMatRatio function is a modification of the function contrMat (multcomp).

Whether the given definitions of contrast matrices for trend test problems in terms of ratios make sense and how they are to be interpreted is to be discussed.

Usage

contrMatRatio(n, type = "Tukey", base = 1)

Arguments

n integer vector of sample sizes

type the type of multiple contrasts
   • "Dunnett": many to one comparisons, with the control group in the denominator
   • "Tukey": all-pair comparisons
   • "Sequen": comparison of consecutive groups, where the groups of lower order is the denominator
   • "AVE": comparison of each group with average of all others, where the average is taken as denominator
   • "GrandMean": comparison of each group with grand mean of all groups, where the grand mean is taken as denominator
   • "Changepoint": ratio of averages of groups of higher order divided by averages of groups of lower order
   • "Marcus": Marcus contrasts defined for ratios
   • "McDermott": McDermott contrasts for ratios
contrMatRatio

- "Williams": Williams contrasts for ratios
- "UmbrellaWilliams": Umbrella-protected Williams contrasts for ratios, i.e. a sequence of Williams-type contrasts with groups of higher order step-wise omitted

base a single integer specifying the control (i.e. denominator) group for "Dunnett"-type contrasts for calculating the ratios to the control

Details

This is a simple adaption of the contrMat function in the package multcomp for ratio hypotheses.

Value

A list containing:

numC the (named) numerator contrast where rows correspond to contrasts
denC the (named) denominator contrast where rows correspond to contrasts
rnames a character vector with names of the contrasts and the type of contrast as attr.

Author(s)

Frank Schaarschmidt and Daniel Gerhard by modifying the code of contrMat(multcomp)

See Also

contrMat(multcomp)

Examples

library(mratios)

n=c(A=10,B=20,Z=10,D=10)

contrMatRatio(n=n, type="Dunnett", base=1)
contrMatRatio(n=n, type="Dunnett", base=3)
contrMatRatio(n=n, type="Tukey")
contrMatRatio(n=n, type="Sequen")
contrMatRatio(n=n, type="AVE")
contrMatRatio(n=n, type="GrandMean")
contrMatRatio(n=n, type="Williams")
contrMatRatio(n=n, type="UmbrellaWilliams")
gsci.ratio

Test version! Simultaneous confidence intervals for ratios of linear combinations of parameters.

Description

This function calculates simultaneous confidence intervals for ratios of user-defined linear combinations, given a vector parameter estimates and a corresponding variance-covariance matrix. Besides unadjusted intervals, multiplicity adjustments are available using quantiles of a multivariate Normal- or t-distribution. The function provides a more general, but less user-friendly function to calculate ratios of mean parameters from linear (mixed models).

Usage

\[ \text{gsci.ratio(} \text{est, vcmat, Num.Contrast, Den.Contrast,} \]
\[ \text{degfree = NULL, conf.level = 0.95, alternative = "two.sided",} \]
\[ \text{adjusted = TRUE)} \]

Arguments

- **est**: A numeric vector of parameter estimates, for example coefficients of a linear model
- **vcmat**: The corresponding variance-covariance matrix (Number of rows and columns should be the same as the length of the parameter vector)
- **Num.Contrast**: Numerator contrast matrix, where the number of columns must be the same as the length of the parameter vector, and each row represents one contrast
- **Den.Contrast**: Denominator contrast matrix, where the number of columns must be the same as the length of the parameter vector, and each row represents one contrast
- **degfree**: Degrees of freedom used for calculating quantiles of a (multivariate) t-distribution. If NULL, Normal approximations are used
- **conf.level**: Simultaneous confidence level in case of adjusted == TRUE, and comparison-wise confidence level in case of adjusted == FALSE
- **alternative**: a character string: "two.sided" for two-sided intervals, "less" for upper confidence limits, "greater" for lower confidence limits
- **adjusted**: If TRUE, the simultaneous confidence level is controlled, otherwise the comparisonwise confidence level is used

Details

Given a parameter vector and its corresponding covariance matrix from a linear model fit, approximate simultaneous confidence intervals for several ratios of linear combinations of these parameters are calculated. For simultaneous confidence intervals (adjusted=TRUE) the plug-in method is used (plugging the maximum likelihood estimates of the ratios to obtain the correlation matrix for calculating quantiles of a multivariate t or normal distribution).
Linear combinations can be defined by providing matrices for the nominator and the denominator; some pre-defined contrasts can be constructed by the function contrMatRatio. (These may be weighted for different sample sizes.)

**Value**

An object of class "sci.ratio" and "gsci.ratio", containing a list with elements:

- **estimate**  point estimates of the ratios
- **CorrMat.est**  estimate of the correlation matrix
- **Num.Contrast**  matrix of contrasts used for the numerator of ratios
- **Den.Contrast**  matrix of contrasts used for the denominator of ratios
- **conf.int**  confidence interval estimates of the ratios

And some further elements to be passed to print and summary functions.

**Author(s)**

Daniel Gerhard, adapting code of Gemechis Dilba Djira

**References**

The general methodology of constructing inference for ratios of linear model parameters can be found in:


However, when adjusted=TRUE, the quantiles are not obtained as described in Zerbe(1978) or Young et al. (1997), but by adapting the ’plug-in’ method described for the completely randomized one-way layout in


**See Also**

glht(multcomp) for simultaneous CI of differences of means, and function sci.ratio.gen(mratios)
Examples

```r
library(mratios)

# A 90-days chronic toxicity assay:
# Which of the doses (groups 2,3,4) do not show a decrease in
# bodyweight more pronounced than 90 percent of the bodyweight
# in the control group?

data(BW)
boxplot(Weight~Dose,data=BW)

lfit <- lm(Weight~Dose-1, data=BW)
est <- coefficients(lfit)
vc <- vcov(lfit)
CMAT <- contrMatRatio(table(BW$Dose), type="Dunnett")

BWnoninf <- gsci.ratio(est, vc, CMAT$numC, CMAT$denC,
alternative="greater", degfree=lmfit$df.residual)

# the same:
sci.ratio(Weight~Dose, data=BW, type="Dunnett", alternative="greater")

# Plot
plot(BWnoninf, rho=0.9)

### Mixed Model Example

library(nlme)
data(Milk)

# Fit a linear mixed model (maybe there are nicer models available!)

lmefit <- lme(protein ~ Diet-1, data=Milk,
               random=-Time|Cow, correlation=corAR1(form=-Time|Cow))

# Extract the parameter estimates and the corresponding
# variance-covariance matrix

estm <- fixef(lmefit)
vcm <- vcov(lmefit)
```
Mutagenicity

# Define the matrices defining the ratios of interest for
# all-pair comparisons: CM is the numerator matrix and
# DM is the denominator matrix.

CM <- rbind(c(1,0,0),
            c(1,0,0),
            c(0,1,0))
DM <- rbind(c(0,1,0),
            c(0,0,1),
            c(0,0,1))

# Add some row names (This is optional!)
rownames(CM) <- c("b/b+l", "b/l", "b+l/l")

# Calculate and plot simultaneous confidence intervals:
gscimix <- gsci.ratio(estm, vcm, CM, DM, degfree=anova(lmefit)[,2])
plot(gscimix)

Mutagenicity assay

Description

Mutagenicity assay for 4 doses of a compound (hydroquinone) against a negative (vehicle) control and a positive (active) control (cyclophosphamide). Hydroquinone was applied in doses of 30, 50, 70, 100 mg/kg, positive control was applied with 25mg/kg. Counts of micronuclei in polychromatic erythrocytes after 24h are taken as a measure for the potency to induce chromosome damage. Data of male mice are presented (Hauschke et al., 2005).

Usage

data(Mutagenicity)

Format

A data frame with 31 observations on the following 2 variables.

**Treatment**  a factor with levels Cyclo25, Hydro100, Hydro30, Hydro50, Hydro75, Vehicle

**MN**  a numeric vector, giving the counts of micronuclei after 24h

Source

References


Examples

data(Mutagenicity)
str(Mutagenicity)
boxplot(MN-Treatment, data=Mutagenicity)

---

n.ratio

Sample size computation in simultaneous tests for ratios of means

Description

Computes the sample sizes required in simultaneous tests for non-inferiority (or superiority) based on relative margins in multiple comparisons with a control.

Usage

n.ratio(m, rho, Power, cv, rho.star, alpha, Min.power = TRUE)

Arguments

m number of comparisons with a control group
rho relative non-inferiority (or superiority) margin
Power given power (1-beta)
cv coefficient of variation of the control group
rho.star the percentage (of the mean of the control group) to be detected
alpha familywise error rate
Min.power if set to TRUE (by default), the minimal power will be controlled, otherwise complete power

Details

The sample sizes are computed at the least favourable configurations, based on the assumption of no prior information regarding the true configuration of the ratios under the alternative hypotheses. The formula is

\[ n = \frac{((C_1 + C_2)^2)(1 + \rho^2)}{((\rho - \rho^*)^2)CV0^2}, \]

where \( C_1 \) is the lower \( 1 - \alpha \) equi-coordinate percentage point of an m-variate normal distribution and \( C_2 \) is the quantile of univariate (multivariate) normal distribution depending on the type of
power controlled. In tests for non-inferiority (or superiority) with large response values indicating better treatment benefit, $\rho < \rho^*$, where $\rho < 1$ for non-inferiority and $\rho > 1$ for superiority testing. Whereas, if small response values indicate better treatment benefit, $\rho^* < \rho$, where $\rho > 1$ for non-inferiority and $\rho < 1$ for superiority testing.

**Author(s)**

Gemechis Dilba Djira

**References**


**Examples**

```r
# Example 1: Sample size calculation in tests for non-inferiority
# (two-sample case) (Laster and Johnson (2003),
# Statistics in Medicine 22:187-200)

n.ratio(m=1, rho=0.8, Power=0.8, CV0=0.75, rho.star=1,
alpha=0.05)

# Example 2: Sample size calculation in simultaneous tests for
# non-inferiority
# (Dilba et al. (2006), Statistics in Medicine 25:1131-1147)

n.ratio(m=3, rho=0.7, Power=0.8, CV0=0.5, rho.star=0.95,
alpha=0.05)

# Example 3: Controlling complete power

n.ratio(m=5, rho=1.2, Power=0.8, CV0=0.2, rho.star=1.40,
alpha=0.05, Min.power=FALSE)
```

*Penicillin*  
Comparing 6 strains with respect to production of antibiotics
Description

The production of antibiotics of 6 strains (mutants of the same micro organism) was compared. MO were put to holes in agar infected with Bacteria. The diameter of Bacteria-free areas around the colonies of the MO was recorded. Each strain was repeated 8 times.

Usage

data(Penicillinn)

Format

A data frame with 48 observations on the following 2 variables.

- **strain**: a numeric vector, the number identifying the strains
- **diameter**: a numeric vector, size of the diameter of Bacteria-free area around each colony

Source


Examples

library(mratios)
data(Penicillinn)
str(Penicillinn)
boxplot(diameter ~ strain, data=Penicillinn)

---

plot.sci.ratio

Plot output for sci.ratio and sci.ratio.gen

Description

Plot the intervals returned by sci.ratio

Usage

## S3 method for class 'sci.ratio'
plot(x, rho0 = 1, rho0lty=2, rho0lwd=1, rho0col="black",
     CIvert = FALSE, CIlty = 1, CIlwd = 1, CIcex = 1, CIpch=16,
     main = NULL, ylab = NULL, xlab = NULL, sub = NULL, length=NULL, ...)

**plot.sci.ratio**

Arguments

- **x**: an object of class "sci.ratio" as can be obtained by calling the function sci.ratio
- **rho0**: a single numeric value or vector of values defining the hypothesized ratio
- **rho0ltty**: integer values to specify the line type for the rho0 line(s)
- **rho0lwd**: integer values to specify the line width for the rho0 line(s)
- **rho0col**: character vector to specify the colour for the rho0 line(s)
- **CIvert**: logical, CI are plotted horizontal if CIvert=FALSE and vertical otherwise
- **CIltty**: numeric value, giving the line type of the plotted confidence interval, see argument lty in ?par
- **CIlwd**: numeric value, giving the line width of the plotted confidence interval, see argument lwd in ?par
- **CIcex**: a single numeric value: by which amount the symbols in the CI shall be scaled relative to the default (see argument cex in ?par)
- **CIPch**: the symbol to be used for the point estimate, see pch in ?points
- **main**: character string to be plotted as main title of the plot
- **ylab**: character string, label of the y axis (ignored if CIvert=TRUE)
- **xlab**: character string, label of the x axis (ignored if CIvert=FALSE)
- **sub**: as in plot
- **length**: a numeric value, specifying the length/2 of the bars at the ends of the confidence intervals in inches
- **...**: further arguments to be passed to axis()

Details

Too long names of the contrasts/comparisons should be avoided, otherwise use par() to change plot parameters.

Value

A plot of the confidence intervals in the sci.ratio object.

Author(s)

Frank Schaarschmidt

References

plot.hmtest(multcomp)
**print.sci.ratio**

**Examples**

```r
library(mratios)
data(angina)
aCI<-.sci.ratio(response=dose, data=angina, type="Dunnett", alternative="greater")

# Visualize testing for superiority
plot(aCI, rho0=1.25, rho0lty=3)
```

---

**print.sci.ratio**

*Print function for sci.ratio objects*

**Description**

A short print out of the value of a sci.ratio object.

**Usage**

```r
## S3 method for class 'sci.ratio'
print(x, digits=4,...)
```

**Arguments**

- `x`: an object of class "sci.ratio" as can be obtained by calling the function `sci.ratio`
- `digits`: digits for rounding the output
- `...`: arguments to be passed to `print`

**Value**

A print out of the confidence intervals computed by `sci.ratio`.

**See Also**

`plot.sci.ratio`, `summary.sci.ratio`

**Examples**

```r
data(BW)
RES <- sci.ratio(Weight~Dose, data=BW, type="Dunnett", alternative="greater")
print(RES)
```
print.simtest.ratio  

**Print out the results of simtest.ratio**

**Description**
A short print out of the results of simtest.ratio

**Usage**
```r
## S3 method for class 'simtest.ratio'
print(x, digits = 4, ...)
```

**Arguments**
- `x` An object of class "simtest.ratio" as obtained by calling simtest.ratio
- `digits` digits for rounding of the results
- `...` arguments to be passed to print

**Value**
A print out, containing the margins, estimates, teststatistics, and p.values computed by simtest.ratio.

**Examples**
```r
data(BW)
RES <- simtest.ratio(Weight~Dose, data=BW, type="Dunnett",
        Margin.vec=0.9, alternative="greater")
print(RES)
```

**rat.weight**  

*Body weight of rats in a toxicity study*

**Description**
Body weights of male rats were compared between a control group and a group which had received a high dose of a chemical in a toxicity study after a period of recovery

**Usage**
```r
data(rat.weight)
```

**Format**
A data frame with 20 observations on the following 2 variables.

- **group** a factor with two levels, Dosis and Kon, where Dosis is the high dose group, consisting of ten individuals and Kon is the control group, consisting of ten individuals
- **weight** a numeric vector containing the values of response variable, final body weight in gramm
Details
Aim was to test that application of the chemical does not lead to a relevantly lowered or heightened body weight after a time of recovery. 0.8 and 1.25 were defined as relevance boundaries compared to the mean of control group.

Source

Examples
library(mratios)
data(rat.weight)
boxplot(weight~group, data=rat.weight)
boxplot(weight~group, data=rat.weight)

sci.ratio Simultaneous confidence intervals for ratios of linear combinations of means

Description
This function constructs simultaneous confidence intervals for ratios of linear combinations of normal means in a one-way ANOVA model. Different methods are available for multiplicity adjustment.

Usage
sci.ratio(formula, data, type = "Dunnett", base = 1,
           method = "Plug", Num.Contrast = NULL, Den.Contrast = NULL,
           alternative = "two.sided", conf.level = 0.95, names=TRUE)

Arguments
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>formula</td>
<td>A formula specifying a numerical response and a grouping factor as e.g. response ~ treatment</td>
</tr>
<tr>
<td>data</td>
<td>A dataframe containing the response and group variable</td>
</tr>
<tr>
<td>type</td>
<td>type of contrast, with the following options:</td>
</tr>
<tr>
<td></td>
<td>- &quot;Dunnett&quot;: many-to-one comparisons, with the control group in the denominator</td>
</tr>
<tr>
<td></td>
<td>- &quot;Tukey&quot;: all-pair comparisons</td>
</tr>
</tbody>
</table>
• "Sequen": comparison of consecutive groups, where the group with lower order is the denominator
• "AVE": comparison of each group with average of all others, where the average is taken as denominator
• "GrandMean": comparison of each group with grand mean of all groups, where the grand mean is taken as denominator
• "Changepoint": ratio of averages of groups of higher order divided by averages of groups of lower order
• "Marcus": Marcus contrasts as ratios
• "McDermott": McDermott contrasts as ratios
• "Williams": Williams contrasts as ratios
• "UmbrellaWilliams": Umbrella-protected Williams contrasts as ratios

Note: type is ignored, if Num.Contrast and Den.Contrast are specified by the user (See below).

base a single integer specifying the control (i.e. denominator) group for the Dunnett contrasts, ignored otherwise

method character string specifying the method to be used for confidence interval construction:
• "Plug": Plug-in of ratio estimates in the correlation matrix of the multivariate t distribution. This method is the default.
• "Bonf": Simple Bonferroni-adjustment of Fieller confidence intervals for the ratios
• "MtI": Sidak or Slepian- adjustment for two-sided and one-sided confidence intervals, respectively
• "Unadj": Unadjusted Fieller confidence intervals for the ratios (i.e. with comparisonwise confidence level = conf.level)

Num.Contrast Numerator contrast matrix, where columns correspond to groups and rows correspond to contrasts
Den.Contrast Denominator contrast matrix, where columns correspond to groups and rows correspond to contrasts
alternative a character string: "two.sided" for two-sided intervals, "less" for upper confidence limits, "greater" for lower confidence limits
conf.level simultaneous confidence level in case of method="Plug","Bonf", or "MtI", and comparisonwise confidence level in case of method="Unadj"
names logical, indicating whether rownames of the contrast matrices shall be retained in the output

Details

Given a one-way ANOVA model, the interest is in simultaneous confidence intervals for several ratios of linear combinations of the treatment means. It is assumed that the responses are normally distributed with homogeneous variances. Unlike in multiple testing for ratios, the joint distribution of the likelihood ratio statistics has a multivariate t-distribution the correlation matrix of which depends on the unknown ratios. This means that the critical point needed for CI calculations also
depends on the ratios. There are various methods of dealing with this problem (for example, see Dilba et al., 2006). The methods include (i) the unadjusted intervals (Fieller confidence intervals without multiplicity adjustments), (ii) Bonferroni (Fieller intervals with simple Bonferroni adjustments), (iii) MtI (a method based on Sidak and Slepian inequalities for two- and one-sided confidence intervals, respectively), and (iv) plug-in (plugging the maximum likelihood estimates of the ratios in the unknown correlation matrix). The latter method is known to have good simultaneous coverage probabilities. The MtI method consists of replacing the unknown correlation matrix of the multivariate $t$ by an identity matrix of the same dimension.

See the examples for the usage of Numerator and Denominator contrasts. Note that the argument names Num.Contrast and Den.Contrast need to be specified. If numerator and denominator contrasts are plugged in without their argument names, they will not be recognized.

Value

An object of class "sci.ratio", containing a list with elements:

- estimate: point estimates of the ratios
- CorrMat.est: estimate of the correlation matrix (for the plug-in approach)
- Num.Contrast: matrix of contrasts used for the numerator of ratios
- Den.Contrast: matrix of contrasts used for the denominator of ratios
- conf.int: confidence interval estimates of the ratios

And some further elements to be passed to print and summary functions.

Author(s)

Gemechis Dilba Djira

References


See Also

- glht(multcomp) for simultaneous CI of differences of means, plot.sci.ratio for a plotting function of the intervals

Examples

```r
# # #

# Antibiotic activity of 8 different strains of a micro organisms.
# (Horn and Vollandt, 1995):

data(Penicillin)

boxplot(diameter~strain, data=Penicillin)
```
allpairs<-sci.ratio(diameter~strain, data=Penicillin, type="Tukey")
plot(allpairs)
summary(allpairs)

# Comparison to the grand mean of all strains:

CGM<-sci.ratio(diameter~strain, data=Penicillin, type="GrandMean")
plot(CGM)
summary(CGM)

# A 90-days chronic toxicity assay:
# Which of the doses (groups 2,3,4) do not show a decrease in
# bodyweight more pronounced than 90 percent of the bodyweight
# in the control group?

data(BW)

boxplot(Weight~Dose, data=BW)

BWnoninf <- sci.ratio(Weight~Dose, data=BW, type="Dunnett",
alternative="greater")

plot(BWnoninf, rho=0.9)

---

**sci.ratio.gen**

*Simultaneous confidence intervals for ratios of coefficients in the general linear model*

**Description**

Constructs simultaneous confidence intervals for multiple ratios of linear combinations of coefficients in the general linear model.

**Usage**

```r
sci.ratio.gen(Y, X, Num.Contrast, Den.Contrast,
alternative = "two.sided", conf.level = 0.95,
method="Plug")
```

**Arguments**

- **Y** A numerical vector, containing the values of the response variable
- **X** A design matrix for the the linear model, defining the parameters to be estimated, must have same number of rows as `Y`
- **Num.Contrast** Numerator contrast matrix
- **Den.Contrast** Denominator contrast matrix
alternative one of "two.sided", "less", or "greater"
conf.level simultaneous confidence levels
method character string, specifying the method for confidence interval calculation:
  • "Plug": Plug-in of ratio estimates in the correlation matrix of the multivariate t-distribution. This method is the default.
  • "Bonf": Simple Bonferroni-adjustment of Fieller confidence intervals for the ratios
  • "MtI": Sidak or Slepian- adjustment for two-sided and one-sided confidence intervals, respectively
  • "Unadj": Unadjusted Fieller confidence intervals for the ratios (i.e. with comparisonwise confidence level = conf.level)

Details
Given a general linear model, the interest is in simultaneous confidence intervals for several ratios of linear combinations of the coefficients in the model. It is assumed that the responses are normally distributed with homogeneous variances. In this problem, the joint distribution of the likelihood ratio statistics has a multivariate t-distribution the correlation matrix of which depends on the unknown ratios. This means that the critical point needed for CI calculations also depends on the ratios. There are various methods of dealing with this problem (for example, see Dilba et al., 2006). The methods include (i) the unadjusted intervals (Fieller confidence intervals without multiplicity adjustments), (ii) Bonferroni (Fieller intervals with simple Bonferroni adjustments), (iii) MtI (a method based on Sidak and Slepian inequalities for two- and one-sided confidence intervals, respectively), and (iv) plug-in (plugging the maximum likelihood estimates of the ratios in the unknown correlation matrix). The MtI method consists of replacing the unknown correlation matrix by an identity matrix of the same dimension.

Applications include relative potency estimations in multiple parallel line or slope-ratio assays. Users need to define the design matrix of the linear model and the corresponding contrast matrices in an appropriate way.

Value
A list containing

    estimate point estimates for the ratios
CorrMat.est estimates of the correlation matrix (for the plug-in approach)
Num.Contrast matrix of contrasts used for the numerator of ratios
Den.Contrast matrix of contrasts used for the denominator of ratios
conf.int confidence interval estimates of the ratios
    Y response vector
    X design matrix
    fit the model fit, an object of class "lm"

and some further input arguments, to be passed to print and summary functions.
Author(s)
Gemechis Dilba Djira

References


See Also

glht(multcomp) for multiple comparisons of parameters from lm, glm,..., sci.ratio for confidence intervals for ratios of means in a one-way-layout, simtest.ratio for simultaneous tests for ratios of means in a one-way-layout, plot.sci.ratio for plotting the confidence intervals.

Examples

# Slope-ratio assay on data from Jensen(1989),
# Biometrical Journal 31, 841-853.

# Definition of the vector of responses and
# the design matrix can be done directly as
# follows:

Y0 <- c(1.3, 1.7, 2.4, 2.7, 3.6, 3.6, 4.7, 5.0, 6.1, 6.3)
Y1 <- c(2.8, 2.9, 4.1, 3.7, 5.5, 5.5, 6.4, 6.7)
Y2 <- c(2.2, 2.1, 3.2, 3.2, 3.8, 3.9, 4.7, 4.9)
Y3 <- c(2.3, 2.3, 3.2, 3.0, 4.2, 4.2, 4.6, 5.1)
Y <- c(Y0,Y1,Y2,Y3) # the response vector
xi <- rep(1,34)
x0 <- c(0,0, gl(4,2), rep(0,8*3))
x1 <- c(rep(0,10),gl(4,2), rep(0,8*2))
x2 <- c(rep(0,18),gl(4,2), rep(0,8))
x3 <- c(rep(0,26),gl(4,2))
X <- cbind(xi,x0,x1,x2,x3) # the design matrix

# Have a look at the response vector:
Y

# and the design matrix:
X

# Internally in sci.ratio.gen, the following model is fitted

Fiti <- lm(Y ~ X - 1)
Fiti
summary(Fiti)
# In this problem, interest is simultaneous estimation of
# the ratios of slopes relative to the slope of the standard
# treatment. Therefore, the appropriate contrast matrices are:

Num.Contrast <- matrix(c(0,0,1,0,0,0,0,1,0,0,0,0),nrow=3,byrow=TRUE)
Den.Contrast <- matrix(c(0,1,0,0,0,0,0,0,0,0,1,0),nrow=3,byrow=TRUE)

SlopeRatioCI <- sci.ratio.gen(Y=Y, X=X,

# Further details of the fitted model and the contrasts used:
summary(SlopeRatioCI)
plot(SlopeRatioCI)

# If one starts with a dataframe, the function model.matrix
# can be used to create the design matrix:

data(SRAssay)
SRAssay

# Create the design matrix using model.matrix
X <- model.matrix(Response~Treatment:Dose, data=SRAssay)
Response <- SRAssay[,"Response"]

# The response vector and the design matrix are now:
X
Response

# The following coefficients result from fitting this model:
lm(Response~0+X)

# The same contrasts as above are used:
Num.Contrast <- matrix(c(0,0,1,0,0,0,0,0,1,0,0,0),nrow=3,byrow=TRUE)
sciratioVH

0,0,0,0,1), nrow=3, byrow=TRUE)
Den.Contrast <- matrix(c(0,1,0,0,0, 0,1,0,0,0, 0,1,0,0,0), nrow=3, byrow=TRUE)
summary(sciratio.gen(Y=Response, X=X, Num.Contrast, Den.Contrast))

| sciratioVH | Approximate simultaneous confidence intervals for ratios of means when variances are heterogeneous |

**Description**

This function constructs simultaneous confidence intervals for ratios of linear combinations of normal means in a one-way model, allowing that the variances differ among groups. Different methods are available for multiplicity adjustment.

**Usage**

sciratioVH(formula, data,
  type = "Dunnett", base = 1, method = "Plug",
  Num.Contrast = NULL, Den.Contrast = NULL,
  alternative = "two.sided", conf.level = 0.95,
  names = TRUE)

**Arguments**

- **formula**
  - A formula specifying a numerical response and a grouping factor as e.g. response ~ treatment
- **data**
  - A dataframe containing the response and group variable
- **type**
  - type of contrast, with the following options:
    - "Dunnett": many-to-one comparisons, with control in the denominator
    - "Tukey": all-pair comparisons
    - "Sequen": comparison of consecutive groups, where the group with lower order is the denominator
    - "AVE": comparison of each group with average of all others, where the average is taken as denominator
    - "Changepoint": ratio of averages of groups of higher order divided by averages of groups of lower order
    - "Marcus": Marcus contrasts as ratios
    - "McDermott": McDermott contrasts as ratios
    - "Williams": Williams contrasts as ratios

Note: type is ignored, if Num.Contrast and Den.Contrast are specified by the user (See below).
base  a single integer specifying the control (i.e. denominator) group for the Dunnett contrasts, ignored otherwise

method a character string, specifying the method to be used for confidence interval construction:
- "Plug": Plug-in of ratio estimates to obtain the correlation matrix of contrasts (default)
- "Bonf": Simple Bonferroni-adjustment of Fieller confidence intervals for the ratios
- "MtI": Sidak- or Slepian- adjustment for two-sided and one-sided confidence intervals, respectively
- "Unadj": Unadjusted Fieller confidence intervals for the ratios (i.e. with comparisonwise confidence level = conf.level)

Num.Contrast Numerator contrast matrix, where columns correspond to groups and rows correspond to contrasts

Den.Contrast Denominator contrast matrix, where columns correspond to groups and rows correspond to contrasts

alternative a character string
- "two.sided": for two-sided intervals
- "less": for upper confidence limits
- "greater": for lower confidence limits

conf.level simultaneous confidence level in case of method="Plug","Bonf", or "MtI", and comparisonwise confidence level in case of method="Unadj"

names logical, indicating whether rownames of the contrast matrices shall be retained in the output

Details

Given a one-way ANOVA model, the interest is in simultaneous confidence intervals for several ratios of linear combinations of the treatment means. It is assumed that the responses are normally distributed with possibly heterogeneous variances. Multivariate t-distributions are applied with a correlation matrix depending on the unknown ratios and sample variances and degrees of freedom according to Satterthwaite (1946).

Using method="Unadj" results in the methods described in Hasler, Vonk and Hothorn (2007).

Value

An object of class "sci.ratio", containing a list with elements:

- estimate the point estimates of the ratios
- CorrMat.est the estimated correlation matrix
- Num.Contrast matrix of contrasts used for the numerator of ratios
- Den.Contrast matrix of contrasts used for the denominator of ratios
- conf.int the estimated confidence intervals
- NSD a logical indicating whether any denominator occurred, which were not significantly different from 0

and some of the input arguments.
Author(s)
Mario Hasler

References

Simultaneous confidence intervals:
Marginal (unadjusted) confidence intervals:

See Also

plot.sci.ratio for plots of confidence intervals and simtest.ratioVH for raw and multiplicity-adjusted p-values

Examples

data(Mutagenicity, package="mratios")
boxplot(MN~Treatment, data=Mutagenicity)

# Unless it is hard to assume Gaussian distribution
# in this example this is an attempt to take
# heterogeneous variances into account.

# Comparisons to the vehicle control,
# Proof of Hazard, using multiplicity adjusted
# confidence intervals:

sci.ratioVH(MN~Treatment, data=Mutagenicity,
type="Dunnett", base=6, method="Plug")

# Unadjusted confidence intervals for an
# intersection union test to proof safety
# for all doses of the compound.

sci.ratioVH(MN~Treatment, data=Mutagenicity,
type="Dunnett", base=6, method="Unadj", alternative="less")

# # #
# User-defined contrasts:

# Mutagenicity of the doses of the new compound,
# expressed as ratio (DoseX-Vehicle)/(Cyclo25-Vehicle):
# Check the order of the factor levels:
levels(Mutagenicity$Treatment)

# numerators:
NC<-rbind(
  "Hydro30-Vehicle"=c(0,0,1,0,0,-1),
  "Hydro50-Vehicle"=c(0,0,0,1,0,-1),
  "Hydro75-Vehicle"=c(0,0,0,0,1,-1),
  "Hydro100-Vehicle"=c(0,1,0,0,0,-1)
)

DC<-rbind(
  "Cyclo25-Vehicle"=c(1,0,0,0,0,-1),
  "Cyclo25-Vehicle"=c(1,0,0,0,0,-1),
  "Cyclo25-Vehicle"=c(1,0,0,0,0,-1),
  "Cyclo25-Vehicle"=c(1,0,0,0,0,-1)
)

colnames(NC)<-colnames(DC)<-levels(Mutagenicity$Treatment)

NC

DC

CIs<-sci.ratioVH(MN~Treatment, data=Mutagenicity, 
  Num.Contrast=NC, 
  Den.Contrast=DC)

# Unadjusted confidence intervals for multiple ratios 
# of means assuming heterogeneous group variances. 
# The following code produces the results given in Table V of Hasler, Vonk and Hothorn (2007). 
# The upper confidence limits in Table V can produced 
# by calling:

sci.ratioVH(formula=MN~Treatment, data=Mutagenicity, 
  Num.Contrast=NC, Den.Contrast=DC, 
  method="Unadj", alternative="less", conf.level=0.95)
Description

Performs simultaneous tests for several ratios of linear combinations of treatment means in the normal one-way ANOVA model with homogeneous variances.

Usage

simtest.ratio(formula, data, type = "Dunnett", base = 1,
alternative = "two.sided", Margin.vec = NULL, FWER = 0.05,
Num.Contrast = NULL, Den.Contrast = NULL, names = TRUE)

Arguments

formula A formula specifying a numerical response and a grouping factor (e.g., response ~ treatment)
data A dataframe containing the response and group variable
type type of contrast, with the following options:
  • "Dunnett": many-to-one comparisons, with control in the denominator
  • "Tukey": all-pair comparisons
  • "Sequen": comparison of consecutive groups, where the group with lower order is the denominator
  • "AVE": comparison of each group with average of all others, where the average is taken as denominator
  • "GrandMean": comparison of each group with grand mean of all groups, where the grand mean is taken as denominator
  • "Changepoint": ratio of averages of groups of higher order divided by averages of groups of lower order
  • "Marcus": Marcus contrasts as ratios
  • "McDermott": McDermott contrasts as ratios
  • "Williams": Williams contrasts as ratios
  • "UmbrellaWilliams": Umbrella-protected Williams contrasts as ratios
Note: type is ignored if Num.Contrast and Den.Contrast are specified by the user (See below).
base a single integer specifying the control (i.e. denominator) group for the Dunnett contrasts, ignored otherwise
alternative a character string:
  • "two.sided": for two-sided tests
  • "less": for lower tail tests
  • "greater": for upper tail tests
Margin.vec a single numerical value or vector of Margins under the null hypotheses, default is 1
FWER a single numeric value specifying the family-wise error rate to be controlled
Num.Contrast Numerator contrast matrix, where columns correspond to groups and rows correspond to contrasts
Den.Contrast  Denominator contrast matrix, where columns correspond to groups and rows correspond to contrasts
names          a logical value: if TRUE, the output will be named according to names of user defined contrast or factor levels

Details

Given a one-way ANOVA model, the interest is in simultaneous tests for several ratios of linear combinations of the treatment means. Let us denote the ratios by $\gamma_i, i = 1, \ldots, r$, and let $\psi_i, i = 1, \ldots, r$, denote the relative margins against which we compare the ratios. For example, upper-tail simultaneous tests for the ratios are stated as

$$H_0i : \gamma_i \leq \psi_i$$

versus

$$H_1i : \gamma_i > \psi_i, i = 1, \ldots, r$$

The associated likelihood ratio test statistic $T_i$ has a $t$-distribution. For multiplicity adjustments, we use the joint distribution of the $T_i, i = 1, \ldots, r$, which under the null hypotheses follows a central $r$-variate $t$-distribution. Adjusted $p$-values can be calculated by adapting the results of Westfall et al. (1999) for ratio formatted hypotheses.

Value

An object of class simtest.ratio containing:

- estimate    a (named) vector of estimated ratios
- teststat     a (named) vector of the calculated test statistics
- Num.Contrast the numerator contrast matrix
- Den.Contrast the denominator contrast matrix
- CorrMat      the correlation matrix of the multivariate $t$-distribution calculated under the null hypotheses
- critical.pt  the equicoordinate critical value of the multi-variate $t$-distribution for a specified FWER
- p.value.raw  a (named) vector of unadjusted $p$-values
- p.value.adj  a (named) vector of $p$-values adjusted for multiplicity
- Margin.vec   the vector of margins under the null hypotheses

and some other input arguments.

Author(s)

Gemechis Dilba Djira
simtest.ratio

References


See Also

While print.simtest.ratio produces a small default print-out of the results, summary.simtest.ratio can be used to produce a more detailed print-out, which is recommended if user-defined contrasts are used, sci.ratio for constructing simultaneous confidence intervals for ratios in oneway layout.

See summary.glht(multcomp) for multiple tests for parameters of lm, glm.

Examples

```r
library(mratios)

# User-defined contrasts for comparisons
# between Active control, Placebo and three dosage groups:

data(AP)
AP
boxplot(prepost~treatment, data=AP)

# Test whether the differences of doses 50, 100, 150 vs. Placebo
# are non-inferior to the difference of Active control vs. Placebo

# User-defined contrasts:
# Numerator Contrasts:

NC <- rbind(
  "(D100-D0)" = c(0,-1,1,0,0),
  "(D150-D0)" = c(0,-1,0,1,0),
  "(D50-D0)" = c(0,-1,0,0,1))

# Denominator Contrasts:

DC <- rbind(
  "(AC-D0)" = c(1,-1,0,0,0),
  "(AC-D0)" = c(1,-1,0,0,0),
  "(AC-D0)" = c(1,-1,0,0,0))

NC
DC
```
noninf <- simtest.ratio(prepost ~ treatment, data=AP, 
   Num.Contrast=NC, Den.Contrast=DC, Margin.vec=c(0.9,0.9,0.9),
   alternative="greater")
summary( noninf )

# Some more examples on standard multiple comparison procedures
# stated in terms of ratio hypotheses:

# Comparisons vs. Control:
many21 <- simtest.ratio(prepost ~ treatment, data=AP, 
   type="Dunnett")
summary(many21)

# Let the Placebo be the control group, which is the second level
# in alpha-numeric order. A simultaneous test for superiority of
# the three doses and the Active control vs. Placebo could be
# done as:
many21P <- simtest.ratio(prepost ~ treatment, data=AP, 
   type="Dunnett", base=2, alternative="greater", Margin.vec=1.1)
summary(many21P)

# All pairwise comparisons:
allpairs <- simtest.ratio(prepost ~ treatment, data=AP, 
   type="Tukey")
summary(allpairs)

# Comparison to grand mean of all strains
# in the Penicillin example:

data(Penicillin)

CGM <- simtest.ratio(diameter~strain, data=Penicillin, type="GrandMean")
CGM
summary(CGM)

---

simtest.ratioVH  Approximate simultaneous tests for ratios of normal means with heterogeneous variances
Description

Performs simultaneous tests for several ratios of linear combinations of treatment means in a normal one-way layout, assuming normal distribution of the data allowing heterogeneous variances.

Usage

```r
simtest.ratioVH(formula, data,
    type = "Dunnett", base = 1, alternative = "two.sided",
    Margin.vec = NULL, FWER = 0.05,
    Num.Contrast = NULL, Den.Contrast = NULL,
    names = TRUE)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>formula</td>
<td>A formula specifying a numerical response and a grouping factor (e.g., response ~ treatment)</td>
</tr>
<tr>
<td>data</td>
<td>A dataframe containing the response and group variable</td>
</tr>
<tr>
<td>type</td>
<td>type of contrast, with the following options:</td>
</tr>
<tr>
<td></td>
<td>• &quot;Dunnett&quot;: many-to-one comparisons, with control in the denominator</td>
</tr>
<tr>
<td></td>
<td>• &quot;Tukey&quot;: all-pair comparisons</td>
</tr>
<tr>
<td></td>
<td>• &quot;Sequen&quot;: comparison of consecutive groups, where the group with lower order is the denominator</td>
</tr>
<tr>
<td></td>
<td>• &quot;AVE&quot;: comparison of each group with average of all others, where the average is taken as denominator</td>
</tr>
<tr>
<td></td>
<td>• &quot;Changepoint&quot;: ratio of averages of groups of higher order divided by averages of groups of lower order</td>
</tr>
<tr>
<td></td>
<td>• &quot;Marcus&quot;: Marcus contrasts as ratios</td>
</tr>
<tr>
<td></td>
<td>• &quot;McDermott&quot;: McDermott contrasts as ratios</td>
</tr>
<tr>
<td></td>
<td>• &quot;Williams&quot;: Williams contrasts as ratios</td>
</tr>
<tr>
<td></td>
<td>Note: type is ignored if Num.Contrast and Den.Contrast are specified by the user (See below).</td>
</tr>
<tr>
<td>base</td>
<td>a single integer specifying the control (i.e. denominator) group for the Dunnett contrasts, ignored otherwise</td>
</tr>
<tr>
<td>alternative</td>
<td>a character string:</td>
</tr>
<tr>
<td></td>
<td>• &quot;two.sided&quot;: for two-sided tests</td>
</tr>
<tr>
<td></td>
<td>• &quot;less&quot;: for lower tail tests</td>
</tr>
<tr>
<td></td>
<td>• &quot;greater&quot;: for upper tail tests</td>
</tr>
<tr>
<td>Margin.vec</td>
<td>a single numerical value or vector of Margins under the null hypotheses, default is 1</td>
</tr>
<tr>
<td>FWER</td>
<td>a single numeric value specifying the family-wise error rate to be controlled</td>
</tr>
<tr>
<td>Num.Contrast</td>
<td>Numerator contrast matrix, where columns correspond to groups and rows correspond to contrasts</td>
</tr>
<tr>
<td>Den.Contrast</td>
<td>Denominator contrast matrix, where columns correspond to groups and rows correspond to contrasts</td>
</tr>
<tr>
<td>names</td>
<td>a logical value: if TRUE, the output will be named according to names of user defined contrast or factor levels</td>
</tr>
</tbody>
</table>
Details

The associated ratio test statistic $T[i]$ has a t-distribution. Multiplicity adjustment is achieved by using quantiles of $r$ $r$-variate t-distributions, which differ in the degree of freedom and share the correlation structure. The comparison-specific degrees of freedom are derived using the approximation according to Satterthwaite (1946).

Value

An object of class simtest.ratio containing:

- `estimate` a (named) vector of estimated ratios
- `teststat` a (named) vector of the calculated test statistics
- `Num.Contrast` the numerator contrast matrix
- `Den.Contrast` the denominator contrast matrix
- `CorrMat` the correlation matrix of the multivariate t-distribution calculated under the null hypotheses
- `critical.pt` the equicoordinate critical value of the multi-variate t-distribution for a specified FWER
- `p.value.raw` a (named) vector of unadjusted p-values
- `p.value.adj` a (named) vector of p-values adjusted for multiplicity
- `Margin.vec` the vector of margins under the null hypotheses

and some other input arguments.

Author(s)

Mario Hasler

References

Simultaneous tests (adjusted p-values)


Unadjusted tests (raw p-values)


See Also

`sci.ratioVH` for corresponding confidence intervals
Examples

# Unadjusted confidence intervals for multiple ratios
# of means assuming heterogeneous group variances.
# The following code produces the results given in Table V of Hasler, Vonk and Hothorn (2007).
# The upper confidence limits in Table V can produced
# by calling:

# Mutagenicity of the doses of the new compound,
# expressed as ratio (DoseX-Vehicle)/(Cyclo25-Vehicle):

levels(Mutagenicity$Treatment)

# numerators:

NC<-rbind(
  "Hydro30-Vehicle"=c(0,0,1,0,0,-1),
  "Hydro50-Vehicle"=c(0,0,0,1,0,-1),
  "Hydro75-Vehicle"=c(0,0,0,0,1,-1),
  "Hydro100-Vehicle"=c(0,1,0,0,0,-1)
)

DC<-rbind(
  "Cyclo25-Vehicle"=c(1,0,0,0,-1),
  "Cyclo25-Vehicle"=c(1,0,0,0,-1),
  "Cyclo25-Vehicle"=c(1,0,0,0,-1),
  "Cyclo25-Vehicle"=c(1,0,0,0,-1)
)

colnames(NC)<-colnames(DC)<-levels(Mutagenicity$Treatment)

NC

DC
# The raw p-values are those presented in Table V:

```r
simtest.ratioVH(formula=MN~Treatment, data=Mutagenicity, 
Num.Contrast=NC, Den.Contrast=DC, 
alternative="less", Margin.vec=0.5, FWER=0.05)
```

<table>
<thead>
<tr>
<th>SRAssay</th>
<th>Slope ratio assay of panthotenic acid contents in plant tissues</th>
</tr>
</thead>
</table>

**Description**

Content of panthotenic acid in a standard and three unknown samples were measured. The response variable is the titer of a sample to pH 6.8.

**Usage**

data(SRAssay)

**Format**

A data frame with 34 observations on the following 3 variables.

- **Response** a numeric vector, containing the response variable (titer to pH 6.8)
- **Treatment** a factor with levels St, U1, U2 and U3, specifying the standard and 3 unknown samples, respectively
- **Dose** a numeric vector

**Source**


**References**


**Examples**

```r
library(mratios)
data(SRAssay)
str(SRAssay)
plot(Response~Dose, data=SRAssay)
# library(lattice)
```
summary.sci.ratio

Summary function for sci.ratio

Description

Detailed print out for sci.ratio objects.

Usage

```r
## S3 method for class 'sci.ratio'
summary(object, digits=4, ...)
```

Arguments

- `object`: an object of class "sci.ratio" or "sci.ratio.gen" as can be obtained by calling the function `sci.ratio`
- `digits`: digits for rounding the output
- `...`: arguments to be passed to print

Value

A more detailed print output of the results and some computational steps used in `sci.ratio`.

See Also

`print.sci.ratio`, `plot.sci.ratio`

Examples

```r
data(BW)
RES <- sci.ratio(Weight~Dose, data=BW, type="Dunnett", alternative="greater")
summary(RES)
```
**summary.simtest.ratio**  
*Summary function for simtest.ratio*

**Description**
A detailed print out of the results of simtest.ratio

**Usage**
```r
## S3 method for class 'simtest.ratio'
summary(object, digits = 4, ...)
```

**Arguments**
- `object`: An object of class "simtest.ratio" as obtained by calling simtest.ratio
- `digits`: digits for rounding of the results
- `...`: arguments to be passed to print

**Value**
A print out, containing the numerator and denominator contrast matrices, the correlation under the null-hypothesis, margins, estimates, teststatistics, and p.values computed by simtest.ratio.

**Examples**
```r
data(BW)
RES <- simtest.ratio(Weight~Dose, data=BW, type="Dunnett", Margin.vec=0.9, alternative="greater")
summary(RES)
```

---

**t.test.ratio**  
*t-test for the ratio of two means*

**Description**
Performs t-test for the ratio of means of two independent samples from two gaussian distributions. In case of heterogeneous variances a Satterthwaite approximation of the degrees of freedom is used (Tamhane & Logan, 2004).

**Usage**
```r
## Default S3 method:
t.test.ratio(x, y, alternative = "two.sided",
            rho = 1, var.equal = FALSE, conf.level = 0.95,
            iterativeCI=FALSE, ul=1e+10, ll=-1e+10, ...)
## S3 method for class 'formula'
t.test.ratio(formula, data, base=2, ...)
```
t.test.ratio

Arguments

x A numeric vector (group in the numerator of the ratio)
y A numeric vector (group in the denominator of the ratio)
formula A two-sided formula specifying a numeric response variable and a factor with two levels
data A dataframe containing the variables specified in formula. Note: the first group in alpha-numeric order will appear in the denominator of the ratio
alternative character string defining the alternative hypothesis, one of "two.sided", "less" or "greater"
rho a single numeric value: the margin or ratio under the null hypothesis
var.equal logical, if set TRUE, a ratio-t-test assuming equal group variances is performed, otherwise (default) unequal variances are assumed
conf.level confidence level of Fieller's interval for the ratio of two means
base if formula is used: a single numeric value specifying whether the first or second group (according to alpha-numeric order) is to be used as denominator
iterativeCI a single logical, indicating whether the confidence limits shall be found with based on Fieller's formula (default) or by iteratively inverting the test (if TRUE); ignored when var.equal=TRUE
ul a single numeric, defining the upper limit for searching the upper confidence bound in uniroot, if iterativeCI=TRUE and var.equal=FALSE, ignored otherwise
ll a single numeric, defining the lower limit for searching the lower confidence bound in uniroot, if iterativeCI=TRUE and var.equal=FALSE, ignored otherwise
... arguments to be passed to t.test.ratio.default

Details

This function implements the t-test for the ratio of two means and Fieller's confidence interval for the ratio of two means assuming mutually independent Gaussian errors with homogeneous variances, e.g. in Hauschke, Kieser, Hothorn (1999), when the argument var.equal=FALSE (default), the t-test for the ratio of two means assuming mutually independent Gaussian errors and possibly heterogeneous group variances (Tamhane and Logan, 2004) is implemented. When iterativeCI = FALSE (default) the corresponding confidence limits are obtained by using Fieller's formula with plug-in of the Satterthwaites degree of freedom calculated with the sample estimates for ratio and variances (not published). These bounds perform quite well but do not necessarily exactly coincide with the test decision. Setting iterativeCI = TRUE invokes iteratively searching for the confidence limits by inverting Tamhane and Logans test using the function uniroot. If the confidence set is unbounded or gives irregular upper and/or lower bounds, a warning and NAs for the confidence limits are returned.

Note that when the mean of the denominator of the ratio is close to zero, confidence intervals might be degenerated and are not returned.

Value

An object of class "htest"
Author(s)

Frank Schaarschmidt

References


Examples

```r
library(mratios)

# ASAT values of female rats in a toxicity study
# (Hauschke, 1999).
data(ASAT)
ASAT

t.test.ratio(ASAT~group, data=ASAT, alternative="less",
             base=1, rho=1.25, var.equal=TRUE)

# Bodyweights of male rats in a toxicity study.
# Objective was to show equivalence between the high
dose group (Dosis) and the control group (Kon).
# Equivalence margins are set to 0.8 and 1.25. The
# type-I-error to show equivalence is set to alpha=0.05.
data(rat.weight)

# two one-sided tests:
t.test.ratio(weight~group, data=rat.weight, alternative="less",
             rho=1.25, var.equal=TRUE)
t.test.ratio(weight~group, data=rat.weight, alternative="greater",
             rho=0.8, var.equal=TRUE)

# For rho=1, t.test.ratio corresponds to a simple t.test
# with the difference of means under the null set to zero
# (, i.e. mu=0).
```
t.test.ratio

```r
t.test.ratio(ASAT-group, data=ASAT, alternative="less",
        rho=1, var.equal=TRUE)

t.test(ASAT-group, data=ASAT, alternative="less",
        mu=0, var.equal=TRUE)

# Ratio of means between negative and positive control in the
# mutagenicity data set, allowing heterogeneous variances:

data(Mutagenicity)
DM <- subset(Mutagenicity, Treatment=="Vehicle" | Treatment=="Cyclo25")

# 95%-CI using the Fieller formula, Satterthwaite df with plug-in of
# ratio estimate

t.test.ratio(MN-Treatment, data=DM, alternative="two.sided",
        var.equal=FALSE, iterativeCI=FALSE)

# 95%-CI based on directly inverting Tamhane and Logans test
# (Satterthwaite df, avoiding simple plug-in of the ratio estimate)

t.test.ratio(MN-Treatment, data=DM, alternative="two.sided",
        var.equal=FALSE, iterativeCI=TRUE)

t.test.ratio(MN-Treatment, data=DM, alternative="greater", rho=4.589893)$p.value
t.test.ratio(MN-Treatment, data=DM, alternative="less", rho=18.640143)$p.value
```
## Index

<table>
<thead>
<tr>
<th>Topic</th>
<th>Datasets</th>
<th>mratio-package, 2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>angina, 6</td>
<td>Mutagenicity, 15</td>
</tr>
<tr>
<td></td>
<td>AP, 7</td>
<td>n.ratio, 16</td>
</tr>
<tr>
<td></td>
<td>ASAT, 8</td>
<td>Penicillin, 17</td>
</tr>
<tr>
<td></td>
<td>BW, 9</td>
<td>plot.sci.ratio, 18</td>
</tr>
<tr>
<td></td>
<td>Mutagenicity, 15</td>
<td>print.sci.ratio, 20</td>
</tr>
<tr>
<td></td>
<td>Penicillin, 17</td>
<td>print.simtest.ratio, 21</td>
</tr>
<tr>
<td></td>
<td>rat.weight, 21</td>
<td>rat.weight, 21</td>
</tr>
<tr>
<td></td>
<td>SRAssay, 40</td>
<td>sci.ratio, 22, 27</td>
</tr>
<tr>
<td></td>
<td></td>
<td>sci.ratio.gen, 25</td>
</tr>
<tr>
<td></td>
<td></td>
<td>sci.ratioI (sci.ratio), 22</td>
</tr>
<tr>
<td></td>
<td></td>
<td>sci.ratioVH, 29, 38</td>
</tr>
<tr>
<td></td>
<td></td>
<td>simtest.ratio, 27, 32</td>
</tr>
<tr>
<td></td>
<td></td>
<td>simtest.ratioI (simtest.ratio), 32</td>
</tr>
<tr>
<td></td>
<td></td>
<td>simtest.ratioVH, 31, 36</td>
</tr>
<tr>
<td></td>
<td></td>
<td>SRAssay, 40</td>
</tr>
<tr>
<td></td>
<td></td>
<td>summary.sci.ratio, 20, 41</td>
</tr>
<tr>
<td></td>
<td></td>
<td>summary.simtest.ratio, 42</td>
</tr>
<tr>
<td></td>
<td></td>
<td>t.test.ratio, 42</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>Hplot</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>plot.sci.ratio, 18</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>Htest</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>contrMatRatio, 10</td>
</tr>
<tr>
<td></td>
<td>gsci.ratio, 12</td>
</tr>
<tr>
<td></td>
<td>n.ratio, 16</td>
</tr>
<tr>
<td></td>
<td>plot.sci.ratio, 18</td>
</tr>
<tr>
<td></td>
<td>sci.ratio, 22</td>
</tr>
<tr>
<td></td>
<td>sci.ratio.gen, 25</td>
</tr>
<tr>
<td></td>
<td>sci.ratioI (sci.ratio), 22</td>
</tr>
<tr>
<td></td>
<td>sci.ratioVH, 29, 38</td>
</tr>
<tr>
<td></td>
<td>simtest.ratio, 32</td>
</tr>
<tr>
<td></td>
<td>simtest.ratioVH, 36</td>
</tr>
<tr>
<td></td>
<td>t.test.ratio, 42</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>mratios-package, 2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>Print</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>print.sci.ratio, 20</td>
</tr>
<tr>
<td></td>
<td>print.simtest.ratio, 21</td>
</tr>
<tr>
<td></td>
<td>summary.sci.ratio, 41</td>
</tr>
<tr>
<td></td>
<td>summary.simtest.ratio, 42</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>Angina</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>6</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>AP</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>7</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>ASAT</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>8</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>BW</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>9</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>ContrMatRatio</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>10</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>Gsci.ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>12</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Topic</th>
<th>Mratio (mratios-package)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2</td>
</tr>
</tbody>
</table>