Package ‘MBI’

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Later versions will include phylogenetic diversity
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MBI-package

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


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,
       0,5,20,1,4,0,0,0,0,0,10,
       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**

`batch.calculation(test)`

---

**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**


**Examples**

```r
  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, 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


See Also

cn, ct, batch.calculation

Examples

test<-c(90,30,11,5,100,46,19,70,19,1,
       17,0,0,30,4,20,26,12,5,37,
       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,
       36,0,90,45,72,63,54,9,13,10,
       8,5,20,1,4,0,10,0,0,0,10,
       0,0,0,41,4,72,24,7,0,80,1,64,
       0,0,0,41,0,36,0,29,0,40,32,2,0,0)
test<-matrix(test,10,10)
cfull(test)
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

c1(data)

Arguments

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

Author(s)

Youhua Chen <haydi@126.com>

References


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)
c1(test)
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

\texttt{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


See Also

cf, cfull, mn

Examples

```
test<-(90, 30, 11, 5, 100, 46, 19, 70, 19, 1, 17, 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, 20, 1, 4, 0, 0, 0, 0, 0, 10, 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)
```
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

See Also
crich, mrep

Examples
```r
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,
       0,5,20,1,4,0,0,0,0,0,10,
       0,0,1,4,2,4,24,7,80,1,64,
       56,48,0,36,0,29,0,40,32,2,0,0)
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


See Also

crep, mrich

Examples

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

c(t(data)

Arguments

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

Author(s)

Youhua Chen <haydi@126.com>

References


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,
0,5,20,1,4,0,0,0,0,0,10,
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)
test(test)
ct(test)
Calculate Diserud-Odegaard's index

Description


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


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,
56,48,0,36,0,29,0,48,32,32,2,0,0)
test<-(matrix(test,10,10)
do(test)
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

See Also
batch.calculation

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


See Also

data
calculated

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, 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)
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

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**

```r
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**


**See Also**

c1

**Examples**

```r
test <- c(90, 30, 11, 5, 100, 46, 19, 70, 19, 1,
          17, 0, 0, 0, 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, 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

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, 
0,5,20,1,4,0,0,0,0,0,10, 
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


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, 0,0,0,41,4,72,24,7,80,1,64, 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


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,
0,5,20,1,4,0,0,0,0,0,10,
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**

```r
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**


**See Also**

`batch.calculation`

**Examples**

```r
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, 10, 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)
test<-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


See Also

c.t, cfull, mn

Examples

test<-c(90, 30, 11, 5, 100, 46, 19, 70, 19, 1, 17, 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)
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


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,
       0,0,0,41,4,72,24,7,80,1,64,
       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


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,
       0,5,20,1,4,0,0,0,0,0,10,
       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)
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


See Also

batch.calculation

Examples

test<-(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,
  0,5,20,1,4,0,0,0,0,0,10,
  0,0,0,41,4,72,24,7,0,80,1,64,
  56,48,0,36,0,29,0,48,32,32,2,0,0)
test<-matrix(test,10,10)
wnodf(test)
Calculate Williams's turnover index

Description


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


See Also

batch.calculation

Examples

test<-c(90, 30, 11, 5, 100, 46, 19, 70, 19, 1, 17, 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, 0, 10, 0, 0, 4, 4, 7, 0, 80, 1, 64, 56, 48, 0, 36, 0, 29, 0, 40, 32, 32, 2, 0, 0)
test<-matrix(test, 10, 10)
test<-matrix(test, 10, 10)
wt(test)
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