

Package ‘lsbclust’

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Type Package

Title Least-Squares Bilinear Clustering for Three-Way Data

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Description Functions for performing least-squares bilinear clustering of three-way data. The method uses the bilinear decomposition (or bi-additive model) to model two-way matrix slices while clustering over the third way. Up to four different types of clusters are included, one for each term of the bilinear decomposition. In this way, matrices are clustered simultaneously on (a subset of) their overall means, row margins, column margins and row-column interactions. The orthogonality of the bilinear model results in separability of the joint clustering problem into four separate ones. Three of these sub-problems are specific k-means problems, while a special algorithm is implemented for the interactions. Plotting methods are provided, including biplots for the low-rank approximations of the interactions.

License GPL (>= 2)

Depends R (>= 3.4.0), stats, ggplot2

Imports plyr, clue, grid, gridExtra, reshape2, Rcpp, mvtnorm,
graphics, methods, doParallel, foreach, parallel

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lsbclust-package	<i>Least Squares Latent Class Matrix Factorization</i>
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Description

Functions for least squares latent class matrix factorizations.

Author(s)

Pieter C. Schoonees [aut, cre], Patrick J.F. Groenen [aut]

References

Van Rosmalen, J., Van Herk, H., & Groenen, P. J. F. (2010). Identifying response styles: A latent-class bilinear multinomial logit model. *Journal of Marketing Research*, 47(1), 157-172.

akmeans	<i>K-Means Over One Way of An Three-Way Array</i>
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Description

Vectorize matrix slices over a specific way of an three-way array, and conduct [kmeans](#) on it.

Usage

```
akmeans(data, centers, margin = 3L, ndim = NULL, ...)
```

Arguments

data	Three-way data array
centers	Passed to kmeans
margin	Integer indicating which way to cluster over
ndim	The rank of the low dimensional approximation of the matrix slices to construct before clustering (using svd)
...	Additional arguments passed to kmeans

Examples

```
set.seed(1)
res <- akmeans(data = carray(dcars), margin = 3L, centers = 5, nstart = 10)
```

`bicomp`*Bilinear Decomposition of a Matrix*

Description

Decomposes a matrix into an overall mean matrix, row margins matrix, column margins matrix and an interaction matrix, depending on delta.

Usage

```
bicomp(x, delta = c(1, 1, 1, 1), which = 0L:4L)
```

Arguments

<code>x</code>	A matrix to be decomposed.
<code>delta</code>	A vector of length four with 0/1 entries which controls the type of decomposition made.
<code>which</code>	A vector giving the elements to return, with 0 = original data, 1 = overall means, 2 = row means, 3 = column means and 4 = interactions.

Value

An object of class `bicomp`, possible also inheriting from class `data.frame`, which is either a named list with the required components, or a single matrix if a single component is requested. An additional attribute `return_type` gives information on the type of matrices returned.

`carray`*Double-Centre a Three-way Array*

Description

Double-centre the matrix slices of a three-way array.

Usage

```
carray(array, margin = 3L, rows = TRUE, columns = TRUE)
```

Arguments

<code>array</code>	A three-way array
<code>margin</code>	The way of the array over which the centring must be done
<code>rows</code>	Logical indicating whether to centre the rows of the matrix slices
<code>columns</code>	Logical indicating whether to centre the columns of the matrix slices

cfsim	<i>Compare Simulation Results</i>
-------	-----------------------------------

Description

Generic function to compare simulation results in **lsbclust**.

Usage

```
cfsim(fitted, actual, method = c("diag", "cRand"))
```

Arguments

fitted	An object of class <code>lsbclust</code> containing the fitted results.
actual	An object of class <code>lsbclust_sim</code> containing the simulated data.
method	The type of statistics to calculate, passed to cl_agreement

See Also

[cfsim.lsbclust](#), [cfsim.T3Clusf](#)

cfsim.akmeans	<i>Compare LSBCLUST Simulation Results</i>
---------------	--

Description

This function compares cluster membership and parameter estimates for the results of [akmeans](#) on simulated data, constructed using [rlsbclust](#), to the true underlying values.

Usage

```
## S3 method for class 'akmeans'
cfsim(fitted, actual, method = c("diag", "cRand"))
```

Arguments

fitted	An object of class <code>akmeans</code> containing the fitted results.
actual	An object of class <code>lsbclust_sim</code> containing the simulated data.
method	The method for calculating cluster agreement across random starts, passed on to cl_agreement . None is calculated when set to <code>NULL</code> .

Examples

```
## Simulate LSBCLUST data, fit akmeans on double-centered data, and compare
set.seed(1)
dat <- rlsbclust(ndata = 1, nobs = 100, size = c(10, 8), nclust = c(5, 4, 6, 5))
dat[[1]]$data <- carray(dat[[1]]$data)
res <- akmeans(data = dat[[1]]$data, centers = 5, margin = 3, ndim = 2)
cfsim(res, dat[[1]])
```

cfsim.lsbclust *Compare LSBCLUST Simulation Results*

Description

This function compares cluster membership and parameter estimates for the results of `lsbclust` on simulated data to the true underlying values.

Usage

```
## S3 method for class 'lsbclust'
cfsim(fitted, actual, method = c("diag", "cRand"))
```

Arguments

fitted	An object of class <code>lsbclust</code> containing the fitted results.
actual	An object of class <code>lsbclust_sim</code> containing the simulated data.
method	The type of statistics to calculate, passed to <code>c1_agreement</code>

Examples

```
## Simulate LSBCLUST data, fit LSBCLUST, and compare
set.seed(1)
dat <- rlsbclust(ndata = 1, nobs = 100, size = c(10, 8), nclust = c(5, 4, 6, 5))
res <- lsbclust(data = dat[[1]]$data, nclust = c(5, 4, 6, 5))
cfsim(res, dat[[1]])
```

cfsim.T3Clusf *Compare LSBCLUST Simulation Results*

Description

This function compares cluster membership and parameter estimates for the results of `T3Clusf` on simulated data, using `rlsbclust`, to the true underlying values.

Usage

```
## S3 method for class 'T3Clusf'
cfsim(fitted, actual, method = c("diag", "cRand"))
```

Arguments

fitted	An object of class <code>lsbclust</code> containing the fitted results.
actual	An object of class <code>lsbclust_sim</code> containing the simulated data.
method	The method for calculating cluster agreement across random starts, passed on to <code>cl_agreement</code> . None is calculated when set to <code>NULL</code> .

Examples

```
## Simulate LSBCLUST data, fit T3Clusf on double-centered data, and compare
set.seed(1)
dat <- rlsbclust(ndata = 1, nobs = 100, size = c(10, 8), nclust = c(5, 4, 6, 5))
dat[[1]]$data <- carray(dat[[1]]$data)
res <- T3Clusf(X = dat[[1]]$data, Q = 2, G = 5)
cfsim(res, dat[[1]])
```

ClustMeans

C++ Function for Cluster Means

Description

This function calculates the cluster means in vectorized form based on the current value of the clustering vector.

Usage

```
ClustMeans(nclust, start, data)
```

Arguments

nclust	The number of clusters.
start	The current clustering vector.
data	The concatenated data, with $J * K$ rows and N columns

Value

A numeric matrix with `nclust` rows and $J * K$ columns.

```
cl_class_ids.int.lsbclust
      S3 export
```

Description

These export into the framework set out in package **clue**.

Usage

```
## S3 method for class 'int.lsbclust'
cl_class_ids(x)

## S3 method for class 'int.lsbclust'
is.cl_partition(x)

## S3 method for class 'int.lsbclust'
is.cl_hard_partition(x)

## S3 method for class 'lsbclust_sim_part'
cl_class_ids(x)

## S3 method for class 'lsbclust_sim_part'
is.cl_partition(x)

## S3 method for class 'lsbclust_sim_part'
is.cl_hard_partition(x)

## S3 method for class 'T3Clusf'
cl_class_ids(x)

## S3 method for class 'T3Clusf'
is.cl_partition(x)

## S3 method for class 'T3Clusf'
is.cl_hard_partition(x)

## S3 method for class 'akmeans'
cl_class_ids(x)

## S3 method for class 'akmeans'
is.cl_partition(x)

## S3 method for class 'akmeans'
is.cl_hard_partition(x)
```


Arguments

x An object of class `int.lsclust`

cmat *Centring Matrix*

Description

A utility function for calculating centring matrices.

Usage

cmat(k)

Arguments

k An integer determining the dimensions of the centring matrix.

dcars *Dutch Cars Data*

Description

This data set relates to 187 Dutch households rating 10 automobile manufacturers according to 8 variables (original Dutch terms in parentheses): price (prijsniveau), design (vormgeving), safety (veiligheid), operating cost (gebruikskosten), sportiness (sportiviteit), size (modelgrootte), reliability (betrouwbaarheid) and features (uitrusting). A rating scale from 1 to 10 was used.

Usage

dcars

Format

A three-way array with cars in the first dimension, variables in the second and consumers in the third dimension.

The items and labels for the endpoints of the scales are (original Dutch labels in parentheses):

Affordability A rating from 1 = Expensive (duur) to 10 = Cheap (goedkoop)

Attractiveness A rating from 1 = Ugly (lelijk) to 10 = Beautiful (mooi)

Safety A rating from 1 = Bad (slecht) to 10 = Good (goed)

OperatingCost A rating from 1 = Low (laag) to 10 = High (hoog)

Sportiness A rating from 1 = Slow (langzaam) to 10 = Fast (snel)

Size A rating from 1 = Large (groot) to 10 = Small (klein)

Reliability A rating from 1 = Bad (slecht) to 10 = Good (goed)

Features A rating from 1 = Simple (eenvoudig) to 10 = Luxurious (luxe)

Details

The original sample consisted of 188 households. However, one of these households (code 87845) was discarded because it appears that they used a rating scale from 0 to 10 instead of from 1 to 10. Note that all rating scales has been reversed so that higher scores are better for most items. The exceptions are OperatingCost and Size, where larger values mean higher costs and smaller cars respectively.

Source

Tammo Bijmolt, Michel van de Velden

Examples

```
data("dcars")
set.seed(5448)
m <- lsbcclust(data = dcars, delta = c(1, 1, 1, 1), nclust = c(5, 3, 6, 8), nstart = 5,
               nstart.kmeans = 10, parallel = FALSE, fixed = "columns")
```

fitted.akmeans

Extract Fitted Values for akmeans

Description

An S3 method for `fitted` for class "akmeans".

Usage

```
## S3 method for class 'akmeans'
fitted(object, ...)
```

Arguments

object	An object of class "akmeans"
...	Unimplemented

Value

An array approximating the original data

See Also

[akmeans](#)

fitted.lsbclust	<i>Extract Fitted Values for LSBCLUST</i>
-----------------	---

Description

An S3 method for [fitted](#) for class "lsbclust".

Usage

```
## S3 method for class 'lsbclust'  
fitted(object, ...)
```

Arguments

object	An object of class "lsbclust"
...	Unimplemented

Value

An array approximating the original data

See Also

[lsbclust](#)

fitted.T3Clusf	<i>Extract Fitted Values for T3Clusf</i>
----------------	--

Description

An S3 method for [fitted](#) for class "T3Clusf".

Usage

```
## S3 method for class 'T3Clusf'  
fitted(object, ...)
```

Arguments

object	An object of class "T3Clusf"
...	Unimplemented

Value

An array approximating the original data

See Also[T3Clusf](#)

`genproc`*Generalized Procrustes Rotation*

Description

This function finds K orthogonal rotation matrices so that the rotated versions of the input configurations match each other optimally in the least-squares sense. The algorithm depends on the starting values for the rotation matrices. At present identity matrices are used as starting values. Only rotations / reflections are considered – no scaling or translation factors are included.

Usage

```
genproc(configs, maxit = 50L, reltol = 1e-06, random = FALSE)
```

Arguments

<code>configs</code>	A list of original configuration matrices
<code>maxit</code>	The maximum number of iterations allowed
<code>reltol</code>	The relative error tolerance for determining numeric convergence.
<code>random</code>	Logical indicating whether or not to use random starts (only applicable when the dimensionality is two).

References

Gower, J. C., & Dijksterhuis, G. B. (2004). Procrustes problems (Vol. 3). Oxford: Oxford University Press.

`indarr`*Create Array of Indicator Matrices*

Description

This function takes a `matrix` or `data.frame` and the number of rating categories `maxcat` and produces a three-way array of m by `maxcat` indicator matrices, one for each of the n rows. The input `x` must be a `matrix` or `data.frame` of dimensions n by m which contains the ratings on a scale of 1 to `maxcat` for m items. Note that missing values (NA's) will not appear in the columns.

Usage

```
indarr(x, maxcat, na.add = TRUE)
```

Arguments

x	a matrix of data.frame
maxcat	an integer indicating the maximum of the rating scale (which is assumed to start with 1)
na.add	logical indicating whether to add a designated category for missings or not. Defaults to TRUE.

Value

A list of rating by item indicator matrices.

Author(s)

Pieter C. Schoonees

Examples

```
data("lov")
arr <- indarr(lov[1:10, 1:9], maxcat = 9)
str(arr)
```

int.lsbclust

Interaction Clustering in Least Squares Bilinear Clustering

Description

This function implements the interaction clustering part of the Least Squares Bilinear Clustering method of Schoonees, Groenen and Van de Velden (2014).

Usage

```
int.lsbclust(data, margin = 3L, delta, nclust, ndim = 2, fixed = c("none",
  "rows", "columns"), nstart = 50, starts = NULL, alpha = 0.5,
  parallel = FALSE, mc.cores = detectCores() - 1, maxit = 100,
  verbose = 1, method = "diag", minsize = 3L, return_data = FALSE)
```

Arguments

data	A three-way array representing the data.
margin	An integer giving the single subscript of data over which the clustering will be applied.
delta	A four-element binary vector (logical or numeric) indicating which sum-to-zero constraints must be enforced.
nclust	An integer giving the desired number of clusters. If it is a vector, the algorithm will be run for each element.
ndim	The required rank for the approximation of the interactions (a scalar).

<code>fixed</code>	One of "none", "rows" or "columns" indicating whether to fix neither sets of coordinates, or whether to fix the row or column coordinates across clusters respectively. If a vector is supplied, only the first element will be used.
<code>nstart</code>	The number of random starts to use.
<code>starts</code>	A list containing starting configurations for the cluster membership vector. If not supplied, random initializations will be generated.
<code>alpha</code>	Numeric value in [0, 1] which determines how the singular values are distributed between rows and columns.
<code>parallel</code>	Logical indicating whether to parallelize over different starts or not.
<code>mc.cores</code>	The number of cores to use in case <code>parallel = TRUE</code> , passed to <code>makeCluster</code> .
<code>maxit</code>	The maximum number of iterations allowed.
<code>verbose</code>	Integer controlling the amount of information printed: 0 = no information, 1 = Information on random starts and progress, and 2 = information is printed after each iteration for the interaction clustering.
<code>method</code>	The method for calculating cluster agreement across random starts, passed on to <code>cl_agreement</code> . None is calculated when set to NULL.
<code>minsize</code>	Integer giving the minimum size of cluster to uphold when reinitializing empty clusters.
<code>return_data</code>	Logical indicating whether to include the data in the return value or not

Value

An object of class `int.lsb`

Examples

```
data("supermarkets")
out <- int.lsbclust(data = supermarkets, margin = 3, delta = c(1,1,0,0), nclust = 4, ndim = 2,
  fixed = "rows", nstart = 1, alpha = 0)
```

KMeansW

C++ Function for Weighted K-Means

Description

This function does a weighted K-means clustering.

Usage

```
ComputeMeans(cm, data, weight, nclust)
```

```
AssignCluster(data, weight, M, nclust)
```

```
KMeansW(nclust, start, data, weight, eps = 1e-08, IterMax = 100L)
```

Arguments

cm	Numeric vector of class indicators.
data	The concatenated data, with N rows and M columns. Currently, the columns are clustered.
weight	The vector of length nrow(data) with weights with nonnegative elements.
nclust	The number of clusters.
M	Matrix of cluster means.
start	The current cluster membership vector.
eps	Numerical absolute convergence criteria for the K-means.
IterMax	Integer giving the maximum number of iterations allowed for the K-means.

Value

A list with the following values.

centers	the nclust by M matrix centers of cluster means.
cluster	vector of length N with cluster memberships.
loss	vector of length IterMax with the first entries containing the loss.
iterations	the number of iterations used (corresponding to the number of nonzero entries in loss)

Examples

```
set.seed(1)
clustmem <- sample.int(n = 10, size = 100, replace = TRUE)
mat <- rbind(matrix(rnorm(30*4, mean = 3), nrow = 30),
             matrix(rnorm(30*4, mean = -2), nrow = 30),
             matrix(rnorm(40*4, mean = 0), nrow = 40))
wt <- runif(100)
testMeans <- lsyclust:::ComputeMeans(cm = clustmem, data = mat, weight = wt, nclust = 3)
testK <- lsyclust:::KMeansW(start = clustmem, data = mat, weight = wt, nclust = 3)
```

LossMat

C++ Function for Interaction Loss Function

Description

This function calculates the loss function for the interaction clustering for all data slices and clusters means. The inputs are numeric matrices.

Arguments

x	The data matrix, with the N slices strung out as vectors in the columns.
y	The matrix of cluster means, with each mean represented by a row.

Value

A numeric matrix with nclust rows and N columns.

 lov

List-of-values Data Set

Description

This is the list-of-values data set used in Van Rosmalen, Van Herk & Groenen (2010). Column names and factor labels differ slightly from that paper. Missing values are encoded as NA as usual. The first nine columns are items answered on a nine-point rating scale, with rating 1 representing 'very important' and category 9 'not important at all'. The respondents were asked how important each of these items are as a guiding principle in their lives.

Usage

```
data("lov")
```

Format

A data frame with 4514 observations on the following 12 variables.

Belonging a numeric vector; 'a sense of belonging'

Excitement a numeric vector

Relationships a numeric vector; 'warm relationships with others'

Self-fulfilment a numeric vector

Respected a numeric vector; 'being well-respected'

Enjoyment a numeric vector; 'fun and enjoyment'

Security a numeric vector

Self-respect a numeric vector

Accomplishment a numeric vector; 'a sense of accomplishment'

Country a factor with levels Britain, France, Germany, Italy and Spain

Education a factor with levels Low and High

Age a factor with levels -25, 25-39, 40-54 and 55+

Source

Joost van Rosmalen

References

Van Rosmalen, J., Van Herk, H., & Groenen, P. J. (2010). Identifying response styles: A latent-class bilinear multinomial logit model. *Journal of Marketing Research*, 47(1), 157-172.

Examples

```
data("lov")

## Construct array
lovarr <- indarr(lov[, 1:9], maxcat = 9)

## Run analysis
set.seed(13841)
fit <- lsbclust(data = lovarr, margin = 3, delta = c(0, 1, 0, 0), nclust = c(NA, 11, NA, 5),
               fixed = "rows", nstart = 1, iter.max = 50, nstart.kmeans = 10)
```

lsbclust

Least-squares Bilinear Clustering of Three-way Data

Description

This function clusters along one way of a three-way array (as specified by `margin`) while decomposing along the other two dimensions. Four types of clusterings are allowed based on the respective two-way slices of the array: on the overall means, row margins, column margins and the interactions between rows and columns. Which clusterings can be fit is determined by the vector `delta`, with four binary elements. All orthogonal models are fitted. The nonorthogonal case `delta = (1, 1, 0, 0)` returns an error. See the reference for further details.

Usage

```
lsbclust(data, margin = 3L, delta = c(1L, 1L, 1L, 1L), nclust, ndim = 2L,
         fixed = c("none", "rows", "columns"), nstart = 20L, starts = NULL,
         nstart.kmeans = 500L, alpha = 0.5, parallel = FALSE, maxit = 100L,
         verbose = 1, method = "diag", type = NULL, sep.nclust = TRUE, ...)
```

Arguments

<code>data</code>	A three-way array representing the data.
<code>margin</code>	An integer giving the single subscript of <code>data</code> over which the clustering will be applied.
<code>delta</code>	A four-element binary vector (logical or numeric) indicating which sum-to-zero constraints must be enforced.
<code>nclust</code>	A vector of length four giving the number of clusters for the overall mean, the row margins, the column margins and the interactions (in that order) respectively. Alternatively, a vector of length one, in which case all components will have the same number of clusters.
<code>ndim</code>	The required rank for the approximation of the interactions (a scalar).
<code>fixed</code>	One of "none", "rows" or "columns" indicating whether to fix neither sets of coordinates, or whether to fix the row or column coordinates across clusters respectively. If a vector is supplied, only the first element will be used (passed to int.lsbclust).

nstart	The number of random starts to use for the interaction clustering.
starts	A list containing starting configurations for the cluster membership vector. If not supplied, random initializations will be generated (passed to <code>int.lsbclust</code>).
nstart.kmeans	The number of random starts to use in <code>kmeans</code> .
alpha	Numeric value in [0, 1] which determines how the singular values are distributed between rows and columns (passed to <code>int.lsbclust</code>).
parallel	Logical indicating whether to parallel over different starts or not (passed to <code>int.lsbclust</code>).
maxit	The maximum number of iterations allowed in the interaction clustering.
verbose	Integer controlling the amount of information printed: 0 = no information, 1 = Information on random starts and progress, and 2 = information is printed after each iteration for the interaction clustering.
method	The method for calculating cluster agreement across random starts, passed on to <code>cl_agreement</code> (passed to <code>int.lsbclust</code>).
type	One of "rows", "columns" or "overall" (or a unique abbreviation of one of these) indicating whether clustering should be done on row margins, column margins or the overall means of the two-way slices respectively. If more than one option are supplied, the algorithm is run for all (unique) options supplied (passed to <code>orc.lsbclust</code>). This is an optional argument.
sep.nclust	Logical indicating how nclust should be used across different type's. If sep.nclust is TRUE, nclust is recycled so that each type can have a different number of clusters. If sep.nclust is FALSE, the same vector nclust is used for all type's.
...	Additional arguments passed to <code>kmeans</code> .

Value

Returns an object of S3 class `lsbclust` which has slots:

overall	Object of class <code>ovl.kmeans</code> for the overall means clustering
rows	Object of class <code>row.kmeans</code> for the row means clustering
columns	Object of class <code>col.kmeans</code> for the column means clustering
interactions	Object of class <code>int.lsbclust</code> for the interaction clustering
call	The function call used to create the object
delta	The value of delta in the fit
df	Breakdown of the degrees-of-freedom across the different subproblems
loss	Breakdown of the loss across subproblems
time	Time taken in seconds to calculate the solution
cluster	Matrix of cluster membership per observation for all cluster types

References

Schoonees, P.C., Groenen, P.J.F., Van de Velden, M. Least-squares Bilinear Clustering of Three-way Data. Econometric Institute Report, EI2014-23.

See Also

[int.lsbclust](#), [orc.lsbclust](#)

meanbiplot

Biplots of

Description

Construct simple two-dimensional biplots given matrices representing the rows and columns of a two-dimensional matrix using **ggplot2**.

Usage

```
meanbiplot(rows, cols)
```

Arguments

rows A list of matrices representing the rows
 cols A list of matrices representing the columns

Examples

```
set.seed(1)
dat <- rlsbclust(ndata = 1, nobs = 100, size = c(10, 8), nclust = c(5, 4, 6, 5))
meanbiplot(dat[[1]]$interactions$C, dat[[1]]$interactions$D)
```

meanheatmap

Plot Heatmap of A Matrix

Description

Construct a heatmap of a matrix using **ggplot2**.

Usage

```
meanheatmap(x)
```

Arguments

x Matrix or list of matrices to be plotted

Examples

```
set.seed(1)
dat <- rlsbclust(ndata = 1, nobs = 100, size = c(6, 6), nclust = c(5, 4, 6, 5))
meanheatmap(Map(tcrossprod, dat[[1]]$interactions$C, dat[[1]]$interactions$D))
```

orc.lsbclust

*K-means on the Overall Mean, Row Margins or Column Margins***Description**

This function conducts k-means on the overall mean, the row margins or column margins of a set of N matrices. These matrices are two-way slices of a three-dimensional array.

Usage

```
orc.lsbclust(data, margin = 3L, delta, nclust, sep.nclust = TRUE,
             type = NULL, verbose = 1, ...)
```

Arguments

data	A three-way array representing the data.
margin	An integer giving the single subscript of data over which the clustering will be applied.
delta	A four-element binary vector (logical or numeric) indicating which sum-to-zero constraints must be enforced.
nclust	An integer giving the desired number of clusters. In case type specifies more than one method, nclust can be a vector containing the number of clusters to be determined for each type of cluster, and in the correct order as determined by type (after matching the arguments). If type is of length greater than one and nclust is of length one, the behaviour is governed by sep.nclust.
sep.nclust	Logical indicating how nclust should be used across different type's. If sep.nclust is TRUE, nclust is recycled so that each type can have a different number of clusters. If sep.nclust is FALSE, the same vector nclust is used for all type's.
type	One of "overall", "rows" or "columns" (or a unique abbreviation of one of these) indicating whether clustering should be done on row margins, column margins or the overall means of the two-way slices respectively. If more than one option are supplied, the algorithm is run for all (unique) options supplied.
verbose	Integer controlling the amount of information printed: 0 = no information, 1 = Information on random starts and progress, and 2 = information is printed after each iteration for the interaction clustering.
...	Additional arguments passed to kmeans .

Value

A list containing a subset of the classes row.kmeans, col.kmeans and ov1.kmeans which are specific versions of class kmeans. In case type is a vector, a list is returned containing the results for each of the (unique) elements of type, with the same classes as before. See [kmeans](#) for an overview of the structure of these objects.

See Also

[kmeans](#)

plot.bicomp	<i>Plot a bicomp Object</i>
-------------	-----------------------------

Description

Plot method for an object of class bicomp (see [bicomp](#)).

Usage

```
## S3 method for class 'bicomp'
plot(x, which = 0L:4L, arrange = TRUE, col = c("red4",
  "beige", "blue4"), strip.legend = TRUE, add.titles = FALSE, ...)
```

Arguments

x	An object of class bicomp.
which	A numeric vector indicating which matrices to plot, with 0 = original data, 1 = overall means, 2 = row means, 3 = column means and 4 = interactions.
arrange	Logical indicating whether to arrange the plots side-by-side via grid.arrange or not.
col	A character vector of length three giving the parameters low, mid and high for scale_fill_gradient2 .
strip.legend	Logical indicating whether to strip the legend off the plot or not.
add.titles	Logical indicating whether to add titles to the plots or not.
...	Additional arguments to theme .

plot.col.kmeans	<i>Plot method for class 'col.kmeans'</i>
-----------------	---

Description

Simple plot method for object of class 'col.kmeans' as output by [orc.lsbclust](#).

Usage

```
## S3 method for class 'col.kmeans'
plot(x, which = 1L, ...)
```

Arguments

x	An object of class col.kmeans
which	Which type of plot to produce (only 3 types are implemented).
...	additional arguments passed to theme .

Author(s)

Pieter C. Schoonees

Examples

```
data("dcars")
m <- orc.lsbclust(data = dcars, margin = 3, delta = c(1,1,1,1), nclust = 5, type = "columns")
plot(m)
```

plot.int.lsbclust *Plot Method for Class 'int.lsbclust'*

Description

Two-dimensional plot method for object of class 'int.lsbclust' as output by [int.lsbclust](#).

Usage

```
## S3 method for class 'int.lsbclust'
plot(x, which = seq_len(nclust),
     plot.type = c("biplots", "means", "estimates"), segments = NULL,
     biplot.axes = TRUE, nmarkers = 5, alpha = NULL, check.alpha = TRUE,
     fix.alpha = FALSE, probs = 0, arrange = FALSE, fix.limits = TRUE,
     limit.exp = 1.05, lambda.scale = TRUE, procrustes.rotation = x$fixed ==
     "none", fix.lambda = FALSE, labs.grey = TRUE, label.0 = FALSE,
     tick.length = 0.0075 * diff(lims), axis.col = "grey60", label.size = 3,
     axis.size = 0.25, axis.title.size = 4, draw.axis = NULL,
     points.col = list(rows = "red", columns = "blue2"),
     offset.tick.labels = 3.5, offset.axis.title = list(rows = 0.015 *
     max(nchar(rnms)), columns = 0.015 * max(nchar(cnms))),
     axis.arrow = grid::arrow(angle = 20, length = grid::unit(0.0175, "npc")),
     ...)
```

Arguments

x	An object of class <code>int.lsbclust</code> .
which	A vector indicating which item segments to plot.
plot.type	Character string giving the type of plots to produce: either "biplots" for the biplots approximating the cluster means, "means" for level plots of the cluster means themselves or "estimates" for level plots of the low-rank approximations of the cluster means (as represented in the biplots).
segments	A logical vector with two elements, indicating whether the rows and columns should be plotted as line segments or not.
biplot.axes	A logical indicating whether to plot calibrated biplot axes for the line segments indicated in segments or not.

nmarkers	Either a single integer giving the number of desired markers per biplot axis for all axes, or a named list. This is passed as the argument <code>n</code> to <code>pretty</code> . See <code>Details</code> for information on the list option.
alpha	Numeric value in $[0, 1]$ which determines how the singular values are distributed between rows and columns. It will trigger a recomputation of the updates if it does not correspond to the value used when fitting the model.
check.alpha	Logical indicating whether to look for a better alpha. This is only used when <code>alpha = NULL</code> is used.
fix.alpha	Logical indicating whether to fix alpha across all clusters or not when <code>fixed == "none"</code> .
probs	Argument passed to <code>quantile</code> to determine the alpha value. The corresponding quantile of the distances of all points in the biplots to the origin will be used to determine alpha in case <code>check.alpha = TRUE</code> .
arrange	Logical indicating whether to arrange the plots side-by-side via <code>grid.arrange</code> or not.
fix.limits	Logical indicating whether biplot x- and y-limits must be fixed across clusters or not. Note that this is automatically set to <code>TRUE</code> when <code>fixed == "rows"</code> or <code>fixed == "columns"</code> . When limits are fixed, the axis calibrations are also turned off.
limit.exp	A numeric expansion factor applied multiplicatively to the plot limits, but only when <code>fixed</code> equals <code>"rows"</code> or <code>"columns"</code> .
lambda.scale	Logical indicating whether to apply lambda scaling to the coordinates or not. If true, the scaling is done such that the average squared distance to the origin is equal for the row and column coordinates.
procrustes.rotation	Logical indicating whether to do Procrustes rotations so that the location of the axes indicated as segments (see argument <code>segments</code>) are similar across configurations.
fix.lambda	Logical indicating whether to fix lambda across all clusters or not.
labs.grey	Logical indicating whether to apply greying to the text labels or not.
label.0	Logical indicating whether to label the origin or not.
tick.length	The required tick length as a <code>unit</code> object. It defaults to a proportion of the width of the plot region (through lazy evaluation).
axis.col	The colour of the biplot axes.
label.size	The size of the labels for the markers on the biplot axes.
axis.size	Line size for biplot axes.
axis.title.size	Size of biplot axis titles.
draw.axis	A list with up to two components which must be named <code>"rows"</code> and <code>"columns"</code> . Each element contains a vector indicating which biplot axes should be drawn. The vectors can be character vectors containing the names of the axes to be drawn, numeric vectors containing indices indicating which axes to draw, or logical vectors indicating which biplot axes to draw. In case of the default value <code>NULL</code> , the elements of <code>segments</code> are used for the <code>"rows"</code> and <code>"columns"</code> entries.

points.col	A named list containing the colours to use for plotting the sets of points. The elements "rows" and "columns" contain vectors giving the colours for the points. Single element vectors are recycled across the different points, otherwise the vectors must be of the appropriate length.
offset.tick.labels	A numeric value giving the offset factor of the biplot axis marker labels from their respective tick marks. Higher (lower) values lead to labels being further from (nearer to) their respective tick marks.
offset.axis.title	A names list of (up to) two numeric values giving the fixed length offset of the biplot axis title label from the end of the axis segment. The two elements must have names "rows" and "columns".
axis.arrow	An arrow object to be used for the endpoints of biplot axis segment lines. This is passed to geom_segment .
...	Additional arguments passed to theme .

Details

In case `nmarkers` is a list, it can have up to two elements. These are required to be named "rows" and/or "columns", otherwise an error will be thrown. The elements of the list contains either single numeric values each or numeric vectors of the appropriate lengths indicating the `n` argument passed to [pretty](#).

plot.lsbclust	<i>Plot method for class 'lsbclust'</i>
---------------	---

Description

This plot method simply plots each of the components in the list of class `lsbclust`.

Usage

```
## S3 method for class 'lsbclust'
plot(x, type = c("overall", "rows", "columns",
  "interactions"), biplot.axes = TRUE, ...)
```

Arguments

x	An object of class <code>orc.kmeans</code>
type	A character vector indicating which component(s) of <code>x</code> to plot: a combination of "overall", "rows", "columns" and "interactions".
biplot.axes	A logical indicating whether to plot calibrated biplot axes for the line segments indicated in segments or not.
...	additional arguments passed to the plot methods of the respective components, typically to theme . Use e.g. <code>plot(x\$interactions)</code> for more control over the respective plots.

Author(s)

Pieter C. Schoonees

See Also[plot.int.lsbclust](#), [plot.ovl.kmeans](#), [plot.row.kmeans](#), [plot.col.kmeans](#)**Examples**

```
data("dcars")
m <- lsbclust(data = dcars, margin = 3, delta = c(1, 1, 1, 1), nclust = 5, nstart = 1)
plot(m)
```

plot.ovl.kmeans *Plot method for class 'ovl.kmeans'*

Description

Simple plot method for object of class 'ovl.kmeans' as output by [orc.lsbclust](#).

Usage

```
## S3 method for class 'ovl.kmeans'
plot(x, which = 1L, ...)
```

Arguments

x An object of class `ovl.kmeans`

which Which type of plot to produce. Currently only `which = 1` is implemented.

... additional arguments passed to [theme](#).

Author(s)

Pieter C. Schoonees

Examples

```
data("dcars")
m <- orc.lsbclust(data = dcars, margin = 3, delta = c(1,1,1,1), nclust = 5, type = "overall")
plot(m)
```

plot.row.kmeans *Plot method for class 'row.kmeans'*

Description

Simple plot method for object of class 'row.kmeans' as output by [orc.lsbclust](#).

Usage

```
## S3 method for class 'row.kmeans'
plot(x, which = 1L, ...)
```

Arguments

x An object of class row.kmeans
 which Which type of plot to produce (only 3 types are implemented).
 ... additional arguments passed to [theme](#).

Author(s)

Pieter C. Schoonees

Examples

```
data("dcars")
m <- orc.lsbclust(data = dcars, margin = 3, delta = c(1,1,1,1), nclust = 5, type = "rows")
plot(m)
```

plot.step.lsbclust *Plot method for class 'step.lsbclust'*

Description

Plot 'step.lsbclust' objects.

Usage

```
## S3 method for class 'step.lsbclust'
plot(x, which = 1L:5L, col.all = NULL,
     arrange = FALSE, chull = FALSE, ...)
```

Arguments

x	An object of class <code>step.lsbclust</code>
which	Which type of plot to produce.
col.all	A character vector of length one indicating which of "overall", "rows", "columns" or "interactions" should be mapped to colour in the plot for all possible models. Care needs to be taken that the stated component is included in the fit.
arrange	Logical indicating whether to arrange the plots side-by-side via <code>grid.arrange</code> or not.
chull	Logical indicating whether to plot the estimated convex hull or not.
...	additional arguments passed to <code>theme</code> .

Author(s)

Pieter C. Schoonees

plot.T3Clusf

Plot Method for Class 'T3Clusf'

Description

Two-dimensional plot method for object of class 'T3Clusf' as output by `T3Clusf`.

Usage

```
## S3 method for class 'T3Clusf'
plot(x, which = seq_len(nclust), arrange = FALSE, ...)
```

Arguments

x	An object of class <code>T3Clusf</code> .
which	An integer vector indicating which item segments to plot.
arrange	Logical indicating whether to arrange the plots on a single page or not
...	Additional arguments to <code>theme</code>

print.lsbclust	<i>Print method for object of class 'lsbclust'</i>
----------------	--

Description

Print a 'lsbclust' object.

Usage

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

Arguments

x	An object of class 'lsbclust'
...	Unimplemented.

rlsbclust	<i>Simulate from LSBCLUST Model</i>
-----------	-------------------------------------

Description

Simulate three-way arrays adhering to the LSBCLUST framework (see [lsbclust](#)).

Usage

```
rlsbclust(ndata = 50L, nobs, size, nclust, clustsize = NULL,
  delta = rep(1L, 4L), ndim = 2L, alpha = 0.5, fixed = c("none", "rows",
  "columns"), err_sd = 1, svmins = 1, svmax = 6)
```

Arguments

ndata	Integer giving the number of data sets to generate with the same underlying parameters.
nobs	Integer giving the number of observations to sample.
size	Vector with two elements giving the number of rows and columns respectively of each simulated observation.
nclust	A vector of length four giving the number of clusters for the overall mean, the row margins, the column margins and the interactions (in that order) respectively. Alternatively, a vector of length one, in which case all components will have the same number of clusters.

clustsize	A list of length four, with each element containing a vector of the same length as the corresponding entry in <code>nclust</code> , indicating the number of elements to contribute to each sample. Naturally, each of these vectors must sum to <code>nobs</code> , or an error will result. Positional matching are used, in the order "overall", "rows", "columns" and "interactions". If <code>NULL</code> , all clusters will be of equal size.
delta	A four-element binary vector (logical or numeric) indicating which sum-to-zero constraints must be enforced.
ndim	The required rank for the approximation of the interactions (a scalar).
alpha	Numeric value in $[0, 1]$ which determines how the singular values are distributed between rows and columns (passed to <code>int.lsbclust</code>).
fixed	One of "none", "rows" or "columns" indicating whether to fix neither sets of coordinates, or whether to fix the row or column coordinates across clusters respectively. If a vector is supplied, only the first element will be used (passed to <code>int.lsbclust</code>).
err_sd	The standard deviation of the error distribution, as passed to <code>rnorm</code>
svmins	Vector of minimum values for the singular values (as passed to <code>simsv</code>). Optionally, if all minima are equal, a single numeric value which will be expanded to the correct length.
svmax	The maximum possible singular value (as passed to <code>simsv</code>)

Examples

```
## Nothing fixed, balanced classes
set.seed(1)
dat <- rlsbclust(ndata = 1, nobs = 100, size = c(10, 8), nclust = c(5, 4, 6, 5))
res <- lsbclust(data = dat[[1]]$data, nclust = c(5, 4, 6, 5))
cfsim(res, dat[[1]])

## Rows fixed, balanced classes
set.seed(2)
dat <- rlsbclust(ndata = 1, nobs = 100, size = c(10, 8), nclust = c(5, 4, 6, 5),
                fixed = "rows")
res <- lsbclust(data = dat[[1]]$data, nclust = c(5, 4, 6, 5), fixed = "rows")
cfsim(res, dat[[1]])

## Rows fixed, unbalanced classes
set.seed(3)
dat <- rlsbclust(ndata = 1, nobs = 100, size = c(10, 8), nclust = c(5, 4, 6, 5),
                fixed = "columns",
                clustsize = list(NULL, NULL, c(40, 25, 15, 10, 5, 5), c(40, 25, 15, 10, 10)))
res <- lsbclust(data = dat[[1]]$data, nclust = c(5, 4, 6, 5), fixed = "columns")
cfsim(res, dat[[1]])
```

`rorth`*Generate A Random Orthonormal Matrix*

Description

Uniformly sample an orthonormal matrix from the collection of all possible orthonormal matrices of a certain size. The QR decomposition is used on a matrix containing Gaussian random numbers. The QR decomposition might not be the most efficient algorithm under some circumstances.

Usage

```
rorth(nrow, ncol, sd = 1)
```

Arguments

<code>nrow</code>	Integer giving the number of rows required.
<code>ncol</code>	Integer giving the number of columns required.
<code>sd</code>	The standard deviation passed to <code>rnorm</code>

References

Stewart, G. W. (1980). The efficient generation of random orthogonal matrices with an application to condition estimators. *SIAM Journal on Numerical Analysis*, 17(3), 403-409.

Examples

```
set.seed(1)
rorth(5, 2)
```

`simsv`*Randomly Generate Positive Singular Values*

Description

Generate random singular values for a specified number of clusters for use in simulations. A mixture distribution is used with truncation to ensure that the singular values differ between clusters, are ordered, and are nonnegative.

Usage

```
simsv(nclust, ndim = 2, mins = 1, max = 5)
```

Arguments

nclust	Integer giving the number of clusters for which to sample singular values.
ndim	Integer; the number of singular values required.
mins	Numeric vector of length ndim giving the minimum values for the respective singular values.
max	Numeric value giving the maximum possible value for the mean of the cluster-specific singular value distribution, relative to the mins

sim_lsbcust

*Simulate and Analyze LSBCLUST***Description**

Perform a single simulation run for the LSBCLUST model. Multiple data sets are generated for a single set of underlying parameters,

Usage

```
sim_lsbcust(ndata, nobs, size, nclust, clustsize = NULL, delta = rep(1L,
  4L), ndim = 2L, alpha = 0.5, fixed = c("none", "rows", "columns"),
  err_sd = 1, svmins = 0.5, svmax = 5, seed = NULL, parallel = FALSE,
  parallel_data = TRUE, verbose = 0, nstart_T3 = 20L, nstart_ak = 20L,
  mc.cores = detectCores() - 1, include_fits = FALSE,
  include_data = FALSE, nstart, nstart.kmeans)
```

Arguments

ndata	Integer giving the number of data sets to generate with the same underlying parameters.
nobs	Integer giving the number of observations to sample.
size	Vector with two elements giving the number of rows and columns respectively of each simulated observation.
nclust	A vector of length four giving the number of clusters for the overall mean, the row margins, the column margins and the interactions (in that order) respectively. Alternatively, a vector of length one, in which case all components will have the same number of clusters.
clustsize	A list of length four, with each element containing a vector of the same length as the corresponding entry in nclust, indicating the number of elements to contribute to each sample. Naturally, each of these vectors must sum to nobs, or an error will result. Positional matching are used, in the order "overall", "rows", "columns" and "interactions". If NULL, all clusters will be of equal size.
delta	A four-element binary vector (logical or numeric) indicating which sum-to-zero constraints must be enforced.
ndim	The required rank for the approximation of the interactions (a scalar).

alpha	Numeric value in [0, 1] which determines how the singular values are distributed between rows and columns (passed to <code>int.lsbclust</code>).
fixed	One of "none", "rows" or "columns" indicating whether to fix neither sets of coordinates, or whether to fix the row or column coordinates across clusters respectively. If a vector is supplied, only the first element will be used (passed to <code>int.lsbclust</code>).
err_sd	The standard deviation of the error distribution, as passed to <code>rnorm</code>
svmins	Vector of minimum values for the singular values (as passed to <code>simsv</code>). Optionally, if all minima are equal, a single numeric value which will be expanded to the correct length.
svmax	The maximum possible singular value (as passed to <code>simsv</code>)
seed	An optional seed to be set for the random number generator
parallel	Logical indicating whether to parallelize over random starts. Note that <code>parallel_data</code> has precedence over this
parallel_data	Logical indicating whether to parallelize over the data sets. If FALSE, parallelization is done over random starts (depending on <code>parallel</code>).
verbose	Integer giving the number of iterations after which the loss values is printed.
nstart_T3	The number of random starts to use for <code>T3Clustf</code>
nstart_ak	The number of random starts to use for <code>akmeans</code>
mc.cores	The number of cores to use, passed to <code>makeCluster</code>
include_fits	Logical indicating whether to include the model fits, or only the fit statistics
include_data	Logical indicating whether to include the simulated data fitted on, or only the results
nstart	From <code>lsbclust</code>
nstart.kmeans	From <code>lsbclust</code>

Examples

```
set.seed(1)
res <- sim_lsbclust(ndata = 5, nobs = 100, size = c(10, 8), nclust = rep(5, 4),
  verbose = 0, nstart_T3 = 2, nstart_ak = 1, parallel_data = FALSE,
  nstart = 2, nstart.kmeans = 5 )
```

step.lsbclust

Model Search for lsbclust

Description

Fit `lsbclust` models for different numbers of clusters and/or different values of `delta`. The resulting output can be inspected through its `plot` method to facilitate model selection. Each component of the model is fitted separately.

Usage

```
step.lsbclust(data, margin = 3L, delta = c(1, 1, 1, 1), nclust, ndim = 2,
  fixed = c("none", "rows", "columns"), nstart = 20, starts = NULL,
  nstart.kmeans = 500, alpha = 0.5, parallel = FALSE, maxit = 100,
  verbose = -1, type = NULL, ...)
```

Arguments

data	A three-way array representing the data.
margin	An integer giving the single subscript of data over which the clustering will be applied.
delta	A four-element binary vector (logical or numeric) indicating which sum-to-zero constraints must be enforced.
nclust	Either a vector giving the number of clusters which will be applied to each element of the model, that is to (a subset of) the overall mean, row margins, column margins and interactions. If it is a list, arguments are matched by the names "overall", "rows" "columns" and "interactions". If the list does not have names, the components are extracted in the aforementioned order.
ndim	The required rank for the approximation of the interactions (a scalar).
fixed	One of "none", "rows" or "columns" indicating whether to fix neither sets of coordinates, or whether to fix the row or column coordinates across clusters respectively. If a vector is supplied, only the first element will be used (passed to int.lsbclust).
nstart	The number of random starts to use for the interaction clustering.
starts	A list containing starting configurations for the cluster membership vector. If not supplied, random initializations will be generated (passed to int.lsbclust).
nstart.kmeans	The number of random starts to use in kmeans .
alpha	Numeric value in [0, 1] which determines how the singular values are distributed between rows and columns (passed to int.lsbclust).
parallel	Logical indicating whether to parallelize over different starts or not (passed to int.lsbclust).
maxit	The maximum number of iterations allowed in the interaction clustering.
verbose	The number of iterations after which information on progress is provided (passed to int.lsbclust).
type	One of "rows", "columns" or "overall" (or a unique abbreviation of one of these) indicating whether clustering should be done on row margins, column margins or the overall means of the two-way slices respectively. If more than one option are supplied, the algorithm is run for all (unique) options supplied (passed to orc.lsbclust). This is an optional argument.
...	Additional arguments passed to kmeans .

Examples

```

m <- step.lsbclust(data = dcars, margin = 3, delta = c(1, 0, 1, 0), nclust = 4:5,
                  ndim = 2, fixed = "columns", nstart = 1, nstart.kmeans = 100,
                  parallel = FALSE)

## For a list of all deltas
delta <- expand.grid(replicate(4, c(0,1), simplify = FALSE))
delta <- with(delta, delta[!(Var1 == 0 & Var3 == 1), ])
delta <- with(delta, delta[!(Var2 == 0 & Var4 == 1),])
delta <- delta[-4,]
delta <- as.list(as.data.frame(t(delta)))
m2 <- step.lsbclust(data = dcars, margin = 3, delta = delta, nclust = 4:5,
                  ndim = 2, fixed = "columns", nstart = 1, nstart.kmeans = 100,
                  parallel = FALSE)

```

summary.int.lsbclust *Summary Method for Class "int.lsbclust"*

Description

Some goodness-of-fit diagnostics are provided for all three margins.

Usage

```

## S3 method for class 'int.lsbclust'
summary(object, digits = 3, ...)

```

Arguments

object	An object of class 'int.lsbclust'.
digits	The number of digits in the printed output.
...	Unimplemented.

summary.lsbclust *Summary Method for Class "lsbclust"*

Description

Summarize a lsbclust object.

Usage

```

## S3 method for class 'lsbclust'
summary(object, digits = 3, ...)

```

Arguments

object	An object of class 'lsbclust'.
digits	The number of digits in the printed output.
...	Unimplemented.

supermarkets	<i>Dutch Supermarkets Data Set</i>
--------------	------------------------------------

Description

This data set relates to 220 consumers rating 10 Dutch supermarket chains according to 8 variables. A rating scale from 1 to 10 was used.

Usage

```
supermarkets
```

Format

A three-way array with supermarkets in the first dimension, variables in the second and consumers in the third dimension.

Source

Michel van de Velden

Examples

```
data("supermarkets")
fit <- lsbclust(data = supermarkets, nclust = 6, fixed = "rows", nstart = 2)
```

T3Clusf	<i>T3Clusf: Tucker3 Fuzzy Cluster Analysis</i>
---------	--

Description

This is an implementation of the T3Clusf algorithm of Rocci & Vichi (2005).

Usage

```
T3Clusf(X, Q, R = Q, G = 2, margin = 3L, alpha = 1, eps = 1e-08,
maxit = 100L, verbose = 1, nstart = 1L, parallel = TRUE,
mc.cores = detectCores() - 1L, minsize = 3L)
```

Arguments

X	Three-way data array, with no missing values.
Q	Integer giving the number of dimensions required for mode B (variables). This is the first mode of the array, excluding the mode clustered over (see margin).
R	Integer giving the number of dimensions required for mode C (occasions). This is the second mode of the array, excluding the mode clustered over (see margin).
G	Integer giving the number of clusters required.
margin	Integer giving the margin of the array to cluster over. The remaining two modes, in the original order, corresponds to Q and R.
alpha	Numeric value giving the fuzziness parameter.
eps	Small numeric value giving the empirical convergence threshold.
maxit	Integer giving the maximum number of iterations allowed.
verbose	Integer giving the number of iterations after which the loss values are printed.
nstart	Integer giving the number of random starts required.
parallel	Logical indicating whether to parallelize over random starts if nstart > 1.
mc.cores	Argument passed to makeCluster .
minsize	Integer giving the minimum size of cluster to uphold when reinitializing empty clusters.

References

Rocci, R., & Vichi, M. (2005). *Three-mode component analysis with crisp or fuzzy partition of units*. *Psychometrika*, 70(4), 715-736.

Examples

```
data("dcars")
set.seed(13)
res <- T3Clusf(X = carray(dcars), Q = 3, R = 2, G = 3, alpha = 1)
```

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