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

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

NeedsCompilation no

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spaa-package   *SPecies Association Analysis*

Description

Miscellaneous functions for analysis of species association and niche overlap.

Details

Package:	spaa
Type:	Package
Version:	0.2.1
Date:	2013-8-23
License:	GPL-2
LazyLoad:	yes

Author(s)

Author: Jinlong Zhang <jinlongzhang01@gmail.com>

Maintainer: Jinlong Zhang <jinlongzhang01@gmail.com>

Examples

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

## adding information
```

```
## add genera from dataframe B to dataframe A.
add.col(inputA = testdata, inputB = splist, add = "genera",
according = "species")
## add family from dataframe B to dataframe A.
add.col(inputA = testdata, inputB = splist, add = "family",
according = "species")

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

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

# simple network with positive lines in red and negative lines
# in blue
plotnetwork(result$Pearson)
title("Pearson Correlation Network")

# The lower matrix plot illustrating Pearson's 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 carefull in seletion of intervals.

plotlowertri(result$Pearson, int = 0.5, cex=3, interval = 4,
pchlist = c(19, 17, 15, 1, 5), size = TRUE)
title("Pearson Correlation Lower Matrix Plot")

## plot lower matrix
## Using BCI data for lower matrix plot
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")

##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)
```

---

add.col   *Add one column from A to B, according to one column of common*
                                     name.

Description

This function can be used to add one column from dataframe B to dataframe A, according to the
column names speciefied.

Usage

```
add.col(inputA, inputB, add, according)
```

Arguments

inputA   inputA A dataframe which a column to be added according to one row infor-
              mation. Must contain a column name equals to one column name in dataframe
              B at the least.

inputB   inputB A dataframe which a column to be abstracted from, must contain a col-
              umn equals to at least one column name in dataframe A.

add   add the column name in dataframe B to be add to dataframe A. musth be char-
              acter.

according   according the common column name specified to match the data entries from
              dataframe A and dataframe B. must be character.

Details

This function can be used to add one column from dataframe B to dataframe A, according to the
column names specified. Users have to make sure the to dataframes at least share the common
names specified. This function may be an alternative for merge

Author(s)

Jinlong Zhang

See Also

See Also[merge](merge)

Examples

```
data(splist)
data(testdata)
## add genera from dataframe B to dataframe A.
add.col(inputA = testdata, inputB = splist, add = "genera",
according = "species")
## add family from dataframe B to dataframe A.
add.col(inputA = testdata, inputB = splist, add = "family",
according = "species")
```

---

data2mat   *Convert species list data to species matrix*

Description

This function can be used to convert the species list to species matrix. The rows of the output matrix are plots, or sites. The columns are the species.

Usage

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

Arguments

data   The input data

Details

The input data will have to include :species,plots or sites, abundance, specifically, a column named "abundance" must be specified.

Value

Return a species matrix with each row for each plot, and each column for species.

Author(s)

Jinlong Zhang <jinlongzhang01@gmail.com>

References

None

Examples

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

---

datasample *community matrix example*

Description

Community matrix

Usage

```
data(datasample)
```

Format

A data frame with 8 plots on the following 14 species.

Details

including 14 species, 8 plots of Gutianshan Natural Reserve, Zhejiang, China, values are the value of importance in the plot 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)
```

---

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   *Species relative frequency*

Description

This function calculates the species relative frequency which equals to the numbers of occupied plots partitioned by the total number of plots for each species.

Usage

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

Arguments

matr   The standard species matrix

Details

The input data is a standard species matrix with rows for plots and column for species.

Value

Returns a vector that contains relative frequency for each species included in the input matrix.

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 data matrix with each column for each species, and each row for each plot.
method	Index of niche overlap to be specified.

Details

To be added.

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

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

---

niche.overlap.boot   *Boostrap of niche overlap*

Description

Bootstrap of niche overlap between species.

Usage

```
niche.overlap.boot(mat, method = c("pianka", "schoener", "petraitis",
    "czech", "morisita", "levins"), times = 999, quant = c(0.025, 0.975))
```

Arguments

mat	A community data matrix with columns representing species, and rows representing sites.
method	A character string indicating the index of niche overlap to be applied.
times	Interger, Number of bootstrap to be implemented.
quant	Quantile of bootstrap results, the confidence intervals.

Details

This function bootstraps the niche overlap within each pair of species. \ pianka: Pianka's niche overlap index\ 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

Niche overlap boostrap utility function

Description

Compute the bootstrap value between two vectors. This is a internal function called by `niche.overlap.boot`, users are encouraged to use the latter function.

Usage

```
niche.overlap.boot.pair(vectorA, vectorB, method = c("levins",
    "schoener", "petraitis", "pianka", "czech", "morisita"),
     times = 999, quant = c(0.025, 0.975))
```

Arguments

vectorA	A numerical vector including species A's abundance or value of importance.
vectorB	A numerical vector including species B's abundance or value of importance.
method	Niche overlap indeces to be applied.
times	Number of bootstraps
quant	Confidence interval of the bootstrap results.

Details

To do.

Value

This function will return a vector including the following elements:\ "Observed", \ "Boot mean", \ "Boot std", \ "Boot CI1", \ "Boot CI2", \ "times" \

Note

Users are ecouraged to call [niche.overlap.boot](#) rather than this function.

Author(s)

Jinlong Zhang <jinlongzhang01@gmail.com>

References

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

See Also

[niche.overlap.boot](#)

Examples

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

---

niche.overlap.pair   *Niche overlap between one pair of species.*

Description

Compute niche overlap index between one pair of species. Users are encouraged to used [niche.overlap](#) istead of this function.

Usage

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

Arguments

vectA	A numerical vector including species A's abundance or value of importance.
vectB	A numerical vector including species B's abundance or value of importance.
method	Niche overlap index to be applied.

Details

None

Value

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

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

---

niche.width   *Niche width*

Description

Compute niche width of the species in a community.

Usage

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

Arguments

mat	A community data matrix with each column for each species, and each row for each plot.
method	Index of niche width.

Details

To be added

Value

A vetor contains niche width index of species in 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

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

---

plotlowertri   *Plotting lower semi matrix*

Description

Function for plotting lower semi matrix. These plots are often used to illustrate the relationship in Pearson's correlation, similarity or dissimilarity index between sites or species.

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 data, often the results of correlation matrix, can also be class dist object.
valuename	Value name that will be used in the legend.
pchlist	The types of point shape to plot see pch par().
interval	Number of intervals to illustrate the shape of points
cex	Point size
ncex	Text size for the add.number, which appeared at the top of each column.

int	Row space between lines in legend
add.number	Species number for each column.
size	Whether the size of points would change according to value.
add.text	To add value to the grid.
show.legend	Whether the legend should be drawn.
digits	Number of digits of for each interval

Details

If the matrix contains less than 15 rows/columns, you may have to adjust the row space between the text lines in the legend, using argument int. Data in class dist can be include, and will be converted to matrix at first internally.

The lower matrix plot illustrating Pearson's Correlation between each pair of species. Note some value didn't appeared in the plots, may have appeared the legend. This is due to the distribution of data. Be careful in selection of intervals. In this situation you may set show.legend = FALSE, and add the legend manually. This may be fixed in the future.

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   *Correlation network plot*

Description

This function could be used to plot correlation network, with less than 15 sites (recommended). The points lie in a circle with lines connected. Blue lines indicate negative values and the red ones the positive ones.

Usage

```
plotnetwork(datainput, interval = 8, xlim = c(-2.5,5),
ylim=c(-3.2,3.2), lty = c(1,2,3,4,4,3,2,1,5), value = "r",
legendx = 3, legendy = 0, right = 1.2, intcept = 0.22,
left = 0.35, linelength = 0.3, cex = 3, lwd = 1.5,
show.legend = TRUE, digits = 2, dit = 1.2,
number.label = TRUE, text.label = TRUE,
linecol = c("red", "black"), ...)
```

Arguments

`datainput`	The correlation matrix, ex. Pearson's correlation matrix
`interval`	Number of intervals of the values, indicating how to partition the range of input data
`xlim`	The x range of the plot. The users need not to change it.
`ylim`	The y range of the plot. The users need not to change it.
`lty`	Line styles used in connection lines for each interval. Must have number of elements + 1.
`value`	Value of the matrix, should be a character, will used in legend.
`legendx`	Legend position x.
`legendy`	Legend position y.
`right`	Legend position adjustment parameter.
`intcept`	Legend position adjustment. can be used to specify the row space between each line for the legend.
`left`	Legend position adjustment parameter.
`linelength`	Line length in the legend.
`cex`	Point size for each circle.
`lwd`	Line width for each circle.
`...`	Other arguments to be passed from.
`show.legend`	Whether the legend should be drawn.
`digits`	Number of digits displayed in legend.
`dit`	Distance of text labels from each corner.
`number.label`	Whether the number label should be drawn.
`text.label`	Whether the text label should be drawn.
`linecol`	Colours of the lines specified. The positive correlation will be drawn in the first colour specified.

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 red or blue, according the sign of the value of association. Users can adjust the line style and legends based on their requirements.

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("orange", "blue"),
number.label = FALSE)

title("Pearson Correlation Network")
```

---

sp.assoc   *Total species association*

Description

Calculate species association

Usage

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

Arguments

matr   standard species matrix , with rows for plots and columns for species.

Details

Calculate species association using the following formula.

Number of plots.

N

Number of species.

S

Number of plots occupied by certain species.

n

total number of species for each plot.

Tj

mean species number for all the plots.

t

Variance of species relative frequency:

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

Return 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

Calculate species association between each pair of species.

Usage

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

Arguments

matr   Standard species matrix, with rows for plots and columns for species.

Details

Assume we have speciesA and speciesB, a, b, c, d that corresponding to the co-occurrence could be used to conduct the species association analysis between the two species.

a = number of plots both occupied by speciesA and speciesB.

b = number of plots only found speciesA.

c = number of plots only found speciesB.

d = number of plots without speciesA or speciesB.

N = a+b+c+d

This function are using the following formula:

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 b*c>= a*d and d>=a:

AC=(a*d − b*c)/((a+b)*(a+c))

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

AC = (a*d − b*c/((b+d)(d+c))

Point correlation coefficient

(PCC):

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

Value

chisq	chi square matrix
chisqass	chi square matrix information
V	V Value indicating species association is positive or negative
Ochiai	Ochiai's index
Dice	Dice's index
Jaccard	Jaccard's index
Pearson	Pearson's correlation
Spearman	Spearman's rank correlation
PCC	Point correlation coefficient
AC	Association coefficient

Author(s)

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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

Zhou XY, Wang BS, Li MG, Zan QJ.(2000). An analysis of interspecific associations in secondary succession forest communities in Heishiding Nature Reserve, Guangdong Province. Acta Phytoecologica Sinica. 24:332-339.

JIAN Minfei, LIU qijing, ZHU du, YOU hai.(2009). Inter-specific correlations among dorminant populations of tree layer species in evergreen broad-leaved forest in Jiulianshan Mountain of subtropical China. Chinese Journal of Plant Ecology. 33: 672-680

See Also

See Also as sp.assoc for species association for total species.

Examples

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

---

splist   *species list used in function add.col()*

Description

A species check list example to be 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)
## add genera from dataframe B to dataframe A.
add.col(inputA = testdata, inputB = splist, add = "genera",
according = "species")
## add family from dataframe B to dataframe A.
add.col(inputA = testdata, inputB = splist, add = "family",
according = "species")
```

---

sub.sp.matrix *Subset species matrix according to relative frequency*

Description

Subset species matrix according to relative frequency.

Usage

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

Arguments

spmatrix   The spmatrix is a standard species matrix with rows for plots and column for
            species.

freq   The value of relative frequency to be specified, species with higher relative fre-
            quency will be reserved in the output matrix.

common   The number of most common (according to relative frequency) species to be
            specified.

Details

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

Value

A subset matrix with certain number of top 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   *Example Data*

Description

Data used in example in list format.

Usage

```
data(testdata)
```

Format

A data frame 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](lab.mat) for converting the vector to matrix of XY labels.

Examples

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

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