Package ‘clustrd’

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**Type**  Package

**Title**  Methods for Joint Dimension Reduction and Clustering

**Description**  A class of methods that combine dimension reduction and clustering of continuous, categorical or mixed-type data. For continuous data, the package contains implementations of factorial K-means (Vichi and Kiers 2001; <DOI:10.1016/S0167-9473(00)00064-5>) and reduced K-means (De Soete and Carroll 1994; <DOI:10.1007/978-3-642-51175-2_24>); both methods that combine principal component analysis with K-means clustering. For categorical data, the package provides MCA K-means (Hwang, Dillon and Takane 2006; <DOI:10.1007/s11336-004-1173-x>), i-FCB (Iodice D’Enza and Palumbo 2013, <DOI:10.1007/s00180-012-0329-x>) and Cluster Correspondence Analysis (van de Velden, Iodice D’Enza and Palumbo 2017; <DOI:10.1007/s11336-016-9514-0>), which combine multiple correspondence analysis with K-means. For mixed-type data, it provides mixed Reduced K-means and mixed Factorial K-means (van de Velden, Iodice D’Enza and Markos 2019; <DOI:10.1002/wics.1456>), which combine PCA for mixed-type data with K-means.

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**R topics documented:**

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The data set refers to a collection of 55 articles on Bribery cases from central Russian newspapers 1999-2000 (Mirkin, 2005). The variables reflect the following fivefold structure of bribery situations: two interacting sides - the office and the client, their interaction, the corrupt service rendered, and the environment in which it all occurs. These structural aspects can be characterized by eleven variables that have been manually recovered from the newspaper articles.

**Usage**

```r
data("bribery")
```

**Format**

A data frame with 55 observations on 11 categorical variables.

- **Of** Type of Office
- **Cl** Level of Client
- **Serv** Type of service: obstruction of justice, favours, cover-up, change of category, extortion of money for rendering free services
- **Occ** Frequency of occurrence
- **Init** Who initiated the bribery act
- **Brib** Bribe Level in $
- **Typ** Type of corruption
- **Net** Corruption network
- **Con** Condition of corruption
- **Bran** Branch at which the corrupt service occurred
- **Pun** Punishment
References


Examples

data(bribery)

**clusmca**

*Joint dimension reduction and clustering of categorical data.*

Description

This function implements MCA K-means (Hwang, Dillon and Takane, 2006), i-FCB (Iodice D’Enza and Palumbo, 2013) and Cluster Correspondence Analysis (van de Velden, Iodice D’Enza and Palumbo, 2017). The methods combine variants of Correspondence Analysis for dimension reduction with K-means for clustering.

Usage

clusmca(data, nclus, ndim, method=c("clusCA","iFCB","MCAk"), alphak = .5, nstart = 100, smartStart = NULL, gamma = TRUE, inboot = FALSE, seed = NULL)

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

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

## S3 method for class 'clusmca'
fitted(object, mth = c("centers", "classes"), ...)

Arguments

- **data**: Dataset with categorical variables
- **nclus**: Number of clusters (nclus = 1 returns the MCA solution; see Details)
- **ndim**: Dimensionality of the solution
- **method**: Specifies the method. Options are MCAk for MCA K-means, iFCB for Iterative Factorial Clustering of Binary variables and clusCA for Cluster Correspondence Analysis (default = "clusCA")
- **alphak**: Non-negative scalar to adjust for the relative importance of MCA (alphak = 1) and K-means (alphak = 0) in the solution (default = .5). Works only in combination with method = "MCAk"
- **nstart**: Number of random starts (default = 100)
smartStart  If NULL then a random cluster membership vector is generated. Alternatively, a cluster membership vector can be provided as a starting solution.
gamma  Scaling parameter that leads to similar spread in the object and variable scores (default = TRUE)
seed  An integer that is used as argument by set.seed() for offsetting the random number generator when smartStart = NULL. The default value is NULL.
inboot  Used internally in the bootstrap functions to perform bootstrapping on the indicator matrix.
x  For the print method, a class of clusmca
object  For the summary method, a class of clusmca
mth  For the fitted method, a character string that specifies the type of fitted value to return: "centers" for the observations center vector, or "class" for the observations cluster membership value
...  Not used

Details
For the K-means part, the algorithm of Hartigan-Wong is used by default.
The hidden print and summary methods print out some key components of an object of class clusmca.
The hidden fitted method returns cluster fitted values. If method is "classes", this is a vector of cluster membership (the cluster component of the "clusmca" object). If method is "centers", this is a matrix where each row is the cluster center for the observation. The rownames of the matrix are the cluster membership values.
When nclus = 1 the function returns the MCA solution with objects in principal and variables in standard coordinates. plot(object) shows the corresponding asymmetric biplot.

Value
obscoord  Object scores
attcoord  Variable scores
centroid  Cluster centroids
cluster  Cluster membership
criterion  Optimal value of the objective criterion
size  The number of objects in each cluster
nstart  A copy of nstart in the return object
odata  A copy of data in the return object

References
cluspca

Joint dimension reduction and clustering of continuous data.

Description
This function implements Factorial K-means (Vichi and Kiers, 2001) and Reduced K-means (De Soete and Carroll, 1994), as well as a compromise version of these two methods. The methods combine Principal Component Analysis for dimension reduction with K-means for clustering.

Usage
cluspca(data, nclus, ndim, alpha = NULL, method = c("RKM","FKM"), center = TRUE, scale = TRUE, rotation = "none", nstart = 100, smartStart = NULL, seed = NULL)

# S3 method for class 'cluspca'

See Also
cluspca, cluspcamix, tuneclus

Examples
data(cmc)
# Preprocessing: values of wife's age and number of children were categorized # into three groups based on quartiles
cmc$W_AGE = ordered(cut(cmc$W_AGE, c(16,26,39,49), include.lowest = TRUE))
levels(cmc$W_AGE) = c("16-26","27-39","40-49")
cmc$NCHILD = ordered(cut(cmc$NCHILD, c(0,1,4,17), right = FALSE))
levels(cmc$NCHILD) = c("0","1-4","5 and above")

#Cluster Correspondence Analysis solution with 3 clusters in 2 dimensions
#after 10 random starts
outclusCA = clusmca(cmc, 3, 2, method = "clusCA", nstart = 10, seed = 1234)
outclusCA
#Scatterplot (dimensions 1 and 2)
plot(outclusCA)

#MCA K-means solution with 3 clusters in 2 dimensions after 10 random starts
outMCAk = clusmca(cmc, 3, 2, method = "MCAk", nstart = 10, seed = 1234)
outMCAk
#Scatterplot (dimensions 1 and 2)
plot(outMCAk)

#nclus = 1 just gives the MCA solution
#outMCA = clusmca(cmc, 1, 2)
#outMCA
#Scatterplot (dimensions 1 and 2)
#asymmetric biplot with scaling gamma = TRUE
#plot(outMCA)
print(x, ...)  

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

## S3 method for class 'cluspca'
fitted(object, mth = c("centers", "classes"), ...)  

### Arguments

data Dataset with metric variables
nclus Number of clusters (nclus = 1 returns the PCA solution
ndim Dimensionality of the solution
method Specifies the method. Options are RKM for reduced K-means and FKM for factorial K-means (default = "RKM")
alpha Adjusts for the relative importance of RKM and FKM in the objective function; alpha = 0.5 leads to reduced K-means, alpha = 0 to factorial K-means, and alpha = 1 reduces to the tandem approach (PCA followed by K-means)
center A logical value indicating whether the variables should be shifted to be zero centered (default = TRUE)
scale A logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place (default = TRUE)
rotation Specifies the method used to rotate the factors. Options are none for no rotation, varimax for varimax rotation with Kaiser normalization and promax for promax rotation (default = "none")
nstart Number of starts (default = 100)
smartStart If NULL then a random cluster membership vector is generated. Alternatively, a cluster membership vector can be provided as a starting solution
seed An integer that is used as argument by set.seed() for offsetting the random number generator when smartStart = NULL. The default value is NULL.
x For the print method, a class of clusmca
object For the summary method, a class of clusmca
mth For the fitted method, a character string that specifies the type of fitted value to return: "centers" for the observations center vector, or "class" for the observations cluster membership value
... Not used

### Details

For the K-means part, the algorithm of Hartigan-Wong is used by default.

The hidden print and summary methods print out some key components of an object of class cluspca.

The hidden fitted method returns cluster fitted values. If method is "classes", this is a vector of cluster membership (the cluster component of the "cluspca" object). If method is "centers", this
cluspca is a matrix where each row is the cluster center for the observation. The rownames of the matrix are the cluster membership values.

When nclus = 1 the function returns the PCA solution and plot(object) shows the corresponding biplot.

Value

- obscoord: Object scores
- attcoord: Variable scores
- centroid: Cluster centroids
- cluster: Cluster membership
- criterion: Optimal value of the objective function
- size: The number of objects in each cluster
- scale: A copy of scale in the return object
- center: A copy of center in the return object
- nstart: A copy of nstart in the return object
- odata: A copy of data in the return object

References


See Also

clusmca, cluspcamix, tuneclus

Examples

```r
# Reduced K-means with 3 clusters in 2 dimensions after 10 random starts
data(macro)
outRKM = cluspca(macro, 3, 2, method = "RKM", rotation = "varimax", scale = FALSE, nstart = 10)
summary(outRKM)
# Scatterplot (dimensions 1 and 2) and cluster description plot
plot(outRKM, cludesc = TRUE)

# Factorial K-means with 3 clusters in 2 dimensions
# with a Reduced K-means starting solution
outFKM = cluspca(macro, 3, 2, method = "FKM", rotation = "varimax",
scale = FALSE, smartStart = outRKM$cluster)
outFKM
# Scatterplot (dimensions 1 and 2) and cluster description plot
plot(outFKM, cludesc = TRUE)
```
#To get the Tandem approach (PCA(SVD) + K-means)
outTandem = cluspca(macro, 3, 2, alpha = 1, seed = 1234)
plot(outTandem)

#nclus = 1 just gives the PCA solution
#outPCA = cluspca(macro, 1, 2)
#outPCA
#Scatterplot (dimensions 1 and 2)
#plot(outPCA)

cluspcamix

Joint dimension reduction and clustering of mixed-type data.

Description

This function implements clustering and dimension reduction for mixed-type variables, i.e., categorical and metric (see, Yamamoto & Hwang, 2014; van de Velden, Iodice D’Enza, & Markos 2019; Vichi, Vicari, & Kiers, 2019). This framework includes Mixed Reduced K-means and Mixed Factorial K-means, as well as a compromise of these two methods. The methods combine Principal Component Analysis of mixed-data for dimension reduction with K-means for clustering.

Usage

cluspcamix(data, nclus, ndim, method=c("mixedRKM", "mixedFKM"), center = TRUE, scale = TRUE, alpha=NULL, rotation="none", nstart = 100, smartStart=NULL, seed=NULL, inboot = FALSE)

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

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

## S3 method for class 'cluspcamix'
fitted(object, mth = c("centers", "classes"), ...)

Arguments

data Dataset with categorical and metric variables
nclus Number of clusters (nclus = 1 returns the PCAMIX solution)
ndim Dimensionality of the solution
method Specifies the method. Options are mixedRKM for mixed reduced K-means and mixedFKM for mixed factorial K-means (default = "mixedRKM")
center A logical value indicating whether the variables should be shifted to be zero centered (default = TRUE)
### scale
A logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place (default = `TRUE`)

### alpha
Adjusts for the relative importance of Mixed RKM and Mixed FKM in the objective function; `alpha = 0.5` leads to mixed reduced K-means, `alpha = 0` to mixed factorial K-means, and `alpha = 1` reduces to the tandem approach (PCAMIX followed by K-means)

### rotation
Specifies the method used to rotate the factors. Options are `none` for no rotation, `varimax` for varimax rotation with Kaiser normalization and `promax` for promax rotation (default = "none")

### nstart
Number of random starts (default = 100)

### smartStart
If `NULL` then a random cluster membership vector is generated. Alternatively, a cluster membership vector can be provided as a starting solution

### seed
An integer that is used as argument by `set.seed()` for offsetting the random number generator when `smartStart = NULL`. The default value is `NULL`.

### inboot
Used internally in the bootstrap functions to perform bootstrapping on the indicator matrix.

### x
For the print method, a class of `cluspcamix`

### object
For the summary method, a class of `cluspcamix`

### mth
For the fitted method, a character string that specifies the type of fitted value to return: "centers" for the observations center vector, or "class" for the observations cluster membership value

### ...
Not used

### Details
For the K-means part, the algorithm of Hartigan-Wong is used by default.

The hidden print and summary methods print out some key components of an object of class `cluspcamix`.

The hidden fitted method returns cluster fitted values. If method is "classes", this is a vector of cluster membership (the cluster component of the "cluspcamix" object). If method is "centers", this is a matrix where each row is the cluster center for the observation. The rownames of the matrix are the cluster membership values.

When `nclus = 1` the function returns the solution of PCAMIX and `plot(object)` shows the corresponding biplot.

### Value
- **obscoord**: Object scores
- **attcoord**: Variable scores
- **centroid**: Cluster centroids
- **cluster**: Cluster membership
- **criterion**: Optimal value of the objective criterion
- **size**: The number of objects in each cluster
scale  A copy of scale in the return object
center A copy of center in the return object
nstart A copy of nstart in the return object
odata  A copy of data in the return object

References


See Also

cluspca, clusmca, tuneclus

Examples

data(diamond)
#Mixed Reduced K-means solution with 3 clusters in 2 dimensions
#after 10 random starts
outmixedRKM = cluspcamix(diamond, 3, 2, method = "mixedRKM", nstart = 10, seed = 1234)
outmixedRKM
#Scatterplot (dimensions 1 and 2)
plot(outmixedRKM)

#Tandem analysis: PCAMIX followed by K-means solution
#with 3 clusters in 2 dimensions after 10 random starts
outTandem = cluspcamix(diamond, 3, 2, alpha = 1, nstart = 10, seed = 1234)
outTandem
#Scatterplot (dimensions 1 and 2)
plot(outTandem)

#nclus = 1 just gives the PCAMIX solution
#outPCAMIX = cluspcamix(diamond, 1, 2)
#outPCAMIX
#Biplot (dimensions 1 and 2)
#plot(outPCAMIX)
Description

Data of married women in Indonesia who were not pregnant (or did not know they were pregnant) at the time of the survey. The dataset contains demographic and socio-economic characteristics of the women along with their preferred method of contraception (no use, long-term methods, short-term methods).

Usage

data(cmc)

Format

A data frame containing 1,437 observations on the following 10 variables.

W_AGE  wife's age in years.
W_EDU  ordered factor indicating wife's education, with levels "low", "2", "3" and "high".
H_EDU  ordered factor indicating wife's education, with levels "low", "2", "3" and "high".
NCHILD number of children.
W_REL  factor indicating wife's religion, with levels "non-Islam" and "Islam".
W_WORK factor indicating if the wife is working.
H_OCC  factor indicating husband's occupation, with levels "1", "2", "3" and "4". The labels are not known.
SOL  ordered factor indicating the standard of living index with levels "low", "2", "3" and "high".
MEDEXP  factor indicating media exposure, with levels "good" and "not good".
CM  factor indicating the contraceptive method used, with levels "no-use", "long-term" and "short-term".

Source

This dataset is part of the 1987 National Indonesia Contraceptive Prevalence Survey and was created by Tjen-Sien Lim. It has been taken from the UCI Machine Learning Repository at http://archive.ics.uci.edu/ml/.

References


Examples

data(cmc)
Description

Data on 308 diamond stones sold in Singapore. The main attributes are diamond weight, colour, clarity, certification body and price in Singapore $. The weight of a diamond stone is indicated in terms of carat units. Since stones may be divided into 3 clusters due to their size, namely small (less than 0.5 carats), medium (0.5 to less than 1 carat) and large (1 carat and over), following Chu (2001), three binary variables have been built representing the three caratage ranges, and three quantitative variables (denoted Small, Medium, Large) have been derived by multiplying such binary variables by carats. So, the "Small" variable has nonzero values (i.e., the carat values) only for the smallest diamonds (less than 0.5 carats), and likewise for the other two variables. Thus, these variables are weighted binary variables. The colour of a diamond is graded from D (completely colourless), E, F, G, ..., to I (almost colorless). Clarity refers to the diamond’s internal and external imperfections. Clarity is graded on a scale from IF (internally flawless), to very very slightly imperfect (VVS1 or VVS2), and very slightly imperfect, VS1 or VS2. Three certification bodies were used: New York based Gemmological Institute of America (GIA), Antwerp based International Gemmological Institute (IGI) and Hoge Raad Voor Diamant (HRD).

Usage

data(diamond)

Format

A data frame with 308 observations on the following 7 variables.

Small  weighted binary variable with nonzero values (i.e., the carat values) for diamonds with less than 0.5 carats.

Medium weighted binary variable with nonzero values (i.e., the carat values) for diamonds from 0.5 to less than 1 carat.

Large weighted binary variable with nonzero values (i.e., the carat values) for diamonds from 1 carat and over.

Colour  the color of the diamond with a factor with levels (D, E, F, G, H, I).

Clarity  the clarity of the diamond with a factor with levels (IF, VVS1, VVS2, VS1, VS2).

Certification  the certification body with a factor with levels (GIA, IGI, HRD).

Price  the price of a diamond in Singapore $.

References

Global stability assessment of Joint Dimension Reduction and Clustering methods by bootstrapping.

Description

Runs joint dimension and clustering algorithms repeatedly for different numbers of clusters on bootstrap replica of the original data and returns corresponding cluster assignments, and cluster agreement indices comparing pairs of partitions.

Usage

global_bootclus(data, nclusrange = 3:4, ndim = NULL, method = c("RKM","FKM","mixedRKM","mixedFKM","clusCA","MCAk","iFCB"), nboot = 10, alpha = NULL, alphak = NULL, center = TRUE, scale = TRUE, nstart = 100, smartStart = NULL, seed = NULL)

Arguments

data
An integer or an integer vector with the number of clusters or a range of numbers of clusters (should be greater than one)
nclusrange
Continuous, Categorical or Mixed data set
ndim
An integer or an integer vector with the number of clusters or a range of numbers of clusters (should be greater than one)
method
A logical value indicating whether the metric variables should be shifted to be zero centered (default = TRUE)
alpha
A logical value indicating whether the metric variables should be scaled to have unit variance before the analysis takes place (default = TRUE)
nboot
Number of random starts (default = 100)
scale
If NULL then a random cluster membership vector is generated. Alternatively, a cluster membership vector can be provided as a starting solution
smartStart
An integer that is used as argument by set.seed() for offsetting the random number generator when smartStart = NULL. The default value is NULL.
...
Details

The algorithm for assessing global cluster stability is similar to that in Dolnicar and Leisch (2010) and can be summarized in three steps:

Step 1. Resampling: Draw bootstrap samples \( S_i \) and \( T_i \) of size \( n \) from the data and use the original data, \( X \), as evaluation set \( E_i = X \). Apply the clustering method of choice to \( S_i \) and \( T_i \) and obtain \( C^S_i \) and \( C^T_i \).

Step 2. Mapping: Assign each observation \( x_i \) to the closest centers of \( C^S_i \) and \( C^T_i \) using Euclidean distance, resulting in partitions \( C^{XS}_i \) and \( C^{XT}_i \), where \( C^{XS}_i \) is the partition of the original data, \( X \), predicted from clustering bootstrap sample \( S_i \) (same for \( T_i \) and \( C^{XT}_i \)).

Step 3. Evaluation: Use the Adjusted Rand Index (ARI, Hubert & Arabie, 1985) or the Measure of Concordance (MOC, Pfitzner 2008) as measure of agreement and stability. Inspect the distributions of ARI/MOC to assess the global reproducibility of the clustering solutions. While \( n_{boot} = 100 \) is recommended, smaller run numbers could give quite informative results as well, if computation times become too high.

Note that the stability of a clustering solution is assessed, but stability is not the only important validity criterion - clustering solutions obtained by very inflexible clustering methods may be stable but not valid, as discussed in Hennig (2007).

Value

- `nclusrange`: An integer or an integer vector with the number of clusters or a range of numbers of clusters
- `clust1`: Partitions, \( C^{XS}_i \) of the original data, \( X \), predicted from clustering bootstrap sample \( S_i \) (see Details)
- `clust2`: Partitions, \( C^{XT}_i \) of the original data, \( X \), predicted from clustering bootstrap sample \( T_i \) (see Details)
- `index1`: Indices of the original data rows in bootstrap sample \( S_i \)
- `index2`: Indices of the original data rows in bootstrap sample \( T_i \)
- `rand`: Adjusted Rand Index values
- `moc`: Measure of Concordance values

References


See Also

- `local_bootclus`
### Examples

```r
## 3 bootstrap replicates and nstart = 1 for speed in example,
## use at least 20 replicates for real applications
data(diamond)
boot_mixedRKM = global_bootclus(diamond[, -7], nclusrange = 3:4,
method = "mixedRKM", nboot = 3, nstart = 1, seed = 1234)

boxplot(boot_mixedRKM$rand, xlab = "Number of clusters", ylab =
"adjusted Rand Index")

## 5 bootstrap replicates and nstart = 10 for speed in example,
## use more for real applications
#data(macro)
#boot_RKM = global_bootclus(macro, nclusrange = 2:5,
#method = "RKM", nboot = 5, nstart = 10, seed = 1234)

#boxplot(boot_RKM$rand, xlab = "Number of clusters", ylab =
#"adjusted Rand Index")

## 5 bootstrap replicates and nstart = 1 for speed in example,
## use more for real applications
#data(bribery)
#boot_cluCA = global_bootclus(bribery, nclusrange = 2:5,
#method = "clusCA", nboot = 5, nstart = 1, seed = 1234)

#boxplot(boot_cluCA$rand, xlab = "Number of clusters", ylab =
#"adjusted Rand Index")
```

### Data Description

The dataset was collected with an interactive online version of the Humor Styles Questionnaire (HSQ) which assesses four independent ways in which people express and appreciate humor (Martin et al. 2003): affiliative (items with prefix AF), defined as the benign uses of humor to enhance one’s relationships with others; self-enhancing (SE), indicating uses of humor to enhance the self; aggressive (AG), the use of humor to enhance the self at the expense of others; self-defeating (SD), the use of humor to enhance relationships at the expense of oneself. The main part of the questionnaire consisted of 32 statements rated from 1 to 5 according to the respondents’ level of agreement. The number of respondents is 993.

### Usage

```r
data("hsq")
```
Format

A data frame with 993 observations on 32 Likert-type variables (statements) with 5 response categories, ranging from 1 (strong agreement) to 5 (strong disagreement).

AF1  I usually don’t laugh or joke around much with other people
SE2  If I am feeling depressed, I can usually cheer myself up with humor
AG3  If someone makes a mistake, I will often tease them about it
SD4  I let people laugh at me or make fun at my expense more than I should
AF5  I don’t have to work very hard at making other people laugh – I seem to be a naturally humorous person
SE6  Even when I’m by myself, I’m often amused by the absurdities of life
AG7  People are never offended or hurt by my sense of humor
SD8  I will often get carried away in putting myself down if it makes my family or friends laugh
AF9  I rarely make other people laugh by telling funny stories about myself
SE10 If I am feeling upset or unhappy I usually try to think of something funny about the situation to make myself feel better
AG11 When telling jokes or saying funny things, I am usually not very concerned about how other people are taking it
SD12 I often try to make people like or accept me more by saying something funny about my own weaknesses, blunders, or faults
AF13 I laugh and joke a lot with my closest friends
SE14 My humorous outlook on life keeps me from getting overly upset or depressed about things
AG15 I do not like it when people use humor as a way of criticizing or putting someone down
SD16 I don’t often say funny things to put myself down
AF17 I usually don’t like to tell jokes or amuse people
SE18 If I’m by myself and I’m feeling unhappy, I make an effort to think of something funny to cheer myself up
AG19 Sometimes I think of something that is so funny that I can’t stop myself from saying it, even if it is not appropriate for the situation
SD20 I often go overboard in putting myself down when I am making jokes or trying to be funny
AF21 I enjoy making people laugh
SE22 If I am feeling sad or upset, I usually lose my sense of humor
AG23 I never participate in laughing at others even if all my friends are doing it
SD24 When I am with friends or family, I often seem to be the one that other people make fun of or joke about
AF25 I don’t often joke around with my friends
SE26 It is my experience that thinking about some amusing aspect of a situation is often a very effective way of coping with problems
AG27 If I don’t like someone, I often use humor or teasing to put them down
If I am having problems or feeling unhappy, I often cover it up by joking around, so that even my closest friends don’t know how I really feel.

I usually can’t think of witty things to say when I’m with other people.

I don’t need to be with other people to feel amused - I can usually find things to laugh about even when I’m by myself.

Even if something is really funny to me, I will not laugh or joke about it if someone will be offended.

Letting others laugh at me is my way of keeping my friends and family in good spirits.

References


Examples

data(hsq)

---

**local_bootclus**

Cluster-wise stability assessment of Joint Dimension Reduction and Clustering methods by bootstrapping.

**Description**

Assessment of the cluster-wise stability of a joint dimension and clustering method. The data is resampled using bootstrapping and the Jaccard similarities of the original clusters to the most similar clusters in the resampled data are computed. The mean over these similarities is used as an index of the stability of a cluster. The method is similar to the one described in Hennig (2007).

**Usage**

``` r
local_bootclus(data, nclus, ndim = NULL, method = c("RKM","FKM","mixedRKM","mixedFKM","clusCA","MCAk","iFCB"), scale = TRUE, center = TRUE, alpha = NULL, nstart=100, nboot=10, alphak = .5, seed = NULL)
```

**Arguments**

- `data`: Continuous, Categorical or Mixed data set
- `nclus`: Number of clusters
- `ndim`: Dimensionality of the solution
- `method`: Specifies the method. Options are RKM for Reduced K-means, FKM for Factorial K-means, mixedRKM for Mixed Reduced K-means, mixedFKM for Mixed Factorial K-means, MCAk for MCA K-means, iFCB for Iterative Factorial Clustering of Binary variables and clusCA for Cluster Correspondence Analysis.
scale  A logical value indicating whether the metric variables should be scaled to have unit variance before the analysis takes place (default = TRUE)
center A logical value indicating whether the metric variables should be shifted to be zero centered (default = TRUE)
alpha  Adjusts for the relative importance of (mixed) RKM and FKM in the objective function. \( \alpha = 1 \) reduces to PCA/PCAMIX, \( \alpha = 0.5 \) to (mixed) reduced K-means, and \( \alpha = 0 \) to (mixed) factorial K-means
nstart Number of random starts (default = 100)
nboot Number of bootstrap pairs of partitions
alphak Non-negative scalar to adjust for the relative importance of MCA (\( \text{alphak} = 1 \)) and K-means (\( \text{alphak} = 0 \)) in the solution (default = .5). Works only in combination with \text{method} = "MCAk"
seed An integer that is used as argument by \text{set.seed()} for offsetting the random number generator when \text{smartStart} = NULL. The default value is NULL.

Details

The algorithm for assessing local cluster stability is similar to that in Hennig (2007) and can be summarized in three steps:

Step 1. Resampling: Draw bootstrap samples \( S_i \) and \( T_i \) of size \( n \) from the data and use the original data as evaluation set \( E_i = X \). Apply a joint dimension reduction and clustering method to \( S_i \) and \( T_i \) and obtain \( C^S_i \) and \( C^T_i \).

Step 2. Mapping: Assign each observation \( x_i \) to the closest centers of \( C^S_i \) and \( C^T_i \) using Euclidean distance, resulting in partitions \( C^{XS}_i \) and \( C^{XT}_i \).

Step 3. Evaluation: Obtain the maximum Jaccard agreement between each original cluster \( C_k \) and each one of the two bootstrap clusters, \( C^{k'XS}_i \) and \( C^{k'XT}_i \) as measure of agreement and stability, and take the average of each pair.

Inspect the distributions of the maximum Jaccard coefficients to assess the cluster level (local) stability of the solution.

Here are some guidelines for interpretation. Generally, a valid, stable cluster should yield a mean Jaccard similarity value of 0.75 or more. Between 0.6 and 0.75, clusters may be considered as indicating patterns in the data, but which points exactly should belong to these clusters is highly doubtful. Below average Jaccard values of 0.6, clusters should not be trusted. "Highly stable" clusters should yield average Jaccard similarities of 0.85 and above.

While \( B = 100 \) is recommended, smaller run numbers could give quite informative results as well, if computation times become too high.

Note that the stability of a cluster is assessed, but stability is not the only important validity criterion - clusters obtained by very inflexible clustering methods may be stable but not valid, as discussed in Hennig (2007).

Value

nclus An integer with the number of clusters
clust1 Partitions, \( C^{XS}_i \) of the original data, \( X \), predicted from clustering bootstrap sample \( S_i \) (see Details)
clust2: Partitions, $C^{XT \_i}$ of the original data, $X$, predicted from clustering bootstrap sample $T \_i$ (see Details)

index1: Indices of the original data rows in bootstrap sample $S \_i$

index2: Indices of the original data rows in bootstrap sample $T \_i$

Jaccard: Mean Jaccard similarity values

References


See Also

`global_bootclus`

Examples

```r
## 5 bootstrap replicates and nstart = 10 for speed in example, 
## use more for real applications
data(iris)
bootres = local_bootclus(iris[, -5], nclus = 3, ndim = 2, 
method = "RKM", nboot = 5, nstart = 1, seed = 1234)

boxplot(bootres$Jaccard, xlab = "cluster number", ylab = 
"Jaccard similarity")

## 5 bootstrap replicates and nstart = 5 for speed in example, 
## use more for real applications
#data(diamond)
#bootres = local_bootclus(diamond[, -7], nclus = 4, ndim = 3, 
#method = "mixedRKM", nboot = 5, nstart = 10, seed = 1234)

#boxplot(bootres$Jaccard, xlab = "cluster number", ylab = 
#"Jaccard similarity")

## 5 bootstrap replicates and nstart = 1 for speed in example, 
## use more for real applications
#data(bribery)
#bootres = local_bootclus(bribery, nclus = 5, ndim = 4, 
#method = "clusCA", nboot = 10, nstart = 1, seed = 1234)

#boxplot(bootres$Jaccard, xlab = "cluster number", ylab = 
#"Jaccard similarity")
```
**macro**  
*Economic Indicators of 20 OECD countries for 1999*

**Description**

Data on the macroeconomic performance of national economies of 20 countries, members of the OECD (September 1999). The performance of the economies reflects the interaction of six main economic indicators (percentage change from the previous year): gross domestic product (GDP), leading indicator (LI), unemployment rate (UR), interest rate (IR), trade balance (TB), net national savings (NNS).

**Usage**

```r
data(macro)
```

**Format**

A data frame with 20 observations on the following 6 variables.

- GDP numeric
- LI numeric
- UR numeric
- IR numeric
- TB numeric
- NNS numeric

**References**


---

**plot.clusmca**  
*Plotting function for clusmca() output.*

**Description**

Plotting function that creates a scatterplot of the object scores and/or the attribute scores and the cluster centroids. Optionally, the function returns a series of barplots showing the standardized residuals per attribute for each cluster.

**Usage**

```r
## S3 method for class 'clusmca'
plot(x, dims = c(1,2), what = c(TRUE,TRUE),
     cludesc = FALSE, topstdres = 20, objlabs = FALSE, attlabs = NULL, subplot = FALSE, ...)
```
Arguments

- **x**: Object returned by `clusmca()`
- **dims**: Numerical vector of length 2 indicating the dimensions to plot on horizontal and vertical axes respectively; default is first dimension horizontal and second dimension vertical
- **what**: Vector of two logical values specifying the contents of the plots. First entry indicates whether a scatterplot of the objects is displayed in principal coordinates. Second entry indicates whether a scatterplot of the attribute categories is displayed in principal coordinates. Cluster centroids are always displayed. The default is `c(TRUE,TRUE)` and the resultant plot is a biplot of both objects and attribute categories with gamma-based scaling (see van de Velden et al., 2017)
- **cludesc**: A logical value indicating whether a series of barplots is produced showing the largest (in absolute value) standardized residuals per attribute for each cluster (default = `FALSE`)
- **topstdres**: Number of largest standardized residuals used to describe each cluster (default = 20). Works only in combination with `cludesc = TRUE`
- **objlabs**: A logical value indicating whether object labels will be plotted; if `TRUE` row names of the data matrix are used (default = `FALSE`). Warning: when `TRUE`, execution time of the plotting function will increase dramatically as the number of objects gets larger
- **attlabs**: Vector of custom attribute labels; if not provided, default labeling is applied
- **subplot**: A logical value indicating whether a subplot with the full distribution of the standardized residuals will appear at the bottom left corner of the corresponding plots. Works only in combination with `cludesc = TRUE`
- **...**: Further arguments to be transferred to `clusmca()`

Value

The function returns a ggplot2 scatterplot of the solution obtained via `clusmca()` that can be further customized using the `ggplot2` package. When `cludesc = TRUE` the function also returns a series of ggplot2 barplots showing the largest (or all) standardized residuals per attribute for each cluster.

References


See Also

- `plot.cluspca`, `plot.cluspcamix`
Examples

data("hsq")
#Cluster Correspondence Analysis with 3 clusters in 2 dimensions after 10 random starts
outclusCA = clusmca(hsq[,1:8], 3, 2, nstart = 10)
#Save the ggplot2 scatterplot
map = plot(outclusCA)$map
#Customization (adding titles)
map + ggtitle(paste("Cluster CA plot of the hsq data: 3 clusters of sizes ",
paste(outclusCA$size, collapse = ", ", sep = ", ")
+ xlab("Dim. 1") + ylab("Dim. 2")
+ theme(plot.title = element_text(size = 10, face = "bold", hjust = 0.5))

outclusCA = clusmca(hsq[,1:8], 4, 3, method = "iFCB", nstart= 10)
#Scatterlot with the observations only (dimensions 1 and 3)
#and cluster description plots showing the 20 largest std. residuals
#(with the full distribution showing in subplots)
plot(outclusCA, dim = c(1,3), what = c(TRUE, FALSE), cludesc = TRUE,
subplot = TRUE)

plot.cluspca

Plotting function for cluspca() output.

Description

Plotting function that creates a scatterplot of the objects, a correlation circle of the variables or a
biplot of both objects and variables. Optionally, it returns a parallel coordinate plot showing cluster
means.

Usage

## S3 method for class 'cluspca'
plot(x, dims = c(1, 2), cludesc = FALSE,
what = c(TRUE,TRUE), objlabs = FALSE, attlabs, ...)

Arguments

x

Object returned by cluspca()

dims

Numerical vector of length 2 indicating the dimensions to plot on horizontal
and vertical axes respectively; default is first dimension horizontal and second
dimension vertical

what

Vector of two logical values specifying the contents of the plots. First entry
indicates whether a scatterplot of the objects and cluster centroids is displayed
and the second entry whether a correlation circle of the variables is displayed.
The default is c(TRUE,TRUE) and the resultant plot is a biplot of both objects
and variables
cludesc A logical value indicating if a parallel coordinate plot showing cluster means is produced (default = FALSE)

objlabs A logical value indicating whether object labels will be plotted; if TRUE row names of the data matrix are used (default = FALSE). Warning: when TRUE, execution time of the plotting function will increase dramatically as the number of objects gets larger

attlabs Vector of custom attribute labels; if not provided, default labeling is applied

... Further arguments to be transferred to cluspca()

Value

The function returns a ggplot2 scatterplot of the solution obtained via cluspca() that can be further customized using the ggplot2 package. When cludesc = TRUE the function also returns a ggplot2 parallel coordinate plot.

References


See Also

plot.clusmca, plot.cluspcamix

Examples

data("macro")
#Factorial K-means (3 clusters in 2 dimensions) after 100 random starts
outFKM = cluspca(macro, 3, 2, method = "FKM", rotation = "varimax")
#Scatterplot (dimensions 1 and 2) and cluster description plot
plot(outFKM, cludesc = TRUE)

data("iris", package = "datasets")
#Compromise solution between PCA and Reduced K-means
#on the iris dataset (3 clusters in 2 dimensions) after 100 random starts
outclusPCA = cluspca(iris[,,-5], 3, 2, alpha = 0.3, rotation = "varimax")
table(outclusPCA$cluster,iris[,5])
#Save the ggplot2 scatterplot
map = plot(outclusPCA)$map
#Customization (adding titles)
map + ggtitle(paste("A compromise solution between RKM and FKM on the iris: 3 clusters of sizes ", paste(outclusPCA$size, collapse = " ", sep = " ")) + xlab("Dimension 1") + ylab("Dimension 2") + theme(plot.title = element_text(size = 10, face = "bold", hjust = 0.5))
plot.cluspcamix *Plotting function for cluspcamix() output.*

**Description**

Plotting function that creates a scatterplot of the objects, a correlation circle of the variables or a biplot of both objects and variables. Optionally, for metric variables, it returns a parallel coordinate plot showing cluster means and for categorical variables, a series of barplots showing the standardized residuals per attribute for each cluster.

**Usage**

```r
## S3 method for class 'cluspcamix'
plot(x, dims = c(1, 2), cludesc = FALSE,
     topstdres = 20, objlabs = FALSE, attlabs = NULL, subplot = FALSE,
     what = c(TRUE,TRUE), ...)
```

**Arguments**

- `x` Object returned by cluspcamix()
- `dims` Numerical vector of length 2 indicating the dimensions to plot on horizontal and vertical axes respectively; default is first dimension horizontal and second dimension vertical.
- `what` Vector of two logical values specifying the contents of the plots. First entry indicates whether a scatterplot of the objects and cluster centroids is displayed and the second entry whether a correlation circle of the variables is displayed. The default is `c(TRUE,TRUE)` and the resultant plot is a biplot of both objects and variables.
- `cludesc` A logical value indicating if a parallel coordinate plot showing cluster means is produced (default = `FALSE`).
- `topstdres` Number of largest standardized residuals used to describe each cluster (default = 20). Works only in combination with `cludesc = TRUE`.
- `subplot` A logical value indicating whether a subplot with the full distribution of the standardized residuals will appear at the bottom left corner of the corresponding plots. Works only in combination with `cludesc = TRUE`.
- `objlabs` A logical value indicating whether object labels will be plotted; if `TRUE` row names of the data matrix are used (default = `FALSE`). Warning: when `TRUE`, execution time of the plotting function will increase dramatically as the number of objects gets larger.
- `attlabs` Vector of custom attribute labels; if not provided, default labeling is applied.
- `...` Further arguments to be transferred to cluspcamix().
The function returns a ggplot2 scatterplot of the solution obtained via cluspcamix() that can be further customized using the ggplot2 package. When cludesc = TRUE, for metric variables, the function also returns a ggplot2 parallel coordinate plot and for categorical variables, a series of ggplot2 barplots showing the largest (or all) standardized residuals per attribute for each cluster.

References


See Also

plot.clusmca, plot.cluspca

Examples

data(diamond)
# Mixed Reduced K-means solution with 3 clusters in 2 dimensions
# after 10 random starts
outmixedRKM = cluspcamix(diamond, 3, 2, method = "mixedRKM", nstart = 10)
# Scatterplot (dimensions 1 and 2)
plot(outmixedRKM, cludesc = TRUE)

---

**tuneclus**

Cluster quality assessment for a range of clusters and dimensions.

**Description**

This function facilitates the selection of the appropriate number of clusters and dimensions for joint dimension reduction and clustering methods.

**Usage**

tuneclus(data, nclusrange = 3:4, ndimrange = 2:3,
method = c("RKM","FKM","mixedRKM","mixedFKM","clusCA","iFCB","MCAk"),
criterion = "asw", dst = "full", alpha = NULL, alphak = NULL,
center = TRUE, scale = TRUE, rotation = "none", nstart = 100,
smartStart = NULL, seed = NULL)

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

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

fitted(object, mth = c("centers", "classes"), ...)

### Arguments

data
Continuous, Categorical or Mixed data set

nclusrange
An integer vector with the range of numbers of clusters which are to be com-
pared by the cluster validity criteria. Note: the number of clusters should be
greater than one

ndimrange
An integer vector with the range of dimensions which are to be compared by the
cluster validity criteria

method
Specifies the method. Options are RKM for reduced K-means, FKM for factorial
K-means, mixedRKM for mixed reduced K-means, mixedFKM for mixed factorial
K-means, MCAk for MCA K-means, iFCB for Iterative Factorial Clustering of
Binary variables and clusCA for Cluster Correspondence Analysis

criterion
One of asw, ch or crit. Determines whether average silhouette width, Calinski-
Harabasz index or objective value of the selected method is used (default = "asw")

dst
Specifies the data used to compute the distances between objects. Options are
full for the original data (after possible scaling) and low for the object scores
in the low-dimensional space (default = "full")

alpha
Adjusts for the relative importance of (mixed) RKM and FKM in the objective
function; alpha = 1 reduces to PCA, alpha = 0.5 to (mixed) reduced K-means,
and alpha = 0 to (mixed) factorial K-means

alphak
Non-negative scalar to adjust for the relative importance of MCA (alphak = 1)
and K-means (alphak = 0) in the solution (default = .5). Works only in combi-
nation with method = "MCAk"

center
A logical value indicating whether the variables should be shifted to be zero
centered (default = TRUE)

scale
A logical value indicating whether the variables should be scaled to have unit
variance before the analysis takes place (default = TRUE)

rotation
Specifies the method used to rotate the factors. Options are none for no rotation,
varimax for varimax rotation with Kaiser normalization and promax for promax
rotation (default = "none")

nstart
Number of starts (default = 100)

smartStart
If NULL then a random cluster membership vector is generated. Alternatively, a
cluster membership vector can be provided as a starting solution

seed
An integer that is used as argument by set.seed() for offsetting the random
number generator when smartStart = NULL. The default value is NULL.

x
For the print method, a class of clusmca

object
For the summary method, a class of clusmca
tuneclus

mth
For the fitted method, a character string that specifies the type of fitted value
to return: "centers" for the observations center vector, or "class" for the
observations cluster membership value

... Not used

Details

For the K-means part, the algorithm of Hartigan-Wong is used by default.
The hidden print and summary methods print out some key components of an
object of class tuneclus.
The hidden fitted method returns cluster fitted values. If method is "classes", this is a vector of
cluster membership (the cluster component of the "tuneclus" object). If method is "centers", this
is a matrix where each row is the cluster center for the observation. The rownames of the matrix are
the cluster membership values.

Value

clusobjbest The output of the optimal run of cluspca() or clusmca()
nclusbest The optimal number of clusters
ndimbest The optimal number of dimensions
critbest The optimal criterion value for nclusbest clusters and ndimbest dimensions
critgrid Matrix of size nclusrange x ndimrange with the criterion values for the specified
ranges of clusters and dimensions (values are calculated only when the
number of clusters is greater than the number of dimensions; otherwise values
in the grid are left blank)
criterion "asw" for average Silhouette width or "ch" for "Calinski-Harabasz"
cluasw Average Silhouette width values of each cluster, when criterion = "asw"

References


See Also

global_bootclus, local_bootclus

Examples

# Reduced K-means for a range of clusters and dimensions
data(macro)
# Cluster quality assessment based on the average silhouette width in the low dimensional space
# nstart = 1 for speed in example
# use more for real applications
bestRKM = tuneclus(macro, 3:4, 2:3, method = "RKM", "centers")
criterion = "asw", dst = "low", nstart = 1, seed = 1234)
bestRKM
#plot(bestRKM)

# Cluster Correspondence Analysis for a range of clusters and dimensions
data(bribery)
# Cluster quality assessment based on the Callinski-Harabasz index in the full dimensional space
bestclusCA = tuneclus(bribery, 4:5, 3:4, method = "clusCA",
criterion = "ch", nstart = 20, seed = 1234)
bestclusCA
#plot(bestclusCA, cludesc = TRUE)

# Mixed reduced K-means for a range of clusters and dimensions
data(diamond)
# Cluster quality assessment based on the average silhouette width in the low dimensional space
# nstart = 5 for speed in example
# use more for real applications
bestmixedRKM = tuneclus(diamond[, -7], 3:4, 2:3,
method = "mixedRKM", criterion = "asw", dst = "low",
nstart = 5, seed = 1234)
bestmixedRKM
#plot(bestmixedRKM)
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