Principal Coordinate Analysis

Description

Function pcoa.all computes principal coordinate decomposition (also called classical scaling) of a distance matrix D (Gower 1966) and outputs the eigenvectors corresponding to all eigenvalues, positive and negative.

Usage

```
pcoa.all(D, diagonal=0, all=FALSE, include.zero=FALSE, rn=NULL)
```

Arguments

D	A distance matrix of class dist or matrix.
diagonal	In an ordinary dissimilarity or distance matrix, the diagonal is 0. Other constant values can be forced on the diagonal of matrix D. For example, for the construction of db-MEM eigenfunctions, the diagonal contains 4*thresh.
all	If TRUE, the eigenvectors corresponding to all eigenvalues, positive and negative, are shown in the output list. Default value: all=FALSE.
include.zero	If FALSE (default value), the zero eigenvalues as well as their eigenvectors are excluded from the output list. See details.
rn	An optional vector of row names, of length n, for the n objects.

Details

This function was developed to provide principal coordinate decomposition for the function PCNM of this library. It computes the eigenvectors corresponding to all eigenvalues, positive and negative, using matrix algebra. It is faster than cmdscale, which only outputs the positive eigenvalues and corresponding eigenvectors.

Another function in this library, pcoa, offers more options for principal coordinate analysis of ordinary distance matrices computed from community composition or other response data tables. Its companion for the production or ordination diagrams is biplot.pcoa.

In pcoa.all, when there are no negative eigenvalues, the eigenvectors (principal coordinates) are scaled to a length equal to the square root of the corresponding eigenvalues. When negative eigenvalues are present, the eigenvectors are scaled to

length 1 to prevent the production of complex engenvectors. Eigenvectors scaled in that way do not preserve the distances in matrix D among the objects. They should not be used, in particular, to draw ordination graphs.

When `include.zero` is `TRUE`, the null eigenvalue(s) and associated eigenvector(s) are shown in the output list. These eigenvectors are meaningless and should not be used for modelling.

Value

`values`	The eigenvalues.
`rel.values`	The relative eigenvalues.
`rel.cum.values`	The cumulative relative eigenvalues.
`vectors`	The principal coordinates.
`trace`	The trace of the distance matrix. This is also the sum of all eigenvalues, positive and negative.

Author(s)

Pierre Legendre, Universite de Montreal

References

Gower, J. C. 1966. Some distance properties of latent root and vector methods used in multivariate analysis. Biometrika. 53: 325-338.

Legendre, P. and L. Legendre. 1998. Numerical ecology, 2nd English edition. Elsevier Science BV, Amsterdam.

See Also

PCNM, pcoa

Examples

```
# Oribatid mite data from Borcard and Legendre (1994)
library(vegan)
data(mite)       # 70 peat cores, 35 species

mite.D <- vegdist(mite, "bray")
res <- pcoa.all(mite.D)
res <- pcoa.all(mite.D, all=TRUE)
```