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 `data.frame` or `matrix`.

coeff   Family of coefficients to be computed –
- "S" or "Sorensen" – Podani family, Sørensen-based indices.
- "J" or "Jaccard" – Podani family, Jaccard-based indices.
- "BS" – Baselga family, Sørensen-based indices.
- "BJ" – Baselga family, Jaccard-based indices.
- "N" – Podani & Schmera (2011) relativized nestedness index.

The quantitative form in the Sørensen family is the percentage difference index.
The quantitative form in the Jaccard family is the Ruzicka index.

quant   If `quant=TRUE`, compute the quantitative forms of replacement, nestedness and **D**.
If `quant=FALSE`, compute the presence-absence forms of the coefficients.

save.abc   If `save.abc=TRUE`, save the matrices of parameters a, b and c used in presence-absence calculations.

Details

For species presence-absence data, the distance coefficients are Jaccard=(b+c)/(a+b+c) and 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:

`repl`	Replacement matrix, class = `dist`.
`rich`	Richness/abundance difference or nestedness matrix, class = `dist`. With options "BJ", "BS" and "N", `rich` contains nestedness indices. With option "N", the `repl[i,j]` and `rich[i,j]` values do not add up to D[i,j].
`D`	Dissimilarity matrix, class = `dist`.
`part`	Beta diversity partitioning vector – 1. Total beta div. = 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.
`note`	Name of the dissimilarity coefficient.

References

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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?