Package ‘MixMatrix’

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Type Package

Title Classification with Matrix Variate Normal and t Distributions

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variate normal, t, and inverted t distributions; ML estimation for matrix
variate normal and t distributions using the EM algorithm,
including some restrictions on the parameters; and classification by linear and
quadratic discriminant analysis for matrix variate normal and t

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**Description**

generate AR(1) correlation matrices

**Usage**

```r
ARgenerate(n, rho)
```

**Arguments**

- `n` number of columns/rows
- `rho` correlation parameter

**Value**

Toeplitz $n \times n$ matrix with 1 on the diagonal and $rho^k$ on the other diagonals, where $k$ is distance from the main diagonal. Used internally but it is useful for generating your own random matrices.

**See Also**

- `stats::toeplitz()`

**Examples**

```r
ARgenerate(6, .9)
```
CSgenerate

*Generate a compound symmetric correlation matrix*

**Description**

Generate a compound symmetric correlation matrix

**Usage**

CSgenerate(n, rho)

**Arguments**

- **n**: number of dimensions
- **rho**: off-diagonal element - a correlation between -1 and 1. Will warn if less than 0.

**Value**

returns an \( n \times n \) matrix with 1 on the diagonal and \( \rho \) on the off-diagonal.

**Examples**

# generates a covariance matrix with 1 on the main diagonal
# and 0.5 on the off-diagonal elements.
CSgenerate(3, .5)

init_matrixmixture

*Initializing settings for Matrix Mixture Models*

**Description**

Providing this will generate a list suitable for use as the init argument in the matrixmixture function. Either provide data and it will select centers and variance matrices to initialize or provide initial values and it will format them as expected for the function.

**Usage**

init_matrixmixture(
  data,
  prior = NULL,
  K = length(prior),
  centers = NULL,
  U = NULL,
  V = NULL,
  centermethod = "kmeans",
  varmethod = "identity",
)
model = "normal",
init = NULL,
...
)

Arguments

data data, \( p \times q \times n \) array
prior prior probability. One of prior and \( K \) must be provided. They must be consistent if both provided.
\( K \) number of groups
centers (optional) either a matrix or an array of \( p \times p \) matrices for use as the centers argument. If fewer than \( K \) are provided, the remainder are chosen by centermethod.
\( U \) (optional) either a matrix or an array of \( p \times p \) matrices for use as the \( U \) argument. If a matrix is provided, it is duplicated to provide an array. If an array is provided, it should have \( K \) slices.
\( V \) (optional) either a matrix or an array of matrices for use as the \( V \) argument. If a matrix is provided, it is duplicated to provide an array. If an array is provided, it should have \( K \) slices.
centermethod what method to use to generate initial centers. Currently support random start (random) or performing k-means (kmeans) on the vectorized version for a small number of iterations and then converting back. By default, if \( K \) centers are provided, nothing will be done.
varmethod what method to use to choose initial variance matrices. Currently only identity matrices are created. By default, if \( U \) and \( V \) matrices are provided, nothing will be done.
model whether to use a normal distribution or a t-distribution, not relevant for more initialization methods.
init (optional) a (possibly partially-formed) list with some of the components centers, \( U \), and \( V \). The function will complete the list and fill out missing entries.
... Additional arguments to pass to \texttt{kmeans()} if that is centermethod.

Value

a list suitable to use as the \texttt{init} argument in \texttt{matrixmixture}:

\texttt{centers} the group means, a \( p \times q \times K \) array.
\texttt{\( U \)} the between-row covariance matrices, a \( p \times p \times K \) array
\texttt{\( V \)} the between-column covariance matrix, a \( q \times q \times K \) array

See Also

\texttt{matrixmixture()}
Examples

```r
set.seed(20180221)
A <- rmatrixt(30, mean = matrix(0, nrow=3, ncol=4), df = 10)
# 3x4 matrices with mean 0
B <- rmatrixt(30, mean = matrix(2, nrow=3, ncol=4), df = 10)
# 3x4 matrices with mean 2
C <- array(c(A,B), dim = c(3,4,60)) # combine into one array
prior <- c(.5,.5) # equal probability prior
init = init_matrixmixture(C, prior = prior)
# will find two centers using the "kmeans" method on the vectorized matrices
```

---

**matrixlda**  
*LDA for matrix variate distributions*

**Description**

Performs linear discriminant analysis on matrix variate data. This works slightly differently from the LDA function in MASS: it does not sphere the data or otherwise normalize it. It presumes equal variance matrices and probabilities are given as if the data are from a matrix variate normal distribution. The estimated variance matrices are weighted by the prior. However, if there are not enough members of a class to estimate a variance, this may be a problem. The function does not take the formula interface. If `method = 't'` is selected, this performs discrimination using the matrix variate t distribution, presuming equal covariances between classes.

**Usage**

```r
matrixlda(
  x,
  grouping,
  prior,
  tol = 1e-04,
  method = "normal",
  nu = 10,
  ...
)
```

**Arguments**

- `x`  
  3-D array of matrix data indexed by the third dimension
- `grouping`  
  a vector of prior probabilities of the same length as the number of classes
- `prior`  
  by default, `1e-4`. Tolerance parameter checks for 0 variance.
- `method`  
  whether to use the normal distribution (normal) or the t distribution (t). By default, normal.
- `nu`  
  If using the t-distribution, the degrees of freedom parameter. By default, 10.
Arguments passed to or from other methods, such as additional parameters to pass to MLmatrixnorm (e.g., row.mean)

subset  An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)

Value

Returns a list of class matrixlda containing the following components:

- prior  the prior probabilities used.
- counts  the counts of group membership
- means  the group means.
- scaling  the scalar variance parameter
- U  the between-row covariance matrix
- V  the between-column covariance matrix
- lev  levels of the grouping factor
- N  The number of observations used.
- method  The method used.
- nu  The degrees of freedom parameter if the t distribution was used.
- call  The (matched) function call.

References


See Also

predict.matrixlda(), MASS::lda(), MLmatrixnorm() and MLmatrixt() matrixlda(), and matrixmixture()

Examples

set.seed(20180221)
# construct two populations of 3x4 random matrices with different means
A <- rmatrixnorm(30, mean = matrix(0, nrow = 3, ncol = 4))
B <- rmatrixnorm(30, mean = matrix(1, nrow = 3, ncol = 4))
C <- array(c(A, B), dim = c(3, 4, 60)) # combine together
groups <- c(rep(1, 30), rep(2, 30)) # define groups
prior <- c(.5, .5) # set prior
D <- matrixlda(C, groups, prior) # fit model
logLik(D)
print(D)

matrixmixture

Fit a matrix variate mixture model

Description
Clustering by fitting a mixture model using EM with K groups and unconstrained covariance matrices for a matrix variate normal or matrix variate t distribution (with specified degrees of freedom nu).

Usage

matrixmixture(
  x,
  init = NULL,
  prior = NULL,
  K = length(prior),
  iter = 1000,
  model = "normal",
  method = NULL,
  row.mean = FALSE,
  col.mean = FALSE,
  tolerance = 0.1,
  nu = NULL,
  ..., 
  verbose = 0,
  miniter = 5,
  convergence = TRUE
)

Arguments

x data, p \times q \times n array
init a list containing an array of K of p \times q means labeled centers, and optionally p \times p and q \times q positive definite variance matrices labeled U and V. By default, those are presumed to be identity if not provided. If init is missing, it will be provided using the prior or K by init_matrixmix.
prior prior for the K classes, a vector that adds to unity
K number of classes - provide either this or the prior. If this is provided, the prior will be of uniform distribution among the classes.
iter maximum number of iterations.
model: whether to use the normal or t distribution.

method: what method to use to fit the distribution. Currently no options.

row.mean: By default, FALSE. If TRUE, will fit a common mean within each row. If both this and col.mean are TRUE, there will be a common mean for the entire matrix.

col.mean: By default, FALSE. If TRUE, will fit a common mean within each row. If both this and row.mean are TRUE, there will be a common mean for the entire matrix.

tolerance: convergence criterion, using Aitken acceleration of the log-likelihood by default.

nu: degrees of freedom parameter. Can be a vector of length K.

...: pass additional arguments to MLmatrixnorm or MLmatrixt

verbose: whether to print diagnostic output, by default 0. Higher numbers output more results.

miniter: minimum number of iterations

convergence: By default, TRUE, using Aitken acceleration to determine convergence. If false, it instead checks if the change in log-likelihood is less than tolerance. Aitken acceleration may prematurely end in the first few steps, so you may wish to set miniter or select FALSE if this is an issue.

Value

A list of class MixMatrixModel containing the following components:

prior: the prior probabilities used.

init: the initialization used.

K: the number of groups

N: the number of observations

centers: the group means.

U: the between-row covariance matrices

V: the between-column covariance matrix

posterior: the posterior probabilities for each observation

pi: the final proportions

nu: The degrees of freedom parameter if the t distribution was used.

convergence: whether the model converged

logLik: a vector of the log-likelihoods of each iteration ending in the final log-likelihood of the model

model: the model used

method: the method used

call: The (matched) function call.
References


See Also

init_matrixmixture()

Examples

set.seed(20180221)
A <- rmatrixt(20, mean=matrix(0,nrow=3,ncol=4), df = 5)
# 3x4 matrices with mean 0
B <- rmatrixt(20, mean=matrix(1,nrow=3,ncol=4), df = 5)
# 3x4 matrices with mean 1
C <- array(c(A,B), dim=c(3,4,40)) # combine into one array
prior <- c(.5,.5) # equal probability prior
# create an initialization object, starts at the true parameters
init = list(centers = array(c(rep(0,12),rep(1,12)), dim = c(3,4,2)),
          U = array(c(diag(3), diag(3)), dim = c(3,3,2))*20,
          V = array(c(diag(4), diag(4)), dim = c(4,4,2))
)
# fit model
res<-matrixmixture(C, init = init, prior = prior, nu = 5,
                    model = "t", tolerance = 1e-3, convergence = FALSE)
print(res$centers) # the final centers
print(res$pi) # the final mixing proportion
plot(res) # the log likelihood by iteration
logLik(res) # log likelihood of final result
BIC(res) # BIC of final result
predict(res, newdata = C[,,c(1,21)]) # predicted class membership
**matrixqda**

*Quadratic Discriminant Analysis for Matrix Variate Observations*

Description

See matrixlda: quadratic discriminant analysis for matrix variate observations.

Usage

```r
matrixqda(
  x,
  grouping,
  prior,
  tol = 1e-04,
  method = "normal",
  nu = 10,
  ...
)
```

Arguments

- **x**: 3-D array of matrix data indexed by the third dimension
- **grouping**: vector
- **prior**: a vector of prior probabilities of the same length as the number of classes
- **tol**: by default, 1e-4. Tolerance parameter checks for 0 variance.
- **method**: whether to use the normal distribution (normal) or the t distribution (t). By default, normal.
- **nu**: If using the t-distribution, the degrees of freedom parameter. By default, 10.
- **...**: Arguments passed to or from other methods, such as additional parameters to pass to MLmatrixnorm (e.g., row.mean)
- **subset**: An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)

Details

This uses MLmatrixnorm or MLmatrixt to find the means and variances for the case when different groups have different variances.

Value

Returns a list of class matrixqda containing the following components:

- **prior**: the prior probabilities used.
- **counts**: the counts of group membership
means the group means.
U the between-row covariance matrices
V the between-column covariance matrices
lev levels of the grouping factor
N The number of observations used.
method The method used.
u The degrees of freedom parameter if the t-distribution was used.
call The (matched) function call.

References
G Z Thompson, R Maitra, W Q Meeker, A Bastawros (2019),
"Classification with the matrix-variate-t distribution", arXiv
Pierre Dutilleul. The MLE algorithm for the matrix normal distribution.

See Also
predict.matrixqda(), MASS::qda(), MLmatrixnorm(), MLmatrixt(), matrixlda(), and matrixmixture()

Examples
set.seed(20180221)
# construct two populations of 3x4 random matrices with different means
A <- rmatrixnorm(30, mean = matrix(0, nrow = 3, ncol = 4))
B <- rmatrixnorm(30, mean = matrix(1, nrow = 3, ncol = 4))
C <- array(c(A, B), dim = c(3, 4, 60)) # combine together
groups <- c(rep(1, 30), rep(2, 30)) # define groups
prior <- c(.5, .5) # set prior
D <- matrixqda(C, groups, prior)
logLik(D)
print(D)

MixMatrix Classification with Matrix Variate Normal and t Distributions

Description
Provides sampling and density functions for matrix variate normal, t, and inverted t distributions;
ML estimation for matrix variate normal and t distributions using the EM algorithm, including some
restrictions on the parameters; and classification by linear and quadratic discriminant analysis for
matrix variate normal and t distributions described in Thompson et al. (2019). Performs clustering
with matrix variate normal and t mixture models.
Maximum likelihood estimation for matrix normal distributions

Description

Maximum likelihood estimates exist for \( N > \max(p/q, q/p) + 1 \) and are unique for \( N > \max(p, q) \). This finds the estimate for the mean and then alternates between estimates for the \( U \) and \( V \) matrices until convergence. An AR(1), compound symmetry, correlation matrix, or independence restriction can be proposed for either or both variance matrices. However, if they are inappropriate for the data, they may fail with a warning.

Usage

```r
MLmatrixnorm(
  data,
  row.mean = FALSE,
  col.mean = FALSE,
  row.variance = "none",
  col.variance = "none",
  tol = 10 * .Machine$double.eps^0.5,
  max.iter = 100,
  U,
  V,
  ...
)
```

Arguments

data Either a list of matrices or a 3-D array with matrices in dimensions 1 and 2, indexed by dimension 3.
row.mean By default, FALSE. If TRUE, will fit a common mean within each row. If both this and col.mean are TRUE, there will be a common mean for the entire matrix.
col.mean By default, FALSE. If TRUE, will fit a common mean within each row. If both this and row.mean are TRUE, there will be a common mean for the entire matrix.
row.variance Imposes a variance structure on the rows. Either 'none', 'AR(1)', 'CS' for 'compound symmetry', 'Correlation' for a correlation matrix, or 'Independence' for independent and identical variance across the rows. Only positive correlations are allowed for AR(1) and CS covariances. Note that while maximum likelihood estimators are available (and used) for the unconstrained variance matrices, optim is used for any constraints so it may be considerably slower.
col.variance Imposes a variance structure on the columns. Either 'none', 'AR(1)', 'CS', 'Correlation', or 'Independence'. Only positive correlations are allowed for AR(1) and CS.
tol Convergence criterion. Measured against square deviation between iterations of the two variance-covariance matrices.
max.iter Maximum possible iterations of the algorithm.
U (optional) Can provide a starting point for the U matrix. By default, an identity matrix.
V (optional) Can provide a starting point for the V matrix. By default, an identity matrix.
... (optional) additional arguments can be passed to optim if using restrictions on the variance.

Value

Returns a list with the following elements:

mean the mean matrix
scaling the scalar variance parameter (the first entry of the covariances are restricted to unity)
U the between-row covariance matrix
V the between-column covariance matrix
iter the number of iterations
tol the squared difference between iterations of the variance matrices at the time of stopping
logLik vector of log likelihoods at each iteration.
convergence a convergence flag, TRUE if converged.
call The (matched) function call.

References


See Also

rmatrixnorm() and MLmatrixt()

Examples

set.seed(20180202)
# simulating from a given density
A <- rmatrixnorm(
  n = 100, mean = matrix(c(100, 0, -100, 0, 25, -1000), nrow = 2),
  L = matrix(c(2, 1, 0, .1), nrow = 2), list = TRUE
)
# finding the parameters by ML estimation
results <- MLmatrixnorm(A, tol = 1e-5)
print(results)
Maximum likelihood estimation for matrix variate t distributions

Description

For the matrix variate normal distribution, maximum likelihood estimates exist for \( N > \max(p/q, q/p) + 1 \) and are unique for \( N > \max(p, q) \). The number necessary for the matrix variate t has not been worked out but this is a lower bound. This implements an ECME algorithm to estimate the mean, covariance, and degrees of freedom parameters. An AR(1), compound symmetry, or independence restriction can be proposed for either or both variance matrices. However, if they are inappropriate for the data, they may fail with a warning.

Usage

```r
MLmatrixt(data, row.mean = FALSE, col.mean = FALSE, row.variance = "none", col.variance = "none", df = 10, fixed = TRUE, tol = .Machine$double.eps^0.5, max.iter = 5000, U, V, ...)
```

Arguments

data Either a list of matrices or a 3-D array with matrices in dimensions 1 and 2, indexed by dimension 3.

row.mean By default, FALSE. If TRUE, will fit a common mean within each row. If both this and col.mean are TRUE, there will be a common mean for the entire matrix.

col.mean By default, FALSE. If TRUE, will fit a common mean within each row. If both this and row.mean are TRUE, there will be a common mean for the entire matrix.

row.variance Imposes a variance structure on the rows. Either ‘none’, ‘AR(1)’, ‘CS’ for ‘compound symmetry’, ‘Correlation’ for a correlation matrix, or ‘Independence’ for independent and identical variance across the rows. Only positive correlations are allowed for AR(1) and CS and these restrictions may not be guaranteed to converge. Note that while maximum likelihood estimators are available (and used) for the unconstrained variance matrices, optim is used for any constraints so it may be considerably slower.
col.variance  Imposes a variance structure on the columns. Either 'none', 'AR(1)', 'CS', 'Correlation', or 'Independence'. Only positive correlations are allowed for AR(1) and CS.
df  Starting value for the degrees of freedom. If fixed = TRUE, then this is required and not updated. By default, set to 10.
fixed  Whether df is estimated or fixed. By default, TRUE.
tol  Convergence criterion. Measured against square deviation between iterations of the two variance-covariance matrices.
max.iter  Maximum possible iterations of the algorithm.
U  (optional) Can provide a starting point for the U matrix. By default, an identity matrix.
V  (optional) Can provide a starting point for the V matrix. By default, an identity matrix.
...  (optional) additional arguments can be passed to optim if using restrictions on the variance.

Value

Returns a list with the following elements:

mean  the mean matrix
U  the between-row covariance matrix
V  the between-column covariance matrix
var  the scalar variance parameter (the first entry of the covariances are restricted to unity)
nu  the degrees of freedom parameter
iter  the number of iterations
tol  the squared difference between iterations of the variance matrices at the time of stopping
logLik  log likelihood of result.
convergence  a convergence flag, TRUE if converged.
call  The (matched) function call.

References


See Also
rmatrixnorm(), rmatrixt(), MLmatrixnorm()

Examples
set.seed(20180202)
# drawing from a distribution with specified mean and covariance
A <- rmatrixt(
  n = 100, mean = matrix(c(100, 0, -100, 0, 25, -1000), nrow = 2),
  L = matrix(c(2, 1, 0, .1), nrow = 2), list = TRUE, df = 5
)
# fitting maximum likelihood estimates
results <- MLmatrixt(A, tol = 1e-5, df = 5)
print(results)

predict.matrixlda  Classify Matrix Variate Observations by Linear Discrimination

Description
Classify matrix variate observations in conjunction with matrixlda.

Usage
## S3 method for class 'matrixlda'
predict(object, newdata, prior = object$prior, ...)

Arguments
object object of class matrixlda
newdata array or list of new observations to be classified. If newdata is missing, an attempt will be made to retrieve the data used to fit the matrixlda object.
prior The prior probabilities of the classes, by default the proportions in the training set or what was set in the call to matrixlda.
... arguments based from or to other methods
This function is a method for the generic function predict() for class "matrixlda". It can be invoked by calling predict(x) for an object x of the appropriate class.

Returns a list containing the following components:

- class: The MAP classification (a factor)
- posterior: posterior probabilities for the classes

See Also

matrixlda(), matrixqda(), and matrixmixture()

Examples

```r
set.seed(20180221)
# construct two populations of 3x4 random matrices with different means
A <- rmatrixnorm(30, mean = matrix(0, nrow = 3, ncol = 4))
B <- rmatrixnorm(30, mean = matrix(1, nrow = 3, ncol = 4))
C <- array(c(A, B), dim = c(3, 4, 60)) # combine together
groups <- c(rep(1, 30), rep(2, 30)) # define groups
prior <- c(.5, .5) # set prior
D <- matrixlda(C, groups, prior)
predict(D)$posterior[1:10, ]
```

Classify matrix variate observations in conjunction with matrixqda.

## S3 method for class 'matrixlda'

```r
# S3 method for class 'matrixlda'
predict(object, newdata, prior = object$prior, ...)
```

**Arguments**

- **object**: object of class matrixlda
- **newdata**: array or list of new observations to be classified. If newdata is missing, an attempt will be made to retrieve the data used to fit the matrixlda object.
- **prior**: The prior probabilities of the classes, by default the proportions in the training set or what was set in the call to matrixqda.
- **...**: arguments based from or to other methods
Details

This function is a method for the generic function `predict()` for class "matrixqda". It can be invoked by calling `predict(x)` for an object `x` of the appropriate class.

Value

Returns a list containing the following components:

- **class**: The MAP classification (a factor)
- **posterior**: posterior probabilities for the classes

See Also

`matrixlda()`, `matrixqda()`, and `matrixmixture()`

Examples

```r
set.seed(20180221)
# construct two populations of 3x4 random matrices with different means
A <- rmatrixnorm(30, mean = matrix(0, nrow = 3, ncol = 4))
B <- rmatrixnorm(30, mean = matrix(1, nrow = 3, ncol = 4))
C <- array(c(A, B), dim = c(3, 4, 60)) # combine together
groups <- c(rep(1, 30), rep(2, 30)) # define groups
prior <- c(.5, .5) # set prior
D <- matrixqda(C, groups, prior) # fit model
predict(D)$posterior[1:10, ] # predict, show results of first 10
```

---

**rmatrixinvt**

*Distribution functions for matrix variate inverted t distributions*

Description

Generate random samples from the inverted matrix variate t distribution or compute densities.

Usage

```r
rmatrixinvt(
  n,
  df,
  mean,
  L = diag(dim(as.matrix(mean)))[1],
  R = diag(dim(as.matrix(mean)))[2],
  U = L %*% t(L),
  V = t(R) %*% R,
  list = FALSE,
  array = NULL
)```


rmatrixinvt

```r
rmatrixinvt(x, df, mean = matrix(0, p, n), L = diag(p),
R = diag(n), U = L %*% t(L),
V = t(R) %*% R,
log = FALSE)
```

Arguments

- **n** number of observations for generation
- **df** degrees of freedom (> 0, may be non-integer), df = 0, Inf is allowed and will return a normal distribution.
- **mean** $p \times q$ This is really a ‘shift’ rather than a mean, though the expected value will be equal to this if $df > 2$
- **L** $p \times p$ matrix specifying relations among the rows. By default, an identity matrix.
- **R** $q \times q$ matrix specifying relations among the columns. By default, an identity matrix.
- **U** $L L^T - p \times p$ positive definite matrix for rows, computed from $L$ if not specified.
- **V** $R^T R - q \times q$ positive definite matrix for columns, computed from $R$ if not specified.
- **list** Defaults to FALSE. If this is TRUE, then the output will be a list of matrices.
- **array** If $n = 1$ and this is not specified and list is FALSE, the function will return a matrix containing the one observation. If $n > 1$, should be the opposite of list. If list is TRUE, this will be ignored.
- **x** quantile for density
- **log** logical; in dmatrixinvt, if TRUE, probabilities p are given as log(p).

Value

- **rmatrixinvt** returns either a list of $n p \times q$ matrices or a $p \times q \times n$ array.
- **dmatrixinvt** returns the density at x.

References


See Also

`rmatrixnorm()`, `rmatrixt()`, and `stats::Distributions()`.

Examples

```r
# an example of drawing from the distribution and computing the density.
A <- rmatrixinv(n = 2, df = 10, diag(4))
dmatrixinv(A[, , 1], df = 10, mean = diag(4))
```

Description

Density and random generation for the matrix variate normal distribution

Usage

```r
rmatrixnorm(
  n,
  mean,
  L = diag(dim(as.matrix(mean))[[1]]),
  R = diag(dim(as.matrix(mean))[[2]]),
  U = L %% t(L),
  V = t(R) %% R,
  list = FALSE,
  array = NULL,
  force = FALSE
)
```

```r
dmatrixnorm(
  x,
  mean = matrix(0, p, n),
  L = diag(p),
  R = diag(n),
  U = L %% t(L),
  V = t(R) %% R,
  log = FALSE
)
```

Arguments

- `n` number of observations to generate - must be a positive integer.
- `mean` `p × q` matrix of means
- `L` `p × p` matrix specifying relations among the rows. By default, an identity matrix.
- `R` `q × q` matrix specifying relations among the columns. By default, an identity matrix.
**U**

$LL^T$ - $p \times p$ positive definite variance-covariance matrix for rows, computed
from $L$ if not specified.

**V**

$R^T R$ - $q \times q$ positive definite variance-covariance matrix for columns, computed
from $R$ if not specified.

**list**

Defaults to FALSE. If this is TRUE, then the output will be a list of matrices.

**array**

If $n = 1$ and this is not specified and list is FALSE, the function will return a
matrix containing the one observation. If $n > 1$, should be the opposite of list.
If list is TRUE, this will be ignores.

**force**

If TRUE, will take the input of $L$ and/or $R$ directly - otherwise computes $U$ and
$V$ and uses Cholesky decompositions. Useful for generating degenerate normal
distributions. Will also override concerns about potentially singular matrices
unless they are not, in fact, invertible.

**x**

quantile for density

**log**

logical; if TRUE, probabilities p are given as log(p).

**Value**

`rmatrixnorm` returns either a list of $n \times p \times q$ matrices or a $p \times q \times n$ array.

`dmatrixnorm` returns the density at x.

**References**

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**See Also**

`rmatrixt()`, `rmatrixinvt()`, `rnorm()` and `stats::Distributions()`

**Examples**

```r
set.seed(20180202)
# a draw from a matrix variate normal with a certain mean
# and row-wise covariance
rmatrixnorm(
  n = 1, mean = matrix(c(100, 0, -100, 0, 25, -1000), nrow = 2),
  L = matrix(c(2, 1, 0, .1), nrow = 2), list = FALSE
)
set.seed(20180202)
# another way of specifying this - note the output is equivalent
A <- rmatrixnorm(
  n = 10, mean = matrix(c(100, 0, -100, 0, 25, -1000), nrow = 2),
  L = matrix(c(2, 1, 0, .1), nrow = 2), list = TRUE
)
A[[1]]
# demonstrating the dmatrixnorm function
dmatrixnorm(A[[1]],
  mean = matrix(c(100, 0, -100, 0, 25, -1000), nrow = 2),
  L = matrix(c(2, 1, 0, .1), nrow = 2), log = TRUE
)
```
rmatrixt

Distribution functions for the matrix variate t distribution.

Description
Density and random generation for the matrix variate t distribution.

Usage

```r
rmatrixt(
  n,
  df,
  mean,
  L = diag(dim(as.matrix(mean)))[1],
  R = diag(dim(as.matrix(mean)))[2],
  U = L %*% t(L),
  V = t(R) %*% R,
  list = FALSE,
  array = NULL,
  force = FALSE
)
```

```r
dmatrixt(
  x,
  df,
  mean = matrix(0, p, n),
  L = diag(p),
  R = diag(n),
  U = L %*% t(L),
  V = t(R) %*% R,
  log = FALSE
)
```

Arguments

- **n**: number of observations for generation
- **df**: degrees of freedom (> 0, may be non-integer), df = 0, Inf is allowed and will return a normal distribution.
- **mean**: \( p \times q \) This is really a 'shift' rather than a mean, though the expected value will be equal to this if \( df > 2 \)
- **L**: \( p \times p \) matrix specifying relations among the rows. By default, an identity matrix.
- **R**: \( q \times q \) matrix specifying relations among the columns. By default, an identity matrix.
- **U**: \( L L^T \) \( p \times p \) positive definite matrix for rows, computed from \( L \) if not specified.
- **V**: \( R^T R \) \( q \times q \) positive definite matrix for columns, computed from \( R \) if not specified.
**rmatrinx**

list Defaults to FALSE. If this is TRUE, then the output will be a list of matrices.

array If \( n = 1 \) and this is not specified and list is FALSE, the function will return a matrix containing the one observation. If \( n > 1 \), should be the opposite of list. If list is TRUE, this will be ignored.

force In rmatrix: if TRUE, will take the input of R directly - otherwise uses V and uses Cholesky decompositions. Useful for generating degenerate t-distributions. Will also override concerns about potentially singular matrices unless they are not, in fact, invertible.

x quantile for density

log logical; in dmatrixt, if TRUE, probabilities p are given as \( \log(p) \).

**Details**

The matrix \( t \)-distribution is parameterized slightly differently from the univariate and multivariate \( t \)-distributions

- the variance is scaled by a factor of \( 1/df \). In this parameterization, the variance for a \( 1 \times 1 \) matrix variate \( t \)-distributed random variable with identity variance matrices is \( 1/(df - 2) \) instead of \( df/(df - 2) \). A Central Limit Theorem for the matrix variate \( T \) is then that as \( df \) goes to infinity, \( MV T(0, df, I_p, df * I_q) \) converges to \( MV N(0, I_p, I_q) \).

**Value**

rmatrinx returns either a list of \( n \times p \times q \) matrices or a \( p \times q \times n \) array.

dmatrinx returns the density at \( x \).

**References**


**See Also**

rmatrinxnorm(), rmatrixinv(), rt() and stats::Distributions().

**Examples**

```r
set.seed(20180202)
# random matrix with df = 10 and the given mean and L matrix
rmatrinx(
  n = 1, df = 10, mean = matrix(c(100, 0, -100, 0, 25, -1000), nrow = 2),
  L = matrix(c(2, 1, 0, .1), nrow = 2), list = FALSE
)
# comparing 1-D distribution of t to matrix
summary(rt(n = 100, df = 10))
summary(rmatrinx(n = 100, df = 10, matrix(0)))
```
# demonstrating equivalence of 1x1 matrix t to usual t
set.seed(20180204)
x <- rmatrixt(n = 1, mean = matrix(0), df = 1)
dt(x, 1)
dmatrixt(x, df = 1)
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