Package ‘EMCluster’

September 5, 2023

Version 0.2-15
Date 2023-09-03
Title EM Algorithm for Model-Based Clustering of Finite Mixture Gaussian Distribution
Depends R (>= 4.0.0), MASS, Matrix, methods
Enhances RColorBrewer
LazyLoad yes
LazyData yes
Description EM algorithms and several efficient initialization methods for model-based clustering of finite mixture Gaussian distribution with unstructured dispersion in both of unsupervised and semi-supervised learning.
License Mozilla Public License 2.0
BugReports https://github.com/snoweye/EMCluster/issues
URL https://github.com/snoweye/EMCluster
NeedsCompilation yes
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Repository CRAN
Date/Publication 2023-09-05 10:00:02 UTC
EMCluster-package

R topics documented:

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EMCluster-package  EM Algorithm for Model-Based Clustering of Finite Mixture Gaussian Distribution

Description

EMCluster provides EM algorithms and several efficient initialization methods for model-based clustering of finite mixture Gaussian distribution with unstructured dispersion in both of unsupervised and semi-supervised clustering.

Details

The install command is simply as

> R CMD INSTALL EMCluster_0.2-0.tar.gz

from a command mode or

R> install.packages("EMCluster")

inside an R session.
Assign Class

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra

See Also

init.EM, emcluster.

Examples

```r
## Not run:
demo(allinit, 'EMCluster', ask = F, echo = F)
demo(allinit_ss, 'EMCluster', ask = F, echo = F)

## End(Not run)
```

<table>
<thead>
<tr>
<th>Assign Class</th>
<th>Assign Class Id</th>
</tr>
</thead>
</table>

Description

This function assigns cluster id to each observation in \( x \) according to the desired model \( \text{emobj} \) or specified parameters \( \pi, \Mu, \text{and LTSigma} \).

Usage

```r
assign.class(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL,
lab = NULL, return.all = TRUE)
```

Arguments

- \( x \): the data matrix, dimension \( n \times p \).
- \( \text{emobj} \): the desired model which is a list mainly contains \( \pi, \Mu, \text{and LTSigma} \), usually a returned object from init.EM.
- \( \pi \): the mixing proportion, length \( K \).
- \( \Mu \): the centers of clusters, dimension \( K \times p \).
- \( \text{LTSigma} \): the lower triangular matrices of dispersion, dimension \( K \times \frac{p(p + 1)}{2} \).
- \( \text{lab} \): labeled data for semi-supervised clustering, length \( n \).
- \( \text{return.all} \): if returning with a whole \( \text{emobj} \) object.
Details

This function are based either an input emobj or inputs pi, Mu, and LTSigma to assign class id to each observation of x.
If lab is submitted, then the observation with label id greater 0 will not be assigned new class.

Value

This function returns a list containing mainly two new variables: nc (length K numbers of observations in each class) and class (length n class id).

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra

See Also

init.EM, emcluster.

Examples

library(EMCluster, quietly = TRUE)
set.seed(1234)
x2 <- da2$da
ret <- init.EM(x2, nclass = 2)
ret.new <- assign.class(x2, ret, return.all = FALSE)
str(ret.new)

Conversion

Convert Matrices in Different Format

Description

These utility functions are to convert matrices in different formats.

Usage

LTSigma2variance(x)
variance2LTSigma(x)
LTsigma2var(x1, p = NULL)
var2LTsigma(x1)
class2Gamma(class)
Gamma2class(Gamma)
Conversion

Arguments

x  a matrix/array to be converted, the dimension could be $K \times p(p + 1)/2$ or $p \times p \times K$.
x1  a vector/matrix to be converted, the length and dimension could be $p(p + 1)/2$ and $p \times p$.
p  dimension of matrix.
class  id of clusters for each observation, length $n$.
Gamma  containing posterior probabilities if normalized, otherwise containing component densities weighted by mixing proportion, dimension $n \times K$.

Details

LTsigma2variance converts LTsigma format to 3D array, and variance2LTsigma is the inversion function.
LTsigma2var converts LTsigma format to a matrix, and var2LTsigma is the inversion function. Note that LTsigma is one component of LTSigma.
class2Gamma converts id to a Gamma matrix where with probability 1 for the cluster where the observation belongs to, and Gamma2class converts posterior to cluster id where largest posterior is picked for each observation.

Value

A vector/matrix/array is returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra

References

https://www.stat.iastate.edu/people/ranjan-maitra

See Also

init.EM, emcluster.

Examples

## Not run:
library(EMCluster, quietly = TRUE)
x <- da2$LTsigma
class <- da2$class

y <- LTsigma2variance(x)
str(y)
y <- variance2LTsigma(y)
str(y)
sum(x != y)
Gamma <- class2Gamma(class)
class.new <- Gamma2class(Gamma)
sum(class != class.new)

## End(Not run)

### Dataset

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Dataset for demonstrations</th>
</tr>
</thead>
</table>

#### Description

There are four small datasets to test and demonstrate EMCluster.

#### Usage

da1
da2
da3

#### Format

da1, da2, da3 are in list.

#### Details

da1 has 500 observations in two dimensions da1$da$x and da1$da$y, and they are in 10 clusters given in da1$class.
da2 has 2,500 observations in two dimensions, too. The true parameters are given in da1$pi, da1$Mu, and da1$LTSigma. There are 40 clusters given in da1$class for this dataset.
da3 is similar to da2, but with lower overlaps between clusters.

#### Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

#### References

https://www.stat.iastate.edu/people/ranjan-maitra
EM Algorithm

**EM Algorithm** for model-based clustering

**Description**

These are core functions of EMCluster performing EM algorithm for model-based clustering of finite mixture multivariate Gaussian distribution with unstructured dispersion.

**Usage**

```r
emcluster(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL,
lab = NULL, EMC = .EMC, assign.class = FALSE)
shortemcluster(x, emobj = NULL, pi = NULL, Mu = NULL,
LTSigma = NULL, maxiter = 100, eps = 1e-2)
simple.init(x, nclass = 1)
```

**Arguments**

- `x`: the data matrix, dimension $n \times p$.
- `emobj`: the desired model which is a list mainly contains `pi`, `Mu`, and `LTSigma`, usually a returned object from `init.EM`.
- `pi`: the mixing proportion, length $K$.
- `Mu`: the centers of clusters, dimension $K \times p$.
- `LTSigma`: the lower triangular matrices of dispersion, $K \times (p+1)/2$.
- `lab`: labeled data for semi-supervised clustering, length $n$.
- `EMC`: the control for the EM iterations.
- `assign.class`: if assigning class id.
- `maxiter`: maximum number of iterations.
- `eps`: convergent tolerance.
- `nclass`: the desired number of clusters, $K$.

**Details**

The `emcluster` mainly performs EM iterations starting from the given parameters `emobj` without other initializations.

The `shortemcluster` performs short-EM iterations as described in `init.EM`.

**Value**

The `emcluster` returns an object `emobj` with class `emret` which can be used in post-process or other functions such as `e.step`, `m.step`, `assign.class`, `em.ic`, and `dmixmvn`.

The `shortemcluster` also returns an object `emobj` with class `emret` which is the best of several random initializations.

The `simple.init` utilizes `rand.EM` to obtain a simple initial.
**Author(s)**

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

**References**

https://www.stat.iastate.edu/people/ranjan-maitra

**See Also**

init.EM, e.step, m.step, EMControl.

**Examples**

```r
library(EMCluster, quietly = TRUE)
set.seed(1234)
x1 <- da1$da

emobj <- simple.init(x1, nclass = 10)
emobj <- shortemcluster(x1, emobj)
summary(emobj)

ret <- emcluster(x1, emobj, assign.class = TRUE)
summary(ret)
```

---

**EM Control Generator and Controller**

**Description**

The `.EMControl` generates an EM control (.EMC) controlling the options and conditions of EM algorithms, i.e. this function generate a default template. One can either modify `.EMC` or employ this function to control EM algorithms. By default, `.EMC`, `.EMC.Rnd`, and `.EMC.Rndp` are three native controllers as the EMCluster is loaded.

**Usage**

```r
.EMControl(alpha = 0.99, short.iter = 200, short.eps = 1e-2,
            fixed.iter = 1, n.candidate = 3,
            em.iter = 1000, em.eps = 1e-6, exhaust.iter = 5)
.EMC
.EMC.Rnd
.EMC.Rndp
```
EM Control

Arguments

- **alpha**: only used in emgroup for "SVD" initialization.
- **short.iter**: number of short-EM steps, default = 200.
- **short.eps**: tolerance of short-EM steps, default = 1e-2.
- **fixed.iter**: fixed iterations of EM for "RndEM" initialization, default = 1.
- **n.candidate**: reserved for other initialization methods (unimplemented).
- **em.iter**: maximum number of long-EM steps, default = 1000.
- **em.eps**: tolerance of long-EM steps, default = 1e-6.
- **exhaust.iter**: number of iterations for "exhaustEM" initialization, default = 5.

Details

**exhaust.iter** and **fixed.iter** are used to control the iterations of initialization procedures.

**short.iter** and **short.eps** are used to control the short-EM iterations.

**em.iter** and **em.eps** are used to control the long-EM iterations.

Moreover, **short.eps** and **em.eps** are for checking convergence of the iterations.

Value

This function returns a list as .EMC by default.

The .EMC.Rnd is equal to .EMControl(short.eps = Inf) and usually used by the rand.EM method.

The .EMC.Rndp is equal to .EMControl(fixed.iter = 5) where each random initials run 5 EM iterations in the rand.EM method.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra

See Also

- init.EM, emcluster.

Examples

```r
library(EMCluster, quietly = TRUE)
.EMC <- .EMControl()
.EMC.Rnd <- .EMControl(short.eps = Inf)
.EMC.Rndp <- .EMControl(fixed.iter = 5)
```
Description

These functions are tools for compute information criteria for the fitted models.

Usage

em.ic(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL, llhdval = NULL)
em.aic(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL)
em.bic(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL)
em.clc(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL)
em.icl(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL)
em.icl.bic(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL)

Arguments

x
the data matrix, dimension $n \times p$.

emobj
the desired model which is a list mainly contains pi, Mu, and LTSigma, usually a returned object from init.EM.

pi
the mixing proportion, length $K$.

Mu
the centers of clusters, dimension $K \times p$.

LTSigma
the lower triangular matrices of dispersion, $K \times p(p+1)/2$.

llhdval
the total log likelihood value of x given emobj.

Details

The em.ic calls all other functions to compute AIC (em.aic), BIC (em.bic), CLC (em.clc), ICL (em.icl), and ICL.BIC (em.icl.bic). All are useful information criteria for model selections, mainly choosing number of cluster.

Value

em.ic returns a list containing all other information criteria for given the data x and the desired model emobj.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra

References

https://www.stat.iastate.edu/people/ranjan-maitra
Initialization and EM

See Also

init.EM.

Examples

library(EMCluster, quietly = TRUE)
x2 <- da2$da

emobj <- list(pi = da2$pi, Mu = da2$Mu, LTSigma = da2$LTSigma)
em.ic(x2, emobj = emobj)

Description

These functions perform initializations (including em.EM and RndEM) followed by the EM iterations for model-based clustering of finite mixture multivariate Gaussian distribution with unstructured dispersion in both of unsupervised and semi-supervised clusterings.

Usage

init.EM(x, nclass = 1, lab = NULL, EMC = .EMC, stable.solution = TRUE, min.n = NULL, min.n.iter = 10, method = c("em.EM", "Rnd.EM"))
em.EM(x, nclass = 1, lab = NULL, EMC = .EMC, stable.solution = TRUE, min.n = NULL, min.n.iter = 10)
rand.EM(x, nclass = 1, lab = NULL, EMC = .EMC.Rnd, stable.solution = TRUE, min.n = NULL, min.n.iter = 10)
exhaust.EM(x, nclass = 1, lab = NULL, EMC = .EMControl(short.iter = 1, short.eps = Inf), method = c("em.EM", "Rnd.EM"), stable.solution = TRUE, min.n = NULL, min.n.iter = 10);

Arguments

x the data matrix, dimension $n \times p$.
nclass the desired number of clusters, $K$.
lab labeled data for semi-supervised clustering, length $n$.
EMC the control for the EM iterations.
stable.solution if returning a stable solution.
min.n restriction for a stable solution, the minimum number of observations for every final clusters.
min.n.iter  restriction for a stable solution, the minimum number of iterations for trying a stable solution.
method an initialization method.

Details
The init.EM calls either em.EM if method="em.EM" or rand.EM if method="Rnd.EM".

The em.EM has two steps: short-EM has loose convergent tolerance controlled by .EMC$short.eps and try several random initializations controlled by .EMC$short.iter, while long-EM starts from the best short-EM result (in terms of log likelihood) and run to convergence with a tight tolerance controlled by .EMC$em.eps.

The rand.EM also has two steps: first randomly pick several random initializations controlled by .EMC$short.iter, and second starts from the best of the random result (in terms of log likelihood) and run to convergence.

The lab is only for the semi-supervised clustering, and it contains pre-labeled indices between 1 and K for labeled observations. Observations with index 0 is non-labeled and has to be clustered by the EM algorithm. Indices will be assigned by the results of the EM algorithm. See demo(allinit_ss,'EMCluster') for details.

The exhaust.EM also calls the init.EM with different EMC and perform exhaust.iter times of EM algorithm with different initials. The best result is returned.

Value
These functions return an object emobj with class emret which can be used in post-process or other functions such as e.step, m.step, assign.class, em.ic, and dmixmvn.

Author(s)
Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References
https://www.stat.iastate.edu/people/ranjan-maitra

See Also
emcluster, .EMControl.

Examples
## Not run:
library(EMCluster, quietly = TRUE)
set.seed(1234)
x <- da1$da
ret.em <- init.EM(x, nclass = 10, method = "em.EM")
ret.Rnd <- init.EM(x, nclass = 10, method = "Rnd.EM", EMC = .EMC.Rnd)
emobj <- simple.init(x, nclass = 10)
ret.init <- emcluster(x, emobj, assign.class = TRUE)

par(mfrow = c(2, 2))
plotem(ret.em, x)
plotem(ret.Rnd, x)
plotem(ret.init, x)

## End(Not run)

---

### Jaccard Index

#### Description

This function returns the Jaccard index for binary ids.

#### Usage

Jaccard.Index(x, y)

#### Arguments

- `x`  
  true binary ids, 0 or 1.
- `y`  
  predicted binary ids, 0 or 1.

#### Details

All ids, x and y, should be either 0 (not active) or 1 (active). Any value other than 1 will be converted to 0.

#### Value

Return the value of Jaccard index.

#### Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

#### References

[https://www.stat.iastate.edu/people/ranjan-maitra](https://www.stat.iastate.edu/people/ranjan-maitra)
Examples

```r
library(EMCluster, quietly = TRUE)
x.id <- c(1, 1, 1, 0, 0, 0, 3, 3, 3)
y.id <- c(0, 1, 0, 1, 1, 1, 0, 1, 1)
Jaccard.Index(x.id, y.id)
```

Description

This function tests two mixture Gaussian models with unstructured covariance matrices and different numbers of clusters.

Usage

```r
lmt(emobj.0, emobj.a, x, tau = 0.5, n.mc.E.delta = 1000,
    n.mc.E.chi2, verbose = FALSE)
```

Arguments

- `emobj.0`: a `emret` object for the null hypothesis.
- `emobj.a`: a `emret` object for the alternative hypothesis.
- `x`: the data matrix, dimension $n \times p$.
- `tau`: proportion of null and alternative hypotheses.
- `n.mc.E.delta`: number of Monte Carlo simulations for expectation of delta (difference of logL).
- `n.mc.E.chi2`: number of Monte Carlo simulations for expectation of chisquare statistics.
- `verbose`: if verbose.

Details

This function calls several subroutines to compute information, likelihood ratio statistics, degrees of freedom, non-centrality of chi-squared distributions... etc. Based on Monte Carlo methods to estimate parameters of likelihood mixture tests, this function returns a p-value for testing $H_0$: $emobj.0$ v.s. $Ha: emobj.a$.

Value

A list of class `lmt` are returned.
LMT Functions

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra

See Also

init.EM.

Examples

## Not run:
library(EMCluster, quietly = TRUE)
set.seed(1234)

x <- as.matrix(iris[, 1:4])
p <- ncol(x)
min.n <- p * (p + 1) / 2
.EM$short.iter <- 200

ret.2 <- init.EM(x, nclass = 2, min.n = min.n, method = "Rnd.EM")
ret.3 <- init.EM(x, nclass = 3, min.n = min.n, method = "Rnd.EM")
ret.4 <- init.EM(x, nclass = 4, min.n = min.n, method = "Rnd.EM")

(lmt.23 <- lmt(ret.2, ret.3, x))
(lmt.34 <- lmt(ret.3, ret.4, x))
(lmt.24 <- lmt(ret.2, ret.4, x))

## End(Not run)
Density of (Mixture) Multivariate Normal Distribution

Description

These functions are tools for compute density of (mixture) multivariate Gaussian distribution with unstructured dispersion.

Usage

\[
\begin{align*}
dmvn(x, \mu, LTsigma, \text{log} = \text{FALSE}) \\
dlnvn(x, \mu, LTsigma, \text{log} = \text{TRUE}) \\
dmixmvn(x, \text{emobj} = \text{NULL}, \pi = \text{NULL}, \text{Mu} = \text{NULL}, LTSigma = \text{NULL}, \text{log} = \text{FALSE}) \\
\text{logL}(x, \text{emobj} = \text{NULL}, \pi = \text{NULL}, \text{Mu} = \text{NULL}, LTSigma = \text{NULL})
\end{align*}
\]

Arguments

- **x**: the data matrix, dimension \(n \times p\).
- **\mu**: the centers of clusters, length \(p\).
- **LTsigma**: the lower triangular matrices of dispersion, length \(p(p + 1)/2\).
- **\text{log}**: if logarithm returned.
- **\text{emobj}**: the desired model which is a list mainly contains \(\pi\), \(\text{Mu}\), and \(LTsigma\), usually a returned object from \text{init.EM}.
- **\pi**: the mixing proportion, length \(K\).
- **\text{Mu}**: the centers of clusters, dimension \(K \times p\).
- **LTsigma**: the lower triangular matrices of dispersion, \(K \times p(p + 1)/2\).

Details

The \text{dmvn} and \text{dlmn} compute density and log density of multivariate distribution.

The \text{dmixmvn} computes density of mixture multivariate distribution and is based either an input \text{emobj} or inputs \(\pi, \text{Mu},\) and \(LTsigma\) to assign class id to each observation of \(x\).

The \text{logL} returns the value of the observed log likelihood function of the parameters at the current values of the parameters \(\pi, \text{Mu},\) and \(LTsigma\), with the supplied data matrix \(x\).

Value

A density value is returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra
Other Initializations

See Also

init.EM, emcluster.

Examples

```r
library(EMCluster, quietly = TRUE)
x2 <- da2$da
x3 <- da3$da
	emobj2 <- list(pi = da2$pi, Mu = da2$Mu, LTSigma = da2$LTSigma)
emobj3 <- list(pi = da3$pi, Mu = da3$Mu, LTSigma = da3$LTSigma)

logL(x2, emobj = emobj2)
logL(x3, emobj = emobj3)

dmixmvn2 <- dmixmvn(x2, emobj2)
dmixmvn3 <- dmixmvn(x3, emobj3)

dlmvn(da2$da[1,], da2$Mu[1,], da2$LTSigma[1,])
log(dmvn(da2$da[1,], da2$Mu[1,], da2$LTSigma[1,]))
```

Other Initializations

Description

Two more functions with different initialization method.

Usage

```
starts.via.svd(x, nclass = 1, method = c("em", "kmeans"), EMC = .EMC)
emgroup(x, nclass = 1, EMC = .EMC)
```

Arguments

- `x`: the data matrix, dimension $n \times p$.
- `nclass`: the desired number of clusters, $K$.
- `method`: method with the svd initializations.
- `EMC`: the control for the EM iterations.

Details

The `starts.via.svd` utilizes SVD to initial parameters, and the `emgroup` runs the EM algorithm starting from the initial.
Value

The `starts.via.svd` returns an object with class `svd`, and the `emgroup` returns an object `emobj` with class `emret`.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra

See Also

`init.EM`, `EMControl`.

Examples

```r
library(EMCluster, quietly = TRUE)
set.seed(1234)
x1 <- da1$da

emobj <- emgroup(x1, nclass = 10)
summary(emobj)

ret.0 <- starts.via.svd(x1, nclass = 10, method = "kmeans")
summary(ret.0)
```

Description

The functions plot two dimensional data for clusters.

Usage

```r
plotem(emobj, x, main = NULL, xlab = NULL, ylab = NULL, 
...)
plot2d(x, emobj = NULL, k = NULL, color.pch = 1,
append.BN = TRUE, ...)
Arguments

- **emobj**: the desired model which is a list mainly contains \( \pi \), \( \mu \), and \( \Sigma_{LT} \), usually a returned object from `init.EM`.
- **x**: the data matrix, dimension \( n \times p \).
- **main**: title of plot.
- **xlab**: label of x-axis.
- **ylab**: label of y-axis.
- **...**: other parameters to the plot.
- **k**: index for symbols.
- **color.pch**: color and style for symbols.
- **append.BN**: if appending bivariate normal ellipsoid.

Details

This a simple x-y lot.

Value

A plot is returned.

Author(s)

Wei-Chen Chen &lt;wccsnow@gmail.com&gt; and Ranjan Maitra.

References

[https://www.stat.iastate.edu/people/ranjan-maitra](https://www.stat.iastate.edu/people/ranjan-maitra)

See Also

- `init.EM`, `emcluster`.

Examples

```r
## Not run:
library(EMCluster, quietly = TRUE)
x1 <- da1$da

ret.1 <- starts.via.svd(x1, nclass = 10, method = "em")
summary(ret.1)

plotem(ret.1, x1)
## End(Not run)
```
Plot Multivariate Data

Description

The function plots multivariate data for clusters as the parallel coordinates plot.

Usage

plotmd(x, class = NULL, xlab = "Variables", ylab = "Data", ...)

Arguments

- **x**: the data matrix, dimension $n \times p$.
- **class**: class id for all observations.
- **xlab**: label of x-axis.
- **ylab**: label of y-axis.
- **...**: other parameters to the plot.

Details

This a simplified parallel coordinate plot.

Value

A plot is returned.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra

See Also

init.EM, emcluster.
Examples

```r
## Not run:
library(EMCluster, quietly = TRUE)
set.seed(1234)

x <- as.matrix(iris[, 1:4], ncol = 4)
ret <- em.EM(x, nclass = 5)
plotmd(x, ret$class)

## End(Not run)
```

Description

The function plots multivariate data on 2D plane with contour. Typically, the contour is built via projection pursuit or SVD algorithms, such as `project.on.2d()`.

Usage

```r
plotppcontour(da, Pi, Mu, S, class, class.true = NULL, n.grid = 128,
               angle = 0, xlab = "", ylab = "", main = "")
```

Arguments

- `da`: a projected data matrix, dimension $n \times 2$.
- `Pi`: proportion, length $K$.
- `Mu`: the projected centers of cluster, dimension $K \times 2$.
- `S`: projected matrices of dispersion, dimension $p \times p \times K$.
- `class`: id of classifications, length $n$.
- `class.true`: true id of classifications if available, length $n$.
- `n.grid`: number of grid points.
- `angle`: a rotation angle (0 to $2\pi$).
- `xlab`: an option for `plot()` function.
- `ylab`: an option for `plot()` function.
- `main`: an option for `plot()` function.

Details

This function plots projection output of `project.on.2d()`.

da, Mu, and S are projected by some projection matrices obtained via SVD or projection pursuit algorithms. The projection is made on a 2D plane in the direction in which clusters of data $x$ are most distinguishable to visualize.
Value

A 2D projection plot is returned.

Note

Only distinguishable for up to 7 clusters due to the limited color schemes.

Author(s)

Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra

See Also

project.on.2d().

Examples

```r
## Not run:
library(EMCluster, quietly = TRUE)
library(MASS, quietly = TRUE)
set.seed(1234)

### Crabs.
x <- as.matrix(crabs[, 4:8])
ret <- init.EM(x, nclass = 4, min.n = 20)
ret.proj <- project.on.2d(x, ret)

### Plot.
pdf("crabs_ppcontour.pdf", height = 5, width = 5)
plotppcontour(ret.proj$da, ret.proj$Pi, ret.proj$Mu, ret.proj$S,
               ret.proj$class, angle = pi/6, main = "Crabs K = 4")
dev.off()

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

Several classes are declared in `EMCluster`, and these are functions to print and summary objects.

### Usage

```r
## S3 method for class 'emret'
print(x, digits = max(4, getOption("digits") - 3), ...)
## S3 method for class 'emret'
summary(object, ...)
## S3 method for class 'svd'
summary(object, ...)
```

### Arguments

- `x` : an object with the class attributes.
- `digits` : for printing out numbers.
- `object` : an object with the class attributes.
- `...` : other possible options.

### Details

These are useful functions for summarizing and debugging.

### Value

The results will cat or print on the STDOUT by default.

### Author(s)

Wei-Chen Chen &lt;wccsnow@gmail.com&gt; and Ranjan Maitra.

### References

[https://www.stat.iastate.edu/people/ranjan-maitra](https://www.stat.iastate.edu/people/ranjan-maitra)
Projection On 2D

See Also

init.EM, emcluster, starts.via.svd.

Examples

```r
## Not run:
library(EMCluster, quietly = TRUE)
x2 <- da2$da

emobj <- list(pi = da2$pi, Mu = da2$Mu, LTSigma = da2$LTSigma)
eobj <- e.step(x2, emobj = emobj)
emobj <- m.step(x2, emobj = eobj)
summary(emobj)

ret <- starts.via.svd(x2, nclass = 10, method = "kmeans")
summary(ret)

## End(Not run)
```

Description

The function projects multivariate data on 2D plane which can be displayed by `plotppcontour()` later.

Usage

```r
project.on.2d(x, emobj = NULL, pi = NULL, Mu = NULL,
LTSigma = NULL, class = NULL, method = c("PP", "SVD"))
```

Arguments

- `x` the data matrix, dimension $n \times p$.
- `emobj` the desired model which is a list mainly contains `pi`, `Mu`, and `LTSigma`, usually a returned object from `init.EM`.
- `pi` the mixing proportion, length $K$.
- `Mu` the centers of clusters, dimension $K \times p$.
- `LTSigma` the lower triangular matrices of dispersion, $K \times p(p+1)/2$.
- `class` id of classifications, length $n$.
- `method` either projection pursuit or singular value decomposition.

Details

This function produces projection outputs of $x$ and `emobj`. 

---

Projection On 2D  Produce Projection on 2D
Value

A projection is returned which is a list contains

- da is a \(n \times 2\) projected matrix of \(x\).
- \(\Pi\) is the original proportion \(\pi\) of length \(K\).
- \(\mu\) is a \(K \times 2\) projected matrix of \(\mu\).
- \(S\) is a \(2 \times 2 \times K\) projected array of \(\Sigma\).
- class is the original class \(c\).
- proj.mat is the projection matrix of dimension \(p \times 2\).

Author(s)

Wei-Chen Chen \(<wccsnow@gmail.com>\) and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra

See Also

project.on.2d().

Examples

```r
## Not run:
library(EMCluster, quietly = TRUE)
set.seed(1234)

### Iris.
x <- as.matrix(iris[, 1:4])
ret <- init.EM(x, nclass = 3, min.n = 30)
ret.proj <- project.on.2d(x, ret)

### Plot.
pdf("iris_ppcontour.pdf", height = 5, width = 5)
plotppcontour(ret.proj$da, ret.proj$Pi, ret.proj$Mu, ret.proj$S,
              ret.proj$class, main = "Iris K = 3")
dev.off()

## End(Not run)
```
Rand Index

Description

This function returns the Rand index and the adjusted Rand index for given true class ids and predicted class ids.

Usage

RRand(trcl, prcl, lab = NULL)

Arguments

- trcl: true class ids.
- prcl: predicted class ids.
- lab: known ids for semi-supervised clustering.

Details

All ids, trcl and prcl, should be positive integers and started from 1 to K, and the maximums are allowed to be different.

lab used in semi-supervised clustering contains the labels which are known before clustering. It should be positive integer and started from 1 for labeled data and 0 for unlabeled data.

Value

Return a Class RRand contains Rand index and adjusted Rand index.

Author(s)

Wei-Chen Chen (<wccsnow@gmail.com>) and Ranjan Maitra.

References

https://www.stat.iastate.edu/people/ranjan-maitra

Examples

library(EMCluster, quietly = TRUE)

true.id <- c(1, 1, 1, 2, 2, 2, 3, 3, 3)
pred.id <- c(2, 1, 2, 1, 1, 1, 2, 1, 1)
label <- c(0, 0, 0, 0, 1, 0, 2, 0, 0)

RRand(true.id, pred.id)
RRand(true.id, pred.id, lab = label)
Recolor Classification IDs

Description

These functions return new classification IDs.

Usage

```r
recolor(id.target, id.class, scatter.class = NULL, scatter.target = NULL)
rematch(tg.id, cl.id)
recode(id)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id.target</td>
<td>target class ids.</td>
</tr>
<tr>
<td>id.class</td>
<td>original class ids.</td>
</tr>
<tr>
<td>scatter.class</td>
<td>scatter class ids.</td>
</tr>
<tr>
<td>scatter.target</td>
<td>scatter target class ids.</td>
</tr>
<tr>
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<td>class ids.</td>
</tr>
<tr>
<td>tg.id</td>
<td>target class ids.</td>
</tr>
<tr>
<td>cl.id</td>
<td>class ids.</td>
</tr>
</tbody>
</table>

Details

The function `recolor` colors `id.target` in accordance with the most likely candidate in `id.class`. Note that if scatter is present, then the class given by 0 is represented as scatter and it is assumed to be the same for both classifications.

The function `rematch` returns a list as `id.trcl` and `id.prcl`. It is the heart of the recolor function and is usually called from recolor.

The function `recode` reorders classes to eliminate group ids without any members. It is assumed that the group ids are integers.

Value

See Details.

Author(s)

Ranjan Maitra.

References

[https://www.stat.iastate.edu/people/ranjan-maitra](https://www.stat.iastate.edu/people/ranjan-maitra)
Examples

```r
## Not run:
library(EMCluster, quietly = TRUE)

true.id <- c(1, 1, 1, 2, 2, 2, 3, 3, 3)
pred.id <- c(2, 1, 2, 1, 1, 1, 2, 1, 1)
recolor(pred.id, true.id)
## End(Not run)
```

### Description

These functions are single E- and M-step of EM algorithm for model-based clustering of finite mixture multivariate Gaussian distribution with unstructured dispersion.

### Usage

```r
e.step(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL, 
   norm = TRUE)
m.step(x, emobj = NULL, Gamma = NULL, assign.class = FALSE)
```

### Arguments

- **x**
  - the data matrix, dimension $n \times p$.
- **emobj**
  - the desired model which is a list mainly contains pi, Mu, and LTSigma, usually a returned object from `init.EM`.
- **pi**
  - the mixing proportion, length $K$.
- **Mu**
  - the centers of clusters, dimension $K \times p$.
- **LTSigma**
  - the lower triangular matrices of dispersion, $K \times \frac{p(p+1)}{2}$.
- **norm**
  - if returning normalized Gamma.
- **Gamma**
  - containing posterior probabilities if normalized, otherwise containing component densities weighted by mixing proportion, dimension $n \times K$.
- **assign.class**
  - if assigning class id.

### Details

These two functions are mainly used in debugging for development and post process after model fitting.
Value
The e.step returns a list contains Gamma, the posterior probabilities if norm=TRUE, otherwise it contains component densities. This is one E-step and Gamma is used to update emobj in the M-step next.

The m.step returns a new emobj according to the Gamma from the E-step above.

Author(s)
Wei-Chen Chen <wccsnow@gmail.com> and Ranjan Maitra.

References
https://www.stat.iastate.edu/people/ranjan-maitra

See Also
init.EM.

Examples

```r
library(EMCluster, quietly = TRUE)
x2 <- da2$da

emobj <- list(pi = da2$pi, Mu = da2$Mu, LTSigma = da2$LTSigma)
eobj <- e.step(x2, emobj = emobj)
emobj <- m.step(x2, emobj = eobj)
emobj
```
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