

Package ‘betadiv’

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Type Package

Title Estimators of Multiple-Site Dissimilarity Indices for the Assessment of Beta Diversity

Version 1.0.1

Author Mathieu Fortin, Anna Kondratyeva, Rosalinde Van Couwenberghe

Maintainer Mathieu Fortin <mathieu.fortin.re@gmail.com>

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Description Implement the multiple-site dissimilarity indices of Simpson, Sorensen and nestedness, which can be used to assess the beta diversity of a population. These indices were adapted from those developed by Baselga (2010) <doi:10.1111/j.1466-8238.2009.00490.x> in order to have them population size-independent. All the details behind the calculation and estimation of these adapted indices can be found in Fortin et al. (2020) <doi:10.1111/geb.13080>.

URL <https://sourceforge.net/p/mrnfforesttools/divindices/wiki/Home/>

Depends R (>= 3.4.0)

Imports J4R (>= 1.0.8)

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

SystemRequirements Java 8

Suggests testthat

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`getDissimilarityEstimates`*Estimate Dissimilarity Indices*

Description

This function computes estimates of the adapted dissimilarity indices of Simpson, Sorensen and nestedness from a sample.

Usage

```
getDissimilarityEstimates(  
  dataset,  
  plotIdField,  
  speciesIdField,  
  populationSize,  
  memSize = NULL  
)
```

Arguments

<code>dataset</code>	a data.frame object that contains at least two fields: one for the sample plot ids and the other for the species. Each row is actually an observation of a species in a particular plot.
<code>plotIdField</code>	the name of the field that contains the sample plot id in the dataset.
<code>speciesIdField</code>	the name of the field that contains the species in the dataset.
<code>populationSize</code>	the number of units in the population. That is the total number of sample plots that could fit in the population. Under the assumption that the plot size is constant, the population size is calculated as the area of the population divided by the area of a single sample plot.
<code>memSize</code>	the size of the Java Virtual Machine in Mg (if not specified the JVM is instantiated with the default memory size, which depends on the available RAM)

Details

The dissimilarity indices were adapted from those of Baselga (2010). These adapted indices are population size independent so that it is possible to compare the dissimilarity of two populations of unequal sizes.

This function implements estimators of these adapted indices. A sample of plots with species observations must be passed to the function as well as the population size, that is the number of plots that fit in this population. The variance estimation is based on the Jackknife method. The function returns a data.frame object with the estimates of the multiple-site version of Simpson, Sorensen and nestedness as well as their associated standard errors. In addition, the function also provides an estimate of the alpha and gamma diversity. The gamma diversity estimate is based on the Chao2 estimator (Chao and Lin 2012).

Value

a data.frame object with the estimated dissimilarity indices and their standard errors

References

Fortin, M., A. Kondratyeva, and R. Van Couwenberghe. 2020. Improved Beta-diversity estimators based on multiple-site dissimilarity: Distinguishing the sample from the population. *Global Ecology and Biogeography* 29: 1073-1084. <https://doi.org/10.1111/geb.13080>

Baselga, A. 2010. Partitioning the turnover and nestedness components of beta diversity. *Global Ecology and Biogeography* 19:134-143.

Chao A., and C.-W Lin. 2012. Nonparametric lower bounds for species richness and shared species richness under sampling without replacement. *Biometrics* 68: 912-921.

Examples

```
### An example using the subsetUrbanEnvironmentNancy dataset ###
## Not run:
dataRelevés <- betadiv::subsetUrbanEnvironmentNancy

strataList <- unique(dataRelevés$Stratum)
output <- NULL
baselga <- NULL
stratum <- strataList[1]

for (stratum in strataList) {
  releve.s <- dataRelevés[which(dataRelevés$Stratum == stratum),]
  if (stratum == "forest") {
    populationSize <- 3089 * 10000 / (pi * 5^2)
  } else if (stratum == "parking") {
    populationSize <- 501 * 10000 / (pi * 5^2)
  } else {
    populationSize <- 100000
  }

  indices <- getDissimilarityEstimates(releve.s, "CODE_POINT", "Espece",
                                     populationSize, memSize = 500)

  indices$stratum <- stratum
  output <- rbind(output, indices)
}

## End(Not run)
```

subsetUrbanEnvironmentNancy

Data from Urban Environments in Nancy, France

Description

A subset of a two-phase inventory that was carried out in Nancy, Eastern France, in 2015

Usage

```
data(subsetUrbanEnvironmentNancy)
```

Format

An object of class `data.frame` with 287 rows and 8 columns.

Examples

```
data(subsetUrbanEnvironmentNancy)
```

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