Package 'SpeciesPool'

June 16, 2020

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

Version 0.0.1.9001

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 7.1.0

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

R topics documented:

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beals.all	*Beals' smoothing*

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 plot 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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bray.curtis	*Bray-Curtis dissimilarity*

Description

Calculates Bray-Curtis dissimilarity between a target plot, and all the other relevés 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 dissimilarities between the target and all the other relevés in input.data

Author(s)

Francesco Maria Sabatini

Helge Bruelheide

Mij.calc   *Pairwise likelihood of species co-occurrence*

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

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SpeciesPool	*Species pool based on Beal's smoothing*

Description

For each relevé, this function selects all neighbouring relevés 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,
  cutoff = c("iChao2", "Gompertz", "Michaelis"),
  verbose = T,
  species.list = F,
  mycrs = NULL,
  lonlat = NULL
)
```

Arguments

input.data	data.frame of species abundances across relevés. It should have three columns: one with Relevé IDs, one with Species ID, and one with species abundance/cover values

coords	Either a SpatialPointsDataFrame or a DataFrame with the geographic coordinates of all plots. If SpatialPointsDataframe, it should have Relevé IDs and areas defined in the data. If DataFrame, columns 1:2 should be coordinates (Long, Lat), columns 3:4 should be RelevèIDs and plot area, respectively.
Mij	matrix of pairwise likelihood of species co-occurrence (sparse matrices accepted). If not provided, it will be calculated from the data
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 plots of the input.data the function should run
t.radius	threshold of geographic buffer around target relevé
t.bray	threshold of Bray-Curtis dissimilarity for selecting relevés compositionally similar to target relevé
t.plot.number	minimum number of neighbouring relevés for calculating rarefaction curves
cutoff	method used to estimate the size of the species pool. Default is 'iChao2', other possible are 'Gompertz' or 'Michaelis'
verbose	logical
species.list	logical: Should the list of species composing the species pool be returned?
mycrs	a CRS object defining the coordinate reference of coords, if coords is a data.frame
lonlat	Specify whether the CRS is projected (lonlat=T) or unprojected (lonlat=F)

Value

Returns a dataframe containing for each relevé: - Species - the number of species observed across all relevés neighouring the target relevé

- Chao, iChao2, jack1, jack2 - various species richness estimates and 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)

Francesco Maria Sabatini

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