Package ‘fpc’

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Description Various methods for clustering and cluster validation.
        Fixed point clustering. Linear regression clustering. Clustering by
        merging Gaussian mixture components. Symmetric
        and asymmetric discriminant projections for visualisation of the
        separation of groupings. Cluster validation statistics
        for distance based clustering including corrected Rand index.
        Standardisation of cluster validation statistics by random clusterings and
        comparison between many clustering methods and numbers of clusters based on
        this.
        Cluster-wise cluster stability assessment. Methods for estimation of
        the number of clusters: Calinski-Harabasz, Tibshirani and Walther's
        prediction strength, Fang and Wang's bootstrap stability.
        Gaussian/multinomial mixture fitting for mixed
        continuous/categorical variables. Variable-wise statistics for cluster
        interpretation. DBSCAN clustering. Interface functions for many
        clustering methods implemented in R, including estimating the number of
        clusters with kmeans, pam and Clara. Modality diagnosis for Gaussian
        mixtures. For an overview see package?fpc.

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R topics documented:

- fpc-package .................................................. 4
- adecoord .................................................. 6
- ancoord .................................................. 8
- awcoord .................................................. 9
- batcoord .................................................. 11
- bhattacharyya.dist ....................................... 13
- bhattacharyya.matrix ..................................... 14
- calinhara .................................................. 15
- can ....................................................... 16
- cat2bin .................................................... 17
- cdbw ....................................................... 18
- cgrestandard ............................................... 19
- classifdist ............................................... 21
- clucols .................................................... 23
- clujaccard ............................................... 24
- clusexpect ............................................... 25
- clustatsum ............................................... 26
- cluster.magazine .......................................... 28
- cluster.stats .............................................. 30
- cluster.varstats .......................................... 34
- clusterbenchstats ........................................ 36
- clusterboot ............................................... 39
- cmahal ..................................................... 45
- con.comp .................................................. 46
- confusion ................................................ 48
- cov.wml .................................................... 49
- ccuilcluster.stats ....................................... 50
- cvn ....................................................... 56
- cweight .................................................... 57
- dbscan ..................................................... 58
- dipp.tantrum .............................................. 60
- diptest.multi .............................................. 61
- discrcoord ............................................... 62
- discrete.recode .......................................... 63
- discrproj .................................................. 65
- distancefactor ........................................... 67
- distcritmulti .............................................. 68
- distsimilarity ............................................ 70
- dridgeline ................................................ 71
- dudahart2 ................................................ 72
- extract.mixturepars ..................................... 73
- findrep ..................................................... 74
- fixmahal .................................................. 75
- fixreg ..................................................... 82
- flexmixedruns ............................................. 88
- fpclusters ................................................. 90
Description

Here is a list of the main functions in package fpc. Most other functions are auxiliary functions for these.

Clustering methods

- **dbscan** Computes DBSCAN density based clustering as introduced in Ester et al. (1996).
- **fixmahal** Mahalanobis Fixed Point Clustering, Hennig and Christlieb (2002), Hennig (2005).
- **fixreg** Regression Fixed Point Clustering, Hennig (2003).
- **flexmixedruns** This fits a latent class model to data with mixed type continuous/nominal variables. Actually it calls a method for flexmix.
- **mergenormals** Clustering by merging components of a Gaussian mixture, see Hennig (2010).
- **regmix** ML-fit of a mixture of linear regression models, see DeSarbo and Cron (1988).

Cluster validity indexes and estimation of the number of clusters

- **cluster.stats** This computes several cluster validity statistics from a clustering and a dissimilarity matrix including the Calinski-Harabasz index, the adjusted Rand index and other statistics explained in Gordon (1999) as well as several characterising measures such as average between cluster and within cluster dissimilarity and separation. See also calinhara, dudahart2 for specific indexes, and a new version cqcluster.stats that computes some more indexes and statistics used for computing them. There’s also distrsimilarity, which computes within-cluster dissimilarity to the Gaussian and uniform distribution.
- **prediction.strength** Estimates the number of clusters by computing the prediction strength of a clustering of a dataset into different numbers of components for various clustering methods, see Tibshirani and Walther (2005). In fact, this is more flexible than what is in the original paper, because it can use point classification schemes that work better with clustering methods other than k-means.
- **nselectboot** Estimates the number of clusters by bootstrap stability selection, see Fang and Wang (2012). This is quite flexible regarding clustering methods and point classification schemes and also allows for dissimilarity data.
- **clusterbenchstats** This runs many clustering methods (to be specified by the user) with many numbers of clusters on a dataset and produces standardised and comparable versions of many cluster validity indexes (see Hennig 2017, Akhanli and Hennig 2020). This is done by means of producing random clusterings on the given data, see stupidkcentroids and stupidknn. It allows to compare many clusterings based on many different potential desirable features of a clustering. **print.valstat** allows to compute an aggregated index with user-specified weights.
Cluster visualisation and validation

**clucols** Sets of colours and symbols useful for cluster plotting.

**clusterboot** Cluster-wise stability assessment of a clustering. Clusterings are performed on resampled data to see for every cluster of the original dataset how well this is reproduced. See Hennig (2007) for details.

**cluster.varstats** Extracts variable-wise information for every cluster in order to help with cluster interpretation.

**plotcluster** Visualisation of a clustering or grouping in data by various linear projection methods that optimise the separation between clusters, or between a single cluster and the rest of the data according to Hennig (2004) including classical methods such as discriminant coordinates. This calls the function discrproj, which is a bit more flexible but doesn’t produce a plot itself.

**ridgeline.diagnosis** Plots and diagnostics for assessing modality of Gaussian mixtures, see Ray and Lindsay (2005).

**weightplots** Plots to diagnose component separation in Gaussian mixtures, see Hennig (2010).

**localshape** Local shape matrix, can be used for finding clusters in connection with function ics in package ICS, see Hennig’s discussion and rejoinder of Tyler et al. (2009).

Useful wrapper functions for clustering methods

**kmeansCBI** This and other "CBI"-functions (see the kmeansCBI-help page) are unified wrappers for various clustering methods in R that may be useful because they do in one step for what you normally may need to do a bit more in R (for example fitting a Gaussian mixture with noise component in package mclust).

**kmeansruns** This calls kmeans for the k-means clustering method and includes estimation of the number of clusters and finding an optimal solution from several starting points.

**pamk** This calls pam and clara for the partitioning around medoids clustering method (Kaufman and Rouseeuw, 1990) and includes two different ways of estimating the number of clusters.

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References


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**adcoord**

**Asymmetric discriminant coordinates**

---

**Description**

Asymmetric discriminant coordinates as defined in Hennig (2003). Asymmetric discriminant projection means that there are two classes, one of which is treated as the homogeneous class (i.e., it should appear homogeneous and separated in the resulting projection) while the other may be heterogeneous. The principle is to maximize the ratio between the projection of a between classes separation matrix and the projection of the covariance matrix within the homogeneous class.

**Usage**

`adcoord(xd, clvecd, clnum=1)`

**Arguments**

- **xd**: the data matrix; a numerical object which can be coerced to a matrix.
- **clvecd**: integer vector of class numbers; length must equal nrow(xd).
- **clnum**: integer. Number of the homogeneous class.
Details

The square root of the homogeneous classes covariance matrix is inverted by use of \texttt{tdecomp}, which can be expected to give reasonable results for singular within-class covariance matrices.

Value

List with the following components

- \texttt{ev}: eigenvalues in descending order.
- \texttt{units}: columns are coordinates of projection basis vectors. New points \texttt{x} can be projected onto the projection basis vectors by \texttt{x \%*\% units}
- \texttt{proj}: projections of \texttt{xd} onto \texttt{units}.

Author(s)

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References


See Also

\texttt{plotcluster} for straightforward discriminant plots. \texttt{discrproj} for alternatives. \texttt{rFace} for generation of the example data used below.

Examples

```r
set.seed(4634)
face <- rFace(600,dMoNo=2,dNoEy=0)
grface <- as.integer(attr(face,"grouping"))
adcf <- adcoord(face,grface==2)
adcf2 <- adcoord(face,grface==4)
plot(adcf$proj,col=1+(grface==2))
plot(adcf2$proj,col=1+(grface==4))
# ...done in one step by function plotcluster.
```
Asymmetric neighborhood based discriminant coordinates

Description

Asymmetric neighborhood based discriminant coordinates as defined in Hennig (2003). Asymmetric discriminant projection means that there are two classes, one of which is treated as the homogeneous class (i.e., it should appear homogeneous and separated in the resulting projection) while the other may be heterogeneous. The principle is to maximize the ratio between the projection of a between classes covariance matrix, which is defined by averaging the between classes covariance matrices in the neighborhoods of the points of the homogeneous class and the projection of the covariance matrix within the homogeneous class.

Usage

ancoord(xd, clvecd, clnum=1, nn=50, method="mcd", countmode=1000, ...)

Arguments

- **xd**: the data matrix; a numerical object which can be coerced to a matrix.
- **clvecd**: integer vector of class numbers; length must equal nrow(xd).
- **clnum**: integer. Number of the homogeneous class.
- **nn**: integer. Number of points which belong to the neighborhood of each point (including the point itself).
- **method**: one of "mve", "mcd" or "classical". Covariance matrix used within the homogeneous class. "mcd" and "mve" are robust covariance matrices as implemented in cov.rob. "classical" refers to the classical covariance matrix.
- **countmode**: optional positive integer. Every countmode algorithm runs ancoord shows a message.
- **...**: no effect

Details

The square root of the homogeneous classes covariance matrix is inverted by use of tdecomp, which can be expected to give reasonable results for singular within-class covariance matrices.

Value

List with the following components

- **ev**: eigenvalues in descending order.
- **units**: columns are coordinates of projection basis vectors. New points x can be projected onto the projection basis vectors by x %*% units
- **proj**: projections of xd onto units.
awcoord

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References


See Also

plotcluster for straightforward discriminant plots. discrproj for alternatives. rFace for generation of the example data used below.

Examples

```r
set.seed(4634)
face <- rFace(600,dMoNo=2,dNoEy=0)
grface <- as.integer(attr(face,"grouping"))
ancf2 <- ancoord(face,grface==4)
plot(ancf2$proj,col=1+(grface==4))
# ...done in one step by function plotcluster.
```

Description

Asymmetric weighted discriminant coordinates as defined in Hennig (2003). Asymmetric discriminant projection means that there are two classes, one of which is treated as the homogeneous class (i.e., it should appear homogeneous and separated in the resulting projection) while the other may be heterogeneous. The principle is to maximize the ratio between the projection of a between classes separation matrix and the projection of the covariance matrix within the homogeneous class. Points are weighted according to their (robust) Mahalanobis distance to the homogeneous class.

Usage

```r
awcoord(xd, clvecd, clnum=1, mahal="square", method="classical",
        clweight=switch(method, classical=FALSE, TRUE),
        alpha=0.99, subsample=0, countmode=1000, ...)
```
Arguments

xd the data matrix; a numerical object which can be coerced to a matrix.
clvecd integer vector of class numbers; length must equal nrow(xd).
clnum integer. Number of the homogeneous class.
mahal "md" or "square". If "md", the points are weighted by the square root of the alpha-quantile of the corresponding chi squared distribution over the roots of their Mahalanobis distance to the homogeneous class, unless this is smaller than 1. If "square" (which is recommended), the (originally squared) Mahalanobis distance and the unrooted quantile is used.
method one of "mve", "mcd" or "classical". Covariance matrix used within the homogeneous class and for the computation of the Mahalanobis distances. "mcd" and "mve" are robust covariance matrices as implemented in cov.rob. "classical" refers to the classical covariance matrix.
clweight logical. If FALSE, only the points of the heterogeneous class are weighted. This, together with method="classical", computes AWC as defined in Hennig (2003). If TRUE, all points are weighted. This, together with method="mcd", computes ARC as defined in Hennig (2003).
alpha numeric between 0 and 1. The corresponding quantile of the chi squared distribution is used for the downweighting of points. Points with a smaller Mahalanobis distance to the homogeneous class get full weight.
subsample integer. If 0, all points are used. Else, only a subsample of subsample of the points is used.
countmode optional positive integer. Every countmode algorithm runs awcoord shows a message.
... no effect

Details

The square root of the homogeneous classes covariance matrix is inverted by use of tdecomp, which can be expected to give reasonable results for singular within-class covariance matrices.

Value

List with the following components

ev eigenvalues in descending order.
units columns are coordinates of projection basis vectors. New points x can be projected onto the projection basis vectors by x %*% units
proj projections of xd onto units.

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batcoord

References


See Also

plotcluster for straight forward discriminant plots. discrproj for alternatives. rFace for generation of the example data used below.

Examples

set.seed(4634)
face <- rFace(600,dMoNo=2,dNoEy=0)
grface <- as.integer(attr(face,"grouping"))
awcf <- awcoord(face,grface==1)
# awcf2 <- ancoord(face,grface==1, method="mcd")
plot(awcf$proj,col=1+(grface==1))
# plot(awcf2$proj,col=1+(grface==1))
# ...done in one step by function plotcluster.

batcoord

Bhattacharyya discriminant projection

Description

Computes Bhattacharyya discriminant projection coordinates as described in Fukunaga (1990), p. 455 ff.

Usage

batcoord(xd, clvecd, clnum=1, dom="mean")
batvarcoord(xd, clvecd, clnum=1)

Arguments

xd the data matrix; a numerical object which can be coerced to a matrix.
clvecd integer or logical vector of class numbers; length must equal nrow(xd).
clnum integer, one of the values of clvecd, if this is an integer vector. Bhattacharyya projections can only be computed if there are only two classes in the dataset. clnum is the number of one of the two classes. All the points indicated by other values of clvecd are interpreted as the second class.
dom string. dom=“mean” means that the discriminant coordinate for the group means is computed as the first projection direction by `discrcoord` (option pool=“equal”); both classes have the same weight for computing the within-class covariance matrix). Then the data is projected into a subspace orthogonal (w.r.t. the within-class covariance) to the discriminant coordinate, and the projection coordinates to maximize the differences in variance are computed.

dom=“variance” means that the projection coordinates maximizing the difference in variances are computed. Then they are ordered with respect to the Bhattacharyya distance, which takes also the mean differences into account. Both procedures are implemented as described in Fukunaga (1990).

Details

`batvarcoord` computes the optimal projection coordinates with respect to the difference in variances. `batcoord` combines the differences in mean and variance as explained for the argument dom.

Value

`batcoord` returns a list with the components ev, rev, units, proj. `batvarcoord` returns a list with the components ev, rev, units, proj, W, S1, S2.

ev vector of eigenvalues. If dom=“mean”, then first eigenvalue from `discrcoord`. Further eigenvalues are of $S_1^{-1}S_2$, where $S_i$ is the covariance matrix of class i. For batvarcoord or if dom=“variance”, all eigenvalues come from $S_1^{-1}S_2$ and are ordered by rev.


units columns are coordinates of projection basis vectors. New points x can be projected onto the projection basis vectors by x %*% units.

proj projections of xd onto units.

W matrix $S_1^{-1}S_2$.

S1 covariance matrix of the first class.

S2 covariance matrix of the second class.

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References

bhattacharyya.dist

Bhattacharyya distance between Gaussian distributions

Description

Computes Bhattacharyya distance between two multivariate Gaussian distributions. See Fukunaga (1990).

Usage

bhattacharyya.dist(mu1, mu2, Sigma1, Sigma2)

Arguments

mu1 mean vector of component 1.
u2 mean vector of component 2.
Sigma1 covariance matrix of component 1.
Sigma2 covariance matrix of component 2.

Value

The Bhattacharyya distance between the two Gaussian distributions.

Note

Thanks to David Pinto for improving this function.

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References


Examples

`round(bhattacharyya.dist(c(1,1),c(2,5),diag(2),diag(2)),digits=2)`

```
1.41
```

bhattacharyya.matrix  Matrix of pairwise Bhattacharyya distances

Description

Computes Bhattacharyya distances for pairs of components given the parameters of a Gaussian mixture.

Usage

`bhattacharyya.matrix(muarray,Sigmaarray,ipairs="all",misclassification.bound=TRUE)`

Arguments

- `muarray`: matrix of component means (different components are in different columns).
- `Sigmaarray`: three dimensional array with component covariance matrices (the third dimension refers to components).
- `ipairs`: “all” or list of vectors of two integers. If `ipairs="all"`, computations are carried out for all pairs of components. Otherwise, `ipairs` gives the pairs of components for which computations are carried out.
- `misclassification.bound`: logical. If TRUE, upper bounds for misclassification probabilities $\exp(-b)$ are given out instead of the original Bhattacharyya distances $b$.

Value

A matrix with Bhattacharyya distances (or derived misclassification bounds, see above) between pairs of Gaussian distributions with the provided parameters. If `ipairs!="all"`, the Bhattacharyya distance and the misclassification bound are given as NA for pairs not included in `ipairs`.

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References


See Also

bhattacharyya.dist

Examples

```r
muarray <- cbind(c(0,0),c(0,.1),c(10,10))
sigmaarray <- array(c(diag(2),diag(2),diag(2)),dim=c(2,2,3))
bhattacharyya.matrix(muarray,sigmaarray,ipairs=list(c(1,2),c(2,3)))
```

---

calinhara *Calinski-Harabasz index*

Description

Calinski-Harabasz index for estimating the number of clusters, based on an observations/variables-matrix here. A distance based version is available through cluster.stats.

Usage

```r
calinhara(x,clustering,cn=max(clustering))
```

Arguments

- `x`: data matrix or data frame.
- `cn`: integer. Number of clusters.

Value

Calinski-Harabasz statistic, which is \((n-cn)*\text{sum}(\text{diag}(B))/((cn-1)*\text{sum}(\text{diag}(W)))\). \(B\) being the between-cluster means, and \(W\) being the within-clusters covariance matrix.

Author(s)

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References

See Also
cluster.stats

Examples
```r
set.seed(98765)
iriss <- iris[sample(150,20),-5]
km <- kmeans(iriss,3)
round(calinhara(iriss,km$cluster),digits=2)
```

---

**Description**

Generates tuning constants \( ca \) for `fixreg` dependent on the number of points and variables of the dataset.

Only thought for use in `fixreg`.

**Usage**

`can(n, p)`

**Arguments**

- `n` positive integer. Number of points.
- `p` positive integer. Number of independent variables.

**Details**

The formula is \( 3 + 33/(n \* 2^{-(p-1)/2})^{1/3} + 2900000/(n \* 2^{-(p-1)/2})^{3} \). For justification cf. Hennig (2002).

**Value**

A number.

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References


See Also

fixreg

Examples

can(429,3)

cat2bin

Recode nominal variables to binary variables

Description

Recodes a dataset with nominal variables so that the nominal variables are replaced by binary variables for the categories.

Usage

cat2bin(x, categorical=NULL)

Arguments

x
data matrix or data frame. The data need to be organised case-wise, i.e., if there are categorical variables only, and 15 cases with values c(1,1,2) on the 3 variables, the data matrix needs 15 rows with values 1 1 2. (Categorical variables could take numbers or strings or anything that can be coerced to factor levels as values.)
categoricalvector of numbers of variables to be recoded.

Value

A list with components
data data matrix with variables specified in categorical replaced by 0-1 variables, one for each category.
variableinfo list of lists. One list for every variable in the original dataset, with four components each, namely type ("categorical" or "not recoded"), levels (levels of nominal recoded variables in order of binary variable in output dataset), ncat (number of categories for recoded variables), varnum (number of variables in output dataset belonging to this original variable).
CDbw-index for cluster validation

CDbw-index for cluster validation, as defined in Halkidi and Vazirgiannis (2008), Halkidi et al. (2015).

Usage

cdbw(x, clustering, r = 10, s = seq(0.1, 0.8, by = 0.1),
       clusterstdev = TRUE, trace = FALSE)

Arguments

x something that can be coerced into a numerical matrix. Euclidean dataset.
clustering vector of integers with length = nrow(x); indicating the cluster for each observation.
r integer. Number of cluster border representatives.
s numerical vector of shrinking factors (between 0 and 1).
clusterstdev logical. If TRUE, the neighborhood radius for intra-cluster density is the within-cluster estimated squared distance from the mean of the cluster; otherwise it is the average of these over all clusters.
trace logical. If TRUE, results are printed for the steps to compute the index.
Value
List with components (see Halkidi and Vazirgiannis (2008), Halkidi et al. (2015) for details)

- **cdbw**: value of CDbw index (the higher the better).
- **cohesion**: cohesion.
- **compactness**: compactness.
- **sep**: separation.

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References


Examples
```r
options(digits=3)
iris <- as.matrix(iris[c(1:5,51:55,101:105),-5])
iris <- as.numeric(iris[c(1:5,51:55,101:105),5])
cdbw(iris,iris)
```

---

cgrestandard \(\text{Standardise cluster validation statistics by random clustering results}\)

Description
Standardises cluster validity statistics as produced by `clustatsum` relative to results that were achieved by random clusterings on the same data by `randomclustersim`. The aim is to make differences between values comparable between indexes, see Hennig (2017), Akhanli and Hennig (2020).

This is mainly for use within `clusterbenchstats`.

Usage
```r
cgrestandard(clusum, clusim, G, percentage=FALSE, 
             useallmethods=FALSE, 
             useallg=FALSE, othernc=list())
```
Arguments

clusum
object of class "valstat", see clusterbenchstats.
clusim
list; output object of randomclustersim, see there.
G
vector of integers. Numbers of clusters to consider.
percentage
logical. If FALSE, standardisation is done to mean zero and standard deviation 1 using the random clusterings. If TRUE, the output is the percentage of simulated values below the result (more precisely, this number plus one divided by the total plus one).
useallmethods
logical. If FALSE, only random clustering results from clusim are used for standardisation. If TRUE, also clustering results from other methods as given in clusum are used.
useallg
logical. If TRUE, standardisation uses results from all numbers of clusters in G. If FALSE, standardisation of results for a specific number of cluster only uses results from that number of clusters.
othernc
list of integer vectors of length 2. This allows the incorporation of methods that bring forth other numbers of clusters than those in G, for example because a method may have automatically estimated a number of clusters. The first number is the number of the clustering method (the order is determined by argument clustermethod in clusterbenchstats), the second number is the number of clusters. Results specified here are only standardised in useallg=TRUE.

Details

cgrestandard will add a statistic named dmode to the input set of validation statistics, which is defined as 0.75*dindex+0.25*highdgap, aggregating these two closely related statistics, see clustatsum.

Value

List of class "valstat", see valstat.object, with standardised results as explained above.

Author(s)

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References


See Also

valstat.object, clusterbenchstats, stupidkcentroids, stupidknn, \codestupidkfn, stupidkaven, codeclustatsum
Examples

```r
set.seed(20000)
options(digits=3)
face <- rFace(10,dMoNo=2,dNoEy=0,p=2)
dif <- dist(face)
clusum <- list()
clusum[[2]] <- list()
cl12 <- kmeansCBI(face,2)
cl13 <- kmeansCBI(face,3)
cl22 <- claraCBI(face,2)
cl23 <- claraCBI(face,2)
ccl12 <- clustatsum(dif,cl12$partition)
ccl13 <- clustatsum(dif,cl13$partition)
ccl22 <- clustatsum(dif,cl22$partition)
ccl23 <- clustatsum(dif,cl23$partition)
clusum[[1]] <- list()
clusum[[1]][[2]] <- ccl12
clusum[[1]][[3]] <- ccl13
clusum[[2]][[2]] <- ccl22
clusum[[2]][[3]] <- ccl23
clusum$maxG <- 3
clusum$minG <- 2
clusum$method <- c("kmeansCBI","claraCBI")
clusum$name <- c("kmeansCBI","claraCBI")
clusim <- randomclustersim(dist(face),G=2:3,nnruns=1,kmruns=1,
fnruns=1,avenruns=1,monitor=FALSE)
cgr <- cgrestandard(clusum,clusim,2:3)
cgr2 <- cgrestandard(clusum,clusim,2:3,useallg=TRUE)
cgr3 <- cgrestandard(clusum,clusim,2:3,percentage=TRUE)
print(str(cgr))
print(str(cgr2))
print(cgr3[[1]][[2]])
```

classifdist

Classification of unclustered points

Description

Various methods for classification of unclustered points from clustered points for use within functions nselectboot and prediction.strength.

Usage

```r
classifdist(cdist,clustering,
method="averagedist",
centroids=NULL,nnk=1)
```

classifnp(data,clustering,
method="centroid",cdist=NULL,
    centroids=NULL,nnk=1)

Arguments

  cdist  dissimilarity matrix or dist-object. Necessary for classifdist but optional
         for classifnp and there only used if method="averagedist" (if not provided,
         dist is applied to data).
  data  something that can be coerced into an n*p-data matrix.
  clustering integer vector. Gives the cluster number (between 1 and k for k clusters) for
         clustered points and should be -1 for points to be classified.
  method one of "averagedist","centroid","qda","knn". See details.
  centroids for classifnp a k times p matrix of cluster centroids. For classifdist a vector
         of numbers of centroid objects as provided by pam. Only used if method="centroid";
         in that case mandatory for classifdist but optional for classifnp, where
         cluster mean vectors are computed if centroids=NULL.
  nnk  number of nearest neighbours if method="knn".

Details

classifdist is for data given as dissimilarity matrix, classifnp is for data given as n times p data
matrix. The following methods are supported:

  "centroid" assigns observations to the cluster with closest cluster centroid as specified in argument
  centroids (this is associated to k-means and pam/clara-clustering).
  "averagedist" assigns to the cluster to which an observation has the minimum average dissimilar-
  ity to all points in the cluster (this is associated to average linkage clustering).
  "qda" only in classifnp. Classifies by quadratic discriminant analysis (this is associated to Gaussian
  clusters with flexible covariance matrices), calling qda with default settings. If qda gives
  an error (usually because a class was too small), lda is used.
  "knn" classifies by nnk nearest neighbours (for nnk=1, this is associated with single linkage clus-
  tering). Calls knn in classifnp.

Value

  An integer vector giving cluster numbers for all observations; those for the observations already
  clustered in the input are the same as in the input.

Author(s)

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  hennig/en/

See Also

  prediction.strength,nselectboot
Examples

```r
set.seed(20000)
x1 <- rnorm(50)
y <- rnorm(100)
x2 <- rnorm(40, mean=20)
x3 <- rnorm(10, mean=25, sd=100)
x <- cbind(c(x1,x2,x3),y)
truec <- c(rep(1,50),rep(2,40),rep(3,10))
topredict <- c(1,2,51,52,91)
clumin <- truec
clumin[topredict] <- -1

classifnp(x,clumin, method="averagedist")
classifnp(x,clumin, method="qda")
classifdist(dist(x),clumin, centroids=c(3,53,93), method="centroid")
classifdist(dist(x),clumin, method="knn")
```

**clucols**

Sets of colours and symbols for cluster plotting

Description

clucols gives out a vector of different random colours. clugrey gives out a vector of equidistant grey scales. clusym is a vector of different symbols starting from "1", "2", ...

Usage

```r
clucols(i, seed=NULL)
clugrey(i, max=0.9)
clusym
```

Arguments

- `i` integer. Length of output vector (number of clusters).
- `seed` integer. Random seed.
- `max` between 0 and 1. Maximum grey scale value, see `grey` (close to 1 is bright).

Value

clucols gives out a vector of different random colours. clugrey gives out a vector of equidistant grey scales. clusym is a vector of different characters starting from "1", "2", ...

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en
Examples

```r
set.seed(112233)
require(MASS)
require(flexmix)
data(Cars93)
Cars934 <- Cars93[,c(3,5,8,10)]
cc <-
discrete.recode(Cars934,xvarsorted=FALSE,continuous=c(2,3),discrete=c(1,4))
fcc <- flexmix(cc$data~1,k=3,
model=lcmixed(continuous=2,discrete=2,ppdim=c(6,3),diagonal=TRUE))
plot(Cars934[,c(2,3)],col=clucols(3)[fcc@cluster],pch=clusym[fcc@cluster])
```

cliffeaccard

**chureaccard**

_Jaccard similarity between logical vectors_

Description

Jaccard similarity between logical or 0-1 vectors: \( \frac{\text{sum}(c1 \& c2)}{\text{sum}(c1 | c2)} \).

Usage

```r
cliffeaccard(c1,c2,zerobyzero=NA)
```

Arguments

- `c1`: logical or 0-1-vector.
- `c2`: logical or 0-1-vector (same length).
- `zerobyzero`: result if \( \text{sum}(c1 | c2)=0 \).

Value

Numeric between 0 and 1.

Author(s)

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Examples

```r
c1 <- rep(TRUE,10)
c2 <- c(FALSE,rep(TRUE,9))
cliffeaccard(c1,c2)
```
A rough approximation of the expectation of the number of times a well separated fixed point cluster (FPC) of size $n$ is found in $ir$ fixed point iterations of fixreg.

Usage

```r
clusexpect(n, p, cn, ir)
```}

Arguments

- $n$ : positive integer. Total number of points.
- $p$ : positive integer. Number of independent variables.
- $cn$ : positive integer smaller or equal to $n$. Size of the FPC.
- $ir$ : positive integer. Number of fixed point iterations.

Details

The approximation is based on the assumption that a well separated FPC is found iff all $p+2$ points of the initial configuration come from the FPC. The value is $ir$ times the probability for this. For a discussion of this assumption cf. Hennig (2002).

Value

A number.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

fixreg

Examples

```r
round(clusexpect(500,4,150,2000),digits=2)
```
clustatsum

Compute and format cluster validation statistics

Description

clustatsum computes cluster validation statistics by running cqcluster.stats, and potentially distrsimilarity, and collecting some key statistics values with a somewhat different nomenclature.

This was implemented as a helper function for use inside of clusterbenchstats and cgrestandard.

Usage

clustatsum(datadist=NULL, clustering, noisecluster=FALSE, datanp=NULL, npstats=FALSE, dnnk=2, pamcrit=TRUE, ...)

Arguments

datadist

distances on which validation-measures are based, dist object or distance matrix. If NULL, this is computed from datanp; at least one of datadist and datanp must be specified.

clustering

an integer vector of length of the number of cases, which indicates a clustering. The clusters have to be numbered from 1 to the number of clusters.

noisecluster

logical. If TRUE, it is assumed that the largest cluster number in clustering denotes a 'noise class', i.e. points that do not belong to any cluster. These points are not taken into account for the computation of all functions of within and between cluster distances including the validation indexes.

datanp

optional observations times variables data matrix, see npstats.

npstats

logical. If TRUE, distrsimilarity is called and the two statistics computed there are added to the output. These are based on datanp and require datanp to be specified.

dnnk

nnk-argument to be passed on to distrsimilarity.

pamcrit

pamcrit-argument to be passed on to cqcluster.stats.

...

further arguments to be passed on to cqcluster.stats.

Value

clustatsum returns a list. The components, as listed below, are outputs of summary.cquality with default parameters, which means that they are partly transformed versions of those given out by cqcluster.stats, i.e., their range is between 0 and 1 and large values are good. Those from distrsimilarity are computed with largeisgood=TRUE, correspondingly.

avewithin

average distance within clusters (reweighted so that every observation, rather than every distance, has the same weight).
Clustering summary

**mnnnd**
Average distance to n-th nearest neighbour within cluster.

**cvnnd**
Coefficient of variation of dissimilarities to n-th nearest within-cluster neighbour, measuring uniformity of within-cluster densities, weighted over all clusters, see Sec. 3.7 of Hennig (2017).

**maxdiameter**
Maximum cluster diameter.

**widestgap**
Widest within-cluster gap or average of cluster-wise widest within-cluster gap, depending on parameter averagegap.

**sindex**
Separation index, see argument sepindex.

**minsep**
Minimum cluster separation.

**asw**
Average silhouette width. See silhouette.

**dindex**
This index measures to what extent the density decreases from the cluster mode to the outskirts; I-densdec in Sec. 3.6 of Hennig (2017); low values are good.

**denscut**
This index measures whether cluster boundaries run through density valleys; I-densbound in Sec. 3.6 of Hennig (2017); low values are good.

**highdgap**
This measures whether there is a large within-cluster gap with high density on both sides; I-highdgap in Sec. 3.6 of Hennig (2017); low values are good.

**pearsongamma**
Correlation between distances and a 0-1-vector where 0 means same cluster, 1 means different clusters. "Normalized gamma" in Halkidi et al. (2001).

**withinss**
A generalisation of the within clusters sum of squares (k-means objective function), which is obtained if d is a Euclidean distance matrix. For general distance measures, this is half the sum of the within cluster squared dissimilarities divided by the cluster size.

**entropy**
Entropy of the distribution of cluster memberships, see Meila (2007).

**pamc**
Average distance to cluster centroid.

**kdnorm**
Kolmogorov distance between distribution of within-cluster Mahalanobis distances and appropriate chi-squared distribution, aggregated over clusters (I am grateful to Agustin Mayo-Iscar for the idea).

**kdunif**
Kolmogorov distance between distribution of distances to n-th nearest within-cluster neighbor and appropriate Gamma-distribution, see Byers and Raftery (1998), aggregated over clusters.

**Author(s)**

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**References**


See Also
cqcluster.stats, distrsimilarity

Examples

```r
set.seed(20000)
options(digits=3)
face <- rFace(20,dMoNo=2,dNoEy=0,p=2)
dface <- dist(face)
complete3 <- cutree(hclust(dface),3)
clustatsum(dface,complete3)
```

cluster.magazine  
Run many clustering methods on many numbers of clusters

Description

Runs a user-specified set of clustering methods (CBI-functions, see kmeansCBI with several numbers of clusters on a dataset with unified output.

Usage

```
cluster.magazine(data,G,diss = inherits(data, "dist"),
scaling=TRUE, clustermethod,
distmethod=rep(TRUE,length(clustermethod)),
ncinput=rep(TRUE,length(clustermethod)),
clustermethodpars,
trace=TRUE)
```

Arguments

- **data**: data matrix or dist-object.
- **G**: vector of integers. Numbers of clusters to consider.
- **diss**: logical. If TRUE, the data matrix is assumed to be a distance/dissimilarity matrix, otherwise it's observations times variables.
- **scaling**: either a logical or a numeric vector of length equal to the number of columns of data. If FALSE, data won't be scaled, otherwise scaling is passed on to `scale` as argumentscale.
clustermethod vector of strings specifying names of CBI-functions (see kmeansCBI). These are the clustering methods to be applied.

distmethod vector of logicals, of the same length as clustermethod. TRUE means that the clustering method operates on distances. If diss=TRUE, all entries have to be TRUE. Otherwise, if an entry is true, the corresponding method will be applied on dist(data).

cninput vector of logicals, of the same length as clustermethod. TRUE indicates that the corresponding clustering method requires the number of clusters as input and will not estimate the number of clusters itself.

clustermethodpars list of the same length as clustermethod. Specifies parameters for all involved clustering methods. Its jth entry is passed to clustermethod number k. Can be an empty entry in case all defaults are used for a clustering method. The number of clusters does not need to be specified here.

trace logical. If TRUE, some runtime information is printed.

Value
List of lists comprising

output Two-dimensional list. The first list index i is the number of the clustering method (ordering as specified in clustermethod), the second list index j is the number of clusters. This stores the full output of clustermethod i run on number of clusters j.

clustering Two-dimensional list. The first list index i is the number of the clustering method (ordering as specified in clustermethod), the second list index j is the number of clusters. This stores the clustering integer vector (i.e., the partition-component of the CBI-function, see kmeansCBI) of clustermethod i run on number of clusters j.

noise Two-dimensional list. The first list index i is the number of the clustering method (ordering as specified in clustermethod), the second list index j is the number of clusters. List entries are single logicals. If TRUE, the clustering method estimated some noise, i.e., points not belonging to any cluster, which in the clustering vector are indicated by the highest number (number of clusters plus one in case that the number of clusters was fixed).

othernc list of integer vectors of length 2. The first number is the number of the clustering method (the order is determined by argument clustermethod), the second number is the number of clusters for those methods that estimate the number of clusters themselves and estimate a number that is smaller than min(G) or larger than max(G).

Author(s)
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References


See Also

clusterbenchstats, kmeansCBI

Examples

```r
set.seed(20000)
options(digits=3)
face <- rFace(10,dMoNo=2,dNoEy=0,p=2)
clustermethod=c("kmeansCBI","hclustCBI","hclustCBI")
# A clustering method can be used more than once, with different parameters
clustermethodpars <- list()
clustermethodpars[[2]] <- clustermethodpars[[3]] <- list()
clustermethodpars[[2]]$method <- "complete"
clustermethodpars[[3]]$method <- "average"
cmf <- cluster.magazine(face,G=2:3,clustermethod=clustermethod,
distmethod=rep(FALSE,3),clustermethodpars=clustermethodpars)
print(str(cmf))
```

---

**cluster.stats**

*Cluster validation statistics*

**Description**

Computes a number of distance based statistics, which can be used for cluster validation, comparison between clusterings and decision about the number of clusters: cluster sizes, cluster diameters, average distances within and between clusters, cluster separation, biggest within cluster gap, average silhouette widths, the Calinski and Harabasz index, a Pearson version of Hubert's gamma coefficient, the Dunn index and two indexes to assess the similarity of two clusterings, namely the corrected Rand index and Meila's VI.

**Usage**

```r
cluster.stats(d = NULL, clustering, alt.clustering = NULL,
noisecluster=FALSE,
silhouette = TRUE, G2 = FALSE, G3 = FALSE,
wgap=TRUE, sepindex=TRUE, sepprob=0.1,
sepwithnoise=TRUE,
compareonly = FALSE,
aggregateonly = FALSE)
```
Arguments

- **d**: a distance object (as generated by `dist`) or a distance matrix between cases.
- **clustering**: an integer vector of length of the number of cases, which indicates a clustering. The clusters have to be numbered from 1 to the number of clusters.
- **alt.clustering**: an integer vector such as for `clustering`, indicating an alternative clustering. If provided, the corrected Rand index and Meila’s VI for `clustering` vs. `alt.clustering` are computed.
- **noisecluster**: logical. If TRUE, it is assumed that the largest cluster number in `clustering` denotes a 'noise class', i.e. points that do not belong to any cluster. These points are not taken into account for the computation of all functions of within and between cluster distances including the validation indexes.
- **silhouette** logical. If TRUE, the silhouette statistics are computed, which requires package `cluster`.
- **G2** logical. If TRUE, Goodman and Kruskal’s index G2 (cf. Gordon (1999), p. 62) is computed. This executes lots of sorting algorithms and can be very slow (it has been improved by R. Francois - thanks!)
- **G3** logical. If TRUE, the index G3 (cf. Gordon (1999), p. 62) is computed. This executes sort on all distances and can be extremely slow.
- **wgap** logical. If TRUE, the widest within-cluster gaps (largest link in within-cluster minimum spanning tree) are computed. This is used for finding a good number of clusters in Hennig (2013).
- **sepindex** logical. If TRUE, a separation index is computed, defined based on the distances for every point to the closest point not in the same cluster. The separation index is then the mean of the smallest proportion sepprob of these. This allows to formalise separation less sensitive to a single or a few ambiguous points. The output component corresponding to this is `sindex`, not separation! This is used for finding a good number of clusters in Hennig (2013).
- **sepprob** numerical between 0 and 1, see `sepindex`.
- **sepwithnoise** logical. If TRUE and `sepindex` and `noisecluster` are both TRUE, the noise points are incorporated as cluster in the separation index (`sepindex`) computation. Also they are taken into account for the computation for the minimum cluster separation.
- **compareonly** logical. If TRUE, only the corrected Rand index and Meila’s VI are computed and given out (this requires `alt.clustering` to be specified).
- **aggregateonly** logical. If TRUE (and not compareonly), no clusterwise but only aggregated information is given out (this cuts the size of the output down a bit).

Value

`cluster.stats` returns a list containing the components `n`, `cluster.number`, `cluster.size`, `min.cluster.size`, `noisen`, `diameter`, `average.distance`, `median.distance`, `separation`, `average.toother` ... `ss`, `clus.avg.silwidths`, `avg.silwidth`, `g2`, `g3`, `pearson_gamma`, `dunn`, `entropy`, `wb.ratio`, `ch`, `cwidegap`, `widestgap`, `sindex`, `corrected.rand`, `vi` except if `compareonly=TRUE`, in which case only the last two components are computed.

- **n** number of cases.
- **cluster.number** number of clusters.
cluster.size vector of cluster sizes (number of points).
min.cluster.size size of smallest cluster.
noisen number of noise points, see argument noisecluster (noisen=0 if noisecluster=FALSE).
diameter vector of cluster diameters (maximum within cluster distances).
average.distance vector of clusterwise within cluster average distances.
median.distance vector of clusterwise within cluster distance medians.
separation vector of clusterwise minimum distances of a point in the cluster to a point of another cluster.
average.toother vector of clusterwise average distances of a point in the cluster to the points of other clusters.
separation.matrix matrix of separation values between all pairs of clusters.
ave.between.matrix matrix of mean dissimilarities between points of every pair of clusters.
average.between average distance between clusters.
average.within average distance within clusters (rewighted so that every observation, rather than every distance, has the same weight).
n.between number of distances between clusters.
n.within number of distances within clusters.
max.diameter maximum cluster diameter.
min.separation minimum cluster separation.
within.cluster.ss a generalisation of the within clusters sum of squares (k-means objective function), which is obtained if d is a Euclidean distance matrix. For general distance measures, this is half the sum of the within cluster squared dissimilarities divided by the cluster size.
clus.avg.silwidths vector of cluster average silhouette widths. See silhouette.
avg.silwidth average silhouette width. See silhouette.
g3 G3 coefficient. See Gordon (1999, p. 62).
pearsongamma correlation between distances and a 0-1-vector where 0 means same cluster, 1 means different clusters. "Normalized gamma" in Halkidi et al. (2001).
dunn minimum separation / maximum diameter. Dunn index, see Halkidi et al. (2002).
dunn2 minimum average dissimilarity between two cluster / maximum average within cluster dissimilarity, another version of the family of Dunn indexes.
entropy

type: double

Description:

Entropy of the distribution of cluster memberships, see Meila(2007).

wb.ratio

type: double

Description:

Average within/average between.

ch

type: double

Description:

Calinski and Harabasz index (Calinski and Harabasz 1974, optimal in Milligan and Cooper 1985; generalised for dissimilarites in Hennig and Liao 2013).

cwidegap

type: list

Description:

Vector of widest within-cluster gaps.

widestgap

type: double

Description:

Widest within-cluster gap.

sindex

type: double

Description:

Separation index, see argument sepindex.

corrected.rand

type: double

Description:

Corrected Rand index (if alt.clustering has been specified), see Gordon (1999, p. 198).

vi

type: double

Description:

Variation of information (VI) index (if alt.clustering has been specified), see Meila (2007).

Note

Because cluster.stats processes a full dissimilarity matrix, it isn't suitable for large data sets. You may consider distcritmulti in that case.

Author(s)

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References


See Also

cqcluster.stats is a more sophisticated version of cluster.stats with more options. silhouette, dist, calinhara, distcritmulti. clusterboot computes clusterwise stability statistics by re-sampling.

Examples

```r
set.seed(20000)
options(digits=3)
face <- rFace(200,dMoNo=2,dNoEy=0,p=2)
dface <- dist(face)
complete3 <- cutree(hclust(dface),3)
cluster.stats(dface,complete3,
  alt.clustering=as.integer(attr(face,"grouping")))
```

cluster.varstats  Variablewise statistics for clusters

Description

This function gives some helpful variable-wise information for cluster interpretation, given a clustering and a data set. The output object contains some tables. For categorical variables, tables compare clusterwise distributions with overall distributions. Continuous variables are categorised for this.

If desired, tables, histograms, some standard statistics of continuous variables and validation plots as available through discrproj (Hennig 2004) are given out on the fly.

Usage

```r
cluster.varstats(clustering,vardata,contdata=vardata,
  clusterwise=TRUE,
  tablevar=NULL,catvar=NULL,
  quantvar=NULL, catvarcats=10,
  proportions=FALSE,
  projmethod="none",minsize=ncol(contdata)+2,
  ask=TRUE,rangefactor=1)
```

```r
## S3 method for class 'varwisetables'
print(x,digits=3,...)
```

Arguments

- `clustering`  vector of integers. Clustering (needs to be in standard coding, 1,2,...).
- `vardata`  data matrix or data frame of which variables are summarised.
**cluster.varstats**

- **contdata**: variable matrix or data frame, normally all or some variables from vardata, on which cluster visualisation by projection methods is performed unless projmethod="none". It should make sense to interpret these variables in a quantitative (interval-scaled) way.

- **clusterwise**: logical. If FALSE, only the output tables are computed but no more detail and graphs are given on the fly.

- **tablevar**: vector of integers. Numbers of variables treated as categorical (i.e., no histograms and statistics, just tables) if clusterwise=TRUE. Note that an error will be produced by factor type variables unless they are declared as categorical here.

- **catvar**: vector of integers. Numbers of variables to be categorised by proportional quantiles for table computation. Recommended for all continuous variables.

- **quantvar**: vector of integers. Variables for which means, standard deviations and quantiles should be given out if clusterwise=TRUE.

- **catvarcats**: integer. Number of categories used for categorisation of variables specified in quantvar.

- **proportions**: logical. If TRUE, output tables contain proportions, otherwise numbers of observations.

- **projmethod**: one of "none", "dc", "bc", "vbc", "mvdc", "adc", "awc" (recommended if not "none"), "arc", "nc", "wnc", "anc". Cluster validation projection method introduced in Hennig (2004), passed on as method argument in discrproj.

- **minsize**: integer. Projection is not carried out for clusters with fewer points than this. (If this is chosen smaller, it may lead to errors with some projection methods.)

- **ask**: logical. If TRUE, par(ask=TRUE) is set in the beginning to prompt the user before plots and par(ask=FALSE) in the end.

- **rangefactor**: numeric. Factor by which to multiply the range for projection plot ranges.

- **x**: an object of class "varwisetables", output object of cluster.varstats.

- **digits**: integer. Number of digits after the decimal point to print out.

- **...**: not used.

**Value**

An object of class "varwisetables", which is a list with a table for each variable, giving (categorised) marginal distributions by cluster.

**Author(s)**

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**References**

Examples

```r
set.seed(112233)
options(digits=3)
require(MASS)
require(flexmix)
data(Cars93)
Cars934 <- Cars93[,c(3,5,8,10)]
cc <-
   discrete.recode(Cars934,xvarsorted=FALSE,continuous=c(2,3),discrete=c(1,4))
fcc <- flexmix(cc$data-1,k=2,
   model=lcmixed(continuous=2,discrete=2,ppdim=c(6,3),diagonal=TRUE))
cv <-
   cluster.varstats(fcc@cluster,Cars934, contdata=Cars934[,c(2,3)],
   tablevar=c(1,4),catvar=c(2,3),quantvar=c(2,3),projmethod="awc",
   ask=FALSE)
print(cv)
```

clusterbenchstats  Run and validate many clusterings

Description

This runs the methodology explained in Hennig (2017), Akhanli and Hennig (2020). It runs a user-specified set of clustering methods (CBI-functions, see kmeansCBI) with several numbers of clusters on a dataset, and computes many cluster validation indexes. In order to explore the variation of these indexes, random clusterings on the data are generated, and validation indexes are standardised by use of the random clusterings in order to make them comparable and differences between values interpretable.

The function print.valstat can be used to provide weights for the cluster validation statistics, and will then compute a weighted validation index that can be used to compare all clusterings.

Usage

```r
clusterbenchstats(data,G,diss = inherits(data, "dist"),
   scaling=TRUE, clustermethod,
   methodnames=clustermethod, distmethod=rep(TRUE,length(clustermethod)),
   ncinput=rep(TRUE,length(clustermethod)), clustermethodpars,
   npstats=FALSE, trace=TRUE, pamcrit=TRUE,snnk=2,
   dnnk=2, nnruns=100,kmruts=100,fnnruns=100,aenruns=100,
   multicore=FALSE,cores=detectCores()-1, useallmethods=TRUE,
   useallg=FALSE,...)
```
### S3 method for class 'clusterbenchstats'

`print(x,...)`

#### Arguments

- **data**: data matrix or `dist`-object.
- **G**: vector of integers. Numbers of clusters to consider.
- **diss**: logical. If TRUE, the data matrix is assumed to be a distance/dissimilarity matrix, otherwise it's observations times variables.
- **scaling**: either a logical or a numeric vector of length equal to the number of columns of data. If FALSE, data won't be scaled, otherwise scaling is passed on to `scale` as argument `scale`.
- **clustermethod**: vector of strings specifying names of CBI-functions (see `kmeansCBI`). These are the clustering methods to be applied.
- **methodnames**: vector of strings with user-chosen names for clustering methods, one for every method in `clustermethod`. These can be used to distinguish different methods run by the same CBI-function but with different parameter values such as complete and average linkage for `hclustCBI`.
- **distmethod**: vector of logicals, of the same length as `clustermethod`. TRUE means that the clustering method operates on distances. If `diss=TRUE`, all entries have to be TRUE. Otherwise, if an entry is true, the corresponding method will be applied on `dist(data)`.
- **ncinput**: vector of logicals, of the same length as `clustermethod`. TRUE indicates that the corresponding clustering method requires the number of clusters as input and will not estimate the number of clusters itself.
- **clustermethodpars**: list of the same length as `clustermethod`. Specifies parameters for all involved clustering methods. Its jth entry is passed to clustermethod number k. Can be an empty entry in case all defaults are used for a clustering method. The number of clusters does not need to be specified here.
- **npstats**: logical. If TRUE, `distrsimilarity` is called and the two validity statistics computed there are added. These require diss=FALSE.
- **trace**: logical. If TRUE, some runtime information is printed.
- **pamcrit**: logical. If TRUE, the average distance of points to their respective cluster centroids is computed (criterion of the PAM clustering method, validation criterion pamc); centroids are chosen so that they minimise this criterion for the given clustering. Passed on to `cqcluster.stats`.
- **snnk**: integer. Number of neighbours used in coefficient of variation of distance to nearest within cluster neighbour, the cvnnd-statistic (clusters with snnk or fewer points are ignored for this). Passed on to `cqcluster.stats` as argument nnk.
- **dnnk**: integer. Number of nearest neighbors to use for dissimilarity to the uniform in case that npstats=TRUE; nnk-argument to be passed on to `distrsimilarity`.
- **nnruns**: integer. Number of runs of `stupidknn` (random clusterings).
clusterbenchstats

kruns
integer. Number of runs of stupidkcentroids (random clusterings).

fnruns
integer. Number of runs of stupidkfn (random clusterings).

avenruns
integer. Number of runs of stupidkaven (random clusterings).

multicore
logical. If TRUE, parallel computing is used through the function mclapply from package parallel; read warnings there if you intend to use this; it won’t work on Windows.

cores
integer. Number of cores for parallelisation.

useallmethods
logical, to be passed on to cgrestandard. If FALSE, only random clustering results are used for standardisation. If TRUE, clustering results from all methods are used.

useallg
logical to be passed on to cgrestandard. If TRUE, standardisation uses results from all numbers of clusters in G. If FALSE, standardisation of results for a specific number of cluster only uses results from that number of clusters.

... further arguments to be passed on to cqcluster.stats through clustatsum (no effect in print.clusterbenchstats).

x
object of class "clusterbenchstats".

Value

The output of clusterbenchstats is a big list of lists comprising lists cm, stat, sim, qstat, sstat, statistics

cm
output object of cluster.magazine, see there for details. Clustering of all methods and numbers of clusters on the dataset data.

stat
object of class "valstat", see valstat.object for details. Unstandardised cluster validation statistics.

sim
output object of randomclustersim, see there. Validity indexes from random clusterings used for standardisation of validation statistics on data.

qstat
object of class "valstat", see valstat.object for details. Cluster validation statistics standardised by random clusterings, output of cgrestandard based on percentages, i.e., with percentage=TRUE.

sstat
object of class "valstat", see valstat.object for details. Cluster validation statistics standardised by random clusterings, output of cgrestandard based on mean and standard deviation, i.e., with percentage=FALSE.

Note

This may require a lot of computing time and also memory for datasets that are not small, as most indexes require computation and storage of distances.

Author(s)

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References


See Also

`valstat.object`, `cluster.magazine`, `kmeansCBI`, `cqcluster.stats`, `clustatsum`, `cgrestandard`

Examples

```r
set.seed(20000)
options(digits=3)
face <- rFace(10,dMoNo=2,dNoEy=0,p=2)
clustermethod=c("kmeansCBI","hclustCBI")
# A clustering method can be used more than once, with different parameters
clustermethodpars <- list()
clustermethodpars[[2]] <- list()
clustermethodpars[[2]]$method <- "average"
methodname <- c("kmeans","average")
cbs <- clusterbenchstats(face,G=2:3,clustermethod=clustermethod,
                         methodname=methodname,distmethod=rep(FALSE,2),
                         clustermethodpars=clustermethodpars,nnruns=1,kmruns=1,fnruns=1,avenruns=1)
print(cbs)
print(cbs$qstat,aggregate=TRUE,weights=c(1,0,0,0,0,1,0,1,0,1,0,0,1,1,1,1))
# The weights are weights for the validation statistics ordered as in cbs$qstat$statistics for computation of an aggregated index, see
# ?print.valstat.
```

---

`clusterboot`  
*Clusterwise cluster stability assessment by resampling*

Description

Assessment of the clusterwise stability of a clustering of data, which can be cases*variables or dissimilarity data. The data is resampled using several schemes (bootstrap, subsetting, jittering, replacement of points by noise) 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 (other statistics can be computed as well). The methods are described in Hennig (2007).

`clusterboot` is an integrated function that computes the clustering as well, using interface functions for various clustering methods implemented in R (several interface functions are provided, but...
you can implement further ones for your favourite clustering method). See the documentation of the input parameter clustermethod below.

Quite general clustering methods are possible, i.e. methods estimating or fixing the number of clusters, methods producing overlapping clusters or not assigning all cases to clusters (but declaring them as "noise"). Fuzzy clusterings cannot be processed and have to be transformed to crisp clusterings by the interface function.

Usage

clusterboot(data,B=100, distances=(inherits(data, "dist")),
  bootmethod="boot",
  bscompare=TRUE,
  multipleboot=FALSE,
  jittertuning=0.05, noisetuning=c(0.05,4),
  subtuning=floor(nrow(data)/2),
  clustermethod,noisemethod=FALSE,count=TRUE,
  showplots=FALSE,dissolution=0.5,
  recover=0.75,seed=NULL,datatomatrix=TRUE,...)

## S3 method for class 'clboot'
print(x,statistics=c("mean","dissolution","recovery"),...)

## S3 method for class 'clboot'
plot(x,xlim=c(0,1),breaks=seq(0,1,by=0.05),...)

Arguments

data by default something that can be coerced into a (numerical) matrix (data frames with non-numerical data are allowed when using datatomatrix=FALSE, see below). The data matrix - either an n*p-data matrix (or data frame) or an n*n-dissimilarity matrix (or dist-object).

B integer. Number of resampling runs for each scheme, see bootmethod.

distances logical. If TRUE, the data is interpreted as dissimilarity matrix. If data is a dist-object, distances=TRUE automatically, otherwise distances=FALSE by default. This means that you have to set it to TRUE manually if data is a dissimilarity matrix.

bootmethod vector of strings, defining the methods used for resampling. Possible methods: "boot": nonparametric bootstrap (precise behaviour is controlled by parameters bscompare and multipleboot).

"subset": selecting random subsets from the dataset. Size determined by subtuning.

"noise": replacing a certain percentage of the points by random noise, see noisetuning.

"jitter" add random noise to all points, see jittertuning. (This didn't perform well in Hennig (2007), but you may want to get your own experience.)

"bojit" nonparametric bootstrap first, and then adding noise to the points, see jittertuning.
Important: only the methods "boot" and "subset" work with dissimilarity data, or if datatomatrix=FALSE!

The results in Hennig (2007) indicate that "boot" is generally informative and often quite similar to "subset" and "bojit", while "noise" sometimes provides different information. Therefore the default (for distances=FALSE) is to use "boot" and "noise". However, some clustering methods may have problems with multiple points, which can be solved by using "bojit" or "subset" instead of "boot" or by multipleboot=FALSE below.

bscompare logical. If TRUE, multiple points in the bootstrap sample are taken into account to compute the Jaccard similarity to the original clusters (which are represented by their "bootstrap versions", i.e., the points of the original cluster which also occur in the bootstrap sample). If a point was drawn more than once, it is in the "bootstrap version" of the original cluster more than once, too, if bscompare=TRUE. Otherwise multiple points are ignored for the computation of the Jaccard similarities. If multipleboot=FALSE, it doesn’t make a difference.

multipleboot logical. If FALSE, all points drawn more than once in the bootstrap draw are only used once in the bootstrap samples.

jittertuning positive numeric. Tuning for the "jitter"-method. The noise distribution for jittering is a normal distribution with zero mean. The covariance matrix has the same Eigenvectors as that of the original data set, but the standard deviation along the principal directions is determined by the jittertuning-quantile of the distances between neighboring points projected along these directions.

noisetuning A vector of two positive numerics. Tuning for the "noise"-method. The first component determines the probability that a point is replaced by noise. Noise is generated by a uniform distribution on a hyperrectangle along the principal directions of the original data set, ranging from -noisetuning[2] to noisetuning[2] times the standard deviation of the data set along the respective direction. Note that only points not replaced by noise are considered for the computation of Jaccard similarities.

subtuning integer. Size of subsets for "subset".

clustermethod an interface function (the function name, not a string containing the name, has to be provided!). This defines the clustering method. See the "Details"-section for a list of available interface functions and guidelines how to write your own ones.

noisemethod logical. If TRUE, the last cluster is regarded as "noise cluster", which means that for computing the Jaccard similarity, it is not treated as a cluster. The noise cluster of the original clustering is only compared with the noise cluster of the clustering of the resampled data. This means that in the clusterboot-output (and plot), if points were assigned to the noise cluster, the last cluster number refers to it, and its Jaccard similarity values refer to comparisons with estimated noise components in resampled datasets only. (Some cluster methods such as trimmed k-means and mclustBIC produce such noise components.)

count logical. If TRUE, the resampling runs are counted on the screen.

showplots logical. If TRUE, a plot of the first two dimensions of the resampled data set (or the classical MDS solution for dissimilarity data) is shown for every resampling run. The last plot shows the original data set. Ignored if datatomatrix=FALSE.
dissolution numeric between 0 and 1. If the Jaccard similarity between the resampling version of the original cluster and the most similar cluster on the resampled data is smaller or equal to this value, the cluster is considered as "dissolved". Numbers of dissolved clusters are recorded.

recover numeric between 0 and 1. If the Jaccard similarity between the resampling version of the original cluster and the most similar cluster on the resampled data is larger than this value, the cluster is considered as "successfully recovered". Numbers of recovered clusters are recorded.

seed integer. Seed for random generator (fed into set.seed) to make results reproducible. If NULL, results depend on chance.

datatomatrix logical. If TRUE, data is coerced into a (numerical) matrix at the start of clusterboot. FALSE may be chosen for mixed type data including e.g. categorical factors (assuming that the chosen clustermethod allows for this). This disables some features of clusterboot, see parameters bootmethod and showplots.

... additional parameters for the clustermethods called by clusterboot. No effect in print.clboot and plot.clboot.

x object of class clboot.

statistics specifies in print.clboot, which of the three clusterwise Jaccard similarity statistics "mean", "dissolution" (number of times the cluster has been dissolved) and "recovery" (number of times a cluster has been successfully recovered) is printed.

xlim transferred to hist.

breaks transferred to hist.

Details

Here are some guidelines for interpretation. There is some theoretical justification to consider a Jaccard similarity value smaller or equal to 0.5 as an indication of a "dissolved cluster", see Hennig (2008). 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. All of this refers to bootstrap; for the other resampling schemes it depends on the tuning constants, though their default values should grant similar interpretations in most cases.

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). See plotcluster for graphical cluster validation.

Information about interface functions for clustering methods:

The following interface functions are currently implemented (in the present package; note that almost all of these functions require the specification of some control parameters, so if you use one of them, look up their common help page kmeansCBI) first:
kmeansCBI an interface to the function \texttt{kmeans} for k-means clustering. This assumes a cases*variables matrix as input.

hclustCBI an interface to the function \texttt{hclust} for agglomerative hierarchical clustering with optional noise cluster. This function produces a partition and assumes a cases*variables matrix as input.

hclusttreeCBI an interface to the function \texttt{hclust} for agglomerative hierarchical clustering. This function produces a tree (not only a partition; therefore the number of clusters can be huge!) and assumes a cases*variables matrix as input.

disthclustCBI an interface to the function \texttt{hclust} for agglomerative hierarchical clustering with optional noise cluster. This function produces a partition and assumes a dissimilarity matrix as input.

noisemclustCBI an interface to the function \texttt{mclustBIC} for normal mixture model based clustering. This assumes a cases*variables matrix as input. Warning: \texttt{mclustBIC} sometimes has problems with multiple points. It is recommended to use this only together with \texttt{multipleboot=FALSE}.

distnoisemclustCBI an interface to the function \texttt{mclustBIC} for normal mixture model based clustering. This assumes a dissimilarity matrix as input and generates a data matrix by multidimensional scaling first. Warning: \texttt{mclustBIC} sometimes has problems with multiple points. It is recommended to use this only together with \texttt{multipleboot=FALSE}.

claraCBI an interface to the functions \texttt{pam} and \texttt{clara} for partitioning around medoids. This can be used with cases*variables as well as dissimilarity matrices as input.

pamkCBI an interface to the function \texttt{pamk} for partitioning around medoids. The number of cluster is estimated by the average silhouette width. This can be used with cases*variables as well as dissimilarity matrices as input.

trimkmeansCBI an interface to the function \texttt{trimkmeans} for trimmed k-means clustering. This assumes a cases*variables matrix as input.

tclusCBI an interface to the function \texttt{tclust} in the \texttt{tclust} library for trimmed Gaussian clustering. This assumes a cases*variables matrix as input. Note that this function is not currently provided because the \texttt{tclust} package is only available in the CRAN archives, but the code is in the Examples-section of the \texttt{kmeansCBI}-help page.

disttrimkmeansCBI an interface to the function \texttt{trimkmeans} for trimmed k-means clustering. This assumes a dissimilarity matrix as input and generates a data matrix by multidimensional scaling first.

dbscanCBI an interface to the function \texttt{dbscan} for density based clustering. This can be used with cases*variables as well as dissimilarity matrices as input.

mahalCBI an interface to the function \texttt{fixmahal} for fixed point clustering. This assumes a cases*variables matrix as input.

mergenormCBI an interface to the function \texttt{mergenormals} for clustering by merging Gaussian mixture components.

speccCBI an interface to the function \texttt{specc} for spectral clustering.

You can write your own interface function. The first argument of an interface function should preferably be a data matrix (of class "matrix", but it may be a symmetrical dissimilarity matrix). It can be a data frame, but this restricts some of the functionality of \texttt{clusterboot}, see above. Further arguments can be tuning constants for the clustering method. The output of an interface function should be a list containing (at least) the following components:
result clustering result, usually a list with the full output of the clustering method (the precise format doesn’t matter); whatever you want to use later.

nc number of clusters. If some points don’t belong to any cluster but are declared as “noise”, nc includes the noise cluster, and there should be another component nccl, being the number of clusters not including the noise cluster (note that it is not mandatory to define a noise component if not all points are assigned to clusters, but if you do it, the stability of the noise cluster is assessed as well.)

clusterlist this is a list consisting of a logical vectors of length of the number of data points (n) for each cluster, indicating whether a point is a member of this cluster (TRUE) or not. If a noise cluster is included, it should always be the last vector in this list.

partition an integer vector of length n, partitioning the data. If the method produces a partition, it should be the clustering. This component is only used for plots, so you could do something like rep(1,n) for non-partitioning methods. If a noise cluster is included, nc=nccl+1 and the noise cluster is cluster no. nc.

clustermethod a string indicating the clustering method.

Value

clusterboot returns an object of class "clboot", which is a list with components result, partition, nc, clustermethod, B, noisemethod, bootmethod, multipleboot, dissolution, recover, bootresult, bootmean, bootbrd, bootrecover, subsetresult, subsetmean, etc.

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References


See Also
dist, interface functions: kmeansCBI, hclustCBI, hclusttreeCBI, disthclustCBI, noisemclustCBI, distnoisemclustCBI, claraCBI, pamkCBI, trimkmeansCBI, disttrimkmeansCBI, dbscanCBI, mahalCBI

Examples

options(digits=3)
set.seed(20000)
face <- rFace(50,dMoNo=2,dNoEy=0,p=2)
cf1 <- clusterboot(face,B=3,bootmethod=
  c("boot","noise","jitter"),clustermethod=kmeansCBI,
  krange=5,seed=15555)

print(cf1)
plot(cf1)

cf2 <- clusterboot(dist(face),B=3,bootmethod=
  "subset",clustermethod=disthclustCBI,
  k=5, cut="number", method="average", showplots=TRUE, seed=15555)
print(cf2)
d1 <- c("a","b","a","c")
d2 <- c("a","a","a","b")
dx <- as.data.frame(cbind(d1,d2))
cpx <- clusterboot(dx,k=2,B=10,clustermethod=claraCBI,
  multipleboot=TRUE,usepam=TRUE,datatomatrix=FALSE)
print(cpx)

---

**cmahal**

*Generation of tuning constant for Mahalanobis fixed point clusters.*

**Description**

Generates tuning constants CA for fixmahal dependent on the number of points and variables of the current fixed point cluster (FPC).

This is experimental and only thought for use in fixmahal.

**Usage**

`cmahal(n, p, nmin, cmin, nc1, c1 = cmin, q = 1)`

**Arguments**

- `n`: positive integer. Number of points.
- `p`: positive integer. Number of variables.
- `nmin`: integer larger than 1. Smallest number of points for which CA is computed. For smaller FPC sizes, CA is set to the value for `nmin`. 
### con.comp

**Description**

Connectivity components of an undirected graph

**Usage**

`con.comp(comat)`

#### Parameters

- **cmin**
  positive number. Minimum value for \( c_a \).

- **nc1**
  positive integer. Number of points at which \( c_a = c_1 \).

- **c1**
  positive numeric. Tuning constant for `cmahal`. Value for \( c_a \) for FPC size equal to \( nc1 \).

- **q**
  numeric between 0 and 1. 1 for steepest possible descent of \( c_a \) as function of the FPC size. Should presumably always be 1.

#### Details

Some experiments suggest that the tuning constant \( c_a \) should decrease with increasing FPC size and increase with increasing \( p \) in `fixmahal`. This is to prevent too small meaningless FPCs while maintaining the significant larger ones. `cmahal` with \( q=1 \) computes \( c_a \) in such a way that as long as \( c_a > c_{\text{min}} \), the decrease in \( n \) is as steep as possible in order to maintain the validity of the convergence theorem in Hennig and Christlieb (2002).

**Value**

A numeric vector of length \( n \), giving the values for \( c_a \) for all FPC sizes smaller or equal to \( n \).

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**References**


**See Also**

`fixmahal`

**Examples**

```r
plot(1:100, cmahal(100, 3, nmin=5, cmin=qchisq(0.99, 3), nc1=90),
     xlab="FPC size", ylab="cmahal")
```

---

### con.comp

*Connectivity components of an undirected graph*

**Description**

Computes the connectivity components of an undirected graph from a matrix giving the edges.

**Usage**

`con.comp(comat)`
Argument

comat a symmetric logical or 0-1 matrix, where comat[i,j]=TRUE means that there is an edge between vertices i and j. The diagonal is ignored.

Details

The "depth-first search" algorithm of Cormen, Leiserson and Rivest (1990, p. 477) is used.

Value

An integer vector, giving the number of the connectivity component for each vertice.

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References


See Also

hclust, cutree for cutted single linkage trees (often equivalent).

Examples

set.seed(1000)
x <- rnorm(20)
m <- matrix(0,nrow=20,ncol=20)
for(i in 1:20)
  for(j in 1:20)
    m[i,j] <- abs(x[i]-x[j])
d <- m<0.2
cc <- con.comp(d)
max(cc) # number of connectivity components
plot(x,cc)
# The same should be produced by
# cutree(hclust(as.dist(m),method="single"),h=0.2).
Description

Estimates a misclassification probability in a mixture distribution between two mixture components from estimated posterior probabilities regardless of component parameters, see Hennig (2010).

Usage

\texttt{confusion(z,pro,i,j,adjustprobs=FALSE)}

Arguments

\begin{itemize}
  \item \texttt{z} matrix of posterior probabilities for observations (rows) to belong to mixture components (columns), so entries need to sum up to 1 for each row.
  \item \texttt{pro} vector of component proportions, need to sum up to 1.
  \item \texttt{i} integer. Component number.
  \item \texttt{j} integer. Component number.
  \item \texttt{adjustprobs} logical. If \texttt{TRUE}, probabilities are initially standardised so that those for components \texttt{i} and \texttt{j} add up to one (i.e., if they were the only components).
\end{itemize}

Value

Estimated probability that an observation generated by component \texttt{j} is classified to component \texttt{i} by maximum a posteriori rule.

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References


Examples

\begin{verbatim}
set.seed(12345)
m <- rpois(20,lambda=5)
dim(m) <- c(5,4)
pro <- apply(m,2,sum)
pro <- pro/sum(pro)
m <- m/apply(m,1,sum)
round(confusion(m,pro,1,2),digits=2)
\end{verbatim}
Description

Returns a list containing estimates of the weighted covariance matrix and the mean of the data, and optionally of the (weighted) correlation matrix. The covariance matrix is divided by the sum of the weights, corresponding to \( n \) and the ML-estimator in the case of equal weights, as opposed to \( n-1 \) for `cov.wt`.

Usage

```r
cov.wml(x, wt = rep(1/nrow(x), nrow(x)), cor = FALSE, center = TRUE)
```

Arguments

- `x`: a matrix or data frame. As usual, rows are observations and columns are variables.
- `wt`: a non-negative and non-zero vector of weights for each observation. Its length must equal the number of rows of `x`.
- `cor`: A logical indicating whether the estimated correlation weighted matrix will be returned as well.
- `center`: Either a logical or a numeric vector specifying the centers to be used when computing covariances. If `TRUE`, the (weighted) mean of each variable is used, if `FALSE`, zero is used. If `center` is numeric, its length must equal the number of columns of `x`.

Value

A list containing the following named components:

- `cov`: the estimated (weighted) covariance matrix.
- `center`: an estimate for the center (mean) of the data.
- `n.obs`: the number of observations (rows) in `x`.
- `wt`: the weights used in the estimation. Only returned if given as an argument.
- `cor`: the estimated correlation matrix. Only returned if `cor` is `TRUE`.

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See Also

cov.wt, cov, var
Examples

```r
x <- c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10)
y <- c(1, 2, 3, 8, 7, 6, 5, 8, 9, 10)
cov.wml(cbind(x, y), wt = c(0, 0, 0, 1, 1, 1, 1, 1, 0, 0))
cov.wt(cbind(x, y), wt = c(0, 0, 0, 1, 1, 1, 1, 1, 0, 0))
```

---

cqcluster.stats  
Cluster validation statistics (version for use with clusterbenchstats)

Description

This is a more sophisticated version of `cluster.stats` for use with `clusterbenchstats`, see Hennig (2017). Computes a number of distance-based statistics, which can be used for cluster validation, comparison between clusterings and decision about the number of clusters: cluster sizes, cluster diameters, average distances within and between clusters, cluster separation, biggest within cluster gap, average silhouette widths, the Calinski and Harabasz index, a Pearson version of Hubert’s gamma coefficient, the Dunn index, further statistics introduced in Hennig (2017) and two indexes to assess the similarity of two clusterings, namely the corrected Rand index and Meila’s VI.

Usage

```r
cqcluster.stats(d = NULL, clustering, alt.clustering = NULL,  
noisecluster = FALSE,  
silhouette = TRUE, G2 = FALSE, G3 = FALSE, wgap = TRUE, sepindex = TRUE,  
sepprob = 0.1, sepwithnoise = TRUE, compareonly = FALSE,  
aggregateonly = FALSE,  
averagegap = FALSE, pamcrit = TRUE,  
dquantile = 0.1,  
nndist = TRUE, nnk = 2, standardisation = "max", sepall = TRUE, maxk = 10,  
cvstan = sqrt(length(clustering)))
```

## S3 method for class 'cquality'
summary(object, stanbound = TRUE, largeisgood = TRUE, ...)

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

Arguments

d  
a distance object (as generated by `dist`) or a distance matrix between cases.

clustering  
an integer vector of length of the number of cases, which indicates a clustering.  
The clusters have to be numbered from 1 to the number of clusters.

alt.clustering  
an integer vector such as for `clustering`, indicating an alternative clustering.  
If provided, the corrected Rand index and Meila’s VI for `clustering` vs. 
`alt.clustering` are computed.
noisecluster  logical. If TRUE, it is assumed that the largest cluster number in clustering
denotes a 'noise class', i.e. points that do not belong to any cluster. These points
are not taken into account for the computation of all functions of within and
between cluster distances including the validation indexes.
silhouette  logical. If TRUE, the silhouette statistics are computed, which requires package
cluster.
is computed. This executes lots of sorting algorithms and can be very slow (it
has been improved by R. Francois - thanks!)
G3  logical. If TRUE, the index G3 (cf. Gordon (1999), p. 62) is computed. This
executes sort on all distances and can be extremely slow.
wgap  logical. If TRUE, the widest within-cluster gaps (largest link in within-cluster
minimum spanning tree) are computed. This is used for finding a good number
of clusters in Hennig (2013). See also parameter averagegap.
sepindex  logical. If TRUE, a separation index is computed, defined based on the distances
for every point to the closest point not in the same cluster. The separation index
is then the mean of the smallest proportion sepprob of these. This allows to
formalise separation less sensitive to a single or a few ambiguous points. The
output component corresponding to this is sindex, not separation! This is
used for finding a good number of clusters in Hennig (2013). See also parameter
sepall.
sepprob  numerical between 0 and 1, see sepindex.
sepwithnoise  logical. If TRUE and sepindex and noisecluster are both TRUE, the noise
points are incorporated as cluster in the separation index (sepindex) compu-
tation. Also they are taken into account for the computation for the minimum
cluster separation.
compareonly  logical. If TRUE, only the corrected Rand index and Meila’s VI are computed
and given out (this requires alt.clustering to be specified).
aggregateonly  logical. If TRUE (and not compareonly), no clusterwise but only aggregated
information is given out (this cuts the size of the output down a bit).
averagegap  logical. If TRUE, the average of the widest within-cluster gaps over all clusters is
given out, if FALSE, the maximum is given out.
pamcrit  logical. If TRUE, the average distance of points to their respective cluster cen-
troids is computed (criterion of the PAM clustering method); centroids are chosen
so that they minimise this criterion for the given clustering.
dquantile  numerical between 0 and 1; quantile used for kernel density estimator for density
indexes, see Hennig (2017), Sec. 3.6.
nndist  logical. If TRUE, average distance to nmkth nearest neighbour within cluster is
computed.
nnk  integer. Number of neighbours used in average and coefficient of variation of
distance to nearest within cluster neighbour (clusters with nnk or fewer points
are ignored for this).
standardisation  "none", "max", "ave", "q90", or a number. See details.
sepall logical. If TRUE, a fraction of smallest sepprob distances to other clusters is used from every cluster. Otherwise, a fraction of smallest sepprob distances overall is used in the computation of sindex.

maxk numeric. Parsimony is defined as the number of clusters divided by maxk.

cvstan numeric. cvnn is standardised by cvstan if there is standardisation, see Details.

object object of class cquality, output of cqcluster.stats.

x object of class cquality, output of cqcluster.stats.

stanbound logical. If TRUE, all index values larger than 1 will be set to 1, and all values smaller than 0 will be set to 0. This is for preparation in case of largeisgood=TRUE (if values are already suitably standardised within cqcluster.stats, it won’t do harm and can do good).

largeisgood logical. If TRUE, indexes x are transformed to 1-x in case that before transformation smaller values indicate a better clustering (that’s average.within,mnnd,widestgap,within.cluster.ss,dindex,denscut,pamc,max.diameter,highdgap,cvnnd). For this to make sense, cqcluster.stats should be run with standardisation="max" and summary.cquality with stanbound=TRUE.

... no effect.

Details

The standardisation-parameter governs the standardisation of the index values. standardisation="none" means that unstandardised raw values of indexes are given out. Otherwise, entropy will be standardised by the maximum possible value for the given number of clusters; within.cluster.ss and between.cluster.ss will be standardised by the overall sum of squares; mnnd will be standardised by the maximum distance to the nnkth nearest neighbour within cluster; pearsongamma will be standardised by adding 1 and dividing by 2; cvnn will be standardised by cvstan (the default is the possible maximum).

standardisation allows options for the standardisation of average.within,sindex,wgap,pamcrit,max.diameter,min.separation and can be "max" (maximum distance), "ave" (average distance), q90 (0.9-quantile of distances), or a positive number. "max" is the default and standardises all the listed indexes into the range [0,1].

Value

cqcluster.stats with compareonly=FALSE and aggregateonly=FALSE returns a list of type cquality containing the components n,cluster.number,cluster.size,min.cluster.size,noisen,diameter,average.between,average.within,widestgap,... scut,highdgap,npenalty,dpenalty,withindensp,densoc,pdistto,pclosetomode,distto,percwdens,percdensoc,parsimony,cvnnd,cvnndc. Some of these are standardised, see Details. If compareonly=TRUE, only corrected.rand,vi are given out. If aggregateonly=TRUE, only n,cluster.number,min.cluster.size,noisen,diameter,average.between,average.within, widestgap,... scut,highdgap,npenalty,dpenalty,withindensp,densoc,pdistto,pclosetomode,distto,percwdens,percdensoc,parsimony,cvnnd,cvnndc are given out.

summary.cquality returns a list of type summary.cquality with components average.within,nnk,mnnd,avg.silwidth, These are as documented below for cqcluster.stats, but after transformation by stanbound and largeisgood, see arguments.

n number of points.

cluster.number number of clusters.

cluster.size vector of cluster sizes (number of points).
min.cluster.size
size of smallest cluster.

noisen
number of noise points, see argument noisecluster (noisen=0 if noisecluster=FALSE).

diameter
vector of cluster diameters (maximum within cluster distances).

average.distance
vector of clusterwise within cluster average distances.

median.distance
vector of clusterwise within cluster distance medians.

separation
vector of clusterwise minimum distances of a point in the cluster to a point of another cluster.

average.toother
vector of clusterwise average distances of a point in the cluster to the points of other clusters.

separation.matrix
matrix of separation values between all pairs of clusters.

ave.between.matrix
matrix of mean dissimilarities between points of every pair of clusters.

avebetween
average distance between clusters.

avewithin
average distance within clusters (rewighted so that every observation, rather than every distance, has the same weight).

n.between
number of distances between clusters.

n.within
number of distances within clusters.

maxdiameter
maximum cluster diameter.

minsep
minimum cluster separation.

withinss
a generalisation of the within clusters sum of squares (k-means objective function), which is obtained if \( d \) is a Euclidean distance matrix. For general distance measures, this is half the sum of the within cluster squared dissimilarities divided by the cluster size.

clus.avg.silwidths
vector of cluster average silhouette widths. See silhouette.

asw
average silhouette width. See silhouette.

g2

g3

pearsongamma
correlation between distances and a 0-1-vector where 0 means same cluster, 1 means different clusters. "Normalized gamma" in Halkidi et al. (2001).

dunn
minimum separation / maximum diameter. Dunn index, see Halkidi et al. (2002).

dunn2
minimum average dissimilarity between two cluster / maximum average within cluster dissimilarity, another version of the family of Dunn indexes.

entropy
entropy of the distribution of cluster memberships, see Meila(2007).

wb.ratio
average.within/average.between.
ch

Calinski and Harabasz index (Calinski and Harabasz 1974, optimal in Milligan and Cooper 1985; generalised for dissimilarities in Hennig and Liao 2013).

cwidegap

vector of widest within-cluster gaps.

widestgap

widest within-cluster gap or average of cluster-wide widest within-cluster gap, depending on parameter averagegap.

corrected.rand

corrected Rand index (if alt.clustering has been specified), see Gordon (1999, p. 198).

vi

variation of information (VI) index (if alt.clustering has been specified), see Meila (2007).

sindex

separation index, see argument sepindex.

svec

vector of smallest closest distances of points to next cluster that are used in the computation of sindex if sepall=TRUE.

psep

vector of all closest distances of points to next cluster.

stan

value by which som statistics were standardised, see Details.

nnk

value of input parameter nnk.

mnnd

average distance to nnkth nearest neighbour within cluster.

panmc

average distance to cluster centroid.

pancentroids

index numbers of cluster centroids.

dindex

this index measures to what extent the density decreases from the cluster mode to the outskirts; I-densdec in Sec. 3.6 of Hennig (2017); low values are good.

denscut

this index measures whether cluster boundaries run through density valleys; I-densbound in Sec. 3.6 of Hennig (2017); low values are good.

highdgap

this measures whether there is a large within-cluster gap with high density on both sides; I-highdgap in Sec. 3.6 of Hennig (2017); low values are good.

npenalty

vector of penalties for all clusters that are used in the computation of denscut, see Hennig (2017) (these are sums of penalties over all points in the cluster).

depenalty

vector of penalties for all clusters that are used in the computation of dindex, see Hennig (2017) (these are sums of several penalties for density increase when going from the mode outward in the cluster).

withindensp

distance-based kernel density values for all points as computed in Sec. 3.6 of Hennig (2017).

densoc

contribution of points from other clusters than the one to which a point is assigned to the density, for all points; called h_o in Sec. 3.6 of Hennig (2017).

pdistto

list that for all clusters has a sequence of point numbers. These are the points already incorporated in the sequence of points constructed in the algorithm in Sec. 3.6 of Hennig (2017) to which the next point to be joined is connected.

pclosetomode

list that for all clusters has a sequence of point numbers. Sequence of points to be incorporated in the sequence of points constructed in the algorithm in Sec. 3.6 of Hennig (2017).

distto

list that for all clusters has a sequence of differences between the standardised densities (see per.cw.dens) at the new point added and the point to which it is connected (if this is positive, the penalty is this to the square), in the algorithm in Sec. 3.6 of Hennig (2017).
percwdens  
this is withindensp divided by its maximum.

percdensoc  
this is densoc divided by the maximum of withindensp, called h_o^* in Sec. 3.6 of Hennig (2017).

parsimony  
number of clusters divided by maxk.

cvnd  
coefficient of variation of dissimilarities to nnkth nearest within-cluster neighbour, measuring uniformity of within-cluster densities, weighted over all clusters, see Sec. 3.7 of Hennig (2017).

cvndc  
vector of cluster-wise coefficients of variation of dissimilarities to nnkth nearest within-cluster neighbour as required in computation of cvnd.

Note
Because cqcluster.stats processes a full dissimilarity matrix, it isn’t suitable for large data sets. You may consider distcritmulti in that case.

Author(s)
Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References

See Also
cluster.stats, silhouette, dist, calinhara, distcritmulti. clusterboot computes clusterwise stability statistics by resampling.
Examples

```r
set.seed(20000)
options(digits=3)
face <- rFace(200,dMoNo=2,dNoEy=0,p=2)
dface <- dist(face)
complete3 <- cutree(hclust(dface),3)
cqcluster.stats(dface,complete3,
    alt.clustering=as.integer(attr(face,"grouping")))
```

---

**cvnn**

*Cluster validation based on nearest neighbours*

---

**Description**

Cluster validity index based on nearest neighbours as defined in Liu et al. (2013) with a correction explained in Halkidi et al. (2015).

**Usage**

```r
cvnn(d=NULL,clusterings,k=5)
```

**Arguments**

- `d`: dissimilarity matrix or dist-object.
- `clusterings`: list of vectors of integers with length =nrow(d); indicating the cluster for each observation for several clusterings (list elements) to be compared.
- `k`: integer. Number of nearest neighbours.

**Value**

List with components (see Liu et al. (2013), Halkidi et al. (2015) for details)

- `cvnnindex`: vector of index values for the various clusterings, see Liu et al. (2013), the lower the better.
- `sep`: vector of separation values.
- `comp`: vector of compactness values.

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cweight

References


Examples
```r
options(digits=3)
iriss <- as.matrix(iris[c(1:10,51:55,101:105),-5])
irisc <- as.numeric(iris[c(1:10,51:55,101:105),5])
print(cvnn(dist(iriss),list(irisc,rep(1:4,5))))
```

---

cweight

Weight function for AWC

Description
For use in awcoord only.

Usage
```r
cweight(x, ca)
```

Arguments
- `x` numerical.
- `ca` numerical.

Value
`ca/x` if smaller than 1, else 1.

Author(s)
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See Also
- awcoord

Examples
```r
cweight(4,1)
```
dbscan  

**DBSCAN density reachability and connectivity clustering**

**Description**

Generates a density based clustering of arbitrary shape as introduced in Ester et al. (1996).

**Usage**

```r
dbscan(data, eps, MinPts = 5, scale = FALSE, method = c("hybrid", "raw", "dist"), seeds = TRUE, showplot = FALSE, countmode = NULL)
```

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

## S3 method for class 'dbscan'
plot(x, data, ...)

## S3 method for class 'dbscan'
predict(object, data, newdata = NULL, predict.max=1000, ...)
```

**Arguments**

- `data`  
  data matrix, data.frame, dissimilarity matrix or dist-object. Specify method="dist" if the data should be interpreted as dissimilarity matrix or object. Otherwise Euclidean distances will be used.

- `eps`  
  Reachability distance, see Ester et al. (1996).

- `MinPts`  
  Reachability minimum no. of points, see Ester et al. (1996).

- `scale`  
  scale the data if TRUE.

- `method`  
  "dist" treats data as distance matrix (relatively fast but memory expensive), 
  "raw" treats data as raw data and avoids calculating a distance matrix (saves memory but may be slow), "hybrid" expects also raw data, but calculates partial distance matrices (very fast with moderate memory requirements).

- `seeds`  
  FALSE to not include the isseed-vector in the dbscan-object.

- `showplot`  
  0 = no plot, 1 = plot per iteration, 2 = plot per subiteration.

- `countmode`  
  NULL or vector of point numbers at which to report progress.

- `x`  
  object of class dbscan.

- `object`  
  object of class dbscan.

- `newdata`  
  matrix or data.frame with raw data to predict.

- `predict.max`  
  max. batch size for predictions.

- `...`  
  Further arguments transferred to plot methods.
Details

Clusters require a minimum no of points (MinPts) within a maximum distance (eps) around one of its members (the seed). Any point within eps around any point which satisfies the seed condition is a cluster member (recursively). Some points may not belong to any clusters (noise).

We have clustered a 100,000 x 2 dataset in 40 minutes on a Pentium M 1600 MHz.

print.dbscan shows a statistic of the number of points belonging to the clusters that are seeds and border points.

plot.dbscan distinguishes between seed and border points by plot symbol.

Value

predict.dbscan gives out a vector of predicted clusters for the points in newdata.

dbscan gives out an object of class 'dbscan' which is a LIST with components

- `cluster` integer vector coding cluster membership with noise observations (singletons) coded as 0
- `isseed` logical vector indicating whether a point is a seed (not border, not noise)
- `eps` parameter eps
- `MinPts` parameter MinPts

Note

this is a simplified version of the original algorithm (no K-D-trees used), thus we have \( o(n^2) \) instead of \( o(n \times \log(n)) \)

Author(s)

Jens Oehlschlaegel, based on a draft by Christian Hennig.

References


Examples

```r
set.seed(665544)
n <- 600
x <- cbind(runif(10, 0, 10)+rnorm(n, sd=0.2), runif(10, 0, 10)+rnorm(n, sd=0.2))
par(bg="grey40")
ds <- dbscan(x, 0.2)
# run with showplot=1 to see how dbscan works.
plot(ds, x)
```
dipp.tantrum

Simulates p-value for dip test

**Description**

Simulates p-value for dip test (see dip) in the way suggested by Tantrum, Murua and Stuetzle (2003) from the closest unimodal distribution determined by kernel density estimation with bandwidth chosen so that the density just becomes unimodal. This is less conservative (and in fact sometimes anti-conservative) than the values from dip.test.

**Usage**

dipp.tantrum(xdata,d,M=100)

**Arguments**

- **xdata** numeric vector. One-dimensional dataset.
- **d** numeric. Value of dip statistic.
- **M** integer. Number of artificial datasets generated in order to estimate the p-value.

**Value**

List with components

- **p.value** approximated p-value.
- **bw** borderline unimodality bandwith in density with default settings.
- **dv** vector of dip statistic values from simulated artificial data.

**Author(s)**

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References


Examples

# not run, requires package diptest
# x <- runif(100)
# d <- dip(x)
# dt <- dipp.tantrum(x,d,M=10)

---

diptest.multi

*Diptest for discriminant coordinate projection*

Description

Diptest (Hartigan and Hartigan, 1985, see *dip*) for data projected in discriminant coordinate separating optimally two class means (see *discrcoord*) as suggested by Tantrum, Murua and Stuetzle (2003).

Usage

diptest.multi(xdata,class,pvalue="uniform",M=100)

Arguments

- **xdata**: matrix. Potentially multidimensional dataset.
- **class**: vector of integers giving class numbers for observations.
- **pvalue**: "uniform" or "tantrum". Defines whether the p-value is computed from a uniform null model as suggested in Hartigan and Hartigan (1985, using *dip.test*) or as suggested in Tantrum et al. (2003, using *dipp.tantrum*).
- **M**: integer. Number of artificial datasets generated in order to estimate the p-value if pvalue="tantrum".

Value

The resulting p-value.

Author(s)

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References


Examples

```r
require(diptest)
x <- cbind(runif(100),runif(100))
partition <- 1+(x[,1]<0.5)
d1 <- diptest.multi(x,partition)
d2 <- diptest.multi(x,partition,pvalue="tantrum",M=10)
```

```r
discrcoord

Discriminant coordinates/canonical variates

Description

Computes discriminant coordinates, sometimes referred to as "canonical variates" as described in Seber (1984).

Usage

discrcoord(xd, clvecd, pool = "n", ...)

Arguments

- **xd**: the data matrix; a numerical object which can be coerced to a matrix.
- **clvecd**: integer vector of class numbers; length must equal nrow(xd).
- **pool**: string. Determines how the within classes covariance is pooled. "n" means that the class covariances are weighted corresponding to the number of points in each class (default). "equal" means that all classes get equal weight.
- ... no effect

Details

The matrix T (see Seber (1984), p. 270) is inverted by use of `tdecomp`, which can be expected to give reasonable results for singular within-class covariance matrices.

Value

List with the following components

- **ev**: eigenvalues in descending order.
- **units**: columns are coordinates of projection basis vectors. New points x can be projected onto the projection basis vectors by `x %*% units`
- **proj**: projections of xd onto units.
discrete.recode

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

plotcluster for straightforward discriminant plots.

batcoord for discriminating projections for two classes, so that also the differences in variance are shown (discrcoord is based only on differences in mean).

rFace for generation of the example data used below.

Examples

```r
set.seed(4634)
face <- rFace(600,dMoNo=2,dNoEy=0)
grface <- as.integer(attr(face,"grouping"))
dcf <- discrcoord(face,grface)
plot(dcf$proj,col=grface)
# ...done in one step by function plotcluster.
```

---

discrete.recode Recodes mixed variables dataset

Description

Recodes a dataset with mixed continuous and categorical variables so that the continuous variables come first and the categorical variables have standard coding 1, 2, 3,... (in lexicographical ordering of values coerced to strings).

Usage

```r
discrete.recode(x,xvarsorted=TRUE,continuous=0,discrete)
```

Arguments

x data matrix or data frame. The data need to be organised case-wise, i.e., if there are categorical variables only, and 15 cases with values c(1,1,2) on the 3 variables, the data matrix needs 15 rows with values 1 1 2. (Categorical variables could take numbers or strings or anything that can be coerced to factor levels as values.)

xvarsorted logical. If TRUE, the continuous variables are assumed to be the first ones, and the categorical variables to be behind them.
continuous vector of integers giving positions of the continuous variables. If \texttt{xvarsorted=TRUE}, a single integer, number of continuous variables.

discrete vector of integers giving positions of the categorical variables (the variables need to be coded in such a way that \texttt{data.matrix} converts them to something numeric). If \texttt{xvarsorted=TRUE}, a single integer, number of categorical variables.

Value

A list with components

data data matrix with continuous variables first and categorical variables in standard coding behind them.

\texttt{ppdim} vector of categorical variable-wise numbers of categories.

\texttt{discretelevels} list of levels of the categorical variables belonging to what is treated by \texttt{flexmixedruns} as category 1, 2, 3 etc.

\texttt{continuous} number of continuous variables.

\texttt{discrete} number of categorical variables.

Author(s)

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See Also

\texttt{lcmixed}

Examples

\begin{verbatim}
set.seed(776655)
v1 <- rnorm(20)
v2 <- rnorm(20)
d1 <- sample(c(2,4,6,8),20,replace=TRUE)
d2 <- sample(1:4,20,replace=TRUE)
data <- cbind(v1,d1,v2,d2)
lc <-
discrete.recode(ldata,xvarsorted=FALSE,continuous=c(1,3),discrete=c(2,4))
require(MASS)
data(Cars93)
Cars934 <- Cars93[,c(3,5,8,10)]
cc <- discrete.recode(Cars934,xvarsorted=FALSE,continuous=c(2,3),discrete=c(1,4))
\end{verbatim}
**Description**

An interface for ten methods of linear dimension reduction in order to separate the groups optimally in the projected data. Includes classical discriminant coordinates, methods to project differences in mean and covariance structure, asymmetric methods (separation of a homogeneous class from a heterogeneous one), local neighborhood-based methods and methods based on robust covariance matrices.

**Usage**

```r
discrproj(x, clvecd, method="dc", clnum=NULL, ignorepoints=FALSE, ignorenum=0, ...)
```

**Arguments**

- `x` the data matrix; a numerical object which can be coerced to a matrix.
- `clvecd` vector of class numbers which can be coerced into integers; length must equal `nrow(xd)`.
- `method` one of
  - "dc" usual discriminant coordinates, see `discrcoord`,
  - "bc" Bhattacharyya coordinates, first coordinate showing mean differences, second showing covariance matrix differences, see `batcoord`,
  - "vbc" variance dominated Bhattacharyya coordinates, see `batcoord`,
  - "mvdc" added mean and variance differences optimizing coordinates, see `mvdcoord`,
  - "adc" asymmetric discriminant coordinates, see `adcoord`,
  - "awc" asymmetric discriminant coordinates with weighted observations, see `awcoord`,
  - "arc" asymmetric discriminant coordinates with weighted observations and robust MCD-covariance matrix, see `awcoord`,
  - "nc" neighborhood based coordinates, see `ncoord`,
  - "wnc" neighborhood based coordinates with weighted neighborhoods, see `ncoord`,
  - "anc" asymmetric neighborhood based coordinates, see `ancoord`.
  Note that "bc", "vbc", "adc", "awc", "arc" and "anc" assume that there are only two classes.
- `clnum` integer. Number of the class which is attempted to plot homogeneously by "asymmetric methods", which are the methods assuming that there are only two classes, as indicated above.
- `ignorepoints` logical. If TRUE, points with label `ignorenum` in `clvecd` are ignored in the computation for `method` and are only projected afterwards onto the resulting units. If `pch=NULL`, the plot symbol for these points is "N".

ignorenum

one of the potential values of the components of clvecd. Only has effect if
ignorepoints=TRUE, see above.

additional parameters passed to the projection methods.

Value

discrproj returns the output of the chosen projection method, which is a list with at least the com-
ponents ev, units, proj. For detailed informations see the help pages of the projection methods.

ev
eigenvalues in descending order, usually indicating portion of information in the

units
columns are coordinates of projection basis vectors. New points x can be pro-

proj
jections of xd onto units.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.
hennig/en/

References

tional and Graphical Statistics 13, 930-945.


See Also

discrcoord, batcoord, mvdcoord, adcoord, awcoord, ncoord, ancoord.
rFace for generation of the example data used below.

Examples

set.seed(4634)
face <- rFace(300,dMoNo=2,dNoEy=0,p=3)
grface <- as.integer(attr(face,"grouping"))

# The abs in the following is there to unify the output,
# because eigenvectors are defined only up to their sign.
# Statistically it doesn't make sense to compute absolute values.
round(abs(discrproj(face,grface, method="nc")$units),digits=2)
round(abs(discrproj(face,grface, method="wnc")$units),digits=2)
round(abs(discrproj(face,grface, clnum=1, method="arc")$units),digits=2)
distancefactor

\textit{Factor for dissimilarity of mixed type data}

\section*{Description}
Computes a factor that can be used to standardise ordinal categorical variables and binary dummy variables coding categories of nominal scaled variables for Euclidean dissimilarity computation in mixed type data. See Hennig and Liao (2013).

\section*{Usage}
\begin{verbatim}
distancefactor(cat,n=NULL, catsizes=NULL, type="categorical",
    normfactor=2, qfactor=ifelse(type="categorical",1/2,
        1/(1+1/(cat-1))))
\end{verbatim}

\section*{Arguments}
\begin{description}
\item[cat] integer. Number of categories of the variable to be standardised. Note that for type="categorical" the number of categories of the original variable is required, although the distancefactor is used to standardise dummy variables for the categories.
\item[n] integer. Number of data points.
\item[catsizes] vector of integers giving numbers of observations per category. One of n and catsizes must be supplied. If catsizes=NULL, rep(round(n/cat),cat) is used (this may be appropriate as well if numbers of observations of categories are unequal, if the researcher decides that the dissimilarity measure should not be influenced by empirical category sizes.
\item[type] "categorical" if the factor is used for dummy variables belonging to a nominal variable, "ordinal" if the factor is used for an ordinal variable and standard Likert coding.
\item[normfactor] numeric. Factor on which standardisation is based. As a default, this is $E(X_1-X_2)^2=2$ for independent unit variance variables.
\item[qfactor] numeric. Factor q in Hennig and Liao (2013) to adjust for clumping effects due to discreteness.
\end{description}

\section*{Value}
A factor by which to multiply the variable in order to make it comparable to a unit variance continuous variable when aggregated in Euclidean fashion for dissimilarity computation, so that expected effective difference between two realisations of the variable equals qfactor*normfactor.

\section*{Author(s)}
Christian Hennig \texttt{<christian.hennig@unibo.it>} \url{https://www.unibo.it/sitoweb/christian.hennig/en}
References


See Also

lcmixed, pam

Examples

```r
set.seed(776655)
d1 <- sample(1:5,20,replace=TRUE)
d2 <- sample(1:4,20,replace=TRUE)
data <- cbind(d1,d2)
lc <- cat2bin(data,categorical=1)$data
lc[,1:5] <- lc[,1:5]*distancefactor(5,20,type="categorical")
lc[,6] <- lc[,6]*distancefactor(4,20,type="ordinal")
```

---

**distcritmulti**

Distance based validity criteria for large data sets

Description

Approximates average silhouette width or the Pearson version of Hubert’s gamma criterion by hacking the dataset into pieces and averaging the subset-wise values, see Hennig and Liao (2013).

Usage

```r
distcritmulti(x,clustering,part=NULL,ns=10,criterion="asw",
              fun="dist",metric="euclidean",
              count=FALSE,seed=NULL,...)
```

Arguments

- **x**: cases times variables data matrix.
- **clustering**: vector of integers indicating the clustering.
- **part**: vector of integer subset sizes; sum should be smaller or equal to the number of cases of x. If NULL, subset sizes are chosen approximately equal.
- **ns**: integer. Number of subsets, only used if part==NULL.
- **criterion**: "asw" or "pearsongamma", specifies whether the average silhouette width or the Pearson version of Hubert’s gamma is computed.
- **fun**: "dist" or "daisy", specifies which function is used for computing dissimilarities.
- **metric**: passed on to dist (as argument method) or daisy to determine which dissimilarity is used.
**distcritmulti**

- **count** logical. if TRUE, the subset number just processed is printed.
- **seed** integer, random seed. (If NULL, result depends on random numbers.)
- **...** further arguments to be passed on to `dist` or `daisy`.

**Value**

A list with components `crit.overall`, `crit.sub`, `crit.sd`, `part`.

- **crit.overall** value of criterion.
- **crit.sub** vector of subset-wise criterion values.
- **crit.sd** standard deviation of `crit.sub`, can be used to assess stability.
- **subsets** list of case indexes in subsets.

**Author(s)**

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**References**


**See Also**

`cluster.stats`, `silhouette`

**Examples**

```r
set.seed(20000)
options(digits=3)
face <- rFace(50,dMoNo=2,dNoEy=0,p=2)
clustering <- as.integer(attr(face,"grouping"))
distcritmulti(face,clustering,ns=3,seed=100000,criterion="pearsongamma")
```
distrsimilarity

Similarity of within-cluster distributions to normal and uniform

Description

Two measures of dissimilarity between the within-cluster distributions of a dataset and normal or uniform distribution. For the normal it’s the Kolmogorov dissimilarity between the Mahalanobis distances to the center and a chi-squared distribution. For the uniform it is the Kolmogorov distance between the distance to the kth nearest neighbour and a Gamma distribution (this is based on Byers and Raftery (1998)). The clusterwise values are aggregated by weighting with the cluster sizes.

Usage

distrsimilarity(x, clustering, noisecluster = FALSE, distribution = c("normal", "uniform"), nnk = 2, largeisgood = FALSE, messages = FALSE)

Arguments

x
the data matrix; a numerical object which can be coerced to a matrix.

clustering
integer vector of class numbers; length must equal nrow(x), numbers must go from 1 to the number of clusters.

noisecluster
logical. If TRUE, the cluster with the largest number is ignored for the computations.

distribution
vector of "normal", "uniform" or both. Indicates which of the two dissimilarities is/are computed.

nnk
integer. Number of nearest neighbors to use for dissimilarity to the uniform.

largeisgood
logical. If TRUE, dissimilarities are transformed to 1-d (this means that larger values indicate a better fit).

messages
logical. If TRUE, warnings are given if within-cluster covariance matrices are not invertible (in which case all within-cluster Mahalanobis distances are set to zero).

Value

List with the following components

kdnorm
Kolmogorov distance between distribution of within-cluster Mahalanobis distances and appropriate chi-squared distribution, aggregated over clusters (I am grateful to Agustin Mayo-Iscar for the idea).

kdunif
Kolmogorov distance between distribution of distances to nnkth nearest within-cluster neighbor and appropriate Gamma-distribution, see Byers and Raftery (1998), aggregated over clusters.

kdnormc
vector of cluster-wise Kolmogorov distances between distribution of within-cluster Mahalanobis distances and appropriate chi-squared distribution.
kdunifc vector of cluster-wise Kolmogorov distances between distribution of distances to \( nnk \)th nearest within-cluster neighbor and appropriate Gamma-distribution.

xmahal vector of Mahalanobs distances to the respective cluster center.

xdknn vector of distance to \( nnk \)th nearest within-cluster neighbor.

**Note**

It is very hard to capture similarity to a multivariate normal or uniform in a single value, and both used here have their shortcomings. Particularly, the dissimilarity to the uniform can still indicate a good fit if there are holes or it’s a uniform distribution concentrated on several not connected sets.

**Author(s)**

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**References**


**See Also**

cqcluster.stats, cluster.stats for more cluster validity statistics.

**Examples**

```r
set.seed(20000)
options(digits=3)
face <- rFace(200,dMoNo=2,dNoEy=0,p=2)
km3 <- kmeans(face,3)
distrsimilarity(face,km3$cluster)
```

---

**dridgeline**

*Density along the ridgeline*

**Description**

Computes the density of a two-component Gaussian mixture along the ridgeline (Ray and Lindsay, 2005), along which all its density extrema are located.

**Usage**

```r
dridgeline(alpha=seq(0,1,0.001), prop,
    mu1, mu2, Sigma1, Sigma2, showplot=FALSE, ...)
```
Arguments

alpha: sequence of values between 0 and 1 for which the density is computed.
prop: mixture proportion of first component.
mu1: mean vector of component 1.
mu2: mean vector of component 2.
Sigma1: covariance matrix of component 1.
Sigma2: covariance matrix of component 2.
showplot: logical. If TRUE, the density is plotted against alpha.
...
... further arguments to be passed on to plot.

Value

Vector of density values for values of alpha.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


Examples

```r
q <- dridgeline(seq(0,1,0.1),0.5,c(1,1),c(2,5),diag(2),diag(2))
```

---

**dudahart2**  
*Duda-Hart test for splitting*

Description

Duda-Hart test for whether a data set should be split into two clusters.

Usage

```r
dudahart2(x, clustering, alpha=0.001)
```

Arguments

x: data matrix or data frame.
clustering: vector of integers. Clustering into two clusters.
alpha: numeric between 0 and 1. Significance level (recommended to be small if this is used for estimating the number of clusters).
Value

A list with components

- **p.value** p-value against null hypothesis of homogeneity.
- **dh** ratio of within-cluster sum of squares for two clusters and overall sum of squares.
- **compare** critical value for dh at level alpha.
- **cluster1** FALSE if the null hypothesis of homogeneity is rejected.
- **alpha** see above.
- **z** 1-\alpha-quantile of a standard Gaussian.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en

References


See Also

- `cluster.stats`

Examples

```r
options(digits=2)
set.seed(98765)
iriss <- iris[sample(150,20),-5]
km <- kmeans(iriss,2)
dudahart2(iriss,km$cluster)
```

**Description**

Extracts parameters of certain mixture components from the output of `summary.mclustBIC` and updates proportions so that they sum up to 1.

**Usage**

```r
extract.mixturepars(mclustsum,compnumbers,noise=FALSE)
```

**Arguments**

- **mclustsum** output object of `summary.mclustBIC`.
- **compnumbers** vector of integers. Numbers of mixture components.
- **noise** logical. Should be TRUE if a noise component was fitted by `mclustBIC`.  

Value

Object as component parameters of `summary.mclustBIC`-output, but for specified components only. (Orientation information from all components is kept.)

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

Examples

```r
set.seed(98765)
require(mclust)
iriss <- iris[sample(150,20),-5]
irisBIC <- mclustBIC(iriss,G=5,modelNames="VEV")
siris <- summary(irisBIC,iriss)
emp <- extract.mixturepars(siris,2)
emp$pro
round(emp$mean,digits=1)
emp$variance$modelName
round(emp$variance$scale,digits=2)
```

findrep

Finding representatives for cluster border

Description

Finds representative objects for the border of a cluster and the within-cluster variance as defined in the framework of the `cdbw` cluster validation index (and meant to be used in that context).

Usage

```r
findrep(x,xcen,clustering,cluster,r,p=ncol(x),n=nrow(x),
       nc=sum(clustering==cluster))
```

Arguments

- **x**: matrix. Euclidean dataset.
- **xcen**: mean vector of cluster.
- **clustering**: vector of integers with length =nrow(x); indicating the cluster for each observation.
- **cluster**: integer. Number of cluster to be treated.
- **r**: integer. Number of representatives.
- **p**: integer. Number of dimensions.
- **n**: integer. Number of observations.
- **nc**: integer. Number of observations in cluster.
Value

List with components

- `repc`: vector of index of representatives (out of all observations).
- `repx`: vector of index of representatives (out of only the observations in cluster).
- `maxr`: number of representatives (this can be smaller than `r` if fewer pairwise different observations are in cluster).
- `wvar`: estimated average within-cluster squared distance to mean.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

cdbw

Examples

```r
options(digits=3)
iris <- as.matrix(iris[c(1:5,51:55,101:105),-5])
irisx <- as.numeric(iris[c(1:5,51:55,101:105),5])
findrep(iris,colMeans(irisx),irisx,cluster=1,r=2)
```

fixmahal  

*Mahalanobis Fixed Point Clusters*

Description

Computes Mahalanobis fixed point clusters (FPCs), i.e., subsets of the data, which consist exactly of the non-outliers w.r.t. themselves, and may be interpreted as generated from a homogeneous normal population. FPCs may overlap, are not necessarily exhausting and do not need a specification of the number of clusters.

Note that while fixmahal has lots of parameters, only one (or few) of them have usually to be specified, cf. the examples. The philosophy is to allow much flexibility, but to always provide sensible defaults.
Usage

```r
fixmahal(dat, n = nrow(as.matrix(dat)), p = ncol(as.matrix(dat)),
method = "fuzzy", cgen = "fixed",
ca = NA, ca2 = NA,
calpha = ifelse(method=="fuzzy",0.95,0.99),
calpha2 = 0.995,
pointit = TRUE, subset = n,
ncl = 100+20*p,
startn = 18+p, mnc = floor(startn/2),
mer = ifelse(pointit,0.1,0),
distcut = 0.85, maxit = 5*n, iter = n*1e-5,
init.group = list(),
ind.storage = TRUE, countmode = 100,
plot = "none")
```

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

## S3 method for class 'summary.mfpc'
print(x, maxnc=30, ...)

## S3 method for class 'mfpc'
plot(x, dat, no, bw=FALSE, main=c("Representative FPC No. ",no),
  xlab=NULL, ylab=NULL,
  pch=NULL, col=NULL, ...)

## S3 method for class 'mfpc'
fpclusters(object, dat=NA, ca=object$ca, p=object$p, ...)

fpmi(dat, n = nrow(as.matrix(dat)), p = ncol(as.matrix(dat)),
gv, ca, ca2, method = "ml", plot,
maxit = 5*n, iter = n*1e-6)

Arguments

- **dat**
  - something that can be coerced to a numerical matrix or vector. Data matrix, rows are points, columns are variables. `fpclusters.rfpc` does not need specification of `dat` if `fixmahal` has been run with `ind.storage=TRUE`.

- **n**
  - optional positive integer. Number of cases.

- **p**
  - optional positive integer. Number of independent variables.

- **method**
  - a string. method="classical" means 0-1 weighting of observations by Mahalanobis distances and use of the classical normal covariance estimator. method="ml" uses the ML-covariance estimator (division by n instead of n-1) This is used in Hennig and Christlieb (2002). method can also be "mcd" or "mve", to enforce the use of robust centers and covariance matrices, see `cov.rob`. This is experimental, not recommended at the moment, may be very slowly and requires
library lqs. The default is method="fuzzy", where weighted means and covariance matrices are used (Hennig, 2005). The weights are computed by wfu, i.e., a function that is constant 1 for arguments smaller than ca, 0 for arguments larger than ca2 and continuously linear in between. Convergence is only proven for method="ml" up to now.

cgen
optional string. "fixed" means that the same tuning constant ca is used for all iterations. "auto" means that ca is generated dependently on the size of the current data subset in each iteration by cmahal. This is experimental.

ca
optional positive number. Tuning constant, specifying required cluster separation. By default determined as calpha-quantile of the chisquared distribution with p degrees of freedom.

calpa2
optional positive number. Second tuning constant needed if method="fuzzy". By default determined as calpha2-quantile of the chisquared distribution with p degrees of freedom.

calpha
number between 0 and 1. See ca.

calpha2
number between 0 and 1, larger than calpha. See ca2.

pointit
optional logical. If TRUE, subset fixed point algorithms are started from initial configurations, which are built around single points of the dataset, cf. mahalconf. Otherwise, initial configurations are only specified by init.group.

subset
optional positive integer smaller or equal than n. Initial configurations for the fixed point algorithm (cf. mahalconf) are built from a subset of subset points from the data. No effect if pointit=FALSE. Default: all points.

nc1
optional positive integer. Tuning constant needed by cmahal to generate ca automatically. Only needed for cgen="auto".

startn
optional positive integer. Size of the initial configurations. The default value is chosen to prevent that small meaningless FPCs are found, but it should be decreased if clusters of size smaller than the default value are of interest.

mnc
optional positive integer. Minimum size of clusters to be reported.

mer
optional nonnegative number. FPCs (groups of them, respectively, see details) are only reported as stable if the ratio of the number of their findings to their number of points exceeds mer. This holds under pointit=TRUE and subset=n. For subset<n, the ratio is adjusted, but for small subset, the results may extremely vary and have to be taken with care.

distcut
optional value between 0 and 1. A similarity measure between FPCs, given in Hennig (2002), and the corresponding Single Linkage groups of FPCs with similarity larger than distcut are computed. A single representative FPC is selected for each group.

maxit
optional integer. Maximum number of iterations per algorithm run (usually an FPC is found much earlier).

iter
positive number. Algorithm stops when difference between subsequent weight vectors is smaller than iter. Only needed for method="fuzzy".

init.group
optional list of logical vectors of length n. Every vector indicates a starting configuration for the fixed point algorithm. This can be used for datasets with high dimension, where the vectors of init.group indicate cluster candidates found
by graphical inspection or background knowledge, as in Hennig and Christlieb (2002).

**ind.storage**  optional logical. If TRUE, then all indicator vectors of found FPCs are given in the value of fixmahal. May need lots of memory, but is a bit faster.

**countmode**  optional positive integer. Every countmode algorithm runs fixmahal shows a message.

**plot**  optional string. If "start", you get a scatterplot of the first two variables to highlight the initial configuration, "iteration" generates such a plot at each iteration, "both" does both (this may be very time consuming). The default is "none".

**object**  object of class mfpc, output of fixmahal.

**x**  object of class mfpc, output of fixmahal.

**maxnc**  positive integer. Maximum number of FPCs to be reported.

**no**  positive integer. Number of the representative FPC to be plotted.

**bw**  optional logical. If TRUE, plot is black/white, FPC is indicated by different symbol. Else FPC is indicated red.

**main**  plot title.

**xlab**  label for x-axis. If NULL, a default text is used.

**ylab**  label for y-axis. If NULL, a default text is used.

**pch**  plotting symbol, see par. If NULL, the default is used.

**col**  plotting color, see par. If NULL, the default is used.

**gv**  logical vector (or, with method="fuzzy", vector of weights between 0 and 1) of length n. Indicates the initial configuration for the fixed point algorithm.

...  additional parameters to be passed to plot (no effects elsewhere).

**Details**

A (crisp) Mahalanobis FPC is a data subset that reproduces itself under the following operation: Compute mean and covariance matrix estimator for the data subset, and compute all points of the dataset for which the squared Mahalanobis distance is smaller than \( c_a \).

Fixed points of this operation can be considered as clusters, because they contain only non-outliers (as defined by the above mentioned procedure) and all other points are outliers w.r.t. the subset. The current default is to compute fuzzy Mahalanobis FPCs, where the points in the subset have a membership weight between 0 and 1 and give rise to weighted means and covariance matrices. The new weights are then obtained by computing the weight function \( wfu \) of the squared Mahalanobis distances, i.e., full weight for squared distances smaller than \( c_a \), zero weight for squared distances larger than \( c_a^2 \) and decreasing weights (linear function of squared distances) in between. A fixed point algorithm is started from the whole dataset, algorithms are started from the subsets specified in init.group, and further algorithms are started from further initial configurations as explained under subset and in the function mahalconf.

Usually some of the FPCs are unstable, and more than one FPC may correspond to the same significant pattern in the data. Therefore the number of FPCs is reduced: A similarity matrix is computed between FPCs. Similarity between sets is defined as the ratio between 2 times size of intersection and the sum of sizes of both sets. The Single Linkage clusters (groups) of level distcut are
computed, i.e. the connectivity components of the graph where edges are drawn between FPCs with similarity larger than distcut. Groups of FPCs whose members are found often enough (cf. parameter mer) are considered as stable enough. A representative FPC is chosen for every Single Linkage cluster of FPCs according to the maximum expectation ratio ser. ser is the ratio between the number of findings of an FPC and the number of points of an FPC, adjusted suitably if subset<n. Usually only the representative FPCs of stable groups are of interest.

Default tuning constants are taken from Hennig (2005).

Generally, the default settings are recommended for fixmahal. For large datasets, the use of init.group together with pointit=FALSE is useful. Occasionally, mnc and startn may be chosen smaller than the default, if smaller clusters are of interest, but this may lead to too many clusters. Decrease of ca will often lead to too many clusters, even for homogeneous data. Increase of ca will produce only very strongly separated clusters. Both may be of interest occasionally. Singular covariance matrices during the iterations are handled by solvecov.

summary.mfpc gives a summary about the representative FPCs of stable groups.

plot.mfpc is a plot method for the representative FPC of stable group no. no. It produces a scatterplot, where the points belonging to the FPC are highlighted, the mean is and for p<3 also the region of the FPC is shown. For p>=3, the optimal separating projection computed by batcoord is shown.

fpclusters.mfpc produces a list of indicator vectors for the representative FPCs of stable groups.

fpmi is called by fixmahal for a single fixed point algorithm and will usually not be executed alone.

Value

fixmahal returns an object of class mfpc. This is a list containing the components nc, g, means, covs, nfound, er, tsc, ncoll.

summary.mfpc returns an object of class summary.mfpc. This is a list containing the components means, covs, sn, stfound, sn, ser, tsim, tsc, sim, ca, ca2, calpha, mer, method, cgen, pointit.

fpclusters.mfpc returns a list of indicator vectors for the representative FPCs of stable groups.

fpmi returns a list with the components mg, covg, md, gv, coll, method, ca.

nc integer. Number of FPCs.

g list of logical vectors. Indicator vectors of FPCs. FALSE if ind.storage=FALSE.

means list of numerical vectors. Means of FPCs. In summary.mfpc, only for representative FPCs of stable groups and sorted according to ser.

covs list of numerical matrices. Covariance matrices of FPCs. In summary.mfpc, only for representative FPCs of stable groups and sorted according to ser.

nfound vector of integers. Number of findings for the FPCs.

er numerical vector. Ratio of number of findings of FPCs to their size. Under pointit=TRUE, this can be taken as a measure of stability of FPCs.

tsc integer. Number of algorithm runs leading to too small or too seldom found FPCs.

ncoll integer. Number of algorithm runs where collinear covariance matrices occurred.

skc integer. Number of skipped clusters.
vector of integers. Numbers of FPCs to which algorithm runs led, which were
started by init.group.

vector of integers. Size of intersection between FPCs. See sseg.

vector of integers. Similarities between FPCs. See sseg.

integer. Number of representative FPCs of stable groups. In summary.mfpc,
sorted according to ser.

vector of integers. Number of findings of members of all groups of FPCs. In
summary.mfpc, sorted according to ser.

numerical vector. Ratio of number of findings of groups of FPCs to their size.
Under pointit=TRUE, this can be taken as a measure of stability of FPCs. In
summary.mfpc, sorted from largest to smallest.

vector of integers. Numbers of representative FPCs of all groups.

vector of integers of length stn. Numbers of representative FPCs of the stable
groups.

vector of integers. Numbers of groups ordered according to largest ser.

vector of integers. Number of group an FPC belongs to.

see arguments.

see arguments.

see arguments.

see arguments, if cgen has been "fixed". Else numerical vector of length nc
(see below), giving the final values of ca for all FPC. In fpmi, tuning constant
for the iterated FPC.

see arguments.

numerical vector of length n for cgen="auto". The values for the tuning con-
stant ca corresponding to the cluster sizes from 1 to n.

see arguments.

see arguments.

see arguments.

see arguments.

see arguments.

see arguments.

vector of integers. Number of points of representative FPCs.

integer. Number of algorithm runs leading to skipped FPCs.

vector of integers. Size of intersections between representative FPCs of stable
groups. See sseg.

mean vector.

covariance matrix.

Mahalanobis distances.
fixmahal

gv logical (numerical, respectively, if method="fuzzy") indicator vector of iterated FPC.
coll logical. TRUE means that singular covariance matrices occurred during the iterations.

Author(s)
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References

See Also
fixreg for linear regression fixed point clusters.
mahalconf, wfu, cmahal for computation of initial configurations, weights, tuning constants.
sseg for indexing the similarity/intersection vectors computed by fixmahal.
batcoord, cov.rob, solvecov, cov.wml, plotcluster for computation of projections, (inverted) covariance matrices, plotting.
rFace for generation of example data, see below.

Examples

```r
options(digits=2)
set.seed(20000)
face <- rFace(400,dMoNo=2,dNoEy=0, p=3)
# The first example uses grouping information via init.group.
initg <- list()
grface <- as.integer(attr(face,"grouping"))
for (i in 1:5) initg[[i]] <- (grface==i)
ff0 <- fixmahal(face, pointit=FALSE, init.group=initg)
summary(ff0)
cff0 <- fpclusters(ff0)
plot(face, col=1+cff0[[1]])
plot(face, col=1+cff0[[4]]) # Why does this come out as a cluster?
plot(ff0, face, 4) # A bit clearer...
# Without grouping information, examples need more time:
# ff1 <- fixmahal(face)
# summary(ff1)
# cff1 <- fpclusters(ff1)
# plot(face, col=1+cff1[[1]])
# plot(face, col=1+cff1[[6]]) # Why does this come out as a cluster?
```
# plot(ff1, face, 6) # A bit clearer...
# ff2 <- fixmahal(face, method="ml")
# summary(ff2)
# ff3 <- fixmahal(face, method="ml", calpha=0.95, subset=50)
# summary(ff3)
## ...fast, but lots of clusters. mer=0.3 may be useful here.
# set.seed(3000)
# face2 <- rFace(400, doMoNo=2, dNoEy=0)
# ff5 <- fixmahal(face2)
# summary(ff5)
## misses right eye of face data; with p=6,
## initial configurations are too large for 40 point clusters
# ff6 <- fixmahal(face2, startn=30)
# summary(ff6)
# cff6 <- fpclusters(ff6)
# plot(face2, col=1+cff6[[3]])
# plot(ff6, face2, 3)
# x <- c(1,2,3,6,6,7,8,120)
# ff8 <- fixmahal(x)
# summary(ff8)
## misses right eye of face data; with p=6,
## initial configurations are too large for 40 point clusters
# ff9 <- fixmahal(x, mnc=3, startn=3)
# summary(ff9)

---

### fixreg

**Linear Regression Fixed Point Clusters**

**Description**

Computes linear regression fixed point clusters (FPCs), i.e., subsets of the data, which consist exactly of the non-outliers w.r.t. themselves, and may be interpreted as generated from a homogeneous linear regression relation between independent and dependent variable. FPCs may overlap, are not necessarily exhausting and do not need a specification of the number of clusters.

Note that while fixreg has lots of parameters, only one (or few) of them have usually to be specified, cf. the examples. The philosophy is to allow much flexibility, but to always provide sensible defaults.

**Usage**

```r
fixreg(indep=rep(1,n), dep, n=length(dep),
       p=ncol(as.matrix(indep)),
       ca=NA, mnc=NA, mtf=3, ir=NA, irnc=NA,
       irprob=0.95, mncprob=0.5, maxir=20000, maxit=5*n,
       distcut=0.85, init.group=list(),
       ind.storage=FALSE, countmode=100,
       plot=FALSE)
```

## S3 method for class 'rfpc'

```r
## S3 method for class 'rfpc'
```

---

```r
plot(ff1, face, 6) # A bit clearer...
ff2 <- fixmahal(face, method="ml")
summary(ff2)
ff3 <- fixmahal(face, method="ml", calpha=0.95, subset=50)
summary(ff3)
## ...fast, but lots of clusters. mer=0.3 may be useful here.
set.seed(3000)
face2 <- rFace(400, doMoNo=2, dNoEy=0)
ff5 <- fixmahal(face2)
summary(ff5)
## misses right eye of face data; with p=6,
## initial configurations are too large for 40 point clusters
ff6 <- fixmahal(face2, startn=30)
summary(ff6)
cff6 <- fpclusters(ff6)
plot(face2, col=1+cff6[[3]])
plot(ff6, face2, 3)
```
summary(object, ...)

## S3 method for class 'summary.rfpc'
print(x, maxnc=30, ...)

## S3 method for class 'rfpc'
plot(x, indep=rep(1,n), dep, no, bw=TRUE,
     main=c("Representative FPC No. ",no),
     xlab="Linear combination of independents",
     ylab=deparse(substitute(indep)),
     xlim=NULL, ylim=range(dep),
     pch=NULL, col=NULL,...)

## S3 method for class 'rfpc'
fpclusters(object, indep=NA, dep=NA, ca=object$ca, ...)

rfpi(indep, dep, p, gv, ca, maxit, plot)

Arguments

indep numerical matrix or vector. Independent variables. Leave out for clustering one-dimensional data. fpclusters.rfpc does not need specification of indep if fixreg was run with ind.storage=TRUE.

dep numerical vector. Dependent variable. fpclusters.rfpc does not need specification of dep if fixreg was run with ind.storage=TRUE.

n optional positive integer. Number of cases.

p optional positive integer. Number of independent variables.

cxa optional positive number. Tuning constant, specifying required cluster separation. By default determined automatically as a function of n and p, see function can, Hennig (2002a).

mnc optional positive integer. Minimum size of clusters to be reported. By default determined automatically as a function of mncprob. See Hennig (2002a).

mtf optional positive integer. FPCs must be found at least mtf times to be reported by summary.rfpc.

ir optional positive integer. Number of algorithm runs. By default determined automatically as a function of n, p, irnc, irprob, mtf, maxir. See function itnumber and Hennig (2002a).

irnc optional positive integer. Size of the smallest cluster to be found with approximated probability irprob.

irprob optional value between 0 and 1. Approximated probability for a cluster of size irnc to be found.

mncprob optional value between 0 amd 1. Approximated probability for a cluster of size mnc to be found.

maxir optional integer. Maximum number of algorithm runs.

maxit optional integer. Maximum number of iterations per algorithm run (usually an FPC is found much earlier).
A linear regression FPC is a data subset that reproduces itself under the following operation: Compute linear regression and error variance estimator for the data subset, and compute all points of the dataset for which the squared residual is smaller than \( ca \) times the error variance. Fixed points of this operation can be considered as clusters, because they contain only non-outliers (as defined by the above mentioned procedure) and all other points are outliers w.r.t. the subset. \texttt{fixreg} performs \( ir \) fixed point algorithms started from random subsets of size \( p+2 \) to look for FPCs. Additionally an algorithm is started from the whole dataset, and algorithms are started from the subsets specified in \texttt{init.group}.

Usually some of the FPCs are unstable, and more than one FPC may correspond to the same significant pattern in the data. Therefore the number of FPCs is reduced: FPCs with less than \( mnc \) points...
are ignored. Then a similarity matrix is computed between the remaining FPCs. Similarity between sets is defined as the ratio between 2 times size of intersection and the sum of sizes of both sets. The Single Linkage clusters (groups) of level distcut are computed, i.e. the connectivity components of the graph where edges are drawn between FPCs with similarity larger than distcut. Groups of FPCs whose members are found mtf times or more are considered as stable enough. A representative FPC is chosen for every Single Linkage cluster of FPCs according to the maximum expectation ratio ser. ser is the ratio between the number of findings of an FPC and the estimated expectation of the number of findings of an FPC of this size, called expectation ratio and computed by clusexpect.

Usually only the representative FPCs of stable groups are of interest.

The choice of the involved tuning constants such as ca and ir is discussed in detail in Hennig (2002a). Statistical theory is presented in Hennig (2003).

Generally, the default settings are recommended for fixreg. In cases where they lead to a too large number of algorithm runs (e.g., always for p>4), the use of init.group together with mtf=1 and ir=0 is useful. Occasionally, irnc may be chosen smaller than the default, if smaller clusters are of interest, but this may lead to too many clusters and too many algorithm runs. Decrease of ca will often lead to too many clusters, even for homogeneous data. Increase of ca will produce only very strongly separated clusters. Both may be of interest occasionally.

rfpi is called by fixreg for a single fixed point algorithm and will usually not be executed alone.

summary.rfpc gives a summary about the representative FPCs of stable groups.

plot.rfpc is a plot method for the representative FPC of stable group no. no. It produces a scatter-plot of the linear combination of independent variables determined by the regression coefficients of the FPC vs. the dependent variable. The regression line and the region of non-outliers determined by ca are plotted as well.

fpclusters.rfpc produces a list of indicator vectors for the representative FPCs of stable groups.

Value

fixreg returns an object of class rfpc. This is a list containing the components nc, g, coefs, vars, nfound, er, tsc, ncoll, g.

summary.rfpc returns an object of class summary.rfpc. This is a list containing the components coefs, vars, stfound, stn, sn, ser, tsc, sim, ca, ir, mnc, mtf.

fpclusters.rfpc returns a list of indicator vectors for the representative FPCs of stable groups.

rfpi returns a list with the components coef, var, g, coll, ca.

nc integer. Number of FPCs.

g list of logical vectors. Indicator vectors of FPCs. FALSE if ind.storage=FALSE.

coefs list of numerical vectors. Regression coefficients of FPCs. In summary.rfpc, only for representative FPCs of stable groups and sorted according to stfound.

vars list of numbers. Error variances of FPCs. In summary.rfpc, only for representative FPCs of stable groups and sorted according to stfound.

nfound vector of integers. Number of findings for the FPCs.

er numerical vector. Expectation ratios of FPCs. Can be taken as a stability measure.

tsc integer. Number of algorithm runs leading to too small or too seldom found FPCs.
ncoll integer. Number of algorithm runs where collinear regressor matrices occurred.
grto vector of integers. Numbers of FPCs to which algorithm runs led, which were started by init.group.
imatrix vector of integers. Size of intersection between FPCs. See sseg.
smatrix numerical vector. Similarities between FPCs. See sseg.
stn integer. Number of representative FPCs of stable groups. In summary.rfpc sorted according to stfound.
stfound vector of integers. Number of findings of members of all groups of FPCs. In summary.rfpc sorted according to stfound.
sfpc vector of integers. Numbers of representative FPCs.
ssig vector of integers. As sfpc, but only for stable groups.
sto vector of integers. Number of representative FPC of most, 2nd most, ..., often found group of FPCs.
struc vector of integers. Number of group an FPC belongs to.
n see arguments.
p see arguments.
ca see arguments.
ir see arguments.
mnc see arguments.
mtf see arguments.
distcut see arguments.
sn vector of integers. Number of points of representative FPCs.
ser numerical vector. Expectation ratio for stable groups.
sim vector of integers. Size of intersections between representative FPCs of stable groups. See sseg.
coef vector of regression coefficients.
var error variance.
g logical indicator vector of iterated FPC.
coll logical. TRUE means that singular covariance matrices occurred during the iterations.

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References

See Also

`fixmahal` for fixed point clusters in the usual setup (non-regression).

`regmix` for clusterwise linear regression by mixture modeling ML.

`can`, `itnumber` for computation of the default settings.

`clusexpect` for estimation of the expected number of findings of an FPC of given size.

`itnumber` for the generation of the number of fixed point algorithms.

`minsize` for the smallest FPC size to be found with a given probability.

`sseg` for indexing the similarity/intersection vectors computed by `fixreg`.

Examples

```r
set.seed(190000)
options(digits=3)
data(tonedata)
attach(tonedata)
tonefix <- fixreg(stretchratio,tuned,mtf=1,ir=20)
summary(tonefix)
# This is designed to have a fast example; default setting would be better.
# if you want to see more (and you have a bit more time),
# try out the following:
## Not run:
set.seed(1000)
tonefix <- fixreg(stretchratio,tuned)
# Default - good for these data
summary(tonefix)
plot(tonefix,stretchratio,tuned,1)
plot(tonefix,stretchratio,tuned,2)
toneclus <- fpclusters(tonefix,stretchratio,tuned)
plot(stretchratio,tuned,col=1+toneclus[[2]])
tonefix2 <- fixreg(stretchratio,tuned,distcut=1,mtf=1,countmode=50)
# Every found fixed point cluster is reported,
# no matter how unstable it may be.
summary(tonefix2)
tonefix3 <- fixreg(stretchratio,tuned,ca=7)
# ca defaults to 10.07 for these data.
summary(tonefix3)
subset <- c(rep(FALSE,5),rep(TRUE,24),rep(FALSE,121))
tonefix4 <- fixreg(stretchratio,tuned,
                   mtf=1,ir=0,init.group=list(subset))
summary(tonefix4)
## End(Not run)
```
Flexmixedruns fits a latent class mixture (clustering) model where some variables are continuous and modelled within the mixture components by Gaussian distributions and some variables are categorical and modelled within components by independent multinomial distributions. The fit is by maximum likelihood estimation computed with the EM-algorithm. The number of components can be estimated by the BIC.

Note that at least one categorical variable is needed, but it is possible to use data without continuous variable.

Usage

flexmixedruns(x, diagonal=TRUE, xvarsorted=TRUE, continuous, discrete, ppdim=NULL, initial.cluster=NULL, simruns=20, n.cluster=1:20, verbose=TRUE, recode=TRUE, allout=TRUE, control=list(minprior=0.001), silent=TRUE)

Arguments

x data matrix or data frame. The data need to be organised case-wise, i.e., if there are categorical variables only, and 15 cases with values c(1,1,2) on the 3 variables, the data matrix needs 15 rows with values 1 1 2. (Categorical variables could take numbers or strings or anything that can be coerced to factor levels as values.)

diagonal logical. If TRUE, Gaussian models are fitted restricted to diagonal covariance matrices. Otherwise, covariance matrices are unrestricted. TRUE is consistent with the "within class independence" assumption for the multinomial variables.

xvarsorted logical. If TRUE, the continuous variables are assumed to be the first ones, and the categorical variables to be behind them.

continuous vector of integers giving positions of the continuous variables. If xvarsorted=TRUE, a single integer, number of continuous variables.

discrete vector of integers giving positions of the categorical variables. If xvarsorted=TRUE, a single integer, number of categorical variables.

ppdim vector of integers specifying the number of (in the data) existing categories for each categorical variable. If recode=TRUE, this can be omitted and is computed automatically.

initial.cluster this corresponds to the cluster parameter in flexmix and should only be specified if simruns=1 and n.cluster is a single number. Either a matrix with n.cluster columns of initial cluster membership probabilities for each observation; or a factor or integer vector with the initial cluster assignments of observations at the start of the EM algorithm. Default is random assignment into n.cluster clusters.
flexmixedruns

| simruns  | integer. Number of starts of the EM algorithm with random initialisation in order to find a good global optimum. |
| n.cluster | vector of integers, numbers of components (the optimum one is found by minimising the BIC). |
| verbose  | logical. If TRUE, some information about the different runs of the EM algorithm is given out. |
| recode   | logical. If TRUE, the function discrete.recode is applied in order to recode categorical data so that the lcmixed-method can use it. Only set this to FALSE if your data already has that format (even if that case, TRUE doesn't do harm). If recode=FALSE, the categorical variables are assumed to be coded 1,2,3,... |
| allout   | logical. If TRUE, the regular flexmix-output is given out for every single number of clusters, which can create a huge output object. |
| control | list of control parameters for flexmix, for details see the help page of FLXcontrol-class. |
| silent   | logical. This is passed on to the try-function. If FALSE, error messages from failed runs of flexmix are suppressed. (The information that a flexmix-error occurred is still given out if verbose=TRUE). |

Details

Sometimes flexmix produces errors because of degenerating covariance matrices, too small clusters etc. flexmixedruns tolerates these and treats them as non-optimal runs. (Higher simruns or different control may be required to get a valid solution.)

General documentation on flexmix can be found in Friedrich Leisch's "FlexMix: A General Framework for Finite Mixture Models and Latent Class Regression in R", https://CRAN.R-project.org/package=flexmix

Value

A list with components

- `optsummary` summary object for flexmix object with optimal number of components.
- `optimalk` optimal number of components.
- `errcount` vector with numbers of EM runs for each number of components that led to flexmix errors.
- `flexout` if allout=TRUE, list of flexmix output objects for all numbers of components, for details see the help page of flexmix-class. Slots that can be used include for example cluster and components. So if fo is the flexmixedruns-output object, fo$flexout[[fo$optimalk]]@cluster gives a component number vector for the observations (maximum posterior rule), and fo$flexout[[fo$optimalk]]@components gives the estimated model parameters, which for lcmixed and therefore flexmixedruns are called
  - `center` mean vector
  - `cov` covariance matrix
  - `pp` list of categorical variable-wise category probabilities

If allout=FALSE, only the flexmix output object for the optimal number of components, i.e., the [[fo$optimalk]] indexing above can then be omitted.
### fpclusters

**Description**

`fpclusters` is a generic function which extracts the representative fixed point clusters (FPCs) from FPC objects generated by `fixmahal` and `fixreg`. For documentation and examples see `fixmahal` and `fixreg`.

**Usage**

```r
fpclusters(object, ...)```

---

**Arguments**

- `object`: an object of class `FPC` generated by `fixmahal` or `fixreg`.
- `...`: additional arguments passed to the method function.

**Details**

- `bicvals`: vector of values of the BIC for each number of components.
- `ppdim`: vector of categorical variable-wise numbers of categories.
- `discretelevels`: list of levels of the categorical variables belonging to what is treated by `flexmixedruns` as category 1, 2, 3 etc.

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**References**


**See Also**

`lcmixed`, `flexmix`, `FLXcontrol-class`, `flexmix-class`, `discrete.recode`.

**Examples**

```r
options(digits=3)
set.seed(776655)
v1 <- rnorm(100)
v2 <- rnorm(100)
d1 <- sample(1:5,100,replace=TRUE)
d2 <- sample(1:4,100,replace=TRUE)
data <- cbind(v1,v2,d1,d2)
fr <- flexmixedruns(data,
  continuous=2,discrete=2,simruns=2,n.cluster=2:3,allout=FALSE)
print(fr$optimalk)
print(fr$optsummary)
print(fr$flexout@cluster)
print(fr$flexout@components)
```
**Arguments**

- **object**: object of class `rfpc` or `mfpc`.
- ... further arguments depending on the method.

**Value**

a list of logical or numerical vectors indicating or giving the weights of the cluster memberships.

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**See Also**

- `fixmahal`, `fixreg`

---

**itnumber**

*Number of regression fixed point cluster iterations*

**Description**

Computes the number of fixed point iterations needed by `fixreg` to find `mtf` times a fixed point cluster (FPC) of size `cn` with an approximated probability of `prob`.

Thought for use within `fixreg`.

**Usage**

```r
itnumber(n, p, cn, mtf, prob = 0.95, maxir = 20000)
```

**Arguments**

- **n**: positive integer. Total number of points.
- **p**: positive integer. Number of independent variables.
- **cn**: positive integer smaller or equal to `n`. Size of the FPC.
- **mtf**: positive integer.
- **prob**: number between 0 and 1.
- **maxir**: positive integer. `itnumber` is set to this value if it would otherwise be larger.

**Details**

The computation is based on the binomial distribution with probability given by `clusexpect` with `ir=1`. 
Description

Jitters some variables in a data matrix.

Usage

jittervar(x,jitterv=NULL,factor=1)

Arguments

x          data matrix or data frame.
jitterv    vector of numbers of variables to be jittered.
factor     numeric. Passed on to jitter. See the documentation there. The higher, the more jittering.

Value

data matrix or data frame with jittered variables.

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kmeansCBI

See Also

jitter

Examples

```r
set.seed(776655)
v1 <- rnorm(20)
v2 <- rnorm(20)
d1 <- sample(1:5,20,replace=TRUE)
d2 <- sample(1:4,20,replace=TRUE)
ldata <- cbind(v1,v2,d1,d2)
jv <- jittervar(ldata,jitterv=3:4)
```

kmeansCBI

Interface functions for clustering methods

Description

These functions provide an interface to several clustering methods implemented in R, for use together with the cluster stability assessment in clusterboot (as parameter clustermethod; "CBI" stands for "clusterboot interface"). In some situations it could make sense to use them to compute a clustering even if you don't want to run clusterboot, because some of the functions contain some additional features (e.g., normal mixture model based clustering of dissimilarity matrices projected into the Euclidean space by MDS or partitioning around medoids with estimated number of clusters, noise/outlier identification in hierarchical clustering).

Usage

```r
kmeansCBI(data,krange,k,scaling=FALSE,runs=1,criterion="ch",...)
hclustCBI(data,k,cut="number",method,scaling=TRUE,noisecut=0,...)
hclusttreeCBI(data,minlevel=2,method,scaling=TRUE,...)
disthclustCBI(dmatrix,k,cut="number",method,noisecut=0,...)
noisemclustCBI(data,G,k,modelNames,nnk,hcmodel=NULL,Vinv=NULL,summary.out=FALSE,...)
distnoisemclustCBI(dmatrix,G,k,modelNames,nnk,hcmodel=NULL,Vinv=NULL,mdsmethod="classical",mdsdim=4,summary.out=FALSE,points.out=FALSE,...)
claraCBI(data,k,usepam=TRUE,diss=inherits(data,"dist"),...)
```
pamkCBI(data,krange=2:10,k=NULL,criterion="asw", usepam=TRUE, scaling=FALSE,diss=inherits(data,"dist"),...)

tclustCBI(data,k,trim=0.05,...)

dbscanCBI(data,eps,MinPts,diss=inherits(data,"dist"),...)

mahalCBI(data,clusterCut=0.5,...)

mergenormCBI(data, G=NULL, k=NULL, modelName=NULL, nnk=0, hcmodel = NULL, Vinv = NULL, mergemethod="bhat", cutoff=0.1,...)

speccCBI(data,k,...)

pdfclustCBI(data,...)

emskewCBI(data,k,distr="mst",repeats=100,...)

**Arguments**

- **data**
  - a numeric matrix. The data matrix - usually a cases*variables-data matrix. ClaraCBI, pamkCBI and dbscanCBI work with an n*n-dissimilarity matrix as well, see parameter diss.

- **dmatrix**
  - a squared numerical dissimilarity matrix or a dist-object.

- **k**
  - numeric, usually integer. In most cases, this is the number of clusters for methods where this is fixed. For hclustCBI and disthclustCBI see parameter cut below. Some methods have a k parameter on top of a G or krange parameter for compatibility; k in these cases does not have to be specified but if it is, it is always a single number of clusters and overwrites G and krange.

- **scaling**
  - either a logical value or a numeric vector of length equal to the number of variables. If scaling is a numeric vector with length equal to the number of variables, then each variable is divided by the corresponding value from scaling. If scaling is TRUE then scaling is done by dividing the (centered) variables by their root-mean-square, and if scaling is FALSE, no scaling is done before execution.

- **runs**
  - integer. Number of random initializations from which the k-means algorithm is started.

- **criterion**
  - "ch" or "asw". Decides whether number of clusters is estimated by the Calinski-Harabasz criterion or by the average silhouette width.

- **cut**
  - either "level" or "number". This determines how cutree is used to obtain a partition from a hierarchy tree. cut="level" means that the tree is cut at a particular dissimilarity level, cut="number" means that the tree is cut in order to obtain a fixed number of clusters. The parameter k specifies the number of clusters or the dissimilarity level, depending on cut.

- **method**
  - method for hierarchical clustering, see the documentation of hclust.
noisecut numeric. All clusters of size \( \leq \) noisecut in the disthclustCBI/hclustCBI-partition are joined and declared as noise/outliers.

minlevel integer. minlevel=1 means that all clusters in the tree are given out by hclusttreeCBI or disthclusttreeCBI, including one-point clusters (but excluding the cluster with all points). minlevel=2 excludes the one-point clusters. minlevel=3 excludes the two-point cluster which has been merged first, and increasing the value of minlevel by 1 in all further steps means that the remaining earliest formed cluster is excluded.

G vector of integers. Number of clusters or numbers of clusters used by mclustBIC. If G has more than one entry, the number of clusters is estimated by the BIC.

modelName vector of string. Models for covariance matrices, see documentation of mclustBIC.

nnk integer. Tuning constant for NNclean, which is used to estimate the initial noise for noisemclustCBI and distnoisemclustCBI. See parameter k in the documentation of NNclean. nnk=0 means that no noise component is fitted.

hcmodel string or NULL. Determines the initialization of the EM-algorithm for mclustBIC. Documented in hc.

Vinv numeric. See documentation of mclustBIC.

summary.out logical. If TRUE, the result of summary.mclustBIC is added as component mclustsummary to the output of noisemclustCBI and distnoisemclustCBI.

mdsdim integer. Dimensionality of MDS solution.

points.out logical. If TRUE, the matrix of MDS points is added as component points to the output of noisemclustCBI.

usepam logical. If TRUE, the function pam is used for clustering, otherwise clara. pam is better, clara is faster.

diss logical. If TRUE, data will be considered as a dissimilarity matrix. In claraCBI, this requires usepam=TRUE.

krange vector of integers. Numbers of clusters to be compared.

trim numeric between 0 and 1. Proportion of data points trimmed, i.e., assigned to noise. See tclust in the tclust package, trimkmeans.

eps numeric. The radius of the neighborhoods to be considered by dbscan.

MinPts integer. How many points have to be in a neighborhood so that a point is considered to be a cluster seed? See documentation of dbscan.

clustercut numeric between 0 and 1. If fixmahal is used for fuzzy clustering, a crisp partition is generated and points with cluster membership values above clustercut are considered as members of the corresponding cluster.

mergemethod method for merging Gaussians, passed on as method to mergenormals.

cutoff numeric between 0 and 1, tuning constant for mergenormals.

distr one of "mvn", "mvt", "msn", "mst". Defines the family of mixtures (multivariate normal, multivariate t, multivariate skew normal, or multivariate skew t). See EmSkew.
repeats  integer. In case that EmSkew doesn’t give a solution, how often should execution be repeated with new random initialisations? (EmSkew’s own nrandom doesn’t help if an initialisation leads to a NULL output.)

... further parameters to be transferred to the original clustering functions (not required).

Details

All these functions call clustering methods implemented in R to cluster data and to provide output in the format required by clusterboot. Here is a brief overview. For further details see the help pages of the involved clustering methods.

kmeansCBI  an interface to the function kmeansruns calling kmeans for k-means clustering. (kmeansruns allows the specification of several random initializations of the k-means algorithm and estimation of k by the Calinski-Harabasz index or the average silhouette width.)

hclustCBI  an interface to the function hclust for agglomerative hierarchical clustering with noise component (see parameter noisecut above). This function produces a partition and assumes a cases*variables matrix as input.

hclusttreeCBI  an interface to the function hclust for agglomerative hierarchical clustering. This function gives out all clusters belonging to the hierarchy (upward from a certain level, see parameter minlevel above).

disthclustCBI  an interface to the function hclust for agglomerative hierarchical clustering with noise component (see parameter noisecut above). This function produces a partition and assumes a dissimilarity matrix as input.

noisemclustCBI  an interface to the function mclustBIC, for normal mixture model based clustering. Warning: mclustBIC often has problems with multiple points. In clusterboot, it is recommended to use this together with multipleboot=FALSE.

distnoisemclustCBI  an interface to the function mclustBIC for normal mixture model based clustering. This assumes a dissimilarity matrix as input and generates a data matrix by multidimensional scaling first. Warning: mclustBIC often has problems with multiple points. In clusterboot, it is recommended to use this together with multipleboot=FALSE.

claraCBI  an interface to the functions pam and clara for partitioning around medoids.

pamkCBI  an interface to the function pamk calling pam for partitioning around medoids. The number of clusters is estimated by the Calinski-Harabasz index or by the average silhouette width.

tclustCBI  an interface to the function tclust in the tclust package for trimmed Gaussian clustering. This assumes a cases*variables matrix as input.

disttrimkmeansCBI  an interface to the function trimkmeans for trimmed k-means clustering. This assumes a dissimilarity matrix as input and generates a data matrix by multidimensional scaling first.

dbscanCBI  an interface to the function dbscan for density based clustering.

mahalCBI  an interface to the function fixmahal for fixed point clustering. This assumes a cases*variables matrix as input.

mergenormCBI  an interface to the function mergenormals for clustering by merging Gaussian mixture components. Unlike mergenormals, mergenormCBI includes the computation of the initial Gaussian mixture. This assumes a cases*variables matrix as input.
**kmeansCBI**

speccCBI an interface to the function `specc` for spectral clustering. See the `specc` help page for additional tuning parameters. This assumes a cases*variables matrix as input.

pdfclustCBI an interface to the function `pdfCluster` for density-based clustering. See the `pdfCluster` help page for additional tuning parameters. This assumes a cases*variables matrix as input.

emskewCBI an interface to the function `EmSkew` for clustering with the EM-algorithm based on Gaussian, skew Gaussian, t or skew-t mixtures. See help page of `EmSkew`. This assumes a cases*variables matrix as input.

### Value

All interface functions return a list with the following components (there may be some more, see summary.out and points.out above):

- **result** clustering result, usually a list with the full output of the clustering method (the precise format doesn’t matter); whatever you want to use later.
- **nc** number of clusters. If some points don’t belong to any cluster, these are declared "noise". nc includes the "noise cluster", and there should be another component `nc1`, being the number of clusters not including the noise cluster.
- **clusterlist** this is a list consisting of a logical vectors of length of the number of data points (n) for each cluster, indicating whether a point is a member of this cluster (TRUE) or not. If a noise cluster is included, it should always be the last vector in this list.
- **partition** an integer vector of length n, partitioning the data. If the method produces a partition, it should be the clustering. This component is only used for plots, so you could do something like `rep(1,n)` for non-partitioning methods. If a noise cluster is included, `nc=nccl+1` and the noise cluster is cluster no. `nc`.
- **clustermethod** a string indicating the clustering method.

The output of some of the functions has further components:

- **nccl** see nc above.
- **nnk** by noisemclustCBI and distnoisemclustCBI, see above.
- **initnoise** logical vector, indicating initially estimated noise by `NNclean`, called by noisemclustCBI and distnoisemclustCBI.
- **noise** logical. TRUE if points were classified as noise/outliers by disthclustCBI.

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### See Also

`clusterboot, dist, kmeans, kmeansruns, hclust, mclustBIC, pam, pamk, clara, trimkmeans, dbscan, fixmahal, tclust, pdfCluster, EmSkew`
kmeansruns

k-means with estimating k and initialisations

Description
This calls the function `kmeans` to perform a k-means clustering, but initializes the k-means algorithm several times with random points from the data set as means. Furthermore, it is more robust against the occurrence of empty clusters in the algorithm and it estimates the number of clusters by either the Calinski Harabasz index (calinhara) or average silhouette width (see pam.object). The Duda-Hart test (dudahart2) is applied to decide whether there should be more than one cluster (unless 1 is excluded as number of clusters).

Usage
```
kmeansruns(data,krange=2:10,criterion="ch",
iter.max=100,runs=100,
scaledata=FALSE,alpha=0.001,
critout=FALSE,plot=FALSE,...)
```

Arguments

- **data**: A numeric matrix of data, or an object that can be coerced to such a matrix (such as a numeric vector or a data frame with all numeric columns).
- **krange**: integer vector. Numbers of clusters which are to be compared by the average silhouette width criterion. Note: average silhouette width and Calinski-Harabasz can't estimate number of clusters nc=1. If 1 is included, a Duda-Hart test is applied and 1 is estimated if this is not significant.
- **criterion**: one of "asw" or "ch". Determines whether average silhouette width or Calinski-Harabasz is applied.
- **iter.max**: integer. The maximum number of iterations allowed.
- **runs**: integer. Number of starts of the k-means algorithm.
- **scaledata**: logical. If TRUE, the variables are centered and scaled to unit variance before execution.
kmeansruns

alpha numeric between 0 and 1, tuning constant for dudahart2 (only used for 1-cluster test).

critout logical. If TRUE, the criterion value is printed out for every number of clusters.

plot logical. If TRUE, every clustering resulting from a run of the algorithm is plotted.

Value

The output of the optimal run of the kmeans-function with added components bestk and crit. A list with components

cluster A vector of integers indicating the cluster to which each point is allocated.
centers A matrix of cluster centers.
withinss The within-cluster sum of squares for each cluster.
size The number of points in each cluster.
bestk The optimal number of clusters.
crit Vector with values of the criterion for all used numbers of clusters (0 if number not tried).

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References


See Also

kmeans, pamk, calinhara, dudahart2)

Examples

options(digits=3)
set.seed(20000)
face <- rFace(50,dMoNo=2,dNoEy=0,p=2)
pka <- kmeansruns(face,krange=1:5,critout=TRUE,runs=2,criterion="asw")
pkc <- kmeansruns(face,krange=1:5,critout=TRUE,runs=2,criterion="ch")
lcmixed is a method for the flexmix-function in package flexmix. It provides the necessary information to run an EM-algorithm for maximum likelihood estimation for a latent class mixture (clustering) model where some variables are continuous and modelled within the mixture components by Gaussian distributions and some variables are categorical and modelled within components by independent multinomial distributions. lcmixed can be called within flexmix. The function flexmixedruns is a wrapper function that can be run to apply lcmixed.

Note that at least one categorical variable is needed, but it is possible to use data without continuous variable.

There are further format restrictions to the data (see below in the documentation of continuous and discrete), which can be ignored when running lcmixed through flexmixedruns.

Usage

lcmixed( formula = .~., continuous, discrete, ppdim, diagonal = TRUE, pred.ordinal=FALSE, printlik=FALSE )

Arguments

formula a formula to specify response and explanatory variables. For lcmixed this always has the form x~1, where x is a matrix or data frame of all variables to be involved, because regression and explanatory variables are not implemented.

continuous number of continuous variables. Note that the continuous variables always need to be the first variables in the matrix or data frame.

discrete number of categorical variables. Always the last variables in the matrix or data frame. Note that categorical variables always must be coded as integers 1,2,3, etc. without interruption.

ppdim vector of integers specifying the number of (in the data) existing categories for each categorical variable.

diagonal logical. If TRUE, Gaussian models are fitted restricted to diagonal covariance matrices. Otherwise, covariance matrices are unrestricted. TRUE is consistent with the "within class independence" assumption for the multinomial variables.

pred.ordinal logical. If FALSE, the within-component predicted value for categorical variables is the probability mode, otherwise it is the mean of the standard (1,2,3,...) scores, which may be better for ordinal variables.

printlik logical. If TRUE, the loglikelihood is printed out whenever computed.
Details

The data need to be organised case-wise, i.e., if there are categorical variables only, and 15 cases with values c(1,1,2) on the 3 variables, the data matrix needs 15 rows with values 1 1 2.

General documentation on flexmix methods can be found in Chapter 4 of Friedrich Leisch’s "FlexMix: A General Framework for Finite Mixture Models and Latent Class Regression in R", https://CRAN.R-project.org/package=flexmix

Value

An object of class FLXMC (not documented; only used internally by flexmix).

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en

References


See Also

flexmixedruns, flexmix, flexmix-class, discrete.recode, which recodes a dataset into the format required by lcmixed

Examples

```r
set.seed(112233)
options(digits=3)
require(MASS)
require(flexmix)
data(Cars93)
Cars934 <- Cars93[,c(3,5,8,10)]
cc <-
discrete.recode(Cars934,xvarsorted=FALSE,continuous=c(2,3),discrete=c(1,4))
fcc <- flexmix(cc$data~1,k=2,
model=lcmixed(continuous=2,discrete=2,ppdim=c(6,3),diagonal=TRUE))
summary(fcc)
```
Description
This computes a matrix formalising 'local shape', i.e., aggregated standardised variance/covariance in a Mahalanobis neighbourhood of the data points. This can be used for finding clusters when used as one of the covariance matrices in Invariant Coordinate Selection (function ics in package ICS), see Hennig's discussion and rejoinder of Tyler et al. (2009).

Usage
localshape(xdata, proportion=0.1, mscatter="mcd", mcdalpha=0.8, covstandard="det")

Arguments
xdata objects times variables data matrix.
proportion proportion of points to be considered as neighbourhood.
mscatter "mcd" or "cov"; specified minimum covariance determinant or classical covariance matrix to be used for Mahalanobis distance computation.
mcdalpha if mscatter="mcd", this is the alpha parameter to be used by the MCD covariance matrix, i.e. one minus the asymptotic breakdown point, see covMcd.
covstandard one of "trace", "det" or "none", determining by what constant the pointwise neighbourhood covariance matrices are standardised. "det" makes the affine equivariant, as noted in the discussion rejoinder of Tyler et al. (2009).

Value
The local shape matrix.

Author(s)
Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en

References

Examples
options(digits=3)
data(iris)
localshape(iris[, -5], mscatter="cov")
mahalanodisc  

**Mahalanobis for AWC**

**Description**

Vector of Mahalanobis distances or their root. For use in awcoord only.

**Usage**

```r
mahalanodisc(x2, mg, covg, modus="square")
```

**Arguments**

- `x2`: numerical data matrix.
- `mg`: mean vector.
- `covg`: covariance matrix.
- `modus`: "md" (roots of Mahalanobis distances) or "square" (original squared form of Mahalanobis distances).

**Details**

The covariance matrix is inverted by use of `solvecov`, which can be expected to give reasonable results for singular within-class covariance matrices.

**Value**

vector of (rooted) Mahalanobis distances.

**Author(s)**

Christian Hennig <christian.hennig@unibo.it>  [https://www.unibo.it/sitoweb/christian.hennig/en/](https://www.unibo.it/sitoweb/christian.hennig/en/)

**See Also**

- `awcoord`, `solvecov`

**Examples**

```r
options(digits=3)
x <- cbind(rnorm(50),rnorm(50))
mahalanodisc(x,c(0,0),cov(x))
mahalanodisc(x,c(0,0),matrix(0,ncol=2,nrow=2))
```
mahalanofix

Mahalanobis distances from center of indexed points

Description

Computes the vector of (classical or robust) Mahalanobis distances of all points of \( x \) to the center of the points indexed (or weighted) by \( gv \). The latter also determine the covariance matrix.

Thought for use within fixmahal.

Usage

```r
mahalanofix(x, n = nrow(as.matrix(x)), p = ncol(as.matrix(x)), gv = rep(1, times = n), cmax = 1e+10, method = "ml")
mahalanofuz(x, n = nrow(as.matrix(x)), p = ncol(as.matrix(x)),
            gv = rep(1, times=n), cmax = 1e+10)
```

Arguments

- **x**: a numerical data matrix, rows are points, columns are variables.
- **n**: positive integer. Number of points.
- **p**: positive integer. Number of variables.
- **gv**: for mahalanofix a logical or 0-1 vector of length \( n \). For mahalanofuz a numerical vector with values between 0 and 1.
- **cmax**: positive number. used in solvecov if covariance matrix is singular.
- **method**: "ml", "classical", "mcd" or "mve". Method to compute the covariance matrix estimator. See cov.rob, fixmahal.

Details

solvecov is used to invert the covariance matrix. The methods "mcd" and "mve" in mahalanofix do not work properly with point constellations with singular covariance matrices!

Value

A list of the following components:

- **md**: vector of Mahalanobis distances.
- **mg**: mean of the points indexed by \( gv \), weighted mean in mahalanofuz.
- **covg**: covariance matrix of the points indexed by \( gv \), weighted covariance matrix in mahalanofuz.
- **covinv**: covg inverted by solvecov.
- **coll**: logical. If TRUE, covg has been (numerically) singular.
Note

Methods "mcd" and "mve" require library lqs.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

See Also

fixmahal, solvecov, cov.rob

Examples

```r
x <- c(1,2,3,4,5,6,7,8,9,10)
y <- c(1,2,3,8,7,6,5,8,9,10)
mahalanofix(cbind(x,y),gv=c(0,0,0,1,1,1,0,0))
mahalanofix(cbind(x,y),gv=c(0,0,0,1,1,1,0,0),method="mcd")
mahalanofuz(cbind(x,y),gv=c(0,0,0.5,0.5,1,1,0.5,0.5,0))
```

Description

Generates an initial configuration of `startn` points from dataset `x` for the `fixmahal` fixed point iteration.

Thought only for use within `fixmahal`.

Usage

```r
mahalconf(x, no, startn, covall, plot)
```

Arguments

- **x**: numerical matrix. Rows are points, columns are variables.
- **no**: integer between 1 and `nrow(x)`. Number of the first point of the configuration.
- **startn**: integer between 1 and `nrow(x)`.
- **covall**: covariance matrix for the computation of the first Mahalanobis distances.
- **plot**: a string. If equal to "start" or "both", the first two variables and the first `ncol(x)+1` points are plotted.
Details

mahalconf first chooses the \( p \) (number of variables) nearest points to point \( \text{no} \) in terms of the Mahalanobis distance w.r.t. \( \text{covall} \), so that there are \( p + 1 \) points. In every further step, the covariance matrix of the current configuration is computed and the nearest point in terms of the new Mahalanobis distance is added. \text{solvecov} \) is used to invert singular covariance matrices.

Value

A logical vector of length \( nrow(x) \).

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

See Also

\text{fixmahal}, \text{solvecov}

Examples

```r
set.seed(4634)
f <- rFace(600,dMoNo=2,dNoEy=0,p=2)
mahalconf(f, no=200, startn=20, covall=cov(f), plot="start")
```

mergenormals

\text{Clustering by merging Gaussian mixture components}

Description

Clustering by merging Gaussian mixture components; computes all methods introduced in Hennig (2010) from an initial mclust clustering. See details section for details.

Usage

```r
mergenormals(xdata, mclustsummary=NULL, clustering, probs, muarray, Sigmaarray, z, method=NULL, cutoff=NULL, by=0.005, numberstop=NULL, renumber=TRUE, M=50, ...)
```
Arguments

**xdata**
- data (something that can be coerced into a matrix).

**mclustsummary**
- output object from `summary.mclustBIC` for `xdata`. Either `mclustsummary` or all of clustering, `probs`, `muarray`, `Sigmaarray` and `z` need to be specified (the latter are obtained from `mclustsummary` if they are not provided). I am not aware of restrictions of the usage of `mclustBIC` to produce an initial clustering; covariance matrix models can be restricted and a noise component can be included if desired, although I have probably not tested all possibilities.

**clustering**
- vector of integers. Initial assignment of data to mixture components.

**probs**
- vector of component proportions (for all components; should sum up to one).

**muarray**
- matrix of component means (rows).

**Sigmaarray**
- array of component covariance matrices (third dimension refers to component number).

**z**
- matrix of observation- (row-)wise posterior probabilities of belonging to the components (columns).

**method**
- one of "bhat", "ridge.uni", "ridge.ratio", "demp", "dipuni", "diptantrum", "predictive". See details.

**cutoff**
- numeric between 0 and 1. Tuning constant, see details and Hennig (2010). If not specified, the default values given in (9) in Hennig (2010) are used.

**by**
- real between 0 and 1. Interval width for density computation along the ridgeline, used for methods "ridge.uni" and "ridge.ratio". Methods "dipuni" and "diptantrum" require ridgeline computations and use it as well.

**numberstop**
- integer. If specified, `cutoff` is ignored and components are merged until the number of clusters specified here is reached.

**renumber**
- logical. If `TRUE` merged clusters are renumbered from 1 to their number. If not, numbers of the original clustering are used (numbers of components that were merged into others then will not appear).

**M**
- integer. Number of times the dataset is divided into two halves. Used if `method="predictive"`.

... additional optional parameters to pass on to `ridgeline.diagnosis` or `mixpredictive` (in `mergenormals`).

**object**
- object of class `mergenorm`, output of `mergenormals`.

**x**
- object of class `summary.mergenorm`, output of `summary.mergenorm`.

Details

Mixture components are merged in a hierarchical fashion. The merging criterion is computed for all pairs of current clusters and the two clusters with the highest criterion value (lowest, respectively, for `method="predictive"`) are merged. Then criterion values are recomputed for the merged cluster. Merging is continued until the criterion value to merge is below (or above, for `method="predictive"`) the `cutoff` value. Details are given in Hennig (2010). The following criteria are offered, specified by the `method`-argument.

"ridge.uni" components are only merged if their mixture is unimodal according to Ray and Lindsay's (2005) ridgeline theory, see `ridgeline.diagnosis`. This ignores argument `cutoff`.
"ridge.ratio"  ratio between density minimum between components and minimum of density maxima according to Ray and Lindsay’s (2005) ridgeline theory, see ridgeline.diagnosis.
"bhat" Bhattacharyya upper bound on misclassification probability between two components, see bhattacharyya.matrix.
"demp" direct estimation of misclassification probability between components, see Hennig (2010).
"dipuni" this uses method="ridge.ratio" to decide which clusters to merge but stops merging according to the p-value of the dip test computed as in Hartigan and Hartigan (1985), see dip.test.
"dip.tantrum" as "dipuni", but p-value of dip test computed as in Tantrum, Murua and Stuetzle (2003), see dipp.tantrum.
"predictive" this uses method="demp" to decide which clusters to merge but stops merging according to the value of prediction strength (Tibshirani and Walther, 2005) as computed in mixpredictive.

Value

ergenormals gives out an object of class mergenorm, which is a List with components
clustering integer vector. Final clustering.
clusternumbers vector of numbers of remaining clusters. These are given in terms of the original clusters even of renumber=TRUE, in which case they may be needed to understand the numbering of some further components, see below.
defunct.components vector of numbers of components that were "merged away".
valuemerged vector of values of the merging criterion (see details) at which components were merged.
mergedtonumbers vector of numbers of clusters to which the original components weremerged.
parameters a list, if mclustsummary was provided. Entry no. i refers to number i in clusternumbers. The list entry i contains the parameters of the original mixture components that make up cluster i, as extracted by extract.mixturepars.
predvalues vector of prediction strength values for clusternumbers from 1 to the number of components in the original mixture, if method="predictive". See mixpredictive.
orig.decisionmatrix square matrix with entries giving the original values of the merging criterion (see details) for every pair of original mixture components.
new.decisionmatrix square matrix as orig.decisionmatrix, but with final entries; numbering of rows and columns corresponds to clusternumbers; all entries corresponding to other rows and columns can be ignored.
probs final cluster values of probs (see arguments) for merged components, generated by (potentially repeated) execution of mergeparameters out of the original ones. Numbered according to clusternumbers.
muarray final cluster means, analogous to probs.
Sigmaarray final cluster covariance matrices, analogous to probs.
mergenormals

z final matrix of posterior probabilities of observations belonging to the clusters, analogous to probs.

noise logical. If TRUE, there was a noise component fitted in the initial mclust clustering (see help for initialization in mclustBIC). In this case, a cluster number 0 indicates noise. noise is ignored by the merging methods and kept as it was originally.

method as above.

cutoff as above.

summary.mergenorm gives out a list with components clustering, clusternumbers, defunct.components, valuemerged, mergedtonumbers, predvalues, probs, muarray, Sigmaarray, z, noise, method, cutoff as above, plus onc (original number of components) and mnc (number of clusters after merging).

Author(s)

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References


Examples

require(mclust)
require(MASS)
options(digits=3)
data(crabs)
dc <- crabs[,4:8]
cm <- mclustBIC(crabs[,4:8],G=9,modelNames="EEE")
scm <- summary(cm,crabs[,4:8])
cmnbhat <- mergenormals(crabs[,4:8],scm,method="bhat")
summary(cmnbhat)
cmndemp <- mergenormals(crabs[,4:8],scm,method="demp")
summary(cmndemp)
# Other methods take a bit longer, but try them!
# The values of by and M below are still chosen for reasonably fast execution.
# cmnrr <- mergenormals(crabs[,4:8],scm,method="ridge.ratio",by=0.05)
# cmd <- mergenormals(crabs[,4:8],scm,method="dip.tantrum",by=0.05)
# cmp <- mergenormals(crabs[,4:8],scm,method="predictive",M=3)
mergeparameters: New parameters from merging two Gaussian mixture components

Description

Re-computes pointwise posterior probabilities, mean and covariance matrix for a mixture component obtained by merging two mixture components in a Gaussian mixture.

Usage

mergeparameters(xdata, j1, j2, probs, muarray, Sigmaarray, z)

Arguments

- **xdata**: data (something that can be coerced into a matrix).
- **j1**: integer. Number of first mixture component to be merged.
- **j2**: integer. Number of second mixture component to be merged.
- **probs**: vector of component proportions (for all components; should sum up to one).
- **muarray**: matrix of component means (rows).
- **Sigmaarray**: array of component covariance matrices (third dimension refers to component number).
- **z**: matrix of observation- (row-)wise posterior probabilities of belonging to the components (columns).

Value

List with components

- **probs**: see above; sum of probabilities for original components j1 and j2 is now probs[j1]. Note that generally, also for the further components, values for the merged component are in place j1 and values in place j2 are not changed. This means that in order to have only the information for the new mixture after merging, the entries in places j2 need to be suppressed.

- **muarray**: see above; weighted mean of means of component j1 and j2 is now in place j1.

- **Sigmaarray**: see above; weighted covariance matrix handled as above.

- **z**: see above; original entries for columns j1 and j2 are summed up and now in column j1.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/
minsize

References

Examples

```r
options(digits=3)
set.seed(98765)
require(mclust)
iris <- iris[sample(150,20),-5]
irisBIC <- mclustBIC(iris)
siris <- summary(irisBIC,iris)
probs <- siris$parameters$pro
muarray <- siris$parameters$mean
Sigmaarray <- siris$parameters$variance$sigma
z <- siris$z
mpi <- mergeparameters(iris,1,2,probs,muarray,Sigmaarray,z)
mpi$probs
mpi$muarray
```

minsize

Minimum size of regression fixed point cluster

Description
Computes the minimum size of a fixed point cluster (FPC) which is found at least mtf times with approximated probability prob by ir fixed point iterations of fixreg. Thought for use within fixreg.

Usage

```r
minsize(n, p, ir, mtf, prob = 0.5)
```

Arguments

- `n` positive integer. Total number of points.
- `p` positive integer. Number of independent variables.
- `ir` positive integer. Number of fixed point iterations.
- `mtf` positive integer.
- `prob` numerical between 0 and 1.

Details
The computation is based on the binomial distribution with probability given by clusexpect with ir=1.
Value

An integer.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

fixreg, clusexpect, itnumber

Examples

mminsize(500,4,7000,2)

mixdens

Density of multivariate Gaussian mixture, mclust parameterisation

Description

Computes density values for data from a mixture of multivariate Gaussian distributions with parameters based on the way models are specified and parameters are stored in package mclust.

Usage

mixdens(modelName, data, parameters)

Arguments

modelName an mclust model name. See mclustModelNames.
data data matrix; density values are computed for every observation (row).
parameters parameters of Gaussian mixture in the format used in the output of summary.mclustBIC.

Value

Vector of density values for the observations.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/
Examples

```r
set.seed(98765)
require(mclust)
iriss <- iris[sample(150,20),-5]
irisBIC <- mclustBIC(iriss)
siris <- summary(irisBIC,iriss)
round(mixdens(siris$modelName,iriss,siris$parameters),digits=2)
```

Description

Computes the prediction strength of clustering by merging Gaussian mixture components, see `mergenormals`. The predictive strength is defined according to Tibshirani and Walther (2005), carried out as described in Hennig (2010), see details.

Usage

```r
mixpredictive(xdata, Gcomp, Gmix, M=50, ...)
```

Arguments

- **xdata**: data (something that can be coerced into a matrix).
- **Gcomp**: integer. Number of components of the underlying Gaussian mixture.
- **Gmix**: integer. Number of clusters after merging Gaussian components.
- **M**: integer. Number of times the dataset is divided into two halves.
- **...**: further arguments that can potentially arrive in calls but are currently not used.

Details

The prediction strength for a certain number of clusters `Gmix` under a random partition of the dataset in halves `A` and `B` is defined as follows. Both halves are clustered with `Gmix` clusters. Then the points of `A` are classified to the clusters of `B`. This is done by use of the maximum a posteriori rule for mixtures as in Hennig (2010), differently from Tibshirani and Walther (2005). A pair of points `A` in the same `A`-cluster is defined to be correctly predicted if both points are classified into the same cluster on `B`. The same is done with the points of `B` relative to the clustering on `A`. The prediction strength for each of the clusterings is the minimum (taken over all clusters) relative frequency of correctly predicted pairs of points of that cluster. The final mean prediction strength statistic is the mean over all `2M` clusterings.

Value

List with components

- **predcorr**: vector of length `M` with relative frequencies of correct predictions (clusterwise minimum).
- **mean.pred**: mean of `predcorr`.
Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

`prediction.strength` for Tibshirani and Walther’s original method. `mergenormals` for the clustering method applied here.

Examples

```r
set.seed(98765)
iriss <- iris[sample(150,20),-5]
mp <- mixpredictive(iriss,2,2,M=2)
```

---

**mvdcoord**

*Mean/variance differences discriminant coordinates*

**Description**

Discriminant projections as defined in Young, Marco and Odell (1987). The principle is to maximize the projection of a matrix consisting of the differences between the means of all classes and the first mean and the differences between the covariance matrices of all classes and the first covariance matrix.

**Usage**

```r
mvdcoord(xd, clvecd, clnum=1, sphere="mcd", ...)
```

**Arguments**

- `xd` the data matrix; a numerical object which can be coerced to a matrix.
- `clvecd` integer vector of class numbers; length must equal `nrow(xd)`.
- `clnum` integer. Number of the class to which all differences are computed.
- `sphere` a covariance matrix or one of "mve", "mcd", "classical", "none". The matrix used for sphering the data. "mcd" and "mve" are robust covariance matrices as implemented in `cov.rob`. "classical" refers to the classical covariance matrix. "none" means no sphering and use of the raw data.
- ... no effect
Value

List with the following components

- **ev**: eigenvalues in descending order.
- **units**: columns are coordinates of projection basis vectors. New points \( x \) can be projected onto the projection basis vectors by \( x \%*% \text{units} \).
- **proj**: projections of \( x_d \) onto \( \text{units} \).

Author(s)

Christian Hennig

<christian.hennig@unibo.it>

https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

- **plotcluster** for straightforward discriminant plots.
- **discrproj** for alternatives.
- **rFace** for generation of the example data used below.

Examples

```r
set.seed(4634)
face <- rFace(300,dMoNo=2,dNoEy=0,p=3)
grface <- as.integer(attr(face,"grouping"))
mcf <- mvdcoord(face,grface)
plot(mcf$proj,col=grface)
# ...done in one step by function plotcluster.
```

ncoord

*Neighborhood based discriminant coordinates*

Description

Neighborhood based discriminant coordinates as defined in Hastie and Tibshirani (1996) and a robustified version as defined in Hennig (2003). The principle is to maximize the projection of a between classes covariance matrix, which is defined by averaging the between classes covariance matrices in the neighborhoods of all points.

Usage

```r
ncoord(xd, clvecd, nn=50, weighted=FALSE,
       sphere="mcd", orderall=TRUE, countmode=1000, ...)
```
Arguments

- **xd**: the data matrix; a numerical object which can be coerced to a matrix.
- **clvecd**: integer vector of class numbers; length must equal nrow(xd).
- **nn**: integer. Number of points which belong to the neighborhood of each point (including the point itself).
- **weighted**: logical. FALSE corresponds to the original method of Hastie and Tibshirani (1996). If TRUE, the between classes covariance matrices B are weighted by w/trace B, where w is some weight depending on the sizes of the classes in the neighborhood. Division by trace B reduces the effect of outliers. TRUE corresponds to WNC as defined in Hennig (2003).
- **sphere**: a covariance matrix or one of "mve", "mcd", "classical", "none". The matrix used for sphering the data. "mcd" and "mve" are robust covariance matrices as implemented in cov.rob. "classical" refers to the classical covariance matrix. "none" means no sphering and use of the raw data.
- **orderall**: logical. By default, the neighborhoods are computed by ordering all points each time. If FALSE, the neighborhoods are computed by selecting nn times the nearest point from the remaining points, which may be faster sometimes.
- **countmode**: optional positive integer. Every countmode algorithm runs ncoord shows a message.

Value

List with the following components

- **ev**: eigenvalues in descending order.
- **units**: columns are coordinates of projection basis vectors. New points x can be projected onto the projection basis vectors by x %*% units
- **proj**: projections of xd onto units.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

plotcluster for straightforward discriminant plots. discrproj for alternatives. rFace for generation of the example data used below.

Examples

```r
set.seed(4634)
face <- rFace(600,dMoNo=2,dNoEy=0)
grface <- as.integer(attr(face,"grouping"))
ncf <- ncoord(face,grface)
plot(ncf$proj,col=grface)
ncf2 <- ncoord(face,grface,weighted=TRUE)
plot(ncf2$proj,col=grface)
# ...done in one step by function plotcluster.
```

Description

Cluster validity index based on the neg-entropy distances of within-cluster distributions to normal distribution, see Lago-Fernandez and Corbacho (2010).

Usage

```r
neginc(x,clustering)
```

Arguments

- `x` something that can be coerced into a numerical matrix. Euclidean dataset.
- `clustering` vector of integers with length =nrow(x); indicating the cluster for each observation.

Value

Index value, see Lago-Fernandez and Corbacho (2010). The lower (i.e., the more negative) the better.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References

Examples

options(digits=3)
iriss <- as.matrix(iris[c(1:10,51:55,101:105),-5])
irisc <- as.numeric(iris[c(1:10,51:55,101:105),5])
neginc(iriss,irisc)

nselectboot

Selection of the number of clusters via bootstrap

Description

Selection of the number of clusters via bootstrap as explained in Fang and Wang (2012). Several times 2 bootstrap samples are drawn from the data and the number of clusters is chosen by optimising an instability estimation from these pairs.

In principle all clustering methods can be used that have a CBI-wrapper, see clusterboot, kmeansCBI. However, the currently implemented classification methods are not necessarily suitable for all of them, see argument classification.

Usage

nselectboot(data,B=50,distances=inherits(data,"dist"),
            clustermethod=NULL,
            classification="averagedist",krange=2:10,
            count=FALSE,nnk=1, ...)

Arguments

data something that can be coerced into a matrix. The data matrix - either an \(n*p\)-data matrix (or data frame) or an \(n*n\)-dissimilarity matrix (or dist-object).
B integer. Number of resampling runs.
distances logical. If TRUE, the data is interpreted as dissimilarity matrix. If data is a dist-object, distances=TRUE automatically, otherwise distances=FALSE by default. This means that you have to set it to TRUE manually if data is a dissimilarity matrix.
clustermethod an interface function (the function name, not a string containing the name, has to be provided!). This defines the clustering method. See the "Details"-section of clusterboot and kmeansCBI for the format. Clustering methods for nselectboot must have a k-argument for the number of clusters and must otherwise follow the specifications in clusterboot. Note that nselectboot won’t work with CBI-functions that implicitly already estimate the number of clusters such as pamkCBI; use claraCBI if you want to run it for pam/clara clustering.
classification string. This determines how non-clustered points are classified to given clusters. Options are explained in classifdist (if distances=TRUE) and classifnp (otherwise). Certain classification methods are connected to certain clustering methods. classification="averagedist" is recommended for average
nselectboot

linkage, classification="centroid" is recommended for k-means, clara and pam (with distances it will work with claraCBI only), classification="knn" with nnk=1 is recommended for single linkage and classification="qda" is recommended for Gaussian mixtures with flexible covariance matrices.

krange integer vector; numbers of clusters to be tried.

count logical. If TRUE, numbers of clusters and bootstrap runs are printed.

nnk number of nearest neighbours if classification="knn", see classifdist (if distances=TRUE) and classifnp (otherwise).

... arguments to be passed on to the clustering method.

Value

nselectboot returns a list with components kopt, stabk, stab.

kopt optimal number of clusters.

stabhk mean instability values for numbers of clusters.

stab matrix of instability values for all bootstrap runs and numbers of clusters.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

classifdist, classifnp, clusterboot,kmeansCBI

Examples

```
set.seed(20000)
face <- rFace(50,dMoNo=2,dNoEy=0,p=2)
nselectboot(dist(face),B=2,clustermethod=disthclustCBI,
method="average",krange=5:7)
nselectboot(dist(face),B=2,clustermethod=claraCBI,
classification="centroid",krange=5:7)
nselectboot(face,B=2,clustermethod=kmeansCBI,
classification="centroid",krange=5:7)
# Of course use larger B in a real application.
```
Partitioning around medoids with estimation of number of clusters

Description
This calls the function `pam` or `clara` to perform a partitioning around medoids clustering with the number of clusters estimated by optimum average silhouette width (see `pam.object`) or Calinski-Harabasz index (`calinhara`). The Duda-Hart test (`dudahart2`) is applied to decide whether there should be more than one cluster (unless 1 is excluded as number of clusters or data are dissimilarities).

Usage

```
pamk(data,krange=2:10,criterion="asw", usepam=TRUE, scaling=FALSE, alpha=0.001, diss=inherits(data, "dist"), critout=FALSE, ns=10, seed=NULL, ...)
```

Arguments

- `data` a data matrix or data frame or something that can be coerced into a matrix, or dissimilarity matrix or object. See `pam` for more information.
- `krange` integer vector. Numbers of clusters which are to be compared by the average silhouette width criterion. Note: average silhouette width and Calinski-Harabasz can’t estimate number of clusters nc=1. If 1 is included, a Duda-Hart test is applied and 1 is estimated if this is not significant.
- `criterion` one of "asw", "multiasw" or "ch". Determines whether average silhouette width (as given out by `pam/clara`, or as computed by `distcritmulti` if "multiasw" is specified; recommended for large data sets with `usepam=FALSE`) or Calinski-Harabasz is applied. Note that the original Calinski-Harabasz index is not defined for dissimilarities; if dissimilarity data is run with `criterion="ch"`, the dissimilarity-based generalisation in Hennig and Liao (2013) is used.
- `usepam` logical. If `TRUE`, `pam` is used, otherwise `clara` (recommended for large datasets with 2,000 or more observations; dissimilarity matrices can not be used with `clara`).
- `scaling` either a logical value or a numeric vector of length equal to the number of variables. If scaling is a numeric vector with length equal to the number of variables, then each variable is divided by the corresponding value from scaling. If scaling is `TRUE` then scaling is done by dividing the (centered) variables by their root-mean-square, and if scaling is `FALSE`, no scaling is done.
- `alpha` numeric between 0 and 1, tuning constant for `dudahart2` (only used for 1-cluster test).
- `diss` logical flag: if `TRUE` (default for `dist` or dissimilarity-objects), then data will be considered as a dissimilarity matrix (and the potential number of clusters 1 will be ignored). If `FALSE`, then data will be considered as a matrix of observations by variables.
critout logical. If TRUE, the criterion value is printed out for every number of clusters.

ns passed on to distcritmulti if criterion="multiasw".

seed passed on to distcritmulti if criterion="multiasw".

... further arguments to be transferred to pam or clara.

Value

A list with components

pamobject The output of the optimal run of the pam-function.

nc the optimal number of clusters.

crit vector of criterion values for numbers of clusters. crit[1] is the p-value of the Duda-Hart test if 1 is in krange and diss=FALSE.

Note

clara and pam can handle NA-entries (see their documentation) but dudahart2 cannot. Therefore NA should not occur if 1 is in krange.

Author(s)

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References


See Also

pam, clara distcritmulti

Examples

options(digits=3)
set.seed(20000)
face <- rFace(50,dMoNo=2,dNoEy=0,p=2)
pk1 <- pamk(face,krange=1:5,criterion="asw",critout=TRUE)
pk2 <- pamk(face,krange=1:5,criterion="multiasw",ns=2,critout=TRUE)
# "multiasw" is better for larger data sets, use larger ns then.
pk3 <- pamk(face,krange=1:5,criterion="ch",critout=TRUE)
piridge  

**Ridgeline Pi-function**

**Description**

The Pi-function is given in (6) in Ray and Lindsay, 2005. Equating it to the mixture proportion yields locations of two-component Gaussian mixture density extrema.

**Usage**

```r
piridge(alpha, mu1, mu2, Sigma1, Sigma2, showplot=FALSE)
```

**Arguments**

- `alpha` sequence of values between 0 and 1 for which the Pi-function is computed.
- `mu1` mean vector of component 1.
- `mu2` mean vector of component 2.
- `Sigma1` covariance matrix of component 1.
- `Sigma2` covariance matrix of component 2.
- `showplot` logical. If TRUE, the Pi-function is plotted against `alpha`.

**Value**

Vector of values of the Pi-function for values of `alpha`.

**Author(s)**

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**References**


**Examples**

```r
q <- piridge(seq(0, 1, 0.1), c(1, 1), c(2, 5), diag(2), diag(2))
```
Description

By use of the Pi-function in Ray and Lindsay, 2005, locations of two-component Gaussian mixture density extrema or saddlepoints are computed.

Usage

piridge.zeroes(prop, mu1, mu2, Sigma1, Sigma2, alphamin=0, alphamax=1, by=0.001)

Arguments

prop proportion of mixture component 1.
mu1 mean vector of component 1.
mu2 mean vector of component 2.
Sigma1 covariance matrix of component 1.
Sigma2 covariance matrix of component 2.
alphamin minimum alpha value.
alphamax maximum alpha value.
by interval between alpha-values where to look for extrema.

Value

list with components

number.zeroes number of zeroes of Pi-function, i.e., extrema or saddlepoints of density.
estimated.roots estimated alpha-values at which extrema or saddlepoints occur.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


Examples

q <- piridge.zeroes(0.2,c(1,1),c(2,5),diag(2),diag(2),by=0.1)
plot.valstat  

Simulation-standardised plot and print of cluster validation statistics

Description

Visualisation and print function for cluster validation output compared to results on simulated random clusterings. The print method can also be used to compute and print an aggregated cluster validation index.

Unlike for many other plot methods, the additional arguments of plot.valstat are essential. print.valstat should make good sense with the defaults, but for computing the aggregate index aggregate and weights need to be set.

Usage

## S3 method for class 'valstat'
plot(x,simobject=NULL,statistic="sindex",
     xlim=NULL,ylim=c(0,1),
     nmethods=length(x)-5,
     col=1:nmethods,cex=1,pch=c("c","f","a","n"),
     simcol=rep(grey(0.7),4),
     shift=c(-0.1,-1/3,1/3,0.1),include.othernc=NULL,...)

## S3 method for class 'valstat'
print(x,statistics=x$statistics,
      nmethods=length(x)-5,aggregate=FALSE,
      weights=NULL,digits=2,
      include.othernc=NULL,...)

Arguments

x  
object of class "valstat", such as sublists stat,qstat,sstat of clusterbenchstats-output.

simobject  
list of simulation results as produced by randomclustersim and documented there; typically sublist sim of clusterbenchstats-output.

statistic  
one of "avewithin","mnnd","variation","diameter","gap","sindex","minsep","asw","dindex","denscut","highdgap","pg","withinss","entropy","pamc","kdnorm","kdunif","dmode" validation statistic to be plotted.

xlim  
passed on to plot. Default is the range of all involved numbers of clusters, minimum minus 0.5 to maximum plus 0.5.

ylim  
passed on to plot.

nmethods  
integer. Number of clustering methods to involve (these are those from number 1 to nmethods specified in x$name).

col  
colours used for the different clustering methods.
Passed on to `plot`.

Vector of symbols for random clustering results from `stupidkcentroids`, `stupidkfn`, `stupidkaven`, `stupidknn`. To be passed on to `plot`.

Vector of colours used for random clustering results in order `stupidkcentroids`, `stupidkfn`, `stupidkaven`, `stupidknn`.

Numeric vector. Indicates the amount to which the results from `stupidkcentroids`, `stupidkfn`, `stupidkaven`, `stupidknn` are plotted to the right of their respective number of clusters (negative numbers plot to the left).

This indicates whether methods should be included that estimated their number of clusters themselves and gave a result outside the standard range as given by `x$minG` and `x$maxG`. If not `NULL`, this is a list of integer vectors of length 2. The first number is the number of the clustering method (the order is determined by argument `x$name`), the second number is the number of clusters for those methods that estimate the number of clusters themselves and estimated a number outside the standard range. Normally what will be used here, if not `NULL`, is the output parameter `cm$othernc` of `clusterbenchstats`, see also `cluster.magazine`.

Vector of character strings specifying the validation statistics that will be included in the output (unless you want to restrict the output for some reason, the default should be fine).

Logical. If `TRUE`, an aggregate validation statistic will be computed as the weighted mean of the involved statistic. This requires `weights` to be set. In order for this to make sense, values of the validation statistics should be comparable, which is achieved by standardisation in `clusterbenchstats`. Accordingly, `x` should be the `qstat` or `sstat`-component of the `clusterbenchstats`-output rather than the `stat`-component.

Vector of numericals. Weights for computation of the aggregate statistic in case that `aggregate=TRUE`. The order of clustering methods corresponding to the weight vector is given by `x$name`.

Minimal number of significant digits, passed on to `print.table`.

No effect.

Whereas `print.valstat`, at least with `aggregate=TRUE` makes more sense for the `qstat` or `sstat`-component of the `clusterbenchstats`-output rather than the `stat`-component, `plot.valstat` should be run with the `stat`-component if `simobject` is specified, because the simulated cluster validity statistics are unstandardised and need to be compared with unstandardised values on the dataset of interest.

`print.valstats` returns the results table as invisible object.
Author(s)

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References


See Also

`clusterbenchstats, valstat.object, cluster.magazine`

Examples

```r
set.seed(20000)
options(digits=3)
face <- rFace(10,dMoNo=2,dNoEy=0,p=2)
clustermethod=c("kmeansCBI","hclustCBI","hclustCBI")
clustermethodpars <- list()
clustermethodpars[[2]] <- clustermethodpars[[3]] <- list()
clustermethodpars[[2]]$method <- "ward.D2"
clustermethodpars[[3]]$method <- "single"
methodname <- c("kmeans","ward","single")
cbs <- clusterbenchstats(face,G=2:3,clustermethod=clustermethod,
methodname=methodname,distmethod=rep(FALSE,3),
clustermethodpars=clustermethodpars,nmruns=2,kmruns=2,fnruns=2,avenruns=2)
plot(cbs$stat,cbs$sim)
plot(cbs$stat,cbs$sim,statistic="dindex")
plot(cbs$stat,cbs$sim,statistic="avewithin")
print(cbs$sstat,aggregate=TRUE,weights=c(1,0,0,0,0,1,0,0,0,0,1,0,0,0))
```

plotcluster

Discriminant projection plot.

Description

Plots to distinguish given classes by ten available projection methods. Includes classical discriminant coordinates, methods to project differences in mean and covariance structure, asymmetric methods (separation of a homogeneous class from a heterogeneous one), local neighborhood-based methods and methods based on robust covariance matrices. One-dimensional data is plotted against the cluster number.
Usage

plotcluster(x, clvecd, clnum=NULL,
            method=ifelse(is.null(clnum),"dc","awc"), bw=FALSE,
            ignorepoints=FALSE, ignorenum=0, pointsbyclvecd=TRUE,
            xlab=NULL, ylab=NULL,
            pch=NULL, col=NULL, ...)

Arguments

x the data matrix; a numerical object which can be coerced to a matrix.

clvecd vector of class numbers which can be coerced into integers; length must equal nrow(x).

method one of

"dc" usual discriminant coordinates, see discrcoord,
"bc" Bhattacharyya coordinates, first coordinate showing mean differences, second showing covariance matrix differences, see batcoord,
"vbc" variance dominated Bhattacharyya coordinates, see batcoord,
"mvdc" added mean and variance differences optimizing coordinates, see mvdcoord,
"adc" asymmetric discriminant coordinates, see adcoord,
"awc" asymmetric discriminant coordinates with weighted observations, see awcoord,
"arc" asymmetric discriminant coordinates with weighted observations and robust MCD-covariance matrix, see awcoord,
"ne" neighborhood based coordinates, see ncoord,
"wnc" neighborhood based coordinates with weighted neighborhoods, see ncoord,
"anc" asymmetric neighborhood based coordinates, see ancoord.

Note that "bc", "vbc", "adc", "awc", "arc" and "anc" assume that there are only two classes.

clnum integer. Number of the class which is attempted to plot homogeneously by asymmetric methods, which are the methods assuming that there are only two classes, as indicated above. clnum is ignored for methods "dc" and "ne".

bw logical. If TRUE, the classes are distinguished by symbols, and the default color is black/white. If FALSE, the classes are distinguished by colors, and the default symbol is pch=1.

ignorepoints logical. If TRUE, points with label ignorenum in clvecd are ignored in the computation for method and are only projected afterwards onto the resulting units. If pch=NULL, the plot symbol for these points is "N".

ignorenum one of the potential values of the components of clvecd. Only has effect if ignorepoints=TRUE, see above.

pointsbyclvecd logical. If TRUE and pch=NULL and/or col=NULL, some hopefully suitable plot symbols (numbers and letters) and colors are chosen to distinguish the values of clvecd, starting with "1"/"black" for the cluster with the smallest clvecd-code (note that colors for clusters with numbers larger than minimum number
+3 are drawn at random from all available colors). FALSE produces potentially less reasonable (but nonrandom) standard colors and symbols if method is "de" or "nc", and will only distinguish whether clvecd=clnum or not for the other methods.

- **xlab**: label for x-axis. If NULL, a default text is used.
- **ylab**: label for y-axis. If NULL, a default text is used.
- **pch**: plotting symbol, see `par`. If NULL, the default is used.
- **col**: plotting color, see `par`. If NULL, the default is used.
- **...**: additional parameters passed to `plot` or the projection methods.

**Note**

For some of the asymmetric methods, the area in the plot occupied by the "homogeneous class" (see `clnum` above) may be very small, and it may make sense to run `plotcluster` a second time specifying plot parameters `xlim` and `ylim` in a suitable way. It often makes sense to magnify the plot region containing the homogeneous class in this way so that its separation from the rest can be seen more clearly.

**Author(s)**

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**References**


**See Also**

`discrcoord`, `batcoord`, `mvdcoord`, `adcoord`, `awcoord`, `ncoord`, `ancoord`.

`discrproj` is an interface to all these projection methods.

`rFace` for generation of the example data used below.

**Examples**

```r
set.seed(4634)
face <- rFace(300,dMoNo=2,dNoEy=0)
grface <- as.integer(attr(face,"grouping"))
plotcluster(face,grface)
plotcluster(face,grface==1)
plotcluster(face,grface, clnum=1, method="vbc")
```
**prediction.strength**  
*Prediction strength for estimating number of clusters*

**Description**
Computes the prediction strength of a clustering of a dataset into different numbers of components. The prediction strength is defined according to Tibshirani and Walther (2005), who recommend to choose as optimal number of cluster the largest number of clusters that leads to a prediction strength above 0.8 or 0.9. See details.

Various clustering methods can be used, see argument clustermethod. In Tibshirani and Walther (2005), only classification to the nearest centroid is discussed, but more methods are offered here, see argument classification.

**Usage**
```r
prediction.strength(xdata, Gmin=2, Gmax=10, M=50,
clustermethod=kmeansCBI,
    classification="centroid",
    cutoff=0.8,nnk=1,
    distances=inherits(xdata,"dist"),count=FALSE,...)
```
```
## S3 method for class 'predstr'
print(x, ...)
```

**Arguments**
- `xdata`: data (something that can be coerced into a matrix).
- `Gmin`: integer. Minimum number of clusters. Note that the prediction strength for 1 cluster is trivially 1, which is automatically included if GMin>1. Therefore GMin<2 is useless.
- `Gmax`: integer. Maximum number of clusters.
- `M`: integer. Number of times the dataset is divided into two halves.
- `clustermethod`: an interface function (the function name, not a string containing the name, has to be provided!). This defines the clustering method. See the "Details"-section of `clusterboot` and `kmeansCBI` for the format. Clustering methods for prediction.strength must have a k-argument for the number of clusters, must operate on n times p data matrices and must otherwise follow the specifications in `clusterboot` Note that prediction.strength won't work with CBI-functions that implicitly already estimate the number of clusters such as `pamkCBI`; use `claraCBI` if you want to run it for pam/clara clustering.
- `classification`: string. This determines how non-clustered points are classified to given clusters. Options are explained in `classifnp` and `classifdist`, the latter for dissimilarity data. Certain classification methods are connected to certain clustering methods. classification="averagedist" is recommended for average linkage, classification="centroid" is recommended for k-means, clara and pam (with distances it will work with `claraCBI` only), classification="knn"
with \( \text{nnk}=1 \) is recommended for single linkage and \( \text{classification} = \text{"qda"} \) is recommended for Gaussian mixtures with flexible covariance matrices.

**cutoff** numeric between 0 and 1. The optimal number of clusters is the maximum one with prediction strength above \( \text{cutoff} \).

**nnk** number of nearest neighbours if \( \text{classification} = \text{"knn"} \), see \texttt{classifnp}.

**distances** logical. If \texttt{TRUE}, data will be interpreted as dissimilarity matrix, passed on to clustering methods as \texttt{"dist"}-object, and \texttt{classifdist} will be used for classification.

**count** logical. \texttt{TRUE} will print current number of clusters and simulation run number on the screen.

**x** object of class \texttt{predstr}.

**...** arguments to be passed on to the clustering method.

**Details**

The prediction strength for a certain number of clusters \( k \) under a random partition of the dataset into halves A and B is defined as follows. Both halves are clustered with \( k \) clusters. Then the points of A are classified to the clusters of B. In the original paper this is done by assigning every observation in A to the closest cluster centroid in B (corresponding to \( \text{classification} = \text{"centroid"} \)), but other methods are possible, see \texttt{classifnp}. A pair of points A in the same A-cluster is defined to be correctly predicted if both points are classified into the same cluster on B. The same is done with the points of B relative to the clustering on A. The prediction strength for each of the clusterings is the minimum (taken over all clusters) relative frequency of correctly predicted pairs of points of that cluster. The final mean prediction strength statistic is the mean over all \( 2M \) clusterings.

**Value**

\texttt{prediction.strength} gives out an object of class \texttt{predstr}, which is a list with components

- **predcorr** list of vectors of length \( M \) with relative frequencies of correct predictions (clusterwise minimum). Every list entry refers to a certain number of clusters.

- **mean.pred** means of \texttt{predcorr} for all numbers of clusters.

- **optimalk** optimal number of clusters.

- **cutoff** see above.

- **method** a string identifying the clustering method.

- **Gmax** see above.

- **M** see above.

**Author(s)**

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**References**

See Also

kmeansCBI, classifnp

Examples

options(digits=3)
set.seed(98765)
iriss <- iris[sample(150,20),-5]
prediction.strength(iriss,2,3,M=3)
prediction.strength(iriss,2,3,M=3,clustermethod=claraCBI)
# The examples are fast, but of course M should really be larger.

---

### randcmatrix

#### Random partition matrix

**Description**

For use within regmix. Generates a random 0-1-matrix with \( n \) rows and \( cln \) columns so that every row contains exactly one one and every columns contains at least \( p+3 \) ones.

**Usage**

```
randcmatrix(n, cln, p)
```

**Arguments**

- `n` is a positive integer. Number of rows.
- `cln` is a positive integer. Number of columns.
- `p` is a positive integer. See above.

**Value**

An \( n \times cln \)-matrix.

**Author(s)**

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**See Also**

regmix

**Examples**

```
set.seed(111)
randcmatrix(10,2,1)
```
**randomclustersim**

---

**randconf**  
*Generate a sample indicator vector*

**Description**

Generates a logical vector of length \( n \) with \( p \) TRUEs.

**Usage**

```r
randconf(n, p)
```

**Arguments**

- \( n \)  
  positive integer.
- \( p \)  
  positive integer.

**Value**

A logical vector.

**Author(s)**

Christian Hennig &lt;christian.hennig@unibo.it&gt;  

**See Also**

- `sample`

**Examples**

```r
randconf(10,3)
```

---

**randomclustersim**  
*Simulation of validity indexes based on random clusterings*

**Description**

For a given dataset this simulates random clusterings using `stupidkcentroids`, `stupidknn`, `stupidkfn`, and `stupidkaven`. It then computes and stores a set of cluster validity indexes for every clustering.

**Usage**

```r
randomclustersim(datadist, datanp=NULL, npstats=FALSE, 
                   G, nnruns=100, kmruns=100, fnruns=100, avenruns=100, 
                   nnk=4, dnnk=2, 
                   pamcrit=TRUE, 
                   multicore=FALSE, cores=detectCores()-1, monitor=TRUE)
```
Arguments

datadist  distances on which validation-measures are based, dist object or distance matrix.
datanp   optional observations times variables data matrix, see npstats.
npstats logical. If TRUE, distrsimilarity is called and the two statistics computed there are added to the output. These are based on datanp and require datanp to be specified.
G       vector of integers. Numbers of clusters to consider.
nnruns  integer. Number of runs of stupidknn.
kmruns  integer. Number of runs of stupidkcentroids.
fnruns  integer. Number of runs of stupidkfn.
avenruns integer. Number of runs of stupidkaven.
nnk     nnk-argument to be passed on to cqcluster.stats.
nnk     nnk-argument to be passed on to distrsimilarity.
pamcrit pamcrit-argument to be passed on to cqcluster.stats.
multicore logical. If TRUE, parallel computing is used through the function mclapply from package parallel; read warnings there if you intend to use this; it won't work on Windows.
cores   integer. Number of cores for parallelisation.
monitor logical. If TRUE, it will print some runtime information.

Value

List with components

 nn  list, indexed by number of clusters. Every entry is a data frame with nnruns observations for every simulation run of stupidknn. The variables of the data frame are avewithin, mnnd, cvnnd, maxdiameter, widestgap, sindex, minsep, asw, dindex, denscut, if pamcrit=TRUE also pamc, if npstats=TRUE also kdnorm, kdunif. All these are cluster validation indexes; documented as values of clustatsum.

 fn  list, indexed by number of clusters. Every entry is a data frame with fnruns observations for every simulation run of stupidkfn. The variables of the data frame are avewithin, mnnd, cvnnd, maxdiameter, widestgap, sindex, minsep, asw, dindex, denscut, if pamcrit=TRUE also pamc, if npstats=TRUE also kdnorm, kdunif. All these are cluster validation indexes; documented as values of clustatsum.

 aven list, indexed by number of clusters. Every entry is a data frame with avenruns observations for every simulation run of stupidkaven. The variables of the data frame are avewithin, mnnd, cvnnd, maxdiameter, widestgap, sindex, minsep, asw, dindex, denscut, if pamcrit=TRUE also pamc, if npstats=TRUE also kdnorm, kdunif. All these are cluster validation indexes; documented as values of clustatsum.

 km  list, indexed by number of clusters. Every entry is a data frame with kmruns observations for every simulation run of stupidkcentroids. The variables of the data frame are avewithin, mnnd, cvnnd, maxdiameter, widestgap, sindex, minsep, asw, dindex, denscut, if pamcrit=TRUE also pamc, if npstats=TRUE also kdnorm, kdunif. All these are cluster validation indexes; documented as values of clustatsum.
regmix

**Number of Runs**
- `nnruns`: number of involved runs of `stupidknn`
- `fnruns`: number of involved runs of `stupidkfn`
- `avenruns`: number of involved runs of `stupidkaven`
- `kmruns`: number of involved runs of `stupidcentroids`

**Author(s)**
Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

**References**

**See Also**
stupidcentroids, stupidknn, stupidkfn, stupidkaven, clustatsum

**Examples**
```r
set.seed(20000)
options(digits=3)
face <- rFace(10,dMoNo=2,dNoEy=0,p=2)
randomclustersim(dist(face),datanp=face,npstats=TRUE,G=2:3,
nnruns=2,kmruns=2, fnruns=1,avenruns=1,nnk=2)
```

---

**Description**
Computes an ML-estimator for clusterwise linear regression under a regression mixture model with Normal errors. Parameters are proportions, regression coefficients and error variances, all independent of the values of the independent variable, and all may differ for different clusters. Computation is by the EM-algorithm. The number of clusters is estimated via the Bayesian Information Criterion (BIC). Note that package `flexmix` has more sophisticated tools to do the same thing and is recommended. The functions are kept in here only for compatibility reasons.

**Usage**
```r
regmix(indep, dep, ir=1, nclust=1:7, icrit=1.e-5, mnsig=1.e-6, warnings=FALSE)
regem(indep, dep, m, cln, icrit=1.e-5, mnsig=1.e-6, warnings=FALSE)
```
Arguments

- **indep**: numerical matrix or vector. Independent variables.
- **dep**: numerical vector. Dependent variable.
- **ir**: positive integer. Number of iteration runs for every number of clusters.
- **nclust**: vector of positive integers. Numbers of clusters.
- **icrit**: positive numerical. Stopping criterion for the iterations (difference of loglikelihoods).
- **minsig**: positive numerical. Minimum value for the variance parameters (likelihood is unbounded if variances are allowed to converge to 0).
- **warnings**: logical. If TRUE, warnings are given during the EM iteration in case of collinear regressors, too small mixture components and error variances smaller than minimum. In the former two cases, the algorithm is terminated without a result, but an optimal solution is still computed from other algorithm runs (if there are others). In the latter case, the corresponding variance is set to the minimum.
- **cln**: positive integer. (Single) number of clusters.
- **m**: matrix of positive numericals. Number of columns must be cln. Number of rows must be number of data points. Columns must add up to 1. Initial configuration for the EM iteration in terms of a probability vector for every point which gives its degree of membership to every cluster. As generated by `randcmatrix`.

Details

The result of the EM iteration depends on the initial configuration, which is generated randomly by `randcmatrix` for `regmix`. `regmix` calls `regem`. To provide the initial configuration manually, use parameter `m` of `regem` directly. Take a look at the example about how to generate `m` if you want to specify initial parameters.

The original paper DeSarbo and Cron (1988) suggests the AIC for estimating the number of clusters. The use of the BIC is advocated by Wedel and DeSarbo (1995). The BIC is defined here as $2 \times \text{loglik} - \log(n) \times ((p+3) \times \text{cln}-1)$, $p$ being the number of independent variables, i.e., the larger the better.

See the entry for the input parameter `warnings` for the treatment of several numerical problems.

Value

`regmix` returns a list containing the components `clnopt, loglik, bic, coef, var, eps, z, g`.

`regem` returns a list containing the components `loglik, coef, var, z, g, warn`.

- **clnopt**: optimal number of clusters according to the BIC.
- **loglik**: loglikelihood for the optimal model.
- **bic**: vector of BIC values for all numbers of clusters in `nclust`.
- **var**: vector of error variance estimators for the clusters.
eps

vector of cluster proportion estimators.

z

matrix of estimated a posteriori probabilities of the points (rows) to be generated by the clusters (columns). Compare input argument m.

g

integer vector of estimated cluster numbers for the points (via argmax over z).

warn

logical. TRUE if one of the estimated clusters has too few points and/or collinear regressors.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

Regression mixtures can also (and probably better) be computed with the flexmix package, see *flexmix*. (When I first write the regmix-function, flexmix didn’t exist.)

fixreg for fixed point clusters for clusterwise linear regression.

EMclust for Normal mixture model fitting (non-regression).

Examples

```r
## Not run:
# This apparently gives slightly different but data-analytically fine results # on some versions of R.
set.seed(12234)
data(tonedata)
attach(tonedata)
rmt1 <- regmix(stretchratio,tuned,nclust=1:2)
# nclust=1:2 makes the example fast;
# a more serious application would rather use the default.
rmt1$g
round(rmt1$bic,digits=2)
# start with initial parameter values
cln <- 3
n <- 150
initcoef <- cbind(c(2,0),c(0,1),c(0,2.5))
initvar <- c(0.001,0.0001,0.5)
initeps <- c(0.4,0.3,0.3)
# computation of m from initial parameters
m <- matrix(nrow=n, ncol=cln)
stm <- numeric(0)
```
for (i in 1:cln)
for (j in 1:n){
  m[j,i] <- initeps[i]*dnorm(tuned[j], mean=initcoef[1,i]+initcoef[2,i]*stretchratio[j], sd=sqrt(initvar[i]))
}
for (j in 1:n){
  stm[j] <- sum(m[j,])
  for (i in 1:cln)
    m[j,i] <- m[j,i]/stm[j]
}
rmr2 <- regem(stretchratio, tuned, m, cln)

## End(Not run)

rFace

"Face-shaped" clustered benchmark datasets

Description

Generates "face-shaped" clustered benchmark datasets. This is based on a collaboration with Martin Maechler.

Usage

rFace(n, p = 6, nrep.top = 2, smile.coef = 0.6, dMoNo = 1.2, dNoEy = 1)

Arguments

n
integer greater or equal to 10. Number of points.

p
integer greater or equal to 2. Dimension.

nrep.top
integer. Number of repetitions of the hair-top point.

smile.coef
numeric. Coefficient for quadratic term used for generation of mouth-points. Positive values => smile.

dMoNo
number. Distance from mouth to nose.

dNoEy
number. Minimum vertical distance from mouth to eyes.

Details

The function generates a nice benchmark example for cluster analysis. There are six "clusters" in this data, of which the first five are clearly homogeneous patterns, but with different distributional shapes and different qualities of separation. The clusters are distinguished only in the first two dimensions. The attribute grouping is a factor giving the cluster numbers, see below. The sixth group of points corresponds to some hairs, and is rather a collection of outliers than a cluster in itself. This group contains nrep. top+2 points. Of the remaining points, 20% belong to cluster 1, the chin (quadratic function plus noise). 10% belong to cluster 2, the right eye (Gaussian). 30% belong to cluster 3, the mouth (Gaussian/squared Gaussian). 20% belong to cluster 4, the nose (Gaussian/gamma), and 20% belong to cluster 5, the left eye (uniform).
The distributions of the further variables are homogeneous over all points. The third dimension is exponentially distributed, the fourth dimension is Cauchy distributed, all further distributions are Gaussian.

Please consider the source code for exact generation of the clusters.

**Value**

An \( n \times p \) numeric matrix with attributes

- **grouping**: a factor giving the cluster memberships of the points.
- **indexlist**: a list of six vectors containing the indices of points belonging to the six groups.

**Author(s)**

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

**Examples**

```r
set.seed(4634)
face <- rFace(600,dMoNo=2,dNoEy=0)
grface <- as.integer(attr(face,"grouping"))
plot(face, col = grface)
# pairs(face, col = grface, main ="rFace(600,dMoNo=2,dNoEy=0)"
```

---

**ridgeline**

*Ridgeline computation*

**Description**

Computes \((\alpha\Sigma_1^{-1} + (1-\alpha)\Sigma_2^{-1})^{-1} \cdot \alpha(\Sigma_1^{-1}\mu_1) + (1-\alpha)(\Sigma_2^{-1}\mu_2))\) as required for the computation of the ridgeline (Ray and Lindsay, 2005) to find all density extrema of a two-component Gaussian mixture with mean vectors \(\mu_1\) and \(\mu_2\) and covariance matrices \(\Sigma_1\), \(\Sigma_2\).

**Usage**

```r
ridgeline(alpha, mu1, mu2, Sigma1, Sigma2)
```

**Arguments**

- **alpha**: numeric between 0 and 1.
- **mu1**: mean vector of component 1.
- **mu2**: mean vector of component 2.
- **Sigma1**: covariance matrix of component 1.
- **Sigma2**: covariance matrix of component 2.
Value

A vector. See above.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


Examples

```r
ridgeline(0.5,c(1,1),c(2,5),diag(2),diag(2))
```

Description

Computes ridgeline ratios and unimodality checks for pairs of components given the parameters of a Gaussian mixture. Produces ridgeline plots.

Usage

```r
ridgeline.diagnosis (propvector,muarray,Sigmaarray, k=length(propvector), ipairs="all", compute.ratio=TRUE,by=0.001, ratiocutoff=NULL,ridgelineplot="matrix")
```

Arguments

- `propvector` vector of component proportions. Length must be number of components, and must sum up to 1.
- `muarray` matrix of component means (different components are in different columns).
- `Sigmaarray` three dimensional array with component covariance matrices (the third dimension refers to components).
- `k` integer. Number of components.
- `ipairs` "all" or list of vectors of two integers. If `ipairs="all"`, computations are carried out for all pairs of components. Otherwise, `ipairs` gives the pairs of components for which computations are carried out.
- `compute.ratio` logical. If `TRUE`, a matrix of ridgeline ratios is computed, see Hennig (2010a).
by real between 0 and 1. Interval width for density computation along the ridgeline.

ratiocutoff real between 0 and 1. If not NULL, the connection.matrix (see below) is computed by checking whether ridgeline ratios between components are below ratiocutoff.

ridgelineplot one of "none", "matrix", "pairwise". If "matrix", a matrix of pairwise ridgeline plots (see Hennig 2010b) will be plotted. If "pairwise", pairwise ridgeline plots are plotted (you may want to set par(ask=TRUE) to see them all). No plotting if "none".

Value

A list with components

merged.clusters vector of integers, stating for every mixture component the number of the cluster of components that would be merged by merging connectivity components of the graph specified by connection.matrix.

connection.matrix zero-one matrix, in which a one means that the mixture of the corresponding pair of components of the original mixture is either unimodel (if ratiocutoff=NULL) or that their ridgeline ratio is above ratiocutoff. If ipairs!="all", ignored pairs always have 0 in this matrix, same for ratio.matrix.

ratio.matrix matrix with entries between 0 und 1, giving the ridgeline ratio, which is the density minimum of the mixture of the corresponding pair of components along the ridgeline divided by the minimum of the two maxima closest to the beginning and the end of the ridgeline.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References

Hennig, C. (2010a) Methods for merging Gaussian mixture components, Advances in Data Analysis and Classification, 4, 3-34.


See Also

ridgeline, dridgeline, piridge, piridge.zeroes
**Examples**

```r
muarray <- cbind(c(0,0),c(0,0.1),c(10,10))
sigmaarray <- array(c(diag(2),diag(2),diag(2)),dim=c(2,2,3))
rd <-
  ridgeline.diagnosis(c(0.5,0.3,0.2),muarray,sigmaarray,ridgedlineplot="matrix",by=0.1)
  # Much slower but more precise with default by=0.001.
```

---

**Description**

Extracts the information about the size of the intersections between representative Fixed Point Clusters (FPCs) of stable groups from the output of the FPC-functions `fixreg` and `fixmahal`.

**Usage**

```r
simmatrix(fpcobj)
```

**Arguments**

- `fpcobj` an object of class `rfpc` or `mfpc`.

**Value**

A non-negative real-valued vector giving the number of points in the intersections of the representative FPCs of stable groups.

**Note**

The intersection between representative FPCs no. i and j is at position `sseg(i,j)`.

**Author(s)**

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**See Also**

`fixmahal`, `fixreg`, `sseg`

**Examples**

```r
set.seed(190000)
data(tonedata)
  # Note: If you do not use the installed package, replace this by
data(tonedata)
  # tonedata <- read.table("(path/)tonedata.txt", header=TRUE)
  attach(tonedata)
tonefix <- fixreg(stretchratio,tuned,mtf=1,ir=20)
simmatrix(tonefix)[sseg(2,3)]
```
solvecov

*Inversion of (possibly singular) symmetric matrices*

**Description**

Tries to invert a matrix by `solve`. If this fails because of singularity, an eigenvector decomposition is computed, and eigenvalues below $1/cmax$ are replaced by $1/cmax$, i.e., $cmax$ will be the corresponding eigenvalue of the inverted matrix.

**Usage**

```
solvecov(m, cmax = 1e+10)
```

**Arguments**

- `m` a numeric symmetric matrix.
- `cmax` a positive value, see above.

**Value**

A list with the following components:

- `inv` the inverted matrix
- `coll` TRUE if `solve` failed because of singularity.

**Author(s)**

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**See Also**

- `solve`, `eigen`

**Examples**

```r
x <- c(1,0,0,1,0,1,0,0,1)
dim(x) <- c(3,3)
solvecov(x)
```
sseg | Position in a similarity vector

Description

sseg(i, j) gives the position of the similarity of objects i and j in the similarity vectors produced by fixreg and fixmahal. sseg should only be used as an auxiliary function in fixreg and fixmahal.

Usage

sseg(i, j)

Arguments

i positive integer.

j positive integer.

Value

A positive integer.

Author(s)

Christian Hennig \(<\text{christian.hennig@unibo.it}>\) \(\text{https://www.unibo.it/sitoweb/christian.hennig/en/}\)

Examples

sseg(3, 4)

stupidkaven | Stupid average dissimilarity random clustering

Description

Picks k random starting points from given dataset to initialise k clusters. Then, one by one, the point not yet assigned to any cluster with smallest average dissimilarity to the points of any already existing cluster is assigned to that cluster, until all points are assigned. This is a random version of average linkage clustering, see Akhanli and Hennig (2020).

Usage

stupidkaven(d, k)
Arguments

- **d**: dist-object or dissimilarity matrix.
- **k**: integer. Number of clusters.

Value

The clustering vector (values 1 to k, length number of objects behind d).

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

- `stupidkcentroids`, `stupidknn`, `stupidkfn`

Examples

```r
set.seed(20000)
options(digits=3)
face <- rFace(200,dMoNo=2,dNoEy=0,p=2)
stupidkaven(dist(face),3)
```

Description

Picks k random centroids from given dataset and assigns every point to closest centroid. This is called stupid k-centroids in Hennig (2017).

Usage

```r
stupidkcentroids(d,k)
```
stupidkfn

Value

The clustering vector (values 1 to k, length number of objects behind d).

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

References


See Also

stupidknn, stupidkfn, stupidkaven

Examples

```r
set.seed(20000)
options(digits=3)
face <- rFace(200,dMoNo=2,dNoEy=0,p=2)
stupidkcentroids(dist(face),3)
```

---

stupidkfn

**Stupid farthest neighbour random clustering**

Description

Picks k random starting points from given dataset to initialise k clusters. Then, one by one, a point not yet assigned to any cluster is assigned to that cluster, until all points are assigned. The point/cluster pair to be used is picked according to the smallest distance of a point to the farthest point to it in any of the already existing clusters as in complete linkage clustering, see Akhanli and Hennig (2020).

Usage

`stupidkfn(d,k)`

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>d</td>
<td>dist-object or dissimilarity matrix.</td>
</tr>
<tr>
<td>k</td>
<td>integer. Number of clusters.</td>
</tr>
</tbody>
</table>
**stupidknn**

**Value**

The clustering vector (values 1 to k, length number of objects behind d),

**Author(s)**

Christian Hennig &lt;christian.hennig@unibo.it&gt; https://www.unibo.it/sitoweb/christian.hennig/en/

**References**


**See Also**

stupidkcentroids, stupidknn, stupidkaven

**Examples**

```r
set.seed(20000)
options(digits=3)
face <- rFace(200,dMoNo=2,dNoEy=0,p=2)
stupidkfn(dist(face),3)
```

---

```
stupidknn       Stupid nearest neighbour random clustering
```

**Description**

Picks k random starting points from given dataset to initialise k clusters. Then, one by one, the point not yet assigned to any cluster that is closest to an already assigned point is assigned to that cluster, until all points are assigned. This is called stupid nearest neighbour clustering in Hennig (2017).

**Usage**

```
stupidknn(d,k)
```

**Arguments**

- **d**: `dist-object or dissimilarity matrix`
- **k**: `integer. Number of clusters`

**Value**

The clustering vector (values 1 to k, length number of objects behind d),
**tdecomp**

**Author(s)**
Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

**References**


**See Also**
stupidkcentroids, stupidkfn, stupidkaven

**Examples**
```r
set.seed(20000)
options(digits=3)
face <- rFace(200,dMoNo=2,dNoEy=0,p=2)
stupidknn(dist(face),3)
```

---

**tdecomp**

*Root of singularity-corrected eigenvalue decomposition*

**Description**
Computes transposed eigenvectors of matrix $m$ times diagonal of square root of eigenvalues so that eigenvalues smaller than 1e-6 are set to 1e-6.

**Usage**
tdecomp(m)

**Arguments**

- **m**: a symmetric matrix of minimum format 2*2.

**Details**
Thought for use in discrcoord only.

**Value**
a matrix.
Note

Thought for use within `discrcoord` only.

Author(s)

Christian Hennig <christian.hennig@unibo.it> https://www.unibo.it/sitoweb/christian.hennig/en/

Examples

```r
x <- rnorm(10)
y <- rnorm(10)
z <- cov(cbind(x,y))
round(tdecomp(z),digits=2)
```

---

### tonedata

Tone perception data

---

#### Description

The tone perception data stem from an experiment of Cohen (1980) and have been analyzed in de Veaux (1989). A pure fundamental tone was played to a trained musician. Electronically generated overtones were added, determined by a stretching ratio of `stretchratio`. `stretchratio=2.0` corresponds to the harmonic pattern usually heard in traditional definite pitched instruments. The musician was asked to tune an adjustable tone to the octave above the fundamental tone. `tuned` gives the ratio of the adjusted tone to the fundamental, i.e. `tuned=2.0` would be the correct tuning for all `stretchratio`-values. The data analyzed here belong to 150 trials with the same musician. In the original study, there were four further musicians.

#### Usage

```r
data(tonedata)
```

#### Format

A data frame with 2 variables `stretchratio` and `tuned` and 150 cases.

#### Source


#### References

Is a fitted density unimodal or not?

Description

Checks whether a series of fitted density values (such as given out as y-component of \texttt{density}) is unimodal.

Usage

\texttt{unimodal.ind(y)}

Arguments

\texttt{y} numeric vector of fitted density values in order of increasing x-values such as given out as y-component of \texttt{density}.

Value

Logical. \texttt{TRUE} if unimodal.

Author(s)

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Examples

\texttt{unimodal.ind(c(1,3,3,4,2,1,0,0))}

Cluster validation statistics - object

The objects of class "\texttt{valstat}" store cluster validation statistics from various clustering methods run with various numbers of clusters.
Value

A legitimate valstat object is a list. The format of the list relies on the number of involved clustering methods, nmethods, say, i.e., the length of the method-component explained below. The first nmethods elements of the valstat-list are just numbered. These are themselves lists that are numbered between 1 and the maxG-component defined below. Element [[i]][[j]] refers to the clustering from clustering method number i with number of clusters j. Every such element is a list with components avewithin, mnd, cvnnd, maxdiameter, widestgap, sindex, minsep, asw, dindex, denscut, highdgap, pearsongamma.

Further optional components are pamc, kdnorm, kdunif, dmode, aggregated. All these are cluster validation indexes, as follows.

- **avewithin**: average distance within clusters (reweighted so that every observation, rather than every distance, has the same weight).
- **mnd**: average distance to nnkth nearest neighbour within cluster. (nnk is a parameter of cqcluster.stats, default 2.)
- **cvnnd**: coefficient of variation of dissimilarities to nnkth nearest within-cluster neighbour, measuring uniformity of within-cluster densities, weighted over all clusters, see Sec. 3.7 of Hennig (2017). (nnk is a parameter of cqcluster.stats, default 2.)
- **maxdiameter**: maximum cluster diameter.
- **widestgap**: widest within-cluster gap or average of cluster-wise widest within-cluster gap, depending on parameter averagegap of cqcluster.stats, default FALSE.
- **sindex**: separation index. Defined based on the distances for every point to the closest point not in the same cluster. The separation index is then the mean of the smallest proportion sepprob (parameter of cqcluster.stats, default 0.1) of these. See Hennig (2017).
- **minsep**: minimum cluster separation.
- **asw**: average silhouette width. See silhouette.
- **dindex**: this index measures to what extent the density decreases from the cluster mode to the outskirts; Idensdec in Sec. 3.6 of Hennig (2017); low values are good.
- **denscut**: this index measures whether cluster boundaries run through density valleys; Idensbound in Sec. 3.6 of Hennig (2017); low values are good.
- **highdgap**: this measures whether there is a large within-cluster gap with high density on both sides; Ihighdgap in Sec. 3.6 of Hennig (2017); low values are good.
- **pearsongamma**: correlation between distances and a 0-1-vector where 0 means same cluster, 1 means different clusters. "Normalized gamma" in Halkidi et al. (2001).
- **withinss**: a generalisation of the within clusters sum of squares (k-means objective function), which is obtained if d is a Euclidean distance matrix. For general distance measures, this is half the sum of the within cluster squared dissimilarities divided by the cluster size.
- **entropy**: entropy of the distribution of cluster memberships, see Meila(2007).
- **pamc**: average distance to cluster centroid, which is the observation that minimises this average distance.
- **kdnorm**: Kolmogorov distance between distribution of within-cluster Mahalanobis distances and appropriate chi-squared distribution, aggregated over clusters (I am grateful to Agustín Mayo-Iscar for the idea).
kdunif
Kolmogorov distance between distribution of distances to \( dnnk \)th nearest within-cluster neighbor and appropriate Gamma-distribution, see Byers and Raftery (1998), aggregated over clusters. \( dnnk \) is parameter \( nnk \) of \texttt{distrsimilarity}, corresponding to \( nnk \) of \texttt{clusterbenchstats}.

dmode
aggregated density mode index equal to \( 0.75 * \text{dindex} + 0.25 * \text{highdgap} \) before standardisation.

Furthermore, a \texttt{valstat} object has the following list components:

- \texttt{maxG}
  maximum number of clusters.

- \texttt{minG}
  minimum number of clusters (list entries below that number are empty lists).

- \texttt{method}
  vector of names (character strings) of clustering CBI-functions, see \texttt{kmeansCBI}.

- \texttt{name}
  vector of names (character strings) of clustering methods. These can be user-chosen names (see argument \texttt{methodsnames} in \texttt{clusterbenchstats}) and may distinguish different methods run by the same CBI-function but with different parameter values such as complete and average linkage for \texttt{hclustCBI}.

- \texttt{statistics}
  vector of names (character strings) of cluster validation indexes.

**GENERATION**

These objects are generated as part of the \texttt{clusterbenchstats}-output.

**METHODS**

The \texttt{valstat} class has methods for the following generic functions: \texttt{print}, \texttt{plot}, see \texttt{plot.valstat}.

**Author(s)**

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**References**


**See Also**

\texttt{clusterbenchstats, plot.valstat}. 
weightplots  

Ordered posterior plots

Description

Ordered posterior plots for Gaussian mixture components, see Hennig (2010).

Usage

weightplots(z, clusternumbers="all", clustercol=2,  
 allcol=grey(0.2+((1:ncol(z))-1)*  
 0.6/(ncol(z)-1)),  
 lty=rep(1,ncol(z)),clusterlwd=3,  
 legendposition="none",  
 weightcutoff=0.01,ask=TRUE, ...)

Arguments

z  
matrix with rows corresponding to observations and columns corresponding to mixture components. Entries are probabilities that an observation has been generated by a mixture component. These will normally be estimated posteriori probabilities, as generated as component z of the output object from \texttt{summary.mclustBIC}.

clusternumbers  
"all" or vector of integers. Numbers of components for which plots are drawn.

clustercol  
colour used for the main components for which a plot is drawn.

allcol  
colours used for respective other components in plots in which they are not main components.

lty  
line types for components.

clusterlwd  
numeric. Line width for main component.

legendposition  
"none" or vector with two coordinates in the plot, where a legend should be printed.

weightcutoff  
numeric between 0 and 1. Observations are only taken into account for which the posterior probability for the main component is larger than this.

ask  
logical. If TRUE, it sets \texttt{par(ask=TRUE)} in the beginning and \texttt{par(ask=FALSE)} after all plots were showed.

...  
further parameters to be passed on to \texttt{legend}.

Details

Shows posterior probabilities for observations belonging to all mixture components on the y-axis, with points ordered by posterior probability for main component.

Value

Invisible matrix of posterior probabilities z from \texttt{mclustsummary}. 
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References


Examples

```r
require(mclust)
require(MASS)
data(crabs)
dc <- crabs[,4:8]
cm <- mclustBIC(crabs[,4:8],G=9,modelNames="EEE")
scm <- summary(cm,crabs[,4:8])
weightplots(scm$z,clusternumbers=1:3,ask=FALSE)
weightplots(scm$z,clusternumbers=1:3,allcol=1:9, ask=FALSE,
legendposition=c(5,0.7))
# Remove ask=FALSE to have time to watch the plots.
```

wfu

Weight function (for Mahalanobis distances)

Description

Function of the elements of md, which is 1 for arguments smaller than ca, 0 for arguments larger than ca2 and linear (default: continuous) in between.

Thought for use in fixmahal.

Usage

`wfu(md, ca, ca2, a1 = 1/(ca - ca2), a0 = -a1 * ca2)`

Arguments

- `md` vector of positive numericals.
- `ca` positive numerical.
- `ca2` positive numerical.
- `a1` numerical. Slope.
- `a0` numerical. Intercept.

Value

A vector of numericals between 0 and 1.
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See Also

fixmahal

Examples

md <- seq(0,10,by=0.1)
round(wfu(md,ca=5,ca2=8),digits=2)

taxtable

xtable Partition crosstable with empty clusters

Description

This produces a crosstable between two integer vectors (partitions) of the same length with a given maximum vector entry \(k\) so that the size of the table is \(k \times k\) with zeroes for missing entries between 1 and \(k\) (the command \texttt{table} does pretty much the same thing but will leave out missing entries).

Usage

\texttt{xtable(c1,c2,k)}

Arguments

\begin{itemize}
\item \texttt{c1} \ hspace{1cm} vector of integers.
\item \texttt{c2} \ hspace{1cm} vector of integers of same length as \texttt{c1}.
\item \texttt{k} \ hspace{1cm} integer. Must be larger or equal to maximum entry in \texttt{c1} and \texttt{c2}.
\end{itemize}

Value

A matrix of dimensions \(c(k,k)\). Entry \([i,j]\) gives the number of places in which \(c1==i\) & \(c2==j\).

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See Also

\texttt{table}
Examples

```r
c1 <- 1:3
c2 <- c(1,1,2)
xtable(c1,c2,3)
```

---

**zmisclassification.matrix**

*Matrix of misclassification probabilities between mixture components*

**Description**

Matrix of misclassification probabilities in a mixture distribution between two mixture components from estimated posterior probabilities regardless of component parameters, see Hennig (2010).

**Usage**

```
zmisclassification.matrix(z, pro=NULL, clustering=NULL, ipairs="all", symmetric=TRUE, stat="max")
```

**Arguments**

- `z`: matrix of posterior probabilities for observations (rows) to belong to mixture components (columns), so entries need to sum up to 1 for each row.
- `pro`: vector of component proportions, need to sum up to 1. Computed from `z` as default.
- `clustering`: vector of integers giving the estimated mixture components for every observation. Computed from `z` as default.
- `ipairs`: "all" or list of vectors of two integers. If `ipairs="all"`, computations are carried out for all pairs of components. Otherwise, `ipairs` gives the pairs of components for which computations are carried out.
- `symmetric`: logical. If `TRUE`, the matrix is symmetrised, see parameter `stat`.
- `stat`: "max" or "mean". The statistic by which the two misclassification probabilities are aggregated if `symmetric=TRUE`.

**Value**

A matrix with the (symmetrised, if required) misclassification probabilities between each pair of mixture components. If `symmetric=FALSE`, matrix entry `[i,j]` is the estimated probability that an observation generated by component `j` is classified to component `i` by maximum a posteriori rule.

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References


See Also

confusion

Examples

```r
set.seed(12345)
m <- rpois(20, lambda=5)
dim(m) <- c(5,4)
m <- m/apply(m,1,sum)
round(zmisclassification.matrix(m,symmetric=FALSE),digits=2)
```
Index

*Topic arith
  can, 16
cweight, 57
wfu, 153
*Topic array
  con.comp, 46
  solvecov, 142
tdecomp, 147
xtable, 154
*Topic classif
  adcoord, 6
  ancoord, 8
  awcoord, 9
  batcoord, 11
discrcoord, 62
discrproj, 65
distrsimilarity, 70
mvdcoord, 114
ncoord, 115
plotcluster, 126
*Topic cluster
  bhattacharyya.matrix, 14
calinhara, 15
cdbw, 18
cgrestandard, 19
classifdist, 21
c lucrols, 23
clujaccard, 24
clusexpect, 25
clustatsum, 26
clustatsum, 26
cluster.magazine, 28
cluster.stats, 30
cluster.varstats, 34
clusterbenchstats, 36
clusterboot, 39
cmahal, 45
con.comp, 46
confusion, 48
cqcluster.stats, 50
cvnn, 56
dbscan, 58
dippen.tantrum, 60
dipstest.multi, 61
distancefactor, 67
distcritmulti, 68
distrsimilarity, 70
ridgeline, 71
dudahart2, 72
extract.mixturepars, 73
findrep, 74
fixmahal, 75
fixreg, 82
flexmixedruns, 88
fpclusters, 90
itnumber, 91
kmeansCBI, 93
kmeansruns, 98
lcmixed, 100
mahalconf, 105
mergenormals, 106
mergeparameters, 110
mnsize, 111
mixdens, 112
mixpredictive, 113
neginc, 117
nselectboot, 118
pamk, 120
piridge, 122
piridge.zeroes, 123
plot.valstat, 124
prediction.strength, 129
randcmatrix, 131
randomclustersim, 132
regmix, 134
ridgeline, 138
ridgeline.diagno, 139
stupidkaven, 143
stupidkcentroids, 144
stupidkfn, 145
stupidknn, 146
valstat.object, 149
weightplots, 152
zmisclassification.matrix, 155
*Topic **datasets**
tonedata, 148
*Topic **data**
rFace, 137
*Topic **distribution**
randconf, 132
*Topic **manip**
cat2bin, 17
discrete.recode, 63
jittervar, 92
*Topic **multivariate**
adcoord, 6
ancoord, 8
awcoord, 9
batcoord, 11
bhhattacharyya.dist, 13
bhhattacharyya.matrix, 14
cgrestandard, 19
classifdist, 21
clustatsum, 26
cluster.magazine, 28
cluster.stats, 30
clusterbenchstats, 36
clusterboot, 39
confusion, 48
cov.wml, 49
cqcluster.stats, 50
dbscan, 58
diptest.multi, 61
discrcoord, 62
discrproj, 65
distrsimilarity, 70
dridgeline, 71
extract.mixturepars, 73
fixmahal, 75
kmeansCB1, 93
kmeansruns, 98
localshape, 102
mahalanodisc, 103
mahalanofix, 104
mahalconf, 105
mergenormals, 106
mergeparameters, 110
mixdens, 112
mixpredictive, 113
mvdcoord, 113
ncord, 115
nselectboot, 118
pamk, 120
piridge, 122
piridge.zeros, 123
plot.valstat, 124
plotcluster, 126
prediction.strength, 129
randomclustersim, 132
ridgeline, 138
ridgeline.diagnosis, 139
stupidkaven, 143
stupidkcentroids, 144
stupidkfn, 145
stupidknn, 146
weightplots, 152
zmisclassification.matrix, 155
*Topic **regression**
fixreg, 82
regmix, 134
*Topic **robust**
fixmahal, 75
fixreg, 82
*Topic **univar**
clusexpect, 25
itnumber, 91
minsize, 111
unimodal.ind, 149
*Topic **utilities**
simmatrix, 141
ssseg, 143
adcoord, 6, 65, 66, 127, 128
ancoord, 8, 65, 66, 127, 128
awcoord, 9, 57, 65, 66, 103, 127, 128
batcoord, 11, 63, 65, 66, 79, 81, 127, 128
batvarcoord (batcoord), 11
bhhattacharyya.dist, 13, 15
bhhattacharyya.matrix, 14, 108

calinhara, 4, 15, 34, 55, 98, 99, 120
can, 16, 83, 87
cat2bin, 17
cdbw, 18, 74, 75
cgrestandard, 19, 26, 38, 39
INDEX

clara, 5, 43, 95–97, 120, 121
c ClaraCBI, 45, 118, 119, 129
c ClaraCBI (kmeansCBI), 93
classifdist, 21, 118, 119, 129, 130
classifnp, 118, 119, 129–131
classifnp (classifdist), 21
c lucols, 23
clugrey (clucols), 23
clujaccard, 24
clusexpect, 25, 85, 87, 91, 92, 111, 112
clustatsum, 19, 20, 26, 38, 39, 133, 134
cluster. magazine, 28, 38, 39, 125, 126
cluster.stats, 16, 30, 50, 55, 69, 71, 73
c luster. varstats, 34
c lusterbenchmarkstats, 19, 20, 26, 30, 36, 50, 124–126, 151
c lusterboot, 34, 39, 55, 93, 96, 97, 118, 119, 129
c luster sym (clucols), 23
cmvahal, 45, 77, 81
cmdscale, 95
con. comp, 46
c confusion, 48, 156
c ov, 49
c ov. rob, 8, 10, 76, 81, 104, 105, 114, 116
c ov. wml, 49, 81
c ov. w t, 49
covMtdc, 102
cqcluster.stats, 4, 26, 28, 34, 37–39, 50, 71, 133, 150
cutree, 47
cvnn, 56
cweight, 57
daissy, 68, 69
data. matrix, 64
dbscan, 43, 58, 95–97
dbscanCBI, 45
dbscanCBI (kmeansCBI), 93
density, 60, 149
dip, 60, 61
dip. test, 60, 61, 108
dippet. tantrum, 60, 108
dip test, multi, 61
dis CRCord, 12, 13, 62, 65, 66, 127, 128, 148
discrete. recode, 18, 63, 90, 101
discrecproj, 5, 7, 9, 11, 34, 35, 65, 115, 117, 128
dist, 34, 45, 55, 68, 69, 97
distancefactor, 67
distcritmulti, 33, 34, 55, 68, 120, 121
disthclustCBI, 45
disthclustCBI (kmeansCBI), 93
disthclusttreeCBI (kmeansCBI), 93
distnoisemclustCBI, 45
distnoisemclustCBI (kmeansCBI), 93
distrsimilarity, 4, 26, 28, 37, 70, 133, 151
distrtrimkmeansCBI, 45
distrtrimkmeansCBI (kmeansCBI), 93
dridgeline, 71, 140
dudahart2, 4, 72, 98, 99, 120, 121
eigen, 142
eMclust, 136
EmSkew, 95–97
emskewCBI (kmeansCBI), 93
extract. mixturepars, 73, 108
findrep, 74
fixmahal, 43, 45, 46, 75, 87, 90, 91, 95–97, 104–106, 141, 154
fixreg, 16, 17, 25, 81, 82, 90–92, 111, 112, 136, 141
flexmix, 4, 90, 100, 101, 136
flexmixedruns, 88, 100, 101
fpc-package, 4
fpclusters, 90
fpclusters.mfpc (fixmahal), 75
fpclusters.rfpc (fixreg), 82
fpmi (fixmahal), 75
grey, 23
hc, 95
hclust, 47, 94, 96, 97
hclustCBI, 37, 45, 151
hclustCBI (kmeansCBI), 93
hclusttreeCBI, 45
hclusttreeCBI (kmeansCBI), 93
isoMDS, 95
itnumber, 83, 87, 91, 112
jitter, 92, 93
jittervar, 92
kmeans, 5, 43, 96–99
kmeansCBI, 5, 28–30, 36, 37, 39, 42, 43, 45, 93, 118, 119, 129, 131, 151
mergeparameters, 108, 110
minsise, 87, 111
mixdens, 112
mixpredictive, 108, 113
mvcoord, 65, 66, 114, 127, 128
ncoord, 65, 66, 115, 127, 128
neginc, 117
NNclean, 95, 97
noisemclustCBI, 45
noisemclustCBI (kmeansCBI), 93
nselectboot, 22, 118
pam, 5, 22, 43, 68, 95–97, 120, 121
pam.object, 98, 120
pamk, 43, 96, 97, 99, 120
pamkCBI, 45, 118, 129
pamkCBI (kmeansCBI), 93
par, 78, 84, 128
pdfclustCBI (kmeansCBI), 93
pdfCluster, 97
piridge, 122, 140
piridge.zeros, 123, 140
plot.clboot (clusterboot), 39
plot.dbscan (dbscan), 58
plot.mfpc (fixmahal), 75
plot.rfpc (fixreg), 82
plot.valstat, 124, 151
plotcluster, 7, 9, 11, 13, 42, 63, 81, 115, 117, 126
predict.dbscan (dbscan), 58
prediction.strength, 22, 114, 129
print.clboot (clusterboot), 39
print.clusterbenchstats
(clusterbenchstats), 36
print.dbscan (dbscan), 58
print.mfpc (fixmahal), 75
print.predstr (prediction.strength), 129
print.rfpc (fixreg), 82
print.summary.cquality
(cclust.stats), 50
print.summary.mergenorm (mergenormals), 106
print.summary.mfpc (fixmahal), 75
print.summary.rfpc (fixreg), 82
print.table, 125
print.valstat, 4, 36
print.valstat (plot.valstat), 124
print.varwisetables (cluster.varstats), 34
qda, 22
randcmatrix, 131, 135
randconf, 132
randomclustersim, 19, 20, 38, 124, 132
regem (regmix), 134
regmix, 87, 131, 134
rFace, 7, 9, 11, 13, 63, 66, 81, 115, 117, 128, 137
rfpi (fixreg), 82
ridgeline, 138, 140
ridgeline.diagnosis, 107, 108, 139
sammon, 95
sample, 132
scale, 28, 37
silhouette, 27, 32, 34, 53, 55, 69, 150
simmatrix, 141
solve, 142
solvecov, 79, 81, 103–106, 142
specc, 43, 97
speccBCl (kmeansBCl), 93
sseg, 80, 81, 86, 87, 141, 143
stupidkaven, 20, 38, 125, 132–134, 143, 145–147
stupidcentroids, 4, 20, 38, 125, 132–134, 144, 144, 146, 147
stupidkfn, 20, 38, 125, 132–134, 144, 145, 147
stupidknn, 4, 20, 37, 125, 132–134, 144–146, 146
summary.cquality, 26
summary.cquality(cqcluster.stats), 50
summary.mclustBIC, 73, 74, 95, 107, 112, 152
summary.mergenorm(mergenormals), 106
summary.mfpc(fixmahal), 75
summary.rfpc(fixreg), 82
table, 154
tclust, 97
tclustCBI(kmeansCBI), 93
tdecomp, 7, 8, 10, 62, 147
tonedata, 148
trimkmeans, 43, 95–97
trimkmeansCBI, 45
trimkmeansCBI(kmeansCBI), 93
try, 89
unimodal.ind, 149
valstat.object, 20, 38, 39, 126, 149
var, 49
weightplots, 152
wfu, 77, 78, 81, 153
xtable, 154
zmisclassification.matrix, 155