Nonmetric unfolding

Description

Variant of smacof for rectangular matrices (typically ratings, preferences) that allows for nonmetric transformations. Also known as nonmetric unfolding.

Usage

```
unfolding(delta, ndim = 2, type = c("ratio", "interval", "ordinal",
"mspline"),
         conditionality = c("matrix", "row"), lambda = 0.5, omega = 0.1,
         circle = c("none", "row", "column"), weightmat = NULL, init = NULL,
         ties = c("primary", "secondary"), verbose = FALSE, relax = TRUE,
         itmax = 10000, eps = 1e-6, spline.degree = 2, spline.intKnots = 2)

smacofRect(delta, ndim = 2, type = c("ratio", "interval", "ordinal",
"mspline"),
         conditionality = c("matrix", "row"), lambda = 0.5, omega = 0.1,
         circle = c("none", "row", "column"), weightmat = NULL, init = NULL,
         ties = c("primary", "secondary"), verbose = FALSE, relax = TRUE,
         itmax = 10000, eps = 1e-6, spline.degree = 2, spline.intKnots = 2)

prefscal(delta, ndim = 2, type = c("ratio", "interval", "ordinal",
"mspline"),
         conditionality = c("matrix", "row"), lambda = 0.5, omega = 0.1,
         circle = c("none", "row", "column"), weightmat = NULL, init = NULL,
         ties = c("primary", "secondary"), verbose = FALSE, relax = TRUE,
         itmax = 10000, eps = 1e-6, spline.degree = 2, spline.intKnots = 2)
```

Arguments

`delta`	Data frame or matrix of preferences, ratings, dissimilarities.
`ndim`	Number of dimensions
`type`	MDS type: `"interval"`, `"ratio"`, `"ordinal"`, or `"mspline"`
`conditionality`	A single transformations are applied for the entire matrix `"matrix"` or for each row separately `"row"`
`lambda`	Penalty strength balancing the loss contribution of stress and the penalty
`omega`	Penalty width determines for what values of the variation coefficient the penalty should become active.
`circle`	If `"column"`, the column configurations are restricted to be on a circle, if `"row"`, row configurations are on a circle, if `"none"`, there are no restrictions on row and column configurations
`weightmat`	Optional matrix with dissimilarity weights

`init`	Matrix with starting values for configurations (optional)
`ties`	Tie specification for `ordinal` transformations: `primary` unties the ties and `secondary`keeps the ties tied
`verbose`	If `TRUE`, intermediate stress is printed out
`relax`	If `TRUE`, block relaxation is used for majorization after 100 iterations. It tends to reduce the number of iterations by a factor 2.
`itmax`	Maximum number of iterations
`eps`	Convergence criterion
`spline.degree`	Degree of the spline for an `"mspline"` transformation
`spline.intKnots`	Number of interior knots of the spline for a `"mspline"` transformation

Details

Unfolding tries to match a rectangular matrix `delta` of dissimilarities between row and column objects by Euclidean distances between row and column points. Badness of fit is measured by raw Stress as the sum of squared differences between `delta` and the Euclidean distances. Instead of dissimilarities optimal transformations (dhats) can be found. The dhats should be a function of the original `delta` restricted to be `"ratio"`, `"interval"`,`"ordinal"`, or `"mspline"`. These transformations can be the same for the entire matrix (`conditionality = "matrix"`) of data or different per row (`conditionality = "row"`). To avoid a degenerate solution with all dhats and distances equal to 1, the prefscal penalty is is used. A penalty is added based on the variation coefficient of the dhats (mean dhat divided by the standard deviation of the dhats). The penalty width (`omega`) weights the penalty and determines from what value of the variation coefficient of the dhats the penalty should become active. The penalty strength (`lambda`) is needed to ensure that the penalty can be strong enough.

Creates an object of class `smacofR`.

Value

`obsdiss`	Observed dissimilarities, corresponds to `delta`
`confdist`	Configuration dissimilarities
`dhat`	Matrix with optimal transformation of size `delta`
`iord`	List of size 1 for matrix conditional and size `nrow(delta)` for row conditional with the index that orders the dhats. Needed for the Shepard plot
`conf.row`	Matrix of final row configurations
`conf.col`	Matrix of final column configurations
`stress`	Final, normalized stress value
`pstress`	Penalized stress value (the criterion that is minimized)
`spp.row`	Stress per point, rows
`spp.col`	Stress per point, columns

congvec	Vector of congruency coefficients
ndim	Number of dimensions
model	Type of smacof model
niter	Number of iterations
nind	Number of individuals (rows)
trans	Transformation
conditionality	Conditionality of the transformation
nobj	Number of objects (columns)

Author(s)

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References

de Leeuw, J. & Mair, P. (2009). Multidimensional scaling using majorization: The R package smacof. Journal of Statistical Software, 31(3), 1-30, http://www.jstatsoft.org/v31/i03/

Busing, F. M. T. A., Groenen, P. J. F., & Heiser, W. J. (2005). Avoiding degeneracy in multidimensional unfolding by penalizing on the coefficient of variation. Psychometrika, 70, 71-98.

See Also

plot.smacof, smacofConstraint, smacofSym, smacofIndDiff, smacofSphere

Examples

```
## Ratio unfolding
res <- unfolding(breakfast)
res

## various configuration plots0
plot(res)
plot(res, type = "p", pch = 25)
plot(res, type = "p", pch = 25, col.columns = 3,
     label.conf.columns = list(label = TRUE, pos = 3, col = 3),
     col.rows = 8, label.conf.rows = list(label = TRUE, pos = 3, col = 8))

## Shepard plot
plot(res, "Shepard")

## Stress decomposition chart
plot(res, "stressplot")

## Not run:
## Ordinal unfolding row conditional
## Note that ordinal unfolding may need many iterations (several thousands)
```

```
res <- unfolding(breakfast, type = "ordinal", conditionality = "row", omega =
0.1, itmax = 3000)
res
## Shepard plot
plot(res, "Shepard")
plot(res)

## End(Not run)
```