# Package: EMCluster (via r-universe)

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**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

**Maintainer** Wei-Chen Chen <wccsnow@gmail.com>

**Author** Wei-Chen Chen [aut, cre], Ranjan Maitra [aut], Volodymyr Melnykov [ctb], Dan Nettleton [ctb], David Faden [ctb], Rouben Rostamian [ctb], R Core team [ctb] (some functions are modified from the R source code)

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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.

## 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:
demo(allinit, 'EMCluster', ask = F, echo = F)
demo(allinit_ss, 'EMCluster', ask = F, echo = F)

## End(Not run)
```

---

`Assign Class` *Assign Class Id*

---

## Description

This function assigns cluster id to each observation in `x` according to the desired model `emobj` or specified parameters `pi`, `Mu`, and `LTSigma`.

## Usage

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

## Arguments

| | |
|---|---|
| `x` | the data matrix, dimension $n \times p$. |
| `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, dimension $K \times p(p+1)/2$. |
| `lab` | labeled data for semi-supervised clustering, length $n$. |
| `return.all` | if returning with a whole `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)
```

## 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` *Dataset for demonstrations*

---

## 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

```
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, $K \times p(p+1)/2$. |
| 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

```
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 *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 .EC.Rndp are three native controllers as the **EMCluster** is loaded.

### Usage

```
.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
```

## 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.

Moeover, 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

```
library(EMCluster, quietly = TRUE)

.EMC <- .EMControl()
.EMC.Rnd <- .EMControl(short.eps = Inf)
.EMC.Rndp <- .EMControl(fixed.iter = 5)
```

`Information Criteria` *Information Criteria for Model-Based Clustering*

## 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

## 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)
```

---

`Initialization and EM` *Initialization and EM Algorithm*

---

## 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` *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

## Examples

```
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)
```

Likelihood Mixture Tests

*Likelihood Mixture Tests*

## Description

This function test two mixture Gaussian models with unstructured covariance matrix and different numbers of clusters.

## Usage

```
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 return a p-value for testing H0: `emobj.0` v.s. Ha: `emobj.a`.

## Value

A list of class `lmt` are 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`.

### 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
.EMC$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)
```

---

## LMT Functions *Likelihood Mixture Test (LMT) Functions of EMCluster*

---

### Description

All likelihood mixture test (LMT) functions are for testing and can be utilized by advanced developers with caution.

Currently, these are only for workflows.

### Author(s)

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

### References

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

---

## MVN *Density of (Mixture) Multivariate Normal Distribution*

---

### Description

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

## Usage

```
dmvn(x, mu, LTsigma, log = FALSE)
dlmvn(x, mu, LTsigma, log = TRUE)
dmixmvn(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL, log = FALSE)
logL(x, emobj = NULL, pi = NULL, Mu = NULL, LTSigma = NULL)
```

## Arguments

| | |
|---|---|
| x | the data matrix, dimension $n \times p$. |
| mu | the centers of clusters, length $p$. |
| LTsigma | the lower triangular matrices of dispersion, length $p(p+1)/2$. |
| log | if logarithm returned. |
| 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, $K \times p(p+1)/2$. |

## Details

The dmvn and dlmvn compute density and log density of multivariate distribution.

The dmixmvn computes density of mixture multivariate distribution and is based either an input emobj or inputs pi, Mu, and LTSigma to assign class id to each observation of x.

The logL returns the value of the observed log likelihood function of the parameters at the current values of the parameters pi, Mu, and LTSigma, with the suplied 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

## See Also

init.EM, emcluster.

### Examples

```
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 *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 and 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

```
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)
```

---

# Plot EM Results *Plot Two Dimensional Data with clusters*

---

## Description

The functions plot two dimensional data for clusters.

## Usage

```
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 LTSigma, 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 <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)
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

*Plot Multivariate Data*

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## 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

```
## 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)
```

`Plot Projection and Contour`

*Plot Contour*

## 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

```
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` | ture 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

```
## 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)
```

---

Post I Information Functions

*Post I Information Functions of EMCluster*

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### Description

All post I information functions are for computing relative quantities and can be utilized by advanced developers with caution.

Currently, these are only for workflows.

### Author(s)

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

### References

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

`Print and Summary` *Functions for Printing or Summarizing Objects According to Classes*

## Description

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

## Usage

```
## 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 <wccsnow@gmail.com> and Ranjan Maitra.

## References

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

## See Also

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

## Examples

```
## 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)
```

---

`Projection On 2D` *Produce Projection on 2D*

---

## Description

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

## Usage

```
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`.

## 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 emobj$pi of length $K$.
- Mu is a $K \times 2$ projected matrix of emboj$Mu.
- S is a $2 \times 2 \times K$ projected array of emboj$LTSigma.
- class is the original class id emobj$class.
- 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

```
## 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 *Rand Index and Adjusted 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`
*Recolor Classification IDs*

## Description

These functions return new classification IDs.

## Usage

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

## Arguments

| | |
|---|---|
| `id.target` | target class ids. |
| `id.class` | original class ids. |
| `scatter.class` | scatter class ids. |
| `scatter.target` | scatter target class ids. |
| `id` | class ids. |
| `tg.id` | target class ids. |
| `cl.id` | class ids. |

## 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` reoders 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

## Examples

```
## 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)
```

---

`Single Step` *Single E- and M-step*

---

## 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

```
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, $K \times p(p+1)/2$. |
| `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

```
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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