

Package ‘SpeciesPool’

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Title Plot-specific species pools based on Beal's smoothing

Version 0.0.0.9000

Description Function to calculate the plot-specific species pool, based on a vegetation database and Beals' smoothing.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Depends dplyr,
Matrix,
dismo,
tidyr,
reshape2,
SpadeR,
vegan,
parallel,
doParallel,
foreach

R topics documented:

| | |
|-----------------------------|---|
| beals.all | 1 |
| bray.curtis | 2 |
| Mij.calc | 3 |
| SAR.IIIb | 3 |
| SpeciesPool_sPlot | 4 |

| | |
|--------------|----------|
| Index | 5 |
|--------------|----------|

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| beals.all | <i>Beals' smoothing</i> |
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Description

Calculates Beals' smoothing for all species in a target plot, based on Mij matrix

Usage

```
beals.all(x.names, x.cover, Mij)
```

Arguments

`x.names` vector of species names or labels
`x.cover` vector of species presence-absences
`Mij` Matrix of pairwise likelihood of species co-occurrence (Sparse matrices accepted)

Value

A vector of bray-curtis dissimilarity between the target and all the other relevés in `input.data`

Author(s)

Francesco Maria Sabatini
 Helge Bruelheide

References

Ewald, J. (2002) Multiple controls of understorey plant richness in mountain forests of the Bavarian Alps. *Phytocoenologia*, 32, 85-100.

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| <code>bray.curtis</code> | <i>Bray-Curtis dissimilarity</i> |
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Description

Calculates Bray-Curtis dissimilarity between a target plot, and all the other plots in the dataset

Usage

```
bray.curtis(input.data, target.plot.ID)
```

Arguments

`input.data` A species x relevés matrix with abundance values
`target.plot.ID` ID or label of target plot

Value

A vector of bray-curtis dissimilarity between the target and all the other relevés in `input.data`

Author(s)

Francesco Maria Sabatini
 Helge Bruelheide

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| Mij.calc | <i>Pairwise likelihood of species co-occurrence</i> |
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Description

Intermediate step to calculate Beals' smoothing

Usage

```
Mij.calc(dt, verbose = F)
```

Arguments

dt A data.frame with three columns: releve ID, species ID, and abundance

Value

Returns a square matrix of the likelihood of pairwise species co-occurrence

Author(s)

Francesco Maria Sabatini
Helge Bruelheide

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| SAR.IIIb | <i>Rarefaction curves</i> |
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Description

Builds an empirical rarefaction curve

Usage

```
SAR.IIIb(x, areas, n = 10)
```

Arguments

x A vector of species richness
areas A vector of plot sizes
n numeric - number of intervals of rarefaction curve

Value

Returns a dataframe of cumulative richness and pooled plot areas

Author(s)

Francesco Maria Sabatini
Helge Bruelheide

SpeciesPool_sPlot *Species pool based on Beal's smoothing*

Description

For each relevé, this function selects all neighbouring relevé having a similar potential species composition, and fits empirical non-linear functions to rarefaction curves.

Usage

```
SpeciesPool_sPlot(input.data, coords, Mij = NULL, ncores = 1,
  rows = NULL, t.radius = 20000, t.bray = 0.2, t.plot.number = 10L,
  verbose = T, species.list = F)
```

Arguments

| | |
|---------------|--|
| input.data | data.frame of species abundances across relevés. It should have three columns: Relevé ID, Species ID, and species abundance |
| coords | A SpatialPointsDataFrame with the geographic coordinates of all plots. It should have Relevé ID and areas defined in the @data |
| Mij | Matrix of pairwise likelihood of species co-occurrence (Sparse matrices accepted) |
| ncores | integer indicating the number of cores to use. If ncores>1 the calculation will be done in parallel |
| rows | a vector of integers indicating on which rows of input.data the function should run |
| t.radius | Threshold of geographic buffer around target relevé |
| t.bray | Threshold of bray-curtis dissimilarity for selection relevé compositionally similar to target relevé |
| t.plot.number | Minimum number of neighbouring relevés for calculating rarefaction curves |
| verbose | logical |
| species.list | logical - Should the list of species composing the species pool be returned? |

Value

Returns a dataframe containing for each relevé: Species - the number of species observed across all relevé neighbouring the target relevé Chao, iChao2, jack1, jack2 - various species richness estimates, standard errors, as derived from the function SpadeR::ChaoSpecies nplots - number of relevés within a t.radius distance from the target relevé having a bray-curtis dissimilarity lower than t.bray beals.at.chao - cut-off of Beals' occurrence likelihood, selected as the ith species corresponding to chao n.plots.area - number of relevés within a t.radius distance, and t.bray dissimilarity from target relevés for which area data is available arr, gomp, mm, Asymp - parameter estimates for different empirical non-linear functions fitted to rarefaction curves, with relative AIC sp.pool.list - list of species compatible with target relevé, i.e. having a Beals' likelihood lower than beals.at.chao

Author(s)

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Index

beals.all, [1](#)

bray.curtis, [2](#)

Mij.calc, [3](#)

SAR.IIIb, [3](#)

SpeciesPool_sPlot, [4](#)