Package: spaa (via r-universe)

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Type Package

Title SPecies Association Analysis

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Description Miscellaneous functions for analysing species association and niche overlap.

License GPL (>= 2)

LazyLoad yes

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VignetteBuilder knitr

URL `https://github.com/helixcn/spaa`

NeedsCompilation no

Repository https://helixcn.r-universe.dev

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Contents

`spaa-package` *SPecies Association Analysis*

Description

Miscellaneous functions for analysing species association and niche overlap.

Details

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Author(s)

Jinlong Zhang [aut, cre]

Maintainer: Jinlong Zhang <jinlongzhang01@gmail.com>

References

Zhang Jin-tun,(2004) Quantitative Ecology, Science Press, Beijing

Examples

```
library(vegan)
data(BCI)
## select the top 30 species according to relative frequeny.
sub <- sub.sp.matrix(BCI, common = 30)
## Set the digits to 1
plotlowertri(cor(sub), size = TRUE, cex = 3, digits = 1)

## Niche width and niche overlap
data(datasample)
niche.overlap.boot(datasample[,1:3], method = "levins")
niche.overlap(datasample, method = "levins")
niche.width(datasample[,1:3], method = "shannon")
```

`data2mat` *Convert field records to community matrix*

Description

Convert field records to community matrix

Usage

```
data2mat(data = data)
```

Arguments

`data`	A dataframe with the the following columns: `species`, `plots` or `sites`, `abundance`.

Value

Return a community matrix ready for computing diversity indices.

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

None

Examples

```
data(testdata)
spmatrix <- data2mat(testdata)
```

`datasample` *A sample dataset for a community*

Description

A sample community matrix containing 8 plots and 14 species, from Gutianshan, Zhejiang, China.

Usage

```
data(datasample)
```

Details

Values are the importance value for each species.

Source

Hu Zheng-hua, Qian Hai-Yuan, Yu Ming-jian. 2009. The niche of dominant species populations in Castanopsis eyrei forest in Gutian Mountain National Natural Reserve. Acta Ecologica Sinica. Vol.29, 3670-3677

Examples

```
data(datasample)
datasample
```

`freq.calc` *Compute species' relative frequency*

Description

Computing species' relative frequency as defined by the numbers of plots having a species divided by the total number of plots.

Usage

```
freq.calc(matr)
```

Arguments

`matr`	A community matrix

Details

The input should be a standard community matrix with rows representing sites and columns representing species.

Value

A vector containing relative frequency for each species

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

None

Examples

```
data(testdata)
spmatrix <- data2mat(testdata)
freq.calc(spmatrix)
```

`niche.overlap` *Niche overlap between each pair of species*

Description

Compute niche overlap between each pair of species.

Usage

```
niche.overlap(mat, method = c("levins", "schoener",
       "petraitis", "pianka", "czech", "morisita"))
```

Arguments

`mat`	A community matrix with columns representing species, and rows representing plots.
`method`	A string specifying the name of the index.

Details

To add.

Value

A distance matrix contains niche overlap index between each pair of species.

Author(s)

Jinlong Zhang `<jinlongzhang01@gmail.com>`

References

Zhang Jin-tun,(2004) Quantitative Ecology, Science Press, Beijing

Nicholas J. Gotelli. 2000. Null model analysis of species co-occurrence patterns. Ecology 81:2606-2621. http://esapubs.org/archive/ecol/E081/022/EcoSim

See Also

`niche.overlap.pair`

Examples

```
data(datasample)
niche.overlap(datasample, method = "levins")
```

`niche.overlap.boot` *Boostrap niche overlap indices*

Description

Bootstrap niche overlap indices

Usage

```
niche.overlap.boot(mat, method = c("pianka", "schoener", "petraitis",
    "czech", "morisita", "levins"), times = 1000, quant = c(0.025, 0.975))
```

Arguments

`mat`	standard community matrix.
`method`	character string specifying the index.
`times`	Interger, representing the number of bootstrap samples to generate.
`quant`	Quantile of the bootstrap values.

Details

This function bootstraps the following niche overlap indices between each pair of species: \ `schoener`: Schoener's niche overlap index\ `petraitis`: Petraitis' niche overlap index\ `czech`: Czechanowski index \ `morisita`: Morisita's overlap index\ `levins`: Levin's overlap index\ see more information from Gotelli, N(2009).\

Value

a data frame with each row for each pair of species the columns are `"Observed"`, `"Boot mean"`, `"Boot std"`, `"Boot CI1"`, `"Boot CI2"`, `"times"`

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

Zhang Jin-tun,(2004) Quantitative Ecology, Science Press, Beijing\

Nicholas J. Gotelli. 2000. Null model analysis of species co-occurrence patterns. Ecology 81:2606-2621. http://esapubs.org/archive/ecol/E081/022/EcoSim

See Also

`niche.overlap.boot.pair`

Examples

```
data(datasample)
niche.overlap.boot(datasample[,1:4], method = "pianka")
niche.overlap.boot(datasample[,1:4], method = "schoener")
niche.overlap.boot(datasample[,1:4], method = "czech")
niche.overlap.boot(datasample[,1:4], method = "levins")
```

`niche.overlap.boot.pair` *Boostrap the niche overlap indices*

Description

bootstrap the niche overlap indices between a pair of species. This is an internal function used by `niche.overlap.boot`, use `niche.overlap.boot` instead.

Usage

```
niche.overlap.boot.pair(vectorA, vectorB, method = c("levins",
     "schoener", "petraitis", "pianka", "czech", "morisita"),
      times = 1000, quant = c(0.025, 0.975))
```

Arguments

`vectorA`	A numeric vector containing species A's abundance or importance value.
`vectorB`	A numeric vector containing species B's abundance or importance value.
`method`	Name of the index to use.
`times`	Number of bootstraps
`quant`	Confidence intervals of the bootstrap results.

Value

This function will return a vector containing:\ `"Observed"`, \ `"Boot mean"`, \ `"Boot std"`, \ `"Boot CI1"`, \ `"Boot CI2"`, \ `"times"` \

Note

This is an internal function, please use `niche.overlap.boot`.

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

Zhang Jin-tun,(2004) Quantitative Ecology, Science Press, Beijing

See Also

niche.overlap.boot

Examples

```
data(datasample)
niche.overlap.boot.pair(datasample[,1], datasample[,2], method = "levins")
```

`niche.overlap.pair` *Compute niche overlap index between two species*

Description

Compute niche overlap index between two species. This is an internal function, used `niche.overlap` instead.

Usage

```
niche.overlap.pair(vectA, vectB, method = c("pianka",
     "schoener","petraitis","czech","morisita", "levins"))
```

Arguments

`vectA`	A numeric vector containing species A's abundance or importance value
`vectB`	A numeric vector containing species B's abundance or importance value
`method`	Niche overlap index

Details

None

Value

The niche overlap index

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

Zhang Jin-tun,(2004) Quantitative Ecology, Science Press, Beijing

Nicholas J. Gotelli. 2000. Null model analysis of species co-occurrence patterns. Ecology 81:2606-2621. http://esapubs.org/archive/ecol/E081/022/EcoSim

See Also

`niche.overlap`

Examples

```
data(datasample)
niche.overlap.pair(datasample[,1],datasample[,2], method = "levins")
```

`niche.width` *Niche width*

Description

Compute niche width for all the species in a community.

Usage

```
niche.width(mat, method = c("shannon", "levins"))
```

Arguments

`mat`	A community matrix with columns representing species, and rows representing plots.
`method`	Character string showing the name of the index.

Value

A vetor containing niche width for all the species in the community.

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

Zhang Jin-tun,(2004) Quantitative Ecology, Science Press, Beijing

See Also

`niche.overlap` for niche overlap

Examples

```
data(datasample)
niche.width(datasample, method = "levins")
niche.width(datasample, method = "shannon")
```

`plotlowertri` *Generate a graphs showing correlation matrix (lower semi matrix) (Deprecated)*

Description

Generate graphs (lower semi matrix) showing lower semi matrix. These graphs are often used to show the structure of a correlation, similarity or dissimilarity matrix.

Usage

```
plotlowertri(input, valuename = "r",
pchlist = c(19, 17, 15, 1, 5, 2, 7), interval = 6,
cex = 1, ncex = 1, int =1.2, add.number = TRUE,
size = FALSE, add.text = FALSE, show.legend = TRUE,
digits = 2)
```

Arguments

`input`	The `input`, often a correlation or a distance matrix.
`valuename`	Name of the value that to show in the legend.
`pchlist`	A numberic vector specifying the shapes of points, see `pch` `par()`.
`interval`	Types of point shapes to show
`cex`	A number specifying the text size in the legend
`ncex`	Size of the text shown above each column.
`int`	Space between lines within the legend
`add.number`	If the column number should be shown
`size`	Whether the size of points should change with the value
`add.text`	Logical, If the number should be shown in the grid.
`show.legend`	Logical, If the legend should be appear.
`digits`	Number of digits for the label of each interval.

Details

In the legend, space between lines could be adjusted by specifying `int`.

Value

lower matrix plot

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

Zhang Qiaoying, Peng Shaolin, Zhang Sumei, Zhang Yunchun, Hou Yuping.(2008). Association of dormintant species in Guia hill Municipal Park of Macao. Ecology and Environment. 17:1541-1547

See Also

See Also `plotnetwork`

Examples

```
data(testdata)
spmatrix <- data2mat(testdata)
result <- sp.pair(spmatrix)

## Check the legend for 0.00 to 0.33 (Unwanted label)
plotlowertri(result$Pearson, int = 0.5, cex=1.5)
title("Pearson Correlation Lower Matrix Plot")

## Change the size of points and reset the intervals.
## Warning: The lower matrix plot illustrating Pearson
## Correlation between each pair of species. Note the
## triangle didn't appeared in the plots, but have been
## added to the legend. This is due to the distribution
## of data. Be careful in selection of intervals.


plotlowertri(result$Pearson, int = 0.5, cex=1.5,
interval = 4, pchlist = c(19, 17, 15, 1, 5), size = TRUE)

title("Pearson Correlation Lower Matrix Plot")

## "Pure" dots, may have to add legend manually...
plotlowertri(result$Pearson, int = 0.5, cex=2.5,
interval = 4, pchlist = rep(19, 5), size = TRUE,
show.legend = FALSE)

title("Pearson Correlation Lower Matrix Plot")


## Using BCI data
library(vegan)
data(BCI)
## select the top 30 species according to relative frequency.
sub <- sub.sp.matrix(BCI, common = 30)
## Original
plotlowertri(cor(sub))

## Change size
plotlowertri(cor(sub), size = TRUE, cex = 3)

## Set the digits to 1
plotlowertri(cor(sub), size = TRUE, cex = 3, digits = 1,
```

```
ncex = 0.7)
```

`plotnetwork` *Plot correlation network (Deprecated)*

Description

Plotting correlation network showing the relationship between each pair of sites connected by segments. The points are arranged in a circle.

Usage

```
plotnetwork(datainput, n_levels = 6, xlim = c(-2.5, 5),
    ylim = c(-2.5, 2.5), node_size = 3, lwd.var = TRUE,
    lwd = 4, label_dist = 1.2,
    show.node = TRUE, show.text.label = TRUE,
    linecol = c("orange", "blue"),show.legend = TRUE,
    valuename = "r", legendx = 3,
    legendy = -2, legend_line_space = 1,
    legend_linelength = 0.3, adjust_legend_x = 0,
    adjust_legend_y = 0,digits = 2, ... )
```

Arguments

`datainput`	The correlation matrix, usually a lower matrix
`n_levels`	Number of types of segments to show the correlation, note interval should <12
`xlim`	horizontal range of the canvas
`ylim`	vertical range of the canvas
`node_size`	size of the nodes
`lwd.var`	logical, if the segments width should vary with the absolute value
`lwd`	width of the segments for connecting the sites, default 1
`label_dist`	Distance of text labels from each node.
`show.node`	Whether the nodes in the figure should be labeled
`show.text.label`	Whether the text label should be drawn.
`linecol`	Colours showing positve or negative correlation. The lines representing positive correlations use the first element
`show.legend`	If the legend should be shown
`valuename`	Name of the variable shown in the legend
`legendx`	the starting position of the legend x
`legendy`	the starting position of the legend y

`legend_line_space`	the space between the lines in the legend
`legend_linelength`	length of the segment in the legend
`adjust_legend_x`	adjusting the position of legend (x)
`adjust_legend_y`	adjusting the position of legend (y)
`digits`	Number of disgits shown in the legend, it will be used in generating the breaks as well
`...`	other parameters related with plot.default

Details

This function could be used to plot the pairwise connections between less than 20 sites (above 20 is not recommended since there would be too many connections).

The lines will be in orange or blue, according the sign of the value.

Value

Correlation network plots.

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

None

Examples

```
data(testdata)
spmatrix <- data2mat(testdata)
result <- sp.pair(spmatrix)
plotnetwork(result$Pearson)

plotnetwork(result$Pearson, linecol = c("red", "black"))

plotnetwork(result$Pearson, n_levels = 4,  node_size = 4,
    lwd.var = FALSE, label_dist = 0.8, show.node = FALSE,
    show.text.label = FALSE, linecol = c("red", "black"),
    show.legend = TRUE, valuename = "r", legendx = 3,
    legend_line_space = 0.5, legend_linelength = 0.5,
    adjust_legend_x = -1)

title("Pearson Correlation Network")
```

`sp.assoc` *Analyzing species association*

Description

Analyzing species association

Usage

```
sp.assoc(matr)
```

Arguments

`matr`	standard community matrix , with rows representing sites and columns representing species.

Details

Computations are based on the following formula.

If, `N`: Number of plots.

`S`: Number of species.

`n`: Number of plots occupied by certain species.

`Tj`: total number of species for each plot. `s t`: mean species number for all the plots.

Then: Variance of species relative frequency is: `sigma^{2}{T}= sum{i}=1^{s}P{i}(1-P{i})`.

Variance of species number is: `S^{2}{T}=({1}{N})sum{j=1}^{N}(T{j}-t)^{2}` .

Species relative frequency: `P{i}={n{i}}{N}`.

Variance ratio:

If `VR > 1` Positively associated,

If `VR < 1` Negative associated

`VR = {S{T}^{2}}/{sigma{T}^{2}}`

`W`: used in comparison with chi square with n degrees of freedom.

`W = VR * N`

Value

Variance ratio, W, Chisq, etc, see `details`

`pi`	Species frequency
`N`	Number of plots
`S`	Number of species
`Tj`	Total number of species for each plot
`Numspmean`	Mean number of species

`sigmaTsq`	Variance of species relative frequency
`STsq`	Variance of species number
`var.ratio`	Variance ratio
`W`	W statiscit value: used in comparison with chi square.(n)

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

Zhang Qiaoying, Peng Shaolin, Zhang Sumei, Zhang Yunchun, Hou Yuping. (2008) Association of dormintant species in Guia hill Municipal Park of Macao. Ecology and Environment. 17:1541-1547

GUO zhongling, MA yuandan, ZHENG Jiping, LIU Wande , JIN Zefeng.(2004) Biodiversity of tree species,their populations'spatial distribution pattern and interspecific association in mixed deciduous broadleaved forest in Changbai Mountains. Chinese Journal of Applied Ecology. 15:2013-2018

Shi Zuomin, Liu Shirong, Cheng Ruimei, Jiang Youxu.(2001) Interspecific association of plant populations in deciduous broad leaved forest in Baotianman. Scientia Silvae Sinicae. 37:30-35

See Also

See also `sp.pair` for association between each pair of species.

Examples

```
data(testdata)
spmatrix <- data2mat(testdata)
sp.assoc(spmatrix)
```

`sp.pair` *Species association between each pair of species*

Description

Compute species association between each pair of species.

Usage

```
sp.pair(matr)
```

Arguments

`matr`	Standard community matrix, with rows representing sites and columns representing species.

Details

If `a`, `b`, `c`, `d` denote the co-occurrence the two species A and B, where:

`a` = number of plots occupied both by A and B.

`b` = number of plots only have A.

`c` = number of plots only have B.

`d` = number of plots without A or B.

`N` = `a+b+c+d`

Then, it is possible to compute:

Chi square (Yate's correction): `chi^{2}=((((a*d-b*c)-0.5*N)^2)*N)/(a+b)*(a+c)*(b+d)*(c+d)`

V ratio: `V` = `((a+d)-(b+c))/(a + b + c + d)`

Jaccard index: `Jaccard` =`a/(a + b + c)`

Ochiai index: `Ochiai` = `a/sqrt((a+b)*(a+c))`

Dice index: `Dice` = `2*a/(2*a + b + c)`

The Association Coefficient(`AC`):

if `a*d` >= `b*c`:

`AC` = `(a*d - b*c)/((a+b)*(b+d))`

if `a*d` < `b*c` and `a` <= `d`:

`AC` = `(a*d - b*c)/((a+b)*(a+c))`

if `a*d` < `b*c` and `a` > `d`:

`AC` = `(a*d - b*c)/((b+d)*(c+d))`

Point correlation coefficient

(`PCC`):

`PCC` = `{a*d-b*c}/{(a+b)*(a+c)*(c+d)*(b+d)}`

Value

`chisq`	Chi Square matrix
`V`	`V` positive or negative association
`Ochiai`	Ochiai's index
`Dice`	Dice's index
`Jaccard`	Jaccard's index
`Pearson`	Pearson's correlation coefficient
`Spearman`	Spearman's rank correlation coefficient
`PCC`	Point correlation coefficient
`AC`	Association coefficient

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

HURLBERT, S. H. (1969). A coefficient of interspecific association. Ecology, 50(1), 1-9.

WANG, B. S., & PENG S. L. (1985). Studies on the Measuring Techniques of Interspecific Association of Lower-Subtropical Evergreen-Broadleaved Forests. I. The Exploration and the Revision on the Measuring Formulas of Interspecific Association. Chinese Journal of Plant Ecology, 9(4), 274-285.

JIAN, M. F., LIU, Q. J., ZHU, D., & YOU, H. (2009). Inter-specific correlations among dominant populations of tree layer species in evergreen broad-leaved forest in Jiulianshan Mountain of subtropical China. Chinese Journal of Plant Ecology, 33(4), 672-680.

ZHOU, X. Y., WANG, B. S., LI, M. G., & ZAN, Q. J. (2000). An analysis of interspecific associations in secondary succession forest communities in Heishiding Natural Reserve, Guangdong Province. Chinese Journal of Plant Ecology, 24(3), 332-339

See Also

See Also as `sp.assoc` for computing association for all the species.

Examples

```
data(testdata)
spmatrix <- data2mat(testdata)
result <- sp.pair(spmatrix)
```

`splist` *A sample dataframe showing species taxonomic information (Deprecated)*

Description

A sample dataframe containing the checklist of species used in add.col()

Usage

```
data(splist)
```

Format

A data frame with 9 observations on the following 3 variables.

`species` a factor with levels `sp1` to `sp8`

`genera` a factor with levels `gen1` to `gen6`

`family` a factor with levels `fam1` to `fam5`

References

None

Examples

```
data(splist)
data(testdata)
```

`sub.sp.matrix` *Subset species based on relative frequency*

Description

Subset species based on relative frequency.

Usage

```
sub.sp.matrix(spmatrix, freq = 0.5, common = NULL)
```

Arguments

`spmatrix`	a standard community matrix with rows representing sites and columns representing species.
`freq`	The relative frequency, species with higher relative frequency will be kept in the output.
`common`	The number of most common species to keep.

Details

sub.sp.matrix will select the species whose relative frequency above 0.5 (default), or select certain number of species based on relative frequency.

Value

A subset matrix of species with high relative frequency.

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

None

See Also

See Also `subset`

Examples

```
library(vegan)
data(BCI)
## Select the species whose relative frequency
## more than 0.5, from BCI data
sub <- sub.sp.matrix(BCI, freq = 0.5)
## Select the top 30 species according to relative frequency
sub <- sub.sp.matrix(BCI, common = 30)
```

`testdata` *A sample dataset s*

Description

A sample dataset

Usage

```
data(testdata)
```

Format

A dataframe with 11 observations on the following 3 variables.

`plotname` a factor with levels `plot1`, `plot2`, `plot3`.

`species` a factor with levels `sp1` to `sp7`.

`abundance` a numeric vector indicating number of individuals appeared in each plot.

Examples

```
data(testdata)
testdata
```

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