Package ‘Rmixmod’

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Description

Rmixmod is a package based on the existing MIXMOD software. MIXMOD is a tool for fitting a mixture model of multivariate gaussian or multinomial components to a given data set with either a clustering, a density estimation or a discriminant analysis point of view.

Details

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<th>Rmixmod</th>
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The general purpose of the package is to discover, or explain, group structures in multivariate data sets with unknown (cluster analysis or clustering) or known class discriminant analysis or classification. It is an exploratory data analysis tool for solving clustering and classification problems. But it can also be regarded as a semi-parametric tool to estimate densities with Gaussian mixture distributions and multinomial distributions.

Mathematically, mixture probability density function (pdf) $f$ is a weighted sum of $K$ components densities:

$$f(x|\theta) = \sum_{k=1}^{K} p_k h(x|\lambda_k)$$

where $h(.|\lambda_k)$ denotes a $d$-dimensional distribution parametrized by $\lambda_k$. The parameters are the mixing proportions $p_k$ and the component of the distribution $\lambda_k$.

In the Gaussian case, $h$ is the density of a Gaussian distribution with mean $\mu_k$ and variance matrix $\Sigma_k$, and thus $\lambda_k = (\mu_k, \Sigma_k)$.

In the qualitative case, $h$ is a multinomial distribution and $\lambda_k = (a_k, \epsilon_k)$ is the parameter of the distribution.

Estimation of the mixture parameters is performed either through maximum likelihood via the EM (Expectation Maximization, Dempster et al. 1977), the SEM (Stochastic EM, Celeux and Diebolt 1985) algorithm or through classification maximum likelihood via the CEM algorithm (Clustering EM, Celeux and Govaert 1992). These three algorithms can be chained to obtain original fitting strategies (e.g. CEM then EM with results of CEM) to use advantages of each of them in the estimation process. As mixture problems usually have multiple relative maxima, the program will produce different results, depending on the initial estimates supplied by the user. If the user does
Rmixmod-package

not input his own initial estimates, some initial estimates procedures are proposed (random centers for instance).

It is possible to constrain some input parameters. For example, dispersions can be equal between classes, etc.

In the Gaussian case, fourteen models are implemented. They are based on the eigenvalue decomposition, are most generally used. They depend on constraints on the variance matrix such as same variance matrix between clusters, spherical variance matrix... and they are suitable for data sets in any dimension.

In the qualitative case, five multinomial models are available. They are based on a reparametrization of the multinomial probabilities.

In both cases, the models and the number of clusters can be chosen by different criteria : BIC (Bayesian Information Criterion), ICL (Integrated Completed Likelihood, a classification version of BIC), NEC (Entropy Criterion), or Cross-Validation (CV).

Author(s)

Author: Remi Lebret and Serge Iovleff and Florent Langrognet, with contributions from C. Biernacki and G. Celeux and G. Govaert <contact@mixmod.org>

References


Examples

## Clustering Analysis

```r
# load quantitative data set
data(geyser)

# Clustering in gaussian case
xem1 <- mixmodCluster(geyser, 3)
summary(xem1)
plot(xem1)
hist(xem1)

# load qualitative data set
data(birds)

# Clustering in multinomial case
xem2 <- mixmodCluster(birds, 2)
summary(xem2)
barplot(xem2)
```

## Discriminant Analysis

```r
# start by extract 10 observations from iris data set
remaining.obs <- sample(1:nrow(iris), 10)

# then run a mixmodLearn() analysis without those 10 observations
learn <- mixmodLearn(iris[-remaining.obs, 1:4], iris$Species[-remaining.obs])

# create a MixmodPredict to predict those 10 observations
prediction <- mixmodPredict(data = iris[remaining.obs, 1:4], classificationRule = learn$"bestResult")
```
# show results
prediction
# compare prediction with real results
as.integer(iris$Species[remaining.obs]) == prediction["partition"]

asQualitative

Convert a data frame containing integers to a qualitative data set with factors.

Description

Convert a data frame containing integers to a qualitative data set with factors.

Usage

asQualitative(x)

Arguments

x

a vector or a matrix or a data frame

Value

a qualitative data set with factors

barplot

Barplot of a class [Mixmod]

Description

Barplot of qualitative data from a [Mixmod] object using parameters to plot probabilities of modalities.

Arguments

x

an object of class [Mixmod]

... further arguments passed to or from other methods

Details

Each line corresponds to one variable. Barplot is drawn for each cluster with the probabilities for each modality to be in that cluster.

See Also

barplot
**Examples**

```r
data(birds)
xem2 <- mixmodCluster(birds, 2)
barplot(xem2)
```

---

**Description**

Barplot of qualitative data object using parameters from a `MixmodResults` to plot probabilities of modalities.

**Usage**

```r
barplotCluster(x, data, variables = colnames(data),
               main = paste("Barplot of", variables), ...)
```

**Arguments**

- `x` an object of class `MixmodResults`
- `data` a vector, matrix or data frame containing a qualitative data set.
- `variables` list of variables names to compute a barplot. All variables from data by default.
- `main` a list of title for the barplot. `main` must have the same length than `variables`.
- `...` further arguments passed to or from other methods

**Details**

Each line corresponds to one variable. A barplot is drawn for each cluster with the probabilities for each modality to be in that cluster.

**See Also**

- `barplot`

**Examples**

```r
data(birds)
xem2 <- mixmodCluster(birds, 2)
barplotCluster(xem2["bestResult"], birds)
```
**birds**

*Qualitative data: morphological description of birds*

**Description**

The dataset contains details on the morphology of birds (puffins). Each individual (bird) is described by 6 qualitative variables. One variable for the gender and 5 variables giving a morphological description of the birds. There is 69 puffins divided in 2 sub-classes: lherminieri (34) and subalaris (35).

**Format**

A data frame with 69 observations on the following 5 variables.

- **gender**: a numeric vector defining the gender (2 modalities, male or female). 
- **eyebrow**: a numeric vector describing the eyebrow stripe (4 modalities). 
- **collar**: a numeric vector describing the collar (5 modalities). 
- **sub-caudal**: a numeric vector describing the sub-caudal (5 modalities). 
- **border**: a numeric vector describing the border (3 modalities).

**Source**


**Examples**

```r
data(birds)
```

**car**

*Qualitative data: Car Evaluation*

**Description**

Car Evaluation Database was derived from a simple hierarchical decision model originally developed for the demonstration of DEX, M. Bohanec, V. Rajkovic: Expert system for decision making.

**Format**

A data frame with 1728 observations on the following 6 variables.

- **buying**: the buying price (4 modalities: vhigh, high, med, low). 
- **maint**: the price of the maintenance (4 modalities: vhigh, high, med, low). 
- **doors**: the number of doors (4 modalities: 2, 3, 4, 5more). 
- **persons**: the capacity in terms of persons to carry (3 modalities: 2, 4, more). 
- **lug_boot**: the size of luggage boot (3 modalities: small, med, big). 
- **safety**: the estimated safety of the car (3 modalities: low, med, high). 
- **acceptability**: the car acceptability (4 modalities: unacc, acc, good, vgood).
**Source**

Creator: Marko Bohanec
Donors: Marko Bohanec & Blaz Zupan

**Examples**

```r
data(car)
```

---

**finance**

*Quantitative data: Financial health of companies*

**Description**

This data set is made up of 216 healthy firms and 212 bankruptcy firms (year 2002) and also 241 healthy firms and 220 bankruptcy firms (year 2003). Companies are described by four financial ratios expected to provide some meaningful information about their health: EBITDA/Total Assets, Value Added/Total Sales, Quick Ratio, Accounts Payable/Total Sales. This data set offers the possibility to predict the company’s ability to cover its financial obligations and also to study its stability over the years.

**Format**

A data frame with 889 companies (rows) and 6 variables (columns).

- **Year** categorical variable with two modalities (2002 & 2003).
- **Health** categorical variable with two modalities (bankruptcy & healthy).
- **EBITDA/Total Assets** numeric variable.
- **Value Added/Total Sales** numeric variable.
- **Quick Ratio** numeric variable.
- **Accounts Payable/Total Sales** numeric variable.

**Source**


**Examples**

```r
data(finance)
summary(finance)
```
**GaussianModel-class**  
*Constructor of [GaussianModel] class*

**Description**
This class defines a gaussian Model. Inherits the [Model] class.

**Details**
- **family** character defining a family of models.

**Examples**
```r
new("GaussianModel")
new("GaussianModel",family="general")
getSlots("GaussianModel")
```

---

**GaussianParameter-class**  
*Constructor of [GaussianParameter] class*

**Description**
This class defines parameters of a Gaussian Mixture Model. Inherits the [Parameter] class.

**Details**
- **mean** a numeric vector containing mean of each cluster.
- **variance** a vector of matrix containing variance matrix of each cluster.

**Examples**
```r
new("GaussianParameter")
getSlots("GaussianParameter")
```
Description

The file geyser.rda contains 272 observations from the Old Faithful Geyser in the Yellowstone National Park. Each observation consists of two measurements: the duration (in minutes) of the eruption and the waiting time (in minutes) to the next eruption.

Format

A data frame with 272 observations on the following 2 variables.

Duration a numeric vector containing the duration (in minutes) of the eruption
Waiting.Time a numeric vector containing the waiting time (in minutes) to the next eruption

Details

Old Faithful erupts more frequently than any other big geyser, although it is not the largest nor the most regular geyser in the park. Its average interval between two eruptions is about 76 minutes, varying from 45 - 110 minutes. An eruption lasts from 1.1/2 to 5 minutes, expels 3,700 - 8,400 gallons (14,000 - 32,000 liters) of boiling water, and reaches heights of 106 - 184 feet (30 - 55m). It was named for its consistent performance by members of the Washburn Expedition in 1870. Old Faithful is still as spectacular and predictable as it was a century ago.

Source


References


Examples

data(geyser)
**hist**  
*Histograms of a class* [Mixmod]

**Description**

Histograms of quantitative data from a [Mixmod] object using parameters to plot densities.

**Arguments**

- `x` an object of class [Mixmod]
- `...` further arguments passed to or from other methods

**Details**

Data with the density of each cluster and the mixture density are drawn for each variable.

**See Also**

hist

**Examples**

```r
data(geyser)
  xem1 <- mixmodCluster(geyser,3)
  hist(xem1)
```

**histCluster**  
*Histogram of a class* [MixmodResults]

**Description**

Histograms of data object using parameters from a [MixmodResults] to plot densities.

**Usage**

```r
histCluster(x, data, variables = colnames(data),
  xlab = rep("", length(variables)),
  main = paste("Histogram of", variables), ...)
```
Arguments

- **x**: an object of class `MixmodResults`
- **data**: a vector, matrix or data frame containing a quantitative data set.
- **variables**: list of variables names to compute a histogram. All variables from data by default.
- **xlab**: a list of title for the x axis. xlab must have the same length than variables.
- **main**: a list of title for the histogram. main must have the same length than variables.
- **...**: further arguments passed to or from other methods

Details

Data with the density of each cluster and the mixture density are drawn for each variable.

See Also

- hist

Examples

```r
data(geyser)
xem1 <- mixmodCluster(geyser,3)
histCluster(xem1["bestResult"], geyser)
```

---

**isQualitative**  Say if a data frame contains only qualitative variables.

Description

Say if a data frame contains only qualitative variables.

Usage

```r
isQualitative(x)
```

Arguments

- **x**: a vector or a matrix or a data frame

Value

- a boolean
Mixmod-class

Constructor of [Mixmod] class

Description

This is a class to run mixmod library.

Details

- **data** numeric vector, matrix, or data frame of observations. Either qualitative or quantitative.
- **dataType** character. It defines whether data are quantitative or qualitative.
- **nbCluster** integer. It indicates the number of classes.
- **knownLabels** numeric. It contains the known labels.
- **weight** numeric vector with n (number of individuals) rows. Weight is optional. This option is to be used when weight is associated to the data.
- **nbVariable** integer. The number of variables.
- **nbSample** integer. The number of observations.
- **criterion** list of character. This option permits to select the criterion giving the best configuration of an execution.
- **models** a S4 [Model] object. Defining the list of models to be tested.
- **error** logical. Say if at least one model finished with no error in MIXMOD.
- **results** a list of S4 [MixmodResults] object containing all results. Results are sorted into a ascending order according to the first criterion (descending order for the CV criterion). This order can be changed by using the sortByCriterion() method.

Examples

getSlots("Mixmod")

mixmodCluster

Create an instance of the [MixmodCluster] class

Description

This function computes an optimal mixture model according to the criteria furnished, and the list of model defined in [Model], using the algorithm specified in [Strategy].

Usage

mixmodCluster(data, nbCluster, dataType = NULL, models = NULL, strategy = mixmodStrategy(), criterion = "BIC", weight = NULL, knownLabels = NULL)
Arguments

data matrix or data frame containing quantitative or qualitative data. Rows correspond to observations and columns correspond to variables.
nbCluster numeric listing the number of clusters.
dataType character. Type of data is either "quantitative" or "qualitative". Set as NULL by default, type will be guessed depending on variables type.
models a [Model] object defining the list of models to run. For quantitative data, the model "Gaussian_pk_Lk_C" is called (see mixmodGaussianModel() to specify other models). For qualitative data, the model "Binary_pk_Ekjh" is called (see mixmodMultinomialModel() to specify other models).
strategy a [Strategy] object containing the strategy to run. Call mixmodStrategy() method by default.
criterion list of character defining the criterion to select the best model. The best model is the one with the lowest criterion value. Possible values: "BIC", "ICL", "NEC", c("BIC", "ICL", "NEC"). Default is "BIC".
weight numeric vector with n (number of individuals) rows. Weight is optionnal. This option is to be used when weight is associated to the data.
knownLabels vector of size nbSample. it will be used for semi-supervised classification when labels are known. Each cell corresponds to a cluster affectation.

Value

Returns an instance of the [MixmodCluster] class. Those two attributes will contain all outputs:

results a list of [MixmodResults] object containing all the results sorted in ascending order according to the given criterion.
bestResult a S4 [MixmodResults] object containing the best model results.

Author(s)

Remi Lebret and Serge Iovleff and Florent Langrognet, with contributions from C. Biernacki and G. Celeux and G. Govaert <contact@mixmod.org>

Examples

```r
## A quantitative example with the famous geyser data set
data(geyser)
## with default values
mixmodCluster(geyser, nbCluster=2:6)

## An example with the birds data set
data(birds)
mixmodCluster(data=birds, nbCluster = 2:5, criterion= c("BIC","ICL","NEC"), model = mixmodMultinomialModel())

## use graphics functions
xem <- mixmodCluster(data=geyser, nbCluster=3)
plot(xem)
```
MixmodCluster-class

Constructor of \([\text{MixmodCluster}]\) class

Description

This is a class to run clustering with mixmod. Inherits the \([\text{Mixmod}]\) class.

Details

- **strategy** a S4 \([\text{Strategy}]\) object. Defining the strategy used to run MIXMOD.
- **bestResult** a S4 \([\text{MixmodResults}]\) object containing the best model results.

Examples

```r
## A quantitative example with the famous iris data set
data(iris)
## with default values
new("MixmodCluster", data=iris[1:4], nbCluster=3)

getSlots("MixmodCluster")
```

MixmodDAResults-class  Constructor of \([\text{MixmodDAResults}]\) class

Description

This is a class to contain results after a discriminant analysis with MIXMOD. Inherits the \([\text{MixmodResults}]\) class.

Details

- **CVLabel** vector of integers containing labels defined by cross validation.
- **CVClassification** classification table after cross validation.
- **MAPEErrorRate** error rate done by MAP algorithm.
- **MAPClassification** classification table after MAP algorithm.

Examples

```r
getSlots("MixmodDAResults")
```
mixmodGaussianModel  

Create an instance of the [GaussianModel] class

Description

Define a list of Gaussian model to test in MIXMOD.

Usage

```r
mixmodGaussianModel(family = "all", listModels = NULL, 
                   free.proportions = TRUE, equal.proportions = TRUE)
```

Arguments

- `family` character defining a family of models. "general" for the general family, "diagonal" for the diagonal family, "spherical" for the spherical family and "all" for all families. Default is "general".
- `listModels` a list of characters containing a list of models. It is optional.
- `free.proportions` logical to include models with free proportions. Default is TRUE.
- `equal.proportions` logical to include models with equal proportions. Default is TRUE.

Details

In the Gaussian mixture model, following Banfield and Raftery (1993) and Celeux and Govaert (1995), we consider a parameterization of the variance matrices of the mixture components consisting of expressing the variance matrix \( \Sigma_k \) in terms of its eigenvalue decomposition

\[
\Sigma_k = \lambda_k D_k A_k D_k^\prime
\]

where \( \lambda_k = |\Sigma_k|^{1/d} \), \( D_k \) is the matrix of eigenvectors of \( \Sigma_k \) and \( A_k \) is a diagonal matrix, such that \( |A_k| = 1 \), with the normalized eigenvalues of \( \Sigma_k \) on the diagonal in a decreasing order. The parameter \( \lambda_k \) determines the volume of the \( k \)th cluster, \( D_k \) its orientation and \( A_k \) its shape. By allowing some but not all of these quantities to vary between clusters, we obtain parsimonious and easily interpreted models which are appropriate to describe various clustering situations.

In general family, we can allow the volumes, the shapes and the orientations of clusters to vary or to be equal between clusters. Variations on assumptions on the parameters \( \lambda_k, D_k \) and \( A_k \) (1 \( \leq \) \( k \) \( \leq \) \( K \)) lead to 8 general models of interest. For instance, we can assume different volumes and keep the shapes and orientations equal by requiring that \( A_k = A \) (\( A \) unknown) and \( D_k = D \) (\( D \) unknown) for \( k = 1, \ldots, K \). We denote this model \( [\lambda_k DAD']\). With this convention, writing \( [\lambda D_k A D_k'] \) means that we consider the mixture model with equal volumes, equal shapes and different orientations. In diagonal family, we assume that the variance matrices \( \Sigma_k \) are diagonal. In the parameterization, it means that the orientation matrices \( D_k \) are permutation matrices. We write \( \Sigma_k = \lambda_k B_k \) where \( B_k \) is a diagonal matrix with \( |B_k| = 1 \). This particular parameterization gives rise to 4 models: \( [\lambda B] \), \( [\lambda_k B] \), \( [\lambda B_k] \) and \( [\lambda_k B_k] \).

In spherical family, we assume spherical shapes, namely \( A_k = I, I \) denoting the identity matrix. In such a case, two parsimonious models are in competition: \( [\lambda I] \) and \( [\lambda_k I] \).
mixmodGaussianModel

Value

an object of [GaussianModel] which contains some of the 28 Gaussian Models:

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<th>Family</th>
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<th>Shape</th>
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<td>Axes</td>
<td></td>
</tr>
<tr>
<td>Gaussian_pk_Lk_Bk</td>
<td></td>
<td></td>
<td>Free</td>
<td>Axes</td>
<td></td>
</tr>
<tr>
<td>Gaussian_pk_L_I</td>
<td>Spherical</td>
<td>Free</td>
<td>Equal</td>
<td>NA</td>
<td></td>
</tr>
<tr>
<td>Gaussian_pk_Lk_I</td>
<td></td>
<td></td>
<td>Free</td>
<td>NA</td>
<td></td>
</tr>
</tbody>
</table>

Author(s)

Remi Lebret and Serge Iovleff and Florent Langrognet, with contributions from C. Biernacki and G. Celeux and G. Govaert <contact@mixmod.org>

References


Examples

mixmodGaussianModel()
mixmodGaussianModel(family="all",free.proportions=FALSE)
Create an instance of the `MixmodLearn` class

**Description**

This function computes the first step of a discriminant analysis. It will find the best classification rule by running an M step from the training observations.

**Usage**

```r
mixmodLearn(data, knownLabels, dataType = NULL,
models = NULL, criterion = "CV", nbCVBlocks = 10,
weight = NULL)
```

**Arguments**

- `data` matrix or data frame containing quantitative or qualitative data. Rows correspond to observations and columns correspond to variables.
- `knownLabels` vector of size number of observations. Each cell corresponds to a cluster affection. So the maximum value is the number of clusters.
- `dataType` character. Type of data is either "quantitative" or "qualitative". Set as NULL by default, type will be guessed depending on variables type.
- `models` a `Model` object defining the list of models to run. For quantitative data, the model "Gaussian_pk_Lk_C" is called (see `mixmodGaussianModel()` to specify other models). For qualitative data, the model "Binary_pk_Ekjh" is called (see `mixmodMultinomialModel()` to specify other models).
- `criterion` list of character defining the criterion to select the best model. Possible values: "BIC", "CV" or c("CV","BIC"). Default is "CV".
- `nbCVBlocks` integer which defines the number of block to perform the Cross Validation. This value will be ignored if the CV criterion is not choosen. Default value is 10.
- `weight` numeric vector with n (number of individuals) rows. Weight is optionnal. This option is to be used when weight is associated to the data.

**Value**

Returns an instance of the `MixmodLearn` class. Those two attributes will contain all outputs:

- `results` a list of `MixmodResults` object containing all the results sorted in ascending order according to the given criterion.
- `bestResult` a S4 `MixmodResults` object containing the best model results.

**Author(s)**

Remi Lebret and Serge Iovleff and Florent Langrognet, with contributions from C. Biernacki and G. Celeux and G. Govaert <contact@mixmod.org>
MixmodLearn-class

Constructor of [MixmodLearn] class

Description

This is a class to run discriminant analysis with mixmod. Inherits the [Mixmod] class.

Details

- **bestResult** a S4 [MixmodDAResults] object containing the best model results.
- **nbCVBlocks** integer which defines the number of block to perform the Cross Validation.

Examples

```r
## A quantitative example with the famous iris data set
learn.iris<-mixmodLearn(iris[1:4], iris$Species)
## get summary
summary(learn.iris)

## An example with the famous birds data set
data(birds)
birds.partition<-c(rep(1,34),rep(2,35))
learn.birds<-mixmodLearn(data=birds, knownLabels=birds.partition)
## get summary
summary(learn.birds)
```

mixmodMultinomialModel

Create an instance of the [MultinomialModel] class

Description

Define a list of multinomial model to test in MIXMOD.

Usage

```r
mixmodMultinomialModel(listModels = NULL,
  free.proportions = TRUE, equal.proportions = TRUE,
  variable.independency = NULL,
  component.independency = NULL)
```
Arguments

listModels a list of characters containing a list of models. It is optional.

free.proportions logical to include models with free proportions. Default is TRUE.

equal.proportions logical to include models with equal proportions. Default is FALSE.

variable.independency logical to include models where \( \varepsilon^j_k \) is independent of the variable \( j \). Optional.

cOMPONENT.Independence logical to include models where \( \varepsilon^j_k \) is independent of the component \( k \). Optional.

Details

In the multinomial mixture model, the multinomial distribution is associated to the \( j \)th variable of the \( k \)th component is reparameterized by a center \( a_k^j \) and the dispersion \( \varepsilon_k^j \) around this center. Thus, it allows us to give an interpretation similar to the center and the variance matrix used for continuous data in the Gaussian mixture context. In the following, this model will be denoted by \( \varepsilon_k^j \). In this context, three other models can be easily deduced. We note \( \varepsilon_k^j \) the model where \( \varepsilon_k^j \) is independent of the variable \( j \), [\( \varepsilon^j \)] the model where \( \varepsilon_k^j \) is independent of the component \( k \) and, finally, [\( \varepsilon \)] the model where \( \varepsilon_k^j \) is independent of both the variable \( j \) and the component \( k \). In order to maintain some unity in the notation, we will denote also \( \varepsilon_k^{jh} \) the most general model introduced at the previous section.

Value

an object of \([\texttt{MultinomialModel}]\) containing some of the 10 Binary Models:

<table>
<thead>
<tr>
<th>Model</th>
<th>Prop.</th>
<th>Var.</th>
<th>Comp.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Binary_p_E</td>
<td>Equal</td>
<td>TRUE</td>
<td>TRUE</td>
</tr>
<tr>
<td>Binary_p_Ej</td>
<td>FALSE</td>
<td>TRUE</td>
<td></td>
</tr>
<tr>
<td>Binary_p_Ek</td>
<td>TRUE</td>
<td>FALSE</td>
<td></td>
</tr>
<tr>
<td>Binary_p_Ekj</td>
<td>FALSE</td>
<td>FALSE</td>
<td></td>
</tr>
<tr>
<td>Binary_p_Ekjh</td>
<td>FALSE</td>
<td>FALSE</td>
<td></td>
</tr>
<tr>
<td>Binary_pk_E</td>
<td>Free</td>
<td>TRUE</td>
<td>TRUE</td>
</tr>
<tr>
<td>Binary_pk_Ej</td>
<td>FALSE</td>
<td>TRUE</td>
<td></td>
</tr>
<tr>
<td>Binary_pk_Ek</td>
<td>TRUE</td>
<td>FALSE</td>
<td></td>
</tr>
<tr>
<td>Binary_pk_Ekj</td>
<td>FALSE</td>
<td>FALSE</td>
<td></td>
</tr>
<tr>
<td>Binary_pk_Ekjh</td>
<td>FALSE</td>
<td>FALSE</td>
<td></td>
</tr>
</tbody>
</table>

Author(s)

Remi Lebret and Serge Iovleff and Florent Langrognet, with contributions from C. Biernacki and G. Celeux and G. Govaert <contact@mixmod.org>
References


Examples

mixmodMultinomialModel()
mixmodMultinomialModel(equal.proportions=TRUE)
mixmodMultinomialModel( listModels=c(“Binary_pk_E”, “Binary_p_E”) )

mixmodPredict(data, classificationRule)

Description

This function computes the second step of a discriminant analysis. The aim of this step is to assign remaining observations to one of the groups.

Usage

mixmodPredict(data, classificationRule)

Arguments

data matrix or data frame containing quantitative or qualitative data. Rows correspond to observations and columns correspond to variables.
classificationRule a [MixmodResults] object which contains the classification rule computed in the mixmodLearn() or mixmodCluster() step.

Value

Returns an instance of the [MixmodPredict] class which contains predicted partition and probabilities.

Author(s)

Remi Lebret and Serge Iovleff and Florent Langrognet, with contributions from C. Biernacki and G. Celeux and G. Govaert <contact@mixmod.org>
MixmodPredict-class

Constructor of [MixmodPredict] class

Description

This is a class to run discriminant analysis with mixmod.

Details

data  numeric vector, matrix, or data frame of observations. Either qualitative or quantitative.
dataType  character. It defines whether data are quantitative or qualitative.
nbVariable  integer. The number of variables.
nbSample  integer. The number of observations.
error  a character. The mixmod error.
classificationRule  a [MixmodResults] object containing the classification rule.
partition  a matrix containing observations to predict.
proba  a matrix of probabilities.

Examples

# start by extract 10 observations from iris data set
remaining.obs<-sample(1:nrow(iris),10)
# then run a mixmodLearn() analysis without those 10 observations
learn<-mixmodLearn(iris[-remaining.obs,1:4], iris$Species[-remaining.obs])
# create a MixmodPredict to predict those 10 observations
prediction <- mixmodPredict(data=iris[remaining.obs,1:4], classificationRule=learn["bestResult"])
# show results
prediction
# compare prediction with real results
as.integer(iris$Species[remaining.obs]) == prediction["partition"]
MixmodResults-class

Constructor of [MixmodResults] class

Description

This is a class to contain results from MIXMOD library.

Details

nbCluster integer. It indicates the number of components.
model character. Name of the model.
criterion list of character. This option permits to select the criterion giving the best configuration of an execution.
criterionValue numeric. Values of the criterion.
parameters a S4 [Parameter] object. The best model parameters.
likelihood numeric. The model likelihood.
partition vector of integers defining the partition.
proba a matrix of probabilities.
error a character. The mixmod error.

Examples

getSlots("MixmodResults")

mixmodStrategy

Create an instance of [Strategy] class

Description

This class will contain all the parameters needed by the estimation algorithms.

Usage

mixmodStrategy(algo = "EM", nbTry = 1,
               initMethod = "smallEM", nbTryInInit = 50,
               nbIterationInInit = 5, nbIterationInAlgo = 200,
               epsilonInInit = 0.001, epsilonInAlgo = 0.001)
Arguments

**algo**
- list of character string with the estimation algorithm. Possible values: "EM", "SEM", "CEM", c("EM","SEM"). Default value is "EM".

**nbTry**
- integer defining the number of tries. nbTry must be a positive integer. Option available only if init is "random" or "smallEM" or "CEM" or "SEMMax". Default value: 1.

**initMethod**
- a character string with the method of initialization of the algorithm specified in the algo argument. Possible values: "random", "smallEM", "CEM", "SEMMax". Default value: "smallEM".

**nbTryInInit**
- integer defining number of tries in initMethod algorithm. nbTryInInit must be a positive integer. Option available only if init is "smallEM" or "CEM". Default value: 50.

**nbIterationInInit**
- integer defining the number of "EM" or "SEM" iterations in initMethod. nbIterationInInit must be a positive integer. Only available if initMethod is "smallEM" or "SEMMax". Default values: 5 if initMethod is "smallEM" and 100 if initMethod is "SEMMax".

**nbIterationInAlgo**
- list of integers defining the number of iterations if you want to use nbIteration as rule to stop the algorithm(s). Default value: 200.

**epsilonInInit**
- real defining the epsilon value in the initialization step. Only available if initMethod is "smallEM". Default value: 0.001.

**epsilonInAlgo**
- list of reals defining the epsilon value for the algorithm. Warning: epsilonInAlgo doesn't have any sens if algo is SEM, so it needs to be set as NaN in that case. Default value: 0.001.

Details

There are different ways to initialize an algorithm:

**random**
- Initialization from a random position is a standard way to initialize an algorithm. This random initial position is obtained by choosing at random centers in the data set. This simple strategy is repeated 5 times (the user can choose the number of times) from different random positions and the position that maximises the likelihood is selected.

**smallEM**
- A maximum of 50 iterations of the EM algorithm according to the process : ni numbers of iterations of EM are done (with random initialization) until the smallEM stop criterion value has been reached. This action is repeated until the sum of ni reaches 50 iterations (or if in one action 50 iterations are reached before the stop criterion value). It appears that repeating runs of EM is generally profitable since using a single run of EM can often lead to suboptimal solutions.

**CEM**
- 10 repetitions of 50 iterations of the CEM algorithm are done. One advantage of initializing an algorithm with CEM lies in the fact that CEM converges generally in a small number of iterations. Thus, without consuming a large amount of CPU times, several runs of CEM are performed. Then EM is run with the best solution among the 10 repetitions.

**SEMMax**
- A run of 500 iterations of SEM. The idea is that an SEM sequence is expected to enter rapidly in the neighbourhood of the global maximum of the likelihood function.
Defining the algorithms used in the strategy, the stopping rule and when to stop.

- **Algorithms**:
  - EM  Expectation Maximisation
  - CEM  Classification EM
  - SEM  Stochastic EM

- **Stopping rules for the algorithm**:
  - `nbIterationInAlgo`  Sets the maximum number of iterations
  - `epsilonInAlgo`  Sets relative increase of the log-likelihood criterion

- Default values are 200 `nbIterationInAlgo` of EM with an `epsilonInAlgo` value of $10^{-3}$.

**Value**

A `Strategy` object

**Author(s)**

Rémi Lebret and Serge Iovlev and Florent Langrognet, with contributions from C. Biernacki and G. Celeux and G. Govaert <contact@mixmod.org>

**References**


**Examples**

```R
mixmodStrategy()
mixmodStrategy(algo="CEM",initMethod="random",nbTry=10,epsilonInInit=0.00001)
mixmodStrategy(algo=c("SEM","EM"), nbIterationInAlgo=c(200,100), epsilonInAlgo=c(NA,0.00001))
```

---

**Description**

This class defines the Mixmod models.

**Details**

- `listModels`  character containing a list of models.
- `free.proportions`  logical to include models with free proportions. Default is TRUE.
- `equal.proportions`  logical to include models with equal proportions. Default is FALSE.

**Examples**

```R
getSlots("Model")
```
MultinomialModel-class

Constructor of [MultinomialModel] class

Description

This class defines a multinomial Model. Inherits the [Model] class.

Details

variable.independency logical
component.independency logical

Examples

new("MultinomialModel")
new("MultinomialModel", listModels=c("Binary_pk_E","Binary_p_E") )
new("MultinomialModel", free.proportions=FALSE, variable.independency=TRUE )

getSlots("MultinomialModel")

MultinomialParameter-class

Constructor of [MultinomialParameter] class

Description

This class defines parameters of a Multinomial Mixture Model. Inherits the [Parameter] class.

Details

center a numeric vector containing center of each cluster.
scatter a vector of matrix containing dispersion matrix of each cluster.
factor a character vector containing the modalities.

Examples

new("MultinomialParameter")

getSlots("MultinomialParameter")
nbFactorFromData

Get the number of modalities for each column of a categorical data set

Description

Get the number of modalities for each column of a categorical data set

Usage

nbFactorFromData(x)

Arguments

x a vector or a matrix or a data frame containing factors

Value

a vector containing the number of modalities for each column

Parameter-class

Constructor of [Parameter] class

Description

This class defines parameters of a Mixture Model.

Details

proportions a numeric vector containing proportions of the mixture model.

Examples

getslots("Parameter")
Description

Plotting data from a [Mixmod] object using parameters and partition to distinguish the different clusters.

Arguments

- **x**: an object of class [Mixmod]
- **...**: further arguments passed to or from other methods

Details

For quantitative case, ellipsoids (i.e. linear transformations of hyperspheres) centered at the mean are drawn using the parameters computed by MIXMOD. The directions of the principal axes of the ellipsoids are given by the eigenvectors of the covariance matrix $\Sigma$. The squared relative lengths of the principal axes are given by the corresponding eigenvalues. A 1-dimensional representation of variables with the densities is drawn on the diagonal.

For qualitative case, a Multiple Correspondance Analysis is performed to get a 2-dimensional representation of the data set. Bigger symbol means that observations are similar.

See Also

- plot

Examples

```r
## for quantitative case
data(geyser)
xem <- mixmodCluster(geyser,3)
plot(xem)

## for qualitative case
data(birds)
xem2 <- mixmodCluster(birds,2)
plot(xem2)
```
Description

Biplot of two variables from a quantitative data set. Use parameters and partition from a [MixmodResults] object to distinguish the different clusters.

Usage

```r
plotCluster(x, data, variable1 = colnames(data)[1], variable2 = colnames(data)[2], col = x@partition + 1, pch = x@partition, xlab = variable1, ylab = variable2, add.ellipse = TRUE, ...)
```

Arguments

- **x**: an object of class [MixmodResults]
- **data**: a matrix or a data frame containing a quantitative data set.
- **variable1**: character containing the name of the first variable. First column of data by default.
- **variable2**: character containing the name of the second variable. Second column of data by default.
- **col**: a specification for the default plotting color. By default partition is used to separate clusters with different colors.
- **pch**: either an integer specifying a symbol or a single character to be used as the default in plotting points. By default partition is used to separate clusters with different symbols.
- **xlab**: a title for the x axis. Variable1 by default.
- **ylab**: a title for the y axis. Variable2 by default.
- **add.ellipse**: a boolean. Add ellipses to graph. TRUE by default.
- **...**: further arguments passed to or from other methods

Details

Ellipsoids (i.e. linear transformations of hyperspheres) centered at the mean can be drawn using the parameters computed by MIXMOD. The directions of the principal axes of the ellipsoids are given by the eigenvectors of the covariance matrix \( \Sigma \). The squared relative lengths of the principal axes are given by the corresponding eigenvalues.

See Also

- `plot`
Examples

```r
data(geyser)
xem <- mixmodCluster(geyser, 3)
plotCluster(xem["bestResult"], geyser)
```

---

**print**

Print a Rmixmod class to standard output.

**Description**

Print a Rmixmod class to standard output.

**Arguments**

- `x`: a Rmixmod object: a `Strategy`, a `Model`, a `GaussianParameter`, a `MultinomialParameter`, a `MixmodResults`, a `MixmodCluster`, a `MixmodLearn` or a `MixmodPredict`.
- `...`: further arguments passed to or from other methods

**Value**

NULL. Prints to standard out.

**See Also**

`print`

**Examples**

```r
## for strategy
strategy <- mixmodStrategy()
print(strategy)

## for Gaussian models
gmodel <- mixmodGaussianModel()
print(gmodel)

## for multinomial models
mmodel <- mixmodMultinomialModel()
print(mmodel)

## for clustering
data(geyser)
xem <- mixmodCluster(geyser, 3)
print(xem)

## for Gaussian parameters
print(xem["bestResult"]["parameters"])

## for discriminant analysis
# start by extract 10 observations from iris data set
iris.partition <- sample(1:nrow(iris), 10)
```
# then run a mixmodLearn() analysis without those 10 observations
learn<-mixmodLearn(iris[-iris.partition,1:4], iris$Species[-iris.partition])
# print learn results
print(learn)
# create a MixmodPredict to predict those 10 observations
prediction <- mixmodPredict(data=iris[iris.partition,1:4], classificationRule=learn["bestResult"])
# print prediction results
print(prediction)

---

**show**

Show description of a Rmixmod class to standard output.

**Description**

Show description of a Rmixmod class to standard output.

**Arguments**

- `object`: a Rmixmod object: a `Strategy`, a `Model`, a `GaussianParameter`, a `MultinomialParameter`, a `MixmodResults`, a `MixmodCluster`, a `MixmodLearn` or a `MixmodPredict`.

**Value**

NULL. Prints to standard out.

**See Also**

- `show`

**Examples**

```r
## for strategy
strategy <- mixmodStrategy()
show(strategy)

## for Gaussian models
gmodel <- mixmodGaussianModel()
show(gmodel)
## for multinomial models
mmodel <- mixmodMultinomialModel()
show(mmodel)

## for clustering
data(geyser)
xem <- mixmodCluster(geyser,3)
show(xem)
## for Gaussian parameters
show(xem["bestResult"]["parameters"])

## for discriminant analysis
```
# start by extract 10 observations from iris data set
iris.partition<-sample(1:nrow(iris),10)
# then run a mixmodLearn() analysis without those 10 observations
learn<-mixmodLearn(iris[-iris.partition,1:4], iris$Species[-iris.partition])
# create a MixmodPredict to predict those 10 observations
prediction <- mixmodPredict(data=iris[iris.partition,1:4], classificationRule=learn["bestResult"])
# show results
show(prediction)

sortByCriterion  Sorting results of a [Mixmod] object by a given criterion

Description

After calling the mixmodCluster() or mixmodLearn() method, results will be sorted into ascending order according to the first given criterion (descending order for CV criterion). This method is able to reorder the list of results according to a given criterion.

Arguments

object a [Mixmod] object
criterion a string containing the criterion name

Value

a modified [Mixmod] object

Examples

x<-mixmodCluster(iris[1:4],2:10,criterion=c("BIC","ICL"))
icl<-sortByCriterion(x,"ICL")
icl["results"]

Strategy-class  Constructor of [Strategy] class

Description

This class defines the Mixmod strategies.
Summary

Produce result summaries of a Rmixmod class

Description

Produce result summaries of a Rmixmod class

Arguments

x Either a Mixmod object, a Parameter object or a MixmodResults object.

Value

NULL. Summaries to standard out.

See Also

summary
### Examples
```
data(geyser)
xem <- mixmodCluster(geyser,3)
summary(xem)
summary(xem["bestResult"])  
summary(xem["bestResult"]["parameters"])
```

---

### titanic

**Qualitative data: Survival of passengers on the Titanic**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Class</td>
<td>0 = crew, 1 = first, 2 = second, 3 = third, which denote the economic status of the subject</td>
</tr>
<tr>
<td>Age</td>
<td>1 = adult, 0 = child, which denote if the subject is an adult or a child</td>
</tr>
<tr>
<td>Sex</td>
<td>1 = male, 0 = female, which denote the sex of the subject</td>
</tr>
<tr>
<td>Survived</td>
<td>1 = yes, 0 = no, which denote if the subject lived through the fatal maiden voyage of the ocean liner Titanic</td>
</tr>
</tbody>
</table>

### Description
For each person on board the fatal maiden voyage of the ocean liner Titanic, this dataset records: sex, age [adult/child], economic status [first/second/third class, or crew] and whether or not that person survived. Values are aligned and delimited by blanks. There are no missing values.

### Format
A data frame with 2201 observations on the following 4 variables.

- **Class**: 0 = crew, 1 = first, 2 = second, 3 = third, which denote the economic status of the subject
- **Age**: 1 = adult, 0 = child, which denote if the subject is an adult or a child
- **Sex**: 1 = male, 0 = female, which denote the sex of the subject
- **Survived**: 1 = yes, 0 = no, which denote if the subject lived through the fatal maiden voyage of the ocean liner Titanic

### Details
The sinking of the Titanic is a famous event, and new books are still being published about it. Many well-known facts-from the proportions of first-class passengers to the "women and children first" policy, and the fact that that policy was not entirely successful in saving the women and children in the third class-are reflected in the survival rates for various classes of passenger.

These data were originally collected by the British Board of Trade in their investigation of the sinking. Note that there is not complete agreement among primary sources as to the exact numbers on board, rescued, or lost.

Due in particular to the very successful film "Titanic", the last years saw a rise in public interest in the Titanic. Very detailed data about the passengers is now available on the Internet, at sites such as "Encyclopedia Titanica" ([http://www.rmplc.co.uk/eduweb/sites/phind](http://www.rmplc.co.uk/eduweb/sites/phind)).

### Source
The source provides a data set recording class, sex, age, and survival status for each person on board of the Titanic, and is based on data originally collected by the British Board of Trade and reprinted in: British Board of Trade (1990), "Report on the Loss of the Titanic (S.S.)". British Board of Trade Inquiry Report (reprint). Gloucester, UK: Allan Sutton Publishing.
Examples

data(titanic)

[  
  Extract parts of a Rmixmod class

Description

Extract parts of a Rmixmod class

Arguments

x  object from which to extract element(s) or in which to replace element(s).
i  the name of the element we want to extract or replace.
j  if the element designing by i is complex, j specifying elements to extract or replace.
drop  For matrices and arrays. If TRUE the result is coerced to the lowest possible dimension (see the examples). This only works for extracting elements, not for the replacement. See drop for further details.
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