Package 'fmdu'

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Type Package

Title (Restricted) [external] Multidimensional Unfolding

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Description Functions for performing (external) multidimensional unfolding.
Restrictions (fixed coordinates or model restrictions) are available for both row and column coordinates in all combinations.

Depends R (>= 3.0.2)

Imports smacof

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Encoding UTF-8

NeedsCompilation yes

RoxygenNote 7.2.3

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R topics documented:

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external   *Multidimensional External Unfolding Function*

Description

external performs multidimensional external unfolding.

Usage

```
external(
  x,
  w = NULL,
  fixed = NULL,
  z = NULL,
  MAXITER = 1024,
  FCRIT = 1e-08,
  error.check = FALSE,
  echo = FALSE
)
```

Arguments

x	an n by m rectangular matrix containing dissimilarities or distances.
w	an identical sized matrix containing nonnegative weights (all ones when omitted).
fixed	fixed column coordinates (m x p).
z	null or initial row coordinates (n by p).
MAXITER	maximum number of iterations (default = 1024).
FCRIT	relative convergence criterion (default = 0.00000001).
error.check	extensive check validity input parameters (default = FALSE).
echo	print intermediate algorithm results (default = FALSE).

Value

x original n by m matrix with dissimilarities or distances.

w original n by m matrix with dissimilarity weights.

fixed original m x p fixed column coordinates.

z final n by p matrix with row coordinates.

d final n by m matrix with distances between rows of z and rows of fixed.

last.iteration final iteration number.

last.difference final function difference used for convergence testing.

mse final mean squared error function value.

rmse final root mean squared error function value.

References

de Leeuw, J., and Heiser, W. J. (1980). Multidimensional scaling with restrictions on the configuration. In P.R. Krishnaiah (Ed.), Multivariate analysis (Vol. 5, pp. 501–522). Amsterdam, The Netherlands: North-Holland Publishing Company.

Heiser,W. J. (1987a). Joint ordination of species and sites: The unfolding technique. In P. Legendre and L. Legendre (Eds.), Developments in numerical ecology (pp. 189–221). Berlin, Heidelberg: Springer-Verlag.

Busing, F.M.T.A. (2010). Advances in multidimensional unfolding. Unpublished doctoral dissertation, Leiden University, Leiden, the Netherlands.

Examples

```
## Not run:
library( smacof )
data( "breakfast" )
x <- as.matrix( breakfast )
n <- nrow( x )
m <- ncol( x )
d.col <- as.matrix( dist( t( x ) ) )
r <- smacofSym( d.col )
print( r$conf )
e <- external( x, fixed = r$conf )
print( e$z )

## End(Not run)
```

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fastmdu   *(Restricted) Multidimensional Unfolding Function*

Description

`fastmdu` performs three types of multidimensional unfolding in different combination for row and column objects. The function follows algorithms given by de Leeuw and Heiser (1980), Heiser (1987), and Busing (2010).

Usage

```
fastmdu(
  delta,
  w = NULL,
  p = 2,
  x = NULL,
  rx = NULL,
  y = NULL,
  ry = NULL,
  MAXITER = 1024,
```

```
    FCRIT = 1e-08,
    error.check = FALSE,
    echo = FALSE
)
```

Arguments

`delta`	an n by m rectangular matrix containing dissimilarities.
`w`	an identical sized matrix containing nonnegative weights (all ones when omitted).
`p`	dimensionality (default = 2).
`x`	either initial or fixed row coordinates (n by p) or independent row variables (n by hx).
`rx`	Row restriction. If omitted, x is free and x contains the initial row coordinates. If logical valued, x (n by p) contains the initial row coordinates and rx (n by p) indicates free (false) and fixed (true) row coordinates. If real valued, x (n by hx) contains hx independent row variables and rx (hx by p) contains the initial row regression coefficients.
`y`	either initial or fixed column coordinates (m by p) or independent column variables (n by hy).
`ry`	Column restriction. If omitted, y is free and y contains the initial column coordinates. If logical valued, y (m by p) contains the initial column coordinates and ry (m by p) indicated free (false) and fixed (true) column coordinates. If real valued, y (n by hy) contains hy independent column variables and ry (hy by p) contains the initial column regression coefficients.
`MAXITER`	maximum number of iterations (default = 1024).
`FCRIT`	relative convergence criterion (default = 0.00000001).
`error.check`	extensive check validity input parameters (default = FALSE).
`echo`	print intermediate algorithm results (default = FALSE).

Value

data original n by m matrix with dissimilarities.

weights original n by m matrix with dissimilarity weights.

row.coordinates final n by p matrix with row coordinates.

col.coordinates final m by p matrix with column coordinates.

row.coefficients if rx is real valued, final hx by p matrix with row regression coefficients.

col.coefficients if ry is real valued, final hy by p matrix with column regression coefficients.

distances final n by m matrix with distances.

last.iteration final iteration number.

last.difference final function difference used for convergence testing.

n.stress final normalized stress value.

stress.1 final stress-1 value.

call function call

References

de Leeuw, J., and Heiser, W. J. (1980). Multidimensional scaling with restrictions on the configuration. In P.R. Krishnaiah (Ed.), Multivariate analysis (Vol. 5, pp. 501–522). Amsterdam, The Netherlands: North-Holland Publishing Company.

Heiser,W. J. (1987a). Joint ordination of species and sites: The unfolding technique. In P. Legendre and L. Legendre (Eds.), Developments in numerical ecology (pp. 189–221). Berlin, Heidelberg: Springer-Verlag.

Busing, F.M.T.A. (2010). Advances in multidimensional unfolding. Unpublished doctoral dissertation, Leiden University, Leiden, the Netherlands.

Examples

```
## Not run:
library( smacof )
data( "breakfast" )
breakfast <- as.matrix( breakfast )
n <- nrow( breakfast )
m <- ncol( breakfast )
p <- 2
w <- matrix( 1, n, m )
x <- matrix( runif( n * p ), n, p )
y <- matrix( runif( m * p ), m, p )
r <- fastmdu( breakfast, w, p, x, NULL, y, NULL )
print( r )

## End(Not run)
```

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plot.fmdu   *Visualisation of a fmdu objects*

Description

Plot method for a `fmdu` object. The plot shows the result of `fmdu`.

Usage

```
## S3 method for class 'fmdu'
plot(x, ...)
```

Arguments

x   An fmdu object .

...   additional arguments to pass

Value

No return value, called for side effects (plot)

---

print.fmdu	*Print method for all fmdu objects*

Description

Print the results of a fmdu object

Usage

```
## S3 method for class 'fmdu'
print(x, ...)
```

Arguments

x	object of class `fmdu`.
...	additional arguments to be passed.

Value

No return value, called for side effects (print)

---

summary.fmdu	*Summary method for all fmdu objects*

Description

Summary method for all fmdu objects

Usage

```
## S3 method for class 'fmdu'
summary(object, ...)
```

Arguments

object	object of class `fmdu`.
...	additional arguments to be passed.

Value

No return value, called for side effects (summary)

Index