

# Package ‘SpeciesPool’

August 12, 2019

**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,  
sp,  
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.

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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

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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

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,
  cutoff = c("Chao", "Gompertz", "Michaelis"), 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 <code>SpatialPointsDataFrame</code> with the geographic coordinates of all plots. It should have Relevé ID and areas defined in the <code>@data</code>
<code>Mij</code>	Matrix of pairwise likelihood of species co-occurrence (Sparse matrices accepted). If not provided, it will be calculated from the data
<code>ncores</code>	integer indicating the number of cores to use. If <code>ncores&gt;1</code> the calculation will be done in parallel
<code>rows</code>	a vector of integers indicating on which rows of <code>input.data</code> 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>cutoff</code>	Which method to use to set the size of the species pool. Default is 'iChao2', other possible are 'Gompertz' or 'Michaelis'
<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 *i*th 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

Helge Bruelheide

**Examples**

```
load(GVRD_test_data.RData) ## data provided separately, make sure it's in working directory
aa <- SpeciesPool(DT.fb, mycoords, ncores=3, rows=1:100, t.radius=20000, t.bray=0.2, t.plot.number=10L, verbose=
```

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