Package 'mclust'

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Title Gaussian Mixture Modelling for Model-Based Clustering, Classification, and Density Estimation

Description Gaussian finite mixture models fitted via EM algorithm for model-based clustering, classification, and density estimation, including Bayesian regularization, dimension reduction for visualisation, and resampling-based inference.

Depends R (>= 3.0)

Imports stats, utils, graphics, grDevices

Suggests knitr (>= 1.12), rmarkdown (>= 0.9), mix (>= 1.0), geometry (>= 0.3-6), MASS

License GPL (>= 2)

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VignetteBuilder knitr

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Author Chris Fraley [aut],
Adrian E. Raftery [aut] (<https://orcid.org/0000-0002-6589-301X>),
Luca Scrucca [aut, cre] (<https://orcid.org/0000-0003-3826-0484>),
Thomas Brendan Murphy [ctb] (<https://orcid.org/0000-0002-5668-7046>),
Michael Fop [ctb] (<https://orcid.org/0000-0003-3936-2757>)

Maintainer Luca Scrucca <luca.scrucca@unipg.it>

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R topics documented:

`mclust-package` *Gaussian Mixture Modelling for Model-Based Clustering, Classification, and Density Estimation*

Description

Finite Gaussian mixture modelling fitted via EM algorithm for model-based clustering, classification, and density estimation, including Bayesian regularization and dimension reduction.

Details

For a quick introduction to **mclust** see the vignette A quick tour of mclust.

Author(s)

Chris Fraley, Adrian Raftery and Luca Scrucca.

Maintainer: Luca Scrucca <luca.scrucca@unipg.it>

References

Scrucca L., Fop M., Murphy T. B. and Raftery A. E. (2016) mclust 5: clustering, classification and density estimation using Gaussian finite mixture models, *The R Journal*, 8/1, pp. 205-233.

Fraley C. and Raftery A. E. (2002) Model-based clustering, discriminant analysis and density estimation, *Journal of the American Statistical Association*, 97/458, pp. 611-631.

Fraley C., Raftery A. E., Murphy T. B. and Scrucca L. (2012) mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. *Technical Report* No. 597, Department of Statistics, University of Washington.

Examples

```
# Clustering
mod1 <- Mclust(iris[,1:4])
summary(mod1)
plot(mod1,  what = c("BIC", "classification"))

# Classification
data(banknote)
mod2 <- MclustDA(banknote[,2:7], banknote$Status)
summary(mod2)
plot(mod2)

# Density estimation
mod3 <- densityMclust(faithful$waiting)
summary(mod3)
plot(mod3, faithful$waiting)
```

`acidity` *Acidity data*

Description

Acidity index measured in a sample of 155 lakes in the Northeastern United States. The data are on the log scale, as analysed by Crawford et al. (1992, 1994). The data were also used to fit mixture of gaussian distributions by Richardson and Green (1997), and by McLachlan and Peel (2000, Sec. 6.6.2).

Usage

```
data(acidity)
```

Source

http://www.stats.bris.ac.uk/~peter/mixdata

References

Crawford, S. L. (1994) An application of the Laplace method to finite mixture distribution. *Journal of the American Statistical Association*, 89, 259–267.

Crawford, S. L., DeGroot, M. H., Kadane, J. B., and Small, M. J. (1994) Modeling lake chemistry distributions: Approximate Bayesian methods for estimating a finite mixture model. *Technometrics*, 34, 441–453.

McLachlan, G. and Peel, D. (2000) *Finite Mixture Models*. Wiley, New York.

Richardson, S. and Green, P. J. (1997) On Bayesian analysis of mixtures with unknown number of components (with discussion). *Journal of the Royal Statistical Society, Series B*, 59, 731–792.

`adjustedRandIndex` *Adjusted Rand Index*

Description

Computes the adjusted Rand index comparing two classifications.

Usage

```
adjustedRandIndex(x, y)
```

Arguments

`x`	A numeric or character vector of class labels.
`y`	A numeric or character vector of class labels. The length of `y` should be the same as that of `x`.

Value

The adjusted Rand index comparing the two partitions (a scalar). This index has zero expected value in the case of random partition, and it is bounded above by 1 in the case of perfect agreement between two partitions.

References

L. Hubert and P. Arabie (1985) Comparing Partitions, *Journal of the Classification*, 2, pp. 193-218.

See Also

`classError`, `mapClass`, `table`

Examples

```
a <- rep(1:3, 3)
a
b <- rep(c("A", "B", "C"), 3)
b
adjustedRandIndex(a, b)

a <- sample(1:3, 9, replace = TRUE)
a
b <- sample(c("A", "B", "C"), 9, replace = TRUE)
b
adjustedRandIndex(a, b)

a <- rep(1:3, 4)
a
b <- rep(c("A", "B", "C", "D"), 3)
b
```

```
adjustedRandIndex(a, b)

irisHCvvv <- hc(modelName = "VVV", data = iris[,-5])
cl3 <- hclass(irisHCvvv, 3)
adjustedRandIndex(cl3,iris[,5])

irisBIC <- mclustBIC(iris[,-5])
adjustedRandIndex(summary(irisBIC,iris[,-5])$classification,iris[,5])
adjustedRandIndex(summary(irisBIC,iris[,-5],G=3)$classification,iris[,5])
```

---

banknote *Swiss banknotes data*

Description

The data set contains six measurements made on 100 genuine and 100 counterfeit old-Swiss 1000-franc bank notes.

Usage

```
data(banknote)
```

Format

A data frame with the following variables:

Status the status of the banknote: `genuine` or `counterfeit`

Length Length of bill (mm)

Left Width of left edge (mm)

Right Width of right edge (mm)

Bottom Bottom margin width (mm)

Top Top margin width (mm)

Diagonal Length of diagonal (mm)

Source

Flury, B. and Riedwyl, H. (1988). *Multivariate Statistics: A practical approach.* London: Chapman & Hall, Tables 1.1 and 1.2, pp. 5-8.

`Baudry_etal_2010_JCGS_examples` *Simulated Example Datasets From Baudry et al. (2010)*

Description

Simulated datasets used in Baudry et al. (2010) to illustrate the proposed mixture components combining method for clustering.

Please see the cited article for a detailed presentation of these datasets. The data frame with name exN.M is presented in Section N.M in the paper.

Test1D (not in the article) has been simulated from a Gaussian mixture distribution in R.

ex4.1 and ex4.2 have been simulated from a Gaussian mixture distribution in R^2.

ex4.3 has been simulated from a mixture of a uniform distribution on a square and a spherical Gaussian distribution in R^2.

ex4.4.1 has been simulated from a Gaussian mixture model in R^2

ex4.4.2 has been simulated from a mixture of two uniform distributions in R^3.

Usage

```
data(Baudry_etal_2010_JCGS_examples)
```

Format

`ex4.1` is a data frame with 600 observations on 2 real variables.

`ex4.2` is a data frame with 600 observations on 2 real variables.

`ex4.3` is a data frame with 200 observations on 2 real variables.

`ex4.4.1` is a data frame with 800 observations on 2 real variables.

`ex4.4.2` is a data frame with 300 observations on 3 real variables.

`Test1D` is a data frame with 200 observations on 1 real variable.

References

J.-P. Baudry, A. E. Raftery, G. Celeux, K. Lo and R. Gottardo (2010). Combining mixture components for clustering. *Journal of Computational and Graphical Statistics, 19(2):332-353.*

Examples

```
## Not run:
data(Baudry_etal_2010_JCGS_examples)

output <- clustCombi(data = ex4.4.1)
output # is of class clustCombi

# plots the hierarchy of combined solutions, then some "entropy plots" which
```

```
# may help one to select the number of classes
plot(output)

## End(Not run)
```

---

bic *BIC for Parameterized Gaussian Mixture Models*

Description

Computes the BIC (Bayesian Information Criterion) for parameterized mixture models given the loglikelihood, the dimension of the data, and number of mixture components in the model.

Usage

```
bic(modelName, loglik, n, d, G, noise=FALSE, equalPro=FALSE, ...)
```

Arguments

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.
loglik	The log-likelihood for a data set with respect to the Gaussian mixture model specified in the modelName argument.
n	The number of observations in the data used to compute loglik.
d	The dimension of the data used to compute loglik.
G	The number of components in the Gaussian mixture model used to compute loglik.
noise	A logical variable indicating whether or not the model includes an optional Poisson noise component. The default is to assume no noise component.
equalPro	A logical variable indicating whether or not the components in the model are assumed to be present in equal proportion. The default is to assume unequal mixing proportions.
...	Catches unused arguments in an indirect or list call via do.call.

Value

The BIC or Bayesian Information Criterion for the given input arguments.

See Also

mclustBIC, nVarParams, mclustModelNames.

Examples

```
## Not run:
n <- nrow(iris)
d <- ncol(iris)-1
G <- 3

emEst <- me(modelName="VVI", data=iris[,-5], unmap(iris[,5]))
names(emEst)

args(bic)
bic(modelName="VVI", loglik=emEst$loglik, n=n, d=d, G=G)
# do.call("bic", emEst)    ## alternative call

## End(Not run)
```

`BrierScore` *Brier score to assess the accuracy of probabilistic predictions*

Description

The Brier score is a proper score function that measures the accuracy of probabilistic predictions.

Usage

```
BrierScore(z, class)
```

Arguments

`z`	a matrix containing the predicted probabilities of each observation to be classified in one of the classes. Thus, the number of rows must match the length of `class`, and the number of columns the number of known classes.
`class`	a numeric, character vector or factor containing the known class labels for each observation. If `class` is a factor, the number of classes is `nlevels(class)` with classes `levels(class)`. If `class` is a numeric or character vector, the number of classes is equal to the number of classes obtained via `unique(class)`.

Details

The Brier Score is the mean square difference between the true classes and the predicted probabilities.

This function implements the original multi-class definition by Brier (1950), normalized to $[0, 1]$ as in Kruppa et al (2014). The formula is the following:

$$BS = \frac{1}{2n} \sum_{i=1}^{n} \sum_{k=1}^{K} (C_{ik} - p_{ik})^2$$

where n is the number of observations, K the number of classes, $C_{ik} = \{0, 1\}$ the indicator of class k for observation i, and p_{ik} is the predicted probability of observation i to belong to class k.

The above formulation is applicable to multi-class predictions, including the binary case. A small value of the Brier Score indicates high prediction accuracy.

The Brier Score is a strictly proper score (Gneiting and Raftery, 2007), which means that it takes its minimal value only when the predicted probabilities match the empirical probabilities.

References

Brier, G.W. (1950) Verification of forecasts expressed in terms of probability. *Monthly Weather Review*, 78 (1): 1-3.

Gneiting, G. and Raftery, A. E. (2007) Strictly proper scoring rules, prediction, and estimation. *Journal of the American Statistical Association* 102 (477): 359-378.

Kruppa, J., Liu, Y., Diener, H.-C., Holste, T., Weimar, C., Koonig, I. R., and Ziegler, A. (2014) Probability estimation with machine learning methods for dichotomous and multicategory outcome: Applications. *Biometrical Journal*, 56 (4): 564-583.

See Also

cvMclustDA

Examples

```
# multi-class case
class <- factor(c(5,5,5,2,5,3,1,2,1,1), levels = 1:5)
probs <- matrix(c(0.15, 0.01, 0.08, 0.23, 0.01, 0.23, 0.59, 0.02, 0.38, 0.45,
                  0.36, 0.05, 0.30, 0.46, 0.15, 0.13, 0.06, 0.19, 0.27, 0.17,
                  0.40, 0.34, 0.18, 0.04, 0.47, 0.34, 0.32, 0.01, 0.03, 0.11,
                  0.04, 0.04, 0.09, 0.05, 0.28, 0.27, 0.02, 0.03, 0.12, 0.25,
                  0.05, 0.56, 0.35, 0.22, 0.09, 0.03, 0.01, 0.75, 0.20, 0.02),
                nrow = 10, ncol = 5)
cbind(class, probs, map = map(probs))
BrierScore(probs, class)

# two-class case
class <- factor(c(1,1,1,2,2,1,1,2,1,1), levels = 1:2)
probs <- matrix(c(0.91, 0.4, 0.56, 0.27, 0.37, 0.7, 0.97, 0.22, 0.68, 0.43,
                  0.09, 0.6, 0.44, 0.73, 0.63, 0.3, 0.03, 0.78, 0.32, 0.57),
                nrow = 10, ncol = 2)
cbind(class, probs, map = map(probs))
BrierScore(probs, class)

# two-class case when predicted probabilities are constrained to be equal to
# 0 or 1, then the (normalized) Brier Score is equal to the classification
# error rate
probs <- ifelse(probs > 0.5, 1, 0)
cbind(class, probs, map = map(probs))
BrierScore(probs, class)
classError(map(probs), class)$errorRate

# plot Brier score for predicted probabilities in range [0,1]
class <- factor(rep(1, each = 100), levels = 0:1)
prob  <- seq(0, 1, by = 0.01)
```

```
brier <- sapply(prob, function(p)
  { z <- matrix(c(1-p,p), nrow = length(class), ncol = 2, byrow = TRUE)
    BrierScore(z, class)
  })
plot(prob, brier, type = "l", main = "Scoring all one class",
     xlab = "Predicted probability", ylab = "Brier score")

# brier score for predicting balanced data with constant prob
class <- factor(rep(c(1,0), each = 50), levels = 0:1)
prob  <- seq(0, 1, by = 0.01)
brier <- sapply(prob, function(p)
  { z <- matrix(c(1-p,p), nrow = length(class), ncol = 2, byrow = TRUE)
    BrierScore(z, class)
  })
plot(prob, brier, type = "l", main = "Scoring balanced classes",
     xlab = "Predicted probability", ylab = "Brier score")

# brier score for predicting unbalanced data with constant prob
class <- factor(rep(c(0,1), times = c(90,10)), levels = 0:1)
prob  <- seq(0, 1, by = 0.01)
brier <- sapply(prob, function(p)
  { z <- matrix(c(1-p,p), nrow = length(class), ncol = 2, byrow = TRUE)
    BrierScore(z, class)
  })
plot(prob, brier, type = "l", main = "Scoring unbalanced classes",
     xlab = "Predicted probability", ylab = "Brier score")
```

---

cdens *Component Density for Parameterized MVN Mixture Models*

Description

Computes component densities for observations in MVN mixture models parameterized by eigenvalue decomposition.

Usage

```
cdens(modelName, data, logarithm = FALSE, parameters, warn = NULL, ...)
```

Arguments

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.
data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
logarithm	A logical value indicating whether or not the logarithm of the component densities should be returned. The default is to return the component densities, obtained from the log component densities by exponentiation.

`parameters` The parameters of the model:

`mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model.

`variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.

`warn` A logical value indicating whether or not a warning should be issued when computations fail. The default is `warn=FALSE`.

`...` Catches unused arguments in indirect or list calls via `do.call`.

Value

A numeric matrix whose `[i,k]`th entry is the density or log density of observation *i* in component *k*. The densities are not scaled by mixing proportions.

Note

When one or more component densities are very large in magnitude, it may be possible to compute the logarithm of the component densities but not the component densities themselves due to overflow.

See Also

`cdensE`, ..., `cdensVVV`, `dens`, `estep`, `mclustModelNames`, `mclustVariance`, `mclust.options`, `do.call`

Examples

```
z2 <- unmap(hclass(hcVVV(faithful),2)) # initial value for 2 class case

model <- me(modelName = "EEE", data = faithful, z = z2)
cdens(modelName = "EEE", data = faithful, logarithm = TRUE,
      parameters = model$parameters)[1:5,]

data(cross)
odd <- seq(1, nrow(cross), by = 2)
oddBIC <- mclustBIC(cross[odd,-1])
oddModel <- mclustModel(cross[odd,-1], oddBIC) ## best parameter estimates
names(oddModel)

even <- odd + 1
densities <- cdens(modelName = oddModel$modelName, data = cross[even,-1],
                   parameters = oddModel$parameters)
cbind(class = cross[even,1], densities)[1:5,]
```

cdensE *Component Density for a Parameterized MVN Mixture Model*

Description

Computes component densities for points in a parameterized MVN mixture model.

Usage

```
cdensE(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensV(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensX(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensEII(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensVII(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensEEI(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensVEI(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensEVI(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensVVI(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensEEE(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensEEV(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensVEV(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensVVV(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensEVE(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensEVV(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensVEE(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensVVE(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensXII(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensXXI(data, logarithm = FALSE, parameters, warn = NULL, ...)
cdensXXX(data, logarithm = FALSE, parameters, warn = NULL, ...)
```

Arguments

`data`	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
`logarithm`	A logical value indicating whether or not the logarithm of the component densities should be returned. The default is to return the component densities, obtained from the log component densities by exponentiation.
`parameters`	The parameters of the model:
	`mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model.
	`variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.

pro	Mixing proportions for the components of the mixture. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components.
warn	A logical value indicating whether or not a warning should be issued when computations fail. The default is warn=FALSE.
...	Catches unused arguments in indirect or list calls via do.call.

Value

A numeric matrix whose [i,j]th entry is the density of observation *i* in component *j*. The densities are not scaled by mixing proportions.

Note

When one or more component densities are very large in magnitude, then it may be possible to compute the logarithm of the component densities but not the component densities themselves due to overflow.

See Also

cdens, dens, mclustVariance, mstep, mclust.options, do.call.

Examples

```
## Not run:
z2 <- unmap(hclass(hcVVV(faithful),2)) # initial value for 2 class case

model <- meVVV(data=faithful, z=z2)
cdensVVV(data=faithful, logarithm = TRUE, parameters = model$parameters)

data(cross)
z2 <- unmap(cross[,1])

model <- meEEV(data = cross[,-1], z = z2)

EEVdensities <- cdensEEV( data = cross[,-1], parameters = model$parameters)

cbind(cross[,-1],map(EEVdensities))
## End(Not run)
```

---

cdfMclust *Cumulative Distribution and Quantiles for a univariate Gaussian mixture distribution*

Description

Compute the cumulative density function (cdf) or quantiles from an estimated one-dimensional Gaussian mixture fitted using densityMclust.

Usage

```
cdfMclust(object, data, ngrid = 100, ...)
quantileMclust(object, p, ...)
```

Arguments

object	a densityMclust model object.
data	a numeric vector of evaluation points.
ngrid	the number of points in a regular grid to be used as evaluation points if no data are provided.
p	a numeric vector of probabilities.
...	further arguments passed to or from other methods.

Details

The cdf is evaluated at points given by the optional argument data. If not provided, a regular grid of length ngrid for the evaluation points is used.

The quantiles are computed using interpolating splines on an adaptive finer grid.

Value

cdfMclust returns a list of x and y values providing, respectively, the evaluation points and the estimated cdf.

quantileMclust returns a vector of quantiles.

Author(s)

Luca Scrucca

See Also

densityMclust, plot.densityMclust.

Examples

```
x <- c(rnorm(100), rnorm(100, 3, 2))
dens <- densityMclust(x)
summary(dens, parameters = TRUE)
cdf <- cdfMclust(dens)
str(cdf)
q <- quantileMclust(dens, p = c(0.01, 0.1, 0.5, 0.9, 0.99))
cbind(quantile = q, cdf = cdfMclust(dens, q)$y)
plot(cdf, type = "l", xlab = "x", ylab = "CDF")
points(q, cdfMclust(dens, q)$y, pch = 20, col = "red3")

par(mfrow = c(2,2))
dens.waiting <- densityMclust(faithful$waiting)
plot(dens.waiting)
```

```
plot(cdfMclust(dens.waiting), type = "l",
     xlab = dens.waiting$varname, ylab = "CDF")
dens.eruptions <- densityMclust(faithful$eruptions)
plot(dens.eruptions)
plot(cdfMclust(dens.eruptions), type = "l",
     xlab = dens.eruptions$varname, ylab = "CDF")
par(mfrow = c(1,1))
```

---

chevron *Simulated minefield data*

Description

A set of simulated bivariate minefield data (1104 observations).

Usage

```
data(chevron)
```

References

A. Dasgupta and A. E. Raftery (1998). Detecting features in spatial point processes with clutter via model-based clustering. *Journal of the American Statistical Association 93:294-302*.

C. Fraley and A.E. Raftery (1998). *Computer Journal 41:578-588*.

G. J. McLachlan and D. Peel (2000). *Finite Mixture Models*, Wiley, pages 110-112.

---

classError *Classification error*

Description

Computes the errore rate of a given classification relative to the known classes, and the location of misclassified data points.

Usage

```
classError(classification, class)
```

Arguments

`classification`	A numeric, character vector or factor specifying the predicted class labels. Must have the same length as `class`.
`class`	A numeric, character vector or factor of known true class labels. Must have the same length as `classification`.

Details

If more than one mapping between predicted classification and the known truth corresponds to the minimum number of classification errors, only one possible set of misclassified observations is returned.

Value

A list with the following two components:

`misclassified`	The indexes of the misclassified data points in a minimum error mapping between the predicted classification and the known true classes.
`errorRate`	The error rate corresponding to a minimum error mapping between the predicted classification and the known true classes.

See Also

`map` `mapClass`, `table`

Examples

```
(a <- rep(1:3, 3))
(b <- rep(c("A", "B", "C"), 3))
classError(a, b)

(a <- sample(1:3, 9, replace = TRUE))
(b <- sample(c("A", "B", "C"), 9, replace = TRUE))
classError(a, b)

class <- factor(c(5,5,5,2,5,3,1,2,1,1), levels = 1:5)
probs <- matrix(c(0.15, 0.01, 0.08, 0.23, 0.01, 0.23, 0.59, 0.02, 0.38, 0.45,
                  0.36, 0.05, 0.30, 0.46, 0.15, 0.13, 0.06, 0.19, 0.27, 0.17,
                  0.40, 0.34, 0.18, 0.04, 0.47, 0.34, 0.32, 0.01, 0.03, 0.11,
                  0.04, 0.04, 0.09, 0.05, 0.28, 0.27, 0.02, 0.03, 0.12, 0.25,
                  0.05, 0.56, 0.35, 0.22, 0.09, 0.03, 0.01, 0.75, 0.20, 0.02),
                nrow = 10, ncol = 5)
cbind(class, probs, map = map(probs))
classError(map(probs), class)
```

---

classPriorProbs *Estimation of class prior probabilities by EM algorithm*

Description

A simple procedure to improve the estimation of class prior probabilities when the training data does not reflect the true a priori probabilities of the target classes. The EM algorithm used is described in Saerens et al (2002).

Usage

```
classPriorProbs(object, newdata = object$data,
                itmax = 1e3, eps = sqrt(.Machine$double.eps))
```

Arguments

object	an object of class 'MclustDA' resulting from a call to MclustDA.
newdata	a data frame or matrix giving the data. If missing the train data obtained from the call to MclustDA are used.
itmax	an integer value specifying the maximal number of EM iterations.
eps	a scalar specifying the tolerance associated with deciding when to terminate the EM iterations.

Details

The estimation procedure employes an EM algorithm as described in Saerens et al (2002).

Value

A vector of class prior estimates which can then be used in the predict.MclustDA to improve predictions.

References

Saerens, M., Latinne, P. and Decaestecker, C. (2002) Adjusting the outputs of a classifier to new a priori probabilities: a simple procedure, *Neural computation*, 14 (1), 21–41.

See Also

MclustDA, predict.MclustDA

Examples

```
## Not run:
# generate data from a mixture f(x) = 0.9 * N(0,1) + 0.1 * N(3,1)
n <- 10000
mixpro <- c(0.9, 0.1)
class <- factor(sample(0:1, size = n, prob = mixpro, replace = TRUE))
x <- ifelse(class == 1, rnorm(n, mean = 3, sd = 1),
                        rnorm(n, mean = 0, sd = 1))

hist(x[class==0], breaks = 11, xlim = range(x), main = "", xlab = "x",
     col = adjustcolor("dodgerblue2", alpha.f = 0.5), border = "white")
hist(x[class==1], breaks = 11, add = TRUE,
     col = adjustcolor("red3", alpha.f = 0.5), border = "white")
box()

# generate training data from a balanced case-control sample, i.e.
# f(x) = 0.5 * N(0,1) + 0.5 * N(3,1)
n_train <- 1000
```

```
class_train <- factor(sample(0:1, size = n_train, prob = c(0.5, 0.5), replace = TRUE))
x_train <- ifelse(class_train == 1, rnorm(n_train, mean = 3, sd = 1),
                                    rnorm(n_train, mean = 0, sd = 1))

hist(x_train[class_train==0], breaks = 11, xlim = range(x_train),
     main = "", xlab = "x",
     col = adjustcolor("dodgerblue2", alpha.f = 0.5), border = "white")
hist(x_train[class_train==1], breaks = 11, add = TRUE,
     col = adjustcolor("red3", alpha.f = 0.5), border = "white")
box()

# fit a MclustDA model
mod <- MclustDA(x_train, class_train)
summary(mod, parameters = TRUE)

# test set performance
pred <- predict(mod, newdata = x)
classError(pred$classification, class)$error
BrierScore(pred$z, class)

# compute performance over a grid of prior probs
priorProp <- seq(0.01, 0.99, by = 0.01)
CE <- BS <- rep(as.double(NA), length(priorProp))
for(i in seq(priorProp))
{
  pred <- predict(mod, newdata = x, prop = c(1-priorProp[i], priorProp[i]))
  CE[i] <- classError(pred$classification, class = class)$error
  BS[i] <- BrierScore(pred$z, class)
}

# estimate the optimal class prior probs
(priorProbs <- classPriorProbs(mod, x))
pred <- predict(mod, newdata = x, prop = priorProbs)
# compute performance at the estimated class prior probs
classError(pred$classification, class = class)$error
BrierScore(pred$z, class)

matplot(priorProp, cbind(CE,BS), type = "l", lty = 1, lwd = 2,
        xlab = "Class prior probability", ylab = "", ylim = c(0,max(CE,BS)),
        panel.first =
          { abline(h = seq(0,1,by=0.05), col = "grey", lty = 3)
            abline(v = seq(0,1,by=0.05), col = "grey", lty = 3)
          })
abline(v = mod$prop[2], lty = 2)              # training prop
abline(v = mean(class==1), lty = 4)           # test prop (usually unknown)
abline(v = priorProbs[2], lty = 3, lwd = 2)      # estimated prior probs
legend("topleft", legend = c("ClassError", "BrierScore"),
       col = 1:2, lty = 1, lwd = 2, inset = 0.02)

# Summary of results:
priorProp[which.min(CE)] # best prior of class 1 according to classification error
priorProp[which.min(BS)] # best prior of class 1 according to Brier score
priorProbs               # optimal estimated class prior probabilities
```

```
## End(Not run)
```

---

clPairs *Pairwise Scatter Plots showing Classification*

Description

Creates a scatter plot for each pair of variables in given data. Observations in different classes are represented by different colors and symbols.

Usage

```
clPairs(data, classification, symbols, colors,
        labels = dimnames(data)[[2]], cex.labels = 1.5,
        gap = 0.2, ...)

clPairsLegend(x, y, class, col, pch, box = TRUE, ...)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
classification	A numeric or character vector representing a classification of observations (rows) of data.
symbols	Either an integer or character vector assigning a plotting symbol to each unique class in classification. Elements in symbols correspond to classes in order of appearance in the sequence of observations (the order used by the function unique). The default is given by mclust.options("classPlotSymbols").
colors	Either an integer or character vector assigning a color to each unique class in classification. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function unique). The default is given by mclust.options("classPlotColors").
labels	A vector of character strings for labelling the variables. The default is to use the column dimension names of data.
cex.labels	An argument specifying the size of the text labels.
gap	An argument specifying the distance between subplots (see pairs).
x,y	The x and y co-ordinates with respect to a graphic device having plotting region coordinates par("usr" = c(0,1,0,1)).
class	The class labels.
box	A logical, if TRUE then a box is drawn around the current plot figure.
col, pch	The colors and plotting symbols appearing in the legend.
...	For a clPairs call may be additional arguments to be passed to pairs. For a clPairsLegend call may be additional arguments to be passed to legend.

Details

The function `clPairs()` draws scatter plots on the current graphics device for each combination of variables in `data`. Observations of different classifications are labeled with different symbols.

The function `clPairsLegend()` can be used to add a legend. See examples below.

Value

The function `clPairs()` invisibly returns a list with the following components:

`class`	A character vector of class labels.
`col`	A vector of colors used for each class.
`pch`	A vector of plotting symbols used for each class.

See Also

`pairs`, `coordProj`, `mclust.options`

Examples

```
clPairs(iris[,1:4], cl = iris$Species)

clp <- clPairs(iris[,1:4], cl = iris$Species, lower.panel = NULL)
clPairsLegend(0.1, 0.4, class = clp$class,
              col = clp$col, pch = clp$pch,
              title = "Iris data")
```

---

clustCombi *Combining Gaussian Mixture Components for Clustering*

Description

Provides a hierarchy of combined clusterings from the EM/BIC Gaussian mixture solution to one class, following the methodology proposed in the article cited in the references.

Usage

```
clustCombi(object = NULL, data = NULL, ...)
```

Arguments

`object`	An object returned by `Mclust` giving the optimal (according to BIC) parameters, conditional probabilities, and log-likelihood, together with the associated classification and its uncertainty. If not provided, the `data` argument must be specified.

`data` A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables. If the `object` argument is not provided, the function `Mclust` is applied to the given `data` to fit a mixture model.

`...` Optional arguments to be passed to called functions. Notably, any argument (such as the numbers of components for which the BIC is computed; the models to be fitted by EM; initialization parameters for the EM algorithm, ...) to be passed to `Mclust` in case `object = NULL`. Please see the `Mclust` documentation for more details.

Details

Mclust provides a Gaussian mixture fitted to the data by maximum likelihood through the EM algorithm, for the model and number of components selected according to BIC. The corresponding components are hierarchically combined according to an entropy criterion, following the methodology described in the article cited in the references section. The solutions with numbers of classes between the one selected by BIC and one are returned as a `clustCombi` class object.

Value

A list of class `clustCombi` giving the hierarchy of combined solutions from the number of components selected by BIC to one. The details of the output components are as follows:

`classification` A list of the data classifications obtained for each combined solution of the hierarchy through a MAP assignment

`combiM` A list of matrices. `combiM[[K]]` is the matrix used to combine the components of the (K+1)-classes solution to get the K-classes solution. Please see the examples.

`combiz` A list of matrices. `combiz[[K]]` is a matrix whose [i,k]th entry is the probability that observation i in the data belongs to the kth class according to the K-classes combined solution.

`MclustOutput` A list of class `Mclust`. Output of a call to the Mclust function (as provided by the user or the result of a call to the Mclust function) used to initiate the combined solutions hierarchy: please see the `Mclust` function documentation for details.

Author(s)

J.-P. Baudry, A. E. Raftery, L. Scrucca

References

J.-P. Baudry, A. E. Raftery, G. Celeux, K. Lo and R. Gottardo (2010). Combining mixture components for clustering. *Journal of Computational and Graphical Statistics, 19(2):332-353.*

See Also

`plot.clustCombi`

Examples

```
data(Baudry_etal_2010_JCGS_examples)

# run Mclust using provided data
output <- clustCombi(data = ex4.1)
## Not run:
# or run Mclust and then clustcombi on the returned object
mod <- Mclust(ex4.1)
output <- clustCombi(mod)

## End(Not run)

output
summary(output)

## Not run:
# run Mclust using provided data and any further optional argument provided
output <- clustCombi(data = ex4.1, modelName = "EEV", G = 1:15)

## End(Not run)

# plot the hierarchy of combined solutions
plot(output, what = "classification")
# plot some "entropy plots" which may help one to select the number of classes
plot(output, what = "entropy")
# plot the tree structure obtained from combining mixture components
plot(output, what = "tree")

# the selected model and number of components obtained from Mclust using BIC
output$MclustOutput

# the matrix whose [i,k]th entry is the probability that i-th observation in
# the data belongs to the k-th class according to the BIC solution
head( output$combiz[[output$MclustOutput$G]] )
# the matrix whose [i,k]th entry is the probability that i-th observation in
# the data belongs to the k-th class according to the first combined solution
head( output$combiz[[output$MclustOutput$G-1]] )
# the matrix describing how to merge the 6-classes solution to get the
# 5-classes solution
output$combiM[[5]]
# for example the following code returns the label of the class (in the
# 5-classes combined solution) to which the 4th class (in the 6-classes
# solution) is assigned. Only two classes in the (K+1)-classes solution
# are assigned the same class in the K-classes solution: the two which
# are merged at this step...
output$combiM[[5]]
# recover the 5-classes soft clustering from the 6-classes soft clustering
# and the 6 -> 5 combining matrix
all( output$combiz[[5]] == t( output$combiM[[5]] %*% t(output$combiz[[6]]) ) )
# the hard clustering under the 5-classes solution
head( output$classification[[5]] )
```

`clustCombiOptim` *Optimal number of clusters obtained by combining mixture components*

Description

Return the optimal number of clusters by combining mixture components based on the entropy method discussed in the reference given below.

Usage

```
clustCombiOptim(object, reg = 2, plot = FALSE, ...)
```

Arguments

`object`	An object of class `'clustCombi'` resulting from a call to `clustCombi`.
`reg`	The number of parts of the piecewise linear regression for the entropy plots. Choose 2 for a two-segment piecewise linear regression model (i.e. 1 change-point), and 3 for a three-segment piecewise linear regression model (i.e. 3 change-points).
`plot`	Logical, if `TRUE` an entropy plot is also produced.
`...`	Further arguments passed to or from other methods.

Value

The function returns a list with the following components:

`numClusters.combi`	The estimated number of clusters.
`z.combi`	A matrix whose *[i,k]*th entry is the probability that observation *i* in the data belongs to the *k*th cluster.
`cluster.combi`	The clustering labels.

Author(s)

J.-P. Baudry, A. E. Raftery, L. Scrucca

References

J.-P. Baudry, A. E. Raftery, G. Celeux, K. Lo and R. Gottardo (2010). Combining mixture components for clustering. *Journal of Computational and Graphical Statistics, 19(2):332-353.*

See Also

`combiPlot`, `entPlot`, `clustCombi`

Examples

```
data(Baudry_etal_2010_JCGS_examples)
output <- clustCombi(data = ex4.1)
combiOptim <- clustCombiOptim(output)
str(combiOptim)

# plot optimal clustering with alpha color transparency proportional to uncertainty
zmax <- apply(combiOptim$z.combi, 1, max)
col <- mclust.options("classPlotColors")[combiOptim$cluster.combi]
vadjustcolor <- Vectorize(adjustcolor)
alphacol = (zmax - 1/combiOptim$numClusters.combi)/(1-1/combiOptim$numClusters.combi)
col <- vadjustcolor(col, alpha.f = alphacol)
plot(ex4.1, col = col, pch = mclust.options("classPlotSymbols")[combiOptim$cluster.combi])
```

`combiPlot` *Plot Classifications Corresponding to Successive Combined Solutions*

Description

Plot classifications corresponding to successive combined solutions.

Usage

```
combiPlot(data, z, combiM, ...)
```

Arguments

`data`	The data.
`z`	A matrix whose [i,k]th entry is the probability that observation i in the data belongs to the kth class, for the initial solution (ie before any combining). Typically, the one returned by `Mclust`/BIC.
`combiM`	A "combining matrix" (as provided by `clustCombi`), ie a matrix whose kth row contains only zeros, but in columns corresponding to the labels of the classes in the initial solution to be merged together to get the combined solution.
`...`	Other arguments to be passed to the `Mclust` plot functions.

Value

Plot the classifications obtained by MAP from the matrix `t(combiM %*% t(z))`, which is the matrix whose [i,k]th entry is the probability that observation i in the data belongs to the kth class, according to the combined solution obtained by merging (according to `combiM`) the initial solution described by `z`.

Author(s)

J.-P. Baudry, A. E. Raftery, L. Scrucca

References

J.-P. Baudry, A. E. Raftery, G. Celeux, K. Lo and R. Gottardo (2010). Combining mixture components for clustering. *Journal of Computational and Graphical Statistics, 19(2):332-353.*

See Also

clustCombi, combMat, clustCombi

Examples

```
## Not run:
data(Baudry_etal_2010_JCGS_examples)
MclustOutput <- Mclust(ex4.1)

MclustOutput$G # Mclust/BIC selected 6 classes

par(mfrow=c(2,2))

combiM0 <- diag(6) # is the identity matrix
# no merging: plot the initial solution, given by z
combiPlot(ex4.1, MclustOutput$z, combiM0, cex = 3)
title("No combining")

combiM1 <- combMat(6, 1, 2) # let's merge classes labeled 1 and 2
combiM1
combiPlot(ex4.1, MclustOutput$z, combiM1)
title("Combine 1 and 2")

# let's merge classes labeled 1 and 2, and then components labeled (in this
# new 5-classes combined solution...) 1 and 2
combiM2 <- combMat(5, 1, 2) %*% combMat(6, 1, 2)
combiM2
combiPlot(ex4.1, MclustOutput$z, combiM2)
title("Combine 1, 2 and then 1 and 2 again")

plot(0,0,type="n", xlab = "", ylab = "", axes = FALSE)
legend("center", legend = 1:6,
       col = mclust.options("classPlotColors"),
       pch = mclust.options("classPlotSymbols"),
       title = "Class labels:")
## End(Not run)
```

---

combiTree *Tree structure obtained from combining mixture components*

Description

The method implemented in clustCombi can be used for combining Gaussian mixture components for clustering. This provides a hierarchical structure which can be graphically represented as a tree.

Usage

```
combiTree(object, type = c("triangle", "rectangle"),
                  yaxis = c("entropy", "step"),
                  edgePar = list(col = "darkgray", lwd = 2),
                  ...)
```

Arguments

object	An object of class 'clustCombi' resulting from a call to clustCombi.
type	A string specifying the dendrogram's type. Possible values are "triangle" (default), and "rectangle".
yaxis	A string specifying the quantity used to draw the vertical axis. Possible values are "entropy" (default), and "step".
edgePar	A list of plotting parameters. See dendrogram.
...	Further arguments passed to or from other methods.

Value

The function always draw a tree and invisibly returns an object of class 'dendrogram' for fine tuning.

Author(s)

L. Scrucca

See Also

clustCombi

Examples

```
## Not run:
data(Baudry_etal_2010_JCGS_examples)
output <- clustCombi(data = ex4.1)
combiTree(output)
combiTree(output, type = "rectangle")
combiTree(output, yaxis = "step")
combiTree(output, type = "rectangle", yaxis = "step")

## End(Not run)
```

combMat *Combining Matrix*

Description

Create a combining matrix

Usage

```
combMat(K, l1, l2)
```

Arguments

K	The original number of classes: the matrix will define a combining from K to (K-1) classes.
l1	Label of one of the two classes to be combined.
l2	Label of the other class to be combined.

Value

If z is a vector (length *K*) whose *k*th entry is the probability that an observation belongs to the *k*th class in a *K*-classes classification, then combiM %*% z is the vector (length *K-1*) whose *k*th entry is the probability that the observation belongs to the *k*th class in the *K-1*-classes classification obtained by merging classes l1 and l2 in the initial classification.

Author(s)

J.-P. Baudry, A. E. Raftery, L. Scrucca

See Also

clustCombi, combiPlot

coordProj *Coordinate projections of multidimensional data modeled by an MVN mixture.*

Description

Plots coordinate projections given multidimensional data and parameters of an MVN mixture model for the data.

Usage

```
coordProj(data, dimens = c(1,2), parameters = NULL, z = NULL,
          classification = NULL, truth = NULL, uncertainty = NULL,
          what = c("classification", "error", "uncertainty"),
          addEllipses = TRUE, fillEllipses = mclust.options("fillEllipses"),
          symbols = NULL, colors = NULL, scale = FALSE,
          xlim = NULL, ylim = NULL, CEX = 1, PCH = ".", main = FALSE, ...)
```

Arguments

`data`	A numeric matrix or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
`dimens`	A vector of length 2 giving the integer dimensions of the desired coordinate projections. The default is `c(1,2)`, in which the first dimension is plotted against the second.
`parameters`	A named list giving the parameters of an *MCLUST* model, used to produce superimposing ellipses on the plot. The relevant components are as follows: `mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. `variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.
`z`	A matrix in which the `[i,k]`th entry gives the probability of observation *i* belonging to the *k*th class. Used to compute `classification` and `uncertainty` if those arguments aren't available.
`classification`	A numeric or character vector representing a classification of observations (rows) of `data`. If present argument `z` will be ignored.
`truth`	A numeric or character vector giving a known classification of each data point. If `classification` or `z` is also present, this is used for displaying classification errors.
`uncertainty`	A numeric vector of values in *(0,1)* giving the uncertainty of each data point. If present argument `z` will be ignored.
`what`	Choose from one of the following three options: `"classification"` (default), `"error"`, `"uncertainty"`.
`addEllipses`	A logical indicating whether or not to add ellipses with axes corresponding to the within-cluster covariances in case of `"classification"` or `"uncertainty"` plots.
`fillEllipses`	A logical specifying whether or not to fill ellipses with transparent colors when `addEllipses = TRUE`.
`symbols`	Either an integer or character vector assigning a plotting symbol to each unique class in `classification`. Elements in `colors` correspond to classes in order of appearance in the sequence of observations (the order used by the function `unique`). The default is given by `mclust.options("classPlotSymbols")`.

colors	Either an integer or character vector assigning a color to each unique class in classification. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function unique). The default is given by mclust.options("classPlotColors").
scale	A logical variable indicating whether or not the two chosen dimensions should be plotted on the same scale, and thus preserve the shape of the distribution. Default: scale=FALSE
xlim, ylim	Arguments specifying bounds for the ordinate, abscissa of the plot. This may be useful for when comparing plots.
CEX	An argument specifying the size of the plotting symbols. The default value is 1.
PCH	An argument specifying the symbol to be used when a classification has not been specified for the data. The default value is a small dot ".".
main	A logical variable or NULL indicating whether or not to add a title to the plot identifying the dimensions used.
...	Other graphics parameters.

Value

A plot showing a two-dimensional coordinate projection of the data, together with the location of the mixture components, classification, uncertainty, and/or classification errors.

See Also

clPairs, randProj, mclust2Dplot, mclust.options

Examples

```
## Not run:
est <- meVVV(iris[,-5], unmap(iris[,5]))
par(pty = "s", mfrow = c(1,1))
coordProj(iris[,-5], dimens=c(2,3), parameters = est$parameters, z = est$z,
          what = "classification", main = TRUE)
coordProj(iris[,-5], dimens=c(2,3), parameters = est$parameters, z = est$z,
          truth = iris[,5], what = "error", main = TRUE)
coordProj(iris[,-5], dimens=c(2,3), parameters = est$parameters, z = est$z,
          what = "uncertainty", main = TRUE)

## End(Not run)
```

---

covw *Weighted means, covariance and scattering matrices conditioning on a weighted matrix*

Description

Compute efficiently (via Fortran code) the means, covariance and scattering matrices conditioning on a weighted or indicator matrix

Usage

```
covw(X, Z, normalize = TRUE)
```

Arguments

X	A (nxp) data matrix, with n observations on p variables.
Z	A (nxG) matrix of weights, with G number of groups.
normalize	A logical indicating if rows of Z should be normalized to sum to one.

Value

A list with the following components:

mean	A (pxG) matrix of weighted means.
S	A $(pxpxG)$ array of weighted covariance matrices.
W	A $(pxpxG)$ array of weighted scattering matrices.

Author(s)

M. Fop and L. Scrucca

Examples

```
# Z as an indicator matrix
X <- iris[,1:4]
Z <- unmap(iris$Species)
str(covw(X, Z))
# Z as a matrix of weights
mod <- Mclust(X, G = 3, modelNames = "VVV")
str(covw(X, mod$z))
```

---

cross *Simulated Cross Data*

Description

A 500 by 3 matrix in which the first column is the classification and the remaining columns are two data from a simulation of two crossed elliptical Gaussians.

Usage

```
data(cross)
```

Examples

```
# This dataset was created as follows
## Not run:
n <- 250
set.seed(0)
cross <- rbind(matrix(rnorm(n*2), n, 2) %*% diag(c(1,9)),
               matrix(rnorm(n*2), n, 2) %*% diag(c(1,9))[,2:1])
cross <- cbind(c(rep(1,n),rep(2,n)), cross)

## End(Not run)
```

---

cvMclustDA *MclustDA cross-validation*

Description

K-fold cross-validation for discriminant analysis based on Gaussian finite mixture modeling.

Usage

```
cvMclustDA(object, nfold = 10,
           metric = c("error", "brier"),
           prop = object$prop,
           verbose = interactive(), ...)
```

Arguments

object	An object of class 'MclustDA' resulting from a call to MclustDA.
nfold	An integer specifying the number of folds.
metric	A character string specifying the statistic to be used in the cross-validation resampling process. Possible values are "error" for the classification error, and "brier" for the Brier score.
prop	A vector of class prior probabilities, which if not provided default to the class proportions in the training data.
verbose	A logical controlling if a text progress bar is displayed during the cross-validation procedure. By default is TRUE if the session is interactive, and FALSE otherwise.
...	Further arguments passed to or from other methods.

Value

The function returns a list with the following components:

classification	a factor of cross-validated class labels.
z	a matrix containing the cross-validated probabilites for class assignement.
error	the cross-validation classification error if metric = "error", NA otherwise.
brier	the cross-validation Brier score if metric = "brier", NA otherwise.
se	the standard error of the cross-validated statistic.

Author(s)

Luca Scrucca

See Also

summary.MclustDA, plot.MclustDA, predict.MclustDA, classError, BrierScore

Examples

```
## Not run:
X <- iris[,-5]
Class <- iris[,5]

# common EEE covariance structure (which is essentially equivalent to linear discriminant analysis)
irisMclustDA <- MclustDA(X, Class, modelType = "EDDA", modelNames = "EEE")
cv <- cvMclustDA(irisMclustDA)  # default 10-fold CV
cv[c("error", "se")]

cv <- cvMclustDA(irisMclustDA, nfold = length(Class))  # LOO-CV
cv[c("error", "se")]

cv <- cvMclustDA(irisMclustDA, metric = "brier")  # 10-fold CV with Brier score metric
cv[c("brier", "se")]

# general covariance structure selected by BIC
irisMclustDA <- MclustDA(X, Class)
cv <- cvMclustDA(irisMclustDA)  # default 10-fold CV
cv[c("error", "se")]
cv <- cvMclustDA(irisMclustDA, metric = "brier")  # 10-fold CV with Brier score metric
cv[c("brier", "se")]

## End(Not run)
```

`decomp2sigma` *Convert mixture component covariances to matrix form*

Description

Converts covariances from a parameterization by eigenvalue decomposition or cholesky factorization to representation as a 3-D array.

Usage

```
decomp2sigma(d, G, scale, shape, orientation, ...)
```

Arguments

d	The dimension of the data.
G	The number of components in the mixture model.
scale	Either a G-vector giving the scale of the covariance (the dth root of its determinant) for each component in the mixture model, or a single numeric value if the scale is the same for each component.
shape	Either a G by d matrix in which the kth column is the shape of the covariance matrix (normalized to have determinant 1) for the kth component, or a d-vector giving a common shape for all components.
orientation	Either a d by d by G array whose [,,k]th entry is the orthonomal matrix whose columns are the eigenvectors of the covariance matrix of the kth component, or a d by d orthonormal matrix if the mixture components have a common orientation. The orientation component of decomp can be omitted in spherical and diagonal models, for which the principal components are parallel to the coordinate axes so that the orientation matrix is the identity.
...	Catches unused arguments from an indirect or list call via do.call.

Value

A 3-D array whose [,,k]th component is the covariance matrix of the kth component in an MVN mixture model.

See Also

sigma2decomp

Examples

```
meEst <- meVEV(iris[,-5], unmap(iris[,5]))
names(meEst)
meEst$parameters$variance

dec <- meEst$parameters$variance
decomp2sigma(d=dec$d, G=dec$G, shape=dec$shape, scale=dec$scale,
             orientation = dec$orientation)
## Not run:
do.call("decomp2sigma", dec)  ## alternative call

## End(Not run)
```

---

defaultPrior *Default conjugate prior for Gaussian mixtures*

Description

Default conjugate prior specification for Gaussian mixtures.

Usage

```
defaultPrior(data, G, modelName, ...)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
G	The number of mixture components.
modelName	A character string indicating the model: "E": equal variance (univariate) "V": variable variance (univariate) "EII": spherical, equal volume "VII": spherical, unequal volume "EEI": diagonal, equal volume and shape "VEI": diagonal, varying volume, equal shape "EVI": diagonal, equal volume, varying shape "VVI": diagonal, varying volume and shape "EEE": ellipsoidal, equal volume, shape, and orientation "EEV": ellipsoidal, equal volume and equal shape "VEV": ellipsoidal, equal shape "VVV": ellipsoidal, varying volume, shape, and orientation. A description of the models above is provided in the help of mclustModelNames. Note that in the multivariate case only 10 out of 14 models may be used in conjunction with a prior, i.e. those available in *MCLUST* up to version 4.4.
...	One or more of the following: dof The degrees of freedom for the prior on the variance. The default is d + 2, where d is the dimension of the data. scale The scale parameter for the prior on the variance. The default is var(data)/G^(2/d), where d is the dimension of the data. shrinkage The shrinkage parameter for the prior on the mean. The default value is 0.01. If 0 or NA, no prior is assumed for the mean. mean The mean parameter for the prior. The default value is colMeans(data).

Details

defaultPrior is a function whose default is to output the default prior specification for EM within *MCLUST*.
Furthermore, defaultPrior can be used as a template to specify alternative parameters for a conjugate prior.

Value

A list giving the prior degrees of freedom, scale, shrinkage, and mean.

References

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association* 97:611-631.

C. Fraley and A. E. Raftery (2005, revised 2009). Bayesian regularization for normal mixture estimation and model-based clustering. Technical Report, Department of Statistics, University of Washington.

C. Fraley and A. E. Raftery (2007). Bayesian regularization for normal mixture estimation and model-based clustering. *Journal of Classification* 24:155-181.

See Also

mclustBIC, me, mstep, priorControl

Examples

```
# default prior
irisBIC <- mclustBIC(iris[,-5], prior = priorControl())
summary(irisBIC, iris[,-5])

# equivalent to previous example
irisBIC <- mclustBIC(iris[,-5],
                     prior = priorControl(functionName = "defaultPrior"))
summary(irisBIC, iris[,-5])

# no prior on the mean; default prior on variance
irisBIC <- mclustBIC(iris[,-5], prior = priorControl(shrinkage = 0))
summary(irisBIC, iris[,-5])

# equivalent to previous example
irisBIC <- mclustBIC(iris[,-5], prior =
                     priorControl(functionName="defaultPrior", shrinkage=0))
summary(irisBIC, iris[,-5])

defaultPrior( iris[-5], G = 3, modelName = "VVV")
```

---

dens *Density for Parameterized MVN Mixtures*

Description

Computes densities of observations in parameterized MVN mixtures.

Usage

```
dens(modelName, data, logarithm = FALSE, parameters, warn=NULL, ...)
```

Arguments

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.
data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
logarithm	A logical value indicating whether or not the logarithm of the component densities should be returned. The default is to return the component densities, obtained from the log component densities by exponentiation.
parameters	The parameters of the model: pro The vector of mixing proportions for the components of the mixture. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details.
warn	A logical value indicating whether or not a warning should be issued when computations fail. The default is warn=FALSE.
...	Catches unused arguments in indirect or list calls via do.call.

Value

A numeric vector whose *i*th component is the density of the *ith* observation in data in the MVN mixture specified by parameters.

See Also

cdens, mclust.options, do.call

Examples

```
## Not run:
faithfulModel <- Mclust(faithful)
Dens <- dens(modelName = faithfulModel$modelName, data = faithful,
             parameters = faithfulModel$parameters)
Dens

## alternative call
do.call("dens", faithfulModel)
## End(Not run)
```

`densityMclust` *Density Estimation via Model-Based Clustering*

Description

Produces a density estimate for each data point using a Gaussian finite mixture model from `Mclust`.

Usage

```
densityMclust(data, ...)
```

Arguments

`data`	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
`...`	Additional arguments for the `Mclust` function. In particular, setting the arguments `G` and `modelNames` allow to specify the number of mixture components and the type of model to be fitted. By default an "optimal" model is selected based on the BIC criterion.

Value

An object of class `densityMclust`, which inherits from `Mclust`, is returned with the following slot added:

`density`	The density evaluated at the input `data` computed from the estimated model.

Author(s)

Revised version by Luca Scrucca based on the original code by C. Fraley and A.E. Raftery.

References

Scrucca L., Fop M., Murphy T. B. and Raftery A. E. (2016) mclust 5: clustering, classification and density estimation using Gaussian finite mixture models, *The R Journal*, 8/1, pp. 205-233.

Fraley C. and Raftery A. E. (2002) Model-based clustering, discriminant analysis and density estimation, *Journal of the American Statistical Association*, 97/458, pp. 611-631.

Fraley C., Raftery A. E., Murphy T. B. and Scrucca L. (2012) mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. *Technical Report* No. 597, Department of Statistics, University of Washington.

See Also

`plot.densityMclust`, `Mclust`, `summary.Mclust`, `predict.densityMclust`.

Examples

```
dens <- densityMclust(faithful$waiting)
summary(dens)
summary(dens, parameters = TRUE)
plot(dens, what = "BIC", legendArgs = list(x = "topright"))
plot(dens, what = "density", data = faithful$waiting)

dens <- densityMclust(faithful, modelNames = "EEE", G = 3)
summary(dens)
summary(dens, parameters = TRUE)
plot(dens, what = "density", data = faithful,
     drawlabels = FALSE, points.pch = 20)
plot(dens, what = "density", type = "hdr")
plot(dens, what = "density", type = "hdr", prob = c(0.1, 0.9))
plot(dens, what = "density", type = "hdr", data = faithful)
plot(dens, what = "density", type = "persp")

## Not run:
dens <- densityMclust(iris[,1:4], G = 2)
summary(dens, parameters = TRUE)
plot(dens, what = "density", data = iris[,1:4],
     col = "slategrey", drawlabels = FALSE, nlevels = 7)
plot(dens, what = "density", type = "hdr", data = iris[,1:4])
plot(dens, what = "density", type = "persp", col = grey(0.9))

## End(Not run)
```

---

densityMclust.diagnostic

Diagnostic plots for `mclustDensity` *estimation*

Description

Diagnostic plots for density estimation. Only available for the one-dimensional case.

Usage

```
densityMclust.diagnostic(object, type = c("cdf", "qq"),
                         col = c("black", "black"),
                         lwd = c(2,1), lty = c(1,1),
                         legend = TRUE, grid = TRUE,
                         ...)
```

Arguments

`object`	An object of class `'mclustDensity'` obtained from a call to `densityMclust` function.
`type`	The type of graph requested:

	`"cdf"` = a plot of the estimated CDF versus the empirical distribution function. `"qq"` = a Q-Q plot of sample quantiles versus the quantiles obtained from the inverse of the estimated cdf.
`col`	A pair of values for the color to be used for plotting, respectively, the estimated CDF and the empirical cdf.
`lwd`	A pair of values for the line width to be used for plotting, respectively, the estimated CDF and the empirical cdf.
`lty`	A pair of values for the line type to be used for plotting, respectively, the estimated CDF and the empirical cdf.
`legend`	A logical indicating if a legend must be added to the plot of fitted CDF vs the empirical CDF.
`grid`	A logical indicating if a `grid` should be added to the plot.
`...`	Additional arguments.

Details

The two diagnostic plots for density estimation in the one-dimensional case are discussed in Loader (1999, pp- 87-90).

Author(s)

Luca Scrucca

References

Loader C. (1999), Local Regression and Likelihood. New York, Springer.

C. Fraley, A. E. Raftery, T. B. Murphy and L. Scrucca (2012). mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. Technical Report No. 597, Department of Statistics, University of Washington.

See Also

`densityMclust`, `plot.densityMclust`.

Examples

```
## Not run:
x <- faithful$waiting
dens <- densityMclust(x)
plot(dens, x, what = "diagnostic")
# or
densityMclust.diagnostic(dens, type = "cdf")
densityMclust.diagnostic(dens, type = "qq")

## End(Not run)
```

diabetes *Diabetes data*

Description

The data set contains three measurements made on 145 non-obese adult patients classified into three groups.

Usage

```
data(diabetes)
```

Format

A data frame with the following variables:

class The type of diabete: `Normal`, `Overt`, and `Chemical`.

glucose Area under plasma glucose curve after a three hour oral glucose tolerance test (OGTT).

insulin Area under plasma insulin curve after a three hour oral glucose tolerance test (OGTT).

sspg Steady state plasma glucose.

Source

Reaven, G. M. and Miller, R. G. (1979). An attempt to define the nature of chemical diabetes using a multidimensional analysis. *Diabetologia* 16:17-24.

dmvnorm *Density of multivariate Gaussian distribution*

Description

Efficiently computes the densities of observations for a generic multivariate Gaussian distribution

Usage

```
dmvnorm(data, mean, sigma, log = FALSE)
```

Arguments

`data`	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
`mean`	A vector of means for each variable.
`sigma`	A positive definite covariance matrix.
`log`	A logical value indicating whether or not the logarithm of the densities should be returned.

Value

A numeric vector whose *i*th component is the density of the *ith* observation in `data` in the MVN mixture specified by `parameters`.

See Also

dnorm, dens

Examples

```
# univariate
ngrid <- 101
x <- seq(-5, 5, length = ngrid)
dens <- dmvnorm(x, mean = 1, sigma = 5)
plot(x, dens, type = "l")

# bivariate
ngrid <- 101
x1 <- x2 <- seq(-5, 5, length = ngrid)
mu <- c(1,0)
sigma <- matrix(c(1,0.5,0.5,2), 2, 2)
dens <- dmvnorm(as.matrix(expand.grid(x1, x2)), mu, sigma)
dens <- matrix(dens, ngrid, ngrid)
image(x1, x2, dens)
contour(x1, x2, dens, add = TRUE)
```

---

em *EM algorithm starting with E-step for parameterized Gaussian mixture models*

Description

Implements the EM algorithm for parameterized Gaussian mixture models, starting with the expectation step.

Usage

```
em(modelName, data, parameters, prior = NULL, control = emControl(),
   warn = NULL, ...)
```

Arguments

`modelName`	A character string indicating the model. The help file for mclustModelNames describes the available models.
`data`	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
`parameters`	A names list giving the parameters of the model. The components are as follows:

`pro` Mixing proportions for the components of the mixture. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components.

`mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model.

`variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.

`Vinv` An estimate of the reciprocal hypervolume of the data region. If set to NULL or a negative value, the default is determined by applying function `hypvol` to the data. Used only when `pro` includes an additional mixing proportion for a noise component.

`prior` Specification of a conjugate prior on the means and variances. The default assumes no prior.

`control` A list of control parameters for EM. The defaults are set by the call `emControl()`.

`warn` A logical value indicating whether or not a warning should be issued when computations fail. The default is `warn=FALSE`.

`...` Catches unused arguments in indirect or list calls via `do.call`.

Value

A list including the following components:

`modelName` A character string identifying the model (same as the input argument).

`n` The number of observations in the data.

`d` The dimension of the data.

`G` The number of mixture components.

`z` A matrix whose `[i,k]`th entry is the conditional probability of the *i*th observation belonging to the *k*th component of the mixture.

`parameters`

`pro` A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components.

`mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model.

`variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.

`Vinv` The estimate of the reciprocal hypervolume of the data region used in the computation when the input indicates the addition of a noise component to the model.

`loglik` The log likelihood for the data in the mixture model.

`control` The list of control parameters for EM used.

prior	The specification of a conjugate prior on the means and variances used, NULL if no prior is used.
Attributes:	"info" Information on the iteration. "WARNING" An appropriate warning if problems are encountered in the computations.

See Also

emE, ..., emVVV, estep, me, mstep, mclust.options, do.call

Examples

```
## Not run:
msEst <- mstep(modelName = "EEE", data = iris[,-5],
               z = unmap(iris[,5]))
names(msEst)

em(modelName = msEst$modelName, data = iris[,-5],
   parameters = msEst$parameters)

do.call("em", c(list(data = iris[,-5]), msEst))   ## alternative call

## End(Not run)
```

---

emControl *Set control values for use with the EM algorithm*

Description

Supplies a list of values including tolerances for singularity and convergence assessment, for use functions involving EM within *MCLUST*.

Usage

```
emControl(eps, tol, itmax, equalPro)
```

Arguments

eps	A scalar tolerance associated with deciding when to terminate computations due to computational singularity in covariances. Smaller values of eps allow computations to proceed nearer to singularity. The default is the relative machine precision .Machine$double.eps, which is approximately $2e-16$ on IEEE-compliant machines.
tol	A vector of length two giving relative convergence tolerances for the log-likelihood and for parameter convergence in the inner loop for models with iterative M-step ("VEI", "EVE", "VEE", "VVE", "VEV"), respectively. The default is c(1.e-5,sqrt(.Machine$double.eps)). If only one number is supplied, it is used as the tolerance for the outer iterations and the tolerance for the inner iterations is as in the default.

itmax	A vector of length two giving integer limits on the number of EM iterations and on the number of iterations in the inner loop for models with iterative M-step ("VEI", "EVE", "VEE", "VVE", "VEV"), respectively. The default is c(.Machine$integer.max, .Machine$integer.max) allowing termination to be completely governed by tol. If only one number is supplied, it is used as the iteration limit for the outer iteration only.
equalPro	Logical variable indicating whether or not the mixing proportions are equal in the model. Default: equalPro = FALSE.

Details

emControl is provided for assigning values and defaults for EM within *MCLUST*.

Value

A named list in which the names are the names of the arguments and the values are the values supplied to the arguments.

See Also

em, estep, me, mstep, mclustBIC

Examples

```
irisBIC <- mclustBIC(iris[,-5], control = emControl(tol = 1.e-6))
summary(irisBIC, iris[,-5])
```

---

emE *EM algorithm starting with E-step for a parameterized Gaussian mixture model*

Description

Implements the EM algorithm for a parameterized Gaussian mixture model, starting with the expectation step.

Usage

```
emE(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emV(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emX(data, prior = NULL, warn = NULL, ...)
emEII(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emVII(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emEEI(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emVEI(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emEVI(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emVVI(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emEEE(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
```

```
emEEV(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emVEV(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emVVV(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emEVE(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emEVV(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emVEE(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emVVE(data, parameters, prior = NULL, control = emControl(), warn = NULL, ...)
emXII(data, prior = NULL, warn = NULL, ...)
emXXI(data, prior = NULL, warn = NULL, ...)
emXXX(data, prior = NULL, warn = NULL, ...)
```

Arguments

`data`	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
`parameters`	The parameters of the model: `pro` Mixing proportions for the components of the mixture. There should one more mixing proportion than the number of Gaussian components if the mixture model includes a Poisson noise term. `mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. `variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details. `Vinv` An estimate of the reciprocal hypervolume of the data region. The default is determined by applying function `hypvol` to the data. Used only when `pro` includes an additional mixing proportion for a noise component.
`prior`	The default assumes no prior, but this argument allows specification of a conjugate prior on the means and variances through the function `priorControl`.
`control`	A list of control parameters for EM. The defaults are set by the call `emControl()`.
`warn`	A logical value indicating whether or not a warning should be issued whenever a singularity is encountered. The default is given in `mclust.options("warn")`.
`...`	Catches unused arguments in indirect or list calls via `do.call`.

Value

A list including the following components:

`modelName`	A character string identifying the model (same as the input argument).
`z`	A matrix whose `[i,k]`th entry is the conditional probability of the *i*th observation belonging to the *k*th component of the mixture.
`parameters`	`pro` A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components.

`mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model.

`variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.

`Vinv` The estimate of the reciprocal hypervolume of the data region used in the computation when the input indicates the addition of a noise component to the model.

`loglik` The log likelihood for the data in the mixture model.

`Attributes:` `"info"` Information on the iteration.
`"WARNING"` An appropriate warning if problems are encountered in the computations.

See Also

`me`, `mstep`, `mclustVariance`, `mclust.options`.

Examples

```
## Not run:
msEst <- mstepEEE(data = iris[,-5], z = unmap(iris[,5]))
names(msEst)

emEEE(data = iris[,-5], parameters = msEst$parameters)
## End(Not run)
```

---

entPlot *Plot Entropy Plots*

Description

Plot "entropy plots" to help select the number of classes from a hierarchy of combined clusterings.

Usage

```
entPlot(z, combiM, abc = c("standard", "normalized"), reg = 2, ...)
```

Arguments

`z` A matrix whose `[i,k]`th entry is the probability that observation *i* in the data belongs to the *k*th class, for the initial solution (ie before any combining). Typically, the one returned by `Mclust`/BIC.

`combiM` A list of "combining matrices" (as provided by `clustCombi`), ie `combiM[[K]]` is the matrix whose *k*th row contains only zeros, but in columns corresponding to the labels of the classes in the *(K+1)*-classes solution to be merged to get the *K*-classes combined solution. `combiM` must contain matrices from `K` = number of classes in `z` to one.

abc	Choose one or more of: "standard", "normalized", to specify whether the number of observations involved in each combining step should be taken into account to scale the plots or not.
reg	The number of parts of the piecewise linear regression for the entropy plots. Choose one or more of: 2 (for 1 change-point), 3 (for 2 change-points).
...	Other graphical arguments to be passed to the plot functions.

Details

Please see the article cited in the references for more details. A clear elbow in the "entropy plot" should suggest the user to consider the corresponding number(s) of class(es).

Value

if `abc = "standard"`, plots the entropy against the number of clusters and the difference between the entropy of successive combined solutions against the number of clusters. if `abc = "normalized"`, plots the entropy against the cumulated number of observations involved in the successive combining steps and the difference between the entropy of successive combined solutions divided by the number of observations involved in the corresponding combining step against the number of clusters.

Author(s)

J.-P. Baudry, A. E. Raftery, L. Scrucca

References

J.-P. Baudry, A. E. Raftery, G. Celeux, K. Lo and R. Gottardo (2010). Combining mixture components for clustering. *Journal of Computational and Graphical Statistics, 19(2):332-353.*

See Also

`plot.clustCombi`, `combiPlot`, `clustCombi`

Examples

```
## Not run:
data(Baudry_etal_2010_JCGS_examples)
# run Mclust to get the MclustOutput
output <- clustCombi(data = ex4.2, modelNames = "VII")

entPlot(output$MclustOutput$z, output$combiM, reg = c(2,3))
# legend: in red, the single-change-point piecewise linear regression;
#         in blue, the two-change-point piecewise linear regression.

## End(Not run)
```

errorBars *Draw error bars on a plot*

Description

Draw error bars at x from upper to lower. If `horizontal = FALSE` (default) bars are drawn vertically, otherwise horizontally.

Usage

```
errorBars(x, upper, lower, width = 0.1, code = 3, angle = 90, horizontal = FALSE, ...)
```

Arguments

x	A vector of values where the bars must be drawn.
upper	A vector of upper values where the bars must end.
lower	A vector of lower values where the bars must start.
width	A value specifying the width of the end-point segment.
code	An integer code specifying the kind of arrows to be drawn. For details see arrows.
angle	A value specifying the angle at the arrow edge. For details see arrows.
horizontal	A logical specifying if bars should be drawn vertically (default) or horizontally.
...	Further arguments are passed to arrows.

Examples

```
par(mfrow=c(2,2))
# Create a simple example dataset
x <- 1:5
n <- c(10, 15, 12, 6, 3)
se <- c(1, 1.2, 2, 1, .5)
# upper and lower bars
b <- barplot(n, ylim = c(0, max(n)*1.5))
errorBars(b, lower = n-se, upper = n+se, lwd = 2, col = "red3")
# one side bars
b <- barplot(n, ylim = c(0, max(n)*1.5))
errorBars(b, lower = n, upper = n+se, lwd = 2, col = "red3", code = 1)
#
plot(x, n, ylim = c(0, max(n)*1.5), pch = 0)
errorBars(x, lower = n-se, upper = n+se, lwd = 2, col = "red3")
#
dotchart(n, labels = x, pch = 19, xlim = c(0, max(n)*1.5))
errorBars(x, lower = n-se, upper = n+se, col = "red3", horizontal = TRUE)
```

estep *E-step for parameterized Gaussian mixture models.*

Description

Implements the expectation step of EM algorithm for parameterized Gaussian mixture models.

Usage

```
estep( modelName, data, parameters, warn = NULL, ...)
```

Arguments

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.
data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
parameters	A names list giving the parameters of the model. The components are as follows: pro Mixing proportions for the components of the mixture. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details. Vinv An estimate of the reciprocal hypervolume of the data region. If set to NULL or a negative value, the default is determined by applying function hypvol to the data. Used only when pro includes an additional mixing proportion for a noise component.
warn	A logical value indicating whether or not a warning should be issued when computations fail. The default is warn=FALSE.
...	Catches unused arguments in indirect or list calls via do.call.

Value

A list including the following components:

modelName	A character string identifying the model (same as the input argument).
z	A matrix whose [i,k]th entry is the conditional probability of the *i*th observation belonging to the *k*th component of the mixture.
parameters	The input parameters.
loglik	The log-likelihood for the data in the mixture model.
Attributes	"WARNING": an appropriate warning if problems are encountered in the computations.

See Also

estepE, ..., estepVVV, em, mstep, mclust.options mclustVariance

Examples

```
## Not run:
msEst <- mstep(modelName = "VVV", data = iris[,-5], z = unmap(iris[,5]))
names(msEst)

estep(modelName = msEst$modelName, data = iris[,-5],
      parameters = msEst$parameters)
## End(Not run)
```

---

estepE *E-step in the EM algorithm for a parameterized Gaussian mixture model.*

Description

Implements the expectation step in the EM algorithm for a parameterized Gaussian mixture model.

Usage

```
estepE(data, parameters, warn = NULL, ...)
estepV(data, parameters, warn = NULL, ...)
estepEII(data, parameters, warn = NULL, ...)
estepVII(data, parameters, warn = NULL, ...)
estepEEI(data, parameters, warn = NULL, ...)
estepVEI(data, parameters, warn = NULL, ...)
estepEVI(data, parameters, warn = NULL, ...)
estepVVI(data, parameters, warn = NULL, ...)
estepEEE(data, parameters, warn = NULL, ...)
estepEEV(data, parameters, warn = NULL, ...)
estepVEV(data, parameters, warn = NULL, ...)
estepVVV(data, parameters, warn = NULL, ...)
estepEVE(data, parameters, warn = NULL, ...)
estepEVV(data, parameters, warn = NULL, ...)
estepVEE(data, parameters, warn = NULL, ...)
estepVVE(data, parameters, warn = NULL, ...)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
parameters	The parameters of the model:

`pro` Mixing proportions for the components of the mixture. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components.

mu The mean for each component. If there is more than one component, this is a matrix whose columns are the means of the components.

`variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.

`Vinv` An estimate of the reciprocal hypervolume of the data region. If not supplied or set to a negative value, the default is determined by applying function `hypvol` to the data. Used only when `pro` includes an additional mixing proportion for a noise component.

`warn` A logical value indicating whether or certain warnings should be issued. The default is given by `mclust.options("warn")`.

`...` Catches unused arguments in indirect or list calls via `do.call`.

Value

A list including the following components:

`modelName` Character string identifying the model.

`z` A matrix whose `[i,k]`th entry is the conditional probability of the *i*th observation belonging to the *k*th component of the mixture.

`parameters` The input parameters.

`loglik` The logliklihood for the data in the mixture model.

`Attribute` `"WARNING"`: An appropriate warning if problems are encountered in the computations.

See Also

`estep`, `em`, `mstep`, `do.call`, `mclustVariance`, `mclust.options`.

Examples

```
## Not run:
msEst <- mstepEII(data = iris[,-5], z = unmap(iris[,5]))
names(msEst)

estepEII(data = iris[,-5], parameters = msEst$parameters)
## End(Not run)
```

EuroUnemployment *Unemployment data for European countries in 2014*

Description

The data set contains unemployment rates for 31 European countries for the year 2014.

Usage

```
data(EuroUnemployment)
```

Format

A data frame with the following variables:

TUR Total unemployment rate, i.e. percentage of unemployed persons aged 15-74 in the economically active population.

YUR Youth unemployment rate, i.e. percentage of unemployed persons aged 15-24 in the economically active population.

LUR Long-term unemployment rate, i.e. percentage of unemployed persons who have been unemployed for 12 months or more.

Source

EUROSTAT (http://ec.europa.eu/eurostat/web/lfs/data/database)

gmmhd *Identifying Connected Components in Gaussian Finite Mixture Models for Clustering*

Description

Starting with the density estimate obtained from a fitted Gaussian finite mixture model, cluster cores are identified from the connected components at a given density level. Once cluster cores are identified, the remaining observations are allocated to those cluster cores for which the probability of cluster membership is the highest.

Usage

```
gmmhd(object,
      ngrid = min(round((log(nrow(data)))*10), nrow(data)),
      dr = list(d = 3, lambda = 1, cumEvalues = NULL, mindir = 2),
      classify = list(G = 1:5,
                      modelNames = mclust.options("emModelNames")[-c(8, 10)]),
      ...)

## S3 method for class 'gmmhd'
plot(x, what = c("mode", "cores", "clusters"), ...)
```

Arguments

object	An object returned by Mclust.
ngrid	An integer specifying the number of grid points used to compute the density levels.
dr	A list of parameters used in the dimension reduction step.
classify	A list of parameters used in the classification step.
x	An object of class 'gmmhd' as returned by the function gmmhd.
what	A string specifying the type of plot to be produced. See Examples section.
...	further arguments passed to or from other methods.

Details

Model-based clustering associates each component of a finite mixture distribution to a group or cluster. An underlying implicit assumption is that a one-to-one correspondence exists between mixture components and clusters. However, a single Gaussian density may not be sufficient, and two or more mixture components could be needed to reasonably approximate the distribution within a homogeneous group of observations.

This function implements the methodology proposed by Scrucca (2016) based on the identification of high density regions of the underlying density function. Starting with an estimated Gaussian finite mixture model, the corresponding density estimate is used to identify the cluster cores, i.e. those data points which form the core of the clusters. These cluster cores are obtained from the connected components at a given density level c. A mode function gives the number of connected components as the level c is varied. Once cluster cores are identified, the remaining observations are allocated to those cluster cores for which the probability of cluster membership is the highest.

The method usually improves the identification of non-Gaussian clusters compared to a fully parametric approach. Furthermore, it enables the identification of clusters which cannot be obtained by merging mixture components, and it can be straightforwardly extended to cases of higher dimensionality.

Value

A list of class gmmhd with the following components:

Mclust	The input object of class "Mclust" representing an estimated Gaussian finite mixture model.
MclustDA	An object of class "MclustDA" containing the model used for the classification step.
MclustDR	An object of class "MclustDR" containing the dimension reduction step if performed, otherwise NULL.
x	The data used in the algorithm. This can be the input data or a projection if a preliminary dimension reduction step is performed.
density	The density estimated from the input Gaussian finite mixture model evaluated at the input data.
con	A list of connected components at each step.

nc	A vector giving the number of connected components (i.e. modes) at each step.
pn	Vector of values over a uniform grid of proportions of length ngrid.
qn	Vector of density quantiles corresponding to proportions pn.
pc	Vector of empirical proportions corresponding to quantiles qn.
clusterCores	Vector of cluster cores numerical labels; NAs indicate that an observation does not belong to any cluster core.
clusterCores	Vector of numerical labels giving the final clustering.
numClusters	An integer giving the number of clusters.

Author(s)

Luca Scrucca <luca.scrucca@unipg.it>

References

Scrucca, L. (2016) Identifying connected components in Gaussian finite mixture models for clustering. *Computational Statistics & Data Analysis*, 93, 5-17.

See Also

Mclust

Examples

```
## Not run:
data(faithful)
mod <- Mclust(faithful)
summary(mod)
plot(as.densityMclust(mod), faithful, what = "density",
     points.pch = mclust.options("classPlotSymbols")[mod$classification],
     points.col = mclust.options("classPlotColors")[mod$classification])

GMMHD <- gmmhd(mod)
summary(GMMHD)

plot(GMMHD, what = "mode")
plot(GMMHD, what = "cores")
plot(GMMHD, what = "clusters")

## End(Not run)
```

GvHD *GvHD Dataset*

Description

GvHD (Graft-versus-Host Disease) data of Brinkman et al. (2007). Two samples of this flow cytometry data, one from a patient with the GvHD, and the other from a control patient. The GvHD positive and control samples consist of 9083 and 6809 observations, respectively. Both samples include four biomarker variables, namely, CD4, CD8b, CD3, and CD8. The objective of the analysis is to identify CD3+ CD4+ CD8b+ cell sub-populations present in the GvHD positive sample.

A treatment of this data by combining mixtures is proposed in Baudry et al. (2010).

Usage

```
data(GvHD)
```

Format

GvHD.pos (positive patient) is a data frame with 9083 observations on the following 4 variables, which are biomarker measurements.

CD4

CD8b

CD3

CD8

GvHD.control (control patient) is a data frame with 6809 observations on the following 4 variables, which are biomarker measurements.

CD4

CD8b

CD3

CD8

References

R. R. Brinkman, M. Gasparetto, S.-J. J. Lee, A. J. Ribickas, J. Perkins, W. Janssen, R. Smiley and C. Smith (2007). High-content flow cytometry and temporal data analysis for defining a cellular signature of Graft-versus-Host Disease. *Biology of Blood and Marrow Transplantation, 13: 691-700.*

K. Lo, R. R. Brinkman, R. Gottardo (2008). Automated gating of flow cytometry data via robust model-based clustering. *Cytometry A, 73: 321-332.*

J.-P. Baudry, A. E. Raftery, G. Celeux, K. Lo and R. Gottardo (2010). Combining mixture components for clustering. *Journal of Computational and Graphical Statistics, 19(2):332-353.*

Examples

```
## Not run:
data(GvHD)
dat <- GvHD.pos[1:500,] # only a few lines for a quick example
output <- clustCombi(data = dat)
output # is of class clustCombi
# plot the hierarchy of combined solutions
plot(output, what = "classification")
# plot some "entropy plots" which may help one to select the number of classes
plot(output, what = "entropy")
# plot the tree structure obtained from combining mixture components
plot(output, what = "tree")

## End(Not run)
```

---

hc *Model-based Agglomerative Hierarchical Clustering*

Description

Agglomerative hierarchical clustering based on maximum likelihood criteria for Gaussian mixture models parameterized by eigenvalue decomposition.

Usage

```
hc(data,
   modelName = mclust.options("hcModelName"),
   use = mclust.options("hcUse"), ...)

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

## S3 method for class 'hc'
as.dendrogram(object, ...)

## S3 method for class 'hc'
as.hclust(x, ...)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations (n) and columns correspond to variables (d).
modelName	A character string indicating the model to be used. Possible models are: "E" equal variance (one-dimensional)

	"V" spherical, variable variance (one-dimensional) "EII" spherical, equal volume "VII" spherical, unequal volume "EEE" ellipsoidal, equal volume, shape, and orientation "VVV" ellipsoidal, varying volume, shape, and orientation. By default the model provided by mclust.options("hcModelName") is used. See mclust.options.
use	A string or a vector of character strings specifying the type of input variables/data transformation to be used for model-based hierarchical clustering. By default the method specified in mclust.options("hcUse") is used. See mclust.options.
...	Arguments for the method-specific hc functions. See for example hcE.
object, x	An object of class 'hc' resulting from a call to hc().

Details

Most models have memory usage of the order of the square of the number groups in the initial partition for fast execution. Some models, such as equal variance or "EEE", do not admit a fast algorithm under the usual agglomerative hierarchical clustering paradigm. These use less memory but are much slower to execute.

Value

The function hc() returns a numeric two-column matrix in which the *i*th row gives the minimum index for observations in each of the two clusters merged at the *i*th stage of agglomerative hierarchical clustering. Several other informations are also returned as attributes.

The plotting function plot.hc() draws a dendrogram by first converting the input object from class 'hc' to class 'dendrogram' and then plot the transformed object using plot.dendrogram.

The functions as.dendrogram.hc() and as.hclust.hc() are used to convert the input object from class 'hc' to class, respectively, 'dendrogram' and 'hclust'.

Note

If modelName = "E" (univariate with equal variances) or modelName = "EII" (multivariate with equal spherical covariances), then the method is equivalent to Ward's method for hierarchical clustering.

References

J. D. Banfield and A. E. Raftery (1993). Model-based Gaussian and non-Gaussian Clustering. *Biometrics 49:803-821*.

C. Fraley (1998). Algorithms for model-based Gaussian hierarchical clustering. *SIAM Journal on Scientific Computing 20:270-281*.

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association 97:611-631*.

See Also

hcE,..., hcVVV, hclass, mclust.options

Examples

```
hcTree <- hc(modelName = "VVV", data = iris[,-5])
cl <- hclass(hcTree,c(2,3))

## Not run:
par(pty = "s", mfrow = c(1,1))
clPairs(iris[,-5],cl=cl[,"2"])
clPairs(iris[,-5],cl=cl[,"3"])

par(mfrow = c(1,2))
dimens <- c(1,2)
coordProj(iris[,-5], dimens = dimens, classification=cl[,"2"])
coordProj(iris[,-5], dimens = dimens, classification=cl[,"3"])

## End(Not run)
```

---

hcE *Model-based Hierarchical Clustering*

Description

Agglomerative hierarchical clustering based on maximum likelihood for a Gaussian mixture model parameterized by eigenvalue decomposition.

Usage

```
hcE(data, partition, minclus=1, ...)
hcV(data, partition, minclus = 1, alpha = 1, ...)
hcEII(data, partition, minclus = 1, ...)
hcVII(data, partition, minclus = 1, alpha = 1, ...)
hcEEE(data, partition, minclus = 1, ...)
hcVVV(data, partition, minclus = 1, alpha = 1, beta = 1, ...)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
partition	A numeric or character vector representing a partition of observations (rows) of data. If provided, group merges will start with this partition. Otherwise, each observation is assumed to be in a cluster by itself at the start of agglomeration.
minclus	A number indicating the number of clusters at which to stop the agglomeration. The default is to stop when all observations have been merged into a single cluster.

`alpha, beta`	Additional tuning parameters needed for initializatiion in some models. For details, see Fraley 1998. The defaults provided are usually adequate.
`...`	Catch unused arguments from a `do.call` call.

Details

Most models have memory usage of the order of the square of the number groups in the initial partition for fast execution. Some models, such as equal variance or `"EEE"`, do not admit a fast algorithm under the usual agglomerative hierachical clustering paradigm. These use less memory but are much slower to execute.

Value

A numeric two-column matrix in which the *i*th row gives the minimum index for observations in each of the two clusters merged at the *i*th stage of agglomerative hierarchical clustering.

References

J. D. Banfield and A. E. Raftery (1993). Model-based Gaussian and non-Gaussian Clustering. *Biometrics 49:803-821*.

C. Fraley (1998). Algorithms for model-based Gaussian hierarchical clustering. *SIAM Journal on Scientific Computing 20:270-281*.

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association 97:611-631*.

See Also

`hc`, `hclass` `randomPairs`

Examples

```
hcTree <- hcEII(data = iris[,-5])
cl <- hclass(hcTree,c(2,3))

## Not run:
par(pty = "s", mfrow = c(1,1))
clPairs(iris[,-5],cl=cl[,"2"])
clPairs(iris[,-5],cl=cl[,"3"])

par(mfrow = c(1,2))
dimens <- c(1,2)
coordProj(iris[,-5], classification=cl[,"2"], dimens=dimens)
coordProj(iris[,-5], classification=cl[,"3"], dimens=dimens)

## End(Not run)
```

hclass *Classifications from Hierarchical Agglomeration*

Description

Determines the classifications corresponding to different numbers of groups given merge pairs from hierarchical agglomeration.

Usage

```
hclass(hcPairs, G)
```

Arguments

hcPairs	A numeric two-column matrix in which the *i*th row gives the minimum index for observations in each of the two clusters merged at the *i*th stage of agglomerative hierarchical clustering.
G	An integer or vector of integers giving the number of clusters for which the corresponding classfications are wanted.

Value

A matrix with `length(G)` columns, each column corresponding to a classification. Columns are indexed by the character representation of the integers in `G`.

See Also

hc, hcE

Examples

```
hcTree <- hc(modelName="VVV", data = iris[,-5])
cl <- hclass(hcTree,c(2,3))

## Not run:
par(pty = "s", mfrow = c(1,1))
clPairs(iris[,-5],cl=cl[,"2"])
clPairs(iris[,-5],cl=cl[,"3"])

## End(Not run)
```

`hdrlevels` *Highest Density Region (HDR) Levels*

Description

Compute the levels of Highest Density Regions (HDRs) for any density and probability levels.

Usage

```
hdrlevels(density, prob)
```

Arguments

`density`	A vector of density values computed on a set of (observed) evaluation points.
`prob`	A vector of probability levels in the range $[0, 1]$.

Details

From Hyndman (1996), let $f(x)$ be the density function of a random variable X. Then the $100(1-\alpha)\%$ HDR is the subset $R(f_\alpha)$ of the sample space of X such that

$$R(f_\alpha) = x : f(x) \geq f_\alpha$$

where f_α is the largest constant such that $Pr(X \in R(f_\alpha)) \geq 1 - \alpha$

Value

The function returns a vector of density values corresponding to HDRs at given probability levels.

Author(s)

L. Scrucca

References

Rob J. Hyndman (1996) Computing and Graphing Highest Density Regions. *The American Statistician*, 50(2):120-126.

See Also

`plot.densityMclust`

Examples

```
# Example: univariate Gaussian
x <- rnorm(1000)
f <- dnorm(x)
a <- c(0.5, 0.25, 0.1)
(f_a <- hdrlevels(f, prob = 1-a))

plot(x, f)
abline(h = f_a, lty = 2)
text(max(x), f_a, labels = paste0("f_", a), pos = 3)

mean(f > f_a[1])
range(x[which(f > f_a[1])])
qnorm(1-a[1]/2)

mean(f > f_a[2])
range(x[which(f > f_a[2])])
qnorm(1-a[2]/2)

mean(f > f_a[3])
range(x[which(f > f_a[3])])
qnorm(1-a[3]/2)

# Example 2: univariate Gaussian mixture
set.seed(1)
cl <- sample(1:2, size = 1000, prob = c(0.7, 0.3), replace = TRUE)
x <- ifelse(cl == 1,
            rnorm(1000, mean = 0, sd = 1),
            rnorm(1000, mean = 4, sd = 1))
f <- 0.7*dnorm(x, mean = 0, sd = 1) + 0.3*dnorm(x, mean = 4, sd = 1)

a <- 0.25
(f_a <- hdrlevels(f, prob = 1-a))

plot(x, f)
abline(h = f_a, lty = 2)
text(max(x), f_a, labels = paste0("f_", a), pos = 3)

mean(f > f_a)

# find the regions of HDR
ord <- order(x)
f <- f[ord]
x <- x[ord]
x_a <- x[f > f_a]
j <- which.max(diff(x_a))
region1 <- x_a[c(1,j)]
region2 <- x_a[c(j+1,length(x_a))]
plot(x, f, type = "l")
abline(h = f_a, lty = 2)
abline(v = region1, lty = 3, col = 2)
abline(v = region2, lty = 3, col = 3)
```

hypvol *Aproximate Hypervolume for Multivariate Data*

Description

Computes a simple approximation to the hypervolume of a multivariate data set.

Usage

```
hypvol(data, reciprocal=FALSE)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
reciprocal	A logical variable indicating whether or not the reciprocal hypervolume is desired rather than the hypervolume itself. The default is to return the hypervolume.

Value

Returns the minimum of the hypervolume computed from simple variable bounds and that computed from variable bounds of the principal component scores. Used for the default hypervolume parameter for the noise component when observations are designated as noise in `Mclust` and `mclustBIC`.

References

A. Dasgupta and A. E. Raftery (1998). Detecting features in spatial point processes with clutter via model-based clustering. *Journal of the American Statistical Association 93:294-302*.

C. Fraley and A.E. Raftery (1998). *Computer Journal 41:578-588*.

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association 97:611-631*.

See Also

`mclustBIC`

Examples

```
hypvol(iris[,-5])
```

icl *ICL for an estimated Gaussian Mixture Model*

Description

Computes the ICL (Integrated Complete-data Likelihood) for criterion for a Gaussian Mixture Model fitted by Mclust.

Usage

```
icl(object, ...)
```

Arguments

object	An object of class 'Mclust' resulting from a call to Mclust.
...	Further arguments passed to or from other methods.

Value

The ICL for the given input MCLUST model.

References

Biernacki, C., Celeux, G., Govaert, G. (2000). Assessing a mixture model for clustering with the integrated completed likelihood. *IEEE Trans. Pattern Analysis and Machine Intelligence*, 22 (7), 719-725.

See Also

Mclust, mclustBIC, mclustICL, bic.

Examples

```
mod <- Mclust(iris[,1:4])
icl(mod)
```

imputeData *Missing data imputation via the* **mix** *package*

Description

Imputes missing data using the **mix** package.

Usage

```
imputeData(data, categorical = NULL, seed = NULL, verbose = interactive())
```

Arguments

data	A numeric vector, matrix, or data frame of observations containing missing values. Categorical variables are allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
categorical	A logical vectors whose *i*th entry is TRUE if the *i*th variable or column of data is to be interpreted as categorical and FALSE otherwise. The default is to assume that a variable is to be interpreted as categorical only if it is a factor.
seed	A seed for the function rngseed that is used to initialize the random number generator in **mix**. By default, a seed is chosen uniformly in the interval (.Machine$integer.max/1024, .Machine$integer.max).
verbose	A logical, if TRUE reports info about iterations of the algorithm.

Value

A dataset of the same dimensions as data with missing values filled in.

References

Schafer J. L. (1997). Analysis of Imcomplete Multivariate Data, Chapman and Hall.

See Also

imputePairs

Examples

```
## Not run:
# Note that package 'mix' must be installed
data(stlouis, package = "mix")

# impute the continuos variables in the stlouis data
stlimp <- imputeData(stlouis[,-(1:3)])

# plot imputed values
imputePairs(stlouis[,-(1:3)], stlimp)

## End(Not run)
```

imputePairs *Pairwise Scatter Plots showing Missing Data Imputations*

Description

Creates a scatter plot for each pair of variables in given data, allowing display of imputations for missing values in different colors and symbols than non missing values.

Usage

```
imputePairs(data, dataImp,
            symbols = c(1,16), colors = c("black", "red"), labels,
            panel = points, ..., lower.panel = panel, upper.panel = panel,
            diag.panel = NULL, text.panel = textPanel, label.pos = 0.5 +
            has.diag/3, cex.labels = NULL, font.labels = 1, row1attop = TRUE,
            gap = 0.2)
```

Arguments

data	A numeric vector, matrix, or data frame of observations containing missing values. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
dataImp	The dataset data with missing values imputed.
symbols	Either an integer or character vector assigning plotting symbols to the nonmissing data and impued values, respectively. The default is a closed circle for the nonmissing data and an open circle for the imputed values.
colors	Either an integer or character vector assigning colors to the nonmissing data and impued values, respectively. The default is black for the nonmissing data and red for the imputed values.
labels	As in function pairs.
panel	As in function pairs.
...	As in function pairs.
lower.panel	As in function pairs.
upper.panel	As in function pairs.
diag.panel	As in function pairs.
text.panel	As in function pairs.
label.pos	As in function pairs.
cex.labels	As in function pairs.
font.labels	As in function pairs.
row1attop	As in function pairs.
gap	As in function pairs.

Value

A pairs plot displaying the location of missing and nonmissing values.

References

Schafer J. L. (1997). Analysis of Imcomplete Multivariate Data, Chapman and Hall.

See Also

pairs, imputeData

Examples

```
## Not run:
# Note that package 'mix' must be installed
data(stlouis, package = "mix")

# impute the continuos variables in the stlouis data
stlimp <- imputeData(stlouis[,-(1:3)])

# plot imputed values
imputePairs(stlouis[,-(1:3)], stlimp)

## End(Not run)
```

---

logLik.Mclust *Log-Likelihood of a* Mclust *object*

Description

Returns the log-likelihood for a 'Mclust' object.

Usage

```
  ## S3 method for class 'Mclust'
logLik(object, ...)
```

Arguments

object	an object of class 'Mclust' resulting from a call to Mclust.
...	further arguments passed to or from other methods.

Value

Returns an object of class 'logLik' with an element providing the maximized log-likelihood, and further arguments giving the number of (estimated) parameters in the model ("df") and the sample size ("nobs").

Author(s)

Luca Scrucca

See Also

Mclust.

Examples

```
## Not run:
irisMclust <- Mclust(iris[,1:4])
summary(irisMclust)
logLik(irisMclust)

## End(Not run)
```

---

logLik.MclustDA *Log-Likelihood of a* MclustDA *object*

Description

Returns the log-likelihood for a MclustDA object.

Usage

```
  ## S3 method for class 'MclustDA'
logLik(object, data, ...)
```

Arguments

object	an object of class 'MclustDA' resulting from a call to MclustDA.
data	the data for which the log-likelihood must be computed. If missing, the observed data from the 'MclustDA' object is used.
...	further arguments passed to or from other methods.

Value

Returns an object of class 'logLik' with an element providing the maximized log-likelihood, and further arguments giving the number of (estimated) parameters in the model ("df") and the sample size ("nobs").

Author(s)

Luca Scrucca

See Also

MclustDA.

Examples

```
## Not run:
irisMclustDA <- MclustDA(iris[,1:4], iris$Species)
summary(irisMclustDA)
logLik(irisMclustDA)

## End(Not run)
```

---

majorityVote *Majority vote*

Description

A function to compute the majority vote (some would say plurality) label in a vector of labels, breaking ties at random.

Usage

```
majorityVote(x)
```

Arguments

x	A vector of values, either numerical or not.

Value

A list with the following components:

table	A table of votes for each unique value of x.
ind	An integer specifying which unique value of x corresponds to the majority vote.
majority	A string specifying the majority vote label.

Author(s)

L. Scrucca

Examples

```
x <- c("A", "C", "A", "B", "C", "B", "A")
majorityVote(x)
```

map *Classification given Probabilities*

Description

Converts a matrix in which each row sums to 1 to an integer vector specifying for each row the column index of the maximum.

Usage

```
map(z, warn = mclust.options("warn"), ...)
```

Arguments

z	A matrix (for example a matrix of conditional probabilities in which each row sums to 1 as produced by the E-step of the EM algorithm).
warn	A logical variable indicating whether or not a warning should be issued when there are some columns of z for which no row attains a maximum.
...	Provided to allow lists with elements other than the arguments can be passed in indirect or list calls with do.call.

Value

A integer vector with one entry for each row of z, in which the *i*-th value is the column index at which the *i*-th row of z attains a maximum.

See Also

unmap, estep, em, me.

Examples

```
emEst <- me(modelName = "VVV", data = iris[,-5], z = unmap(iris[,5]))

map(emEst$z)
```

mapClass *Correspondence between classifications*

Description

Best correspondence between classes given two vectors viewed as alternative classifications of the same object.

Usage

```
mapClass(a, b)
```

Arguments

a	A numeric or character vector of class labels.
b	A numeric or character vector of class labels. Must have the same length as a.

Value

A list with two named elements, aTOb and bTOa which are themselves lists. The aTOb list has a component corresponding to each unique element of a, which gives the element or elements of b that result in the closest class correspondence.

The bTOa list has a component corresponding to each unique element of b, which gives the element or elements of a that result in the closest class correspondence.

See Also

mapClass, classError, table

Examples

```
a <- rep(1:3, 3)
a
b <- rep(c("A", "B", "C"), 3)
b
mapClass(a, b)
a <- sample(1:3, 9, replace = TRUE)
a
b <- sample(c("A", "B", "C"), 9, replace = TRUE)
b
mapClass(a, b)
```

Mclust *Model-Based Clustering*

Description

Model-based clustering based on parameterized finite Gaussian mixture models. Models are estimated by EM algorithm initialized by hierarchical model-based agglomerative clustering. The optimal model is then selected according to BIC.

Usage

```
Mclust(data, G = NULL, modelNames = NULL,
     prior = NULL,
     control = emControl(),
     initialization = NULL,
     warn = mclust.options("warn"),
     x =  NULL,
     verbose = interactive(), ...)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations (n) and columns correspond to variables (d).
G	An integer vector specifying the numbers of mixture components (clusters) for which the BIC is to be calculated. The default is `G=1:9`.
modelNames	A vector of character strings indicating the models to be fitted in the EM phase of clustering. The default is: • for univariate data ($d = 1$): `c("E", "V")` • for multivariate data ($n > d$): all the models available in `mclust.options("emModelNames")` • for multivariate data ($n <= d$): the spherical and diagonal models, i.e. `c("EII", "VII", "EEI", "EVI", "VEI", "VVI")` The help file for `mclustModelNames` describes the available models.
prior	The default assumes no prior, but this argument allows specification of a conjugate prior on the means and variances through the function `priorControl`. Note that, as described in `defaultPrior`, in the multivariate case only 10 out of 14 models may be used in conjunction with a prior, i.e. those available in *MCLUST* up to version 4.4.
control	A list of control parameters for EM. The defaults are set by the call `emControl()`.
initialization	A list containing zero or more of the following components: `hcPairs` A matrix of merge pairs for hierarchical clustering such as produced by function `hc`. For multivariate data, the default is to compute a hierarchical agglomerative clustering tree by applying function `hc` with model specified by `mclust.options("hcModelName")`, and data transformation set by `mclust.options("hcUse")`. All the input or a subset as indicated by the `subset` argument is used for initial clustering. The hierarchical clustering results are then used to start the EM algorithm from a given partition. For univariate data, the default is to use quantiles to start the EM algorithm. However, hierarchical clustering could also be used by calling `hc` with model specified as `"V"` or `"E"`. `subset` A logical or numeric vector specifying a subset of the data to be used in the initial hierarchical clustering phase. By default no subset is used unless the number of observations exceeds the value specified by `mclust.options("subset")`.

Note that to guarantee exact reproducibility of results a seed must be specified (see set.seed).

noise A logical or numeric vector indicating an initial guess as to which observations are noise in the data. If numeric the entries should correspond to row indexes of the data. If supplied, a noise term will be added to the model in the estimation.

warn A logical value indicating whether or not certain warnings (usually related to singularity) should be issued. The default is controlled by mclust.options.

x An object of class 'mclustBIC'. If supplied, BIC values for models that have already been computed and are available in x are not recomputed. All arguments, with the exception of data, G and modelName, are ignored and their values are set as specified in the attributes of x. Defaults for G and modelNames are taken from x.

verbose A logical controlling if a text progress bar is displayed during the fitting procedure. By default is TRUE if the session is interactive, and FALSE otherwise..

... Catches unused arguments in indirect or list calls via do.call.

Value

An object of class 'Mclust' providing the optimal (according to BIC) mixture model estimation.

The details of the output components are as follows:

call The matched call

data The input data matrix.

modelName A character string denoting the model at which the optimal BIC occurs.

n The number of observations in the data.

d The dimension of the data.

G The optimal number of mixture components.

BIC All BIC values.

bic Optimal BIC value.

loglik The log-likelihood corresponding to the optimal BIC.

df The number of estimated parameters.

hypvol The hypervolume parameter for the noise component if required, otherwise set to NULL (see hypvol).

parameters A list with the following components:

pro A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If missing, equal proportions are assumed.

mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model.

variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details.

z	A matrix whose *[i,k]*th entry is the probability that observation *i* in the test data belongs to the *k*th class.
classification	The classification corresponding to z, i.e. map(z).
uncertainty	The uncertainty associated with the classification.

References

Scrucca L., Fop M., Murphy T. B. and Raftery A. E. (2016) mclust 5: clustering, classification and density estimation using Gaussian finite mixture models, *The R Journal*, 8/1, pp. 205-233.

Fraley C. and Raftery A. E. (2002) Model-based clustering, discriminant analysis and density estimation, *Journal of the American Statistical Association*, 97/458, pp. 611-631.

Fraley C., Raftery A. E., Murphy T. B. and Scrucca L. (2012) mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. *Technical Report* No. 597, Department of Statistics, University of Washington.

C. Fraley and A. E. Raftery (2007) Bayesian regularization for normal mixture estimation and model-based clustering. *Journal of Classification*, 24, 155-181.

See Also

summary.Mclust, plot.Mclust, priorControl, emControl, hc, mclustBIC, mclustModelNames, mclust.options

Examples

```
mod1 <- Mclust(iris[,1:4])
summary(mod1)

mod2 <- Mclust(iris[,1:4], G = 3)
summary(mod2, parameters = TRUE)

# Using prior
mod3 <- Mclust(iris[,1:4], prior = priorControl())
summary(mod3)

mod4 <- Mclust(iris[,1:4], prior = priorControl(functionName="defaultPrior", shrinkage=0.1))
summary(mod4)

# Clustering of faithful data with some artificial noise added
nNoise <- 100
set.seed(0) # to make it reproducible
Noise <- apply(faithful, 2, function(x)
             runif(nNoise, min = min(x)-.1, max = max(x)+.1))
data <- rbind(faithful, Noise)
plot(faithful)
points(Noise, pch = 20, cex = 0.5, col = "lightgrey")
set.seed(0)
NoiseInit <- sample(c(TRUE,FALSE), size = nrow(faithful)+nNoise,
          replace = TRUE, prob = c(3,1)/4)
mod5 <- Mclust(data, initialization = list(noise = NoiseInit))
summary(mod5, parameter = TRUE)
```

```
plot(mod5, what = "classification")
```

`mclust-deprecated` *Deprecated Functions in mclust package*

Description

These functions are provided for compatibility with older versions of the **mclust** package only, and may be removed eventually.

Usage

```
cv.MclustDA(...)
cv1EMtrain(data, labels, modelNames=NULL)
bicEMtrain(data, labels, modelNames=NULL)
```

Arguments

`...`	pass arguments down.
`data`	A numeric vector or matrix of observations.
`labels`	Labels for each element or row in the dataset.
`modelNames`	Vector of model names that should be tested. The default is to select all available model names.

See Also

`deprecated`

`mclust.options` *Default values for use with MCLUST package*

Description

Set or retrieve default values for use with MCLUST package.

Usage

```
mclust.options(...)
```

Arguments

`...`	one or more arguments provided in the `name = value` form, or no argument at all may be given. Available arguments are described in the Details section below.

Details

`mclust.options` is provided for assigning or retrieving default values used by various functions in `MCLUST`.

Available options are:

`emModelNames` A vector of 3-character strings that are associated with multivariate models for which EM estimation is available in MCLUST.
The current default is all of the multivariate mixture models supported in MCLUST. The help file for `mclustModelNames` describes the available models.

`hcModelName` A string associated with multivariate models for which model-based hierarchical clustering is available in MCLUST.
The available models are the following:

- `"EII"` spherical, equal volume
- `"EEE"` ellipsoidal, equal volume, shape, and orientation
- `"VII"` spherical, unequal volume
- `"VVV"` ellipsoidal, varying volume, shape, and orientation.

The `"VVV"` is used as default for initialization of EM algorithm.

`hcUse` A string or a vector of character strings specifying the type of input variables to be used in model-based hierarchical clustering to start the EM algorithm. Possible values are:

- `"VARS"` original variables;
- `"STD"` standardized variables;
- `"SPH"` sphered variables (centered, scaled, uncorrelated) computed using SVD;
- `"PCS"` principal components computed using SVD on centered variables (i.e. using the covariance matrix);
- `"PCR"` principal components computed using SVD on standardized (center and scaled) variables (i.e. using the correlation matrix);
- `"SVD"` scaled SVD transformation;
- `"RND"` no transformation is applied but a random hierarchical structure is returned (see `randomPairs`).

For further details see Scrucca and Raftery (2015), Scrucca et al. (2016).

`subset` A value specifying the maximal sample size to be used in the model-based hierarchical clustering to start the EM algorithm. If data sample size exceeds this value, a random sample is drawn of size specified by `subset`.

`fillEllipses` A logical value specifying whether or not to fill with transparent colors ellipses corresponding to the within-cluster covariances in case of `"classification"` plot for `'Mclust'` objects, or `"scatterplot"` graphs for `'MclustDA'` objects.

`bicPlotSymbols` A vector whose entries correspond to graphics symbols for plotting the BIC values output from `Mclust` and `mclustBIC`. These are displayed in the legend which appears at the lower right of the BIC plots.

`bicPlotColors` A vector whose entries correspond to colors for plotting the BIC curves from output from `Mclust` and `mclustBIC`. These are displayed in the legend which appears at the lower right of the BIC plots.

`classPlotSymbols` A vector whose entries are either integers corresponding to graphics symbols or single characters for indicating classifications when plotting data. Classes are assigned symbols in the given order.

`classPlotColors` A vector whose entries correspond to colors for indicating classifications when plotting data. Classes are assigned colors in the given order.

`warn` A logical value indicating whether or not to issue certain warnings. Most of these warnings have to do with situations in which singularities are encountered. The default is `warn = FALSE`.

The parameter values set via a call to this function will remain in effect for the rest of the session, affecting the subsequent behaviour of the functions for which the given parameters are relevant.

Value

If the argument list is empty the function returns the current list of values. If the argument list is not empty, the returned list is invisible.

References

Scrucca L. and Raftery A. E. (2015) Improved initialisation of model-based clustering using Gaussian hierarchical partitions. *Advances in Data Analysis and Classification*, 9/4, pp. 447-460.

Scrucca L., Fop M., Murphy T. B. and Raftery A. E. (2016) mclust 5: clustering, classification and density estimation using Gaussian finite mixture models, *The R Journal*, 8/1, pp. 205-233.

See Also

`Mclust`, `MclustDA`, `densityMclust`, `emControl`

Examples

```
opt <- mclust.options() # save default values
irisBIC <- mclustBIC(iris[,-5])
summary(irisBIC, iris[,-5])

mclust.options(emModelNames = c("EII", "EEI", "EEE"))
irisBIC <- mclustBIC(iris[,-5])
summary(irisBIC, iris[,-5])

mclust.options(opt)    # restore default values
mclust.options()

oldpar <- par(mfrow = c(2,1), no.readonly = TRUE)
n <- with(mclust.options(),
          max(sapply(list(bicPlotSymbols, bicPlotColors),length)))
plot(seq(n), rep(1,n), ylab = "", xlab = "", yaxt = "n",
     pch = mclust.options("bicPlotSymbols"),
     col = mclust.options("bicPlotColors"))
title("mclust.options(\"bicPlotSymbols\") \n mclust.options(\"bicPlotColors\")")
n <- with(mclust.options(),
          max(sapply(list(classPlotSymbols, classPlotColors),length)))
plot(seq(n), rep(1,n), ylab = "", xlab = "", yaxt = "n",
     pch = mclust.options("classPlotSymbols"),
```

```
     col = mclust.options("classPlotColors"))
title("mclust.options(\"classPlotSymbols\") \n mclust.options(\"classPlotColors\")")
par(oldpar)
```

`mclust1Dplot` *Plot one-dimensional data modeled by an MVN mixture.*

Description

Plot one-dimensional data given parameters of an MVN mixture model for the data.

Usage

```
mclust1Dplot(data, parameters = NULL, z = NULL,
             classification = NULL, truth = NULL, uncertainty = NULL,
             what = c("classification", "density", "error", "uncertainty"),
             symbols = NULL, colors = NULL, ngrid = length(data),
             xlab = NULL, ylab = NULL,
             xlim = NULL, ylim = NULL,
             CEX = 1, main = FALSE, ...)
```

Arguments

`data`	A numeric vector of observations. Categorical variables are not allowed.
`parameters`	A named list giving the parameters of an *MCLUST* model, used to produce superimposing ellipses on the plot. The relevant components are as follows: `pro` Mixing proportions for the components of the mixture. There should one more mixing proportion than the number of Gaussian components if the mixture model includes a Poisson noise term. `mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. `variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.
`z`	A matrix in which the `[i,k]`th entry gives the probability of observation *i* belonging to the *k*th class. Used to compute `classification` and `uncertainty` if those arguments aren't available.
`classification`	A numeric or character vector representing a classification of observations (rows) of `data`. If present argument `z` will be ignored.
`truth`	A numeric or character vector giving a known classification of each data point. If `classification` or `z` is also present, this is used for displaying classification errors.
`uncertainty`	A numeric vector of values in *(0,1)* giving the uncertainty of each data point. If present argument `z` will be ignored.

what	Choose from one of the following options: "classification" (default), "density", "error", "uncertainty".
symbols	Either an integer or character vector assigning a plotting symbol to each unique class classification. Elements in symbols correspond to classes in classification in order of appearance in the observations (the order used by the function unique). The default is to use a single plotting symbol |. Classes are delineated by showing them in separate lines above the whole of the data.
colors	Either an integer or character vector assigning a color to each unique class classification. Elements in colors correspond to classes in order of appearance in the observations (the order used by the function unique). The default is given is mclust.options("classPlotColors").
ngrid	Number of grid points to use for density computation over the interval spanned by the data. The default is the length of the data set.
xlab, ylab	An argument specifying a label for the axes.
xlim, ylim	An argument specifying bounds of the plot. This may be useful for when comparing plots.
CEX	An argument specifying the size of the plotting symbols. The default value is 1.
main	A logical variable or NULL indicating whether or not to add a title to the plot identifying the dimensions used.
...	Other graphics parameters.

Value

A plot showing location of the mixture components, classification, uncertainty, density and/or classification errors. Points in the different classes are shown in separated levels above the whole of the data.

See Also

mclust2Dplot, clPairs, coordProj

Examples

```
## Not run:
n <- 250 ## create artificial data
set.seed(1)
y <- c(rnorm(n,-5), rnorm(n,0), rnorm(n,5))
yclass <- c(rep(1,n), rep(2,n), rep(3,n))

yModel <- Mclust(y)

mclust1Dplot(y, parameters = yModel$parameters, z = yModel$z,
             what = "classification")

mclust1Dplot(y, parameters = yModel$parameters, z = yModel$z,
             what = "error", truth = yclass)

mclust1Dplot(y, parameters = yModel$parameters, z = yModel$z,
```

```
              what = "density")

mclust1Dplot(y, z = yModel$z, parameters = yModel$parameters,
             what = "uncertainty")


## End(Not run)
```

`mclust2Dplot` *Plot two-dimensional data modelled by an MVN mixture*

Description

Plot two-dimensional data given parameters of an MVN mixture model for the data.

Usage

```
mclust2Dplot(data, parameters = NULL, z = NULL,
             classification = NULL, truth = NULL, uncertainty = NULL,
             what = c("classification", "uncertainty", "error"),
             addEllipses = TRUE, fillEllipses = mclust.options("fillEllipses"),
             symbols = NULL, colors = NULL,
             xlim = NULL, ylim = NULL, xlab = NULL, ylab = NULL,
             scale = FALSE, CEX  = 1, PCH = ".",
             main = FALSE, swapAxes = FALSE, ...)
```

Arguments

`data` A numeric matrix or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables. In this case the data are two dimensional, so there are two columns.

`parameters` A named list giving the parameters of an *MCLUST* model, used to produce superimposing ellipses on the plot. The relevant components are as follows:

- `pro` Mixing proportions for the components of the mixture. There should one more mixing proportion than the number of Gaussian components if the mixture model includes a Poisson noise term.
- `mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model.
- `variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.

`z` A matrix in which the `[i,k]`th entry gives the probability of observation *i* belonging to the *k*th class. Used to compute `classification` and `uncertainty` if those arguments aren't available.

classification	A numeric or character vector representing a classification of observations (rows) of data. If present argument z will be ignored.
truth	A numeric or character vector giving a known classification of each data point. If classification or z is also present, this is used for displaying classification errors.
uncertainty	A numeric vector of values in *(0,1)* giving the uncertainty of each data point. If present argument z will be ignored.
what	Choose from one of the following three options: "classification" (default), "error", "uncertainty".
addEllipses	A logical indicating whether or not to add ellipses with axes corresponding to the within-cluster covariances.
fillEllipses	A logical specifying whether or not to fill ellipses with transparent colors when addEllipses = TRUE.
symbols	Either an integer or character vector assigning a plotting symbol to each unique class in classification. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function unique). The default is given by mclust.options("classPlotSymbols").
colors	Either an integer or character vector assigning a color to each unique class in classification. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function unique). The default is given is mclust.options("classPlotColors").
xlim, ylim	Optional argument specifying bounds for the ordinate, abscissa of the plot. This may be useful for when comparing plots.
xlab, ylab	Optional argument specifying labels for the x-axis and y-axis.
scale	A logical variable indicating whether or not the two chosen dimensions should be plotted on the same scale, and thus preserve the shape of the distribution. Default: scale=FALSE
CEX	An argument specifying the size of the plotting symbols. The default value is 1.
PCH	An argument specifying the symbol to be used when a classificatiion has not been specified for the data. The default value is a small dot ".".
main	A logical variable or NULL indicating whether or not to add a title to the plot identifying the dimensions used.
swapAxes	A logical variable indicating whether or not the axes should be swapped for the plot.
...	Other graphics parameters.

Value

A plot showing the data, together with the location of the mixture components, classification, uncertainty, and/or classification errors.

See Also

surfacePlot, clPairs, coordProj, mclust.options

Examples

```
## Not run:
faithfulModel <- Mclust(faithful)

mclust2Dplot(faithful, parameters=faithfulModel$parameters,
             z=faithfulModel$z, what = "classification", main = TRUE)

mclust2Dplot(faithful, parameters=faithfulModel$parameters,
             z=faithfulModel$z, what = "uncertainty", main = TRUE)

## End(Not run)
```

---

mclustBIC *BIC for Model-Based Clustering*

Description

BIC for parameterized Gaussian mixture models fitted by EM algorithm initialized by model-based hierarchical clustering.

Usage

```
mclustBIC(data, G = NULL, modelNames = NULL,
          prior = NULL, control = emControl(),
          initialization = list(hcPairs = NULL,
                                subset = NULL,
                                noise = NULL),
          Vinv = NULL, warn = mclust.options("warn"),
          x = NULL, verbose = interactive(),
          ...)
```

Arguments

`data`	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
`G`	An integer vector specifying the numbers of mixture components (clusters) for which the BIC is to be calculated. The default is `G=1:9`, unless the argument `x` is specified, in which case the default is taken from the values associated with `x`.
`modelNames`	A vector of character strings indicating the models to be fitted in the EM phase of clustering. The help file for `mclustModelNames` describes the available models. The default is: `c("E", "V")` for univariate data `mclust.options("emModelNames")` for multivariate data (n > d) `c("EII", "VII", "EEI", "EVI", "VEI", "VVI")` the spherical and diagonal models for multivariate data (n <= d)

unless the argument x is specified, in which case the default is taken from the values associated with x.

prior — The default assumes no prior, but this argument allows specification of a conjugate prior on the means and variances through the function priorControl.

control — A list of control parameters for EM. The defaults are set by the call emControl().

initialization — A list containing zero or more of the following components:

hcPairs A matrix of merge pairs for hierarchical clustering such as produced by function hc.
For multivariate data, the default is to compute a hierarchical agglomerative clustering tree by applying function hc with model specified by mclust.options("hcModelName"), and data transformation set by mclust.options("hcUse").
All the input or a subset as indicated by the subset argument is used for initial clustering.
The hierarchical clustering results are then used to start the EM algorithm from a given partition.
For univariate data, the default is to use quantiles to start the EM algorithm. However, hierarchical clustering could also be used by calling hc with model specified as "V" or "E".

subset A logical or numeric vector specifying a subset of the data to be used in the initial hierarchical clustering phase. By default no subset is used unless the number of observations exceeds the value specified by mclust.options("subset"). The subset argument is ignored if hcPairs are provided. Note that to guarantee exact reproducibility of results a seed must be specified (see set.seed).

noise A logical or numeric vector indicating an initial guess as to which observations are noise in the data. If numeric the entries should correspond to row indexes of the data. If supplied, a noise term will be added to the model in the estimation.

Vinv — An estimate of the reciprocal hypervolume of the data region. The default is determined by applying function hypvol to the data. Used only if an initial guess as to which observations are noise is supplied.

warn — A logical value indicating whether or not certain warnings (usually related to singularity) should be issued when estimation fails. The default is controlled by mclust.options.

x — An object of class 'mclustBIC'. If supplied, mclustBIC will use the settings in x to produce another object of class 'mclustBIC', but with G and modelNames as specified in the arguments. Models that have already been computed in x are not recomputed. All arguments to mclustBIC except data, G and modelName are ignored and their values are set as specified in the attributes of x. Defaults for G and modelNames are taken from x.

verbose — A logical controlling if a text progress bar is displayed during the fitting procedure. By default is TRUE if the session is interactive, and FALSE otherwise..

... — Catches unused arguments in indirect or list calls via do.call.

Value

Return an object of class 'mclustBIC' containing the Bayesian Information Criterion for the specified mixture models numbers of clusters. Auxiliary information returned as attributes.

The corresponding print method shows the matrix of values and the top models according to the BIC criterion.

References

Scrucca L., Fop M., Murphy T. B. and Raftery A. E. (2016) mclust 5: clustering, classification and density estimation using Gaussian finite mixture models, *The R Journal*, 8/1, pp. 205-233.

Fraley C. and Raftery A. E. (2002) Model-based clustering, discriminant analysis and density estimation, *Journal of the American Statistical Association*, 97/458, pp. 611-631.

Fraley C., Raftery A. E., Murphy T. B. and Scrucca L. (2012) mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. *Technical Report* No. 597, Department of Statistics, University of Washington.

See Also

priorControl, emControl, mclustModel, summary.mclustBIC, hc, me, mclustModelNames, mclust.options

Examples

```
irisBIC <- mclustBIC(iris[,-5])
irisBIC
plot(irisBIC)

## Not run:
subset <- sample(1:nrow(iris), 100)
irisBIC <- mclustBIC(iris[,-5], initialization=list(subset = subset))
irisBIC
plot(irisBIC)

irisBIC1 <- mclustBIC(iris[,-5], G=seq(from=1,to=9,by=2),
                    modelNames=c("EII", "EEI", "EEE"))
irisBIC1
plot(irisBIC1)
irisBIC2  <- mclustBIC(iris[,-5], G=seq(from=2,to=8,by=2),
                       modelNames=c("VII", "VVI", "VVV"), x= irisBIC1)
irisBIC2
plot(irisBIC2)

## End(Not run)

nNoise <- 450
set.seed(0)
poissonNoise <- apply(apply( iris[,-5], 2, range), 2, function(x, n)
                      runif(n, min = x[1]-.1, max = x[2]+.1), n = nNoise)
set.seed(0)
noiseInit <- sample(c(TRUE,FALSE),size=nrow(iris)+nNoise,replace=TRUE,
                    prob=c(3,1))
```

```
irisNdata <- rbind(iris[,-5], poissonNoise)
irisNbic <- mclustBIC(data = irisNdata, G = 1:5,
                      initialization = list(noise = noiseInit))
irisNbic
plot(irisNbic)
```

`mclustBICupdate` *Update BIC values for parameterized Gaussian mixture models*

Description

Update the BIC (Bayesian Information Criterion) for parameterized Gaussian mixture models by taking the best from BIC results as returned by `mclustBIC`.

Usage

```
mclustBICupdate(BIC, ...)
```

Arguments

`BIC`	Object of class `'mclustBIC'` containing the BIC values as returned by a call to `mclustBIC`.
`...`	Further objects of class `'mclustBIC'` to be merged.

Value

An object of class `'mclustBIC'` containing the best values obtained from merging the input arguments. Attributes are also updated according to the best BIC found, so calling `Mclust` on the resulting ouput will return the corresponding best model (see example).

See Also

`mclustBIC`, `Mclust`.

Examples

```
## Not run:
data(galaxies, package = "MASS")
galaxies <- galaxies / 1000

# use several random starting points
BIC <- NULL
for(j in 1:100)
{
  rBIC <- mclustBIC(galaxies, verbose = FALSE,
                    initialization = list(hcPairs = randomPairs(galaxies)))
  BIC <- mclustBICupdate(BIC, rBIC)
}
pickBIC(BIC)
```

```
plot(BIC)

mod <- Mclust(galaxies, x = BIC)
summary(mod)

## End(Not run)
```

MclustBootstrap *Resampling-based Inference for Gaussian finite mixture models*

Description

Bootstrap or jackknife estimation of standard errors and percentile bootstrap confidence intervals for the parameters of a Gaussian mixture model.

Usage

```
MclustBootstrap(object, nboot = 999, type = c("bs", "wlbs", "pb", "jk"),
                max.nonfit = 10*nboot, verbose = interactive(),
                ...)
```

Arguments

object	An object of class 'Mclust' or 'densityMclust' providing an estimated Gaussian mixture model.
nboot	The number of bootstrap replications.
type	A character string specifying the type of resampling to use: "bs" nonparametric bootstrap "wlbs" weighted likelihood bootstrap "pb" parametric bootstrap "jk" jackknife
max.nonfit	The maximum number of non-estimable models allowed.
verbose	A logical controlling if a text progress bar is displayed during the resampling procedure. By default is TRUE if the session is interactive, and FALSE otherwise.
...	Further arguments passed to or from other methods.

Details

For a fitted Gaussian mixture model with object$G mixture components and covariances parameterisation object$modelName, this function returns either the bootstrap distribution or the jackknife distribution of mixture parameters. In the former case, the nonparametric bootstrap or the weighted likelihood bootstrap approach could be used, so the the bootstrap procedure generates nboot bootstrap samples of the same size as the original data by resampling with replacement from the observed data. In the jackknife case, the procedure considers all the samples obtained by omitting one observation at time.

The resulting resampling distribution can then be used to obtain standard errors and percentile confidence intervals by the use of summary.MclustBootstrap function.

Value

An object of class 'MclustBootstrap' with the following components:

n	The number of observations in the data.
d	The dimension of the data.
G	A value specifying the number of mixture components.
modelName	A character string specifying the mixture model covariances parameterisation (see mclustModelNames).
parameters	A list of estimated parameters for the mixture components with the following components: pro a vector of mixing proportions. mean a matrix of means for each component. variance an array of covariance matrices for each component.
nboot	The number of bootstrap replications if type = "bs" or type = "wlbs". The sample size if type = "jk".
type	The type of resampling approach used.
nonfit	The number of resamples that did not convergence during the procedure.
pro	A matrix of dimension (nboot x G) containing the bootstrap distribution for the mixing proportion.
mean	An array of dimension (nboot x d x G), where d is the dimension of the data, containing the bootstrap distribution for the component means.
variance	An array of dimension (nboot x d x d x G), where d is the dimension of the data, containing the bootstrap distribution for the component covariances.

References

Davison, A. and Hinkley, D. (1997) *Bootstrap Methods and Their Applications*. Cambridge University Press.

McLachlan, G.J. and Peel, D. (2000) *Finite Mixture Models*. Wiley.

O'Hagan A., Murphy T. B., Gormley I. C. and Scrucca L. (2015) On Estimation of Parameter Uncertainty in Model-Based Clustering. Submitted to *Computational Statistics*.

See Also

summary.MclustBootstrap, plot.MclustBootstrap, Mclust, densityMclust.

Examples

```
## Not run:
data(diabetes)
X <- diabetes[,-1]
modClust <- Mclust(X)
bootClust <- MclustBootstrap(modClust)
summary(bootClust, what = "se")
summary(bootClust, what = "ci")
```

```
data(acidity)
modDens <- densityMclust(acidity)
modDens <- MclustBootstrap(modDens)
summary(modDens, what = "se")
summary(modDens, what = "ci")

## End(Not run)
```

`mclustBootstrapLRT` *Bootstrap Likelihood Ratio Test for the Number of Mixture Components*

Description

Perform the likelihood ratio test (LRT) for assessing the number of mixture components in a specific finite mixture model parameterisation. The observed significance is approximated by using the (parametric) bootstrap for the likelihood ratio test statistic (LRTS).

Usage

```
mclustBootstrapLRT(data, modelName = NULL, nboot = 999, level = 0.05, maxG = NULL,
                   verbose = interactive(), ...)

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

## S3 method for class 'mclustBootstrapLRT'
plot(x, G = 1, hist.col = "grey", hist.border = "lightgrey", breaks = "Scott",
    col = "forestgreen", lwd = 2, lty = 3, main = NULL, ...)
```

Arguments

`data`	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
`modelName`	A character string indicating the mixture model to be fitted. The help file for `mclustModelNames` describes the available models.
`nboot`	The number of bootstrap replications to use (by default 999).
`level`	The significance level to be used to terminate the sequential bootstrap procedure.
`maxG`	The maximum number of mixture components G to test. If not provided the procedure is stopped when a test is not significant at the specified `level`.
`verbose`	A logical controlling if a text progress bar is displayed during the bootstrap procedure. By default is `TRUE` if the session is interactive, and `FALSE` otherwise.
`...`	Further arguments passed to or from other methods. In particular, see the optional arguments in `mclustBIC`.

x	An 'mclustBootstrapLRT' object.
G	A value specifying the number of components for which to plot the bootstrap distribution.
hist.col	The colour to be used to fill the bars of the histogram.
hist.border	The color of the border around the bars of the histogram.
breaks	See the argument in function hist.
col, lwd, lty	The color, line width and line type to be used to represent the observed LRT statistic.
main	The title for the graph.

Details

The implemented algorithm for computing the LRT observed significance using the bootstrap is the following. Let G_0 be the number of mixture components under the null hypothesis versus $G_1 = G_0 + 1$ under the alternative. Bootstrap samples are drawn by simulating data under the null hypothesis. Then, the p-value may be approximated using eq. (13) on McLachlan and Rathnayake (2014). Equivalently, using the notation of Davison and Hinkley (1997) it may be computed as

$$\text{p-value} = \frac{1 + \#\{LRT_b^* \geq LRTS_{obs}\}}{B + 1}$$

where
B = number of bootstrap samples
LRT_{obs} = LRTS computed on the observed data
LRT_b^* = LRTS computed on the bth bootstrap sample.

Value

An object of class 'mclustBootstrapLRT' with the following components:

G	A vector of number of components tested under the null hypothesis.
modelName	A character string specifying the mixture model as provided in the function call (see above).
obs	The observed values of the LRTS.
boot	A matrix of dimension nboot x the number of components tested containing the bootstrap values of LRTS.
p.value	A vector of p-values.

References

Davison, A. and Hinkley, D. (1997) *Bootstrap Methods and Their Applications*. Cambridge University Press.

McLachlan G.J. (1987) On bootstrapping the likelihood ratio test statistic for the number of components in a normal mixture. *Applied Statistics*, 36, 318-324.

McLachlan, G.J. and Peel, D. (2000) *Finite Mixture Models*. Wiley.

McLachlan, G.J. and Rathnayake, S. (2014) On the number of components in a Gaussian mixture model. *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery*, 4(5), pp. 341-355.

See Also

mclustBIC, mclustICL, Mclust

Examples

```
## Not run:
data(faithful)
faithful.boot = mclustBootstrapLRT(faithful, model = "VVV")
faithful.boot
plot(faithful.boot, G = 1)
plot(faithful.boot, G = 2)

## End(Not run)
```

MclustDA *MclustDA discriminant analysis*

Description

Discriminant analysis based on Gaussian finite mixture modeling.

Usage

```
MclustDA(data, class, G = NULL, modelNames = NULL,
         modelType = c("MclustDA", "EDDA"),
         prior = NULL,
         control = emControl(),
         initialization = NULL,
         warn = mclust.options("warn"),
         verbose = interactive(),
         ...)
```

Arguments

data	A data frame or matrix giving the training data.
class	A vector giving the class labels for the observations in the training data.
G	An integer vector specifying the numbers of mixture components (clusters) for which the BIC is to be calculated within each class. The default is G = 1:5. A different set of mixture components for each class can be specified by providing this argument with a list of integers for each class. See the examples below.
modelNames	A vector of character strings indicating the models to be fitted by EM within each class (see the description in mclustModelNames). A different set of mixture models for each class can be specified by providing this argument with a list of character strings. See the examples below.

`modelType` A character string specifying whether the models given in `modelNames` should fit a different number of mixture components and covariance structures for each class (`"MclustDA"`, the default) or should be constrained to have a single component for each class with the same covariance structure among classes (`"EDDA"`). See Details section and the examples below.

`prior` The default assumes no prior, but this argument allows specification of a conjugate prior on the means and variances through the function `priorControl`.

`control` A list of control parameters for EM. The defaults are set by the call `emControl()`.

`initialization` A list containing zero or more of the following components:

`hcPairs` A matrix of merge pairs for hierarchical clustering such as produced by function `hc`. The default is to compute a hierarchical clustering tree by applying function `hc` with `modelName = "E"` to univariate data and `modelName = "VVV"` to multivariate data or a subset as indicated by the `subset` argument. The hierarchical clustering results are used as starting values for EM.

`subset` A logical or numeric vector specifying a subset of the data to be used in the initial hierarchical clustering phase.

`warn` A logical value indicating whether or not certain warnings (usually related to singularity) should be issued when estimation fails. The default is controlled by `mclust.options`.

`verbose` A logical controlling if a text progress bar is displayed during the fitting procedure. By default is `TRUE` if the session is interactive, and `FALSE` otherwise..

`...` Further arguments passed to or from other methods.

Details

The `"EDDA"` method for discriminant analysis is described in Bensmail and Celeux (1996), while `"MclustDA"` in Fraley and Raftery (2002).

Value

An object of class `'MclustDA'` providing the optimal (according to BIC) mixture model.

The details of the output components are as follows:

`call` The matched call.

`data` The input data matrix.

`class` The input class labels.

`type` A character string specifying the `modelType` estimated.

`models` A list of `Mclust` objects containing information on fitted model for each class.

`n` The total number of observations in the data.

`d` The dimension of the data.

`bic` Optimal BIC value.

`loglik` Log-likelihood for the selected model.

`df` Number of estimated parameters.

Author(s)

Luca Scrucca

References

Scrucca L., Fop M., Murphy T. B. and Raftery A. E. (2016) mclust 5: clustering, classification and density estimation using Gaussian finite mixture models, *The R Journal*, 8/1, pp. 205-233.

Fraley C. and Raftery A. E. (2002) Model-based clustering, discriminant analysis and density estimation, *Journal of the American Statistical Association*, 97/458, pp. 611-631.

Fraley C., Raftery A. E., Murphy T. B. and Scrucca L. (2012) mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. *Technical Report* No. 597, Department of Statistics, University of Washington.

Bensmail, H., and Celeux, G. (1996) Regularized Gaussian Discriminant Analysis Through Eigenvalue Decomposition.*Journal of the American Statistical Association*, 91, 1743-1748.

See Also

summary.MclustDA, plot.MclustDA, predict.MclustDA, classError

Examples

```
odd <- seq(from = 1, to = nrow(iris), by = 2)
even <- odd + 1
X.train <- iris[odd,-5]
Class.train <- iris[odd,5]
X.test <- iris[even,-5]
Class.test <- iris[even,5]

# common EEE covariance structure (which is essentially equivalent to linear discriminant analysis)
irisMclustDA <- MclustDA(X.train, Class.train, modelType = "EDDA", modelNames = "EEE")
summary(irisMclustDA, parameters = TRUE)
summary(irisMclustDA, newdata = X.test, newclass = Class.test)

# common covariance structure selected by BIC
irisMclustDA <- MclustDA(X.train, Class.train, modelType = "EDDA")
summary(irisMclustDA, parameters = TRUE)
summary(irisMclustDA, newdata = X.test, newclass = Class.test)

# general covariance structure selected by BIC
irisMclustDA <- MclustDA(X.train, Class.train)
summary(irisMclustDA, parameters = TRUE)
summary(irisMclustDA, newdata = X.test, newclass = Class.test)

plot(irisMclustDA)
plot(irisMclustDA, dimens = 3:4)
plot(irisMclustDA, dimens = 4)

plot(irisMclustDA, what = "classification")
plot(irisMclustDA, what = "classification", newdata = X.test)
plot(irisMclustDA, what = "classification", dimens = 3:4)
```

```
plot(irisMclustDA, what = "classification", newdata = X.test, dimens = 3:4)
plot(irisMclustDA, what = "classification", dimens = 4)
plot(irisMclustDA, what = "classification", dimens = 4, newdata = X.test)

plot(irisMclustDA, what = "train&test", newdata = X.test)
plot(irisMclustDA, what = "train&test", newdata = X.test, dimens = 3:4)
plot(irisMclustDA, what = "train&test", newdata = X.test, dimens = 4)

plot(irisMclustDA, what = "error")
plot(irisMclustDA, what = "error", dimens = 3:4)
plot(irisMclustDA, what = "error", dimens = 4)
plot(irisMclustDA, what = "error", newdata = X.test, newclass = Class.test)
plot(irisMclustDA, what = "error", newdata = X.test, newclass = Class.test, dimens = 3:4)
plot(irisMclustDA, what = "error", newdata = X.test, newclass = Class.test, dimens = 4)

## Not run:
# simulated 1D data
n <- 250
set.seed(1)
triModal <- c(rnorm(n,-5), rnorm(n,0), rnorm(n,5))
triClass <- c(rep(1,n), rep(2,n), rep(3,n))
odd <- seq(from = 1, to = length(triModal), by = 2)
even <- odd + 1
triMclustDA <- MclustDA(triModal[odd], triClass[odd])
summary(triMclustDA, parameters = TRUE)
summary(triMclustDA, newdata = triModal[even], newclass = triClass[even])
plot(triMclustDA, what = "scatterplot")
plot(triMclustDA, what = "classification")
plot(triMclustDA, what = "classification", newdata = triModal[even])
plot(triMclustDA, what = "train&test", newdata = triModal[even])
plot(triMclustDA, what = "error")
plot(triMclustDA, what = "error", newdata = triModal[even], newclass = triClass[even])

# simulated 2D cross data
data(cross)
odd <- seq(from = 1, to = nrow(cross), by = 2)
even <- odd + 1
crossMclustDA <- MclustDA(cross[odd,-1], cross[odd,1])
summary(crossMclustDA, parameters = TRUE)
summary(crossMclustDA, newdata = cross[even,-1], newclass = cross[even,1])
plot(crossMclustDA, what = "scatterplot")
plot(crossMclustDA, what = "classification")
plot(crossMclustDA, what = "classification", newdata = cross[even,-1])
plot(crossMclustDA, what = "train&test", newdata = cross[even,-1])
plot(crossMclustDA, what = "error")
plot(crossMclustDA, what = "error", newdata =cross[even,-1], newclass = cross[even,1])

## End(Not run)
```

`MclustDR` *Dimension reduction for model-based clustering and classification*

Description

A dimension reduction method for visualizing the clustering or classification structure obtained from a finite mixture of Gaussian densities.

Usage

```
MclustDR(object, lambda = 0.5, normalized = TRUE, Sigma,
         tol = sqrt(.Machine$double.eps))
```

Arguments

object	An object of class 'Mclust' or 'MclustDA' resulting from a call to, respectively, Mclust or MclustDA.
lambda	A tuning parameter in the range [0,1] described in Scrucca (2014). The default 0.5 gives equal importance to differences in means and covariances among clusters/classes. To recover the directions that mostly separate the estimated clusters or classes set this parameter to 1.
normalized	Logical. If TRUE directions are normalized to unit norm.
Sigma	Marginal covariance matrix of data. If not provided is estimated by the MLE of observed data.
tol	A tolerance value.

Details

The method aims at reducing the dimensionality by identifying a set of linear combinations, ordered by importance as quantified by the associated eigenvalues, of the original features which capture most of the clustering or classification structure contained in the data.

Information on the dimension reduction subspace is obtained from the variation on group means and, depending on the estimated mixture model, on the variation on group covariances (see Scrucca, 2010).

Observations may then be projected onto such a reduced subspace, thus providing summary plots which help to visualize the underlying structure.

The method has been extended to the supervised case, i.e. when the true classification is known (see Scrucca, 2013).

This implementation doesn't provide a formal procedure for the selection of dimensionality. A future release will include one or more methods.

Value

An object of class 'MclustDR' with the following components:

call	The matched call
type	A character string specifying the type of model for which the dimension reduction is computed. Currently, possible values are "Mclust" for clustering, and "MclustDA" or "EDDA" for classification.
x	The data matrix.

Sigma	The covariance matrix of the data.
mixcomp	A numeric vector specifying the mixture component of each data observation.
class	A factor specifying the classification of each data observation. For model-based clustering this is equivalent to the corresponding mixture component. For model-based classification this is the known classification.
G	The number of mixture components.
modelName	The name of the parameterization of the estimated mixture model(s). See mclustModelNames.
mu	A matrix of means for each mixture component.
sigma	An array of covariance matrices for each mixture component.
pro	The estimated prior for each mixture component.
M	The kernel matrix.
lambda	The tuning parameter.
evalues	The eigenvalues from the generalized eigen-decomposition of the kernel matrix.
raw.evectors	The raw eigenvectors from the generalized eigen-decomposition of the kernel matrix, ordered according to the eigenvalues.
basis	The basis of the estimated dimension reduction subspace.
std.basis	The basis of the estimated dimension reduction subspace standardized to variables having unit standard deviation.
numdir	The dimension of the projection subspace.
dir	The estimated directions, i.e. the data projected onto the estimated dimension reduction subspace.

Author(s)

Luca Scrucca

References

Scrucca, L. (2010) Dimension reduction for model-based clustering. *Statistics and Computing*, 20(4), pp. 471-484.

Scrucca, L. (2014) Graphical Tools for Model-based Mixture Discriminant Analysis. *Advances in Data Analysis and Classification*, 8(2), pp. 147-165.

See Also

summary.MclustDR, plot.MclustDR, Mclust, MclustDA.

Examples

```
# clustering
data(diabetes)
mod <- Mclust(diabetes[,-1])
summary(mod)

dr <- MclustDR(mod)
```

```
summary(dr)
plot(dr, what = "scatterplot")
plot(dr, what = "evalues")

# adjust the tuning parameter to show the most separating directions
dr1 <- MclustDR(mod, lambda = 1)
summary(dr1)
plot(dr1, what = "scatterplot")
plot(dr1, what = "evalues")

# classification
data(banknote)

da <- MclustDA(banknote[,2:7], banknote$Status, modelType = "EDDA")
dr <- MclustDR(da)
summary(dr)

da <- MclustDA(banknote[,2:7], banknote$Status)
dr <- MclustDR(da)
summary(dr)
```

`MclustDRsubsel` *Subset selection for GMMDR directions based on BIC*

Description

Implements a subset selection method for selecting the relevant directions spanning the dimension reduction subspace for visualizing the clustering or classification structure obtained from a finite mixture of Gaussian densities.

Usage

```
MclustDRsubsel(object, G = 1:9,
                       modelNames = mclust.options("emModelNames"),
                       ...,
                       bic.stop = 0, bic.cutoff = 0,
                       mindir = 1,
                       verbose = interactive())
```

Arguments

`object`	An object of class `'MclustDR'` resulting from a call to `MclustDR`.
`G`	An integer vector specifying the numbers of mixture components or clusters.
`modelNames`	A vector of character strings indicating the models to be fitted. See `mclustModelNames` for a description of the available models.
`...`	Further arguments passed through `Mclust` or `MclustDA`.

`bic.stop` A criterion to terminate the search. If maximal BIC difference is less than `bic.stop` then the algorithm stops.
Two tipical values are:

`0`: algorithm stops when the BIC difference becomes negative (default)

`-Inf`: algorithm continues until all directions have been selected

`bic.cutoff` A value specifying how to select simplest "best" model within `bic.cutoff` from the maximum value achieved. Setting this to `0` (default) simply select the model with the largest BIC difference.

`mindir` An integer value specifying the minimum number of directions to be estimated.

`verbose` A logical or integer value specifying if and how much detailed information should be reported during the iterations of the algorithm.
Possible values are:

`0` or `FALSE`: no trace info is shown;

`1` or `TRUE`: a trace info is shown at each step of the search;

`2`: a more detailed trace info is is shown.

Details

The GMMDR method aims at reducing the dimensionality by identifying a set of linear combinations, ordered by importance as quantified by the associated eigenvalues, of the original features which capture most of the clustering or classification structure contained in the data. This is implemented in `MclustDR`.

The `MclustDRsubsel` function implements the greedy forward search algorithm discussed in Scrucca (2010) to prune the set of all GMMDR directions. The criterion used to select the relevant directions is based on the BIC difference between a clustering model and a model in which the feature proposal has no clustering relevance. The steps are the following:

1. Select the first feature to be the one which maximizes the BIC difference between the best clustering model and the model which assumes no clustering, i.e. a single component.

2. Select the next feature amongst those not previously included, to be the one which maximizes the BIC difference.

3. Iterate the previous step until all the BIC differences for the inclusion of a feature become less than `bic.stop`.

At each step, the search over the model space is performed with respect to the model parametrisation and the number of clusters.

Value

An object of class `'MclustDRsubsel'` which inherits from `'MclustDR'`, so it has the same components of the latter plus the following:

`basisx` The basis of the estimated dimension reduction subspace expressed in terms of the original variables.

`std.basisx` The basis of the estimated dimension reduction subspace expressed in terms of the original variables standardized to have unit standard deviation.

Author(s)

Luca Scrucca

References

Scrucca, L. (2010) Dimension reduction for model-based clustering. *Statistics and Computing*, 20(4), pp. 471-484.

Scrucca, L. (2014) Graphical Tools for Model-based Mixture Discriminant Analysis. *Advances in Data Analysis and Classification*, 8(2), pp. 147-165

See Also

MclustDR, Mclust, MclustDA.

Examples

```
## Not run:
# clustering
data(crabs, package = "MASS")
x <- crabs[,4:8]
class <- paste(crabs$sp, crabs$sex, sep = "|")
mod <- Mclust(x)
table(class, mod$classification)
dr <- MclustDR(mod)
summary(dr)
plot(dr)
drs <- MclustDRsubsel(dr)
summary(drs)
table(class, drs$classification)
plot(drs, what = "scatterplot")
plot(drs, what = "pairs")
plot(drs, what = "contour")
plot(drs, what = "boundaries")
plot(drs, what = "evalues")

# classification
data(banknote)
da <- MclustDA(banknote[,2:7], banknote$Status)
table(banknote$Status, predict(da)$class)
dr <- MclustDR(da)
summary(dr)
drs <- MclustDRsubsel(dr)
summary(drs)
table(banknote$Status, predict(drs)$class)
plot(drs, what = "scatterplot")
plot(drs, what = "classification")
plot(drs, what = "boundaries")
## End(Not run)
```

mclustICL *ICL Criterion for Model-Based Clustering*

Description

ICL (Integrated Complete-data Likelihood) for parameterized Gaussian mixture models fitted by EM algorithm initialized by model-based hierarchical clustering.

Usage

```
mclustICL(data, G = NULL, modelNames = NULL,
          initialization = list(hcPairs = NULL,
                                subset = NULL,
                                noise = NULL),
          x = NULL, ...)

## S3 method for class 'mclustICL'
summary(object, G, modelNames, ...)
```

Arguments

`data`	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
`G`	An integer vector specifying the numbers of mixture components (clusters) for which the criteria should be calculated. The default is `G = 1:9`.
`modelNames`	A vector of character strings indicating the models to be fitted in the EM phase of clustering. The help file for `mclustModelNames` describes the available models. The default is: `c("E", "V")` for univariate data `mclust.options("emModelNames")` for multivariate data (n > d) `c("EII", "VII", "EEI", "EVI", "VEI", "VVI")` the spherical and diagonal models for multivariate data (n <= d)
`initialization`	A list containing zero or more of the following components: `hcPairs` A matrix of merge pairs for hierarchical clustering such as produced by function `hc`. For multivariate data, the default is to compute a hierarchical clustering tree by applying function `hc` with `modelName = "VVV"` to the data or a subset as indicated by the `subset` argument. The hierarchical clustering results are to start EM. For univariate data, the default is to use quantiles to start EM. `subset` A logical or numeric vector specifying a subset of the data to be used in the initial hierarchical clustering phase.
`x`	An object of class `'mclustICL'`. If supplied, `mclustICL` will use the settings in `x` to produce another object of class `'mclustICL'`, but with `G` and `modelNames` as specified in the arguments. Models that have already been computed in `x` are

not recomputed. All arguments to mclustICL except data, G and modelName are ignored and their values are set as specified in the attributes of x. Defaults for G and modelNames are taken from x.

... Futher arguments used in the call to Mclust. See also mclustBIC.

object An integer vector specifying the numbers of mixture components (clusters) for which the criteria should be calculated. The default is G = 1:9.

Value

Returns an object of class 'mclustICL' containing the the ICL criterion for the specified mixture models and numbers of clusters.

The corresponding print method shows the matrix of values and the top models according to the ICL criterion. The summary method shows only the top models.

References

Biernacki, C., Celeux, G., Govaert, G. (2000). Assessing a mixture model for clustering with the integrated completed likelihood. *IEEE Trans. Pattern Analysis and Machine Intelligence*, 22 (7), 719-725.

Scrucca L., Fop M., Murphy T. B. and Raftery A. E. (2016) mclust 5: clustering, classification and density estimation using Gaussian finite mixture models, *The R Journal*, 8/1, pp. 205-233.

See Also

plot.mclustICL, Mclust, mclustBIC, mclustBootstrapLRT, bic, icl

Examples

```
data(faithful)
faithful.ICL <- mclustICL(faithful)
faithful.ICL
summary(faithful.ICL)
plot(faithful.ICL)
## Not run:
# compare with
faithful.BIC <- mclustBIC(faithful)
faithful.BIC
plot(faithful.BIC)

## End(Not run)
```

mclustLoglik — *Log-likelihood from a table of BIC values for parameterized Gaussian mixture models*

Description

Compute the maximal log-likelihood from a table of BIC values contained in a `'mclustBIC'` object as returned by function `mclustBIC`.

Usage

```
mclustLoglik(object, ...)
```

Arguments

`object`	An object of class `'mclustBIC'` containing the BIC values as returned by a call to `mclustBIC`.
`...`	Catches unused arguments in an indirect or list call via `do.call`.

Value

An object of class `'mclustLoglik'` containing the maximal log-likelihood values for the Gaussian mixture models provided as input.

See Also

`mclustBIC`.

Examples

```
## Not run:
BIC <- mclustBIC(iris[,1:4])
mclustLoglik(BIC)

## End(Not run)
```

mclustModel — *Best model based on BIC*

Description

Determines the best model from clustering via `mclustBIC` for a given set of model parameterizations and numbers of components.

Usage

```
mclustModel(data, BICvalues, G, modelNames, ...)
```

Arguments

data	The matrix or vector of observations used to generate 'object'.
BICvalues	An 'mclustBIC' object, which is the result of applying mclustBIC to data.
G	A vector of integers giving the numbers of mixture components (clusters) from which the best model according to BIC will be selected (as.character(G) must be a subset of the row names of BICvalues). The default is to select the best model for all numbers of mixture components used to obtain BICvalues.
modelNames	A vector of integers giving the model parameterizations from which the best model according to BIC will be selected (as.character(model) must be a subset of the column names of BICvalues). The default is to select the best model for parameterizations used to obtain BICvalues.
...	Not used. For generic/method consistency.

Value

A list giving the optimal (according to BIC) parameters, conditional probabilities z, and log-likelihood, together with the associated classification and its uncertainty.

The details of the output components are as follows:

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.
n	The number of observations in the data.
d	The dimension of the data.
G	The number of components in the Gaussian mixture model corresponding to the optimal BIC.
bic	The optimal BIC value.
loglik	The log-likelihood corresponding to the optimal BIC.
parameters	A list with the following components: pro A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If missing, equal proportions are assumed. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details. Vinv The estimate of the reciprocal hypervolume of the data region used in the computation when the input indicates the addition of a noise component to the model.
z	A matrix whose *[i,k]*th entry is the probability that observation *i* in the test data belongs to the *k*th class.

See Also

mclustBIC

Examples

```
irisBIC <- mclustBIC(iris[,-5])
mclustModel(iris[,-5], irisBIC)
mclustModel(iris[,-5], irisBIC, G = 1:6, modelNames = c("VII", "VVI", "VVV"))
```

`mclustModelNames` *MCLUST Model Names*

Description

Description of model names used in the *MCLUST* package.

Usage

```
mclustModelNames(model)
```

Arguments

`model`	A string specifying the model.

Details

The following models are available in package **mclust**:

univariate mixture

`"E"` equal variance (one-dimensional)

`"V"` variable/unqual variance (one-dimensional)

multivariate mixture

`"EII"` spherical, equal volume

`"VII"` spherical, unequal volume

`"EEI"` diagonal, equal volume and shape

`"VEI"` diagonal, varying volume, equal shape

`"EVI"` diagonal, equal volume, varying shape

`"VVI"` diagonal, varying volume and shape

`"EEE"` ellipsoidal, equal volume, shape, and orientation

`"EVE"` ellipsoidal, equal volume and orientation (*)

`"VEE"` ellipsoidal, equal shape and orientation (*)

`"VVE"` ellipsoidal, equal orientation (*)

`"EEV"` ellipsoidal, equal volume and equal shape

"VEV" ellipsoidal, equal shape

"EVV" ellipsoidal, equal volume (*)

"VVV" ellipsoidal, varying volume, shape, and orientation

single component

"X" univariate normal

"XII" spherical multivariate normal

"XXI" diagonal multivariate normal

"XXX" ellipsoidal multivariate normal

(*) new models in **mclust** version >= 5.0.0.

Value

Returns a list with the following components:

model	a character string indicating the model (as in input).
type	the description of the indicated model (see Details section).

See Also

Mclust, mclustBIC

Examples

```
mclustModelNames("E")
mclustModelNames("EEE")
mclustModelNames("VVV")
mclustModelNames("XXI")
```

---

mclustVariance *Template for variance specification for parameterized Gaussian mixture models*

Description

Specification of variance parameters for the various types of Gaussian mixture models.

Usage

```
mclustVariance(modelName, d = NULL, G = 2)
```

Arguments

modelName	A character string specifying the model.
d	A integer specifying the dimension of the data.
G	An integer specifying the number of components in the mixture model.

Details

The variance component in the parameters list from the output to e.g. me or mstep or input to e.g. estep may contain one or more of the following arguments, depending on the model:

modelName A character string indicating the model.

d The dimension of the data.

G The number of components in the mixture model.

sigmasq for the one-dimensional models ("E", "V") and spherical models ("EII", "VII"). This is either a vector whose *k*th component is the variance for the *k*th component in the mixture model ("V" and "VII"), or a scalar giving the common variance for all components in the mixture model ("E" and "EII").

Sigma For the equal variance models "EII", "EEI", and "EEE". A *d* by *d* matrix giving the common covariance for all components of the mixture model.

cholSigma For the equal variance model "EEE". A *d* by *d* upper triangular matrix giving the Cholesky factor of the common covariance for all components of the mixture model.

sigma For all multidimensional mixture models. A *d* by *d* by *G* matrix array whose [,,k]th entry is the covariance matrix for the *k*th component of the mixture model.

cholsigma For the unconstrained covariance mixture model "VVV". A *d* by *d* by *G* matrix array whose [,,k]th entry is the upper triangular Cholesky factor of the covariance matrix for the *k*th component of the mixture model.

scale For diagonal models "EEI", "EVI", "VEI", "VVI" and constant-shape models "EEV" and "VEV". Either a *G*-vector giving the scale of the covariance (the *d*th root of its determinant) for each component in the mixture model, or a single numeric value if the scale is the same for each component.

shape For diagonal models "EEI", "EVI", "VEI", "VVI" and constant-shape models "EEV" and "VEV". Either a *G* by *d* matrix in which the *k*th column is the shape of the covariance matrix (normalized to have determinant 1) for the *k*th component, or a *d*-vector giving a common shape for all components.

orientation For the constant-shape models "EEV" and "VEV". Either a *d* by *d* by *G* array whose [,,k]th entry is the orthonomal matrix whose columns are the eigenvectors of the covariance matrix of the *k*th component, or a *d* by *d* orthonormal matrix if the mixture components have a common orientation. The orientation component is not needed in spherical and diagonal models, since the principal components are parallel to the coordinate axes so that the orientation matrix is the identity.

In all cases, the value -1 is used as a placeholder for unknown nonzero entries.

---

me *EM algorithm starting with M-step for parameterized MVN mixture models*

Description

Implements the EM algorithm for MVN mixture models parameterized by eignevalue decomposition, starting with the maximization step.

Usage

```
me(modelName, data, z, prior = NULL, control = emControl(),
   Vinv = NULL, warn = NULL, ...)
```

Arguments

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.
data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
z	A matrix whose [i,k]th entry is an initial estimate of the conditional probability of the ith observation belonging to the *k*th component of the mixture.
prior	Specification of a conjugate prior on the means and variances. See the help file for priorControl for further information. The default assumes no prior.
control	A list of control parameters for EM. The defaults are set by the call emControl().
Vinv	If the model is to include a noise term, Vinv is an estimate of the reciprocal hypervolume of the data region. If set to a negative value or 0, the model will include a noise term with the reciprocal hypervolume estimated by the function hypvol. The default is not to assume a noise term in the model through the setting Vinv=NULL.
warn	A logical value indicating whether or not certain warnings (usually related to singularity) should be issued when the estimation fails. The default is set in mclust.options("warn").
...	Catches unused arguments in indirect or list calls via do.call.

Value

A list including the following components:

modelName	A character string identifying the model (same as the input argument).
n	The number of observations in the data.
d	The dimension of the data.
G	The number of mixture components.
z	A matrix whose [i,k]th entry is the conditional probability of the *i*th observation belonging to the *k*th component of the mixture.
parameters	pro A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model.

`variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.

`Vinv` The estimate of the reciprocal hypervolume of the data region used in the computation when the input indicates the addition of a noise component to the model.

`loglik` The log likelihood for the data in the mixture model.

`control` The list of control parameters for EM used.

`prior` The specification of a conjugate prior on the means and variances used, `NULL` if no prior is used.

`Attributes:` `"info"` Information on the iteration.
`"WARNING"` An appropriate warning if problems are encountered in the computations.

See Also

`meE`,..., `meVVV`, `em`, `mstep`, `estep`, `priorControl`, `mclustModelNames`, `mclustVariance`, `mclust.options`

Examples

```
## Not run:
me(modelName = "VVV", data = iris[,-5], z = unmap(iris[,5]))
## End(Not run)
```

---

me.weighted *EM algorithm with weights starting with M-step for parameterized MVN mixture models*

Description

Implements the EM algorithm for fitting MVN mixture models parameterized by eigenvalue decomposition, when observations have weights, starting with the maximization step.

Usage

```
me.weighted(modelName, data, z, weights = NULL, prior = NULL,
            control = emControl(), Vinv = NULL, warn = NULL, ...)
```

Arguments

`modelName` A character string indicating the model. The help file for `mclustModelNames` describes the available models.

`data` A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.

z	A matrix whose [i,k]th entry is an initial estimate of the conditional probability of the ith observation belonging to the *k*th component of the mixture.
weights	A vector of positive weights, where the [i]th entry is the weight for the ith observation. If any of the weights are greater than one, then they are scaled so that the maximum weight is one.
prior	Specification of a conjugate prior on the means and variances. See the help file for priorControl for further information. The default assumes no prior.
control	A list of control parameters for EM. The defaults are set by the call emControl.
Vinv	If the model is to include a noise term, Vinv is an estimate of the reciprocal hypervolume of the data region. If set to a negative value or 0, the model will include a noise term with the reciprocal hypervolume estimated by the function hypvol. The default is not to assume a noise term in the model through the setting Vinv=NULL.
warn	A logical value indicating whether or not certain warnings (usually related to singularity) should be issued when the estimation fails. The default is set by warn using mclust.options.
...	Catches unused arguments in indirect or list calls via do.call.

Value

A list including the following components:

modelName	A character string identifying the model (same as the input argument).
z	A matrix whose [i,k]th entry is the conditional probability of the *i*th observation belonging to the *k*th component of the mixture.
parameters	pro A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details. Vinv The estimate of the reciprocal hypervolume of the data region used in the computation when the input indicates the addition of a noise component to the model.
loglik	The log likelihood for the data in the mixture model.
Attributes:	"info" Information on the iteration. "WARNING" An appropriate warning if problems are encountered in the computations.

Author(s)

Thomas Brendan Murphy

See Also

me, meE,..., meVVV, em, mstep, estep, priorControl, mclustModelNames, mclustVariance, mclust.options

Examples

```
## Not run:
w <- rep(1,150)
w[1] <- 0
me.weighted(modelName = "VVV", data = iris[,-5], z = unmap(iris[,5]),weights=w)
## End(Not run)
```

---

meE *EM algorithm starting with M-step for a parameterized Gaussian mixture model*

Description

Implements the EM algorithm for a parameterized Gaussian mixture model, starting with the maximization step.

Usage

```
meE(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meV(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meX(data, prior = NULL, warn = NULL, ...)
meEII(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meVII(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meEEI(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meVEI(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meEVI(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meVVI(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meEEE(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meEVE(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meVEE(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meVVE(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meEEV(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meVEV(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meEVV(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meVVV(data, z, prior=NULL, control=emControl(), Vinv=NULL, warn=NULL, ...)
meXII(data, prior = NULL, warn = NULL, ...)
meXXI(data, prior = NULL, warn = NULL, ...)
meXXX(data, prior = NULL, warn = NULL, ...)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.

z	A matrix whose [i,k]th entry is the conditional probability of the ith observation belonging to the *k*th component of the mixture.
prior	Specification of a conjugate prior on the means and variances. The default assumes no prior.
control	A list of control parameters for EM. The defaults are set by the call emControl().
Vinv	An estimate of the reciprocal hypervolume of the data region, when the model is to include a noise term. Set to a negative value or zero if a noise term is desired, but an estimate is unavailable — in that case function hypvol will be used to obtain the estimate. The default is not to assume a noise term in the model through the setting Vinv=NULL.
warn	A logical value indicating whether or not certain warnings (usually related to singularity) should be issued when the estimation fails. The default is given by mclust.options("warn").
...	Catches unused arguments in indirect or list calls via do.call.

Value

A list including the following components:

modelName	A character string identifying the model (same as the input argument).
z	A matrix whose [i,k]th entry is the conditional probability of the *i*th observation belonging to the *k*th component of the mixture.
parameters	pro A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details. Vinv The estimate of the reciprocal hypervolume of the data region used in the computation when the input indicates the addition of a noise component to the model.
loglik	The log likelihood for the data in the mixture model.
Attributes:	"info" Information on the iteration. "WARNING" An appropriate warning if problems are encountered in the computations.

See Also

em, me, estep, mclust.options

Examples

```
meVVV(data = iris[,-5], z = unmap(iris[,5]))
```

mstep *M-step for parameterized Gaussian mixture models*

Description

Maximization step in the EM algorithm for parameterized Gaussian mixture models.

Usage

```
mstep(modelName, data, z, prior = NULL, warn = NULL, ...)
```

Arguments

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.
data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
z	A matrix whose [i,k]th entry is the conditional probability of the ith observation belonging to the *k*th component of the mixture. In analyses involving noise, this should not include the conditional probabilities for the noise component.
prior	Specification of a conjugate prior on the means and variances. The default assumes no prior.
warn	A logical value indicating whether or not certain warnings (usually related to singularity) should be issued when the estimation fails. The default is given by mclust.options("warn").
...	Catches unused arguments in indirect or list calls via do.call.

Value

A list including the following components:

modelName	A character string identifying the model (same as the input argument).
parameters	pro A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details.
Attributes:	"info" For those models with iterative M-steps ("VEI" and "VEV"), information on the iteration. "WARNING" An appropriate warning if problems are encountered in the computations.

Note

This function computes the M-step only for MVN mixtures, so in analyses involving noise, the conditional probabilities input should exclude those for the noise component.

In contrast to `me` for the EM algorithm, computations in `mstep` are carried out unless failure due to overflow would occur. To impose stricter tolerances on a single `mstep`, use `me` with the *itmax* component of the `control` argument set to 1.

See Also

`mstepE`, ..., `mstepVVV`, `emControl`, `me`, `estep`, `mclust.options`.

Examples

```
## Not run:
mstep(modelName = "VII", data = iris[,-5], z = unmap(iris[,5]))
## End(Not run)
```

`mstepE` *M-step for a parameterized Gaussian mixture model*

Description

Maximization step in the EM algorithm for a parameterized Gaussian mixture model.

Usage

```
mstepE( data, z, prior = NULL, warn = NULL, ...)
mstepV( data, z, prior = NULL, warn = NULL, ...)
mstepEII( data, z, prior = NULL, warn = NULL, ...)
mstepVII( data, z, prior = NULL, warn = NULL, ...)
mstepEEI( data, z, prior = NULL, warn = NULL, ...)
mstepVEI( data, z, prior = NULL, warn = NULL, control = NULL, ...)
mstepEVI( data, z, prior = NULL, warn = NULL, ...)
mstepVVI( data, z, prior = NULL, warn = NULL, ...)
mstepEEE( data, z, prior = NULL, warn = NULL, ...)
mstepEEV( data, z, prior = NULL, warn = NULL, ...)
mstepVEV( data, z, prior = NULL, warn = NULL, control = NULL,...)
mstepVVV( data, z, prior = NULL, warn = NULL, ...)
mstepEVE( data, z, prior = NULL, warn = NULL, control = NULL, ...)
mstepEVV( data, z, prior = NULL, warn = NULL, ...)
mstepVEE( data, z, prior = NULL, warn = NULL, control = NULL, ...)
mstepVVE( data, z, prior = NULL, warn = NULL, control = NULL, ...)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
z	A matrix whose [i,k]th entry is the conditional probability of the ith observation belonging to the *k*th component of the mixture. In analyses involving noise, this should not include the conditional probabilities for the noise component.
prior	Specification of a conjugate prior on the means and variances. The default assumes no prior.
warn	A logical value indicating whether or not certain warnings (usually related to singularity) should be issued when the estimation fails. The default is given by mclust.options("warn").
control	Values controlling termination for models "VEI" and "VEV" that have an iterative M-step. This should be a list with components named *itmax* and *tol*. These components can be of length 1 or 2; in the latter case, mstep will use the second value, under the assumption that the first applies to an outer iteration (as in the function me). The default uses the default values from the function emControl, which sets no limit on the number of iterations, and a relative tolerance of sqrt(.Machine$double.eps) on successive iterates.
...	Catches unused arguments in indirect or list calls via do.call.

Value

A list including the following components:

modelName	A character string identifying the model (same as the input argument).
parameters	pro A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If the model includes a Poisson term for noise, there should be one more mixing proportion than the number of Gaussian components. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details.
Attributes:	"info" For those models with iterative M-steps ("VEI" and "VEV"), information on the iteration. "WARNING" An appropriate warning if problems are encountered in the computations.

Note

This function computes the M-step only for MVN mixtures, so in analyses involving noise, the conditional probabilities input should exclude those for the noise component.

In contrast to me for the EM algorithm, computations in mstep are carried out unless failure due to overflow would occur. To impose stricter tolerances on a single mstep, use me with the *itmax* component of the control argument set to 1.

See Also

mstep, me, estep, mclustVariance, priorControl, emControl.

Examples

```
## Not run:
mstepVII(data = iris[,-5], z = unmap(iris[,5]))
## End(Not run)
```

---

mvn *Univariate or Multivariate Normal Fit*

Description

Computes the mean, covariance, and log-likelihood from fitting a single Gaussian to given data (univariate or multivariate normal).

Usage

```
mvn( modelName, data, prior = NULL, warn = NULL, ...)
```

Arguments

modelName	A character string representing a model name. This can be either "Spherical", "Diagonal", or "Ellipsoidal" or else "X" for one-dimensional data, "XII" for a spherical Gaussian, "XXI" for a diagonal Gaussian "XXX" for a general ellipsoidal Gaussian
data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
prior	Specification of a conjugate prior on the means and variances. The default assumes no prior.
warn	A logical value indicating whether or not a warning should be issued whenever a singularity is encountered. The default is given by mclust.options("warn").
...	Catches unused arguments in indirect or list calls via do.call.

Value

A list including the following components:

`modelName`	A character string identifying the model (same as the input argument).
`parameters`	`mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. `variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.
`loglik`	The log likelihood for the data in the mixture model.
`Attributes:`	`"WARNING"` An appropriate warning if problems are encountered in the computations.

See Also

`mvnX`, `mvnXII`, `mvnXXI`, `mvnXXX`, `mclustModelNames`

Examples

```
n <- 1000

set.seed(0)
x <- rnorm(n, mean = -1, sd = 2)
mvn(modelName = "X", x)

mu <- c(-1, 0, 1)

set.seed(0)
x <- sweep(matrix(rnorm(n*3), n, 3) %*% (2*diag(3)),
           MARGIN = 2, STATS = mu, FUN = "+")
mvn(modelName = "XII", x)
mvn(modelName = "Spherical", x)

set.seed(0)
x <- sweep(matrix(rnorm(n*3), n, 3) %*% diag(1:3),
           MARGIN = 2, STATS = mu, FUN = "+")
mvn(modelName = "XXI", x)
mvn(modelName = "Diagonal", x)

Sigma <- matrix(c(9,-4,1,-4,9,4,1,4,9), 3, 3)
set.seed(0)
x <- sweep(matrix(rnorm(n*3), n, 3) %*% chol(Sigma),
           MARGIN = 2, STATS = mu, FUN = "+")
mvn(modelName = "XXX", x)
mvn(modelName = "Ellipsoidal", x)
```

mvnX *Univariate or Multivariate Normal Fit*

Description

Computes the mean, covariance, and log-likelihood from fitting a single Gaussian (univariate or multivariate normal).

Usage

```
mvnX(data, prior = NULL, warn = NULL, ...)
mvnXII(data, prior = NULL, warn = NULL, ...)
mvnXXI(data, prior = NULL, warn = NULL, ...)
mvnXXX(data, prior = NULL, warn = NULL, ...)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
prior	Specification of a conjugate prior on the means and variances. The default assumes no prior.
warn	A logical value indicating whether or not a warning should be issued whenever a singularity is encountered. The default is given by `mclust.options("warn")`.
...	Catches unused arguments in indirect or list calls via `do.call`.

Details

`mvnXII` computes the best fitting Gaussian with the covariance restricted to be a multiple of the identity.

`mvnXXI` computes the best fitting Gaussian with the covariance restricted to be diagonal.

`mvnXXX` computes the best fitting Gaussian with ellipsoidal (unrestricted) covariance.

Value

A list including the following components:

modelName	A character string identifying the model (same as the input argument).
parameters	`mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. `variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.
loglik	The log likelihood for the data in the mixture model.
Attributes:	`"WARNING"` An appropriate warning if problems are encountered in the computations.

See Also

mvn, mstepE

Examples

```
## Not run:
n <- 1000

set.seed(0)
x <- rnorm(n, mean = -1, sd = 2)
mvnX(x)

mu <- c(-1, 0, 1)

set.seed(0)
x <- sweep(matrix(rnorm(n*3), n, 3) %*% (2*diag(3)),
           MARGIN = 2, STATS = mu, FUN = "+")
mvnXII(x)

set.seed(0)
x <- sweep(matrix(rnorm(n*3), n, 3) %*% diag(1:3),
           MARGIN = 2, STATS = mu, FUN = "+")
mvnXXI(x)

Sigma <- matrix(c(9,-4,1,-4,9,4,1,4,9), 3, 3)
set.seed(0)
x <- sweep(matrix(rnorm(n*3), n, 3) %*% chol(Sigma),
           MARGIN = 2, STATS = mu, FUN = "+")
mvnXXX(x)

## End(Not run)
```

---

nMclustParams *Number of Estimated Parameters in Gaussian Mixture Models*

Description

Gives the number of estimated parameters for parameterizations of the Gaussian mixture model that are used in MCLUST.

Usage

```
nMclustParams(modelName, d, G, noise = FALSE, equalPro = FALSE, ...)
```

Arguments

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.

d	The dimension of the data. Not used for models in which neither the shape nor the orientation varies.
G	The number of components in the Gaussian mixture model used to compute loglik.
noise	A logical variable indicating whether or not the model includes an optional Poisson noise component.
equalPro	A logical variable indicating whether or not the components in the model are assumed to be present in equal proportion.
...	Catches unused arguments in indirect or list calls via do.call.

Details

To get the total number of parameters in model, add G*d for the means and G-1 for the mixing proportions if they are unequal.

Value

The number of variance parameters in the corresponding Gaussian mixture model.

See Also

bic, nVarParams.

Examples

```
mapply(nMclustParams, mclust.options("emModelNames"), d = 2, G = 3)
```

---

nVarParams *Number of Variance Parameters in Gaussian Mixture Models*

Description

Gives the number of variance parameters for parameterizations of the Gaussian mixture model that are used in MCLUST.

Usage

```
nVarParams(modelName, d, G, ...)
```

Arguments

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.
d	The dimension of the data. Not used for models in which neither the shape nor the orientation varies.
G	The number of components in the Gaussian mixture model used to compute loglik.
...	Catches unused arguments in indirect or list calls via do.call.

Details

To get the total number of parameters in model, add `G*d` for the means and `G-1` for the mixing proportions if they are unequal.

Value

The number of variance parameters in the corresponding Gaussian mixture model.

References

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association 97:611:631*.

C. Fraley, A. E. Raftery, T. B. Murphy and L. Scrucca (2012). mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. Technical Report No. 597, Department of Statistics, University of Washington.

See Also

`bic`, `nMclustParams`.

Examples

```
mapply(nVarParams, mclust.options("emModelNames"), d = 2, G = 3)
```

---

partconv *Numeric Encoding of a Partitioning*

Description

Converts a vector interpreted as a classification or partitioning into a numeric vector.

Usage

```
partconv(x, consec=TRUE)
```

Arguments

`x`	A vector interpreted as a classification or partitioning.
`consec`	Logical value indicating whether or not to consecutive class numbers should be used .

Value

Numeric encoding of `x`. When `consec = TRUE`, the distinct values in `x` are numbered by the order in which they appear. When `consec = FALSE`, each distinct value in `x` is numbered by the index corresponding to its first appearance in `x`.

See Also

partuniq

Examples

```
partconv(iris[,5])

set.seed(0)
cl <- sample(LETTERS[1:9], 25, replace=TRUE)
partconv(cl, consec=FALSE)
partconv(cl, consec=TRUE)
```

---

partuniq *Classifies Data According to Unique Observations*

Description

Gives a one-to-one mapping from unique observations to rows of a data matrix.

Usage

```
partuniq(x)
```

Arguments

x	Matrix of observations.

Value

A vector of length `nrow(x)` with integer entries. An observation `k` is assigned an integer `i` whenever observation `i` is the first row of `x` that is identical to observation `k` (note that `i <= k`).

See Also

partconv

Examples

```
set.seed(0)

mat <- data.frame(lets = sample(LETTERS[1:2],9,TRUE), nums = sample(1:2,9,TRUE))
mat

ans <- partuniq(mat)
ans

partconv(ans,consec=TRUE)
```

`plot.clustCombi` *Plot Combined Clusterings Results*

Description

Plot combined clusterings results: classifications corresponding to `Mclust`/BIC and to the hierarchically combined classes, "entropy plots" to help to select a number of classes, and the tree structure obtained from combining mixture components.

Usage

```
## S3 method for class 'clustCombi'
plot(x, what = c("classification", "entropy", "tree"), ...)
```

Arguments

`x`	Object returned by `clustCombi` function.
`what`	Type of plot.
`...`	Other arguments to be passed to other functions: `combiPlot`, `entPlot`, `combiTree`. Please see the corresponding documentations.

Value

Classifications are plotted with `combiPlot`, which relies on the `Mclust` plot functions. Entropy plots are plotted with `entPlot` and may help to select a number of classes: please see the article cited in the references. Tree plots are produced by `combiTree` and graph the tree structure implied by the clusters combining process.

Author(s)

J.-P. Baudry, A. E. Raftery, L. Scrucca

References

J.-P. Baudry, A. E. Raftery, G. Celeux, K. Lo and R. Gottardo (2010). Combining mixture components for clustering. *Journal of Computational and Graphical Statistics, 19(2):332-353.*

See Also

`combiPlot`, `entPlot`, `combiTree`, `clustCombi`.

Examples

```
## Not run:
data(Baudry_etal_2010_JCGS_examples)

## 1D Example
output <- clustCombi(data = Test1D, G=1:15)

# plots the hierarchy of combined solutions, then some "entropy plots" which
# may help one to select the number of classes (please see the article cited
# in the references)
plot(output)

## 2D Example
output <- clustCombi(data = ex4.1)

# plots the hierarchy of combined solutions, then some "entropy plots" which
# may help one to select the number of classes (please see the article cited
# in the references)
plot(output)

## 3D Example
output <- clustCombi(data = ex4.4.2)

# plots the hierarchy of combined solutions, then some "entropy plots" which
# may help one to select the number of classes (please see the article cited
# in the references)
plot(output)

## End(Not run)
```

`plot.densityMclust` *Plots for Mixture-Based Density Estimate*

Description

Plotting methods for an object of class `'mclustDensity'`. Available graphs are plot of BIC values and density for univariate and bivariate data. For higher data dimensionality a scatterplot matrix of pairwise densities is drawn.

Usage

```
## S3 method for class 'densityMclust'
plot(x, data = NULL, what = c("BIC", "density", "diagnostic"), ...)

plotDensityMclust1(x, data = NULL, hist.col = "lightgrey",
                   hist.border = "white",  breaks = "Sturges", ...)

plotDensityMclust2(x, data = NULL, nlevels = 11, levels = NULL,
```

```
                    prob = c(0.25, 0.5, 0.75),
                    points.pch = 1, points.col = 1, points.cex = 0.8, ...)

plotDensityMclustd(x, data = NULL, nlevels = 11, levels = NULL,
                    prob = c(0.25, 0.5, 0.75),
                    points.pch = 1, points.col = 1, points.cex = 0.8,
                    gap = 0.2, ...)
```

Arguments

`x`	An object of class `'mclustDensity'` obtained from a call to `densityMclust` function.
`data`	Optional data points.
`what`	The type of graph requested: `"density"` = a plot of estimated density; if `data` is also provided the density is plotted over data points (see Details section). `"BIC"` = a plot of BIC values for the estimated models versus the number of components. `"diagnostic"` = diagnostic plots (only available for the one-dimensional case, see `densityMclust.diagnostic`)
`hist.col`	The color to be used to fill the bars of the histogram.
`hist.border`	The color of the border around the bars of the histogram.
`breaks`	See the argument in function `hist`.
`points.pch, points.col, points.cex`	The character symbols, colors, and magnification to be used for plotting `data` points.
`nlevels`	An integer, the number of levels to be used in plotting contour densities.
`levels`	A vector of density levels at which to draw the contour lines.
`prob`	A vector of probability levels for computing HDR. Only used if `type = "hdr"` and supersede previous `nlevels` and `levels` arguments.
`gap`	Distance between subplots, in margin lines, for the matrix of pairwise scatterplots.
`...`	Additional arguments passed to `surfacePlot`.

Details

The function `plot.densityMclust` allows to obtain the plot of estimated density or the graph of BIC values for evaluated models.

If `what = "density"` the produced plot dependes on the dimensionality of the data.

For one-dimensional data a call with no `data` provided produces a plot of the estimated density over a sensible range of values. If `data` is provided the density is over-plotted on a histogram for the observed data.

For two-dimensional data further arguments available are those accepted by the `surfacePlot` function. In particular, the density can be represented through `"contour"`, `"hdr"`, `"image"`, and

"persp" type of graph. For type = "hdr" Highest Density Regions (HDRs) are plotted for probability levels prob. See hdrlevels for details.

For higher dimensionality a scatterplot matrix of pairwise projected densities is drawn.

Author(s)

Luca Scrucca

See Also

densityMclust, surfacePlot, densityMclust.diagnostic, Mclust.

Examples

```
## Not run:
dens <- densityMclust(faithful$waiting)
summary(dens)
summary(dens, parameters = TRUE)
plot(dens, what = "BIC", legendArgs = list(x = "topright"))
plot(dens, what = "density", data = faithful$waiting)

dens <- densityMclust(faithful)
summary(dens)
summary(dens, parameters = TRUE)
plot(dens, what = "density", data = faithful,
     drawlabels = FALSE, points.pch = 20)
plot(dens, what = "density", type = "hdr")
plot(dens, what = "density", type = "hdr", prob = seq(0.1, 0.9, by = 0.1))
plot(dens, what = "density", type = "hdr", data = faithful)
plot(dens, what = "density", type = "persp")

dens <- densityMclust(iris[,1:4])
summary(dens, parameters = TRUE)
plot(dens, what = "density", data = iris[,1:4],
     col = "slategrey", drawlabels = FALSE, nlevels = 7)
plot(dens, what = "density", type = "hdr", data = iris[,1:4])
plot(dens, what = "density", type = "persp", col = grey(0.9))

## End(Not run)
```

---

plot.Mclust *Plotting method for Mclust model-based clustering*

Description

Plots for model-based clustering results, such as BIC, classification, uncertainty and density.

Usage

```
## S3 method for class 'Mclust'
plot(x, what = c("BIC", "classification", "uncertainty", "density"),
     dimens = NULL, xlab = NULL, ylab = NULL, ylim = NULL,
     addEllipses = TRUE, main = FALSE, ...)
```

Arguments

x	Output from Mclust.
what	A string specifying the type of graph requested. Available choices are: "BIC" plot of BIC values used for choosing the number of clusters. "classification" = a plot showing the clustering. For data in more than two dimensions a pairs plot is produced, followed by a coordinate projection plot using specified dimens. Ellipses corresponding to covariances of mixture components are also drawn if addEllipses = TRUE. "uncertainty" a plot of classification uncertainty. For data in more than two dimensions a coordinate projection plot is drawn using specified dimens. "density" a plot of estimated density. For data in more than two dimensions a matrix of contours for coordinate projection plot is drawn using specified dimens. If not specified, in interactive sessions a menu of choices is proposed.
dimens	A vector of integers specifying the dimensions of the coordinate projections in case of "classification", "uncertainty", or "density" plots.
xlab, ylab	Optional labels for the x-axis and the y-axis.
ylim	Optional limits for the vertical axis of the BIC plot.
addEllipses	A logical indicating whether or not to add ellipses with axes corresponding to the within-cluster covariances in case of "classification" or "uncertainty" plots.
main	A logical or NULL indicating whether or not to add a title to the plot identifying the type of plot drawn.
...	Other graphics parameters.

Details

For more flexibility in plotting, use mclust1Dplot, mclust2Dplot, surfacePlot, coordProj, or randProj.

See Also

Mclust, plot.mclustBIC, plot.mclustICL, mclust1Dplot, mclust2Dplot, surfacePlot, coordProj, randProj.

Examples

```
## Not run:
precipMclust <- Mclust(precip)
plot(precipMclust)

faithfulMclust <- Mclust(faithful)
plot(faithfulMclust)

irisMclust <- Mclust(iris[,-5])
plot(irisMclust)

## End(Not run)
```

---

plot.mclustBIC *BIC Plot for Model-Based Clustering*

Description

Plots the BIC values returned by the mclustBIC function.

Usage

```
## S3 method for class 'mclustBIC'
plot(x, G = NULL, modelNames = NULL,
     symbols = NULL, colors = NULL,
     xlab = NULL, ylab = "BIC", ylim = NULL,
     legendArgs = list(x = "bottomright", ncol = 2, cex = 1, inset = 0.01),
     ...)
```

Arguments

x	Output from mclustBIC.
G	One or more numbers of components corresponding to models fit in x. The default is to plot the BIC for all of the numbers of components fit.
modelNames	One or more model names corresponding to models fit in x. The default is to plot the BIC for all of the models fit.
symbols	Either an integer or character vector assigning a plotting symbol to each unique class in classification. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function unique). The default is given by mclust.options("classPlotSymbols").
colors	Either an integer or character vector assigning a color to each unique class in classification. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function unique). The default is given by mclust.options("classPlotColors").
xlab	Optional label for the horizontal axis of the BIC plot.
ylab	Label for the vertical axis of the BIC plot.

ylim	Optional limits for the vertical axis of the BIC plot.
legendArgs	Arguments to pass to the legend function. Set to NULL for no legend.
...	Other graphics parameters.

Value

A plot of the BIC values.

See Also

mclustBIC

Examples

```
## Not run:
plot(mclustBIC(precip), legendArgs =  list(x = "bottomleft"))

plot(mclustBIC(faithful))

plot(mclustBIC(iris[,-5]))

## End(Not run)
```

---

plot.MclustBootstrap *Plot of bootstrap distributions for mixture model parameters*

Description

Plots the bootstrap distribution of parameters as returned by the MclustBootstrap function.

Usage

```
## S3 method for class 'MclustBootstrap'
plot(x, what = c("pro", "mean", "var"),
     show.parest = TRUE, show.confint = TRUE,
     hist.col = "grey", hist.border = "lightgrey", breaks = "Sturges",
     col = "forestgreen", lwd = 2, lty = 3,
     xlab = NULL, xlim = NULL, ylim = NULL, ...)
```

Arguments

x	Object returned by MclustBootstrap.
what	Character string specifying if mixing proportions ("pro"), component means ("mean") or component variances ("var") should be drawn.
show.parest	A logical specifying if the parameter estimate should be drawn as vertical line.

show.confint	A logical specifying if the resampling-based confidence interval should be drawn at the bottom of the graph. Confidence level can be provided as further argument conf.level; see summary.MclustBootstrap.
hist.col	The color to be used to fill the bars of the histograms.
hist.border	The color of the border around the bars of the histograms.
breaks	See the argument in function hist.
col, lwd, lty	The color, line width and line type to be used to represent the estimated parameters and confidence intervals.
xlab	Optional label for the horizontal axis.
xlim, ylim	A two-values vector of axis range for, respectively, horizontal and vertical axis.
...	Other graphics parameters.

Value

A plot for each variable/component of the selected parameters.

See Also

MclustBootstrap

Examples

```
## Not run:
data(diabetes)
X <- diabetes[,-1]
modClust <- Mclust(X, G = 3, modelNames = "VVV")
bootClust <- MclustBootstrap(modClust, nboot = 99)
par(mfrow = c(1,3), mar = c(4,2,2,0.5))
plot(bootClust, what = "pro")
par(mfrow = c(3,3), mar = c(4,2,2,0.5))
plot(bootClust, what = "mean")

## End(Not run)
```

---

plot.MclustDA *Plotting method for MclustDA discriminant analysis*

Description

Plots for model-based mixture discriminant analysis results, such as scatterplot of training and test data, classification of train and test data, and errors.

Usage

```
## S3 method for class 'MclustDA'
plot(x, what = c("scatterplot", "classification", "train&test", "error"),
     newdata, newclass, dimens = NULL,
     symbols, colors, main = NULL, ...)
```

Arguments

x	An object of class 'MclustDA' resulting from a call to MclustDA.
what	A string specifying the type of graph requested. Available choices are: "scatterplot" = a plot of training data with points marked based on the known classification. Ellipses corresponding to covariances of mixture components are also drawn. "classification" = a plot of data with points marked on based the predicted classification; if newdata is provided then the test set is shown otherwise the training set. "train&test" = a plot of training and test data with points marked according to the type of set. "error" = a plot of training set (or test set if newdata and newclass are provided) with misclassified points marked. If not specified, in interactive sessions a menu of choices is proposed.
newdata	A data frame or matrix for test data.
newclass	A vector giving the class labels for the observations in the test data (if known).
dimens	A vector of integers giving the dimensions of the desired coordinate projections for multivariate data. The default is to take all the the available dimensions for plotting.
symbols	Either an integer or character vector assigning a plotting symbol to each unique class. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function factor). The default is given by mclust.options("classPlotSymbols").
colors	Either an integer or character vector assigning a color to each unique class in classification. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function factor). The default is given by mclust.options("classPlotColors").
main	A logical, a character string, or NULL (default) for the main title. If NULL or FALSE no title is added to a plot. If TRUE a default title is added identifying the type of plot drawn. If a character string is provided, this is used for the title.
...	further arguments passed to or from other methods.

Details

For more flexibility in plotting, use mclust1Dplot, mclust2Dplot, surfacePlot, coordProj, or randProj.

Author(s)

Luca Scrucca

See Also

MclustDA, surfacePlot, coordProj, randProj

Examples

```
## Not run:
odd <- seq(from = 1, to = nrow(iris), by = 2)
even <- odd + 1
X.train <- iris[odd,-5]
Class.train <- iris[odd,5]
X.test <- iris[even,-5]
Class.test <- iris[even,5]

# common EEE covariance structure (which is essentially equivalent to linear discriminant analysis)
irisMclustDA <- MclustDA(X.train, Class.train, modelType = "EDDA", modelNames = "EEE")
summary(irisMclustDA, parameters = TRUE)
summary(irisMclustDA, newdata = X.test, newclass = Class.test)

# common covariance structure selected by BIC
irisMclustDA <- MclustDA(X.train, Class.train, modelType = "EDDA")
summary(irisMclustDA, parameters = TRUE)
summary(irisMclustDA, newdata = X.test, newclass = Class.test)

# general covariance structure selected by BIC
irisMclustDA <- MclustDA(X.train, Class.train)
summary(irisMclustDA, parameters = TRUE)
summary(irisMclustDA, newdata = X.test, newclass = Class.test)

plot(irisMclustDA)
plot(irisMclustDA, dimens = 3:4)
plot(irisMclustDA, dimens = 4)

plot(irisMclustDA, what = "classification")
plot(irisMclustDA, what = "classification", newdata = X.test)
plot(irisMclustDA, what = "classification", dimens = 3:4)
plot(irisMclustDA, what = "classification", newdata = X.test, dimens = 3:4)
plot(irisMclustDA, what = "classification", dimens = 4)
plot(irisMclustDA, what = "classification", dimens = 4, newdata = X.test)

plot(irisMclustDA, what = "train&test", newdata = X.test)
plot(irisMclustDA, what = "train&test", newdata = X.test, dimens = 3:4)
plot(irisMclustDA, what = "train&test", newdata = X.test, dimens = 4)

plot(irisMclustDA, what = "error")
plot(irisMclustDA, what = "error", dimens = 3:4)
plot(irisMclustDA, what = "error", dimens = 4)
plot(irisMclustDA, what = "error", newdata = X.test, newclass = Class.test)
plot(irisMclustDA, what = "error", newdata = X.test, newclass = Class.test, dimens = 3:4)
plot(irisMclustDA, what = "error", newdata = X.test, newclass = Class.test, dimens = 4)

# simulated 1D data
n <- 250
set.seed(1)
triModal <- c(rnorm(n,-5), rnorm(n,0), rnorm(n,5))
triClass <- c(rep(1,n), rep(2,n), rep(3,n))
odd <- seq(from = 1, to = length(triModal), by = 2)
```

```
even <- odd + 1
triMclustDA <- MclustDA(triModal[odd], triClass[odd])
summary(triMclustDA, parameters = TRUE)
summary(triMclustDA, newdata = triModal[even], newclass = triClass[even])
plot(triMclustDA)
plot(triMclustDA, what = "classification")
plot(triMclustDA, what = "classification", newdata = triModal[even])
plot(triMclustDA, what = "train&test", newdata = triModal[even])
plot(triMclustDA, what = "error")
plot(triMclustDA, what = "error", newdata = triModal[even], newclass = triClass[even])

# simulated 2D cross data
data(cross)
odd <- seq(from = 1, to = nrow(cross), by = 2)
even <- odd + 1
crossMclustDA <- MclustDA(cross[odd,-1], cross[odd,1])
summary(crossMclustDA, parameters = TRUE)
summary(crossMclustDA, newdata = cross[even,-1], newclass = cross[even,1])
plot(crossMclustDA)
plot(crossMclustDA, what = "classification")
plot(crossMclustDA, what = "classification", newdata = cross[even,-1])
plot(crossMclustDA, what = "train&test", newdata = cross[even,-1])
plot(crossMclustDA, what = "error")
plot(crossMclustDA, what = "error", newdata =cross[even,-1], newclass = cross[even,1])

## End(Not run)
```

`plot.MclustDR` *Plotting method for dimension reduction for model-based clustering and classification*

Description

Graphs data projected onto the estimated subspace for model-based clustering and classification.

Usage

```
## S3 method for class 'MclustDR'
plot(x, dimens,
     what = c("scatterplot", "pairs", "contour", "classification",
              "boundaries", "density", "evalues"),
     symbols, colors, col.contour = gray(0.7), col.sep = grey(0.4),
     ngrid = 200, nlevels = 5, asp = NULL, ...)
```

Arguments

`x`	An object of class `'MclustDR'` resulting from a call to `MclustDR`.
`dimens`	A vector of integers giving the dimensions of the desired coordinate projections for multivariate data.

`what` The type of graph requested:

- `"scatterplot"` = a two-dimensional plot of data projected onto the first two directions specified by `dimens` and with data points marked according to the corresponding mixture component. By default, the first two directions are selected for plotting.
- `"pairs"` = a scatterplot matrix of data projected onto the estimated subspace and with data points marked according to the corresponding mixture component. By default, all the available directions are used, unless they have been specified by `dimens`.
- `"contour"` = a two-dimensional plot of data projected onto the first two directions specified by `dimens` (by default, the first two directions) with density contours for classes or clusters and data points marked according to the corresponding mixture component.
- `"classification"` = a two-dimensional plot of data projected onto the first two directions specified by `dimens` (by default, the first two directions) with classification region and data points marked according to the corresponding mixture component.
- `"boundaries"` = a two-dimensional plot of data projected onto the first two directions specified by `dimens` (by default, the first two directions) with uncertainty boundaries and data points marked according to the corresponding mixture component. The uncertainty is shown using a greyscale with darker regions indicating higher uncertainty.
- `"density"` = a one-dimensional plot of estimated density for the first direction specified by `dimens` (by default, the first one). A set of box-plots for each estimated cluster or known class are also shown at the bottom of the graph.

`symbols` Either an integer or character vector assigning a plotting symbol to each unique mixture component. Elements in `colors` correspond to classes in order of appearance in the sequence of observations (the order used by the function `factor`). The default is given by `mclust.options("classPlotSymbols")`.

`colors` Either an integer or character vector assigning a color to each unique cluster or known class. Elements in `colors` correspond to classes in order of appearance in the sequence of observations (the order used by the function `factor`). The default is given by `mclust.options("classPlotColors")`.

`col.contour` The color of contours in case `what = "contour"`.

`col.sep` The color of classification boundaries in case `what = "classification"`.

`ngrid` An integer specifying the number of grid points to use in evaluating the classification regions.

`nlevels` The number of levels to use in case `what = "contour"`.

`asp` For scatterplots the y/x aspect ratio, see `plot.window`.

`...` further arguments passed to or from other methods.

Author(s)

Luca Scrucca

References

Scrucca, L. (2010) Dimension reduction for model-based clustering. *Statistics and Computing*, 20(4), pp. 471-484.

See Also

MclustDR

Examples

```
## Not run:
mod <- Mclust(iris[,1:4], G = 3)
dr <- MclustDR(mod)
plot(dr, what = "evalues")
plot(dr, what = "pairs")
plot(dr, what = "scatterplot", dimens = c(1,3))
plot(dr, what = "contour")
plot(dr, what = "classification", ngrid = 200)
plot(dr, what = "boundaries", ngrid = 200)
plot(dr, what = "density")
plot(dr, what = "density", dimens = 2)

data(banknote)
da <- MclustDA(banknote[,2:7], banknote$Status, G = 1:3)
dr <- MclustDR(da)
plot(dr, what = "evalues")
plot(dr, what = "pairs")
plot(dr, what = "contour")
plot(dr, what = "contour", dimens = c(1,3))
plot(dr, what = "classification", ngrid = 200)
plot(dr, what = "boundaries", ngrid = 200)
plot(dr, what = "density")
plot(dr, what = "density", dimens = 2)

## End(Not run)
```

---

plot.mclustICL *ICL Plot for Model-Based Clustering*

Description

Plots the ICL values returned by the mclustICL function.

Usage

```
## S3 method for class 'mclustICL'
plot(x, ylab = "ICL", ...)
```

Arguments

x	Output from mclustICL.
ylab	Label for the vertical axis of the plot.
...	Further arguments passed to the plot.mclustBIC function.

Value

A plot of the ICL values.

See Also

mclustICL

Examples

```
## Not run:
data(faithful)
faithful.ICL = mclustICL(faithful)
plot(faithful.ICL)

## End(Not run)
```

---

predict.densityMclust *Density estimate of multivariate observations by Gaussian finite mixture modeling*

Description

Compute density estimation for multivariate observations based on Gaussian finite mixture models estimated by densityMclust.

Usage

```
  ## S3 method for class 'densityMclust'
predict(object, newdata, what = c("dens", "cdens", "z"), logarithm = FALSE, ...)
```

Arguments

object	an object of class 'densityMclust' resulting from a call to densityMclust.
newdata	a vector, a data frame or matrix giving the data. If missing the density is computed for the input data obtained from the call to densityMclust.
what	a character string specifying what to retrieve: "dens" returns a vector of values for the mixture density; "cdens" returns a matrix of component densities for each mixture component (along the columns); "z" returns a matrix of conditional probabilities of each data point to belong to a mixture component.
logarithm	A logical value indicating whether or not the logarithm of the density or component densities should be returned.
...	further arguments passed to or from other methods.

Value

Returns a vector or a matrix of densities evaluated at `newdata` depending on the argument `what` (see above).

Author(s)

Luca Scrucca

See Also

`Mclust`.

Examples

```
## Not run:
x <- faithful$waiting
dens <- densityMclust(x)
x0 <- seq(50, 100, by = 10)
d0 <- predict(dens, x0)
plot(dens)
points(x0, d0, pch = 20)

## End(Not run)
```

`predict.Mclust` *Cluster multivariate observations by Gaussian finite mixture modeling*

Description

Cluster prediction for multivariate observations based on Gaussian finite mixture models estimated by `Mclust`.

Usage

```
  ## S3 method for class 'Mclust'
predict(object, newdata, ...)
```

Arguments

`object`	an object of class `'Mclust'` resulting from a call to `Mclust`.
`newdata`	a data frame or matrix giving the data. If missing the clustering data obtained from the call to `Mclust` are classified.
`...`	further arguments passed to or from other methods.

Value

Returns a list of with the following components:

`classification`	a factor of predicted cluster labels for `newdata`.
`z`	a matrix whose *[i,k]*th entry is the probability that observation *i* in `newdata` belongs to the *k*th cluster.

Author(s)

Luca Scrucca

See Also

`Mclust`.

Examples

```
model <- Mclust(faithful)

# predict cluster for the observed data
pred <- predict(model)
str(pred)
pred$z              # equal to model$z
pred$classification # equal to
plot(faithful, col = pred$classification, pch = pred$classification)

# predict cluster over a grid
grid <- apply(faithful, 2, function(x) seq(min(x), max(x), length = 50))
grid <- expand.grid(eruptions = grid[,1], waiting = grid[,2])
pred <- predict(model, grid)
plot(grid, col = mclust.options("classPlotColors")[pred$classification], pch = 15, cex = 0.5)
points(faithful, pch = model$classification)
```

---

predict.MclustDA — *Classify multivariate observations by Gaussian finite mixture modeling*

Description

Classify multivariate observations based on Gaussian finite mixture models estimated by `MclustDA`.

Usage

```
  ## S3 method for class 'MclustDA'
predict(object, newdata, prop = object$prop, ...)
```

Arguments

object	an object of class 'MclustDA' resulting from a call to MclustDA.
newdata	a data frame or matrix giving the data. If missing the train data obtained from the call to MclustDA are classified.
prop	the class proportions or prior class probabilities to belong to each class; by default, this is set at the class proportions in the training data.
...	further arguments passed to or from other methods.

Value

Returns a list of with the following components:

classification	a factor of predicted class labels for newdata.
z	a matrix whose *[i,k]*th entry is the probability that observation *i* in newdata belongs to the *k*th class.

Author(s)

Luca Scrucca

See Also

MclustDA.

Examples

```
## Not run:
odd <- seq(from = 1, to = nrow(iris), by = 2)
even <- odd + 1
X.train <- iris[odd,-5]
Class.train <- iris[odd,5]
X.test <- iris[even,-5]
Class.test <- iris[even,5]

irisMclustDA <- MclustDA(X.train, Class.train)

predTrain <- predict(irisMclustDA)
predTrain
predTest <- predict(irisMclustDA, X.test)
predTest

## End(Not run)
```

`predict.MclustDR` *Classify multivariate observations on a dimension reduced subspace by Gaussian finite mixture modeling*

Description

Classify multivariate observations on a dimension reduced subspace estimated from a Gaussian finite mixture model.

Usage

```
  ## S3 method for class 'MclustDR'
predict(object, dim = 1:object$numdir, newdata, eval.points, ...)
```

Arguments

`object`	an object of class `'MclustDR'` resulting from a call to `MclustDR`.
`dim`	the dimensions of the reduced subspace used for prediction.
`newdata`	a data frame or matrix giving the data. If missing the data obtained from the call to `MclustDR` are used.
`eval.points`	a data frame or matrix giving the data projected on the reduced subspace. If provided `newdata` is not used.
`...`	further arguments passed to or from other methods.

Value

Returns a list of with the following components:

`dir`	a matrix containing the data projected onto the `dim` dimensions of the reduced subspace.
`density`	densities from mixture model for each data point.
`z`	a matrix whose *[i,k]*th entry is the probability that observation *i* in `newdata` belongs to the *k*th class.
`uncertainty`	The uncertainty associated with the classification.
`classification`	A vector of values giving the MAP classification.

Author(s)

Luca Scrucca

References

Scrucca, L. (2010) Dimension reduction for model-based clustering. *Statistics and Computing*, 20(4), pp. 471-484.

See Also

MclustDR.

Examples

```
mod = Mclust(iris[,1:4])
dr = MclustDR(mod)
pred = predict(dr)
str(pred)

data(banknote)
mod = MclustDA(banknote[,2:7], banknote$Status)
dr = MclustDR(mod)
pred = predict(dr)
str(pred)
```

---

priorControl *Conjugate Prior for Gaussian Mixtures.*

Description

Specify a conjugate prior for Gaussian mixtures.

Usage

```
priorControl(functionName = "defaultPrior", ...)
```

Arguments

functionName	The name of the function specifying the conjugate prior. By default the function defaultPrior is used, and this can also be used as a template for alternative specification.
...	Optional named arguments to the function specified in functionName together with their values.

Details

The function priorControl is used to specify a conjugate prior for EM within *MCLUST*.
Note that, as described in defaultPrior, in the multivariate case only 10 out of 14 models may be used in conjunction with a prior, i.e. those available in *MCLUST* up to version 4.4.

Value

A list with the function name as the first component. The remaining components (if any) consist of a list of arguments to the function with assigned values.

References

C. Fraley and A. E. Raftery (2007). Bayesian regularization for normal mixture estimation and model-based clustering. *Journal of Classification 24:155-181*.

See Also

mclustBIC, me, mstep, defaultPrior

Examples

```
# default prior
irisBIC <- mclustBIC(iris[,-5], prior = priorControl())
summary(irisBIC, iris[,-5])

# no prior on the mean; default prior on variance
irisBIC <- mclustBIC(iris[,-5], prior = priorControl(shrinkage = 0))
summary(irisBIC, iris[,-5])
```

---

randomOrthogonalMatrix

Random orthogonal matrix

Description

Generate a random orthogonal basis matrix of dimension (nxd) using the method in Heiberger (1978).

Usage

```
randomOrthogonalMatrix(n, d)
```

Arguments

n	the number of rows of the resulting orthogonal matrix.
d	the number of columns of the resulting orthogonal matrix.

Value

An orthogonal matrix of dimension nxd such that each column is orthogonal to the other and has unit lenght.

References

Heiberger R. (1978) Generation of random orthogonal matrices. *Journal of the Royal Statistical Society. Series C (Applied Statistics)*, 27(2), 199-206.

See Also

coordProj

Examples

```
B <- randomOrthogonalMatrix(10,3)
zapsmall(crossprod(B))
```

---

randomPairs *Random hierarchical structure*

Description

Create a hierarchical structure using a random partition of the data.

Usage

```
randomPairs(data, seed, ...)
```

Arguments

data	A numeric matrix or data frame of observations. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
seed	Optional single value, interpreted as an integer, specifying the seed for random partition.
...	Catches unused arguments in indirect or list calls via do.call.

Value

A numeric two-column matrix in which the *i*th row gives the minimum index for observations in each of the two clusters merged at the *i*th stage of a random agglomerative hierarchical clustering.

See Also

hc, hclass hcVVV

Examples

```
data <- iris[,1:4]
randPairs <- randomPairs(data)
str(randPairs)
# start model-based clustering from a random partition
mod <- Mclust(data, initialization = list(hcPairs = randPairs))
summary(mod)
```

randProj *Random projections of multidimensional data modeled by an MVN mixture*

Description

Plots random projections given multidimensional data and parameters of an MVN mixture model for the data.

Usage

```
randProj(data, seeds = NULL, parameters = NULL, z = NULL,
         classification = NULL, truth = NULL, uncertainty = NULL,
         what = c("classification", "error", "uncertainty"),
         quantiles = c(0.75, 0.95),
         addEllipses = TRUE, fillEllipses = mclust.options("fillEllipses"),
         symbols = NULL, colors = NULL, scale = FALSE,
         xlim = NULL, ylim = NULL, xlab = NULL, ylab = NULL,
         CEX = 1, PCH = ".", main = FALSE, ...)
```

Arguments

data	A numeric matrix or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
seeds	An integer value or a vector of integer values to be used as seed for random number generation. If multiple values are provided, then each seed should produce a different projection. By default, a single seed is drawn randomnly, so each call of `randProj()` produces different projections.
parameters	A named list giving the parameters of an *MCLUST* model, used to produce superimposing ellipses on the plot. The relevant components are as follows: `mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. `variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.
z	A matrix in which the `[i,k]`th entry gives the probability of observation *i* belonging to the *k*th class. Used to compute `classification` and `uncertainty` if those arguments aren't available.
classification	A numeric or character vector representing a classification of observations (rows) of `data`. If present argument `z` will be ignored.
truth	A numeric or character vector giving a known classification of each data point. If `classification` or `z` is also present, this is used for displaying classification errors.

uncertainty	A numeric vector of values in *(0,1)* giving the uncertainty of each data point. If present argument z will be ignored.
what	Choose from one of the following three options: "classification" (default), "error", "uncertainty".
quantiles	A vector of length 2 giving quantiles used in plotting uncertainty. The smallest symbols correspond to the smallest quantile (lowest uncertainty), medium-sized (open) symbols to points falling between the given quantiles, and large (filled) symbols to those in the largest quantile (highest uncertainty). The default is *(0.75,0.95)*.
addEllipses	A logical indicating whether or not to add ellipses with axes corresponding to the within-cluster covariances in case of "classification" or "uncertainty" plots.
fillEllipses	A logical specifying whether or not to fill ellipses with transparent colors when addEllipses = TRUE.
symbols	Either an integer or character vector assigning a plotting symbol to each unique class in classification. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function unique). The default is given by mclust.options("classPlotSymbols").
colors	Either an integer or character vector assigning a color to each unique class in classification. Elements in colors correspond to classes in order of appearance in the sequence of observations (the order used by the function unique). The default is given by mclust.options("classPlotColors").
scale	A logical variable indicating whether or not the two chosen dimensions should be plotted on the same scale, and thus preserve the shape of the distribution. Default: scale=FALSE
xlim, ylim	Optional arguments specifying bounds for the ordinate, abscissa of the plot. This may be useful for when comparing plots.
xlab, ylab	Optional arguments specifying the labels for, respectively, the horizontal and vertical axis.
CEX	An argument specifying the size of the plotting symbols. The default value is 1.
PCH	An argument specifying the symbol to be used when a classificatiion has not been specified for the data. The default value is a small dot ".".
main	A logical variable or NULL indicating whether or not to add a title to the plot identifying the dimensions used.
...	Other graphics parameters.

Value

A plot showing a random two-dimensional projection of the data, together with the location of the mixture components, classification, uncertainty, and/or classification errors.

The function also returns an invisible list with components basis, the randomnly generated basis of the projection subspace, data, a matrix of projected data, and mu and sigma the component parameters transformed to the projection subspace.

See Also

clPairs, coordProj, mclust2Dplot, mclust.options

Examples

```
## Not run:
est <- meVVV(iris[,-5], unmap(iris[,5]))
par(pty = "s", mfrow = c(1,1))
randProj(iris[,-5], seeds=1:3, parameters = est$parameters, z = est$z,
         what = "classification", main = TRUE)
randProj(iris[,-5], seeds=1:3, parameters = est$parameters, z = est$z,
         truth = iris[,5], what = "error", main = TRUE)
randProj(iris[,-5], seeds=1:3, parameters = est$parameters, z = est$z,
         what = "uncertainty", main = TRUE)

## End(Not run)
```

---

sigma2decomp *Convert mixture component covariances to decomposition form.*

Description

Converts a set of covariance matrices from representation as a 3-D array to a parameterization by eigenvalue decomposition.

Usage

```
sigma2decomp(sigma, G = NULL, tol = sqrt(.Machine$double.eps), ...)
```

Arguments

sigma	Either a 3-D array whose [,,k]th component is the covariance matrix for the kth component in an MVN mixture model, or a single covariance matrix in the case that all components have the same covariance.
G	The number of components in the mixture. When sigma is a 3-D array, the number of components can be inferred from its dimensions.
tol	Tolerance for determining whether or not the covariances have equal volume, shape, and or orientation. The default is the square root of the relative machine precision, sqrt(.Machine$double.eps), which is about 1.e-8.
...	Catches unused arguments from an indirect or list call via do.call.

Value

The covariance matrices for the mixture components in decomposition form, including the following components:

modelName	A character string indicating the infered model. The help file for mclustModelNames describes the available models.

d	The dimension of the data.
G	The number of components in the mixture model.
scale	Either a G-vector giving the scale of the covariance (the dth root of its determinant) for each component in the mixture model, or a single numeric value if the scale is the same for each component.
shape	Either a G by d matrix in which the kth column is the shape of the covariance matrix (normalized to have determinant 1) for the kth component, or a d-vector giving a common shape for all components.
orientation	Either a d by d by G array whose `[,,k]`th entry is the orthonomal matrix whose columns are the eigenvectors of the covariance matrix of the kth component, or a d by d orthonormal matrix if the mixture components have a common orientation. The `orientation` component of `decomp` can be omitted in spherical and diagonal models, for which the principal components are parallel to the coordinate axes so that the orientation matrix is the identity.

See Also

decomp2sigma

Examples

```
meEst <- meEEE(iris[,-5], unmap(iris[,5]))
names(meEst$parameters$variance)
meEst$parameters$variance$Sigma

sigma2decomp(meEst$parameters$variance$Sigma, G = length(unique(iris[,5])))
```

---

sim *Simulate from Parameterized MVN Mixture Models*

Description

Simulate data from parameterized MVN mixture models.

Usage

```
sim(modelName, parameters, n, seed = NULL, ...)
```

Arguments

modelName	A character string indicating the model. The help file for mclustModelNames describes the available models.
parameters	A list with the following components:
	pro A vector whose kth component is the mixing proportion for the kth component of the mixture model. If missing, equal proportions are assumed.

`mean` The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model.

`variance` A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for `mclustVariance` for details.

`n` An integer specifying the number of data points to be simulated.

`seed` An optional integer argument to `set.seed` for reproducible random class assignment. By default the current seed will be used. Reproducibility can also be achieved by calling `set.seed` before calling `sim`.

`...` Catches unused arguments in indirect or list calls via `do.call`.

Details

This function can be used with an indirect or list call using `do.call`, allowing the output of e.g. `mstep`, `em`, `me`, `Mclust` to be passed directly without the need to specify individual parameters as arguments.

Value

A matrix in which first column is the classification and the remaining columns are the `n` observations simulated from the specified MVN mixture model.

`Attributes:` `"modelName"` A character string indicating the variance model used for the simulation.

See Also

`simE`, `...`, `simVVV`, `Mclust`, `mstep`, `do.call`

Examples

```
irisBIC <- mclustBIC(iris[,-5])
irisModel <- mclustModel(iris[,-5], irisBIC)
names(irisModel)
irisSim <- sim(modelName = irisModel$modelName,
               parameters = irisModel$parameters,
               n = nrow(iris))

## Not run:
  do.call("sim", irisModel) # alternative call

## End(Not run)

par(pty = "s", mfrow = c(1,2))

dimnames(irisSim) <- list(NULL, c("dummy", (dimnames(iris)[[2]])[-5]))

dimens <- c(1,2)
lim1 <- apply(iris[,dimens],2,range)
```

```
lim2 <- apply(irisSim[,dimens+1],2,range)
lims <- apply(rbind(lim1,lim2),2,range)
xlim <- lims[,1]
ylim <- lims[,2]

coordProj(iris[,-5], parameters=irisModel$parameters,
          classification=map(irisModel$z),
          dimens=dimens, xlim=xlim, ylim=ylim)

coordProj(iris[,-5], parameters=irisModel$parameters,
          classification=map(irisModel$z), truth = irisSim[,-1],
          dimens=dimens, xlim=xlim, ylim=ylim)

irisModel3 <- mclustModel(iris[,-5], irisBIC, G=3)
irisSim3 <- sim(modelName = irisModel3$modelName,
               parameters = irisModel3$parameters, n = 500, seed = 1)
## Not run:
 irisModel3$n <- NULL
 irisSim3 <- do.call("sim",c(list(n=500,seed=1),irisModel3)) # alternative call

## End(Not run)
clPairs(irisSim3[,-1], cl = irisSim3[,1])
```

---

simE *Simulate from a Parameterized MVN Mixture Model*

Description

Simulate data from a parameterized MVN mixture model.

Usage

```
simE(parameters, n, seed = NULL, ...)
simV(parameters, n, seed = NULL, ...)
simEII(parameters, n, seed = NULL, ...)
simVII(parameters, n, seed = NULL, ...)
simEEI(parameters, n, seed = NULL, ...)
simVEI(parameters, n, seed = NULL, ...)
simEVI(parameters, n, seed = NULL, ...)
simVVI(parameters, n, seed = NULL, ...)
simEEE(parameters, n, seed = NULL, ...)
simEEV(parameters, n, seed = NULL, ...)
simVEV(parameters, n, seed = NULL, ...)
simVVV(parameters, n, seed = NULL, ...)
simEVE(parameters, n, seed = NULL, ...)
simEVV(parameters, n, seed = NULL, ...)
simVEE(parameters, n, seed = NULL, ...)
simVVE(parameters, n, seed = NULL, ...)
```

Arguments

parameters	A list with the following components: pro A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If missing, equal proportions are assumed. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details.
n	An integer specifying the number of data points to be simulated.
seed	An optional integer argument to set.seed for reproducible random class assignment. By default the current seed will be used. Reproducibility can also be achieved by calling set.seed before calling sim.
...	Catches unused arguments in indirect or list calls via do.call.

Details

This function can be used with an indirect or list call using do.call, allowing the output of e.g. mstep, em me, Mclust, to be passed directly without the need to specify individual parameters as arguments.

Value

A matrix in which first column is the classification and the remaining columns are the n observations simulated from the specified MVN mixture model.

Attributes:	"modelName" A character string indicating the variance model used for the simulation.

See Also

sim, Mclust, mstepE, mclustVariance.

Examples

```
## Not run:
d <- 2
G <- 2
scale <- 1
shape <- c(1, 9)

O1 <- diag(2)
O2 <- diag(2)[,c(2,1)]
O <- array(cbind(O1,O2), c(2, 2, 2))
O

variance <- list(d= d, G = G, scale = scale, shape = shape, orientation = O)
mu <- matrix(0, d, G) ## center at the origin
```

```
simdat <- simEEV( n = 200,
                  parameters = list(pro=c(1,1),mean=mu,variance=variance),
                  seed = NULL)

cl <- simdat[,1]

sigma <- array(apply(O, 3, function(x,y) crossprod(x*y),
                y = sqrt(scale*shape)), c(2,2,2))
paramList <- list(mu = mu, sigma = sigma)
coordProj( simdat, paramList = paramList, classification = cl)

## End(Not run)
```

---

summary.Mclust *Summarizing Gaussian Finite Mixture Model Fits*

Description

Summary method for class "Mclust".

Usage

```
## S3 method for class 'Mclust'
summary(object, parameters = FALSE, classification = FALSE, ...)
## S3 method for class 'summary.Mclust'
print(x, digits = getOption("digits"), ...)
```

Arguments

object	An object of class 'Mclust' resulting of a call to Mclust or densityMclust.
x	An object of class 'summary.Mclust', usually, a result of a call to summary.Mclust.
parameters	Logical; if TRUE, the parameters of mixture components are printed.
classification	Logical; if TRUE, the MAP classification/clustering of observations is printed.
digits	The number of significant digits to use when printing.
...	Further arguments passed to or from other methods.

Author(s)

Luca Scrucca

See Also

Mclust, densityMclust.

Examples

```
mod1 = Mclust(iris[,1:4])
summary(mod1)
summary(mod1, parameters = TRUE, classification = TRUE)

mod2 = Mclust(iris[,1:4], G = 1)
summary(mod2, parameters = TRUE, classification = TRUE)

mod3 = Mclust(iris[,1:4], prior = priorControl())
summary(mod3)

mod4 = Mclust(iris[,1:4], prior = priorControl(functionName="defaultPrior", shrinkage=0.1))
summary(mod4, parameters = TRUE, classification = TRUE)
```

---

summary.mclustBIC *Summary function for model-based clustering via BIC*

Description

Optimal model characteristics and classification for model-based clustering via `mclustBIC`.

Usage

```
## S3 method for class 'mclustBIC'
summary(object, data, G, modelNames, ...)
```

Arguments

`object`	An `'mclustBIC'` object, which is the result of applying `mclustBIC` to `data`.
`data`	The matrix or vector of observations used to generate 'object'.
`G`	A vector of integers giving the numbers of mixture components (clusters) from which the best model according to BIC will be selected (`as.character(G)` must be a subset of the row names of `object`). The default is to select the best model for all numbers of mixture components used to obtain `object`.
`modelNames`	A vector of integers giving the model parameterizations from which the best model according to BIC will be selected (`as.character(model)` must be a subset of the column names of `object`). The default is to select the best model for parameterizations used to obtain `object`.
`...`	Not used. For generic/method consistency.

Value

A list giving the optimal (according to BIC) parameters, conditional probabilities `z`, and log-likelihood, together with the associated classification and its uncertainty.

The details of the output components are as follows:

`modelName`	A character string denoting the model corresponding to the optimal BIC.

n	The number of observations in the data.
d	The dimension of the data.
G	The number of mixture components in the model corresponding to the optimal BIC.
bic	The optimal BIC value.
loglik	The log-likelihood corresponding to the optimal BIC.
parameters	A list with the following components: pro A vector whose *k*th component is the mixing proportion for the *k*th component of the mixture model. If missing, equal proportions are assumed. mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details.
z	A matrix whose *[i,k]*th entry is the probability that observation *i* in the data belongs to the *k*th class.
classification	map(z): The classification corresponding to z.
uncertainty	The uncertainty associated with the classification.
Attributes:	"bestBICvalues" Some of the best bic values for the analysis. "prior" The prior as specified in the input. "control" The control parameters for EM as specified in the input. "initialization" The parameters used to initial EM for computing the maximum likelihood values used to obtain the BIC.

See Also

mclustBIC mclustModel

Examples

```
irisBIC <- mclustBIC(iris[,-5])
summary(irisBIC, iris[,-5])
summary(irisBIC, iris[,-5], G = 1:6, modelNames = c("VII", "VVI", "VVV"))
```

---

summary.MclustBootstrap

Summary Function for Bootstrap Inference for Gaussian Finite Mixture Models

---

Description

Summary of bootstrap distribution for the parameters of a Gaussian mixture model providing either standard errors or percentile bootstrap confidence intervals.

Usage

```
## S3 method for class 'MclustBootstrap'
summary(object, what = c("se", "ci", "ave"), conf.level = 0.95, ...)
```

Arguments

object	An object of class 'MclustBootstrap' as returned by MclustBootstrap.
what	A character string: "se" for the standard errors; "ci" for the confidence intervals; "ave" for the averages.
conf.level	A value specifying the confidence level of the interval.
...	Further arguments passed to or from other methods.

Details

For details about the procedure used to obtain the bootstrap distribution see MclustBootstrap.

See Also

MclustBootstrap.

Examples

```
## Not run:
data(diabetes)
X = diabetes[,-1]
modClust = Mclust(X)
bootClust = MclustBootstrap(modClust)
summary(bootClust, what = "se")
summary(bootClust, what = "ci")

data(acidity)
modDens = densityMclust(acidity)
modDens = MclustBootstrap(modDens)
summary(modDens, what = "se")
summary(modDens, what = "ci")

## End(Not run)
```

---

summary.MclustDA *Summarizing discriminant analysis based on Gaussian finite mixture modeling*

Description

Summary method for class "MclustDA".

Usage

```
## S3 method for class 'MclustDA'
summary(object, parameters = FALSE, newdata, newclass, ...)
## S3 method for class 'summary.MclustDA'
print(x, digits = getOption("digits"), ...)
```

Arguments

object	An object of class 'MclustDA' resulting from a call to MclustDA.
x	An object of class 'summary.MclustDA', usually, a result of a call to summary.MclustDA.
parameters	Logical; if TRUE, the parameters of mixture components are printed.
newdata	A data frame or matrix giving the test data.
newclass	A vector giving the class labels for the observations in the test data.
digits	The number of significant digits to use when printing.
...	Further arguments passed to or from other methods.

Value

The function summary.MclustDA computes and returns a list of summary statistics of the estimated MclustDA or EDDA model for classification.

Author(s)

Luca Scrucca

See Also

MclustDA, plot.MclustDA.

Examples

```
mod = MclustDA(data = iris[,1:4], class = iris$Species)
summary(mod)
summary(mod, parameters = TRUE)
```

---

summary.MclustDR *Summarizing dimension reduction method for model-based clustering and classification*

Description

Summary method for class "MclustDR".

Usage

```
## S3 method for class 'MclustDR'
summary(object, numdir, std = FALSE, ...)
## S3 method for class 'summary.MclustDR'
print(x, digits = max(5, getOption("digits") - 3), ...)
```

Arguments

object	An object of class 'MclustDR' resulting from a call to MclustDR.
x	An object of class 'summary.MclustDR', usually, a result of a call to summary.MclustDR.
numdir	An integer providing the number of basis directions to be printed.
std	if TRUE the coefficients basis are scaled such that all predictors have unit standard deviation.
digits	The number of significant digits to use when printing.
...	Further arguments passed to or from other methods.

Author(s)

Luca Scrucca

See Also

MclustDR, plot.MclustDR

---

surfacePlot *Density or uncertainty surface for bivariate mixtures*

Description

Plots a density or uncertainty surface given bivariate data and parameters of a MVN mixture model for the data.

Usage

```
surfacePlot(data, parameters,
            what = c("density", "uncertainty"),
            type = c("contour", "hdr", "image", "persp"),
            transformation = c("none", "log", "sqrt"),
            grid = 200, nlevels = 11, levels = NULL,
            prob = c(0.25, 0.5, 0.75),
            col = gray(0.7),
            col.palette = function(...) hcl.colors(..., "blues", rev = TRUE),
            hdr.palette = blue2grey.colors,
            xlim = NULL, ylim = NULL, xlab = NULL, ylab = NULL,
            main = FALSE, scale = FALSE, swapAxes = FALSE,
            verbose = FALSE, ...)
```

Arguments

data	A matrix, or data frame of bivariate observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
parameters	A named list giving the parameters of an *MCLUST* model, used to produce superimposing ellipses on the plot. The relevant components are as follows: mean The mean for each component. If there is more than one component, this is a matrix whose kth column is the mean of the *k*th component of the mixture model. variance A list of variance parameters for the model. The components of this list depend on the model specification. See the help file for mclustVariance for details.
what	Choose from one of the following options: "density" (default), "uncertainty" indicating what to plot.
type	Choose from one of the following three options: "contour" (default), "hdr", "image", and "persp" indicating the plot type.
transformation	Choose from one of the following three options: "none" (default), "log", "sqrt" indicating a transformation to be applied before plotting.
grid	The number of grid points (evenly spaced on each axis). The mixture density and uncertainty is computed at grid x grid points to produce the surface plot. Default: 100.
nlevels	The number of levels to use for a contour plot. Default: 11.
levels	A vector of levels at which to draw the lines in a contour plot.
prob	A vector of probability levels for computing HDR. Only used if type = "hdr" and supersede previous nlevels and levels arguments.
col	A string specifying the colour to be used for type = "contour" and type = "persp" plots.
col.palette	A function which defines a palette of colours to be used for type = "image" plots.
hdr.palette	A function which defines a palette of colours to be used for type = "hdr" plots.
xlim, ylim	Optional argument specifying bounds for the ordinate, abscissa of the plot. This may be useful for when comparing plots.
xlab, ylab	Optional argument specifying labels for the x-axis and y-axis.
main	A logical variable or NULL indicating whether or not to add a title to the plot identifying the dimensions used.
scale	A logical variable indicating whether or not the two dimensions should be plotted on the same scale, and thus preserve the shape of the distribution. The default is not to scale.
swapAxes	A logical variable indicating whether or not the axes should be swapped for the plot.
verbose	A logical variable telling whether or not to print an indication that the function is in the process of computing values at the grid points, which typically takes some time to complete.
...	Other graphics parameters.

Details

For an image plot, a color scheme may need to be selected on the display device in order to view the plot.

Value

A plots showing (a transformation of) the density or uncertainty for the given mixture model and data.

The function also returns an invisible list with components `x`, `y`, and `z` in which `x` and `y` are the values used to define the grid and `z` is the transformed density or uncertainty at the grid points.

References

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association 97:611-631*.

C. Fraley, A. E. Raftery, T. B. Murphy and L. Scrucca (2012). mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation. Technical Report No. 597, Department of Statistics, University of Washington.

See Also

`mclust2Dplot`

Examples

```
## Not run:
faithfulModel <- Mclust(faithful)
surfacePlot(faithful, parameters = faithfulModel$parameters,
            type = "contour", what = "density", transformation = "none",
            drawlabels = FALSE)
surfacePlot(faithful, parameters = faithfulModel$parameters,
            type = "persp", what = "density", transformation = "log")
surfacePlot(faithful, parameters = faithfulModel$parameters,
            type = "contour", what = "uncertainty", transformation = "log")

## End(Not run)
```

---

thyroid *Thyroid gland data*

Description

Data on five laboratory tests administered to a sample of 215 patients. The tests are used to predict whether a patient's thyroid can be classified as euthyroidism (normal thyroid gland function), hypothyroidism (underactive thyroid not producing enough thyroid hormone) or hyperthyroidism (overactive thyroid producing and secreting excessive amounts of the free thyroid hormones T3 and/or thyroxine T4). Diagnosis of thyroid operation was based on a complete medical record, including anamnesis, scan, etc..

Usage

```
data(thyroid)
```

Format

A data frame with the following variables:

Diagnosis Diagnosis of thyroid operation: `Hypo`, `Normal`, and `Hyper`.

RT3U T3-resin uptake test (percentage).

T4 Total Serum thyroxin as measured by the isotopic displacement method.

T3 Total serum triiodothyronine as measured by radioimmuno assay.

TSH Basal thyroid-stimulating hormone (TSH) as measured by radioimmuno assay.

DTSH Maximal absolute difference of TSH value after injection of 200 micro grams of thyrotropin-releasing hormone as compared to the basal value.

Source

UCI ftp://ftp.ics.uci.edu/pub/machine-learning-databases/thyroid-disease/

References

Coomans, D., Broeckaert, M. Jonckheer M. and Massart D.L. (1983) Comparison of Multivariate Discriminant Techniques for Clinical Data - Application to the Thyroid Functional State, *Meth. Inform. Med.* 22, pp. 93-101.

Coomans, D. and I. Broeckaert (1986) *Potential Pattern Recognition in Cemical and Medical Decision Making*, Research Studies Press, Letchworth, England.

---

uncerPlot *Uncertainty Plot for Model-Based Clustering*

Description

Displays the uncertainty in converting a conditional probablility from EM to a classification in model-based clustering.

Usage

```
uncerPlot(z, truth, ...)
```

Arguments

`z`	A matrix whose *[i,k]*th entry is the conditional probability of the ith observation belonging to the *k*th component of the mixture.
`truth`	A numeric or character vector giving the true classification of the data.
`...`	Provided to allow lists with elements other than the arguments can be passed in indirect or list calls with `do.call`.

Details

When truth is provided and the number of classes is compatible with z, the function compareClass is used to to find best correspondence between classes in truth and z.

Value

A plot of the uncertainty profile of the data, with uncertainties in increasing order of magnitude. If truth is supplied and the number of classes is the same as the number of columns of z, the uncertainty of the misclassified data is marked by vertical lines on the plot.

See Also

mclustBIC, em, me, mapClass

Examples

```
irisModel3 <-  Mclust(iris[,-5], G = 3)

uncerPlot(z = irisModel3$z)

uncerPlot(z = irisModel3$z, truth = iris[,5])
```

---

unmap *Indicator Variables given Classification*

Description

Converts a classification into a matrix of indicator variables.

Usage

```
unmap(classification, groups=NULL, noise=NULL, ...)
```

Arguments

classification	A numeric or character vector. Typically the distinct entries of this vector would represent a classification of observations in a data set.
groups	A numeric or character vector indicating the groups from which classification is drawn. If not supplied, the default is to assumed to be the unique entries of classification.
noise	A single numeric or character value used to indicate the value of groups corresponding to noise.
...	Catches unused arguments in indirect or list calls via do.call.

Value

An *n* by *m* matrix of *(0,1)* indicator variables, where *n* is the length of `classification` and *m* is the number of unique values or symbols in `classification`. Columns are labeled by the unique values in `classification`, and the `[i,j]`th entry is *1* if `classification[i]` is the *j*th unique value or symbol in sorted order `classification`. If a `noise` value of symbol is designated, the corresponding indicator variables are relocated to the last column of the matrix.

See Also

`map`, `estep`, `me`

Examples

```
z <- unmap(iris[,5])
z[1:5, ]

emEst <- me(modelName = "VVV", data = iris[,-5], z = z)
emEst$z[1:5,]

map(emEst$z)
```

---

wdbc *Wisconsin diagnostic breast cancer (WDBC) data*

Description

The data set provides data for 569 patients on 30 features of the cell nuclei obtained from a digitized image of a fine needle aspirate (FNA) of a breast mass. For each patient the cancer was diagnosed as malignant or benign.

Usage

```
data(wdbc)
```

Format

A data frame with 569 observations on the following variables:

`ID` ID number

`Diagnosis` cancer diagnosis: `M` = malignant, `B` = benign

`Radius_mean` a numeric vector

`Texture_mean` a numeric vector

`Perimeter_mean` a numeric vector

`Area_mean` a numeric vector

`Smoothness_mean` a numeric vector

`Compactness_mean` a numeric vector

`Concavity_mean` a numeric vector
`Nconcave_mean` a numeric vector
`Symmetry_mean` a numeric vector
`Fractaldim_mean` a numeric vector
`Radius_se` a numeric vector
`Texture_se` a numeric vector
`Perimeter_se` a numeric vector
`Area_se` a numeric vector
`Smoothness_se` a numeric vector
`Compactness_se` a numeric vector
`Concavity_se` a numeric vector
`Nconcave_se` a numeric vector
`Symmetry_se` a numeric vector
`Fractaldim_se` a numeric vector
`Radius_extreme` a numeric vector
`Texture_extreme` a numeric vector
`Perimeter_extreme` a numeric vector
`Area_extreme` a numeric vector
`Smoothness_extreme` a numeric vector
`Compactness_extreme` a numeric vector
`Concavity_extreme` a numeric vector
`Nconcave_extreme` a numeric vector
`Symmetry_extreme` a numeric vector
`Fractaldim_extreme` a numeric vector

Details

The recorded features are:

- `Radius` as mean of distances from center to points on the perimeter
- `Texture` as standard deviation of gray-scale values
- `Perimeter` as cell nucleus perimeter
- `Area` as cell nucleus area
- `Smoothness` as local variation in radius lengths
- `Compactness` as cell nucleus compactness, perimeter^2 / area - 1
- `Concavity` as severity of concave portions of the contour
- `Nconcave` as number of concave portions of the contour
- `Symmetry` as cell nucleus shape
- `Fractaldim` as fractal dimension, "coastline approximation" - 1

For each feature the recorded values are computed from each image as `<feature_name>_mean`, `<feature_name>_se`, and `<feature_name>_extreme`, for the mean, the standard error, and the mean of the three largest values.

Source

UCI http://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+(Diagnostic)

References

Mangasarian, O. L., Street, W. N., and Wolberg, W. H. (1995) Breast cancer diagnosis and prognosis via linear programming. *Operations Research*, 43(4), pp. 570-577.

---

wreath *Data Simulated from a 14-Component Mixture*

Description

A dataset consisting of 1000 observations drawn from a 14-component normal mixture in which the covariances of the components have the same size and shape but differ in orientation.

Usage

```
data(wreath)
```

References

C. Fraley, A. E. Raftery and R. Wehrens (2005). Incremental model-based clustering for large datasets with small clusters. *Journal of Computational and Graphical Statistics 14:1:18.*

Index