Package ‘inecolr’

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Title Modeling and Plotting for Ecologist

Version 0.1.0

Description It provides multiple functions that are useful for ecological research and teaching statistics to ecologists. It is based on data analysis courses offered at the Instituto de Ecología AC (INECOL). For references and published evidence see, Manrique-Ascencio, et al (2024) <doi:10.1111/gcb.17282>, Manrique-Ascencio et al (2024) <doi:10.1111/plb.13683>, Ruiz-Guerra et al(2017) <doi:10.17129/botsci.812>, Juarez-Fragoso et al (2024) <doi:10.1007/s10980-024-01809-z>, Papaqui-Bello et al (2024) <doi:10.13102/sociobiology.v71i2.10503>.

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Repository CRAN

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Contents

`betacomp` *Beta Base on Complementarity of Ecological Communities*

Description

Estimate beta diversity based on the Bray-Curtis index estiumates of complementarity (an assymetric meassures) betweb pairs of ecological communities.

Usage

```
betacomp(M)
```

Arguments

`M`	A numeric matrix with at least two columns (sites) and r rows (species).

Value

Return a list of matrixes of the complementarities between pairs of communities and the beta diversity between them.

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Aguirre, A., Guevara, R., García, M. and López, J.C. (2010), Fate of epiphytes on phorophytes with different architectural characteristics along the perturbation gradient of Sabal mexicana forests in Veracruz, Mexico. Journal of Vegetation Science, 21: 6-15. https://doi.org/10.1111/j.1654-1103.2009.01131.x

Examples

```
library(vegan)
data(dune)
betacomp(t(dune[1:4,]))
```

`fbeta4me` *Functional Beta Biversity for MacroEcology*

Description

It estimates the phylogenetic beta diversity of focal cells within a SpatVector object by considering neighboring cells located within a specified buffer.

Usage

```
fbeta4me(PAM, TRAITS, SHP, width = 10000, index.family="sorensen", verbose=TRUE)
```

Arguments

`PAM`	A presence/absence matrix where sites are organized in rows and species in columns.
`TRAITS`	A species x Traits matrix or a PCoA scores of functional traits. The row labels must exactly match the species names in the presence/absence matrix (PAM).
`SHP`	A SpatVector object representing cells distributed over a geographic space
`width`	Refers to the radius of the buffer. If the SpatVector object uses a latitude/longitude projection, the width is specified in meters.
`index.family`	Choose either the 'sorensen' or 'jaccard' dissimilarity index.
`verbose`	Logical, indicating whether messages and the progress bar are shown. The default is TRUE.

Value

The function returns a data frame that includes turnover, nestedness, total beta diversity, and the number of cells contributing to the mean diversity of the focal cell. The IDs of the cells are used as the row names of the data frame.

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Yang, J., Swenson, N. G., Zhang, G., Ci, X., Cao, M., Sha, L., ... & Lin, L. (2015). Local-scale partitioning of functional and phylogenetic beta diversity in a tropical tree assemblage. Scientific Reports, 5(1), 12731.

Examples

```
data(TRAITS)
data(PAM)
SHP <- terra::vect(paste(system.file("extdata", package = "inecolr"),
"/test.shp", sep=""))
SHP <- SHP[1:10]
f_beta <- fbeta4me(PAM, TRAITS, SHP, width = 10000, index.family="sorensen")
head(f_beta)

data(TRAITS)
data(PAM)
SHP <- terra::vect(paste(system.file("extdata", package = "inecolr"),
"/test.shp", sep=""))
SHP <- SHP[1:10]
f_beta <- fbeta4me(PAM, TRAITS, SHP, width = 10000, index.family="sorensen", verbose=FALSE)
head(f_beta)
```

`hcsrt` *Homocedasticity test*

Description

Test of homocedasticity for lm glm and glmer models based on the trend of the squared residuals as a function of the fitted values

Usage

```
hcsrt(M)
```

Arguments

`M`	A lm, glm or glmer model.

Value

Returns the ANOVA table for the test. Nonsignificant effects mean there is no evidence to reject the null hypothesis that variability is the same across the fitted values range.

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Rohlf, F. (1981). Biometry the principles and practice of statistics in biological research. Zar, J. H. (1999). Biostatistical analysis. Pearson Education India.

Examples

```
y <- sort(rnorm(20, 5, 2))
x <- c(1:20)
M <- lm(y~x)
hcsrt(M)
```

`ks.rnorte` *Kolmogrov-Smirnov model's Residuals Normality Test*

Description

Performed a normality test of the model residuals agains a randon normal sample with as many data as the length of the residuals, mean zero and standar deviation equals to that of the residuals

Usage

```
ks.rnorte(M, quantiles=TRUE)
```

Arguments

`M`	M, a linear or glm model.
`quantiles`	quantiles, logical weather the test is based on quentiles rathern that raw data, defualt is TRUE.

Value

Returs the ks.test. No significant effect means that residuals behave as a normal variable

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Rohlf, F. (1981). Biometry the principles and practice of statistics in biological research. Zar, J. H. (1999). Biostatistical analysis. Pearson Education India.

Examples

```
x <- c(1,3,5,7,9, 11)
y<- c(3.3, 5.8, 10, 12, 16, 17.8)
M <- lm(y~x)
ks.rnorte(M)
```

`meanerrba` *Mean and error intervals*

Description

Mean and error intervals, either represent the mean values as a character (e.g., dot, solid square, etc.) or the height of bars. Error intervals are back-transformed from regular link functions included in «glm», but the user can customize the back transformation by introducing a function in the form of, «function(x)log1p(x)»

Usage

```
meanerrba(means, error, link=NA, backtrans=NULL, bars= FALSE,
legend.text=FALSE, ylab="Mean and error", xlab="Groups", main="", pch=19,
cex = 1, cex.pt=1, cex.axis = 1, cex.lab = 1, cex.main = 2, col= "grey",
border= "grey30", density=NULL, angle=NULL, lwd=1, axis.lty=0,
names.arg = colnames(means), las = 1, ylim = FALSE, axes = TRUE, xpd = FALSE,
add = FALSE)
```

Arguments

`means`	A vector or matrix with mean values. If a matrix, each column of values is grouped in the figure
`error`	A vector or matrix with error values. If a matrix, each column of values is grouped in the figure
`link`	Specified the scale of the linear predictor used to calculate the mean and error values and apply the corresponding back transformation in the plot.
`backtrans`	Define the customized back transformation if needed.
`bars`	Logical values to whether bars should be represented in the plot. The default option is FALSE, and mean values are represented with character, e.g., dot, open square, etc., as defined with the «pch» argument.
`legend.text`	Optional when bars=TRUE: A character vector to ID bars in the groups. The length of the vector must match the number of rows in the means matrix or the length of the means vector.
`ylab`	Label for the y-axis.
`xlab`	Label for the x-axis.
`main`	Label for the heading of the figure.
`pch`	Character to represent the mean values when teh bars argumen is FALSE.
`cex`	Character expansion factor for the names of the groups.
`cex.pt`	Expansion factor for the character representing the mean value.
`cex.axis`	Expansion factor for the axis values.
`cex.lab`	Expansion factor for the axis labels.
`cex.main`	Expansion factor for the heading of the figure.

`col`	A vector for the color of the elements in each group of means.
`border`	A vector for the color of the border when bars are displayed.
`density`	Numeric vector for the densitity of lines of the bars.
`angle`	Numeric vector for the angle of lines of the bars.
`lwd`	Numeric vector for the width of lines of error intervals. Also affects the lines of characters as in function points().
`axis.lty`	Numeric vector for the line type of the x-axis.
`names.arg`	Character vectors are used to name the groups of means taken as the column names of the means matrix or names of means vector elements. When names are not available, they take consecutive capital letter values.
`las`	Integer value (0 to 1) to fix the orientation of values in the y-axis.
`ylim`	Limits of the y-axis, a vector of two elements for the lower and upper limits of the axis, respectively.
`axes`	Logical, wheather the y-axis should appear in the plot. Default value is TRUE
`xpd`	Logical, wheather bars are expanded beyond the ylim.
`add`	Logical, wheather mean and error bars should be added to an existing plot. Default option is FALSE and can not be change for now.

Value

No values returned.

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Rohlf, F. (1981). Biometry the principles and practice of statistics in biological research. Zar, J. H. (1999). Biostatistical analysis. Pearson Education India.

Examples

```
set.seed(42)
means <- matrix(rpois(6, 10), 2, 3)
error <- matrix(runif(6)*2, 2, 3)
meanerrba(means,error,col=c("red", "blue", "purple"), ylim=c(6, 18), xlab="")
abline(h=6, lwd=2)
legend("topright", c("2024", "2024", "2025"), col=c("red", "blue", "purple"),
bty="n", pch=19, ncol=3)

set.seed(42)
means <- matrix(runif(6)*sample(c(1,-1),size=6, replace=TRUE), 2, 3)
error <- matrix(runif(6), 2, 3)/5
meanerrba(t(means),t(error), link="logit", ylim=c(0.2, 0.8),
names=paste("Group",1:3, sep="-"), col=c("blue", "purple"), xlab="")
abline(h=0.2, lwd=2)
```

```
legend("topleft", c("Condition A", "Condition B"), col=c("blue", "purple"),
bty="n", pch=c(19,15))

set.seed(42)
means <- matrix(runif(6)*sample(c(1,-1),size=6, replace=TRUE), 2, 3)
error <- matrix(runif(6), 2, 3)/5
meanerrba(t(means),t(error), link="logit", ylim=c(0.2, 0.8),
names=paste("Group",1:3, sep="-"), col="blue", pch=c(0,5), xlab="")
legend("topleft", c("2024", "2025"), col="blue", bty="n", pch=c(0,5))

set.seed(42)
means <- matrix(runif(6)*sample(c(1,-1),size=6, replace=TRUE), 2, 3)
error <- matrix(runif(6), 2, 3)/5
meanerrba(t(means),t(error), link="logit", bars=TRUE, col=c("navy", "gold2"),
ylim=c(0.2, 0.8), xlab="")
legend("topleft", c("2024", "2025"), fill=c("navy", "gold2"), bty="n")
```

`PAM` *A presence/absebce matrux*

Description

Sites (cells) are in the orws and columns are species. Species names must match those in PHYLO

Usage

```
data("PAM")
```

Format

A data frame with 1000 observations on the following 43 variables.

`Specis_1` a numeric vector

`Specis_2` a numeric vector

`Specis_3` a numeric vector

`Specis_4` a numeric vector

`Specis_5` a numeric vector

`Specis_6` a numeric vector

`Specis_7` a numeric vector

`Specis_8` a numeric vector

`Specis_9` a numeric vector

`Specis_10` a numeric vector

`Specis_11` a numeric vector

`Specis_12` a numeric vector

`Specis_13` a numeric vector

`Specis_14`	a numeric vector
`Specis_15`	a numeric vector
`Specis_16`	a numeric vector
`Specis_17`	a numeric vector
`Specis_18`	a numeric vector
`Specis_19`	a numeric vector
`Specis_20`	a numeric vector
`Specis_21`	a numeric vector
`Specis_22`	a numeric vector
`Specis_23`	a numeric vector
`Specis_24`	a numeric vector
`Specis_25`	a numeric vector
`Specis_26`	a numeric vector
`Specis_27`	a numeric vector
`Specis_28`	a numeric vector
`Specis_29`	a numeric vector
`Specis_30`	a numeric vector
`Specis_31`	a numeric vector
`Specis_32`	a numeric vector
`Specis_33`	a numeric vector
`Specis_34`	a numeric vector
`Specis_35`	a numeric vector
`Specis_36`	a numeric vector
`Specis_37`	a numeric vector
`Specis_38`	a numeric vector
`Specis_39`	a numeric vector
`Specis_40`	a numeric vector
`Specis_41`	a numeric vector
`Specis_42`	a numeric vector
`Specis_43`	a numeric vector

Examples

```
data(PAM)
```

`pbeta4me` *Phylogenetic Beta Biversity for MacroEcology*

Description

It estimates the phylogenetic beta diversity of focal cells within a SpatVector object by considering neighboring cells located within a specified buffer.

Usage

```
pbeta4me(PAM, PHYLO, SHP, width = 10000, index.family="sorensen", verbose =TRUE)
```

Arguments

`PAM`	A presence/absence matrix where sites are organized in rows and species in columns.
`PHYLO`	A phylogenetic rooted tree, which includes branch lengths, is required. The tip labels must exactly match the species names in the presence/absence matrix (PAM).
`SHP`	A SpatVector object representing cells distributed over a geographic space
`width`	Refers to the radius of the buffer. If the SpatVector object uses a latitude/longitude projection, the width is specified in meters.
`index.family`	Choose either the 'sorensen' or 'jaccard' dissimilarity index.
`verbose`	Logical, indicating whether messages and the progress bar are shown. The default is TRUE.

Value

The function returns a data frame that includes turnover, nestedness, total beta diversity, and the number of cells contributing to the mean diversity of the focal cell. The IDs of the cells are used as the row names of the data frame.

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Graham, C. H., & Fine, P. V. (2008). Phylogenetic beta diversity: linking ecological and evolutionary processes across space in time. Ecology letters, 11(12), 1265-1277.

Examples

```
data(PHYLO)
data(PAM)
SHP <- terra::vect(paste(system.file("extdata", package = "inecolr"),
"/test.shp", sep=""))
SHP <- SHP[1:10]
pb_beta <- pbeta4me(PAM, PHYLO, SHP, width = 10000, index.family="sorensen")
head(pb_beta)

data(PHYLO)
data(PAM)
SHP <- terra::vect(paste(system.file("extdata", package = "inecolr"),
"/test.shp", sep=""))
SHP <- SHP[1:10]
pb_beta <- pbeta4me(PAM, PHYLO, SHP, width = 10000, index.family="sorensen",
verbose=FALSE)
head(pb_beta)
```

`PHYLO` *Phylogenetic tree*

Description

A rooted phylogenetic tree with branch lengths. Tip names must math those in PAM's columns

Usage

```
data("PHYLO")
```

Format

The format is: List of 4 $ edge : int [1:84, 1:2] 44 45 46 47 48 49 50 50 51 52 ... $ edge.length: num [1:84] 26.2 81.9 32.6 26.7 100.1 ... $ Nnode : int 42 $ tip.label : chr [1:43] "Specis_43" "Specis_28" "Specis_26" "Specis_27" ... - attr(*, "class")= chr "phylo" - attr(*, "order")= chr "cladewise"

Examples

```
data(PHYLO)
## maybe str(PHYLO) ; plot(PHYLO) ...
```

`ranfor` *Random Forest*

Description

Create the most pasimonious groupping hipothesis based on N classification trees (the forest)

Usage

```
ranfor(data, repetitions=1000, prop=0.85, n.digits = 5, plot=TRUE)
```

Arguments

`data`	A dataframe where the first column is the response (dependent) variable and the rest serve to classify
`repetitions`	Number of iterations
`prop`	Proportion of rows included in each iteration
`n.digits`	N digits to display in the summary table
`plot`	Logical, wheather to plat the result, defualt is TRUE

Value

Retur a matrix ... .

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Rohlf, F. (1981). Biometry the principles and practice of statistics in biological research. Zar, J. H. (1999). Biostatistical analysis. Pearson Education India.

Examples

```
data("iris")
ranfor(iris[,c(5,1:4)])
```

`se` *Stadard Error*

Description

Estimate the stadard error of a numeric or integer vector or colums in a matrix.

Usage

```
se(x)
```

Arguments

`x`	A numeric or integer vector or matrix.

Value

retur satandar error values based on th formula se = sqrt(var(x)/length(x)).

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Rohlf, F. (1981). Biometry the principles and practice of statistics in biological research. Zar, J. H. (1999). Biostatistical analysis. Pearson Education India.

Examples

```
set.seed(42)
data <- matrix(round(rnorm(6, 10, 3),2), 2, 3)
colnames(data)<- LETTERS[1:3]
se <- se(data)
se
```

`simpmod` *Model simplification*

Description

Simplifies models based on the residual sum of squares

Usage

```
simpmod(M, alpha=0.05)
```

Arguments

`M`	A lm, glm.
`alpha`	Crital value to reject the null hypothis when less than or equal to 0.05, the default value..

Value

Returns a list of simplification steps up to the sipliest model in a list object.

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Crawley, the R book

Examples

```
y <- sort(rnorm(20, 5, 2))
x <- c(1:20)
M <- lm(y~x)
simpmod(M)
```

`tbeta4me` *Taxonomic Beta Biversity for MacroEcology*

Description

It estimates the taxonomic beta diversity of focal cells within a SpatVector object by considering neighboring cells located within a specified buffer.

Usage

```
tbeta4me(PAM, SHP, width = 10000, index.family="sorensen", verbose=TRUE)
```

Arguments

`PAM`	A presence/absence matrix where sites are organized in rows and species in columns.
`SHP`	A SpatVector object representing cells distributed over a geographic space
`width`	Refers to the radius of the buffer. If the SpatVector object uses a latitude/longitude projection, the width is specified in meters.
`index.family`	Choose either the 'sorensen' or 'jaccard' dissimilarity index.
`verbose`	Logical, indicating whether messages and the progress bar are shown. The default is TRUE.

Value

The function returns a data frame that includes turnover, nestedness, total beta diversity, and the number of cells contributing to the mean diversity of the focal cell. The IDs of the cells are used as the row names of the data frame.

Author(s)

Guevara, R., roger.guevara@inecol.mx

References

Yang, J., Swenson, N. G., Zhang, G., Ci, X., Cao, M., Sha, L., ... & Lin, L. (2015). Local-scale partitioning of functional and phylogenetic beta diversity in a tropical tree assemblage. Scientific Reports, 5(1), 12731.

Examples

```
data(PAM)
SHP <- terra::vect(paste(system.file("extdata", package = "inecolr"),
"/test.shp", sep=""))
SHP <- SHP[1:10]
t_beta <- tbeta4me(PAM, SHP, width = 10000, index.family="sorensen")
head(t_beta)

data(PAM)
SHP <- terra::vect(paste(system.file("extdata", package = "inecolr"),
"/test.shp", sep=""))
SHP <- SHP[1:10]
t_beta <- tbeta4me(PAM, SHP, width = 10000, index.family="sorensen", verbose=FALSE)
head(t_beta)
```

`TRAITS` *Functional traits of species*

Description

Matrix of five functional traits (columns) of species (rows). Species names must match those in PAM

Usage

```
data("TRAITS")
```

Format

A data frame with 43 observations on the following 5 variables.

`FT1`	a numeric vector
`FT2`	a numeric vector
`FT3`	a numeric vector
`FT4`	a numeric vector
`FT5`	a numeric vector

Examples

```
data(TRAITS)
```

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