

# Package ‘spaa’

August 29, 2016

**Type** Package

**Title** SPecies Association Analysis

**Version** 0.2.2

**Date** 2016-06-09

**Author** Jinlong Zhang [aut, cre]

**Maintainer** Jinlong Zhang <jinlongzhang01@gmail.com>

**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

**Repository** CRAN

**Date/Publication** 2016-06-09 19:59:58

## R topics documented:

spaa-package . . . . .	2
add.col . . . . .	4
data2mat . . . . .	5
datasample . . . . .	6
deg2dec . . . . .	6
dist2list . . . . .	7
freq.calc . . . . .	8
geodist . . . . .	9
lab.mat . . . . .	10
lgeodist . . . . .	11
list2dist . . . . .	12
niche.overlap . . . . .	13
niche.overlap.boot . . . . .	14

niche.overlap.boot.pair . . . . .	15
niche.overlap.pair . . . . .	16
niche.width . . . . .	17
plotlowertri . . . . .	18
plotnetwork . . . . .	20
sp.assoc . . . . .	22
sp.pair . . . . .	24
splist . . . . .	26
sub.sp.matrix . . . . .	27
testdata . . . . .	28
turnover . . . . .	28
XYname . . . . .	30

<b>Index</b>	<b>31</b>
--------------	-----------

---

spaa-package	<i>SPecies Association Analysis</i>
--------------	-------------------------------------

---

## 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	<i>Add one column from A to B, according to one column of common name.</i>
---------	--

---

### Description

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

### Usage

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

### Arguments

inputA	inputA A dataframe which a column to be added according to one row information. 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 column 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 character.
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](#)

**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	<i>community matrix example</i>
------------	---------------------------------

---

**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	<i>Degree to decimal</i>
---------	--------------------------

---

**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 indicates 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	<i>Convert pairwise list to distance matrix</i>
-----------	---

---

## 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	<i>Niche overlap between each pair of species</i>
---------------	---

---

## 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      *Bootstrap 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	Integer, 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 bootstrap utility function*

---

**Description**

Compute the bootstrap value between two vectors. This is an 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**

<code>vectorA</code>	A numerical vector including species A's abundance or value of importance.
<code>vectorB</code>	A numerical vector including species B's abundance or value of importance.
<code>method</code>	Niche overlap indices to be applied.
<code>times</code>	Number of bootstraps
<code>quant</code>	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 encouraged 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](#) instead 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	<i>Niche width</i>
-------------	--------------------

---

**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 vector 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, valuenam = "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.
valuenam	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 dormant 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.
legeny	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.

T<sub>j</sub>

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:

$$S^2\{T\} = \left(\frac{1}{N}\right) \sum_{j=1}^N (T\{j\} - t)^2 .$$

Species relative frequency

$$P\{i\} = \frac{n\{i\}}{N}.$$

Variance ratio:

If  $VR > 1$  Positively associated,

If  $VR < 1$  Negative associated

$$VR = \frac{S\{T\}^2}{\sigma^2\{T\}}$$

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 statistic 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 dormant 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):

$$\chi^2 = \frac{(((a*d-b*c)-0.5*N)^2)*N}{(a+b)*(a+c)*(b+d)*(c+d)}$$

V ratio:

$$V = \frac{((a+d)-(b+c))}{(a + b + c + d)}$$

Jaccard index:

$$\text{Jaccard} = \frac{a}{(a + b + c)}$$

Ochiai index:

$$\text{Ochiai} = \frac{a}{\sqrt{(a+b)*(a+c)}}$$

Dice index:

$$\text{Dice} = \frac{2*a}{(2*a + b + c)}$$

The Association Coefficient(AC):



if  $a*d \geq b*c$ :

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

if  $b*c \geq a*d$  and  $d \geq a$ :

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

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)

Jinlong Zhang <jinlongzhang01@gmail.com>

### References

Zhang Qiaoying, Peng Shaolin, Zhang Sumei, Zhang Yunchun, Hou Yuping.(2008). Association of dormant 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 Phytocologica Sinica. 24:332-339.

JIAN Minfei, LIU qijing, ZHU du, YOU hai.(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: 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	<i>species list used in function add.col()</i>
--------	--

---

**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	<i>Subset species matrix according to relative frequency</i>
---------------	--

---

### 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 frequency 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](#)

**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

- \*Topic **\textasciitildekwd1**
    - niche.overlap, 13
  - \*Topic **\textasciitildekwd2**
    - niche.overlap, 13
  - \*Topic **add**
    - add.col, 4
  - \*Topic **association**
    - sp.assoc, 22
    - sp.pair, 24
    - spaa-package, 2
  - \*Topic **bootstrap**
    - niche.overlap.boot, 14
    - niche.overlap.boot.pair, 15
  - \*Topic **datasets**
    - datasample, 6
    - splist, 26
    - testdata, 28
  - \*Topic **decimal**
    - deg2dec, 6
  - \*Topic **distance**
    - dist2list, 7
    - geodist, 9
    - lgeodist, 11
    - list2dist, 12
  - \*Topic **frequency**
    - freq.calc, 8
    - sub.sp.matrix, 27
  - \*Topic **list**
    - dist2list, 7
  - \*Topic **lower**
    - plotlowertri, 18
  - \*Topic **matrix**
    - data2mat, 5
    - plotlowertri, 18
    - sub.sp.matrix, 27
  - \*Topic **network**
    - plotnetwork, 20
  - \*Topic **niche**
    - niche.overlap.boot, 14
    - niche.overlap.boot.pair, 15
    - niche.overlap.pair, 16
    - niche.width, 17
  - \*Topic **overlap**
    - niche.overlap.boot, 14
    - niche.overlap.boot.pair, 15
    - niche.overlap.pair, 16
  - \*Topic **plot**
    - plotnetwork, 20
  - \*Topic **semimatrix**
    - plotlowertri, 18
  - \*Topic **species**
    - data2mat, 5
    - freq.calc, 8
    - sp.assoc, 22
    - sp.pair, 24
    - spaa-package, 2
  - \*Topic **sub**
    - sub.sp.matrix, 27
  - \*Topic **turnover**
    - lab.mat, 10
    - turnover, 28
    - XYname, 30
- add.col, 4
- data2mat, 5
- datasample, 6
- deg2dec, 6
- dist2list, 7, 12
- freq.calc, 8
- geodist, 9, 11
- lab.mat, 10, 29, 30
- lgeodist, 10, 11
- list2dist, 8, 12
- merge, 4, 5

niche.overlap, [13](#), [16–18](#)  
niche.overlap.boot, [14](#), [15](#), [16](#)  
niche.overlap.boot.pair, [15](#), [15](#)  
niche.overlap.pair, [13](#), [16](#)  
niche.width, [17](#)

plotlowertri, [18](#)  
plotnetwork, [19](#), [20](#)

sp.assoc, [22](#), [25](#)  
sp.pair, [23](#), [24](#)  
spaa (spaa-package), [2](#)  
spaa-package, [2](#)  
splist, [26](#)  
sub.sp.matrix, [27](#)  
subset, [27](#)

testdata, [28](#)  
turnover, [11](#), [28](#)

XYname, [29](#), [30](#)