

Package ‘SpeciesPool’

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

Version 0.0.0.9000

Description Set of functions 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

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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.

bray.curtis	<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

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

SAR.IIIb

Rarefaction curves

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

Species pool based on Beal's smoothing

Description

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

Usage

```
SpeciesPool(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

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