

Package ‘betapart’

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Type Package

Title Partitioning Beta Diversity into Turnover and Nestedness
Components

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Imports ape, geometry, picante, rccd

Suggests vegan

Description Functions to compute pair-wise dissimilarities (distance matrices) and multiple-site dissimilarities, separating the turnover and nestedness-resultant components of taxonomic (incidence and abundance based), functional and phylogenetic beta diversity.

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bbsData	<i>BBS data by state for two timeslices</i>
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Description

The data consists of binary presence/absence matrices for 569 bird species across 49 US states for two time slices (1980 - 1985 and 2000 - 2005). Only species (identified by AOU number) recorded during both time periods are included. The data are taken from the North American Breeding Bird Survey dataset and from a version of the database downloaded in May 2009.

Usage

```
data(bbsData)
```

Format

Two matrices (bbs1980 and bbs2000) of identical structure showing the presence/absence of the species as binary data.

state US states by USPS two letter codes.

aou Species identity by AOU species ID numbers.

Source

<http://www.pwrc.usgs.gov/BBS/>

Examples

```
data(bbsData)
str(bbs1980)
str(bbs2000)
```

beta.multi	<i>Multiple-site dissimilarities</i>
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Description

Computes 3 multiple-site dissimilarities accounting for the spatial turnover and the nestedness components of beta diversity, and the sum of both values

Usage

```
beta.multi(x, index.family="sorensen")
```

Arguments

x	data frame, where rows are sites and columns are species. Alternatively x can be a betapart object derived from the betapart.core function
index.family	family of dissimilarity indices, partial match of "sorensen" or "jaccard".

Value

The function returns a list with the three multiple site dissimilarity values.

For index.family="sorensen" the three indices are:

beta.SIM	value of the turnover component, measured as Simpson dissimilarity
beta.SNE	value of the nestedness component, measured as Nestedness-resultant fraction of Sorensen dissimilarity
beta.SOR	value of the overall beta diversity, measured as Sorensen dissimilarity

For index.family="jaccard" the three indices are:

beta.JTU	value of the turnover component, measured as turnover fraction of Jaccard dissimilarity
beta.JNE	value of the nestedness component, measured as Nestedness-resultant fraction of Jaccard dissimilarity
beta.JAC	value of the overall beta diversity, measured as Jaccard dissimilarity

Author(s)

Andrés Baselga and David Orme

References

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

Baselga, A. 2012. The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232

See Also

[beta.pair](#), [beta.sample](#), [betapart.core](#), [beta.temp](#)

Examples

```
data(ceram.s)
ceram.beta<-beta.multi(ceram.s, index.family="sor")
```

beta.multi.abund	<i>Abundance-based multiple-site dissimilarities</i>
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Description

Computes 3 multiple-site dissimilarities accounting for the (i) balanced variation and (ii) abundance gradient components of dissimilarity, and the sum of both values (i.e. total abundance-based dissimilarity)

Usage

```
beta.multi.abund(x, index.family="bray")
```

Arguments

x	data frame, where rows are sites and columns are species. Alternatively x can be a <code>betapart.abund</code> object derived from the <code>betapart.core.abund</code> function
index.family	family of dissimilarity indices, partial match of "bray" or "ruzicka".

Value

The function returns a list with the three multiple site dissimilarity values.

For `index.family="bray"` the three indices are:

beta.BRAY.BAL	value of the balanced variation component of Bray-Curtis multiple-site dissimilarity
beta.BRAY.GRA	value of the abundance-gradient component of Bray-Curtis multiple-site dissimilarity
beta.BRAY	value of the overall dissimilarity, measured as Bray-Curtis multiple-site dissimilarity

For `index.family="ruzicka"` the three indices are:

beta.RUZ.BAL	value of the balanced variation component of Ruzicka multiple-site dissimilarity
beta.RUZ.GRA	value of the abundance-gradient component of Ruzicka multiple-site dissimilarity
beta.RUZ	value of the overall dissimilarity, measured as Ruzicka multiple-site dissimilarity

Author(s)

Andrés Baselga

References

Baselga, A. 2017. Partitioning abundance-based multiple-site dissimilarity into components: balanced variation in abundance and abundance gradients. *Methods in Ecology and Evolution*, in press

See Also

[beta.pair.abund](#), [beta.sample.abund](#), [betapart.core.abund](#), [beta.multi](#)

Examples

```
require(vegan)
data(BCI)
beta.multi.abund(BCI, index.family="bray")
```

beta.pair

Incidence-based pair-wise dissimilarities

Description

Computes 3 distance matrices accounting for the (i) turnover (replacement), (ii) nestedness-resultant component, and (iii) total dissimilarity (i.e. the sum of both components).

Usage

```
beta.pair(x, index.family = "sorensen")
```

Arguments

`x` data frame, where rows are sites and columns are species. Alternatively `x` can be a `betapart` object derived from the `betapart.core` function

`index.family` family of dissimilarity indices, partial match of "sorensen" or "jaccard".

Value

The function returns a list with three dissimilarity matrices. For `index.family="sorensen"` the three matrices are:

`beta.sim` `dist` object, dissimilarity matrix accounting for spatial turnover (replacement), measured as Simpson pair-wise dissimilarity

`beta.sne` `dist` object, dissimilarity matrix accounting for nestedness-resultant dissimilarity, measured as the nestedness-fraction of Sorensen pair-wise dissimilarity

`beta.sor` `dist` object, dissimilarity matrix accounting for total dissimilarity, measured as Sorensen pair-wise dissimilarity (a monotonic transformation of beta diversity)

For `index.family="jaccard"` the three matrices are:

<code>beta.jtu</code>	dist dissimilarity matrix accounting for spatial turnover, measured as the turnover-fraction of Jaccard pair-wise dissimilarity
<code>beta.jne</code>	dist object, dissimilarity matrix accounting for nestedness-resultant dissimilarity, measured as the nestedness-fraction of Jaccard pair-wise dissimilarity
<code>beta.jac</code>	dist object, dissimilarity matrix accounting for beta diversity, measured as Jaccard pair-wise dissimilarity (a monotonic transformation of beta diversity)

Author(s)

Andrés Baselga and David Orme

References

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

Baselga, A. 2012. The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232

See Also

[beta.pair.abund](#), [codebeta.multi](#), [beta.sample](#), [betapart.core](#), [beta.temp](#)

Examples

```
data(ceram.s)
ceram.dist<-beta.pair(ceram.s, index.family="jac")
```

<code>beta.pair.abund</code>	<i>Abundance-based pair-wise dissimilarities</i>
------------------------------	--

Description

Computes 3 distance matrices accounting for the (i) balanced variation in abundances, (ii) abundance gradients, and (iii) total dissimilarity (i.e. the sum of both components).

Usage

```
beta.pair.abund(x, index.family = "bray")
```

Arguments

<code>x</code>	data frame, where rows are sites and columns are species. Alternatively <code>x</code> can be a <code>betapart.abund</code> object derived from the <code>betapart.core.abund</code> function
<code>index.family</code>	family of dissimilarity indices, partial match of "bray" or "ruzicka".

Value

The function returns a list with three dissimilarity matrices. For `index.family="bray"` the three matrices are:

<code>beta.bray.bal</code>	dist object, dissimilarity matrix accounting for the dissimilarity derived from balanced variation in abundance between sites
<code>beta.bray.gra</code>	dist object, dissimilarity matrix accounting for the dissimilarity derived from unidirectional abundance gradients
<code>beta.bray</code>	dist object, dissimilarity matrix accounting for total abundance-based dissimilarity between sites, measured as the Bray-Curtis index

For `index.family="ruzicka"` the three matrices are:

<code>beta.ruz.bal</code>	dist object, dissimilarity matrix accounting for the dissimilarity derived from balanced variation in abundance between sites
<code>beta.ruz.gra</code>	dist object, dissimilarity matrix accounting for the dissimilarity derived from unidirectional abundance gradients
<code>beta.ruz</code>	dist object, dissimilarity matrix accounting for total abundance-based dissimilarity between sites, measured as the Ruzicka index

Author(s)

Andrés Baselga

References

Baselga, A. 2013. Separating the two components of abundance-based dissimilarity: balanced changes in abundance vs. abundance gradients. *Methods in Ecology and Evolution* 4: 552–557

Legendre, P. 2014. Interpreting the replacement and richness difference components of beta diversity. *Global Ecology and Biogeography*, 23: 1324–1334

See Also

[beta.multi.abund](#), [beta.sample.abund](#), [betapart.core.abund](#), [beta.pair](#)

Examples

```
require(vegan)
data(BCI)
BCI.pair<-beta.pair.abund(BCI, index.family="bray")
```

beta.sample	<i>Resampling multiple-site dissimilarity for n sites</i>
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Description

Resamples the 3 multiple-site dissimilarities (turnover, nestedness-resultant fraction, and overall beta diversity) for a subset of sites of the original data frame.

Usage

```
beta.sample(x, index.family="sorensen", sites=nrow(x$data), samples = 1)
```

Arguments

x	data frame, where rows are sites and columns are species. Alternatively x can be a betapart object derived from the betapart.core function.
index.family	family of dissimilarity indices, partial match of "sorensen" or "jaccard".
sites	number of sites for which multiple-site dissimilarities will be computed. If not specified, default is all sites.
samples	number of repetitions. If not specified, default is 1.

Value

The function returns a list with a dataframe with the resampled 3 multiple-site dissimilarities (turnover fraction, nestedness-resultant fraction and overall dissimilarity; see [beta.multi](#)), a vector with the respective means and a vector with the respective standard deviation.

For index.family="sorensen":

sampled.values	dataframe containing beta.SIM, beta.SNE and beta.SOR for all samples
mean.values	vector containing the mean values of beta.SIM, beta.SNE and beta.SOR among samples
sd.values	vector containing the sd values of beta.SIM, beta.SNE and beta.SOR among samples

For index.family="jaccard":

sampled.values	dataframe containing beta.JTU, beta.JNE and beta.JAC for all samples
mean.values	vector containing the mean values of beta.JTU, beta.JNE and beta.JAC among samples
sd.values	vector containing the sd values of beta.JTU, beta.JNE and beta.JAC among samples

Author(s)

Andrés Baselga and David Orme

References

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

Baselga, A. 2012. The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232

See Also

[beta.multi](#), [beta.sample](#), [beta.temp](#)

Examples

```
# Read the data for Northern and Southern European cerambycids
data(ceram.s)
data(ceram.n)

# Resample 100 times the multiple-site dissimilarities
# for 10 countries.
beta.ceram.s<-beta.sample(ceram.s, index.family="sor", sites=10, samples=100)
beta.ceram.n<-beta.sample(ceram.n, index.family="sor", sites=10, samples=100)

# Plot the distributions of beta.SIM in Southern Europe (red)
# and Northern Europe (blue)
plot(density(beta.ceram.s$sampled.values$beta.SIM), col="red", xlim=c(0,1))
lines(density(beta.ceram.n$sampled.values$beta.SIM), col="blue")

# Compute the p-value of difference in beta.SIM between South and North
# (i.e. the probability of finding in the North a higher value than
# in the South)
p.value.beta.SIM<-length(which(beta.ceram.s$sampled.values$beta.SIM<
beta.ceram.n$sampled.values$beta.SIM))/100

p.value.beta.SIM
# The result is 0 and we used 100 samples, so p<0.01
```

beta.sample.abund *Resampling abundance-based multiple-site dissimilarity for n sites*

Description

Resamples the 3 abundance-based multiple-site dissimilarities (balanced variation fraction, abundance-gradient fraction, and overall dissimilarity) for a subset of sites of the original data frame.

Usage

```
beta.sample.abund(x, index.family="bray", sites = nrow(x), samples = 1)
```

Arguments

<code>x</code>	data frame, where rows are sites and columns are species
<code>index.family</code>	family of dissimilarity indices, partial match of "bray" or "ruzicka".
<code>sites</code>	number of sites for which multiple-site dissimilarities will be computed. If not specified, default is all sites.
<code>samples</code>	number of repetitions. If not specified, default is 1.

Value

The function returns a list with a dataframe with the resampled 3 multiple-site dissimilarities (balanced variation fraction, abundance-gradient fraction and overall dissimilarity; see [beta.multi.abund](#)), a vector with the respective means and a vector with the respective standard deviation.

For `index.family="bray"`:

<code>sampled.values</code>	dataframe containing <code>beta.BRAY.BAL</code> , <code>beta.BRAY.GRA</code> and <code>beta.BRAY</code> for all samples
<code>mean.values</code>	vector containing the mean values of <code>beta.BRAY.BAL</code> , <code>beta.BRAY.GRA</code> and <code>beta.BRAY</code> among samples
<code>sd.values</code>	vector containing the sd values of <code>beta.BRAY.BAL</code> , <code>beta.BRAY.GRA</code> and <code>beta.BRAY</code> among samples

For `index.family="ruzicka"`:

<code>sampled.values</code>	dataframe containing <code>beta.RUZ.BAL</code> , <code>beta.RUZ.GRA</code> and <code>beta.RUZ</code> for all samples
<code>mean.values</code>	vector containing the mean values of <code>beta.RUZ.BAL</code> , <code>beta.RUZ.GRA</code> and <code>beta.RUZ</code> among samples
<code>sd.values</code>	vector containing the sd values of <code>beta.RUZ.BAL</code> , <code>beta.RUZ.GRA</code> and <code>beta.RUZ</code> among samples

Author(s)

Andrés Baselga

References

Baselga, A. 2017. Partitioning abundance-based multiple-site dissimilarity into components: balanced variation in abundance and abundance gradients. *Methods in Ecology and Evolution*, in press

See Also

[beta.multi.abund](#), [beta.sample](#)

Examples

```
require(vegan)
data(BCI)
beta.sample.abund(BCI, index.family="bray", sites=10, samples=100)
```

beta.temp	<i>Temporal change in community composition</i>
-----------	---

Description

Computes the dissimilarity for each locality between time 1 and time 2, considering the turnover and nestedness components of temporal change, and the sum of both values (overall change)

Usage

```
beta.temp(x, y, index.family="sorensen")
```

Arguments

x	data frame for time 1, where rows are sites and columns are species
y	data frame for time 2, where rows are sites and columns are species. x and y must contain exactly the same sites and species
index.family	family of dissimilarity indices, partial match of "sorensen" or "jaccard".

Value

The function returns a data frame where rows are sites and columns are pairwise dissimilarity values between cell composition in time 1 and time 2. For `index.family="sorensen"` the indices are `beta.sim`, `beta.sne`, and `beta.sor`. For `index.family="jaccard"` the indices are `beta.jtu`, `beta.sne`, and `beta.jac`.

Author(s)

Andrés Baselga and David Orme

References

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

Baselga, A. 2012. The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232

See Also

[beta.multi](#), [beta.pair](#), [beta.sample](#), [betapart.core](#),

Examples

```
data(bbsData)
bbs.t <- beta.temp(bbs1980, bbs2000, index.family="sor")
```

Description

betapart allows computing pair-wise dissimilarities (distance matrices) and multiple-site dissimilarities, separating the turnover and nestedness-resultant components of taxonomic (incidence and abundance based), functional and phylogenetic beta diversity.

Details

The partitioning of incidence-based dissimilarity can be performed for two different families of indices: Sorensen and Jaccard. The pairwise function `beta.pair` yields 3 distance matrices accounting for the spatial turnover and the nestedness components of beta-diversity. The third distance matrix accounts for the sum of both components, i.e. total dissimilarity (a monotonic transformation of beta diversity). The multiple site function `beta.multi` yields the spatial turnover and the nestedness components of overall dissimilarity, and the sum of both components, total dissimilarity. The basic calculations for all these multiple-site measures and pairwise dissimilarity matrices can be computed using the function `betapart.core`, which returns an object of class `betapart`. This is useful for large datasets as the consuming calculations are done only once, and its result can then be used for computing many indices. The multiple-site values can be randomly sampled a specified number of times for a specified number of sites using the function `beta.sample`. The aforementioned indices used for assessing spatial patterns can also be used for measuring temporal changes in community composition with the function `beta.temp`. Likewise, an analogous framework has been implemented for separating the two components of abundance-based dissimilarity (balanced changes in abundance vs. abundance gradients) using commands `beta.pair.abund`, `beta.multi.abund`, `betapart.core.abund`, and `beta.sample.abund`. The framework has been extended for functional beta diversity with commands `functional.betapart.core`, `functional.beta.pair` and `functional.beta.multi`, and for phylogenetic beta diversity with commands `phylo.betapart.core`, `phylo.beta.pair` and `phylo.beta.multi`.

Author(s)

Andrés Baselga, David Orme, Sébastien Vileger, Julien De Bortoli and Fabien Leprieur

References

- Baselga, A. 2010. Partitioning the turnover and nestedness components of beta diversity. *Global Ecology and Biogeography* 19:134-143
- Baselga, A. 2012. The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232
- Baselga, A. 2013. Separating the two components of abundance-based dissimilarity: balanced changes in abundance vs. abundance gradients. *Methods in Ecology and Evolution*, 4: 552-557
- Baselga, A. 2017. Partitioning abundance-based multiple-site dissimilarity into components: balanced variation in abundance and abundance gradients. *Methods in Ecology and Evolution*, in press

Baselga A, Leprieur, F. 2015. Comparing methods to separate components of beta diversity. *Methods in Ecology and Evolution* 6: 1069-1079

Baselga A, Orme CDL. 2012. betapart: an R package for the study of beta diversity. *Methods Ecol. Evol.* 3: 808-812

Legendre P. 2014. Interpreting the replacement and richness difference components of beta diversity. *Global Ecology and Biogeography*, 23: 1324–1334

Leprieur F, Albouy C, De Bortoli J, Cowman PF, Belwood DR, Mouillot D. 2012. Quantifying phylogenetic beta diversity: distinguishing between "true" turnover of lineages and phylogenetic diversity gradients. *PLoS One* 7(8): e42760

Villéger, S. Grenouillet, G., Brosse, S. 2013. Decomposing functional beta-diversity reveals that low functional beta-diversity is driven by low functional turnover in European fish assemblages. *Global Ecology and Biogeography*, 22: 671-681

betapart.core

Core calculations of betapart

Description

Computes the basic quantities needed for computing the multiple-site beta diversity measures and pairwise dissimilarity matrices.

Usage

```
betapart.core(x)
```

Arguments

x data frame, where rows are sites and columns are species

Value

The function returns an object of class `betapart` with the following elements:

sumSi	the sum of the species richness values of all sites
St	the total richness in the dataset
a	the multiple-site analog of the shared species term
shared	a matrix containing the number of species shared between pairs of sites
not.shared	a matrix containing the number of species not shared between pairs of sites: b, c
sum.not.shared	a matrix containing the total number of species not shared between pairs of sites: b+c
max.not.shared	a matrix containing the total maximum number of species not shared between pairs of sites: max(b,c)
min.not.shared	a matrix containing the total minimum number of species not shared between pairs of sites: min(b,c)

Author(s)

Andrés Baselga and David Orme

References

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

Baselga, A. 2012. The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232

See Also

[beta.multi](#), [beta.pair](#), [beta.sample](#), [beta.temp](#),

Examples

```
data(ceram.s)
ceram.core.s<-betapart.core(ceram.s)
ceram.dist.jac<-beta.pair(ceram.core.s, index.family="jac")
ceram.dist.sor<-beta.pair(ceram.core.s, index.family="sor")
ceram.multi.jac<-beta.multi(ceram.core.s, index.family="jac")
ceram.multi.sor<-beta.multi(ceram.core.s, index.family="sor")
```

betapart.core.abund *Core calculations of betapart for abundance-based dissimilarity measures*

Description

Computes the basic quantities needed for computing the abundance-based multiple-site dissimilarity measures and pairwise dissimilarity matrices.

Usage

```
betapart.core.abund(x)
```

Arguments

x data frame, where rows are sites and columns are species

Value

The function returns an object of class `betapart.abund` with the following elements:

`multiple.shared.abund`
the multiple-site interesection component in terms of abundances (AM)

`pair.shared.abund`
a matrix containing the agreement in abundance between pairs of sites (A)

`min.not.shared.abund`
a matrix containing the minimum disagreement in abundance between pairs of sites: $\min(B,C)$

`max.not.shared.abund`
a matrix containing the maximum disagreement in abundance between pairs of sites between pairs of sites: $\max(B,C)$

`pair.not.shared.abund`
a matrix containing the total disagreement in abundance between pairs of sites: $B+C$

Author(s)

Andrés Baselga

References

- Baselga, A. 2013. Separating the two components of abundance-based dissimilarity: balanced changes in abundance vs. abundance gradients. *Methods in Ecology and Evolution* 4: 552–557
- Legendre, P. 2014. Interpreting the replacement and richness difference components of beta diversity. *Global Ecology and Biogeography*, 23: 1324–1334
- Baselga, A. 2017. Partitioning abundance-based multiple-site dissimilarity into components: balanced variation in abundance and abundance gradients. *Methods in Ecology and Evolution*, in press

See Also

[beta.multi.abund](#), [beta.pair.abund](#), [beta.sample.abund](#), [betapart.core](#)

Examples

```
require(vegan)
data(BCI)
core.BCI<-betapart.core.abund(BCI)
pair.BCI<-beta.pair.abund(core.BCI)
multi.BCI<-beta.multi.abund(core.BCI)
```

`bray.part`*Partitioning pair-wise Bray-Curtis dissimilarities*

Description

Computes 3 distance matrices accounting for the balanced variation and abundance gradient components of Bray-Curtis dissimilarity, and the sum of both values (i.e. Bray-Curtis dissimilarity)

Usage

```
bray.part(x)
```

Arguments

`x` data frame of species abundances, where rows are sites and columns are species.

Value

The function returns a list with three dissimilarity matrices.

<code>bray.bal</code>	<code>dist</code> object, dissimilarity matrix accounting for the dissimilarity derived from balanced variation in abundance between sites
<code>bray.gra</code>	<code>dist</code> object, dissimilarity matrix accounting for the dissimilarity derived from unidirectional abundance gradients
<code>bray</code>	<code>dist</code> object, dissimilarity matrix accounting for total abundance-based dissimilarity between sites, measured as the Bray-Curtis index

Author(s)

Andrés Baselga

References

Baselga, A. in press. Separating the two components of abundance-based dissimilarity: balanced changes in abundance vs. abundance gradients. *Methods in Ecology and Evolution*. DOI: 10.1111/2041-210X.12029

See Also

[beta.pair](#)

Examples

```
require(vegan)
data(BCI)
BCI.matrices<-bray.part(BCI)
```

ceram.n

Cerambycidae from Northern European Countries

Description

The `ceram.n` data frame has 19 rows and 634 columns. Columns are presence/absence values of 634 species. The variable names are formed from the scientific names. The case names are standard country abbreviations, excepting RSS (Southern European Russia), RSC (Central European Russia) and RSN (Northern European Russia).

Usage

```
data(ceram.n)
```

Source

<http://www.cerambycidae.net/>

References

1. Danilevsky, M. L. 2007. A check-list of Longicorn Beetles (Coleoptera, Cerambycoidea) of Europe. Available at <http://www.cerambycidae.net/>
2. Baselga, A. 2008. Determinants of species richness, endemism and turnover in European longhorn beetles. *Ecography* 31:263-271

ceram.s

Cerambycidae from Southern European Countries

Description

The `ceram.s` data frame has 15 rows and 634 columns. Columns are presence/absence values of 634 species. The variable names are formed from the scientific names. The case names are standard country abbreviations, excepting SS (Serbia) and CBH (Croatia and Bosnia-Herzegovina).

Usage

```
data(ceram.s)
```

Source

<http://www.cerambycidae.net/>

References

1. Danilevsky, M. L. 2007. A check-list of Longicorn Beetles (Coleoptera, Cerambycoidea) of Europe. Available at <http://www.cerambycidae.net/>
2. Baselga, A. 2008. Determinants of species richness, endemism and turnover in European longhorn beetles. *Ecography* 31:263-271

functional.beta.multi *Multiple-site functional dissimilarities*

Description

Computes 3 multiple-site functional dissimilarities accounting for the spatial turnover and the nestedness components of functional beta diversity, and the sum of both values. Functional dissimilarities are based on volume of convex hulls intersections in a multidimensional functional space.

Usage

```
functional.beta.multi(x, traits, index.family="sorensen", warning.time=TRUE)
```

Arguments

x	data frame, where rows are sites and columns are species. Alternatively x can be a functional.betapart object derived from the functional.betapart.core function
traits	if x is not a functional.betapart object, a data frame, where rows are species and columns are functional space dimensions (i.e. quantitative traits or synthetic axes after PCoA). Number of species in each site must be strictly higher than number of dimensions. Number of dimensions should not exceed 4 and number of sites should not exceed 10. See Details.
index.family	family of dissimilarity indices, partial match of "sorensen" or "jaccard".
warning.time	a logical value indicating whether computation of multiple-site dissimilarities would stop if number of dimensions exceeds 4 or if number of sites exceeds 10. If turn to FALSE, computation process can be tracked in the step.fbc.txt file, see Details.

Details

For multiple-site dissimilarities metrics ($N > 2$ sites), the volume of the union of the N convex hulls is computed using the inclusion-exclusion principle (Villéger et al., 2011). It requires to compute the volume of all the intersections between 2 to N convex hulls. Intersection between $k > 2$ convex hulls is computed as the intersection between the two convex hulls shaping intersections between the corresponding $k-1$ convex hulls, e.g. $V(A_n B_n C) = V((A_n B_n) \cap (B_n C))$. For N sites, computing multiple-site dissimilarity metrics thus requires computing $2^N - (N+1)$ pair-wise intersections between convex hulls in a multidimensional functional space. Computation time of the intersection between two convex hulls increases with the number of dimensions (D) of the functional space. Therefore, to prevent from running very long computation process `warning.time` is set by default

to stop the function if $D > 4$ or $N > 10$. Computation progress can be tracked in the "step.fbc.txt" file written in the working directory. This table shows proportion of steps completed for computing convex hull volume shaping each site ("FRi") and intersections between them ("intersection_k").

Value

The function returns a list with the three multiple site functional dissimilarity values.

For `index.family="sorensen"` the three indices are:

<code>beta.SIM</code>	value of the functional turnover component, measured as Simpson derived functional dissimilarity
<code>beta.SNE</code>	value of the functional nestedness component, measured as Nestedness-resultant fraction of Sorensen derived functional dissimilarity
<code>beta.SOR</code>	value of the overall functional beta diversity, measured as Sorensen derived functional dissimilarity

For `index.family="jaccard"` the three indices are:

<code>beta.JTU</code>	value of the functional turnover component, measured as turnover fraction of Jaccard derived functional dissimilarity
<code>beta.JNE</code>	value of the functional nestedness component, measured as Nestedness-resultant fraction of Jaccard derived functional dissimilarity
<code>beta.JAC</code>	value of the overall functional beta diversity, measured as Jaccard derived functional dissimilarity

Author(s)

Sébastien Villéger, Andrés Baselga and David Orme

References

- Villéger S., Novack-Gottshal P. & Mouillot D. 2011. The multidimensionality of the niche reveals functional diversity changes in benthic marine biotas across geological time. *Ecology Letters*. 14, 561–568
- Baselga, A. 2012. The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232
- Villéger, S. Grenouillet, G., Brosse, S. 2013. Decomposing functional beta-diversity reveals that low functional beta-diversity is driven by low functional turnover in European fish assemblages. *Global Ecology and Biogeography*, 22: 671-681

See Also

[functional.beta.pair](#), [functional.betapart.core](#), [beta.multi](#)

Examples

```
##### 4 communities in a 2D functional space (convex hulls are rectangles)
traits.test<-cbind( c(1,1,1,2,2,3,3,4,4,5,5) , c(1,2,4,1,2,3,5,1,4,3,5) )
dimnames(traits.test)<-list(paste("sp",1:11,sep="") , c("Trait 1","Trait 2") )

comm.test<-matrix(0,4,11,dimnames=list( c("A","B","C","D") , paste("sp",1:11,sep="") ) )
comm.test["A",c(1,2,4,5)]<-1
comm.test["B",c(1,3,8,9)]<-1
comm.test["C",c(6,7,10,11)]<-1
comm.test["D",c(2,4,7,9)]<-1

plot(5,5,xlim=c(0,6), ylim=c(0,6), type="n", xlab="Trait 1",ylab="Trait 2")
points(traits.test[,1],traits.test[,2], pch=21,cex=1.5,bg="black")
rect(1,1,4,4, col="#458B0050", border="#458B00") ; text(2.5,2.5,"B",col="#458B00",cex=1.5)
polygon(c(2,1,3,4), c(1,2,5,4), col="#DA70D650", border="#DA70D6") ;
text(2.5,3,"D",col="#DA70D6",cex=1.5)
rect(1,1,2,2, col="#FF000050", border="#FF0000") ; text(1.5,1.5,"A",col="#FF0000",cex=1.5)
rect(3,3,5,5, col="#1E90FF50", border="#1E90FF") ; text(4,4.2,"C",col="#1E90FF",cex=1.5)

test.multi<-functional.beta.multi(x=comm.test, traits=traits.test, index.family = "jaccard" )
test.multi

test.multi.ABC<-functional.beta.multi(x=comm.test[c("A","B","C"),], traits=traits.test,
index.family = "jaccard" )
test.multi.ABC

test.multi.ABD<-functional.beta.multi(x=comm.test[c("A","B","D"),], traits=traits.test,
index.family = "jaccard" )
test.multi.ABD
```

functional.beta.pair *Pair-wise functional dissimilarities*

Description

Computes 3 distance matrices accounting for the spatial turnover and nestedness components of functional beta diversity, and the sum of both values. Functional dissimilarities are based on volume of convex hulls intersections in a multidimensional functional space.

Usage

```
functional.beta.pair(x, traits, index.family="sorensen")
```

Arguments

x data frame, where rows are sites and columns are species. Alternatively x can be a functional.betapart object derived from the functional.betapart.core function

- `traits` if `x` is not a `functional.betapart` object, a data frame, where rows are species and columns are functional space dimensions (i.e. quantitative traits or synthetic axes after PCoA). Number of species in each site must be strictly higher than number of dimensions.
- `index.family` family of dissimilarity indices, partial match of "sorensen" or "jaccard".

Value

The function returns a list with three functional dissimilarity matrices.

For `index.family="sorensen"` the three matrices are:

- `funct.beta.sim` dist object, dissimilarity matrix accounting for functional turnover, measured as Simpson derived pair-wise functional dissimilarity
- `funct.beta.sne` dist object, dissimilarity matrix accounting for nestedness-resultant functional dissimilarity, measured as the nestedness-fraction of Sorensen derived pair-wise functional dissimilarity
- `funct.beta.sor` dist object, dissimilarity matrix accounting for functional beta diversity, measured as Sorensen derived pair-wise functional dissimilarity

For `index.family="jaccard"` the three matrices are:

- `funct.beta.jtu` dist object, dissimilarity matrix accounting for functional turnover, measured as the turnover-fraction of Jaccard derived pair-wise functional dissimilarity
- `funct.beta.jne` dist object, dissimilarity matrix accounting for nestedness-resultant functional dissimilarity, measured as the nestedness-fraction of Jaccard derived pair-wise functional dissimilarity
- `funct.beta.jac` dist object, dissimilarity matrix accounting for functional beta diversity, measured as Jaccard derived pair-wise functional dissimilarity

Author(s)

Sébastien Villéger, Andrés Baselga and David Orme

References

- Villéger S., Novack-Gottshal P. & Mouillot D. 2011. The multidimensionality of the niche reveals functional diversity changes in benthic marine biotas across geological time. *Ecology Letters*. 14, 561–568
- Baselga, A. 2012. The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232
- Villéger, S. Grenouillet, G., Brosse, S. 2013. Decomposing functional beta-diversity reveals that low functional beta-diversity is driven by low functional turnover in European fish assemblages. *Global Ecology and Biogeography*, 22: 671-681

See Also

[functional.beta.multi](#), [functional.betapart.core](#), [beta.pair](#)

Examples

```
##### 4 communities in a 2D functional space (convex hulls are rectangles)
traits.test<-cbind( c(1,1,1,2,2,3,3,4,4,5,5) , c(1,2,4,1,2,3,5,1,4,3,5) )
dimnames(traits.test)<-list(paste("sp",1:11,sep="") , c("Trait 1","Trait 2") )

comm.test<-matrix(0,4,11,dimnames=list( c("A","B","C","D") , paste("sp",1:11,sep="") ) )
comm.test["A",c(1,2,4,5)]<-1
comm.test["B",c(1,3,8,9)]<-1
comm.test["C",c(6,7,10,11)]<-1
comm.test["D",c(2,4,7,9)]<-1

plot(5,5,xlim=c(0,6), ylim=c(0,6), type="n", xlab="Trait 1",ylab="Trait 2")
points(traits.test[,1],traits.test[,2], pch=21,cex=1.5,bg="black")
rect(1,1,4,4, col="#458B0050", border="#458B00") ; text(2.5,2.5,"B",col="#458B00",cex=1.5)
polygon(c(2,1,3,4), c(1,2,5,4), col="#DA70D650", border="#DA70D6") ;
text(2.5,3,"D",col="#DA70D6",cex=1.5)
rect(1,1,2,2, col="#FF000050", border="#FF0000") ; text(1.5,1.5,"A",col="#FF0000",cex=1.5)
rect(3,3,5,5, col="#1E90FF50", border="#1E90FF") ; text(4,4.2,"C",col="#1E90FF",cex=1.5)

test.pair<-functional.beta.pair(x=comm.test, traits=traits.test, index.family = "jaccard" )
lapply(test.pair,round,2)
```

functional.betapart.core

Core calculations of functional dissimilarities metrics

Description

Computes the basic quantities needed for computing the multiple-site functional beta diversity measures and pairwise functional dissimilarity matrices.

Usage

```
functional.betapart.core(x, traits, multi=TRUE, warning.time=TRUE, return.details=FALSE)
```

Arguments

x	data frame, where rows are sites and columns are species.
traits	data frame, where rows are species and columns are functional space dimensions (i.e. quantitative traits or synthetic axes after PCoA). Number of species in each site must be strictly higher than number of dimensions.
multi	a logical value indicating whether basic quantities for multiple-site functional beta-diversity should be computed. See Details.
warning.time	a logical value indicating whether computation of multiple-site dissimilarities would stop if number of dimensions exceeds 4 or if number of sites exceeds 10. If turn to FALSE, computation process can be tracked in the step.fbc.txt file, see Details.

`return.details` a logical value indicating whether volume and coordinates of vertices of convex hulls shaping each site and their intersections in the functional space should be returned.

Details

For multiple-site dissimilarities metrics ($N > 2$ sites), the volume of the union of the N convex hulls is computed using the inclusion-exclusion principle (Villéger et al., 2011). It requires to compute the volume of all the intersections between 2 to N convex hulls. Intersection between $k > 2$ convex hulls is computed as the intersection between the two convex hulls shaping intersections between the corresponding $k-1$ convex hulls, e.g. $V(A_n B_n C) = V((A_n B)_n (B_n C))$. For N sites, computing multiple-site dissimilarity metrics thus requires computing $2^N - (N+1)$ pair-wise intersections between convex hulls in a multidimensional functional space. Computation time of the intersection between two convex hulls increases with the number of dimensions (D) of the functional space. Therefore, to prevent from running very long computation process `warning.time` is set by default to stop the function if $D > 4$ or $N > 10$. Computation progress can be tracked in the "step.fbc.txt" file written in the working directory. This table shows proportion of steps completed for computing convex hull volume shaping each site ("FRi") and intersections between them ("intersection_k").

Value

The function returns an object of class `betapart` with the following elements:

<code>sumFRi</code>	the sum of the functional richness values of all sites
<code>FRt</code>	the total functional richness in the dataset
<code>a</code>	the multiple-site analog of the shared functional richness term
<code>shared</code>	a matrix containing the functional richness shared between pairs of sites
<code>not.shared</code>	a matrix containing the functional richness not shared between pairs of sites: b, c
<code>sum.not.shared</code>	a matrix containing the total functional richness not shared between pairs of sites: b+c
<code>max.not.shared</code>	a matrix containing the total maximum functional richness not shared between pairs of sites: max(b,c)
<code>min.not.shared</code>	a matrix containing the total minimum functional richness not shared between pairs of sites: min(b,c)
<code>details</code>	if <code>return.details=TRUE</code> a list of two lists: <code>\$CH</code> a list with a vector (FRi) of functional richness in each site (i.e. convex hull volume) and <code>coord_vertices</code> a list of N matrices with the coordinates of species being vertices in the D -dimensions functional space. <code>\$intersections</code> a list of 3 lists: <code>\$combinations</code> , $N-1$ matrices with all combinations of 2 to N sites (numbers are rank of sites in x); <code>\$volumes</code> , $N-1$ vectors with the volume inside the intersection between each combination of sites; <code>\$coord_vertices</code> , list of $N-1$ matrices with the coordinates of the vertices shaping these intersections (NA if no intersection).

Author(s)

Sébastien Villéger, Andrés Baselga and David Orme

References

- Villéger S., Novack-Gottshal P. & Mouillot D. 2011. The multidimensionality of the niche reveals functional diversity changes in benthic marine biotas across geological time. *Ecology Letters*. 14, 561–568
- Baselga, A. 2012. The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232
- Villéger, S. Grenouillet, G., Brosse, S. 2013. Decomposing functional beta-diversity reveals that low functional beta-diversity is driven by low functional turnover in European fish assemblages. *Global Ecology and Biogeography*, 22: 671-681

See Also

[functional.beta.multi](#), [functional.beta.pair](#), [betapart.core](#)

Examples

```
##### 4 communities in a 2D functional space (convex hulls are rectangles)
traits.test<-cbind( c(1,1,1,2,2,3,3,4,4,5,5) , c(1,2,4,1,2,3,5,1,4,3,5) )
dimnames(traits.test)<-list(paste("sp",1:11,sep="") , c("Trait 1","Trait 2") )

comm.test<-matrix(0,4,11,dimnames=list( c("A","B","C","D") , paste("sp",1:11,sep="") ) )
comm.test["A",c(1,2,4,5)]<-1
comm.test["B",c(1,3,8,9)]<-1
comm.test["C",c(6,7,10,11)]<-1
comm.test["D",c(2,4,7,9)]<-1

plot(5,5,xlim=c(0,6), ylim=c(0,6), type="n", xlab="Trait 1",ylab="Trait 2")
points(traits.test[,1],traits.test[,2], pch=21,cex=1.5,bg="black")
rect(1,1,4,4, col="#458B0050", border="#458B00") ; text(2.5,2.5,"B",col="#458B00",cex=1.5)
polygon(c(2,1,3,4), c(1,2,5,4), col="#DA70D650", border="#DA70D6") ;
text(2.5,3,"D",col="#DA70D6",cex=1.5)
rect(1,1,2,2, col="#FF000050", border="#FF0000") ; text(1.5,1.5,"A",col="#FF0000",cex=1.5)
rect(3,3,5,5, col="#1E90FF50", border="#1E90FF") ; text(4,4.2,"C",col="#1E90FF",cex=1.5)

test.core<-functional.betapart.core(x=comm.test, traits=traits.test, multi=TRUE,
return.details=FALSE)
test.core

# using functional.betapart.core to get details on intersections
# when only pairwise dissimilarity is computed
test.core.pair<-functional.betapart.core(x=comm.test, traits=traits.test, multi=FALSE,
return.details=TRUE)
test.core.pair

# for multiple dissimilarity
test.core.multi<-functional.betapart.core(x=comm.test, traits=traits.test, multi=TRUE,
return.details=TRUE)
test.core.multi

# using core outputs to compute pairwise and multiple functional dissimilarities
```



```
functional.beta.pair(x=test.core.pair, index.family = "jaccard" )
functional.beta.multi(x=test.core.multi, index.family = "jaccard" )
```

phylo.beta.multi *Multiple-site phylogenetic dissimilarities*

Description

Computes 3 distance values accounting for the multiple-site phylogenetic turnover and nestedness components of phylogenetic beta diversity, and the sum of both values. Phylogenetic dissimilarities are based on Faith's phylogenetic diversity.

Usage

```
phylo.beta.multi(x, tree, index.family="sorensen")
```

Arguments

x	a community matrix or data frame, where rows are sites and columns are species. Alternatively x can be a phylo.betapart object derived from the phylo.betapart.core function
tree	a phylogenetic tree of class phylo with tips names identic to species names from the community matrix.
index.family	family of dissimilarity indices, partial match of "sorensen" or "jaccard".

Details

The Sorensen dissimilarity index allows computing the PhyloSor index (Bryant et al. 2008) whereas the Jaccard dissimilarity index allows computing the UniFrac index (Lozupone & Knight 2005).

Value

The function returns a list with three phylogenetic dissimilarity values.

For index.family="sorensen" the three values are:

phylo.beta.sim	dist object, dissimilarity value accounting for phylogenetic turnover, measured as Simpson derived multiple-site phylogenetic dissimilarity
phylo.beta.sne	dist object, dissimilarity value accounting for nestedness-resultant phylogenetic dissimilarity, measured as the nestedness-fraction of Sorensen derived multiple-site phylogenetic dissimilarity
phylo.beta.sor	dist object, dissimilarity value accounting for phylogenetic beta diversity, measured as Sorensen derived multiple-site phylogenetic dissimilarity

For index.family="jaccard" the three values are:

- phylo.beta.jtu dist object, dissimilarity value accounting for phylogenetic turnover, measured as the turnover-fraction of Jaccard derived multiple-site phylogenetic dissimilarity
- phylo.beta.jne dist object, dissimilarity value accounting for nestedness-resultant phylogenetic dissimilarity, measured as the nestedness-fraction of Jaccard derived multiple-site phylogenetic dissimilarity
- phylo.beta.jac dist object, dissimilarity value accounting for phylogenetic beta diversity, measured as Jaccard derived multiple-site phylogenetic dissimilarity

Author(s)

Julien De Bortoli (juldebortoli@yahoo.fr), Fabien Leprieur (fabien.leprieur@univ-montp2.fr), Andrés Baselga and David Orme

References

- Baselga A. (2012) The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232
- Bryant JA, Lamanna C, Morlon H, Kerkhoff AJ, Enquist BJ, et al. (2008) Microbes on mountainsides: Contrasting elevational patterns of bacterial and plant diversity. *Proceedings of the National Academy of Sciences of the United States of America* 105: 11505-11511.
- Faith DP, Lozupone CA, Nipperess D, Knight R (2009) The Cladistic Basis for the Phylogenetic Diversity (PD) Measure Links Evolutionary Features to Environmental Gradients and Supports Broad Applications of Microbial Ecology's "Phylogenetic Beta Diversity" Framework. *Int J Mol Sci* 10: 4723-4741. doi: 10.3390/ijms10114723.
- Leprieur F, Albouy C, De Bortoli J, Cowman PF, Bellwood DR, et al. (2012) Quantifying Phylogenetic Beta Diversity: Distinguishing between "True" Turnover of Lineages and Phylogenetic Diversity Gradients. *PLoS ONE* 7(8): e42760. doi:10.1371/journal.pone.0042760
- Lozupone C, Knight R (2005) UniFrac: a new phylogenetic method for comparing microbial communities. *Applied and Environmental Microbiology* 71: 8228-8235.

See Also

[phylo.betapart.core](#), [beta.multi](#)

Examples

```
# toy tree for 6 species (sp1 to sp6)
require(ape)
toy.tree<-read.tree(text="(((sp1:1,sp2:1):5,(sp3:3,sp4:3):3):2,(sp5:7,sp6:7):1);")
plot(toy.tree)

# toy community table with 6 assemblages (A to F) with 6 species (sp1 to sp6)
toy.comm<-matrix(nrow=6, ncol=6)
rownames(toy.comm)<-c("A", "B", "C", "D", "E", "F")
colnames(toy.comm)<-c("sp1", "sp2", "sp3", "sp4", "sp5", "sp6")
toy.comm[1,]<-c(1,1,1,0,0,0)
```

```

toy.comm[2,]<-c(0,1,1,1,0,0)
toy.comm[3,]<-c(0,0,1,1,1,0)
toy.comm[4,]<-c(0,0,1,1,1,1)
toy.comm[5,]<-c(0,0,0,1,1,1)
toy.comm[6,]<-c(1,0,0,1,1,1)

toy.phylobetamulti<-phylo.beta.multi(toy.comm, toy.tree, index.family="sor")
toy.betamulti<-beta.multi(toy.comm, index.family="sor")

```

phylo.beta.pair *Pair-wise phylogenetic dissimilarities*

Description

Computes 3 distance matrices accounting for the phylogenetic turnover and nestedness components of phylogenetic beta diversity, and the sum of both values. Phylogenetic dissimilarities are based on Faith's phylogenetic diversity.

Usage

```
phylo.beta.pair(x, tree, index.family="sorensen")
```

Arguments

x	a community matrix or data frame, where rows are sites and columns are species. Alternatively x can be a phylo.betapart object derived from the phylo.betapart.core function
tree	a phylogenetic tree of class phylo with tips names identic to species names from the community matrix.
index.family	family of dissimilarity indices, partial match of "sorensen" or "jaccard".

Details

The Sorensen dissimilarity index allows computing the PhyloSor index (Bryant et al. 2008) whereas the Jaccard dissimilarity index allows computing the UniFrac index (Lozupone & Knight 2005).

Value

The function returns a list with three phylogenetic dissimilarity matrices.

For index.family="sorensen" the three matrices are:

phylo.beta.sim	dist object, dissimilarity matrix accounting for phylogenetic turnover, measured as Simpson derived pair-wise phylogenetic dissimilarity
phylo.beta.sne	dist object, dissimilarity matrix accounting for nestedness-resultant phylogenetic dissimilarity, measured as the nestedness-fraction of Sorensen derived pair-wise phylogenetic dissimilarity

phylo.beta.sor dist object, dissimilarity matrix accounting for phylogenetic beta diversity, measured as Sorensen derived pair-wise phylogenetic dissimilarity

For index.family="jaccard" the three matrices are:

phylo.beta.jtu dist object, dissimilarity matrix accounting for phylogenetic turnover, measured as the turnover-fraction of Jaccard derived pair-wise phylogenetic dissimilarity

phylo.beta.jne dist object, dissimilarity matrix accounting for nestedness-resultant phylogenetic dissimilarity, measured as the nestedness-fraction of Jaccard derived pair-wise phylogenetic dissimilarity

phylo.beta.jac dist object, dissimilarity matrix accounting for phylogenetic beta diversity, measured as Jaccard derived pair-wise phylogenetic dissimilarity

Author(s)

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References

Baselga A. (2012) The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232

Bryant JA, Lamanna C, Morlon H, Kerkhoff AJ, Enquist BJ, et al. (2008) Microbes on mountainsides: Contrasting elevational patterns of bacterial and plant diversity. *Proceedings of the National Academy of Sciences of the United States of America* 105: 11505-11511.

Faith DP, Lozupone CA, Nipperess D, Knight R (2009) The Cladistic Basis for the Phylogenetic Diversity (PD) Measure Links Evolutionary Features to Environmental Gradients and Supports Broad Applications of Microbial Ecology's "Phylogenetic Beta Diversity" Framework. *Int J Mol Sci* 10: 4723-4741. doi: 10.3390/ijms10114723.

Leprieur F, Albouy C, De Bortoli J, Cowman PF, Bellwood DR, et al. (2012) Quantifying Phylogenetic Beta Diversity: Distinguishing between "True" Turnover of Lineages and Phylogenetic Diversity Gradients. *PLoS ONE* 7(8): e42760. doi:10.1371/journal.pone.0042760

Lozupone C, Knight R (2005) UniFrac: a new phylogenetic method for comparing microbial communities. *Applied and Environmental Microbiology* 71: 8228-8235.

See Also

[phylo.betapart.core](#), [beta.pair](#)

Examples

```
# toy tree for 6 species (sp1 to sp6)
require(ape)
toy.tree<-read.tree(text="(((sp1:1,sp2:1):5,(sp3:3,sp4:3):3):2,(sp5:7,sp6:7):1);")
plot(toy.tree)

# toy community table with 6 assemblages (A to F) with 6 species (sp1 to sp6)
```

```

toy.comm<-matrix(nrow=6, ncol=6)
rownames(toy.comm)<-c("A", "B", "C", "D", "E", "F")
colnames(toy.comm)<-c("sp1", "sp2", "sp3", "sp4", "sp5", "sp6")
toy.comm[1,]<-c(1,1,1,0,0,0)
toy.comm[2,]<-c(0,1,1,1,0,0)
toy.comm[3,]<-c(0,0,1,1,1,0)
toy.comm[4,]<-c(0,0,1,1,1,1)
toy.comm[5,]<-c(0,0,0,1,1,1)
toy.comm[6,]<-c(1,0,0,1,1,1)

toy.phylobetapair<-phylo.beta.pair(toy.comm, toy.tree, index.family="sor")
toy.betapair<-beta.pair(toy.comm, index.family="sor")
plot(toy.betapair$beta.sim,toy.phylobetapair$phylo.beta.sim)
plot(toy.betapair$beta.sne,toy.phylobetapair$phylo.beta.sne)

```

phylo.betapart.core *Core calculations of phylogenetic dissimilarities metrics*

Description

Computes the basic quantities needed for computing the multiple-site phylogenetic beta diversity measures and pairwise phylogenetic dissimilarity matrices.

Usage

```
phylo.betapart.core(x, tree)
```

Arguments

x	a community matrix or data frame, where rows are sites and columns are species.
tree	a phylogenetic tree of class phylo with tips names identic to species names from the community matrix.

Value

The function returns a list with:

sumSi	the sum of the phylogenetic diversity values of all sites
St	the total phylogenetic diversity in the dataset
shared	a matrix containing the phylogenetic diversity shared between pairs of sites
sum.not.shared	a matrix containing the total phylogenetic diversity not shared between pairs of sites: $b+c$
max.not.shared	a matrix containing the total maximum phylogenetic diversity not shared between pairs of sites: $\max(b,c)$
min.not.shared	a matrix containing the total minimum phylogenetic diversity not shared between pairs of sites: $\min(b,c)$

Author(s)

Julien De Bortoli (juldebortoli@yahoo.fr), Fabien Leprieur (fabien.leprieur@univ-montp2.fr), Andrés Baselga and David Orme

References

- Baselga A. (2012) The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography* 21, 1223-1232
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See Also

[phylo.beta.pair](#), [phylo.beta.multi](#)

Examples

```
# toy tree for 6 species (sp1 to sp6)
require(ape)
toy.tree<-read.tree(text="(((sp1:1,sp2:1):5,(sp3:3,sp4:3):3):2,(sp5:7,sp6:7):1);")
plot(toy.tree)

# toy community table with 6 assemblages (A to F) with 6 species (sp1 to sp6)
toy.comm<-matrix(nrow=6, ncol=6)
rownames(toy.comm)<-c("A","B","C","D","E","F")
colnames(toy.comm)<-c("sp1","sp2","sp3","sp4","sp5","sp6")
toy.comm[1,]<-c(1,1,1,0,0,0)
toy.comm[2,]<-c(0,1,1,1,0,0)
toy.comm[3,]<-c(0,0,1,1,1,0)
toy.comm[4,]<-c(0,0,1,1,1,1)
toy.comm[5,]<-c(0,0,0,1,1,1)
toy.comm[6,]<-c(1,0,0,1,1,1)

toy.phylocore<-phylo.betapart.core(toy.comm, toy.tree)
```

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