

# Decompose D in replacement and richness diff. components

## Description

Podani-family and Baselga-family decompositions of the Jaccard and Sørensen dissimilarity coefficients and their quantitative forms (Ruzicka and %difference) into replacement and richness difference components, for species presence-absence or abundance data, as described in Legendre (2014).

## Usage

```
beta.div.comp(mat, coef="J", quant=FALSE, save.abc=FALSE)
```

## Arguments

- |          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| mat      | Community composition data. The file class can be either <code>data.frame</code> or <code>matrix</code> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| coef     | Family of coefficients to be computed – <ul style="list-style-type: none"> <li>• "S" or "Sorensen" – Podani family, Sørensen-based indices.</li> <li>• "J" or "Jaccard" – Podani family, Jaccard-based indices.</li> <li>• "BS" – Baselga family, Sørensen-based indices.</li> <li>• "BJ" – Baselga family, Jaccard-based indices.</li> <li>• "N" – Podani &amp; Schmera (2011) relativized nestedness index.</li> </ul> The quantitative form in the Sørensen family is the percentage difference index.<br>The quantitative form in the Jaccard family is the Ruzicka index. |
| quant    | If <code>quant=TRUE</code> , compute the quantitative forms of replacement, nestedness and <b>D</b> .<br>If <code>quant=FALSE</code> , compute the presence-absence forms of the coefficients.                                                                                                                                                                                                                                                                                                                                                                                 |
| save.abc | If <code>save.abc=TRUE</code> , save the matrices of parameters a, b and c used in presence-absence calculations.                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

## Details

For species presence-absence data, the distance coefficients are  $\text{Jaccard} = (b+c)/(a+b+c)$  and  $\text{Sørensen} = (b+c)/(2*a+b+c)$  with the usual  $\{a,b,c\}$  notation.

For species abundance data, the distance coefficients are the Ruzicka index  $= (B+C)/(A+B+C)$  and Odum's percentage difference  $= (B+C)/(2A+B+C)$  (incorrectly called Bray-Curtis in some packages), where

- A = sum of the intersections (or minima) of species abundances at two sites,
- B = sum of abundances at site 1 minus A,
- C = sum of abundances at site 2 minus A.

The binary (quant=FALSE) and quantitative (quant=TRUE) forms of the S and J indices return the same values when computed for presence-absence data.

## Value

Function `beta.div.comp()` returns a list containing the following results:

<code>repl</code>	Replacement matrix, class = <code>dist</code> .
<code>rich</code>	Richness/abundance difference or nestedness matrix, class = <code>dist</code> . With options "BJ", "BS" and "N", <code>rich</code> contains nestedness indices. With option "N", the <code>repl[i, j]</code> and <code>rich[i, j]</code> values do not add up to <code>D[i, j]</code> .
<code>D</code>	Dissimilarity matrix, class = <code>dist</code> .
<code>part</code>	Beta diversity partitioning vector – 1. <code>BDtotal</code> (total beta diversity) = $\sum(D_{ij})/(n*(n-1))$ (Legendre & De Cáceres 2013). This is equal to $\sum(d_{ij}^2)/(n*(n-1))$ where $d_{ij} = \sqrt{D_{ij}}$ . The dissimilarities are square-rooted because the Jaccard, Sørensen, Ruzicka and %difference indices are not Euclidean. 2. Total replacement diversity. 3. Total richness difference diversity (or nestedness). 4. Total replacement diversity/Total beta diversity. 5. Total richness difference diversity (or nestedness)/Total beta diversity.
<code>note</code>	Name of the dissimilarity coefficient.

The Jaccard and Sørensen dissimilarity coefficients and their quantitative forms, the Ruzicka and %difference indices, all have upper bounds ( $D_{\max}$ ) of 1. Hence, when all sites contain a different set of species with no species in common, the maximum value that `BDtotal` can take is 0.5. See Legendre & De Cáceres (2013, p. 958), section *Maximum value of BD*.

This differs from the values produced by function `beta.div()`: with methods "hellinger", "chord" and "profiles", which have maximum values of  $\sqrt{2}$ , `BDtotal` has a maximum value of 1.

## 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.
- Carvalho, J.C., Cardoso, P., Borges, P.A.V., Schmera, D. & Podani, J. (2013) Measuring fractions of beta diversity and their relationships to nestedness: a theoretical and empirical comparison of novel approaches. *Oikos*, 122, 825–834.
- Legendre, P. 2014. Interpreting the replacement and richness difference components of beta diversity. *Global Ecology and Biogeography*, 23, 1324–1334.

Legendre, P. and M. De Cáceres. 2013. Beta diversity as the variance of community data: dissimilarity coefficients and partitioning. *Ecology Letters* 16: 951-963.

Podani, J., Ricotta, C. & Schmera, D. (2013) A general framework for analyzing beta diversity, nestedness and related community-level phenomena based on abundance data. *Ecological Complexity*, 15, 52-61.

Podani, J. & Schmera, D. 2011. A new conceptual and methodological framework for exploring and explaining pattern in presence-absence data. *Oikos*, 120, 1625–1638.

## Author

Pierre Legendre, Département de sciences biologiques, Université de Montréal.  
License: GPL-2.

## Example

### Example: the Doubs river fish data. They are available in the ade4 package.

```
require(ade4)
```

```
data(doubs)
```

```
fish.sp = doubs$fish[-8,] # Fish data; site 8 is removed because no fish were caught
```

```
# Compute and partition a matrix of Jaccard indices (presence-absence data)
```

```
out1 = beta.div.comp(fish.sp, coef="J", quant=FALSE)
```

```
out1$part
```

```
# Compute and partition a matrix of %difference indices (quantitative form of Sørensen index)
```

```
out2 = beta.div.comp(fish.sp, coef="S", quant=TRUE)
```

```
out2$part
```

```
# In paragraph Value, see the description of the 5 elements of vector part.
```

```
# Is the fish beta diversity dominated by replacement or richness/abundance difference?
```