Package ‘pgmm’

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**Coffee**

**Description**

Data on the chemical composition of coffee samples collected from around the world, comprising 43 samples from 29 countries. Each sample is either of the Arabica or Robusta variety. Twelve of the thirteen chemical constituents reported in the study are given. The omitted variable is total chlorogenic acid; it is generally the sum of the chlorogenic, neochlorogenic and isochlorogenic acid values.

**Usage**

`data(coffee)`

**Format**

A data frame with 43 observations and 14 columns. The first two columns contain Variety and Country, respectively, while the remaining 12 columns contain the chemical properties. The Variety is either (1) Arabica or (2) Robusta.

**Note**

The German to English translations of the variable names were carried out by Dr. Sharon M. McNicholas.

**Source**


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**Italian Olive Oil**

**Description**

Data on the percentage composition of eight fatty acids found by lipid fraction of 572 Italian olive oils. The data come from three regions: Southern Italy, Sardinia, and Northern Italy. Within each region there are a number of different areas. Southern Italy comprises North Apulia, Calabria, South Apulia, and Sicily. Sardinia is divided into Inland Sardinia and Costal Sardinia. Northern Italy comprises Umbria, East Liguria, and West Liguria.

**Usage**

`data(olive)`
Format

A data frame with 572 observations and 10 columns. The first column gives the region: (1) Southern Italy, (2) Sardinia, or (3) Northern Italy. The second column gives the area: (1) North Apulia, (2) Calabria, (3) South Apulia, (4) Sicily, (5) Inland Sardinia, (6) Costal Sardinia, (7) East Liguria, (8) West Liguria, and (9) Umbria. The other eight columns contain the variables.

Source

These data are available within the GGobi software (Swayne et al., 2006).

References


Description

An implementation of model-based clustering and model-based classification using parsimonious Gaussian mixture models.

Details

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This package contains the function pgmmEM plus three data sets.

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See Also

Details, examples, and references are given under `pgmmEM`.

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**Description**

Carries out model-based clustering or classification using parsimonious Gaussian mixture models. AECP algorithms are used for parameter estimation. The BIC or the ICL is used for model selection.

**Usage**

```r
pgmmEM(x, rG=1:2, rq=1:2, class=NULL, icl=FALSE, zstart=2, cccStart=TRUE, loop=3, zlist=NULL, modelSubset=NULL, seed=123456, tol=0.1, relax=FALSE)
```

**Arguments**

- `x` A matrix or data frame such that rows correspond to observations and columns correspond to variables.
- `rG` The range of values for the number of components.
- `rq` The range of values for the number of factors.
- `class` If `NULL` then model-based clustering is performed. If a vector with length equal to the number of observations, then model-based classification is performed. In this latter case, the ith entry of `class` is either zero, indicating that the component membership of observation i is unknown, or it corresponds to the component membership of observation i. See Examples below.
- `icl` If `TRUE` then the ICL is used for model selection. Otherwise, the BIC is used for model selection.
- `zstart` A number that controls what starting values are used: (1) Random; (2) k-means; or (3) user-specified via `zlist`.
- `cccStart` If `TRUE` then random starting values are put through the CCC model and the resulting group memberships are used as starting values for the models specified in `modelSubset`. Only relevant for `zstart=1`. See Examples.
- `loop` A number specifying how many different random starts should be used. Only relevant for `zstart=1`.
- `zlist` A list comprising vectors of initial classifications such that `zlist[[g]]` gives the g-component starting values. Only relevant for `zstart=3`. See Examples.
- `modelSubset` A vector of strings giving the models to be used.
- `seed` A number giving the pseudo-random number seed to be used.
tol  A number specifying the epsilon value for the convergence criteria used in the AECM 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. Values of \( \text{tol} \) greater than the default are not accepted.

relax  By default, the number of factors cannot exceed half the number of variables. Setting \( \text{relax}=\text{TRUE} \) relaxes this constraint and allows the number of factors to take any value up to three-quarters the number of variables.

Details

The data \( x \) are either clustered using the PGMM approach of McNicholas & Murphy (2005, 2008, 2010) or classified using the method described by McNicholas (2010). In either case, all 12 covariance structures given by McNicholas & Murphy (2010) are available. Parameter estimation is carried out using AECM algorithms, as described in McNicholas et al. (2010). Either the BIC or the ICL is used for model-selection. The number of AECM algorithms to be run depends on the range of values for the number of components \( r_g \), the range of values for the number of factors \( r_q \), and the number of models in \( \text{modelsubset} \). 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 \text{pgmm} is a list with components:

- \text{map}  A vector of integers, taking values in the range \( r_g \), indicating the maximum \textit{a posteriori} classifications for the best model.
- \text{model}  A string giving the name of the best model.
- \text{g}  The number of components for the best model.
- \text{q}  The number of factors for the best model.
- \text{zhat}  A matrix giving the raw values upon which \text{map} is based.
- \text{load}  The factor loadings matrix (\( \Lambda \)) for the best model.
- \text{noisev}  The \( \Psi \) matrix for the best model.
- \text{plot_info}  A list that stores information to enable \text{plot}.
- \text{summ_info}  A list that stores information to enable \text{summary}.

In addition, the object will contain one of the following, depending on the value of \text{icl}.

- \text{bic}  A number giving the BIC for each model.
- \text{icl}  A number giving the ICL for each model.

Note

Dedicated \text{print}, \text{plot}, and \text{summary} functions are available for objects of class \text{pgmm}.
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References


Examples
```r
# Not run:  
# Wine clustering example with three random starts and the CUU model.
# data("wine")
x<-wine[,,-1]
x<-scale(x)
wine_clust<-pgmmEM(x,rG=1:4,rq=1:4,zstart=1,loop=3,modelSubset=c("CUU"))
table(wine[,1],wine_clust$map)

# Wine clustering example with custom starts and the CUU model.
# data("wine")
x<-wine[,,-1]
x<-scale(x)
hcl<-hclust(dist(x))
z<-list()
for(g in 1:4){
z[[g]]<-cutree(hcl,k=g)
}
wine_clust2<-pgmmEM(x,1:4,1:4,zstart=3,modelSubset=c("CUU"),zlist=z)
table(wine[,1],wine_clust2$map)
print(wine_clust2)
summary(wine_clust2)

# Olive oil classification by region (there are three regions), with two-thirds of
# the observations taken as having known group memberships, using the CUC, CUU and
# UCU models.
data("olive")
x<-olive[,-c(1,2)]
x<-scale(x)
```

### Italian Wine

**Description**

Data on 27 chemical and physical properties of three types of wine (Barolo, Grignolino, Barbera) from the Piedmont region of Italy. The study did include one further variable but the sulphur measurements were not available.
Usage
data(wine)

Format
A data frame with 178 observations and 28 columns. The first column gives the type of wine: (1) Barolo, (2) Grignolino, or (3) Barbera. The other 27 columns contain the variables.

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