Package ‘FisherEM’

October 11, 2018

Type Package

Title The FisherEM Algorithm to Simultaneously Cluster and Visualize High-Dimensional Data

Version 1.5.1

Date 2018-10-11

Author Charles Bouveyron and Camille Brunet

Maintainer Charles Bouveyron <charles.bouveyron@gmail.com>

Depends MASS, parallel, elasticnet

Description The FisherEM algorithm, proposed by Bouveyron & Brunet (201) <doi:10.1007/s11222-011-9249-9>, is an efficient method for the clustering of high-dimensional data. FisherEM models and clusters the data in a discriminative and low-dimensional latent subspace. It also provides a low-dimensional representation of the clustered data. A sparse version of Fisher-EM algorithm is also provided.

License GPL-2

LazyLoad yes

NeedsCompilation no

Repository CRAN

Date/Publication 2018-10-11 10:10:07 UTC

R topics documented:

FisherEM-package .............................................. 2
fem .......................................................... 2
fem.ari .................................................... 5
plot.fem ................................................... 6
print.fem ................................................... 6
sfem ......................................................... 7

Index 10
Description

The FisherEM algorithm, proposed by Bouveyron & Brunet (201) \(<\text{doi:10.1007/s11222-011-9249-9}>\), is an efficient method for the clustering of high-dimensional data. FisherEM models and clusters the data in a discriminative and low-dimensional latent subspace. It also provides a low-dimensional representation of the clustered data. A sparse version of Fisher-EM algorithm is also provided.

Details

<table>
<thead>
<tr>
<th>Package</th>
<th>FisherEM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>Package</td>
</tr>
<tr>
<td>Version</td>
<td>1.2</td>
</tr>
<tr>
<td>Date</td>
<td>2012-07-09</td>
</tr>
<tr>
<td>License</td>
<td>GPL-2</td>
</tr>
<tr>
<td>LazyLoad</td>
<td>yes</td>
</tr>
</tbody>
</table>

Author(s)

Charles Bouveyron and Camille Brunet

Maintainer: Charles Bouveyron <charles.bouveyron@gmail.com>

References


Description

The Fisher-EM algorithm is a subspace clustering method for high-dimensional data. It is based on the Gaussian Mixture Model and on the idea that the data lives in a common and low dimensional subspace. An EM-like algorithm estimates both the discriminative subspace and the parameters of the mixture model.

Usage

fem(Y,K=2:6,model='AkjBk',method='svd',crit='icl',maxit=50,eps=1e-4,init='kmeans',
nstart=5,Tinit=c(),kernel='',disp=FALSE,mc.cores=(detectCores()-1))

Arguments

Y The data matrix. Categorical variables and missing values are not allowed.
K An integer vector specifying the numbers of mixture components (clusters) among which the model selection criterion will choose the most appropriate number of groups. Default is 2:6.
model A vector of discriminative latent mixture (DLM) models to fit. There are 12 different models: "DkBk", "DkB", "DBk", "DB", "AkjBk", "AkjB", "AkBk", "AkBk", "AjBk", "AjB", "ABk", "AB". The option "all" executes the Fisher-EM algorithm on the 12 DLM models and select the best model according to the maximum value obtained by model selection criterion.
method The method use for the fitting of the projection matrix associated to the discriminative subspace. Three methods are available: 'svd', 'reg' and 'gs'. The 'reg' method is the default.
crit The model selection criterion to use for selecting the most appropriate model for the data. There are 3 possibilities: "bic", "aic" or "icl". Default is "icl".
maxit The maximum number of iterations before the stop of the Fisher-EM algorithm.
eps The threshold value for the likelihood differences to stop the Fisher-EM algorithm.
init The initialization method for the Fisher-EM algorithm. There are 4 options: "random" for a randomized initialization, "kmeans" for an initialization by the kmeans algorithm, "hclust" for hierarchical clustering initialization or "user" for a specific initialization through the parameter "Tinit". Default is "kmeans". Notice that for "kmeans" and "random", several initializations are asked and the initialization associated with the highest likelihood is kept (see "nstart").
nstart The number of restart if the initialization is "kmeans" or "random". In such a case, the initialization associated with the highest likelihood is kept.
Tinit A n x K matrix which contains posterior probabilities for initializing the algorithm (each line corresponds to an individual).
kernel It enables to deal with the n < p problem. By default, no kernel (""") is used. But the user has the choice between 3 options for the kernel: "linear", "sigmoid" or "rbf".
disp If true, some messages are printed during the clustering. Default is false.
mc.cores The number of CPUs to use to fit in parallel the different models (only for non-Windows platforms). Default is the number of available cores minus 1.
Value

A list is returned:

- **K**: The number of groups.
- **cls**: The group membership of each individual estimated by the Fisher-EM algorithm.
- **P**: The posterior probabilities of each individual for each group.
- **U**: The loading matrix which determines the orientation of the discriminative subspace.
- **mean**: The estimated mean in the subspace.
- **my**: The estimated mean in the observation space.
- **prop**: The estimated mixture proportion.
- **D**: The covariance matrices in the subspace.
- **aic**: The value of the Akaike information criterion.
- **bic**: The value of the Bayesian information criterion.
- **icl**: The value of the integrated completed likelihood criterion.
- **loglik**: The log-likelihood values computed at each iteration of the FEM algorithm.
- **ll**: The log-likelihood value obtained at the last iteration of the FEM algorithm.
- **method**: The method used.
- **call**: The call of the function.
- **plot**: Some information to pass to the plot.fem function.
- **crit**: The model selection criterion used.

Author(s)

Charles Bouveyron and Camille Brunet

References


See Also

sfem, plot.fem, fem.ari, summary.fem
Examples

data(iris)
res = fem(iris[, -5], K = 3, model = 'DbBk', method = 'reg')
res
plot(res)
fem.ari(res, as.numeric(iris[, 5]))

# Fit several models and numbers of groups (use by default on non-Windows # platforms the parallel computing).
res = fem(iris[, -5], K = 2:6, model = 'all', method = 'svd')
res
plot(res)
fem.ari(res, as.numeric(iris[, 5]))

<table>
<thead>
<tr>
<th>fem.ari</th>
<th>Adjusted Rand index</th>
</tr>
</thead>
</table>

Description

The function computes the adjusted Rand index (ARI) which allows to compare two clustering partitions.

Usage

fem.ari(x, y)

Arguments

x A 'fem' object containing the first partition to compare.
y The second partition to compare (as vector).

Value

ari The value of the ARI.

See Also

fem, sfem, plot.fem, summary.fem

Examples

data(iris)
res = fem(iris[, -5], K = 3, model = 'DbBk', method = 'reg')
res
plot(res)
fem.ari(res, as.numeric(iris[, 5]))
**plot.fem**  
*The plot function for 'fem' objects.*

**Description**

This function plots different information about 'fem' objects such as model selection, log-likelihood evolution and visualization of the clustered data into the discriminative subspace fitted by the Fisher-EM algorithm.

**Usage**

```r
## S3 method for class 'fem'
plot(x, frame=0, crit=c(),...)  
```

**Arguments**

- `x`: The fem object.
- `frame`: 0: all plots; 1: selection of the number of groups; 2: log-likelihood; projection of the data into the discriminative subspace.
- `crit`: The model selection criterion to display. Default is the criterion used in the 'fem' function ('icl' by default).
- `...`: Additional options to pass to the plot function.

**See Also**

fem, sfem, fem.ari, summary.fem

**Examples**

```r
data(iris)
res = fem(iris[, -5], K=3, model='DkBk', method='reg')
res
plot(res)
fem.ari(res, as.numeric(iris[,5]))
```

---

**print.fem**  
*The print function for 'fem' objects.*

**Description**

This function summarizes 'fem' objects. It in particular indicates which DLM model has been chosen and displays the loading matrix 'U' if the original dimension is smaller than 10.
Usage

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

Arguments

- `x` The fem object.
- `...` Additional options to pass to the summary function.

See Also

`fem`, `sfem`, `fem.ari`, `plot.fem`

Examples

```r
data(iris)
res <- fem(iris[,1:5], model='DkBk', method='reg')
res
plot(res)
fem.ari(res, as.numeric(iris[,5]))
```

---

**sfem**

The sparse Fisher-EM algorithm

Description

The sparse Fisher-EM algorithm is a sparse version of the Fisher-EM algorithm. The sparsity is introduced within the F step which estimates the discriminative subspace. The sparsity on U is obtained by adding a l1 penalty to the optimization problem of the F step.

Usage

```r
sfem(Y,K=2:6, obj=NULL, model='AkjBk', method='reg', crit='icl', maxit=50, eps=1e-6,
     init='kmeans', nstart=5, Tinit=c(), kernel='', disp=FALSE, l1=0.1, l2=0, nbit=2)
```

Arguments

- `Y` The data matrix. Categorical variables and missing values are not allowed.
- `K` An integer vector specifying the numbers of mixture components (clusters) among which the model selection criterion will choose the most appropriate number of groups. Default is 2:6.
- `obj` An object of class `fem` previously learned with the `fem` function which will be used as initialization of the sparse FisherEM algorithm.
- `model` A vector of discriminative latent mixture (DLM) models to fit. There are 12 different models: "DkBk", "DkB", "DBk", "DB", "AkjBk", "AkjB", "AkBk", "AkBk", "AjBk", "AjB", "ABk", "ABk", "AB". The option "all" executes the Fisher-EM algorithm on the 12 DLM models and select the best model according to the maximum value obtained by model selection criterion.
method
The method used for the fitting of the projection matrix associated to the discriminative subspace. Three methods are available: 'svd', 'reg' and 'gs'. The 'reg' method is the default.

crit
The model selection criterion to use for selecting the most appropriate model for the data. There are 3 possibilities: "bic", "aic" or "icl". Default is "icl".

maxit
The maximum number of iterations before the stop of the Fisher-EM algorithm.

eps
The threshold value for the likelihood differences to stop the Fisher-EM algorithm.

init
The initialization method for the Fisher-EM algorithm. There are 4 options: "random" for a randomized initialization, "kmeans" for an initialization by the kmeans algorithm, "hclus" for hierarchical clustering initialization or "user" for a specific initialization through the parameter "Tinit". Default is "kmeans". Notice that for "kmeans" and "random", several initializations are asked and the initialization associated with the highest likelihood is kept (see "nstart").

nstart
The number of restart if the initialization is "kmeans" or "random". In such a case, the initialization associated with the highest likelihood is kept.

Tinit
A n x K matrix which contains posterior probabilities for initializing the algorithm (each line corresponds to an individual).

kernel
It enables to deal with the n < p problem. By default, no kernel (" ") is used. But the user has the choice between 3 options for the kernel: "linear", "sigmoid" or "rbf".

disp
If true, some messages are printed during the clustering. Default is false.

l1
The l1 penalty value (lasso) which has to be in [0,1]. A small value (close to 0) leads to a very sparse loading matrix whereas a value equals to 1 corresponds to no sparsity. Default is 0.1.

l2
The l2 penalty value (elasticnet). Defaults is 0 (no regularization).

nbit
The number of iterations for the lasso procedure. Defaults is 2.

Value
A list is returned:

K
The number of groups.

cls
the group membership of each individual estimated by the Fisher-EM algorithm.

P
the posterior probabilities of each individual for each group.

U
The loading matrix which determines the orientation of the discriminative subspace.

mean
The estimated mean in the subspace.

my
The estimated mean in the observation space.

prop
The estimated mixture proportion.

D
The covariance matrices in the subspace.

aic
The value of the Akaike information criterion.

bic
The value of the Bayesian information criterion.
icl    The value of the integrated completed likelihood criterion.
loglik The log-likelihood values computed at each iteration of the FEM algorithm.
ll     the log-likelihood value obtained at the last iteration of the FEM algorithm.
method The method used.
call   The call of the function.
plot   Some information to pass to the plot.fem function.
crit   The model selection criterion used.
l1     The l1 value.
l2     The l2 value.

Author(s)

Charles Bouveyron and Camille Brunet

References


See Also

fem, plot.fem, fem.ari, summary.fem

Examples

data(iris)
res = sfem(iris[, -5], K = 3, model = 'DkBk', l1 = seq(0.1, 0.3, 0.05))
res
plot(res)
fem.ari(res, as.numeric(iris[, 5]))
Index

fem, 2
fem.ari, 5
FisherEM (FisherEM-package), 2
FisherEM-package, 2
plot.fem, 6
print.fem, 6

sfem, 7