Package 'MBI'

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Type Package

Title (M)ultiple-site (B)iodiversity (I)ndices Calculator

Version 1.0

Date 2012-10-17

Author Youhua Chen

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Description Over 20 multiple-site diversity indices can be calculated.
Later versions will include phylogenetic diversity

License GPL-2

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`MBI-package` *MBI: (M)ultiple-site (B)iodiversity (I)ndices Calculator*

Description

Over 20 multiple-site beta diversity indices can be calculated. Later versions will include phylogenetic diversity

Details

Package:	MBI
Type:	Package
Version:	1.0
Date:	2012-10-17
License:	GPL-2

Author(s)

Author: Youhua Chen

Maintainer: Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
```

```
batch.calculation(test)
```

`batch.calculation` *calculate all diversity indices at the same time*

Description

calculate all diversity indices at the same time,will return a table, each column indicates one index

Usage

```
batch.calculation(mat)
```

Arguments

`mat`	mat can be in a form of a single matrix, or a list of matrices for batch handling. rows of the data are sites, while columns of the data are species

Details

will return a table, each column indicates one index

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
batch.calculation(test)
```

`cfull` *calculate Baselga's biodiversity index (nestdness+turnover)*

Description

calculate Baselga's biodiversity index (nestdness+turnover)

Usage

```
cfull(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

See Also

`cn`, `ct`, `batch.calculation`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
cfull(test)
```

`cl` *calculate Lennon's multiple-site richness index*

Description

this is a multiple-site version without calculating pairwise Lennon's richness index, see the average version of pairwise Lennon's richness index for comparison: ml()

Usage

```
cl(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Lennon J, Koleff P, Greenwood J, Gaston K (2001) The geographical structure of British bird distributions: diversity, spatial turnover and scale. Journal of Animal Ecology, 70, 966-979.

See Also

`ml`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
cl(test)
```

`cn` *Calculate Baselga's multiple-site nestedness index*

Description

another version is the average of Baselga's pairwise-site nestedness index, see the function of mn()

Usage

```
cn(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Baselga A (2010) Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography, 19, 134-143.

See Also

`ct`, `cfull`, `mn`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
cn(test)
```

`crep` *Calculate Carvalho's multiple-site replacement index*

Description

Another version is the average of Carvalho's pairwise-site replacement index across all pairs of sites, see the function of mrep()

Usage

```
crep(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Carvalho J, Cardoso P, Gomes P (2012) Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. Global Ecology and Biogeography, 21, 760-771.

See Also

`crich`, `mrep`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
crep(test)
```

`crich` *Calculate Carvalho's multiple-site richness difference index*

Description

Another version is the average of Carvalho's pairwise-site richness difference index across all pairs of sites, see the function of mrich()

Usage

```
crich(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Carvalho J, Cardoso P, Gomes P (2012) Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. Global Ecology and Biogeography, 21, 760-771.

See Also

`crep`, `mrich`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
crich(test)
```

`ct` *Calculate Baselga's multiple-site turnover index*

Description

another version is the average of Baselga's pairwise-site turnover index, see the function of mt()

Usage

```
ct(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Baselga A (2010) Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography, 19, 134-143.

See Also

`cn`, `cfull`, `mt`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
ct(test)
```

`do` *Calculate Diserud-Odegaard's index*

Description

See Chen (2012),or Baselga (2010) Diserud and Odegaard (2007) for introduction of the index

Usage

```
do(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Baselga A (2010) Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography, 19, 134-143.

Diserud O, Odegaard F (2007) A multiple-site similarity measure. Biology Letters, 3, 20-22.

See Also

`batch.calculation`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
do(test)
```

`harrison` *Calculate Harrison's dissimilarity index*

Description

See Chen (2012) or Baselga (2010) for introduction of the index

Usage

```
harrison(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Baselga A (2010) Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography, 19, 134-143.

See Also

`batch.calculation`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
harrison(test)
```

`ht` *Calculate Harrison's turnover index*

Description

See Chen (2012) or Baselga (2010) for introduction of the index

Usage

```
ht(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Baselga A (2010) Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography, 19, 134-143.

See Also

`batch.calculation`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
ht(test)
```

`mjaccard` *Calculate the average of Jaccard pairwise-site dissimilarity index across all pairs of sites*

Description

Calculate the average of Jaccard pairwise-site dissimilarity index across all pairs of sites

Usage

```
mjaccard(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

See Also

`batch.calculation`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
mjaccard(test)
```

`ml` *calculate the average Lennon's pairwise-site richness index*

Description

this is the average version of pairwise Lennon's richness index, see a multiple-site version without calculating pairwise Lennon's richness index for comparison: cl()

Usage

```
ml(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Lennon J, Koleff P, Greenwood J, Gaston K (2001) The geographical structure of British bird distributions: diversity, spatial turnover and scale. Journal of Animal Ecology, 70, 966-979.

See Also

`cl`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
ml(test)
```

`mn` *Calculate the average of Baselga's pairwise-site nestedness index across all pairs of sites*

Description

Another version is Baselga's multiple-site nestedness index across all pairs of sites, see the function of cn()

Usage

```
mn(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Baselga A (2010) Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography, 19, 134-143.

See Also

`cn`, `cfull`, `mt`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
mn(test)
```

`mrep` *Calculate the average of Carvalho's pairwise-site replacement index across all pairs of sites*

Description

Another version is Carvalho's multiple-site replacement index, see the function of crep()

Usage

```
mrep(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Carvalho J, Cardoso P, Gomes P (2012) Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. Global Ecology and Biogeography, 21, 760-771.

See Also

`crep`, `mrich`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
mrep(test)
```

`mrich` *Calculate the average of Carvalho's pairwise-site richness difference index across all pairs of sites*

Description

Another version is Carvalho's multiple-site richness difference index, see the function of crich()

Usage

```
mrich(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Carvalho J, Cardoso P, Gomes P (2012) Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. Global Ecology and Biogeography, 21, 760-771.

See Also

`crich`, `mrep`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
mrich(test)
```

`msorensen` *Calculate the average of Sorensen pairwise-site dissimilarity index across all pairs of sites*

Description

Calculate the average of Sorensen pairwise-site dissimilarity index across all pairs of sites

Usage

```
msorensen(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

See Also

`batch.calculation`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
msorensen(test)
```

`mt` *Calculate the average of Baselga's pairwise-site turnover index across all pairs of sites*

Description

Another version is Baselga's multiple-site turnover index across all pairs of sites, see the function of ct()

Usage

```
mt(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Baselga A (2010) Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography, 19, 134-143.

See Also

`ct`, `cfull`, `mn`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
mt(test)
```

`rarity` *Calculate rarity degrees (decided by the argument "percent") based on distributional ranges of species and abundance of species*

Description

argument "percent" determines the rarity degree you want to calculate

Usage

```
rarity(data, percent = 0.3)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species
`percent`	determines the rarity degree you want to calculate. default is .3, meaning that species have distributional sites less than 30

Details

This index is not beta diversity index, thus not being included in the batch.calculation() function

Value

return two percentage values, one denotes the range rarity percentage, another denotes the abundance rarity percentage

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
rarity(test,percent=.3)
```

`wbeta` *Calculate Whittaker's beta diversity index*

Description

See Chen (2012) and Baselga (2010) for introduction of the index, this index can have value larger than 1.

Usage

```
wbeta(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Baselga A (2010) Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography, 19, 134-143.

See Also

`batch.calculation`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
wbeta(test)
```

`wnodf` *Calculate Almeida-Neto and Ulrich's nestedness index*

Description

Calculate Almeida-Neto and Ulrich's nestedness index, can handle both abundance and occurrence situations automatically

Usage

```
wnodf(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Almeida-Neto M, Ulrich W (2011) A straightforward computational approach for measuring nestedness using quantitative matrices. Environmental Modelling and Software, 26, 173-178.

Almeida-Neto M, Guimaraes P, Guimaraes P, Loyola R, Ulrich W (2008) A consistent metric for nestedness analysis in ecological systems: reconciling concept and measurement. Oikos, 117, 1227-1239.

See Also

batch.calculation

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
wnodf(test)
```

`wt` *Calculate Williams's turnover index*

Description

See Chen (2012) or Baselga (2010) for introduction of the index

Usage

```
wt(data)
```

Arguments

`data`	rows of the data are sites, while columns of the data are species

Author(s)

Youhua Chen <haydi@126.com>

References

Chen Y (2012) MBI: an R package for calculating multiple-site biodiversity indices. Submitted.

Baselga A (2010) Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography, 19, 134-143.

See Also

`batch.calculation`

Examples

```
test<-c(90,30,11,5,100,46,19,70,19,1,
        17,0,0,0,30,4,20,26,12,5,37,
0,25,0,60,30,29,42,36,19,32,
12,0,0,50,6,39,35,18,0,35,0,
28,0,70,35,56,49,42,0,81,15,
36,0,90,45,72,63,54,9,13,0,
0,5,20,1,4,0,0,0,0,0,0,0,10,
0,0,0,41,4,72,24,7,0,80,1,64,
56,48,0,36,0,29,0,40,32,32,2,0,0)
test<-matrix(test,10,10)
wt(test)
```

Index