Compute LCBD from any D matrix

Description

Compute LCBD indices (Legendre & De Cáceres 2013) from a symmetric dissimilarity matrix (**D**) or from a beta component matrix (Repl, RichDiff or AbDiff, or Nes) (Legendre 2014).

Usage

```
LCBD.comp(D, sqrt.D=TRUE, save.D=FALSE)
```

Arguments

D	A dissimilarity or beta diversity component matrix, class=`dist` or `matrix`.
sqrt.D	Take the square root of the dissimilarities in matrix **D** before computing the LCBD indices.
save.D	If `save.D=TRUE`, the dissimilarity matrix will appear in the output list.

Details

Use `sqrt.D=TRUE` when computing LCBD indices for most of the replacement and richness/abundance difference indices computed by function beta.div.comp(), as well as for the corresponding **D** matrices. See Table S1.4 in Appendix S1 of Legendre (2014) to identify the matrices that are Euclidean without taking the square root of the individual values. Only the $RichDiff_S$ (for presence-absence data) and $AbDiff_{\%diff}$ indices (for abundance data) of the Sørensen group in the Podani family have that property. In all other cases, use `sqrt.D=TRUE`.

When computing LCBD from a **D** matrix, use sqrt=TRUE if the **D** matrix is not Euclidean. The Euclidean property can be checked with function is.euclid() of ade4.

`BDtotal` statistics are comparable among data sets having the same or different numbers of sampling units (*n*), provided that the sampling units are of the same size or represent the same sampling effort and that `BDtotal` is computed with the same **D** index.

Function LCBD.comp() produces the same (SStotal, BDtotal, LCBD) results as function beta.div(). Note, however, that the latter produces other interesting results (p.LCBD, SCBD). Function LCBD.comp should then only be used to compute LCBD indices from dissimilarity matrices that cannot be computed by function beta.div(), e.g. genetic **D** matrices, or from replacement and richness difference matrices produced by function beta.div.comp(). Significance of the LCBD indices cannot be tested when their calculation starts from a **D** matrix because the testing procedure involves permutation of the columns of raw data.

Value

Function LCBD.comp() returns a list containing the following results:

SStotal_BDtotal	Total sum of squares and total beta diversity [= Var($\mathbf{Y}$)] of the data matrix.
LCBD	Vector of *Local contributions to beta diversity* (LCBD) for the sites.
D	The input dissimilarity matrix, class = dist; only if save.D=TRUE.

References

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

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

Author

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

Example

```
### Example 1: the mite data are available in the vegan package.
### Compute the Hellinger distance, then the LCBD indices.
require(vegan)
data(mite)
mite.hel = decostand(mite, "hellinger")
mite.D = dist(mite.hel)
out.mite.D = LCBD.comp(mite.D, sqrt.D=FALSE)

### Example 2: the Doubs river fish data are available in the ade4 package.
### Load function beta.div.comp()
require(ade4)
data(doubs)
fish.sp = doubs$fish[-8,]   # Fish data; site 8 is removed because no fish were caught

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

out.fish.D = LCBD.comp(out.comp$D, sqrt.D=TRUE)   # out.comp.D is not Euclidean
out.fish.D$SStotal_BDtotal
out.fish.Repl = LCBD.comp(out.comp$repl, sqrt.D=TRUE)   # out.comp$repl is not Euclidean
out.fish.Repl$SStotal_BDtotal
out.fish.AbDiff = LCBD.comp(out.comp$rich, sqrt.D=FALSE)   # out.comp$rich is Euclidean
out.fish.AbDiff$SStotal_BDtotal
```

Plot maps of the LCBD indices
fish.xy = doubs$xy[-8,]   # Geographic coordinates; site 8 removed because no fish were caught
par(mfrow=c(1,3))
# Map of LCBD indices for %difference dissimilarity
plot(fish.xy, asp=1, type="n", xlab="x coordinates (km)", ylab="y coordinates (km)", main="
Doubs fish LCBD, %difference D")
points(fish.xy, pch=21, col="white", bg="brown", cex=50*out.fish.D$LCBD)

Map of LCBD indices for replacement component of %difference dissimilarity
plot(fish.xy, asp=1, type="n", xlab="x coordinates (km)", ylab="y coordinates (km)", main="
Doubs fish replacement LCBD")
points(fish.xy, pch=21, col="white", bg="brown", cex=50*out.fish.Repl$LCBD)

Map of LCBD indices for abundance difference component of %difference dissimilarity
plot(fish.xy, asp=1, type="n", xlab="x coordinates (km)", ylab="y coordinates (km)", main="
Doubs fish abundance diff. LCBD")
points(fish.xy, pch=21, col="white", bg="brown", cex=50*out.fish.AbDiff$LCBD)