

Package ‘rrMixture’

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Type Package

Title Reduced-Rank Mixture Models

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Description We implement full-ranked, rank-penalized, and adaptive nuclear norm penalized estimation methods using multivariate mixture models proposed by Kang, Chen, and Yao (2022+).

Depends R ($\geq 3.4.0$)

Imports MASS, Rcpp ($\geq 1.0.8$), Matrix, matrixcalc, gtools, utils

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VignetteBuilder knitr

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| | |
|-----------------|--|
| initialize.para | <i>Initialization of Parameter Estimates</i> |
|-----------------|--|

Description

'initialize.para' is used to initialize parameter estimates.

Usage

```
initialize.para(K, X, Y, ind0 = NULL,
               seed = NULL, km.nstart = 20, kmscale = FALSE, n.init = 100,
               commonvar = FALSE)
```

Arguments

| | |
|-----------|--|
| K | number of mixture components. |
| X | n by p design matrix where n is the number of observations and p is the number of predictors. |
| Y | n by q response matrix where n is the number of observations and q is the number of responses. |
| ind0 | vector of length n, specifying the initial assignment of the mixture membership of n observations when there is prior information on the membership. If 'NULL', K-means clustering technique is used to assign the membership for n observations. Default is 'NULL'. |
| seed | seed number for the reproducibility of results. Default is 'NULL'. |
| km.nstart | number of random sets considered to perform K-means clustering. Only used for K-means clustering. Default is 20. |
| kmscale | logical value, indicating whether Y is scaled prior to K-means clustering. Only used for K-means clustering. Default is 'FALSE'. |
| n.init | number of initializations to try. Two methods for initial clustering are used: K-means and random clustering. |
| commonvar | logical value, indicating the homogeneity assumption of variance-covariance matrices across K mixture components. Default is 'FALSE'. |

Value

| | |
|------|---|
| para | array of length K. It consists of K lists, each of which contains initial estimates of membership probability, coefficient matrix, and variance- covariance matrix. |
|------|---|

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References

Kang, S., Chen, K., and Yao, W. (2022+). "Reduced rank estimation in mixtures of multivariate linear regression".

See Also

[rrmix.sim.norm](#)

Examples

```
#-----#
# Simulation 1: Two Components Case
#-----#
K2mod <- rrmix.sim.norm(K = 2, n = 100, p = 5, q = 5, rho = .5,
  b = 1, shift = 1, r.star = c(1, 3), sigma = c(1, 1),
  pr = c(.5, .5), seed = 1215)
K2ini <- initialize.para(K = 2, X = K2mod$X, Y = K2mod$Y,
  seed = 100)

#-----#
# Simulation 2: Four Components Case
#-----#

K4mod <- rrmix.sim.norm(K = 4, n = 600, p = 15, q = 15,
  rho = .5, b = 1, shift = 1, r.star = c(1, 1, 3, 3),
  sigma = c(1, 1, 1, 1), pr = c(.25, .25, .25, .25),
  seed = 1215)
K4ini <- initialize.para(K = 4, X = K4mod$X, Y = K4mod$Y,
  seed = 100)
```

plot

Visualize rrmix Objects

Description

S3 methods visualizing results for some objects generated by `rrmix` and `tune.rrmix`.

Usage

```
## S3 method for class 'rrmix'
plot(
  x,
  pch.L = 1,
  pch.F = 2,
  col.L = "red",
  col.F = "blue",
  lty.L = 1,
  lty.F = 1,
```

```

    type = "b",
    ...
)

## S3 method for class 'tune.rrmix'
plot(
  x,
  metric = c("bic", "soft.class.err", "hard.class.err", "est.err", "pred.err"),
  col = "blue",
  main = NULL,
  xlab = NULL,
  ylab = NULL,
  swapxy = FALSE,
  transform.x = NULL,
  transform.y = NULL,
  transform.z = NULL,
  color.palette = hsv_palette(),
  nlevels = 20,
  ...
)

```

Arguments

| | |
|--|--|
| <code>x</code> | an object of class <code>rrmix</code> or <code>tune.rrmix</code> . |
| <code>pch.L</code> | symbol to use for displaying log-likelihood. |
| <code>pch.F</code> | symbol to use for displaying penalized log-likelihood. |
| <code>col.L</code> | color code or name for displaying log-likelihood. |
| <code>col.F</code> | color code or name displaying penalized log-likelihood. |
| <code>lty.L</code> | line type for displaying log-likelihood. |
| <code>lty.F</code> | line type for displaying penalized log-likelihood. |
| <code>type</code> | character indicating the type of plotting. |
| <code>...</code> | Other arguments for future usage. |
| <code>metric</code> | performance metric to use for finding best 'rrmix' model. 'soft.class.err', 'hard.class.err', 'est.err', and 'pred.err' can only be used when true parameter values are known. |
| <code>col</code> | the color(s) of the surface facets. Transparent colors are ignored. |
| <code>main</code> | main title. |
| <code>xlab</code> | title for the x-axis. |
| <code>ylab</code> | title for the y-axis. |
| <code>swapxy</code> | if TRUE, the parameter axes are swaped (only used in case of two parameters). |
| <code>transform.x, transform.y, transform.z</code> | functions to transform the parameters (x and y) and the error measures (z). Ignored if NULL. |
| <code>color.palette</code> | color palette used in contour plot. |
| <code>nlevels</code> | number of levels used in contour plot. |

Description

'rrmix' is used to estimate parameters of reduced-rank mixture models in multivariate linear regression using the full-ranked, rank-penalized, and adaptive nuclear norm penalized estimators proposed by Kang et. al. (2022+).

Usage

```
rrmix(K = 2, X, Y, est = c("FR", "RP", "ANNP"),
      lambda = 0, gamma = 2, ind0 = NULL, para0 = NULL, seed = NULL,
      kmscale = FALSE, km.nstart = 20, n.init = 100, commonvar = FALSE,
      maxiter = 1000, maxiter.int = 100, thres = 1e-05, thres.int = 1e-05,
      visible = FALSE, para.true = NULL, ind.true = NULL)
```

Arguments

| | |
|-----------|--|
| K | number of mixture components. |
| X | n by p design matrix where n is the number of observations and p is the number of predictors. |
| Y | n by q response matrix where n is the number of observations and q is the number of responses. |
| est | character, specifying the estimation method. 'FR', 'RP', and 'ANNP' refers to as the full-ranked, rank-penalized, and adaptive nuclear norm penalized method, respectively. |
| lambda | numerical value, specifying tuning parameter. Only used in the estimation method of 'RP' and 'ANNP'. If 0, all estimation methods ('FR', 'RP', and 'ANNP') provide the same estimation results. |
| gamma | numerical value, specifying additional tuning parameter, only used in the estimation method of 'ANNP'. It must be nonnegative. |
| ind0 | vector of length n, specifying the initial assignment of the mixture membership of n observations when there is prior information on the membership. If 'NULL', K-means clustering technique is used to assign the membership for n observations. Default is 'NULL'. |
| para0 | array of length K. It consists of K lists, each of which contains initial values of membership probability, coefficient matrix, and variance-covariance matrix. |
| seed | seed number for the reproducibility of initialization results in the EM algorithm. Default is 'NULL'. |
| kmscale | logical value, indicating whether Y is scaled prior to K-means clustering for initialization. Default is 'FALSE'. |
| km.nstart | number of random sets considered to perform K-means clustering for initialization. Default is 20. |

| | |
|--------------------------|--|
| <code>n.init</code> | number of initializations to try. Two methods for initial clustering are used: K-means and random clustering. |
| <code>commonvar</code> | logical value, indicating the homogeneity assumption of variance-covariance matrices across K mixture components. Default is 'FALSE'. |
| <code>maxiter</code> | maximum number of iterations for external iterative algorithm, used in all estimation methods. |
| <code>maxiter.int</code> | maximum number of iterations for internal iterative algorithm, only used in the estimation method of 'ANNP'. |
| <code>thres</code> | threshold value for external EM algorithm, used in all estimation methods. It controls the termination of the EM algorithm. |
| <code>thres.int</code> | threshold value for internal iterative algorithm, only used in the estimation method of 'ANNP'. It controls the termination of the internal algorithm. |
| <code>visible</code> | logical value, indicating whether the outputs from each iteration are printed. Useful when the whole algorithm takes long. Default is 'FALSE'. |
| <code>para.true</code> | array of length K. It consists of K lists, each of which contains a coefficient matrix and its true rank. Only used when true models are known, e.g., in a simulation study. |
| <code>ind.true</code> | vector of length n, specifying the true mixture membership for n observations. Only used when true models are known, e.g., in a simulation study. |

Value

An object of class `rrmix` containing the fitted model, including:

| | |
|------------------------|--|
| <code>call</code> | original function call. |
| <code>seed</code> | seed number which is set for the initialization. |
| <code>n.est</code> | vector of length K, specifying the estimated number of observations in each mixture components. |
| <code>para</code> | array of length K. It consists of K lists, each of which contains final estimates of membership probability, coefficient matrix, and variance-covariance matrix. |
| <code>est.rank</code> | vector of length K, specifying the estimated ranks of coefficient matrices. |
| <code>npar</code> | number of parameters in the model, used to estimate the BIC. |
| <code>n.iter</code> | number of iterations (external EM algorithm). |
| <code>lambda</code> | tuning parameter for the estimation method of 'RP' or 'ANNP'. |
| <code>gamma</code> | tuning parameter for the estimation method of 'ANNP'. |
| <code>ind</code> | vector of length n, specifying the estimated mixture membership for n observations. |
| <code>ind.true</code> | vector of length n, specifying the true mixture membership for n observations. Only returned when the true models are known. |
| <code>loglik</code> | log-likelihood of the final model. |
| <code>penloglik</code> | penalized log-likelihood of the final model. |
| <code>penalty</code> | penalty in the penalized log-likelihood of the final model. |

| | |
|-------------|---|
| bic | BIC of the final model. |
| avg.nn.iter | average number of iterations for internal iterative algorithm, only returned for the estimation method of 'ANNP'. |
| resmat | matrix containing the information for each iteration of the EM algorithm, e.g., iteration number, log-likelihood, penalized log-likelihood, difference between penalized log-likelihood values from two consecutive iterations, and computing time. |
| class.err | Soft and hard classification errors for mixture membership. Only returned when the true models are known. |
| est.err | estimation error from the comparison between the estimated and true coefficient matrices. Only returned when the true models are known. |
| pred.err | prediction error. Only returned when the true models are known. |

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References

Kang, S., Chen, K., and Yao, W. (2022+). "Reduced rank estimation in mixtures of multivariate linear regression".

See Also

[rrmix.sim.norm](#), [initialize.para](#)

Examples

```
library(rrMixture)

#-----#
# Real Data Example: Tuna Data
#-----#
require(bayesm)
data(tuna)
tunaY <- log(tuna[, c("MOVE1", "MOVE2", "MOVE3", "MOVE4",
                    "MOVE5", "MOVE6", "MOVE7")])
tunaX <- tuna[, c("NSALE1", "NSALE2", "NSALE3", "NSALE4",
                "NSALE5", "NSALE6", "NSALE7",
                "LPRICE1", "LPRICE2", "LPRICE3", "LPRICE4",
                "LPRICE5", "LPRICE6", "LPRICE7")]
tunaX <- cbind(intercept = 1, tunaX)

# Rank-penalized estimation

tuna.rp <- rrmix(K = 2, X = tunaX, Y = tunaY, lambda = 3, est = "RP",
               seed = 100, n.init = 100)
summary(tuna.rp)
plot(tuna.rp)
```

```

# Adaptive nuclear norm penalized estimation

tuna.annp <- rrmix(K = 2, X = tunaX, Y = tunaY, lambda = 3, gamma = 2, est = "ANNP",
                 seed = 100, n.init = 100)
summary(tuna.annp)
plot(tuna.annp)

#-----#
# Simulation: Two Components Case
#-----#
# Simulation Data
K2mod <- rrmix.sim.norm(K = 2, n = 100, p = 5, q = 5, rho = .5,
                      b = 1, shift = 1, r.star = c(1, 3), sigma = c(1, 1),
                      pr = c(.5, .5), seed = 1215)

# Rank-penalized estimation

K2.rp <- rrmix(K = 2, X = K2mod$X, Y = K2mod$Y, lambda = 1,
              seed = 17, est = "RP", ind.true = K2mod$ind.true,
              para.true = K2mod$para.true, n.init = 100)
summary(K2.rp)
plot(K2.rp)

# Adaptive nuclear norm penalized estimation

K2.annp <- rrmix(K = 2, X = K2mod$X, Y = K2mod$Y, lambda = 1,
                seed = 17, est = "ANNP", ind.true = K2mod$ind.true,
                para.true = K2mod$para.true, n.init = 100)
summary(K2.annp)
plot(K2.annp)

```

rrmix.sim.norm

Simulation Data Generator

Description

‘rrmix.sim.norm’ is used to create synthetic data from the multivariate normal distribution, which is used in a numerical study of Kang et. al. (2022+).

Usage

```

rrmix.sim.norm(
  K = 2,
  n = 100,
  p = 5,
  q = 5,
  rho = 0.5,
  b = 1,
  shift = 1,

```



```

    r.star = NULL,
    sigma = NULL,
    pr = NULL,
    seed = NULL
  )

```

Arguments

| | |
|--------|--|
| K | number of mixture components. |
| n | number of observations. |
| p | number of predictors including an intercept. |
| q | number of responses. |
| rho | correlation between predictors used to make a design matrix. |
| b | signal strength which controls the magnitude of coefficient matrices. |
| shift | mean shift which measures how separate the mixture components are. |
| r.star | vector of length K, specifying the true ranks of K coefficient matrices. |
| sigma | vector of length K, specifying the noise strength of K multivariate normal distributions. |
| pr | vector of length K, specifying the multinomial probabilities for the K mixture components. |
| seed | seed number for the reproducibility of results. Default is 'NULL'. |

Value

| | |
|-----------|---|
| X | n by p design matrix. |
| Y | n by q response matrix. |
| E | p by q error matrix. |
| ind.true | vector of length n, specifying the true mixture membership for n observations. |
| para.true | array of length K. It consists of K lists, each of which contains a coefficient matrix and its true rank. |

Author(s)

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References

Kang, S., Chen, K., and Yao, W. (2022+). "Reduced rank estimation in mixtures of multivariate linear regression".

Examples

```

#-----#
# Simulation 1: Two Components Case
#-----#
K2mod <- rrmix.sim.norm(K = 2, n = 100, p = 5, q = 5, rho = .5,
  b = 1, shift = 1, r.star = c(1, 3), sigma = c(1, 1),
  pr = c(.5, .5), seed = 1215)

#-----#
# Simulation 2: Four Components Case
#-----#
K4mod <- rrmix.sim.norm(K = 4, n = 600, p = 15, q = 15,
  rho = .5, b = 1, shift = 1, r.star = c(1, 1, 3, 3),
  sigma = c(1, 1, 1, 1), pr = c(.25, .25, .25, .25),
  seed = 1215)

```

rrMixture

rrMixture: Reduced-Rank Mixture Models.

Description

The rrMixture package provides three important functions currently: rrmix, rrmix.sim.norm, and initialize.para.

summary

Summarize rrmix Objects

Description

S3 methods summarizing objects generated by rrmix and tune.rrmix.

Usage

```

## S3 method for class 'rrmix'
summary(object, ...)

## S3 method for class 'tune.rrmix'
summary(
  object,
  metric = c("bic", "soft.class.err", "hard.class.err", "est.err", "pred.err"),
  ...
)

```

Arguments

| | |
|--------|--|
| object | Object generated from rrmix or tune.rrmix. |
| ... | Other arguments for future usage. |
| metric | performance metric to use for finding best 'rrmix' model. 'soft.class.err', 'hard.class.err', 'est.err', and 'pred.err' can only be used when true parameter values are known. |

| | |
|------------|---|
| tune.rrmix | <i>Reduced-rank mixture models with optimal tuning parameter(s)</i> |
|------------|---|

Description

Reduced-rank mixture models with optimal tuning parameter(s)

Usage

```
tune.rrmix(K = NULL, K.max = NULL, X, Y, est = c("FR", "RP", "ANNP"),
           lambda = NULL, n.lambda = 20, gamma = 2,
           ind0 = NULL, para0 = NULL, seed = NULL, kmscale = FALSE, km.nstart = 20,
           n.init = 100, commonvar = FALSE, maxiter = 1000, maxiter.int = 100,
           thres = 1e-05, thres.int = 1e-05,
           para.true = NULL, ind.true = NULL)
```

Arguments

| | |
|----------|--|
| K | number of mixture components. Required when K.max is 'NULL'. |
| K.max | maximum of mixture components. Default is 'NULL'. When provided, the argument K is ignored. |
| X | n by p design matrix where n is the number of observations and p is the number of predictors. |
| Y | n by q response matrix where n is the number of observations and q is the number of responses. |
| est | character, specifying the estimation method. 'FR', 'RP', and 'ANNP' refers to as the full-ranked, rank-penalized, and adaptive nuclear norm penalized method, respectively. |
| lambda | vector consisting of lambda candidates. Only used in the estimation method of 'RP' and 'ANNP'. If 0, all estimation methods ('FR', 'RP', and 'ANNP') provide the same estimation results. Default is 'NULL'. If 'NULL', data-adaptive range of lambda will be provided internally. |
| n.lambda | number of lambda candidates to explore. Only used when 'lambda' is 'NULL'. Default is 20. |
| gamma | numerical value, specifying additional tuning parameter, only used in the estimation method of 'ANNP'. It must be nonnegative. |

| | |
|--------------------------|---|
| <code>ind0</code> | vector of length n , specifying the initial assignment of the mixture membership of n observations when there is prior information on the membership. If 'NULL', K-means clustering technique is used to assign the membership for n observations. Default is 'NULL'. |
| <code>para0</code> | array of length K . It consists of K lists, each of which contains initial values of membership probability, coefficient matrix, and variance-covariance matrix. |
| <code>seed</code> | seed number for the reproducibility of results. Default of 'NULL'. |
| <code>kmscale</code> | logical value, indicating whether Y is scaled prior to K-means clustering for initialization. Default is 'FALSE'. |
| <code>km.nstart</code> | number of random sets considered to perform K-means clustering for initialization. Default is 20. |
| <code>n.init</code> | number of initializations to try. Two methods for initial clustering are used: K-means and random clustering. |
| <code>commonvar</code> | logical value, indicating the homogeneity assumption of variance-covariance matrices across K mixture components. Default is 'FALSE'. |
| <code>maxiter</code> | maximum number of iterations for external iterative algorithm, used in all estimation methods. |
| <code>maxiter.int</code> | maximum number of iterations for internal iterative algorithm, only used in the estimation method of 'ANNP'. |
| <code>thres</code> | threshold value for external EM algorithm, used in all estimation methods. It controls the termination of the EM algorithm. |
| <code>thres.int</code> | threshold value for internal iterative algorithm, only used in the estimation method of 'ANNP'. It controls the termination of the internal algorithm. |
| <code>para.true</code> | array of length K . It consists of K lists, each of which contains a coefficient matrix and its true rank. Only used when true models are known, e.g., in a simulation study. |
| <code>ind.true</code> | vector of length n , specifying the true mixture membership for n observations. Only used when true models are known, e.g., in a simulation study. |

Value

| | |
|--------------------------|--|
| <code>lambda.cand</code> | lambda values used as input. |
| <code>penloglik</code> | penalized log-likelihood values corresponding to the set of lambda values. |
| <code>bic</code> | BIC values corresponding to the set of lambda values. |
| <code>est.rank</code> | estimated ranks corresponding to the set of lambda values. |

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References

Kang, S., Chen, K., and Yao, W. (2022+). "Reduced rank estimation in mixtures of multivariate linear regression".

See Also[rrmix](#)**Examples**

```
#-----#
# Real Data Example: Tuna Data
#-----#
require(bayesm)
data(tuna)
tunaY <- log(tuna[, c("MOVE1", "MOVE2", "MOVE3", "MOVE4",
                    "MOVE5", "MOVE6", "MOVE7")])
tunaX <- tuna[, c("NSALE1", "NSALE2", "NSALE3", "NSALE4",
                "NSALE5", "NSALE6", "NSALE7",
                "LPRICE1", "LPRICE2", "LPRICE3", "LPRICE4",
                "LPRICE5", "LPRICE6", "LPRICE7")]
tunaX <- cbind(intercept = 1, tunaX)

tuna.tune <- tune.rrmix(K.max = 3, X = tunaX, Y = tunaY, est = "RP",
                      lambda = exp(seq(0, log(100), length = 20)),
                      seed = 100, n.init = 100)
summary(tuna.tune)
plot(tuna.tune, transform.y = log, ylab = "log(lambda)")
```

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