

# Package ‘mixture’

February 13, 2018

**Type** Package

**Title** Finite Gaussian Mixture Models for Clustering and Classification

**Version** 1.5

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**Author** Ryan P. Browne, Aisha ElSherbiny and Paul D. McNicholas

**Maintainer** Ryan Browne <rbrowne@math.mcmaster.ca>

**Description** An implementation of all 14 Gaussian parsimonious clustering models (GPCMs) for model-based clustering and model-based classification.

**License** GPL (>= 2)

**LazyLoad** yes

**NeedsCompilation** yes

**Repository** CRAN

**SystemRequirements** GNU make

**Date/Publication** 2018-02-13 22:07:56 UTC

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 e.step

*E-Step*


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### Description

Carries out the E-step for EM algorithm

### Usage

```
e.step(data=NULL, gpar=NULL, labels=NULL, v=1)
```

### Arguments

data	A matrix or data frame such that rows correspond to observations and columns correspond to variables. Note that this function currently only works with multivariate data $p > 1$ .
gpar	A list of the model parameters.
labels	A vector of groups labels. If NULL none are known.
v	The value for deterministic annealing. If $v=1$ the standard estimate is used.

### Details

Carries out the E-step for EM algorithm

### Value

A  $n \times G$  matrix of weights.

### Examples

```
data("x2")
u0 = runif(nrow(x2))
m0 = m.step(data=x2, covtype="VVV", w=cbind(u0,1-u0), D=NULL, mtol=1e-8, mmax=10)
w0 = e.step(data=x2, gpar=m0, labels=NULL, v=1)
```

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 gpcm

*Gaussian Parsimonious Clustering Models*


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### Description

Carries out model-based clustering or classification using some or all of the 14 parsimonious Gaussian clustering models (GPCM).

**Usage**

```
gpcm(data=NULL, G=1:3, mnames=NULL, start=0, label=NULL, veo=FALSE,
      nmax=1000, atol=1e-8, mtol=1e-8, mmax=10, pprogress=FALSE, pwarning=FALSE)
```

**Arguments**

<code>data</code>	A matrix or data frame such that rows correspond to observations and columns correspond to variables. Note that this function currently only works with multivariate data $p > 1$ .
<code>G</code>	A sequence of integers giving the number of components to be used.
<code>mnames</code>	The models (i.e., covariance structures) to be used. If <code>NULL</code> then all 14 are fitted.
<code>start</code>	If $\emptyset$ then the <code>kmeans</code> function is used for initialization. If a positive value is inputted then best out of <code>ceiling(k)</code> random initializations are used. If <code>is.vector</code> then deterministic annealing is used with the given sequence of values in <code>[0,1]</code> ; cf. Zhou and Lange (2010). If <code>is.matrix</code> then matrix is used as an initialization matrix as long as it has non-negative elements. Note: only models with the same number of columns of this matrix will be fit. If <code>is.function</code> then this function is used for building an initialization matrix. See Examples.
<code>label</code>	If <code>NULL</code> then the data has no known groups. If <code>is.integer</code> then some of the observations have known groups. If <code>label[i]=k</code> then observation belongs to group <code>k</code> . If <code>label[i]=0</code> then observation has no known group. See Examples.
<code>veo</code>	If <code>TRUE</code> then if the number variables in the model exceeds the number of observations the model is still fitted.
<code>nmax</code>	The maximum number of iterations each EM algorithm is allowed to use.
<code>atol</code>	A number specifying the epsilon value for the convergence criteria used in the EM algorithms. For each algorithm, the criterion is based on the difference between the log-likelihood at an iteration and an asymptotic estimate of the log-likelihood at that iteration. This asymptotic estimate is based on the Aitken acceleration and details are given in the References.
<code>mtol</code>	A number specifying the epsilon value for the convergence criteria used in the M-step in the GEM algorithms.
<code>mmax</code>	The maximum number of iterations each M-step is allowed in the GEM algorithms.
<code>pprogress</code>	If <code>TRUE</code> print the progress of the function.
<code>pwarning</code>	If <code>TRUE</code> print the warnings.

**Details**

The data  $x$  are either clustered or classified using Gaussian mixture models with some or all of the 14 parsimonious covariance structures described in Celeux & Govaert (1995). The algorithms given by Celeux & Govaert (1995) is used for 12 of the 14 models; the "EVE" and "VVE" models use the algorithms given in Browne & McNicholas (2012, 2013). Starting values are very important to the successful operation of these algorithms and so care must be taken in the interpretation of results.

**Value**

An object of class `gpcm` is a list with components:

<code>map</code>	A vector of integers indicating the maximum <i>a posteriori</i> classifications for the best model.
<code>gpar</code>	A list of the model parameters.
<code>bicModel</code>	A list containing; the number of groups for the best model, the covariance structure, and Bayesian Information Criterion (BIC) value.
<code>loglik</code>	The log-likelihood values from fitting the best model.
<code>z</code>	A matrix giving the raw values upon which <code>map</code> is based.
<code>BIC</code>	An array containing the log-likelihood ( <code>loglik</code> ), number of model parameters ( <code>npar</code> ) and BIC indexed by the covariance structure and number of components.
<code>start</code>	The value inputted into <code>start</code> .
<code>startobject</code>	The type of object inputted into <code>start</code> .

**Note**

Dedicated `print`, `plot` and `summary` functions are available for objects of class `gpcm`.

**Author(s)**

Ryan P. Browne, Aisha ElSherbiny and Paul D. McNicholas.

Maintainer: Ryan Browne <[rbrowne@uoguelph.ca](mailto:rbrowne@uoguelph.ca)>

**References**

Browne, R.P. and McNicholas, P.D. (2014). Estimating common principal components in high dimensions. *Advances in Data Analysis and Classification* **8**(2), 217-226.

Celeux, G., Govaert, G. (1995). Gaussian parsimonious clustering models. *Pattern Recognition* **28**(5), 781-793.

**Examples**

```
data("x2")

# use k-means starts
ax0 = gpcm(x2, G=1:5, mnames=c("VVV", "EVE"),start=0, pprogress=TRUE, atol=1e-2)
summary(ax0)
ax0

# use 6 random values for starting values
ax6 = gpcm(x2, G=1:5, mnames=c("VVV", "EVE"),start= 2, atol=1e-2)
summary(ax6)
ax6

# use deterministic annealing for starting values
#axNULL = gpcm(x2, G=1:5, mnames=c("VVV", "EVE"), start=NULL, atol=1e-2)
#summary(axNULL)
```

```

#axNULL

# use your own deterministic annealing values for starting values
#vseq0 = rep(seq(.05, 1, length.out=5),each=2)
#axv = gpcm(x2, G=1:5, mnames=c("VVV", "EVE"), start=vseq0, atol=1e-2)
#summary(axv)
#axv

# Initialization using your own function
igparhc <- function(data=NULL, g=NULL,covtype=NULL) {
lw = cutree(hclust(dist(data), "complete"),k=g)
w = matrix(0, nrow=nrow(data), ncol=g)
for (j in 1:ncol(w)) w[,j] = as.numeric( lw ==j )
return(w)
}
axhclust = gpcm(x2, G=1:5, mnames=c("VVV", "EVE"),start= igparhc, atol=1e-2)
summary(axhclust)
axhclust

# Estimate all 14 covariance structures from k-means starts
ax = gpcm(x2, G=1:5, start=0, atol=1e-2)
summary(ax)
ax

# model based classification
x2.label = numeric(nrow(x2))
x2.label[c(10,50, 110, 150, 210, 250)] = c(1,1,2,2,3,3)
plot(x2, col=x2.label)
ax1 = gpcm(x2, G=3:5, mnames=c("VVV", "EVE"), label=x2.label, atol=1e-2)

```

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m.step

*M-Step*


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### Description

Carries out the M-step for EM algorithm

### Usage

```
m.step(data=NULL, covtype=NULL, w=NULL, D=NULL, mtol=NULL, mmax=NULL)
```

### Arguments

data	A matrix or data frame such that rows correspond to observations and columns correspond to variables. Note that this function currently only works with multivariate data $p > 1$ .
covtype	A three letter sequence indicating the covariance structure.
w	A $n \times G$ matrix of weights.

D	An initial value for D. If NULL then the identity matrix is used.
mtol	The convergence criteria for the m.step if an iterative procedure is necessary.
mmax	The maximum number of iterations for an iterative procedure.

**Details**

Carries out the M-step for EM algorithm

**Value**

A list of the model parameters with the mu, sigma, invsigma and logdet for each group.

**Examples**

```
data("x2")
u0 = runif(nrow(x2))
m.step(data=x2, covtype="VVV", w=cbind(u0,1-u0), D=NULL, mtol=1e-8, mmax=10)
```

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mixture

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*Mixture Models for Clustering and Classification*


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**Description**

An implementation of all 14 Gaussian parsimonious clustering models (GPCMs) for model-based clustering and model-based classification.

**Details**

Package: mixture  
Type: Package  
Version: 1.3  
Date: 2015-03-10  
License: GPL (>=2)

This package contains the functions [gpcm](#), [e.step](#), and [m.step](#) as well as one simulated data set.

**Author(s)**

Ryan P. Browne, Aisha ElSherbiny and Paul D. McNicholas.  
Maintainer: Ryan Browne <[rbrowne@math.mcmaster.ca](mailto:rbrowne@math.mcmaster.ca)>

**See Also**

Details, examples, and references are given under [gpcm](#).

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x2

*Simulated Data*

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**Description**

Simulated data, with two variables with three groups, used to illustrate [gpcm](#).

**Usage**

```
data(x2)
```

**Format**

A data frame with 300 observations and 2 columns.

**Source**

These data were simulated using R.

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