Package 'spaa'

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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

Suggests vegan

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Contents

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spaa-package   *SPecies Association Analysis*

Description

Miscellaneous functions for analysis of species association and niche overlap.

Details

Package:	spaa
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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)
```

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 repre-
        senting 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](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)
```

Index