

Package ‘simboot’

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Type Package

Title Simultaneous Inference for Diversity Indices

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Description

Provides estimation of simultaneous bootstrap and asymptotic confidence intervals for diversity indices, namely the Shannon and the Simpson index. Several pre--specified multiple comparison types are available to choose. Further user--defined contrast matrices are applicable. In addition, simboot estimates adjusted as well as unadjusted p--values for two of the three proposed bootstrap methods. Further simboot allows for comparing biological diversities of two or more groups while simultaneously testing a user-defined selection of Hill numbers of orders q , which are considered as appropriate and useful indices for measuring diversity.

License GPL (>= 2)

URL <https://github.com/shearer/simboot>,
<http://shearer.github.io/simboot/>

BugReports <https://github.com/shearer/simboot/issues>

Depends boot, mvtnorm

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simboot-package	<i>Simultaneous inference for diversity indices.</i>
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Description

Package **simboot** provides estimation of simultaneous bootstrap and asymptotic confidence intervals for diversity indices, namely the Shannon and the Simpson index. Several pre-specified multiple-comparison types are available. Further user-defined contrast matrices are applicable. In addition, **simboot** estimates adjusted as well as unadjusted p -values for two of the three proposed bootstrap methods. Further simboot allows for comparing biological diversities of two or more groups with simultaneously testing a user-defined selection of Hill numbers of orders q , which are considered appropriate and useful indices for measuring diversity.

Details

Package:	simboot
Type:	Package
Version:	0.2-8
Date:	2024-02-09
License:	GPL (>= 2)
LazyLoad:	yes

Author(s)

Ralph Scherer\ Philip Pallmann\

References

Scherer, R. and Schaarschmidt, F. (2013) Simultaneous confidence intervals for comparing biodiversity indices estimated from overdispersed count data. *Biometrical Journal* 55, 246–263.

Evaluation of the methods in [sbdiv](#)

Pallmann, P. et al. (2012) Assessing group differences in biodiversity by simultaneously testing a user-defined selection of diversity indices. *Molecular ecology resources* 12, 1068–1078.

Evaluation of the methods in [mcpHill](#)

Westfall, P. H. and Young, S. S. (1993) Resampling-Based Multiple Testing: Examples and Methods for p -Value Adjustment. New York: Wiley.

Corresponding method [sbdiv](#) with method [WYht](#)

Besag, J., Green, P. J., Higdon, D., Mengersen, K. (1995) Bayesian computation and stochastic systems (with discussion). *Statistical Science*, 10, 3–66.

Corresponding method [sbdiv](#) with method [rpht](#)

Beran, R. (1988) Balanced simultaneous confidence sets. *Journal of the American Statistical Association*, 83, 679–686.

Corresponding method [sbdiv](#) with method [tsht](#)

Fritsch, K. S., Hsu, J. C. (1999) Multiple comparison of entropies with application to dinosaur biodiversity. *Biometrics*, 55, 4, 1300–1305.

Rogers, J. A., Hsu, J. C. (2001) Multiple comparisons of biodiversity. *Biometrical Journal*, 43, 5, 617–625.

Corresponding method [sbdiv](#) with method [asht](#)

Jost, L. (2008) G(ST) and its relatives do not measure differentiation. *Molecular Ecology*, 17, 4015–4026.

Corresponding method [mcpHill](#)

asht

Internal function for simultaneous asymptotic intervals

Description

Internal function for simultaneous asymptotic intervals

Note

Only internal function. Use function [sbdiv](#) instead

References

- Fritsch, K. S., Hsu, J. C. (1999) Multiple comparison of entropies with application to dinosaur biodiversity. *Biometrics*, 55, 4, 1300–1305.
- Rogers, J. A., Hsu, J. C. (2001) Multiple comparisons of biodiversity. *Biometrical Journal*, 43, 5, 617–625.

Bacteria

Relative Abundances of Soil Bacteria

Description

Relative abundances of soil bacteria from 27 samples collected in nine forest and 18 grassland sites in Germany. The data set includes abundances of 18 bacterial phyla (including three candidate phyla) and five proteobacterial classes.

Usage

```
data(Bacteria)
```

Format

A data frame with 27 observations on the following 24 variables.

Land use type a factor with levels forest grassland

Acidobacteria a numeric vector

Actinobacteria a numeric vector

Bacteroidetes a numeric vector

Chloroflexi a numeric vector

Cyanobacteria a numeric vector

Deinococcus-Thermus a numeric vector

Fibrobacteres a numeric vector

Firmicutes a numeric vector

Fusobacteria a numeric vector

Gemmatimonadetes a numeric vector

Nitrospira a numeric vector

OP11 a numeric vector

Planctomycetes a numeric vector

Spirochaetes a numeric vector

Tenericutes a numeric vector

TM7 a numeric vector

Verrucomicrobia a numeric vector

WS3 a numeric vector
Alphaproteobacteria a numeric vector
Betaproteobacteria a numeric vector
Deltaproteobacteria a numeric vector
Gammaproteobacteria a numeric vector
Epsilonproteobacteria a numeric vector

Details

Relative abundances of 18 bacterial phyla (including three candidate phyla) and five proteobacterial classes (alpha, beta, gamma, delta and epsilon) from two ecological metagenomics studies (Will et al. 2010, Nacke et al. 2011). There are 27 observations altogether, nine of which stem from forest and 18 from grassland plots in Germany.

One goal of these investigations was to unravel differences in bacterial diversity and community composition between the land use types forest and grassland.

The bacteria's relative abundances were determined by analyzing the V2-V3 region of the 16S rRNA gene via pyrosequencing-based DNA techniques.

Source

Will, C., Thuermer, A., Wollherr, A., et al. (2010) Horizon- specific bacterial community composition of German grassland soils, as revealed by pyrosequencing-based analysis of 16S rRNA genes. *Applied and Environmental Microbiology*, 76, 6751–6759.

Nacke, H., Thuermer, A., Wollherr, A., et al. (2011) Pyrosequencing- based assessment of bacterial community structure along different management types in German forest and grassland soils. *PLoS One*, 6, e17000.

Examples

```
data(Bacteria)
str(Bacteria)

### Assess whether there is a difference in biodiversity and
### community composition species richness (Shannon index,
### Simpson index) between grassland and forest.
### Bootstrap times set to 50 due to example time settings

library(simboot)
mcpHill(dataf=Bacteria[,2:24], fact=Bacteria[,1], boots=50, qual=c(0,1,2))
```

Boutrp	<i>Internal function</i>
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Description

Internal function for method `rpht` in function `sbddiv`

Note

Only for internal use.

CCdrp	<i>Internal function</i>
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Description

Internal function for method `rpht` in `sbddiv`

contrMat	<i>Contrast Matrices</i>
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Description

Computes contrast matrices for several multiple comparison procedures.

Usage

```
contrMat(n, type = c("Dunnett", "Tukey", "Sequen", "AVE",
                    "Changepoint", "Williams", "Marcus",
                    "McDermott", "UmbrellaWilliams", "GrandMean"),
         base = 1)
```

Arguments

n	a (possibly named) vector of sample sizes for each group.
type	type of contrast.
base	an integer specifying which group is considered the baseline group for Dunnett contrasts.

Details

Computes the requested matrix of contrasts for comparisons of mean levels.

Value

The matrix of contrasts with appropriate row names is returned.

Note

Function `contrMat` is adapted from package **multcomp**

References

Frank Bretz, Alan Genz and Ludwig A. Hothorn (2001), On the numerical availability of multiple comparison procedures. *Biometrical Journal*, **43**(5), 645–656.

Examples

```
n <- c(10,20,30,40)
names(n) <- paste("group", 1:4, sep="")
contrMat(n) # Dunnett is default
contrMat(n, base = 2) # use second level as baseline
contrMat(n, type = "Tukey")
contrMat(n, type = "Sequen")
contrMat(n, type = "AVE")
contrMat(n, type = "Changepoint")
contrMat(n, type = "Williams")
contrMat(n, type = "Marcus")
contrMat(n, type = "McDermott")
### Umbrella-protected Williams contrasts, i.e. a sequence of
### Williams-type contrasts with groups of higher order
### stepwise omitted
contrMat(n, type = "UmbrellaWilliams")
### comparison of each group with grand mean of all groups
contrMat(n, type = "GrandMean")
```

corrmatgen

Internal function.

Description

Correlation matrix for confidence intervals assuming multivariate standard normal distribution. Calculates the correlation matrix for method `asci` in function `sbdiv`

Usage

```
corrmatgen(CM, varp)
```

Arguments

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

Value

A matrix of dimension MxM.

estShannon	<i>Estimator for Shannon's index</i>
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Description

Estimation function for Shannon's index. Internal use in [estShannonf](#).

Usage

estShannon(x)

Arguments

x Vector of discrete-scaled numerical values.

Details

Estimator of Shannon-Wiener index with bias correction. Number of Species S in the bias correction does not take zeros into account.

Value

Shannon-Wiener index with bias correction

estShannonf	<i>Estimator for Shannon's index odered by a factorial variable f.</i>
-------------	--

Description

Estimation function for Shannon's index. Internal use in [sbddiv](#) for methods [rpht](#), [tsht](#), [asht](#). Sums up species counts in each columns for every treatment group and estimates Shannon's index with bias correction on the resulting vectors of summed up species counts.

$$\widehat{HBC}_i = \hat{H}_i + (S_i - 1)/(2N_{i\bullet}) - (1 - \sum (1/\hat{p}_{i\bullet s})) / (12N_{i\bullet}^2) - \sum ((1/\hat{p}_{i\bullet s}) - (1/(\hat{p}_{i\bullet s}^2))) / (12N_{i\bullet}^3);$$

$$i = 1, \dots, k; s = 1, \dots, S; p_{i\bullet s} = \frac{\sum_{j=1}^n x_{sj}}{N_{i\bullet}};$$

$$\hat{H}_i = (-1) \sum_{s=1}^S (\hat{p}_{i\bullet s} \log(\hat{p}_{i\bullet s}))$$

$N_{i\bullet} = \sum_{j=1}^n N_{ij}$ Number of observed individuals in treatment i .

Usage

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

Arguments

X *n* times *p* matrix containing species in *p* columns and replicates in *n* rows.
f Factor variable containing treatment groups. Must be of length: replicates times treatment groups.

Value

estimate Estimated Shannon-Wiener index for treatment groups
varest Estimated variance of Shannon-Wiener index for treatment groups

estShannonWY *Estimator for Shannon's index row wise.*

Description

Estimation function for Shannon's index. Internal use in [WYht](#). Calculates Shannon-Wiener index with bias correction

$$\widehat{HBC}_{ij} = \hat{H}_{ij} + (S_{ij} - 1) / (2N_{ij}) - (1 - \sum_{s=1}^S (1/\hat{p}_{ijs})) / (12N_{ij}^2) - \sum_{s=1}^S ((1/\hat{p}_{ijs}) - (1/(\hat{p}_{ijs}^2))) / (12N_{ij}^3);$$

$$\hat{H}_{ij} = (-1) \sum_{s=1}^S (\hat{p}_{ijs} \log(\hat{p}_{ijs}))$$

$i = 1, \dots, k; j = 1, \dots, n; s = 1, \dots, S;$

S_j = Number of observed species in replicate j ;

N_j = Number of observed individuals in replicate j

for every row in a $n \times p$ matrix.

Usage

```
estShannonWY(x)
```

Arguments

x Vector of p numerical species counts.

Value

Shannon-Wiener index with bias correction

estSimpson	<i>Estimator for Simpson's index</i>
------------	--------------------------------------

Description

Estimation function for Simpson's index $1 - p^2 * n / (n - 1)$. Internal use in [estSimpsonf](#).

Usage

```
estSimpson(x)
```

Arguments

x Vector of discrete-scaled numerical values.

Value

Estimator of Simpson's index

estSimpsonf	<i>Estimator for Simpson's index odered by a factorial variable f.</i>
-------------	--

Description

Estimation function for Simpson's index. Internal use in [sbdiv](#) for methods [rpht](#), [tsht](#), [asht](#). Sums up species counts in each columns for every treatment group and estimates Simpson's index on the resulting vectors of summed up species counts.

Usage

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

Arguments

X *n* times *p* matrix containing species in *p* columns and replicates in *nrows*.
 f Factor variable containing treatment groups. Must be of length: replicates times treatment groups.

Value

estimate Estimated Simpson index for treatment groups
 varest Estimated variance of Simpson's index for treatment groups

estThetaRow	<i>Internal function</i>
-------------	--------------------------

Description

Internal function for method `WYht` in function `sbddiv`. Calculates the specified diversity index for every replicated sample in each treatment group.

Usage

```
estThetaRow(X, f, theta)
```

Arguments

<code>X</code>	Matrix with dimension $n \times p$.
<code>f</code>	Factorial variable containing treatment groups.
<code>theta</code>	Shannon or Simpson index

mcpHill	<i>Multiplicity-adjusted p-values for comparing biodiversity via simultaneous inference of a user-defined selection of diversity indices</i>
---------	--

Description

The function `mcpHill` allows for comparing biological diversities of two or more groups. It simultaneously tests a user-defined selection of Hill numbers of orders q , which are considered appropriate and useful indices for measuring diversity (Jost 2008). As an output `mcpHill` gives p-values adjusted for multiplicity according to the method of Westfall & Young (1993).

Usage

```
mcpHill(dataf, fact, align = FALSE, block, boots = 5000, udmat
 = FALSE, usermat, mattype = "Dunnett", dunbase = 1, qval = seq(-1, 3),
 opt = "two.sided")
```

Arguments

<code>dataf</code>	Data frame containing numerical values (e.g. species counts or relative abundances). Rows represent repeated observations of the (two or more) groups, columns represent taxonomic units (usually species, or phyla, classes etc.).
<code>fact</code>	Vector assigning (two or more) factor levels to the observations, i.e. the groups to be compared. The length of <code>fact</code> must equal the number of rows in <code>dataf</code> .
<code>align</code>	Logical indicating whether a block alignment should be carried out. If <code>TRUE</code> , the blocks must be specified as a vector in <code>block</code> . Default is <code>FALSE</code> .

block	Vector assigning which block an observation belongs to. Only required if align=TRUE. The length of block must equal the number of rows in dataf.
boots	Number of bootstrap replications. Values lower than 999 are rejected. Default is 5000.
udmat	Logical indicating whether user-defined contrasts are applied for multiple testing. If TRUE, a contrast matrix has to be specified via usermat. Default is FALSE, meaning that the contrast matrix is specified by a catchword (e.g. "Tukey", "Dunnett" etc.).
usermat	Matrix specifying user-defined multiple testing contrasts. Only required if udmat=TRUE. The row sums in the matrix must equal zero.
matttype	Type of contrast matrix for multiple comparisons of groups. Hence only required for comparisons of more than two groups. Can be specified by the catchwords used in function <code>contrMat</code> (e.g. "Dunnett", "Tukey", "GrandMean", "AVE", "Williams", "Changepoint" etc.). Default is "Dunnett".
dunbase	Integer determining the factor group (in alphanumerical order) to be considered the baseline or control and therefore only needed for Dunnett-type multiple contrasts. Default is 1.
qval	Vector containing the requested selection of q-values in order to specify the Hill numbers of orders q to be investigated. Default is <code>seq(-1,3)</code> .
opt	"greater" performs an upper-tailed test, "less" a lower-tailed test and "two.sided" a two-tailed test. Default is "two.sided".

Value

The output of `mcpHill` is a matrix containing the chosen selection of Hill numbers (their orders q) in the first column. The multiplicity-adjusted p-values for each hypothesis tested are in the second column. The names of the rows denote which groups are being compared.

Author(s)

Philip Pallmann

References

- Pallmann, P. et al. (2012)* Assessing group differences in biodiversity by simultaneously testing a user-defined selection of diversity indices. *Molecular ecology resources* 12, 1068–78.
- Jost, L. (2008)* G(ST) and its relatives do not measure differentiation. *Molecular Ecology*, 17, 4015–4026.
- Westfall, P.H. and Young S.S. (1993)* Resampling-based multiple testing: examples and methods for p-value adjustment. New York: Wiley.

Examples

```
### Multiple testing with user-defined contrasts after block alignment
data(predatGM)
```

```

mymat <- rbind( "GM - S1" = c(1,-1,0,0), "GM - S2" = c(1,0,-1,0), "GM -
  S3" = c(1,0,0,-1), "S1 - S2" = c(0,1,-1,0), "S1 - S3" = c(0,1,0,-1) )

# example runs with only 100 bootstrap steps. For estimation use 2000 or more.
mcpHill(dataf=predatGM[,3:35], fact=predatGM[,2], align=TRUE,
block=predatGM[,1], boots=100, udm=TRUE, usermat=mymat, qual=seq(-1,
3, by=0.5))

# with Dunnett-type contrast matrix
mcpHill(dataf=predatGM[,3:35], fact=predatGM[,2], align=TRUE,
block=predatGM[,1], boots=100, udm=FALSE, mattype = "Dunnett", qual=seq(-1,
3, by=0.5))

```

predatGM

Abundance data of predatory insects

Description

In a field trial with 8 complete blocks, one genetically modified crop variety and three varieties without genetical modification (S1, S2, S3) have been cultivated. Note that S1 is genetically closely related to the GM variety, and mainly differs from GM by not containing the transformation, while S2 and S3 are conventional varieties, which are genetically not closely related to GM and S1. In each of the 24 plots, a certain taxonomic group of predatory insects has been trapped. Trapped individuals have been classified to the species level. A total of 33 different species has been observed. For each plot, the summed counts of each species over one cultivation period is given in the variables Sp1, Sp2,...Sp33. Among others, one question in research was: Does the genetic modified variety effect biodiversity of the (ecologically important, non-target) species?

Usage

```
data(predatGM)
```

Format

A data frame with 32 observations on the following 35 variables.

Block a numeric vector, values 1,...,8 indicate the blocks of the trial

Variety a factor distinguishing the four varieties in the field trial, with levels GM (the genetically modified variety), S1 (the near-isogenic, conventional variety), S2 and S3 (further conventional varieties)

Sp1 a numeric vector, observed counts of species 1

Sp2 a numeric vector, ...

Sp3 a numeric vector

Sp4 a numeric vector

Sp5 a numeric vector

Sp6 a numeric vector
Sp7 a numeric vector
Sp8 a numeric vector
Sp9 a numeric vector
Sp10 a numeric vector
Sp11 a numeric vector
Sp12 a numeric vector
Sp13 a numeric vector
Sp14 a numeric vector
Sp15 a numeric vector
Sp16 a numeric vector
Sp17 a numeric vector
Sp18 a numeric vector
Sp19 a numeric vector
Sp20 a numeric vector
Sp21 a numeric vector
Sp22 a numeric vector
Sp23 a numeric vector
Sp24 a numeric vector
Sp25 a numeric vector
Sp26 a numeric vector
Sp27 a numeric vector
Sp28 a numeric vector
Sp29 a numeric vector
Sp30 a numeric vector
Sp31 a numeric vector
Sp32 a numeric vector
Sp33 a numeric vector

Source

Data set provided by Kai U. Priesnitz, Bavarian State Research Center for Agriculture, Institute for Plant Protection, Freising, Germany.

Examples

```

data(predatGM)

str(predatGM)

# Display data as a mosaicplot

# load("D:/Mueller/Biodiv/data/predatGM.rda")

# Matrix of counts with appropriate names
COUNTS<-as.matrix(predatGM[,3:35])
SPECNAM<-names(predatGM)[3:35]
colnames(COUNTS)<-SPECNAM
rownames(COUNTS)<-predatGM[,"Variety"]

# Assign colors and order by decreasing total abundance
COL<-grey(c(0,2,4,6,8,1,3,5,7)/8)
DMO<-COUNTS[,order(colSums(COUNTS), decreasing=TRUE)]
colnames(DMO)[15:33]<-"."

# Mosaicplot
par(mar=c(4,2,1,1))
mosaicplot(DMO, col=COL, las=2, off=15, main="", cex=1.1)
mtext("A", side=3, line=-1.5, adj=0, cex=2)

```

rpht

Internal function for simultaneous bayesian bootstrap intervals

Description

Internal function for simultaneous bayesian bootstrap intervals

Note

Only internal function. Use function [sbdiv](#) instead

References

Besag, J., Green, P. J., Higdon, D., Mengersen, K. (1995) Bayesian computation and stochastic systems (with discussion) . *Statistical Science*, 10, 3–66.

saproDipGM

*Abundance data of Diptera with saprophagous larvae***Description**

In a field trial with 6 complete blocks, three treatments have been applied: a genetically modified crop variety was cultivated without insecticide treatment (GM), its near-isogenic counterpart (i.e. not genetically modified but otherwise genetically closely related to the GM crop) has been cultivated without insecticide treatment (Iso), and the near-isogenic variety has been cultivated with insecticide treatment (Ins). In each of the 18 plots, two emergence traps have been placed and Diptera with saprophagous larvae were classified to the species level and counted. A total number of 25 different species has been observed and included in the present data set. For each plot, the summed counts of each species over one cultivation period (in 2002) and the two traps is given in the columns Acor, ..., Tnud. Among others, one question in this trial was: Does the genetic modified variety effect biodiversity of the (ecologically important, non-target) species in comparison to the isogenic variety (as a negative control) and in comparison to the insecticide treated plants (as a positive control)?

Usage

```
data(saproDipGM)
```

Format

A data frame with 18 observations on the following 27 variables.

Block a numeric vector, values 1,...,6 indicate the blocks of the trial

Variety a factor, distinguishing the 3 treatment levels: GM (genetically modified, no insecticide), Ins (not genetically modified, insecticide treatment) , and Iso (not genetically modified, no insecticide)

Acor a numeric vector of counts of the first species

Arub a numeric vector...

Aaph a numeric vector

Bbre a numeric vector

Btri a numeric vector

Burt a numeric vector

Bvag a numeric vector

Bill a numeric vector

Ccru a numeric vector

Cmir a numeric vector

Cvag a numeric vector

Dnit a numeric vector

Dand a numeric vector

Lcin a numeric vector
Lcas a numeric vector
Malt a numeric vector
Moli a numeric vector
Mluc a numeric vector
Mtox a numeric vector
Ppha a numeric vector
Sato a numeric vector
Spal a numeric vector
Sate a numeric vector
Sleu a numeric vector
Tnud a numeric vector

Source

Data set provided by Dr. Sabine Prescher, Institute for Biosafety of Genetically Modified Plants, Julius-Kuehn-Institut, Braunschweig, Germany

Examples

```
data(saproDipGM)

str(saproDipGM)

# load("D:/Mueller/Biodiv/data/saproDipGM.rda")

# Display data as a mosaicplot

# Matrix of counts with appropriate names
COUNTS<-as.matrix(saproDipGM[,3:27])
SPECNAM<-names(saproDipGM)[3:27]
colnames(COUNTS)<-SPECNAM
rownames(COUNTS)<-saproDipGM[,"Variety"]

# Assign colors and order by decreasing total abundance
COL<-grey(c(0,2,4,6,8,1,3,5,7)/8)
DMO<-COUNTS[,order(colSums(COUNTS), decreasing=TRUE)]

# Mosaicplot
par(mar=c(4,2,1,1))
mosaicplot(DMO, col=COL, las=2, off=15, main="", cex=1.1)
mtext("A", side=3, line=-1.5, adj=0, cex=2)
```

sbddiv	<i>Perform simultaneous confidence intervals or adjusted p-values for the Shannon and the Simpson index.</i>
--------	---

Description

Function `sbddiv` estimates simultaneous confidence intervals for the Shannon or the Simpson index. This function provides calculation of several pre-defined contrasts for confidence intervals. Further self-defined contrast are applicable. Simultaneous resampling confidence intervals are estimated according to the Algorithm of Besag et al. (1995) using method `rpht`, Westfall et al. (1993) using method `WYht` or similar to Beran (1988) using method `tsht`. Further estimation of simultaneous asymptotic intervals adjusting for heterogeneous variances is provided by method `asht` according to Fritsch and Hsu (1999) and Rogers and Hsu (2001). However, estimation of asymptotic intervals may make no sense in data sets with replicated samples due to overdispersion.

Usage

```
sbddiv(X, f, theta = c("Shannon", "Simpson"),
       type = c("Dunnett", "Tukey", "Sequen", "AVE",
               "Changepoint", "Williams", "Marcus",
               "McDermott", "UmbrellaWilliams", "GrandMean"),
       cmat = NULL, method = c("WYht", "tsht", "rpht", "asht"), conf.level =
       0.95, alternative = c("two.sided", "less", "greater"), R = 2000, base =
       1, ...)
```

Arguments

<code>X</code>	Data frame containing numerical values for counts in columns. Every column represents on species.
<code>f</code>	Vector of factorial variables for treatment groups. Vector length must be equal to the length of treatment groups multiplied with sample replications.
<code>theta</code>	Biodiversity index. Options are Shannon and Simpson index.
<code>type</code>	Type of comparison. Options are Dunnett, Tukey, Sequen, AVE, Changepoint, Williams, Marcus, McDermott, UmbrellaWilliams, GrandMean intervals. We tested only Dunnett and Tukey contrasts in simulations.
<code>cmat</code>	Optional self-defined contrast matrix. In case of using this argument, the type argument is not considered.
<code>method</code>	Possible methods are simultaneous bootstrap confidence intervals: <code>WYht</code> , <code>tsht</code> , <code>rpht</code> and asymptotic simultaneous confidence intervals: <code>asht</code> . Adjusted and unadjusted p -values are estimated with method <code>WYht</code> and method <code>tsht</code> .
<code>conf.level</code>	Pre-defined overall confidence level. Default is 0.95, while two-sided inference is estimated with $(1 - \text{conf.level})/2$ for each side and one-sided inference is estimated with $1 - \text{conf.level}$ for the side of interest.
<code>alternative</code>	Specified type of interval. Could be "one-sided" or "two.sided".

R	Number of bootstrap steps. Default is 2000, which is a good compromise between accuracy and computing time
base	Control group. base = 1 uses the first group in alphabetical order.
...	Further optional arguments for the internal used function boot from package boot . Most importantly, the number of Bootstrap samples can be chosen via the parameter R (default is R=2000); see ?boot for further options.

Details

sbdiv is the main function for estimating the different multiplicity adjusted confidence intervals. Different methods are called from internal functions.

Value

conf.int	estimate: Estimated difference between groups. Estimators differ between the methods due to calculation. lower: Lower bounds of estimated intervals. upper: Upper bounds of estimated intervals.
p.value	adj. p: multiplicity adjusted p-values. raw p: unadjusted p-values
conf.level	Pre-specified confidence level
alternative	Pre-specified alternative

Author(s)

Ralph Scherer

References

- Scherer, R. and Schaarschmidt, F. (2013) Simultaneous confidence intervals for comparing biodiversity indices estimated from overdispersed count data. *Biometrical Journal* 55, 246–263.
 Evaluation of the methods in [sbdiv](#)
- Westfall, P. H. and Young, S. S. (1993) Resampling-Based Multiple Testing: Examples and Methods for p -Value Adjustment. New York: Wiley.
- Corresponding method sbdiv with method [WYht](#)
- Besag, J., Green, P. J., Higdon, D., Mengersen, K. (1995) Bayesian computation and stochastic systems (with discussion). *Statistical Science*, 10, 3–66.
- Corresponding method sbdiv with method [rpht](#)
- Beran, R. (1988) Balanced simultaneous confidence sets. *Journal of the American Statistical Association*, 83, 679–686.
- Corresponding method sbdiv with method [tsht](#)
- Fritsch, K. S., Hsu, J. C. (1999) Multiple comparison of entropies with application to dinosaur biodiversity. *Biometrics*, 55, 4, 1300–1305.
- Rogers, J. A., Hsu, J. C. (2001) Multiple comparisons of biodiversity. *Biometrical Journal*, 43, 5, 617–625.
- Corresponding method sbdiv with method [asht](#)

Examples

```
## For plots of the datasets see the help files for the data sets.

## First dataset
data(predatGM)

## structure of data
str(predatGM)

## remove block variable
datSpec_1 <- predatGM[, -1]
str(datSpec_1)

## Order of factorial variable
datSpec_1$Variety

## argument base = 1 uses GM as control group. Not directly executable
## due to intensive computing time
# sbddiv(X = datSpec_1[, 2:length(datSpec_1)], f = datSpec_1[, 1], theta =
# "Shannon", type = "Dunnett", method = "WYht", conf.level = 0.95,
# alternative = "two.sided", R = 2000, base = 1)

## Directly executable but senseless value for boot steps R
sbddiv(X = datSpec_1[, 2:length(datSpec_1)], f = datSpec_1[, 1], theta =
"Shannon", type = "Dunnett", method = "WYht", conf.level = 0.95,
alternative = "two.sided", R = 100, base = 1)

## Second dataset
data(saproDipGM)

## structure
str(saproDipGM)

## remove block variable
datSpec_2 <- saproDipGM[, -1]
str(datSpec_2)

## Order of factor variable
datSpec_2$Variety

## argument base = 2 uses Ins as control group. Not directly executable
## due to intensive computing time
# sbddiv(X = datSpec_2[, 2:length(datSpec_2)], f = datSpec_2[, 1], theta =
# "Shannon", type = "Dunnett", method = "rpht", conf.level = 0.95,
# alternative = "two.sided", R = 2000, base = 2)

## Directly executable but senseless value for boot steps R
sbddiv(X = datSpec_2[, 2:length(datSpec_2)], f = datSpec_2[, 1], theta =
"Shannon", type = "Dunnett", method = "rpht", conf.level = 0.95,
alternative = "two.sided", R = 100, base = 2)
```

SCIRp	<i>Internal function</i>
-------	--------------------------

Description

Interval estimation in method rpci in function sbci

Note

Internal function. Use [sbdiv](#) instead.

Simpson	<i>Internal function for Simpson estimator</i>
---------	--

Description

Calculates Simpson's index on probability vector p

Usage

Simpson(p)

Arguments

p Probability vector x_s/n

Value

Simpson's index

Note

Only for internal use

tsht	<i>Internal function for simultaenous bootstrap intervals</i>
------	---

Description

Internal function for simultaenous bootstrap intervals based on summed up counts for every species.

Note

Only internal function. Use function [sbdiv](#) instead

References

Beran, R. (1988) Balanced simultaneous confidence sets. *Journal of the American Statistical Association*, 83, 679–686.

waldci	<i>Internal function for Wald intervals</i>
--------	---

Description

Internal function for wald intervals in method [asht](#) in function [sbdiv](#)

Note

Internal function. Use function [sbdiv](#) instead.

WYht	<i>Internal function for simultaneous bootstrap confidence intervals</i>
------	--

Description

Internal function for simultaneous bootstrap confidence intervals based on resampled residuals

Note

Only internal function. Use function [sbdiv](#) instead

References

Westfall, P. H. and Young, S. S. (1993) *Resampling-Based Multiple Testing: Examples and Methods for p -Value Adjustment*. New York: Wiley.

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