

Package ‘BSagri’

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Title Statistical methods for safety assessment in agricultural field trials

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Description Collection of functions, data sets and code examples for evaluations of field trials with the objective of safety assessment.

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alignment

Alignment according to one factor

Description

Subtracts the mean or median from observations belonging to the same level of a factor.

Usage

```
alignment(response, block, type = c("mean", "median"), ...)
```

Arguments

response	a numeric vector
block	a factor of the same length as response
type	type of location measure to calculate and subtract; only the choices "mean" and "median" are supported
...	further arguments to be passed to mean or median

Details

Splits response according to the levels of block, calculates and subtracts the mean or median and returns the resulting vector in appropriate order.

Value

A numeric vector.

BOOTSimpson	<i>Simultaneous confidence intervals for Simpson indices</i>
-------------	--

Description

NOTE: This is a Test-version and is not sufficiently checked for correctness so far. Simultaneous confidence intervals for differences and ratios of Simpsons indices of diversity are calculated from data sets with repeated samples of communities and designs with more than two treatments groups. The intervals are calculated based on a stratified, non-parametric ordinary bootstrap sample of Simpsonindices, and applying the Algorithm of Besag et al.(1995) on the joint empirical distribution of differences (BOOTSimpsonD) or ratios (BOOTSimpsonR) of the original distribution.

Usage

```
BOOTSimpsonD(X, f, type = "Dunnett", cmat = NULL, conf.level = 0.95,
  alternative=c("two.sided", "less", "greater"), madj=TRUE, ...)
```

```
BOOTSimpsonR(X, f, type = "Dunnett", cmat = NULL, conf.level = 0.95,
  alternative=c("two.sided", "less", "greater"), madj=TRUE, ...)
```

Arguments

X	a data.frame of dimension n times p, containing integer entries as species counts of p species from n independent samplings
f	a factor, usually with more than two levels. Must be of length n, when X is an n times p matrix
type	a single character string, defining a contrast type. Supported options are 'Dunnett', 'Tukey', 'Sequen'; for more options, see ?contrMatratio in mratios when using BOOTSimpsonR or contrMat in multcomp when using BOOTSimpsonD

<code>cmat</code>	user defined contrasts: when using <code>BOOTSimpsonD</code> , this should be a numeric contrast matrix, with <code>k</code> columns when the factor <code>f</code> has <code>k</code> levels and should define differences of these levels; when using <code>BOOTSimpsonR</code> , this should be a list with two numeric contrast matrices in the entries <code>numC</code> and <code>denC</code> for numerators and denominator of the ratios, respectively; each having <code>k</code> columns when the factor <code>f</code> has <code>k</code> levels
<code>conf.level</code>	a single numeric value between 0.5 and 1
<code>alternative</code>	a single character string, one of <code>'two.sided'</code> , <code>'less'</code> and <code>'greater'</code>
<code>madj</code>	a single logical value, indicating whether simultaneous (if <code>TRUE</code> , the default) or marginal confidence intervals (if <code>FALSE</code>) shall be computed
<code>...</code>	Further arguments to be passed to the function <code>boot</code> from package boot ; most importantly, the number of Bootstrap samples can be chosen via the parameter <code>R</code> (default is <code>R=999</code>); see <code>?boot</code> for further options.

Details

NOTE: This is a test version!

Value

If `madj=TRUE`, an object of class `"SCSNp"`, see [SCSNp](#) for details. If `madj=FALSE`, an object of class `"CInp"`, see [CInp](#) for details.

Author(s)

Frank Schaarschmidt

See Also

[SCSNp](#), these function internally make use of [CCDiff.boot](#), [CCDiff.default](#), [CCRatio.boot](#), [CCRatio.default](#), [boot](#) and [estSimpsonf](#).

Examples

```
X<-t(rmultinom(n=40,size=100,
  prob=c(0.3,0.2,0.2,0.1,0.1,0.05,0.05)))

colnames(X)<-paste("Sp",1:7,sep="")

DAT<-as.data.frame(X)

f<-as.factor(rep(c("A","B","C","D"),each=10))

SCIdunnettd<-BOOTSimpsonD(X=DAT, f=f, type = "Dunnett",
  conf.level = 0.95, alternative = "two.sided")

SCIdunnettd

SCIdunnettr<-BOOTSimpsonR(X=DAT, f=f, type = "Dunnett",
```

```
conf.level = 0.95, alternative = "two.sided")
SCIdunnettr
```

 Brachycera

Eklektor counts of Brachycera

Description

In a field trial, 4 treatments were arranged in a randomized complete block design with 8 blocks and 32 plots. Soil eklektor traps were placed in each plot, on six dates from 2005-07-12 to 2005-09-25, the number of individuals of Brachycera (Flies, Order Diptera) hatching from soil were counted. The individuals were classified to the family level. Interest was in assessing potential effects of the novel treatment (Novum) on the abundance of Brachycera, compared to a near standard (Standard) and two additional standard treatments, A and B.

Usage

```
data(Brachycera)
```

Format

A data frame with 192 observations on the following 15 variables.

Date a POSIXt variable, the time of counting the individuals in the eklektor trap

Treatment a factor with 4 levels A B Standard Novum, where Novum is the novel treatment of interest in safety assessment, and Standard is the nearest standard treatment which commonly accepted. A and B are two additional standard treatments.

Block a numeric vector, specifying the eight blocks 1-8

Plot a factor with levels A1 A2 to Standard8, indicator of the individuals plots

Agromy a numeric vector, counts of individuals

Anthom a numeric vector, counts of individuals

Callip a numeric vector, counts of individuals

Chloro a numeric vector, counts of individuals

Ephyd a numeric vector, counts of individuals

Droso a numeric vector, counts of individuals

Hybo a numeric vector, counts of individuals

Musci a numeric vector, counts of individuals

Phori a numeric vector, counts of individuals

Sphaer a numeric vector, counts of individuals

Total a numeric vector, counts of individuals

Source

...

Examples

```
data(Brachycera)

par(mar=c(11,5,3,1))

boxplot(Total ~ Treatment*Date, data=Brachycera, las=2,
col=c("white","white","blue","green"))

legend(x=15, y=80, legend=levels(Brachycera$Treatment),
fill=c("white","white","blue","green"))
```

c2compnames	<i>Define row names of a contrast matrix, depending on its column names</i>
-------------	---

Description

Define row names of a contrast matrix, depending on its column names, as can be necessary for contrasts matrices. Currently, two options to do that are available.

Usage

```
c2compnames(cmat, ntype = "aggr")
```

Arguments

cmat	a contrast matrix
ntype	a single character string, defining how to build names from the column names of cmat, currently only "aggr" (aggregates names of groups with negative and positive coefficients), and "sequ"

Details

Improvements of this function are welcome!

Value

The input matrix cmat, with its row names replaced.

See Also

contrMat in **multcomp** to define contrast matrices of different types

Examples

```

# names for interaction contrasts:

n1<-c(10,10,10,10)
names(n1)<-c("A","B","C","D")

n2<-c(3,3,3)
names(n2)<-c(1,2,3)

library(multcomp)

CMT1<-contrMat(n1, type="Tukey")
CMT2<-contrMat(n2, type="Tukey")

IAC<-IAcontrastsCMAT(CMAT1=CMT1, CMAT2=CMT2)

c2compnames(IAC, ntype="aggr")
c2compnames(IAC, ntype="sequ")

#####

# names for Williams-type contrasts:

n1<-c(10,10,10,10)
names(n1)<-c("C0","D1","D5","D10")

CMW<-contrMat(n1, type="Williams")

CMW

c2compnames(CMW, ntype="aggr")
c2compnames(CMW, ntype="sequ")

```

Description

Calculate linear combinations of parameters simulated in BUGS. This is a test version for internal use!

Usage

```
CCDiff(bugs, dat, cmat = NULL,
       type = c("Dunnett", "Tukey", "Sequen", "Williams", "Changepoint"))
```

Arguments

bugs	an object of class bugs, containing N values of the joint posterior distribution of in an N-times-P matrix named muvec
dat	an object of R2Bugsdat1w
cmat	a contrast matrix of dimensions M-times-P
type	a single character string, which type of comparisons to perform, if cmat is not given; this argument is ignored if cmat ist specified

Details

Testversion, for internal use.

Value

An object of class "CCDiff", a list with elements

chains	the N-times-M matrix of the transformed joint posterior distribution
bugs	the bugs object, as input
dat	the object of class "R2Bugsdat1w", as input
cmat	the M-times-P contrast matrix

CCDiff.boot

Compute contrasts of chains of joint empirical distributions.

Description

Compute contrasts of chains of joint empirical distributions obtained by stratified bootstrap. For internal use.

Usage

```
CCDiff.boot(x, cmat = NULL,
           type = c("Dunnett", "Tukey", "Sequen", "Williams",
                  "Changepoint", "McDermott", "GrandMean", "Marcus"))
```

Arguments

x	an object of class "boot" as can be obtained by calling <code>boot</code> in package boot with stratified bootstrap
cmat	an optional contrast matrix, <code>ncol(cmat)</code> should be the same the number of strata in x
type	a single character string, naming a contrast type available in <code>contrMat</code> in package multcomp , see <code>?contrMat</code> for details

Details

Testversion. For internal use.

CCDiff.default *Compute contrasts of chains of joint empirical distributions.*

Description

Compute contrasts of chains of joint empirical distributions. For internal use.

Usage

```
CCDiff.default(x, cmat)
```

Arguments

x	an N times K matrix with numeric entries
cmat	a contrast matrix with K columns

Details

Denote the elements of x by x_{nk} and denote the elements of cmat by c_{mk} . Function `CCDiff.default` simply calculates:

$$\sum_{k=1}^K c_{mk} x_{nk}$$

for each $m=1,\dots,M$ and $n=1,\dots,N$. The result is a N times M matrix.

Examples

```
# What the function does:
# a 10 times 4 matrix

X<-round(cbind(
  rnorm(10,1,1),
  rnorm(10,1,1),
```

```

rnorm(10,1,1),
rnorm(10,1,1)))

# and a x times 4 contrast matrix

CMAT<-rbind(
c(-1,1,0,0),
c(-1,0,1,0),
c(-1,0,0,1)
)

CCDiff.default(x=X, cmat=CMAT)

```

CCRatio

Ratio - contrasts of parameters simulated in BUGS

Description

Calculate ratios of parameters simulated in BUGS. This is a test version for internal use!

Usage

```

CCRatio(bugs, dat, cmat = NULL,
type = c("Dunnett", "Tukey", "Sequen", "Williams", "Changepoint"))

```

Arguments

bugs	an object of class bugs, containing N values of the joint posterior distribution of in an N-times-P matrix named muvec
dat	an object of R2Bugsdat1w
cmat	a list containing two contrast matrices of dimensions M-times-P as elements numC, denC giving the numerator and denominator coefficients for the ratios to be calculated
type	a single character string, which type of comparisons to perform, if cmat is not given; this argument is ignored if cmat ist specified

Details

A testversion.

Value

An object of class "CCRatio", a list with elements

chains	the N-times-M matrix of the transformed joint posterior distribution
bugs	the bugs object, as input
dat	the object of class "R2Bugsdat1w", as input
cmat	the M-times-P contrast matrix

CCRatio.boot *Compute ratio contrasts of chains of joint empirical distributions.*

Description

Compute contrasts of chains of joint empirical distributions. For internal use.

Usage

```
CCRatio.boot(x, cmat = NULL,
             type = c("Dunnett", "Tukey", "Sequen", "Williams",
                    "Changepoint", "McDermott", "GrandMean", "Marcus"))
```

Arguments

x an object of class "boot" as can be obtained by calling `boot` in package **boot** with stratified bootstrap

cmat an optional list of two contrast matrices, in entries `numC` and `denC` of the list; `ncol(numC)` and `ncol(denC)` should be the same the number of strata in `x`

type a single character string, naming a contrast type available in `contrMatRatio` in package **mratio**s, see `?contrMatRatio` for details

Details

Testversion. For internal use.

CCRatio.default *Compute ratio contrasts of chains of joint empirical distributions.*

Description

Compute ratio contrasts of chains of joint empirical distributions. For internal use.

Usage

```
CCRatio.default(x, cmat)
```

Arguments

x an N times K matrix with numeric entries

cmat a list with entries `numC` and `denC`, each containing a contrast matrix with K columns (must be the same K as in `x`!) and M rows (is your choice, the number of contrasts of interest)

Details

Denote the elements of x by x_{nk} . Denote the numerator of cmat by C with elements c_{mk} and the denominator of cmat as D with elements d_{mk} . Function `CCRatio.default` simply calculates

$$\frac{\sum_{k=1}^K c_{mk} x_{nk}}{\sum_{k=1}^K d_{mk} x_{nk}}$$

for each $m=1,\dots,M$ and $n=1,\dots,N$. The result is a N times M matrix.

Examples

```
X<-round(cbind(
  rnorm(10,1,1),
  rnorm(10,1,1),
  rnorm(10,1,1),
  rnorm(10,1,1)))

# and numerator and denominator
# x times 4 contrast matrix

NMAT<-rbind(
  c(1,0,0,0),
  c(1,0,0,0),
  c(1,0,0,0)
)

DMAT<-rbind(
  c(0,1,0,0),
  c(0,0,1,0),
  c(0,0,0,1)
)

CCRatio.default(x=X, cmat=list(numC=NMAT, denC=DMAT) )
```

checkargssim

For internal use.

Description

For internal use. Check the appropriateness of input arguments of function `simplesimint`.

Usage

```
checkargssim(coef, vcov, cmat)
```

Arguments

coef	a vector of parameters
vcov	the corresponding variance-covariance matrix
cmat	a contrast matrix

Cica1	<i>Catches of Planthoppers and Leafhoppers</i>
-------	--

Description

Data of a field trial concerning the impact of a genetically modified variety on the abundance of Planthoppers and Leafhoppers. The trial was designed as a randomized complete block design with 8 blocks (Row). In each block, three treatments were randomized: a conventional variety treated with insecticides (Insecticide), a genetically modified variety (GM), and the near-isogenic line (Iso) the to genetically modified line.

Usage

```
data(Cica1)
```

Format

A data frame with 24 observations on the following 6 variables.

Field a factor with levels 1 2, separating the two major sites of the trial. On field 1, the blocks 1-5 were situated, on field 2, blocks 6-8 were situated.

Row a factor with 8 levels, specifying the blocks:R1 R2 R3 R4 R5 R6 R7 R8

Year a numeric vector, for year 1 of the trial

Treatment a factor with 3 levels, specifying the genetically modified variety GM, the conventional variety treated with insecticides Insecticide, and the variety that was near-isogenic to the GM variety Iso

Au_Bonitur Counts of Auchenorryhacha by visual assessment

Zs_sweep_netting Counts of the major species Zyginidia scutellaris, caught by sweep nets

Source

...

Examples

```

data(Cica1)

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

ylim<-range(Cica1[,c("Au_Bonitur","Zs_sweep_netting")])

boxplot(Au_Bonitur ~ Treatment, data=Cica1,
        main= "Aucherrhyncha, visual assessment", ylim=ylim)

boxplot(Zs_sweep_netting ~ Treatment, data=Cica1,
        main="Z.scutellaris, sweep netting", ylim=ylim)

```

Cica2

Catches of Planthoppers and Leafhoppers

Description

Data of a field trial concerning the impact of a genetically modified variety on the abundance of Planthoppers and Leafhoppers. The trial was designed as a randomized complete block design with 8 blocks (Row). In each block, three treatments were randomized: a conventional variety treated with insecticides (Insecticide), a genetically modified variety (GM), and the near-isogenic line (Iso) the to genetically modified line. These data originate from the second year of the trial in Cica1.

Usage

```
data(Cica2)
```

Format

A data frame with 24 observations on the following 8 variables.

Field a factor with 2 levels, 1 2, separating the two major sites of the trial. On field 1, the blocks 1-5 were situated, on field 2, blocks 6-8 were situated.

Row a factor with 8 levels, specifying the blocks: R1 R2 R3 R4 R5 R6 R7 R8

Year a numeric vector, with value 2 for the second year

Treatment a factor with 3 levels, specifying the genetically modified variety GM, the conventional variety treated with insecticides Insecticide, and the variety that was near-isogenic to the GM variety Iso

Au_Bonitur counts of Auchenorryhncha by visual assessment

Zs_sweep_netting counts of the major species Zyginidia scutellaris, caught by sweep nets

Zs_yellow_traps counts of Zyginidia scutellaris, caught by yellow traps

Zs_stick_traps counts of Zyginidia scutellaris, caught by sticky traps

Source

...

References

See [Cica1](#) for data of the same trial a year earlier

Examples

```
data(Cica2)

# A comparison of the treatments:

dev.new(width=12,height=4)
layout(matrix(1:4,ncol=4))

ylim<-range(Cica2[,c("Au_Bonitur","Zs_sweep_netting", "Zs_yellow_traps", "Zs_stick_traps")])

boxplot(Au_Bonitur ~ Treatment, data=Cica2,
  main= "Aucherrhyncha, visual assessment", ylim=ylim, horizontal=TRUE, las=1)

boxplot(Zs_sweep_netting ~ Treatment, data=Cica2,
  main="Z.scutellaris, sweep netting", ylim=ylim, horizontal=TRUE, las=1)

boxplot(Zs_yellow_traps ~ Treatment, data=Cica2,
  main="Z.scutellaris, yellow traps", ylim=ylim, horizontal=TRUE, las=1)

boxplot(Zs_stick_traps ~ Treatment, data=Cica2,
  main="Z.scutellaris, sticky traps", ylim=ylim, horizontal=TRUE, las=1)

# A comparison of sampling methods:

dev.new(width=10,height=10)

pairs(Cica2[,c("Au_Bonitur","Zs_sweep_netting", "Zs_yellow_traps", "Zs_stick_traps")])
```

CIGLM

Wrapper to compute confidence intervals from glms

Description

Computes confidence intervals from the output of a glm, by calling to `glht(multcomp)`.

Usage

```
CIGLM(x, conf.level = 0.95, method = c("Raw", "Adj", "Bonf"))
```

Arguments

<code>x</code>	a object of class "glm", "gamlss", or "glm.nb" as can be obtained by calling to function <code>glm</code> , function <code>gamlss</code> in package <code>gamlss</code> , or function <code>glm.nb</code> in package <code>MASS</code>
<code>conf.level</code>	confidence level, a single numeric value between 0.5 and 1
<code>method</code>	a single character string, with "Raw" for unadjusted intervals, "Adj" for multiplicity adjusted intervals taking the correlations into account, or "Bonf" for a Bonferroni adjustment

Details

This is just a wrapper to `confint.glm` of package `multcomp`.

Note that except for the simple general linear model with assumption of Gaussian response, the resulting intervals are exact intervals. In other cases, the methods are only asymptotically correct, hence might give misleading results for small sample sizes!

Value

An object of class "confint.glm"

See Also

`confint.glm` in package `multcomp` for the function that is used internally, [UnlogCI](#) for a simple function to bring confidence intervals back to the original scales when there is a log or logit link, with appropriate naming.

Examples

```
data(Diptera)
library(multcomp)

modelfit <- glm(Ges ~ Treatment, data=Diptera, family=quasipoisson)
comps <- glm(modelfit, mcp(Treatment="Tukey"))
CIs<-CIGLM(comps, method="Raw")
CIs

CIsAdj<-CIGLM(comps, method="Adj")
CIsAdj

CIsBonf<-CIGLM(comps, method="Bonf")
CIsBonf

library(gamlss)

modelfit2 <- gamlss(Ges ~ Treatment, data=Diptera, family=NBI)
comps2 <- glm(modelfit2, mcp(Treatment="Tukey"))
CIs2<-CIGLM(comps2, method="Raw")
```


whichp	a single character string, naming an element of the <code>sims.list</code> if <code>x</code> is a bugs object, ignored otherwise
...	currently not used

Details

Construct simple confidence intervals based on order statistics applied to the marginal empirical distributions in `x`.

Value

An object of class "CInp", a list with elements

<code>conf.int</code>	a P-times-2 matrix containing the lower and upper confidence limits
<code>estimate</code>	a numeric vector of length P, containing the medians of the P marginal empirical distributions
<code>x</code>	the input object
<code>k</code>	the number of values outside each confidence interval, i.e. <code>conf.level*N</code>
<code>N</code>	the number of values used to construct each confidence interval
<code>conf.level</code>	a single numeric value, the nominal confidence level, as input
<code>alternative</code>	a single character string, as input

See Also

The function internally used is [quantile](#) with its default settings. See [SCSnP](#) for simultaneous sets.

Examples

```
# Assume a 100 times 4 matrix of 4 mutually independent
# normal variables:

X<-cbind(rnorm(100), rnorm(100), rnorm(100), rnorm(100))

lcits<-CInp(x=X, conf.level=0.95, alternative="two.sided")
lcits

ci1<-lcits$conf.int[1,]
length( which(X[,1]>=ci1[1] & X[,1]<=ci1[2] ) )

ci2<-lcits$conf.int[2,]
length( which(X[,2]>=ci2[1] & X[,2]<=ci2[2] ) )
```

CountRep	<i>Synthetic repeated count data set</i>
----------	--

Description

Synthetic data set of repeated counts on the subject.

Usage

```
data(CountRep)
```

Format

A data frame with 160 observations on the following 4 variables.

Abundance a numeric vector with counts simulated from an overdispersed and autocorrelated Poisson distributions

ID a factor with levels N1 N2 ,..., n40, specifying the subject

Time a factor with levels T1 T2 T3 T4, specifying the time

Treatment a factor with levels N S1 S2 S3

Details

Synthetic data set.

Examples

```
data(CountRep)
```

```
library(lattice)
```

```
xypplot(Abundance ~ Time|Treatment, data=CountRep, subject=~ID)
```

Decomp	<i>A simulated data set</i>
--------	-----------------------------

Description

A simulated data set, mimicking an experiment on the decomposition of plant material from four different varieties in soil.

Usage

```
data(Decomp)
```

Format

A data frame with 1152 observations on the following 5 variables.

Block a numeric vector, giving the names of the Blocks

PID a numeric vector, giving the the number of the experimental unit

Variety a factor with levels N S1 S2 S3, specifying the variety assigned to the experimental unit, randomized within each Block

Time a factor with levels t1 t2 t3 t4 t5 t6, specifying time points at which measurements were taken

Perc a numeric vector, giving the percentage of material

Details

The experiment is a randomized complete block design, with repeated measurements within each experimental unit and additional subsamplings within each time point. Plant material from four different varieties was deposited in bags in soil of 32 experimental units (coded by the variable PID), where the varieties had been grown in the vegetation period before. A total number of 36 bags was placed in each experimental unit. At six different time points, plant material was excavated and the content of the bags was analysed concerning the percentage of decomposition relative to the content at the begin of the experiment. At each time point, six bags were excavated at each experimental unit. Some bags could not be found anymore (data missing). The objective was to assess whether properties of the varieties obstruct the decomposition of plant material in the soil. The variety N is of special interest, while the varieties S1, S2, S3 are standard varieties.

Note, that this data set merely serves as an example to evaluate clustered data. Neither in the mean effects nor in the actual data points it does resemble a true experiment!

Source

Simulated.

References

Mimicking an experiment performed by Sabine Prescher (JKI Braunschweig).

Examples

```
data(Decomp)
```

Diptera

Soil eklektor data for some families of Diptera

Description

Hatching of some families of Diptera was recorded in summer 2005 using eklektors covering 2 square meters of soil surface each. A total of 32 eklektors were arranged in a randomized field trial. Total counts of individuals over the whole season are reported. Aim was to assess the impact of a novel treatment on the abundance of Diptera with larval development in the soil, compared to three standard treatments.

Usage

```
data(Diptera)
```

Format

A data frame with 32 observations on the following 7 variables.

Callip a numeric vector

Chloro a numeric vector

Ephyd a numeric vector

Droso a numeric vector

Ges a numeric vector, total number of species

Chiro a numeric vector

Treatment a factor, specifying the four different treatments, with levels S1 S2 for two standard treatments, SNovum for the standard treatment most similar to the novel treatment, and Novum, for the novel treatment

Source

...

Examples

```
data(Diptera)
```

```
dev.new(width=5, height=12)
```

```
layout(matrix(1:6, nrow=6))
```

```
par(mar=c(2,5,3,1))
```

```
boxplot(Callip~Treatment, data=Diptera, horizontal=TRUE, las=1,  
main="Abundanz Callip", col=c("white","white","blue","red"))
```

```
boxplot(Chloro~Treatment, data=Diptera, horizontal=TRUE, las=1,  
main="Abundanz Chloro", col=c("white","white","blue","red"))
```

```
boxplot(Ephyd~Treatment, data=Diptera, horizontal=TRUE, las=1,
        main="Abundanz Ephyd", col=c("white","white","blue","red"))

boxplot(Droso~Treatment, data=Diptera, horizontal=TRUE, las=1,
        main="Abundanz Droso", col=c("white","white","blue","red"))

boxplot(Chiro~Treatment, data=Diptera, horizontal=TRUE, las=1,
        main="Abundanz Chiro", col=c("white","white","blue","red"))

boxplot(Ges~Treatment, data=Diptera, horizontal=TRUE, las=1,
        main="Abundanz all Diptera", col=c("white","white","blue","red"))
```

ExNBCov

Simulated example data, drawn from a Negative Binomial Distribution

Description

Simulated example data, response drawn from a Negative Binomial Distribution, Covariables follow a multivariate normal distribution.

Usage

```
data(ExNBCov)
```

Format

A data frame with 32 observations on the following 12 variables.

Resp a numeric vector, a response of counts

Group a factor with levels A1 A2 A3 A4, e.g. varieties

X1 a numeric covariable

X2 a numeric covariable

X3 a numeric covariable

X4 a numeric covariable

X5 a numeric covariable

X6 a numeric covariable

X7 a numeric covariable

X8 a numeric covariable

X9 a numeric covariable

X10 a numeric covariable

Examples

```
data(ExNBCov)

boxplot(Resp ~ Group, data=ExNBCov)

pairs(ExNBCov)
```

ExPCov

Simulated example data following a Poisson distribution

Description

Reponse follows a Poisson distribution, the covariables follow a multivariate normal on the log-scale.

Usage

```
data(ExPCov)
```

Format

A data frame with 32 observations on the following 12 variables.

resp a response of counts
A a factor with levels A1 A2 A3 A4, e.g. varieties
C1 a numeric covariable
C2 a numeric covariable
C3 a numeric covariable
C4 a numeric covariable
C5 a numeric covariable
C6 a numeric covariable
C7 a numeric covariable
C8 a numeric covariable
C9 a numeric covariable
C10 a numeric covariable

Examples

```
data(ExPCov)

boxplot(resp ~ A, data=ExPCov)

pairs(ExPCov)
```

fakeIn	<i>A simulated data set of lognormal data</i>
--------	---

Description

A simulated data set of lognormal data, could be concentrations

Usage

```
data(fakeIn)
```

Format

A data frame with 32 observations on the following 2 variables.

Concmug a numeric vector, serving as response variable

Treat a factor with levels N S Sa Sb

Examples

```
data(fakeIn)
boxplot(Concmug ~ Treat, data=fakeIn)
```

Feeding	<i>Pupation and Hatching rate in a feeding experiment with four varieties</i>
---------	---

Description

Larvae of a non-target organism were fed with plant material derived from a novel variety(Novum), material from three standard varieties (NStandard: the standard variety most similar to Novum, and two additional standard varieties S1 and S2). Objective was to assess the impact of Novum on the pupation and hatching rate of an animal that potentially feeds on plant material compared to accepted standard varieties.

Usage

```
data(Feeding)
```

Format

A data frame with 32 observations on the following 5 variables.

Rep a factor with 32 levels indexing the 32 replications

Variety a factor with 4 levels: S1 and S2 are two standard varieties, Novum is a novel variety, and NStandard is the standard variety most similar to Novum

Total the total number of animals in each experimental unit

Pupating number of individuals pupating in each unit, the others died

Hatching number of individuals hatching from the pupae

Source

...

Examples

```
data(Feeding)

# Larval mortality:
Feeding$Lmort <- Feeding$Total - Feeding$Pupating

# Pupae mortality
Feeding$Pmort <- Feeding$Pupating - Feeding$Hatching

# Total mortality
Feeding$Tmort <- Feeding$Total - Feeding$Hatching

fit1<-glm(cbind(Pupating,Lmort)~Variety,data=Feeding, family=quasibinomial)
anova(fit1, test="F")

fit2<-glm(cbind(Hatching,Pmort)~Variety,data=Feeding, family=quasibinomial)
anova(fit2, test="F")

fit3<-glm(cbind(Total,Tmort)~Variety,data=Feeding, family=quasibinomial)
anova(fit3, test="F")
```

Description

Builds a family of interaction contrasts for complete two-factorial designs.

Usage

```
IAcontrasts(type, k)
```

Arguments

type a vector of two character strings, specifying the contrast type, currently, "Tukey", "Dunnett", "Sequence" or "Identity" are accepted

k a vector of two integers, specifying the number of groups in each factor of the two-factorial design

Details

Creates contrast matrices using `contrMat` from package **multcomp**, creates the kronecker product of both and creates suitable columnnames.

Value

A matrix with $k[1]*k[2]$ columns and a number of rows depending on type.

See Also

for 2-way interaction contrasts directly based on 2 contrasts matrices, see [IAcontrastsCMAT](#); two possibilities to specify appropriate rownames are implemented in function [c2compnames](#)

Examples

```
IAC<-IAcontrasts(type=c("Tukey", "Tukey"), k=c(3,4))
IAC
IAC2<-c2compnames(IAC, ntype="sequ")
IAC2
```

IAcontrastsCMAT

Interaction contrasts for a two-factorial design

Description

Builds a family of intercation contrasts for complete two-factorial designs.

Usage

```
IAcontrastsCMAT(CMAT1, CMAT2)
```

Arguments

CMAT1 a (named) contrast matrix
CMAT2 a (named) contrast matrix

Details

Builds the kronecker product of CMAT1 and CMAT2 and creates suitable columnnames. Note that CMAT1 and CMAT2 are not checked, and hence its up to the user to define them suitably.

Value

A matrix with $k[1]*k[2]$ columns.

See Also

for interaction contrasts based on contrast definition and the number of levels of the factors in atwo-way layout, see [IAcontrasts](#); two possibilities to specify appropriate rownames are implemented in function [c2comprnames](#)

Examples

```
library(multcomp)

n1<-c(10,10,10,10)
names(n1)<-c("A", "B", "C", "D")

n2<-c(3,3,3)
names(n2)<-c(1,2,3)

CMT1<-contrMat(n1, type="Tukey")
CMT2<-contrMat(n2, type="Tukey")

IAC<-IAcontrastsCMAT(CMAT1=CMT1, CMAT2=CMT2)

c2comprnames(IAC, ntype="sequ")

###

# In

n1<-c(10,10,10,10)
names(n1)<-c("A", "B", "C", "D")

n2<-c(3,3,3)
names(n2)<-c(1,2,3)
```

```

CMD1<-contrMat(n1, type="Dunnett")
CMD2<-contrMat(n2, type="Dunnett")
IAC<-IAcontrastsCMAT(CMAT1=CMD1, CMAT2=CMD2)
c2compnames(IAC, ntype="sequ")

```

Lepi

Insect counts of 12 Species

Description

Simulated data, inspired by a real field investigating the potential impact of genetically modified crop on several insect species belonging to the same order. The trial was designed as a randomized complete block design with 8 blocks (Block), and a total of 24 plots. In each block, three treatments (Treatment) were randomized: a conventional variety treated with insecticides (Ins), a genetically modified variety (GM) without insecticide treatment, and the near-isogenic variety (Iso) the to genetically modified variety, without insecticide treatment. Individuals were counted (after classification to the species level) in two different dates in each year of the trial, where the the second date was of higher importance for assessment of impacts of GM variety on non-target species. In total 12 Species were observed during the trial.

Usage

```
data(Lepi)
```

Format

A data frame with 144 observations on the following 17 variables.

Year a numeric vector, the year 1, 2, 3

Date a numeric vector, 1 and 2 separating the 2 sampling date in each year

Block a numeric vector, with values 1-8, indicator variable for the 8 blocks

Treatment a factor with three levels identifying the varieties: GM is the genetically modified variety, Ins the conventional variety with insecticide treatment and Iso the near isogenic line without insecticide treatment

Plot a factor with 24 levels, identifying the individual plots

Sp1 counts of taxon 1

Sp2 counts of taxon 2

Sp3 counts of taxon 3

Sp4 counts of taxon 4

Sp5 counts of taxon 5

Sp6 counts of taxon 6
 Sp7 counts of taxon 7
 Sp8 counts of taxon 8
 Sp9 counts of taxon 9
 Sp10 counts of taxon 10
 Sp11 counts of taxon 11
 Sp12 counts of taxon 12

Source

Simulated data.

Examples

```
data(Lepi)
str(Lepi)
summary(Lepi)
SPEC<-names(Lepi)[- (1:5)]
# Occurrence
occur<-lapply(X=Lepi[,SPEC], FUN=function(x){length(which(x>0))})
unlist(occur)
# Species with reasonable occurrence in the whole data:
SPEC2<-SPEC[c(1,2,3,6,8,9,11)]
pairs(Lepi[,SPEC2])
#
layout(matrix(1:2, ncol=1 ))
par(mar=c(2,8,2,1))
boxplot(Sp2 ~ Treatment*Year, data=Lepi, main="Species 2",
  las=1, horizontal=TRUE, col=c("red","white","white"))
boxplot(Sp3 ~ Treatment*Year, data=Lepi, main="Species 3",
  las=1, horizontal=TRUE, col=c("red","white","white"))
layout(matrix(1:3, ncol=1 ))
par(mar=c(2,8,2,1))
```

```
boxplot(Sp1 ~ Treatment*Year, data=Lepi, main="Species 1",
  las=1, horizontal=TRUE, col=c("red","white","white"))
```

```
boxplot(Sp8 ~ Treatment*Year, data=Lepi, main="Species 8",
  las=1, horizontal=TRUE, col=c("red","white","white"))
```

```
boxplot(Sp9 ~ Treatment*Year, data=Lepi, main="Species 9",
  las=1, horizontal=TRUE, col=c("red","white","white"))
```

minus2slash	<i>Replace - by / in character strings</i>
-------------	--

Description

Replace - by / in character strings

Usage

```
minus2slash(x)
```

Arguments

x a vector of character strings

Value

a vector of character strings

MM1	<i>Simulated data set for a simple mixed model</i>
-----	--

Description

Simulated data set for a simple mixed model

Usage

```
data(MM1)
```

Format

A data frame with 160 observations on the following 3 variables.

Y a numeric vector, the response, sampled from a normal distribution

F a factor with levels F1 F2 F3 F4, representing fixed effects

R a factor with levels R1 R2 R3 R4 R5, representing random effects, sampled from a normal distribution

Examples

```
data(MM1)
boxplot(Y~F*R, data=MM1)
```

MMPois*Simulated data for a simple mixed model with Poisson response*

Description

A fixed factor F (four levels) and a random factor (five levels), modifying the mean response (random Intercept) Y is a variable following a Poisson distribution.

Usage

```
data(MMPois)
```

Format

A data frame with 160 observations on the following 3 variables.

Y a numeric vector, the Poisson distributed response.

F a factor with levels F1 F2 F3 F4

R a factor with levels R1 R2 R3 R4 R5

Source

Created by simulation.

Examples

```
data(MMPois)

boxplot(Y~R*F, data=MMPois, las=2)
```

MMPoisRep

Simulated data for a simple mixed model with Poisson response

Description

Simulated data with a fixed factor cult (4 levels), with 8 randomized replications each, a (fixed) factor time (6 levels), which are repeated measurements taken from the same experimental units. The 32 experimental (plotid) units differ in their mean response following a gaussian distribution. The response Y follows a Poisson distribution.

Usage

```
data(MMPoisRep)
```

Format

A data frame with 192 observations on the following 4 variables.

plotid a factor with 32 levels, representing the 32 experimental units (plots)

cult a factor with 4 levels (C1 C2 C3 C4), representing a fixed factor (e.g. the cultivar)

time a factor with 6 levels (T1 T2 T3 T4 T5 T6) specifying repeated measurements on the same experimental units (plotid) over time

Y a numeric vector, following a Poisson distribution

Source

Created by simulation.

Examples

```
data(MMPoisRep)
```

```
boxplot(Y ~ cult*time, data=MMPoisRep, las=TRUE)
```

modelparm.methods

For internal use. Extract model parameters needed for multcomp from objects of class gamlss or geeglm.

Description

Only for internal use with glht in package **multcomp**. Extracts model parameters needed for glht(multcomp) from objects of class gamlss or geeglm.

Usage

```
## S3 method for class 'gamlss'
modelparm(model, coef. = coef, vcov. = vcov.gamlss, df = NULL, ...)
## S3 method for class 'geeglm'
modelparm(model, coef. = coef, vcov. = vcov.geeglm, df = NULL, ...)
```

Arguments

model	an object of class <code>gamlss</code> , as currently is created by calling <code>gamlss</code>
coef.	function to extract coefficients
vcov.	function to extract variance covariance matrix
df	function to extract degrees of freedom
...	further argument to be passed to <code>modelparm.default(multcomp)</code>

Details

Only for internal use. Further checks should be implemented.

Value

As `modelparm.default`.

Author(s)

Daniel Gerhard, code slightly changed from package `multcomp`

See Also

function `glht` in package `multcomp`

Nematocera

Eklektor counts of Nematocera

Description

In a field trial, 4 treatments (A,B, Standard, Novum) were arranged in a randomized complete block design with 8 blocks and 32 plots. In summer 2005 soil eklektor traps were placed in each plot, on six dates from 2005-07-12 to 2005-09-25, the number of individuals of *Nematocera* (gnats, midges and others) hatching from soil were counted. The individuals were classified to the family level. Interest was in assessing potential effects of a novel agricultural practice (Novum) on the abundance of *Nematocera*.

Usage

```
data(Nematocera)
```

Format

A data frame with 192 observations on the following 14 variables.

Date a POSIXt, the time of counting the individuals in the eklektor trap

Treatment a factor with 4 levels, A, B, Standard and Novum, where Novum is the novel treatment, Standard is the standard treatment most similar to Novum, and A and B are additional standard treatments.

Block a numeric vector, specifying the blocks 1-8

Plot a factor with 32 levels A1 to Standard8, indicator variables for the individual eklektors

Biblio a numeric vector, counts of individuals, belonging to the family

Cecido a numeric vector, counts of individuals, belonging to the family

Cerato a numeric vector, counts of individuals, belonging to the family

Chiro a numeric vector, counts of individuals, belonging to the family

Myceto a numeric vector, counts of individuals, belonging to the family

Psycho a numeric vector, counts of individuals, belonging to the family

Scato a numeric vector, counts of individuals, belonging to the family

Sciari a numeric vector, counts of individuals, belonging to the family

Tipuli a numeric vector, counts of individuals, belonging to the family

Total a numeric vector, total count of individuals belonging to the suborder Nematocera

Source

...

Examples

```
data(Nematocera)
```

```
par(mar=c(11,5,3,1))
```

```
boxplot(Total ~ Treatment*Date, data=Nematocera, las=2, col=c("white","white","blue","green"))
legend(x=15, y=100, legend=levels(Nematocera$Treatment), fill=c("white","white","blue","green"))
```

```
pairs(Nematocera[,c("Cecido","Cerato","Chiro","Myceto","Psycho","Sciari")])
```

plotCI.Methods

Plot confidence intervals calculated by pairwiseCI

Description

Plot confidence intervals calculated by calling pairwiseCI or UnlogCI.

Usage

```
## S3 method for class 'pairwiseCI'
plotCI(x, ...)
## S3 method for class 'UnlogCI'
plotCI(x, ...)
## S3 method for class 'simplesimint'
plotCI(x, ...)
```

Arguments

x an object of class "pairwiseCI", "UnlogCI" "simplesimint" as can be obtained by calling pairwiseCI in package **pairwiseCI**, by calling **UnlogCI** or **simplesimint**

... further arguments to be passed to plotCII, see ?plotCII in package **MCPAN** for details

Value

A plot.

Examples

```
data(Cica1)
boxplot(Au_Bonitur~Treatment, data=Cica1)

ZikaNP<-pairwiseCI(Au_Bonitur~Treatment, data=Cica1,
  method="HL.ratio", control="Iso", alternative="two.sided", conf.level=0.9)

plotCI(ZikaNP, lines=c(0.5,1,2), lineslty=c(3,1,3), lineslwd=c(1,2,1),
  ylim=c(0.5,2.5), main="Auchenorhyncha visual assessment" )
```

```
#####
```

print.CInp	<i>Print function for CInp</i>
------------	--------------------------------

Description

Print function for objects of class CInp.

Usage

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

Arguments

x	an object of class CInp as can be obtained by calling CInp
...	further arguments to be passed to print

print.SCSnp	<i>Print function for SCSnp</i>
-------------	---------------------------------

Description

A print function for objects of class "SCSnp"

Usage

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

Arguments

x	an object of class SCSnp as can be obtained by calling SCSnp
...	arguments to be passed to print

print.simplesimint *Print objects of class "simplesimint"*

Description

Print function for objects of class "simplesimint"

Usage

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

Arguments

x an object of class "simplesimint" as can be obtained by calling [simplesimint](#)
... further arguments to be passed to print

Value

Prints to console.

See Also

[summary.simplesimint](#)

print.UnlogCI *Print function for UnlogCI*

Description

Print out the results of UnlogCI.

Usage

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

Arguments

x An object of class "UnlogCI"
... further arguments to be passed to print

Value

A print out.

R2Bugsdat1w	<i>For internal use</i>
-------------	-------------------------

Description

Transform a data set to a dataset appropriate for certain OpenBUGS models.

Usage

```
R2Bugsdat1w(formula, data)
```

Arguments

formula	a formula of the style response ~ treatment, where response is a numeric or integer variable, and treatment is a factor variable in data
data	a data.frame, containing the response- and treatment-variables in formula

Details

For internal use.

Value

a list, containing the elements

bugsdat	a list of variables appropriate for certain BUGS models
parameters	a vector of character strings, naming the parameters to save for a call to OpenBUGS
inits	a vector of initial values for the parameters
data	the original data set
Intercept	a single logical indicating whether an Intercept was used to parameterize the factor variable

R2Bugsdat1w.data.frame	<i>For internal use.</i>
------------------------	--------------------------

Description

Transform a data set to a dataset appropriate for certain OpenBUGS models.

Usage

```
R2Bugsdat1w.data.frame(data, response, treatment, Intercept = FALSE)
```

Arguments

data	a data.frame
response	a single character string, naming a numeric variable in data
treatment	a single character string, naming a factor variable in data
Intercept	a single logical value, defining, whether an Intercept shall be used for the construction of the design matrix

Details

For internal use.

Value

a list, containing the elements

bugsdat	a list of variables appropriate for certain BUGS models
parameters	a vector of character strings, naming the parameters to save for a call to OpenBUGS
inits	a vector of initial values for the parameters
data	the original data set
Intercept	a single logical indicating whether an Intercept was used to parameterize the factor variable

SCSnp

Simultaneous confidence sets from empirical joint distribution.

Description

Calculate simultaneous confidence sets according to Besag et al. (1995) from a empirical joint distribution of a parameter vector. Joint empirical distributions might be obtained from WinBUGS or OpenBUGS calls.

Usage

```
SCSnp(x, ...)

## Default S3 method:
SCSnp(x, conf.level = 0.95,
      alternative = "two.sided", ...)

## S3 method for class 'bugs'
SCSnp(x, conf.level = 0.95,
      alternative = "two.sided", whichp = NULL, ...)
```

```
## S3 method for class 'CCRatio'
SCSnP(x, ...)
```

```
## S3 method for class 'CCDiff'
SCSnP(x, ...)
```

Arguments

<code>x</code>	a matrix N-times-P matrix or an object of class <code>CCRatio</code> or <code>CCDiff</code>
<code>conf.level</code>	a single numeric value between 0.5 and 1, the simultaneous confidence level
<code>alternative</code>	a single character string, one of "two.sided", "less", "greater", for two-sided, upper and lower limits
<code>whichp</code>	a single character string, naming an element of the <code>sims.list</code> if <code>x</code> is a bugs object, ignored otherwise
<code>...</code>	further arguments, currently not used

Details

Let P be the number of parameters in the parameter vector and N be the total number of values obtained for the empirical joint distribution of the parameter vector, e.g. as can be obtained e.g., from Gibbs sampling.

Value

An object of class "SCSnP", a list with elements

<code>conf.int</code>	a P -times-2 matrix containing the lower and upper confidence limits
<code>estimate</code>	a numeric vector of length P , containing the medians of the P marginal empirical distributions
<code>x</code>	the input object
<code>k</code>	the number of values outside the SCS, i.e. $\text{conf.level} * N$
<code>N</code>	the number of values used to construct the confidence set
<code>conf.level</code>	a single numeric value, the nominal confidence level, as input
<code>alternative</code>	a single character string, as input

Author(s)

Frank Schaarschmidt

References

Besag J, Green P, Higdon D, Mengersen K (1995): Bayesian Computation and Stochastic Systems. *Statistical Science* 10 (1), 3-66.

See Also

[CInp](#) for a wrapper to `quantile` to compute elementwise intervals

Examples

```
# Assume a 1000 times 4 matrix of 4 mutually independent
# normal variables:

X<-cbind(rnorm(1000), rnorm(1000), rnorm(1000), rnorm(1000))

SCSts<-SCSNp(x=X, conf.level=0.9, alternative="two.sided")
SCSts

SCS<-SCSts$conf.int

in1<-X[,1]>=SCS[1,1] & X[,1]<=SCS[1,2]

in2<-X[,2]>=SCS[2,1] & X[,2]<=SCS[2,2]

in3<-X[,3]>=SCS[3,1] & X[,3]<=SCS[3,2]

in4<-X[,4]>=SCS[4,1] & X[,4]<=SCS[4,2]

sum(in1*in2*in3*in4)
```

simplesimint

Simultaneous confidence intervals from raw estimates

Description

Calculates simultaneous confidence intervals for multiple contrasts based on a parameter vector, its variance-covariance matrix and (optionally) the degrees of freedom, using quantiles of the multivar

Usage

```
simplesimint(coef, vcov, cmat, df = NULL, conf.level = 0.95,
  alternative = c("two.sided", "less", "greater"))
```

Arguments

coef	a single numeric vector, specifying the point estimates of the parameters of interest
vcov	the variance-covariance matrix corresponding to coef, should be of dimension P-times-P, when coef is of P
cmat	the contrasts matrix specifying the comparisons of interest with respect to coef, should have P columns, when coef is of length p

df	optional, the degree of freedom for the multivariate t-distribution; if specified, quantiles from the multivariate t-distribution are used for confidence interval estimation, if not specified (default), quantiles of the multivariate normal distribution are used
conf.level	a single numeric value between 0.5 and 1.0; the simultaneous confidence level
alternative	a single character string, "two.sided" for intervals, "less" for upper limits, and "greater" for lower limits

Details

Implements the methods formerly available in package **multcomp**, function `csimint`. Input values are a vector of parameter estimates μ of length P , a corresponding estimate for its variance-covariance matrix Σ (P times P), and a contrast matrix C of dimension $M \times P$. The contrasts $L = C\mu$ are computed, the variance-covariance matrix (being a function of C and Σ) and the corresponding correlation matrix R are computed. Finally, confidence intervals for L are computed: if `df` is given, quantiles of an M -dimensional t distribution with correlation matrix R are used, otherwise quantiles of an M -dimensional standard normal distribution with correlation matrix R are used.

Value

An object of class "simplesimint"

estimate	the estimates of the contrasts
lower	the lower confidence limits
upper	the upper confidence limits
cmat	the contrast matrix, as input
alternative	a character string, as input
conf.level	a numeric value, as input
quantile	a numeric value, the quantile used for confidence interval estimation
df	a numeric value or NULL, as input
stderr	the standard error of the contrasts
vcovC	the variance covariance matrix of the contrasts

Note

This is a testversion and has not been checked extensively. Please report bugs.

Author(s)

Frank Schaarschmidt

See Also

See `?coef` and `?vcov` for extracting of parameter vectors and corresponding variance covariance matrices from variou model fits.

Examples

```
# For the simple case of Gaussian response
# variables with homoscedastic variance,
# see the following example

library(mratios)
data(angina)

boxplot(response ~ dose, data=angina)

# Fit a cell means model,

fit<-lm(response ~ 0+dose, data=angina)

# extract cell means, the corresponding
# variance-covariance matrix and the
# residual degree of freedom,

cofi<-coef(fit)
vcofi<-vcov(fit)
dofi<-fit$df.residual

# define an appropriate contrast matrix,
# here, comparisons to control

n<-unlist(lapply(split(angina$response, f=angina$dose), length))
names(n)<-names(cofi)

cmat<-contrMat(n=n, type="Dunnnett")
cmat

#

test<-simplesimint(coef=cofi, vcov=vcofi, df=dofi, cmat=cmat, alternative="greater" )

test

summary(test)

plotCI(test)

### Note, that the same result can be achieved much more conveniently
### using confint.glht in package multcomp
```

Description

Produce a detailed print out for objects of class "simplesimint".

Usage

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

Arguments

object an object of class "simplesimint" as can be obtained by calling [simplesimint](#)
 ... further arguments to be passed to print

Value

Prints to console.

Examples

```
library(multcomp)
data(waste)

anova(lm(waste ~ temp*envir, data=waste))

# a cell-means model instead
# of a two-way-layout

fit <- lm(waste ~ 0 + temp:envir, data=waste)

COEF <- coef(fit)
VCOV <- vcov(fit)

DF <- fit$df.residual

IAC <- IAcontrasts(type=c("Identity", "Dunnett"), k=c(5,3))
IACn <- c2compnames(IAC)

SCI <- simplesimint(coef=COEF, vcov=VCOV, df=DF, cmat=IACn)

# the print function just gives this:

SCI

# the summary function produces some more output:

summary(SCI)

#####

IAC <- IAcontrasts(type=c("Identity", "Dunnett"), k=c(5,3))
```

```
# long names currently give nasty outputs!
colnames(IAC)<-names(COEF)
IACn <- c2compnames(IAC)
SCI<- simplesimint(coef=COEF, vcov=VCOV, df=DF, cmat=IACn)
SCI
# the summary function produces some more output:
summary(SCI)
```

UnlogCI

Transform confidence intervals from glm fits and geeglm fits.

Description

Transform confidence intervals derived from glm and geeglm fits back to original scale and give appropriate names.

Usage

```
## S3 method for class 'glht'
UnlogCI(x)
```

Arguments

x an object of class "confint.glht"

Details

Applies exponential function on the estimates and confidence limits and creates useful names for the comparisons and parameters.

Value

An object of class "UnlogCI".

See Also

[plotCI.UnlogCI](#) for plotting the result

Examples

```

### CI for odds ratios
### for models on the logit-link

data(Feeding)

# Larval mortality:

Feeding$Lmort <- Feeding$Total - Feeding$Pupating

fit1<-glm(cbind(Pupating,Lmort)~Variety,data=Feeding, family=quasibinomial)
anova(fit1, test="F")

library(multcomp)

comp<-glht(fit1, mcp(Variety="Tukey"))

CIraw<-CIGLM(comp,method="Raw")

CIraw

UnlogCI(CIraw)

plotCI(UnlogCI(CIraw), lines=c(0.25,0.5,2,4),
  lineslwd=c(1,2,2,1), linescol=c("red","black","black","red"))

#####

### CI for ratios of means
### for models on the log-link

data(Diptera)

# Larval mortality:

fit2<-glm(Ges~Treatment, data=Diptera, family=quasipoisson)
anova(fit2, test="F")

library(multcomp)

comp<-glht(fit2, mcp(Treatment="Tukey"))

CIadj<-CIGLM(comp,method="Adj")

CIadj

UnlogCI(CIadj)

plotCI(UnlogCI(CIadj), lines=c(0.5,1,2), lineslwd=c(2,1,1))

```

`vcov.gamlss`*Extract variance covariance matrix from objects of class gamlss*

Description

Only for internal use. Extract the variance covariance matrix corresponding to the mu parameters of a gamlss-fit.

Usage

```
## S3 method for class 'gamlss'  
vcov(object, ...)
```

Arguments

<code>object</code>	An object of class "gamlss" as can be created by calling <code>gamlss</code>
<code>...</code>	Currently not used.

Details

Only for internal use. Needs implementation of warnings.

Value

A matrix of dimension $m \times m$, if m is the length of mu-parameters from a gamlss fit.

Author(s)

Daniel Gerhard

See Also

packages `gamlss` and `multcomp`

`vcov.geeglm`*Extract variance covariance matrix from objects of class geeglm*

Description

Only for internal use with function `glht`: Extract the variance covariance matrix corresponding to the `mu` parameters of a `gamlss`-fit. Merely uses the method internally used in function `summary.geeglm`, package `geepack`.

Usage

```
## S3 method for class 'geeglm'  
vcov(object, ...)
```

Arguments

<code>object</code>	An object of class "geeglm" as can be created by calling <code>geeglm</code> in package geepack .
<code>...</code>	Currently not used.

Details

Only for internal use. Needs implementation of warnings.

Value

A matrix of dimension `m` times `m`, if `m` is the length of coefficients from a `geeglm` fit.

See Also

packages `gamlss` and `multcomp`

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