

Seriation of a (dis)similarity matrix

Description

This function maximizes the affinity values near the diagonal of a resemblance matrix (or, more generally, an affinity matrix), as per Beum and Brundage (1950). This method represents an interesting alternative to clustering in the case of non-symmetric resemblance matrices. The method is also described in section 8.10 of Legendre and Legendre (2012).

Usage

```
seriation(mat)
```

Arguments

mat A square, symmetric or non-symmetric similarity or distance matrix. If it is a symmetric dissimilarity matrix of class 'dist', produced for example by `dist {stats}`, `vegdist {vegan}`, or `dist.binary {ade4}`, it will be converted to square similarity matrix form by the function.

Details

The input matrix may be a symmetric or non-symmetric matrix of resemblance containing non-negative values. If it is square and contains distances (0's on the main diagonal), the function transforms the distances to similarities (1's on the diagonal) before the calculation. The diagonal elements are excluded from the seriation calculations.

If the input matrix belongs to class 'dist', it is assumed to contain dissimilarities, which are converted by the function to similarities.

Value

Function *seriation()* returns a list with four elements:

mat	The re-ordered similarity matrix, with the original names for the rows and columns. Distances have been converted to similarities with the range [0,1].
ranking	The vector used to reorder the objects (rows and columns).
dat	The three statistics computed on the matrix: sum.col = column sums; sum.pr = column sums multiplied by 'mult'; pr.ave = sum.pr divided by sum.col.
sdev	standard deviation of the pr.ave values. 'mat' is the reordered matrix with the largest value of 'sdev'.

References

Beum, C. O. Jr. and E. G. Brundage. 1950. A method for analyzing the sociomatrix. *Sociometry* 13: 141-145.

Legendre, P. and Legendre, L. 2012. *Numerical Ecology*, 3rd English ed. Elsevier, Amsterdam.

Author

Translated to R by Sébastien Durand and Pierre Legendre, Département de sciences biologiques, Université de Montréal, from a FORTRAN program written by P. Legendre.

Examples

```
# Non-symmetric matrix from Beum and Brundage (1950)
# The affinity values are 2 (largest affinity), 1, or 0
mat.Beum = matrix(c(1,1,0,0,1,0,2,1,0,0,2,0,0,0,1,2,0,2,0,0,2,1,0,1,1,2,0,0,1,0,0,0,1,1,0,1), 6, 6)
ser.out = seriation(mat.Beum)
ser.out

# Symmetric dissimilarity matrix computed from a table of random numbers.
mat = matrix(rnorm(140),7,20)
mat.D = dist(mat)
ser.out = seriation(mat.D)
ser.out

# Compare with hierarchical clustering results
mat.clust = hclust(mat.D, method="average")
plot(mat.clust)
```