Package ‘EMMIXSSL’

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Type Package

Title Semi-Supervised Gaussian Mixture Model with a Missing-Data
Mechanism

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Description

The algorithm of semi-supervised learning based on finite Gaussian mixture models with a missing-data mechanism is designed for a fitting g-class Gaussian mixture model via maximum likelihood (ML). It is proposed to treat the labels of the unclassified features as missing-data and to introduce a framework for their missing as in the pioneering work of Rubin (1976) for missing in incomplete data analysis. This dependency in the missingness pattern can be leveraged to provide additional information about the optimal classifier as specified by Bayes’ rule.

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Contents

`Classifier_Bayes` *Classifier based on Bayes rule*

Description

A classifier based on Bayes rule, that is maximum a posterior probabilities of class membership

Usage

```
Classifier_Bayes(dat, n, p, g, pi, mu, sigma, ncov = 2)
```

Arguments

`dat`	An $n \times p$ matrix where each row represents an individual observation
`n`	Number of observations.
`p`	Dimension of observation vecor.
`g`	Number of classes.
`pi`	A g-dimensional vector for the initial values of the mixing proportions.
`mu`	A $p \times g$ matrix for the initial values of the location parameters.
`sigma`	A $p \times p$ covariance matrix if `ncov=1`, or a list of g covariance matrices with dimension $p \times p \times g$ if `ncov=2`.
`ncov`	Options of structure of sigma matrix; the default value is 2; `ncov = 1` for a common covariance matrix; `ncov` = 2 for the unequal covariance/scale matrices.

Details

The posterior probability can be expressed as

$$\tau_i(y_j;\theta) = Prob\{z_{ij} = 1|y_j\} = \frac{\pi_i \phi(y_j;\mu_i,\Sigma_i)}{\sum_{h=1}^{g} \pi_h \phi(y_j;\mu_h,\Sigma_h)},$$

where ϕ is a normal probability function with mean μ_i and covariance matrix Σ_i, and z_{ij} is is a zero-one indicator variable denoting the class of origin. The Bayes' Classifier of allocation assigns an entity with feature vector y_j to Class C_k if

$$k = argmax_i \tau_i(y_j;\theta).$$

Value

`cluster`	A vector of the class membership.

Examples

```
n<-150
pi<-c(0.25,0.25,0.25,0.25)
sigma<-array(0,dim=c(3,3,4))
sigma[,,1]<-diag(1,3)
sigma[,,2]<-diag(2,3)
sigma[,,3]<-diag(3,3)
sigma[,,4]<-diag(4,3)
mu<-matrix(c(0.2,0.3,0.4,0.2,0.7,0.6,0.1,0.7,1.6,0.2,1.7,0.6),3,4)
dat<-rmix(n=n,pi=pi,mu=mu,sigma=sigma,ncov=2)
cluster<-Classifier_Bayes(dat=dat$Y,n=150,p=3,g=4,mu=mu,sigma=sigma,pi=pi,ncov=2)
```

`cov2vec` *Transform a variance matrix into a vector*

Description

Transform a variance matrix into a vector i.e., Sigma=R^T*R

Usage

```
cov2vec(sigma)
```

Arguments

`sigma`	A variance matrix

Details

The variance matrix is decomposed by computing the Choleski factorization of a real symmetric positive-definite square matrix. Then, storing the upper triangular factor of the Choleski decomposition into a vector.

Value

par A vector representing a variance matrix

`discriminant_beta` *Discriminant function*

Description

Discriminant function in the particular case of g=2 classes with an equal-covariance matrix

Usage

```
discriminant_beta(pi, mu, sigma)
```

Arguments

`pi` A g-dimensional vector for the initial values of the mixing proportions.

`mu` A $p \times g$ matrix for the initial values of the location parameters.

`sigma` A $p \times p$ covariance matrix if `ncov=1`, or a list of g covariance matrices with dimension $p \times p \times g$ if `ncov=2`.

Details

Discriminant function in the particular case of g=2 classes with an equal-covariance matrix can be expressed

$$d(y_i, \beta) = \beta_0 + \beta_1 y_i,$$

where $\beta_0 = \log \frac{\pi_1}{\pi_2} - \frac{1}{2} \frac{\mu_1^2 - \mu_2^2}{\sigma^2}$ and $\beta_1 = \frac{\mu_1 - \mu_2}{\sigma^2}$.

Value

`beta0` An intercept of discriminant function

`beta` A coefficient of discriminant function

`EMMIXSSL` *Fitting Gaussian mixture models*

Description

Fitting Gaussian mixture model to a complete classified dataset or a incomplete classified dataset with/without the missing-data mechanism.

Usage

```
EMMIXSSL(
  dat,
  zm,
  pi,
  mu,
  sigma,
  ncov,
  xi = NULL,
  type,
  iter.max = 500,
  eval.max = 500,
  rel.tol = 1e-06,
  sing.tol = 1e-20
)
```

Arguments

`dat` An $n \times p$ matrix where each row represents an individual observation

`zm` An n-dimensional vector containing the class labels including the missing-label denoted as NA.

`pi` A g-dimensional vector for the initial values of the mixing proportions.

`mu` A $p \times g$ matrix for the initial values of the location parameters.

`sigma` A $p \times p$ covariance matrix if `ncov=1`, or a list of g covariance matrices with dimension $p \times p \times g$ if `ncov=2`.

`ncov` Options of structure of sigma matrix; the default value is 2; `ncov` = 1 for a common covariance matrix; `ncov` = 2 for the unequal covariance/scale matrices.

`xi` A 2-dimensional vector containing the initial values of the coefficients in the logistic function of the Shannon entropy.

`type` Three types of Gaussian mixture models, 'ign' indicates fitting the model to a partially classified sample on the basis of the likelihood that ignores the missing label mechanism, 'full' indicates fitting the model to a partially classified sample on the basis of the full likelihood, taking into account the missing-label mechanism, and 'com' indicate fitting the model to a completed classified sample.

`iter.max` Maximum number of iterations allowed. Defaults to 500

`eval.max`	Maximum number of evaluations of the objective function allowed. Defaults to 500
`rel.tol`	Relative tolerance. Defaults to 1e-15
`sing.tol`	Singular convergence tolerance; defaults to 1e-20.

Value

`objective`	Value of objective likelihood
`convergence`	Value of convergence
`iteration`	Number of iteration
`pi`	Estimated vector of the mixing proportions.
`mu`	Estimated matrix of the location parameters.
`sigma`	Estimated covariance matrix
`xi`	Estimated coefficient vector for a logistic function of the Shannon entropy

Examples

```
n<-150
pi<-c(0.25,0.25,0.25,0.25)
sigma<-array(0,dim=c(3,3,4))
sigma[,,1]<-diag(1,3)
sigma[,,2]<-diag(2,3)
sigma[,,3]<-diag(3,3)
sigma[,,4]<-diag(4,3)
mu<-matrix(c(0.2,0.3,0.4,0.2,0.7,0.6,0.1,0.7,1.6,0.2,1.7,0.6),3,4)
dat<-rmix(n=n,pi=pi,mu=mu,sigma=sigma,ncov=2)
xi<-c(-0.5,1)
m<-rlabel(dat=dat$Y,pi=pi,mu=mu,sigma=sigma,xi=xi,ncov=2)
zm<-dat$clust
zm[m==1]<-NA
inits<-initialvalue(g=4,zm=zm,dat=dat$Y,ncov=2)
## Not run:
fit_pc<-EMMIXSSL(dat=dat$Y,zm=zm,pi=inits$pi,mu=inits$mu,sigma=inits$sigma,xi=xi,type='full',ncov=2)

## End(Not run)
```

`errorrate` *Error rate of the Bayes rule for two-class Gaussian homoscedastic model*

Description

The optimal error rate of Bayes rule for two-class Gaussian homoscedastic model

Usage

```
errorrate(beta0, beta, pi, mu, sigma)
```

Arguments

`beta0`	An $n \times p$ matrix where each row represents an individual observation
`beta`	Number of observations.
`pi`	A g-dimensional vector for the initial values of the mixing proportions.
`mu`	A $p \times g$ matrix for the initial values of the location parameters.
`sigma`	A $p \times p$ covariance matrix if `ncov=1`, or a list of g covariance matrices with dimension $p \times p \times g$ if `ncov=2`.

Details

The optimal error rate of Bayes rule for two-class Gaussian homoscedastic model can be expressed as

$$err(y_j;\theta) = \pi_1\phi\{-\frac{\beta_0 + \beta_1^T\mu_1}{(\beta_1^T\Sigma\beta_1)^{\frac{1}{2}}}\} + \pi_2\phi\{\frac{\beta_0 + \beta_1^T\mu_2}{(\beta_1^T\Sigma\beta_1)^{\frac{1}{2}}}\}$$

where ϕ is a normal probability function with mean μ_i and covariance matrix Σ_i.

Value

`errval`	A vector of error rate.

`gastrodata` *Gastrointestinal dataset*

Description

The collected dataset is composed of 76 colonoscopic videos (recorded with both White Light (WL) and Narrow Band Imaging (NBI)), the histology (classification ground truth), and the endoscopist's opinion (including 4 experts and 3 beginners). There are $n=76$ observations, and each observation consists of 698 features extracted from colonoscopic videos on patients with gastrointestinal lesions.

References

http://www.depeca.uah.es/colonoscopy_dataset/

`gastro_label_binary` *Gastrointestinal binary labels*

Description

A panel of seven endoscopists viewed the videos and determined which patient needs resection (malignant) or no-resection (benign).

References

http://www.depeca.uah.es/colonoscopy_dataset/

gastro_label_trinary *Gastrointestinal trinary labels*

Description

Gastrointestinal trinary ground truth (Adenoma, Serrated, and Hyperplastic)

References

http://www.depeca.uah.es/colonoscopy_dataset/

get_clusterprobs *Posterior probability*

Description

Get posterior probabilities of class membership

Usage

```
get_clusterprobs(dat, n, p, g, pi, mu, sigma, ncov = 2)
```

Arguments

dat	An $n \times p$ matrix where each row represents an individual observation
n	Number of observations.
p	Dimension of observation vecor.
g	Number of multivariate normal classes.
pi	A g-dimensional vector for the initial values of the mixing proportions.
mu	A $p \times g$ matrix for the initial values of the location parameters.
sigma	A $p \times p$ covariance matrix if ncov=1, or a list of g covariance matrices with dimension $p \times p \times g$ if ncov=2.
ncov	Options of structure of sigma matrix; the default value is 2; ncov = 1 for a common covariance matrix; ncov = 2 for the unequal covariance/scale matrices.

Details

The posterior probability can be expressed as

$$\tau_i(y_j;\theta) = Prob\{z_{ij} = 1|y_j\} = \frac{\pi_i \phi(y_j; \mu_i, \Sigma_i)}{\sum_{h=1}^{g} \pi_h \phi(y_j; \mu_h, \Sigma_h)},$$

where ϕ is a normal probability function with mean μ_i and covariance matrix Σ_i, and z_{ij} is is a zero-one indicator variable denoting the class of origin.

Value

`clusprobs`	Posterior probabilities of class membership for the ith entity

Examples

```
n<-150
pi<-c(0.25,0.25,0.25,0.25)
sigma<-array(0,dim=c(3,3,4))
sigma[,,1]<-diag(1,3)
sigma[,,2]<-diag(2,3)
sigma[,,3]<-diag(3,3)
sigma[,,4]<-diag(4,3)
mu<-matrix(c(0.2,0.3,0.4,0.2,0.7,0.6,0.1,0.7,1.6,0.2,1.7,0.6),3,4)
dat<-rmix(n=n,pi=pi,mu=mu,sigma=sigma,ncov=2)
tau<-get_clusterprobs(dat=dat$Y,n=150,p=3,g=4,mu=mu,sigma=sigma,pi=pi,ncov=2)
```

`get_entropy` *Shannon entropy*

Description

Shannon entropy

Usage

```
get_entropy(dat, n, p, g, pi, mu, sigma, ncov = 2)
```

Arguments

`dat`	An $n \times p$ matrix where each row represents an individual observation
`n`	Number of observations.
`p`	Dimension of observation vecor.
`g`	Number of multivariate normal classes.
`pi`	A g-dimensional vector for the initial values of the mixing proportions.
`mu`	A $p \times g$ matrix for the initial values of the location parameters.
`sigma`	A $p \times p$ covariance matrix if `ncov=1`, or a list of g covariance matrices with dimension $p \times p \times g$ if `ncov=2`.
`ncov`	Options of structure of sigma matrix; the default value is 2; `ncov` = 1 for a common covariance matrix; `ncov` = 2 for the unequal covariance/scale matrices.

Details

The concept of information entropy was introduced by *shannon1948mathematical*. The entropy of y_j is formally defined as

$$e_j(y_j;\theta) = -\sum_{i=1}^{g} \tau_i(y_j;\theta) \log \tau_i(y_j;\theta).$$

Value

clusprobs	The posterior probabilities of the i-th entity that belongs to the j-th group.

Examples

```
n<-150
pi<-c(0.25,0.25,0.25,0.25)
sigma<-array(0,dim=c(3,3,4))
sigma[,,1]<-diag(1,3)
sigma[,,2]<-diag(2,3)
sigma[,,3]<-diag(3,3)
sigma[,,4]<-diag(4,3)
mu<-matrix(c(0.2,0.3,0.4,0.2,0.7,0.6,0.1,0.7,1.6,0.2,1.7,0.6),3,4)
dat<-rmix(n=n,pi=pi,mu=mu,sigma=sigma,ncov=2)
en<-get_entropy(dat=dat$Y,n=150,p=3,g=4,mu=mu,sigma=sigma,pi=pi,ncov=2)
```

initialvalue *Initial values for ECM*

Description

Inittial values for claculating the estimates based on solely on the classified features.

Usage

```
initialvalue(dat, zm, g, ncov = 2)
```

Arguments

dat	An $n \times p$ matrix where each row represents an individual observation
zm	An n-dimensional vector containing the class labels including the missing-label denoted as NA.
g	Number of multivariate normal classes.
ncov	Options of structure of sigma matrix; the default value is 2; ncov = 1 for a common covariance matrix; ncov = 2 for the unequal covariance/scale matrices.

Value

pi	A g-dimensional initial vector of the mixing proportions.
mu	A initial $p \times g$ matrix of the location parameters.
sigma	A $p \times p$ covariance matrix if ncov=1, or a list of g covariance matrices with dimension $p \times p \times g$ if ncov=2.

Examples

```
n<-150
pi<-c(0.25,0.25,0.25,0.25)
sigma<-array(0,dim=c(3,3,4))
sigma[,,1]<-diag(1,3)
sigma[,,2]<-diag(2,3)
sigma[,,3]<-diag(3,3)
sigma[,,4]<-diag(4,3)
mu<-matrix(c(0.2,0.3,0.4,0.2,0.7,0.6,0.1,0.7,1.6,0.2,1.7,0.6),3,4)
dat<-rmix(n=n,pi=pi,mu=mu,sigma=sigma,ncov=2)
xi<-c(-0.5,1)
m<-rlabel(dat=dat$Y,pi=pi,mu=mu,sigma=sigma,xi=xi,ncov=2)
zm<-dat$clust
zm[m==1]<-NA
inits<-initialvalue(g=4,zm=zm,dat=dat$Y,ncov=2)
```

list2par *Transfer a list into a vecor*

Description

Transfer a list into a vector

Usage

```
list2par(
  p,
  g,
  pi,
  mu,
  sigma,
  ncov = 2,
  xi = NULL,
  type = c(”ign”, ”full”, ”com”)
)
```

Arguments

p Dimension of observation vecor.

g Number of multivariate normal classes.

pi A g-dimensional vector for the initial values of the mixing proportions.

mu A $p \times g$ matrix for the initial values of the location parameters.

sigma A $p \times p$ covariance matrix if ncov=1, or a list of g covariance matrices with dimension $p \times p \times g$ if ncov=2.

ncov — Options of structure of sigma matrix; the default value is 2; ncov = 1 for a common covariance matrix; ncov = 2 for the unequal covariance/scale matrices.

xi — A 2-dimensional vector containing the initial values of the coefficients in the logistic function of the Shannon entropy.

type — Three types to fit to the model, 'ign' indicates fitting the model on the basis of the likelihood that ignores the missing label mechanism, 'full' indicates that the model to be fitted on the basis of the full likelihood, taking into account the missing-label mechanism, and 'com' indicate that the model to be fitted to a completed classified sample.

Value

par — a vector including all list information

---

loglk_full *Full log-likelihood function*

Description

Full log-likelihood function with both terms of ignoring and missing

Usage

```
loglk_full(dat, zm, pi, mu, sigma, ncov = 2, xi)
```

Arguments

dat — An $n \times p$ matrix where each row represents an individual observation

zm — An n-dimensional vector containing the class labels including the missing-label denoted as NA.

pi — A g-dimensional vector for the initial values of the mixing proportions.

mu — A $p \times g$ matrix for the initial values of the location parameters.

sigma — A $p \times p$ covariance matrix if ncov=1, or a list of g covariance matrices with dimension $p \times p \times g$ if ncov=2.

ncov — Options of structure of sigma matrix; the default value is 2; ncov = 1 for a common covariance matrix; ncov = 2 for the unequal covariance/scale matrices.

xi — A 2-dimensional vector containing the initial values of the coefficients in the logistic function of the Shannon entropy.

Details

The full log-likelihood function can be expressed as

$$\log L_{PC}^{(full)}(\boldsymbol{\Psi}) = \log L_{PC}^{(ig)}(\theta) + \log L_{PC}^{(miss)}(\theta, \boldsymbol{\xi}),$$

wherelog $L_{PC}^{(ig)}(\theta)$is the log likelihood function formed ignoring the missing in the label of the unclassified features, and $\log L_{PC}^{(miss)}(\theta, \boldsymbol{\xi})$ is the log likelihood function formed on the basis of the missing-label indicator.

Value

`lk`	Log-likelihood value

`loglk_ig` *Log likelihood for partially classified data with ingoring the missing mechanism*

Description

Log likelihood for partially classified data with ingoring the missing mechanism

Usage

```
loglk_ig(dat, zm, pi, mu, sigma, ncov = 2)
```

Arguments

`dat`	An $n \times p$ matrix where each row represents an individual observation
`zm`	An n-dimensional vector containing the class labels including the missing-label denoted as NA.
`pi`	A g-dimensional vector for the initial values of the mixing proportions.
`mu`	A $p \times g$ matrix for the initial values of the location parameters.
`sigma`	A $p \times p$ covariance matrix if `ncov=1`, or a list of g covariance matrices with dimension $p \times p \times g$ if `ncov=2`.
`ncov`	Options of structure of sigma matrix; the default value is 2; `ncov` = 1 for a common covariance matrix; `ncov` = 2 for the unequal covariance/scale matrices.

Details

The log-likelihood function for partially classified data with ingoring the missing mechanism can be expressed as

$$\log L_{PC}^{(ig)}(\theta) = \sum_{j=1}^{n} \left[(1-m_j) \sum_{i=1}^{g} z_{ij} \left\{ \log \pi_i + \log f_i(y_j;\omega_i) \right\} + m_j \log \left\{ \sum_{i=1}^{g} \pi_i f_i(y_j;\omega_i) \right\} \right],$$

where m_j is a missing label indicator, z_{ij} is a zero-one indicator variable defining the known group of origin of each, and $f_i(y_j;\omega_i)$ is a probability density function with parameters ω_i.

Value

`lk`	Log-likelihood value.

loglk_miss *Log likelihood function formed on the basis of the missing-label indicator*

Description

Log likelihood for partially classified data based on the missing mechanism with the Shanon entropy

Usage

```
loglk_miss(dat, zm, pi, mu, sigma, ncov = 2, xi)
```

Arguments

dat	An $n \times p$ matrix where each row represents an individual observation
zm	An n-dimensional vector containing the class labels including the missing-label denoted as NA.
pi	A g-dimensional vector for the initial values of the mixing proportions.
mu	A $p \times g$ matrix for the initial values of the location parameters.
sigma	A $p \times p$ covariance matrix if `ncov=1`, or a list of g covariance matrices with dimension $p \times p \times g$ if `ncov=2`.
ncov	Options of structure of sigma matrix; the default value is 2; `ncov` = 1 for a common covariance matrix; `ncov` = 2 for the unequal covariance/scale matrices.
xi	A 2-dimensional vector containing the initial values of the coefficients in the logistic function of the Shannon entropy.

Details

The log-likelihood function formed on the basis of the missing-label indicator can be expressed by

$$\log L_{PC}^{(miss)}(\theta, \boldsymbol{\xi}) = \sum_{j=1}^{n} \left[(1 - m_j) \log \left\{1 - q(y_j; \theta, \boldsymbol{\xi})\right\} + m_j \log q(y_j; \theta, \boldsymbol{\xi})\right],$$

where $q(y_j; \theta, \boldsymbol{\xi})$ is a logistic function of the Shannon entropy $e_j(y_j; \theta)$, and m_j is a missing label indicator.

Value

lk	loglikelihood value

`logsumexp` *log summation of exponential function*

Description

log summation of exponential variable vector.

Usage

```
logsumexp(x)
```

Arguments

`x`	A variable vector.

Value

`val`	log summation of exponential variable vector.

`makelabelmatrix` *Label matrix*

Description

Convert class indicator into a label maxtrix.

Usage

```
makelabelmatrix(clust)
```

Arguments

`clust`	An n-dimensional vector of class partition.

Value

`Z`	A matrix of class indicator.

Examples

```
cluster<-c(1,1,2,2,3,3)
label_maxtrix<-makelabelmatrix(cluster)
```

neg_objective_function

Negative objective function for EMMIXSSL

Description

Negative objective function for EMMIXSSL

Usage

```
neg_objective_function(
  dat,
  zm,
  g,
  par,
  ncov = 2,
  type = c("ign", "full", "com")
)
```

Arguments

dat	An $n \times p$ matrix where each row represents an individual observation
zm	An n-dimensional vector of group partition including the missing-label, denoted as NA.
g	Number of multivariate Gaussian groups.
par	An informative vector including mu, pi,sigma and xi.
ncov	Options of structure of sigma matrix; the default value is 2; ncov = 1 for a common covariance matrix; ncov = 2 for the unequal covariance/scale matrices.
type	Three types to fit to the model, 'ign' indicates fitting the model on the basis of the likelihood that ignores the missing label mechanism, 'full' indicates that the model to be fitted on the basis of the full likelihood, taking into account the missing-label mechanism, and 'com' indicate that the model to be fitted to a completed classified sample.

Value

val	Value of negatvie objective function.

normalise_logprob *Normalize log-probability*

Description

Normalize log-probability.

Usage

```
normalise_logprob(x)
```

Arguments

x	A variable vector.

Value

val	A normalize log probability of variable vector.

par2list *Transfer a vector into a list*

Description

Transfer a vector into a list

Usage

```
par2list(par, g, p, ncov = 2, type = c("ign", "full"))
```

Arguments

par	A vector with list information.
g	Number of multivariate normal classes.
p	Dimension of observation vecor.
ncov	Options of structure of sigma matrix; the default value is 2; ncov = 1 for a common covariance matrix that sigma is a $p \times p$ matrix. ncov = 2 for the unequal covariance/scale matrices that sigma represents a list of g matrices with dimension $p \times p \times g$.
type	Three types to fit to the model, 'ign' indicates fitting the model on the basis of the likelihood that ignores the missing label mechanism, 'full' indicates that the model to be fitted on the basis of the full likelihood, taking into account the missing-label mechanism, and 'com' indicate that the model to be fitted to a completed classified sample.

Value

`parlist` Return a list including `mu`, `pi`, `sigma` and `xi`.

`pro2vec` *Transfer a probability vector into a vector*

Description

Transfer a probability vector into an informative vector

Usage

```
pro2vec(pro)
```

Arguments

`pro` An propability vector

Value

y An informative vector

`rlabel` *Generation of a missing-data indicator*

Description

Generate the missing label indicator

Usage

```
rlabel(dat, pi, mu, sigma, ncov = 2, xi)
```

Arguments

`dat` An $n \times p$ matrix where each row represents an individual observation.

`pi` A g-dimensional vector for the initial values of the mixing proportions.

`mu` A $p \times g$ matrix for the initial values of the location parameters.

`sigma` A $p \times p$ covariance matrix if `ncov=1`, or a list of g covariance matrices with dimension $p \times p \times g$ if `ncov=2`.

`ncov` Options of structure of sigma matrix; the default value is 2; `ncov` = 1 for a common covariance matrix; `ncov` = 2 for the unequal covariance/scale matrices.

`xi` A 2-dimensional coefficient vector for a logistic function of the Shannon entropy.

Value

`m`	A n-dimensional vector of missing label indicator. The element of outputs `m` represents its label indicator is missing if m equals 1, otherwise its label indicator is available if m equals to 0.

Examples

```
n<-150
pi<-c(0.25,0.25,0.25,0.25)
sigma<-array(0,dim=c(3,3,4))
sigma[,,1]<-diag(1,3)
sigma[,,2]<-diag(2,3)
sigma[,,3]<-diag(3,3)
sigma[,,4]<-diag(4,3)
mu<-matrix(c(0.2,0.3,0.4,0.2,0.7,0.6,0.1,0.7,1.6,0.2,1.7,0.6),3,4)
dat<-rmix(n=n,pi=pi,mu=mu,sigma=sigma,ncov=2)
xi<-c(-0.5,1)
m<-rlabel(dat=dat$Y,pi=pi,mu=mu,sigma=sigma,xi=xi,ncov=2)
```

`rmix` *Normal mixture model generator.*

Description

Generate random observations from the normal mixture distributions.

Usage

```
rmix(n, pi, mu, sigma, ncov = 2)
```

Arguments

`n`	Number of observations.
`pi`	A g-dimensional vector for the initial values of the mixing proportions.
`mu`	A $p \times g$ matrix for the initial values of the location parameters.
`sigma`	A $p \times p$ covariance matrix if `ncov=1`, or a list of g covariance matrices with dimension $p \times p \times g$ if `ncov=2`.
`ncov`	Options of structure of sigma matrix; the default value is 2; `ncov` = 1 for a common covariance matrix; `ncov` = 2 for the unequal covariance/scale matrices.

Value

`Y`	An $n \times p$ numeric matrix with samples drawn in rows.
`Z`	An $n \times g$ numeric matrix; each row represents zero-one indicator variables defining the known class of origin of each.
`clust`	An n-dimensional vector of class partition.

Examples

```
n<-150
pi<-c(0.25,0.25,0.25,0.25)
sigma<-array(0,dim=c(3,3,4))
sigma[,,1]<-diag(1,3)
sigma[,,2]<-diag(2,3)
sigma[,,3]<-diag(3,3)
sigma[,,4]<-diag(4,3)
mu<-matrix(c(0.2,0.3,0.4,0.2,0.7,0.6,0.1,0.7,1.6,0.2,1.7,0.6),3,4)
dat<-rmix(n=n,pi=pi,mu=mu,sigma=sigma,ncov=2)
```

---

vec2cov *Transform a vector into a matrix*

Description

Transform a vector into a matrix i.e., Sigma=R^T*R

Usage

```
vec2cov(par)
```

Arguments

`par`	A vector representing a variance matrix

Details

The variance matrix is decomposed by computing the Choleski factorization of a real symmetric positive-definite square matrix. Then, storing the upper triangular factor of the Choleski decomposition into a vector.

Value

sigma A variance matrix

---

vec2pro *Transfer an informative vector to a probability vector*

Description

Transfer an informative vector to a probability vector

Usage

```
vec2pro(vec)
```

Arguments

`vec`	An informative vector

Value

pro A probability vector

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