

Package ‘inecolr’

July 22, 2025

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 (IN-ECOL). For references and published evidence see, Manrique-Ascencio, et al (2024) <[doi:10.1111/gcb.17282](https://doi.org/10.1111/gcb.17282)>, Manrique-Ascencio et al (2024) <[doi:10.1111/plb.13683](https://doi.org/10.1111/plb.13683)>, Ruiz-Guerra et al(2017) <[doi:10.17129/botsci.812](https://doi.org/10.17129/botsci.812)>, Juarez-Fragoso et al (2024) <[doi:10.1007/s10980-024-01809-z](https://doi.org/10.1007/s10980-024-01809-z)>, Papaqui-Bello et al (2024) <[doi:10.13102/sociobiology.v71i2.10503](https://doi.org/10.13102/sociobiology.v71i2.10503)>.

Date 2025-05-10

Depends R (>= 3.5.0)

Imports ape, betapart, boot, cli, gmodels, gtools, multcomp, stringr, terra, tree, vegan

License GPL-3

Encoding UTF-8

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-05-19 13:20:06 UTC

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betacomp	<i>Beta Base on Complementarity of Ecological Communities</i>
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Description

Estimate beta diversity based on the Bray-Curtis index estimates of complementarity (an asymmetric measures) between 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 Diversity 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 = "inacolr"),
"/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 = "inacolr"),
"/test.shp", sep=""))
SHP <- SHP[1:10]
f_beta <- fbeta4me(PAM, TRAITS, SHP, width = 10000, index.family="sorensen", verbose=FALSE)
head(f_beta)
```

hcsrt	<i>Homocedasticity test</i>
-------	-----------------------------

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@inacol.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 against a random normal sample with as many data as the length of the residuals, mean zero and standard deviation equals to that of the residuals

Usage

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

Arguments

M	M, a linear or glm model.
quantiles	quantiles, logical whether the test is based on quantiles rather than raw data, default is TRUE.

Value

Returns 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 density 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/absence matrix***Description**

Sites (cells) are in the rows 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 Diversity 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 = "incolr"),
"/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 = "incolr"),
"/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 match 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 parsimonious grouping hypothesis based on N classification trees (the forest)

Usage

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

Arguments

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

Value

Return 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	<i>Stadard Error</i>
----	----------------------

Description

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

Usage

```
se(x)
```

Arguments

x A numeric or integer vector or matrix.

Value

retur satandar error values based on th formula $se = \sqrt{\text{var}(x)/\text{length}(x)}$.

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	<i>Model simplification</i>
---------	-----------------------------

Description

Simplifies models based on the residual sum of squares

Usage

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

Arguments

M	A lm, glm.
alpha	Critical value to reject the null hypothesis when less than or equal to 0.05, the default value..

Value

Returns a list of simplification steps up to the simplest 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 Diversity 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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