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License GPL-2

LazyLoad yes

Suggests vegan

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

NeedsCompilation no

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Contents

`spaa-package` *SPecies Association Analysis*

Description

Miscellaneous functions for analysis of species association and niche overlap.

Details

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License:	GPL-2
LazyLoad:	yes

Author(s)

Author: Jinlong Zhang <`jinlongzhang01@gmail.com`>

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Examples

```
data(testdata)
testdata

data(splist)
splist
```

```
### data tranformation
(spmatrix <- data2mat(testdata))
#Species association
sp.assoc(spmatrix)

# Species association between each pair of species
(result <- sp.pair(spmatrix))

#### 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")

##example turnover()
plotlab1 <- XYname(4,6)
xxx <- 1:240
dim(xxx) <- c(24, 10)
rownames(xxx) <- plotlab1

### Distance between each pair of plots
ddd <- dist(xxx)

### label matrix
labmat1 <- lab.mat(plotlab1)
yyy <- turnover(labmat1, ddd)

## geodist() example
## Paris
L1 = deg2dec(-2,20,14)
phi1 = deg2dec(48, 50, 11)
## Washington DC
L2 = deg2dec(77,03,56)
phi2 = deg2dec(38,55,17)

##High precision Great Circle distance
geodist(L1, phi1, L2, phi2)
```

`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
```

`deg2dec` *Degree to decimal*

Description

Convert latitude or longitude from degree to decimal format

Usage

```
deg2dec(h, m, s)
```

Arguments

`h`	Degree
`m`	Minute
`s`	Second

Details

Convert latitude or longitude from degree to decimal format.

Value

Degree of decimal format

Note

Places with eastern hemisphere should have longitude and southern hemisphere less than zero.

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

Examples

```
## deg2dec() example
##Paris
L1 = deg2dec(-2,20,14)
phi1 = deg2dec(48, 50, 11)
##Washington DC
L2 = deg2dec(77,03,56)
phi2 = deg2dec(38,55,17)
```

`dist2list` *Convert distance matrix to pairwised list*

Description

Convert distance matrix to pairwised list

Usage

```
dist2list(dist)
```

Arguments

`dist`	distance matrix

Details

Pairwise list with first column indicates the rows of the original distance matrix, second column indicates the columns indicates the rows of the original distance matrix, and the third indicats the values.

Value

Dataframe with three columns.

Author(s)

Jinlong Zhang `<jinlongzhang01@gmail.com>`

References

Tuomisto, H. (2003). "Dispersal, Environment, and Floristic Variation of Western Amazonian Forests." Science 299(5604): 241-244.

See Also

`list2dist`

Examples

```
##dist2list() example
x <- matrix(rnorm(100), nrow=5)
sampledata <- dist(x)
ddd <- dist2list(sampledata)
```

`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)
```

`geodist` *Hight precision Great circle distance between two places*

Description

Hight precision Great circle distance between two places assuming the earth is elliptic sphere.

Usage

```
geodist(L1, phi1, L2, phi2)
```

Arguments

`L1`	Longitude of first place in decimal format.
`phi1`	Latitude of first place in decimal format.
`L2`	Longitude of second place in decimal format.
`phi2`	Latitude of second place in decimal format.

Details

Hight precision great circle distance between two places assuming the earth is elliptic sphere.

Value

Hight precision great circle distance.

Author(s)

Jinlong Zhang `<jinlongzhang01@gmail.com>`

References

Jean Meeus 1991 Astronomical Algorithms Willmann-Bell 80-83

See Also

`lgeodist`

Examples

```
## geodist() example
## Paris
L1 = deg2dec(-2,20,14)
phi1 = deg2dec(48, 50, 11)
## Washington DC
L2 = deg2dec(77,03,56)
phi2 = deg2dec(38,55,17)
##High precision Great Circle distance
```

```
geodist(L1, phi1, L2, phi2)
```

`lab.mat` *Convert vector of XY labels to label matrix*

Description

Convert vector of XY labels to label matrix

Usage

```
lab.mat(plotlab)
```

Arguments

`plotlab`	Vector of XY labels

Value

XY label matrix

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

See Also

`turnover`

Examples

```
### lab.mat() example
plotlab1 <- XYname(4,6)
labmat <- lab.mat(plotlab1)
```

`lgeodist` *Low precision Great circle distance between two places*

Description

Calculating Great circle distance between two places assuming that the earth is sphere.

Usage

```
lgeodist(L1, phi1, L2, phi2)
```

Arguments

`L1`	Longitude of first place in decimal format.
`phi1`	Latitude of first place in decimal format.
`L2`	Longitude of second place in decimal format.
`phi2`	Latitude of second place in decimal format.

Value

Low precision great circle distance between two places.

Note

This function assuming that the earth is sphere.

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

Jean Meeus 1991 Astronomical Algorithms Willmann-Bell 80-81

See Also

`geodist`

Examples

```
#lgeodist() example
##Paris
L1 = deg2dec(-2,20,14)
phi1 = deg2dec(48, 50, 11)
##Washington DC
L2 = deg2dec(77,03,56)
phi2 = deg2dec(38,55,17)
#Great circle distance
```

```
lgeodist(L1, phi1, L2, phi2)
```

`list2dist` *Convert pairwise list to distance matrix*

Description

Convert pairwise list to distance matrix

Usage

```
list2dist(dat)
```

Arguments

`dat`	dataframe with three columns

Details

Dataframe with first column as the column names in the distance matrix, second column as the rownames in the distance matrix, third column the values.

Value

distance matrix

Author(s)

Jinlong Zhang <`jinlongzhang01@gmail.com`>

References

Tuomisto, H. (2003). "Dispersal, Environment, and Floristic Variation of Western Amazonian Forests." Science 299(5604): 241-244.

See Also

`dist2list`

Examples

```
##list2dist() example
x <- matrix(rnorm(100), nrow=5)
sampledata <- dist(x)
ddd <- dist2list(sampledata)
list2dist(ddd)
```

`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")
```

`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
```

`turnover` *Calculating species turnover*

Description

Calculating species turnover based on the mean value between focus quadrat and their neighbours.

Usage

```
turnover(lab.mat, dist.mat, type = c("quart", "octal"))
```

Arguments

`lab.mat`	matrix of quadrat labels.
`dist.mat`	distance matrix between each pair of quadrats
`type`	"quart" indicates four neighbouring quadrats, "octal" indicate eight neighbouring quadrats.

Details

species turnover based on the mean value between centred quadrat and its neighbours.

Value

matrix with species turnover.

Author(s)

Jinlong Zhang `<jinlongzhang01@gmail.com>`

References

Lennon J. 2001 The geographical structure of British bird distributions - diversity, spatial turnover and scale Journal of Animal Ecology 70,966-979

See Also

`XYname` and `lab.mat`

Examples

```
##example turnover()
plotlab1 <- XYname(4,6)
xxx <- 1:240
dim(xxx) <- c(24, 10)
rownames(xxx) <- plotlab1
### Distance between each pair of plots
ddd <- dist(xxx)
### label matrix
labmat1 <- lab.mat(plotlab1)
yyy <- turnover(labmat1, ddd)
```

`XYname` *Generating vector of XY labels*

Description

Generating vector of XY labels by providing number of rows and columns

Usage

```
XYname(x, y)
```

Arguments

`x`	Number of X labels
`y`	Number of Y labels

Value

Vector of XY labels

Author(s)

Jinlong Zhang `<jinlongzhang01@gmail.com>`

References

None

See Also

`lab.mat` for converting the vector to matrix of XY labels.

Examples

```
## XYname() example
XYname(4,6)
```

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