

Package ‘matrixNormal’

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Title The Matrix Normal Distribution

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1.0), rmarkdown, roxygen2, spelling, testthat

Description Computes densities, probabilities, and random deviates of the Matrix Normal (Iranmanesh et al. (2010) <doi:10.7508/ijmsi.2010.02.004>). Also includes simple but useful matrix functions. See the vignette for more information.

License GPL-3

Encoding UTF-8

LazyData true

BugReports <https://github.com/phargarten2/matrixNormal/issues>

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R topics documented:

is.symmetric.matrix	2
matrixNormal_Distribution	4

special.matrix	6
tr	7
vec	8

Index	9
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is.symmetric.matrix	<i>Is a matrix symmetric or positive-definite?</i>
---------------------	--

Description

Determine if a matrix is square, symmetric, positive-definite, or positive-semi-definite.

Usage

```
is.square.matrix(A)
```

```
is.symmetric.matrix(A, tol = .Machine$double.eps^0.5)
```

```
is.positive.semi.definite(A, tol = .Machine$double.eps^0.5)
```

```
is.positive.definite(A, tol = .Machine$double.eps^0.5)
```

Arguments

A	A numeric matrix.
tol	A numeric tolerance level used to check if a matrix is symmetric; that is if the difference between the matrix and its transpose is between -tol and tol.

Details

A tolerance is added to indicate if a matrix is approximately symmetric. If the matrix is not symmetric, a message as well as the top of the matrix is printed.

- `is.symmetric.matrix` returns TRUE if A is a symmetric square numeric matrix and FALSE otherwise. A matrix is symmetric if the difference between A and its transpose is less than *tol*. If A has any missing values, `is.symmetric.matrix` returns NA.
- `is.positive.semi.definite` returns TRUE if a square symmetric real matrix A is positive semi-definite. A matrix is positive semi-definite if its smallest eigenvalue is greater than or equal to zero. If A has any missing values, `is.symmetric.matrix` returns NA.
- `is.positive.definite` returns TRUE if a square symmetric real matrix A is positive-definite. A matrix is positive-definite if its smallest eigenvalue is greater than zero. If A has any missing values, `is.symmetric.matrix` returns NA.

Note

Functions adapted from Frederick Novomestky's **matrixcalc** package in order to implement `rmatnorm` function. I changed argument `x` to `A` to reflect usual matrix notation. For `is.symmetric`, I added a tolerance so that `A` is symmetric even provided small differences between `A` and its transpose. Useful for `rmatnorm` function, which was used repeatedly to generate `matrixNormal` random variates in a Markov chain. For `is.positive.semi.definite` and `is.positive.definite`, I also saved time by avoiding a `$for-loop$` and instead calculating the minimum of eigenvalues.

Examples

```
## Example 0: Not square matrix
B <- matrix(c(1, 2, 3, 4, 5, 6), nrow = 2, byrow = TRUE)
B
is.square.matrix(B)

## Example 1: Not a matrix. should get an error.
df <- as.data.frame(matrix(c(1, 2, 3, 4, 5, 6), nrow = 2, byrow = TRUE))
df
## Not run:
is.square.matrix(df)

## End(Not run)

## Example 2: Not Symmetric & Compare against matrixcalc
F <- matrix(c(1, 2, 3, 4), nrow = 2, byrow = TRUE); F
is.square.matrix(F)
is.symmetric.matrix(F) # should be FALSE
if (!requireNamespace("matrixcalc", quietly = TRUE)) {
  matrixcalc::is.symmetric.matrix(F)
} else {
  message("you need to install the package matrixcalc to compare this example")
}

## Example 3: Symmetric but negative-definite. same test of functions
##' eigenvalues are 3 -1
G <- matrix(c(1, 2, 2, 1), nrow = 2, byrow = TRUE); G
is.symmetric.matrix(G)
if (!requireNamespace("matrixcalc", quietly = TRUE)) {
  matrixcalc::is.symmetric.matrix(G)
} else {
  message("you need to install the package matrixcalc to compare this example.")
}
isSymmetric.matrix(G)
is.positive.definite(G) # FALSE
is.positive.semi.definite(G) # FALSE
## Example 3b: A missing value in G
G[1, 1] <- NA
is.symmetric.matrix(G) # NA
is.positive.definite(G) # NA

## Example 4: positive definite matrix
# eigenvalues are 3.4142136 2.0000000 0.585786
```

```

Q <- matrix(c(2, -1, 0, -1, 2, -1, 0, -1, 2), nrow = 3, byrow = TRUE)
is.symmetric.matrix(Q)
is.positive.definite(Q)

## Example 5: identity matrix is always positive definite
I <- diag(1, 3)
is.square.matrix(I) # TRUE
is.symmetric.matrix(I) # TRUE
is.positive.definite(I) # TRUE

```

matrixNormal_Distribution

The Matrix Normal Distribution

Description

The density (`dmatnorm()`), cumulative distribution function (CDF, `pmatnorm()`), and generation of 1 random number from the matrix normal (`rmatnorm()`) is produced from

$$A \text{ MatNorm}_{n,p}(M, U, V)$$

Usage

```

dmatnorm(A, M, U, V, tol = .Machine$double.eps^0.5, use.log = TRUE)

pmatnorm(Lower = -Inf, Upper = Inf, M, U, V,
  tol = .Machine$double.eps^0.5, algorithm = mvtnorm::GenzBretz(), ...)

rmatnorm(M, U, V, tol = .Machine$double.eps^0.5, method = "chol")

```

Arguments

A	The numeric $n \times p$ matrix that follows the matrix-normal.
M	The mean $n \times p$ matrix that is numeric and real. Must contain non-missing values.
U	The individual scale $n \times n$ real positive-definite matrix (rows). Must contain non-missing values.
V	The parameter scale $p \times p$ real positive-definite matrix (columns). Must contain non-missing values.
tol	A numeric tolerance level used to check if a matrix is symmetric; that is if the difference between the matrix and its transpose is between $-tol$ and tol .
use.log	Logical; if TRUE, densities d are given as $\log(d)$.
Lower	The $n \times p$ matrix of lower limits for CDF
Upper	The $n \times p$ matrix of upper limits for CDF
algorithm	an object of class GenzBretz , Miwa or TVPACK specifying both the algorithm to be used as well as the associated hyper parameters.

...	additional parameters (currently given to GenzBretz for backward compatibility issues).
method	string specifying the matrix decomposition used to determine the matrix root of sigma. Possible methods are eigenvalue decomposition ("eigen", default), singular value decomposition ("svd"), and Cholesky decomposition ("chol"). The Cholesky is typically fastest, not by much though.

Details

Ideally, both scale matrices are positive-definite. However, they may not appear to be symmetric; you may want to increase the tolerance.

These functions rely heavily on this following property of matrix normal distribution. Let function 'koch()' refer to the Kronecker product of a matrix. For a $n \times p$ matrix A , if $A \sim MatNorm(M, U, V)$, then

$$vec(A) \sim MVN_{np}(M, Sigma = koch(U, V))$$

Thus, we can find the probability that $Lower < A < Upper$ by finding the CDF of $vec(A)$, which is given in `pmvnorm` function in `mvtnorm`. See `algorithms` and `pmvnorm`. Also, we can simulate 1 random matrix A from a matrix normal by sampling $vec(A)$ from `mvtnorm::rmvnorm()` function. This matrix A takes the rownames from U and the colnames from V .

References

Iranmanesh, Anis, M. Arashi, and S. M. M. Tabatabaey On Conditional Applications of Matrix Variate Normal Distribution. *Iranian Journal of Mathematical Sciences and Informatics* 5, no. 2. (November 1, 2010): 33-43. <<https://doi.org/10.7508/ijmsi.2010.02.004>>

Examples

```
#Data Used
A <- datasets::CO2[1:10, 4:5]
M <- cbind(stats::rnorm(10, 435, 296), stats::rnorm(10, 27, 11) )
V <- matrix(c(87, 13, 13, 112), nrow = 2, ncol = 2, byrow = TRUE)
V #Right covariance matrix (2 x 2), say the covariance between parameters.
U <- I(10) #Block of left-covariance matrix ( 84 x 84), say the covariance between subjects.

#PDF
dmatnorm(A, M, U, V )
dmatnorm(A, M, U, V, use.log = FALSE)

#Generating Probability Lower and Upper Bounds (They're matrices )
Lower <- matrix( rep(-1, 20), ncol = 2)
Upper <- matrix( rep(3, 20), ncol = 2)
Lower; Upper
#The probability that a randomly chosen matrix A is between Lower and Upper
pmatnorm( Lower, Upper, M, U, V)
#CDF
pmatnorm( Lower = -Inf, Upper, M, U, V)
#entire domain = 1
```

```
pmatnorm( Lower = -Inf, Upper = Inf, M, U, V)

#Random generation
set.seed(123)
M <- cbind(rnorm(3, 435, 296), rnorm(3, 27, 11) )
U <- diag(1, 3)
V <- matrix(c(10, 5 ,5, 3), nrow = 2)
rmatnorm(M, U, V)
## Not run:  #M has a different sample size than U; will return an error.
M <- cbind(rnorm(4, 435, 296), rnorm(4, 27, 11) )
rmatnorm(M, U, V)

## End(Not run)
```

special.matrix

Generating Special Matrices

Description

Creates Identity Matrix I and Matrix of Ones J.

Usage

I(n)

J(n, m = n)

Arguments

n number of rows in I or J.

m number of columns in J. Default: same as number of rows.

Details

Create an Identity Matrix where the number of columns is n. This is a diagonal matrix with all equal to one (1). An identity matrix is usually written as I. To make an identity matrix with r rows and columns, use I.

A J matrix is a general matrix of any number of rows and columns, but in which all elements in the matrix are equal to one (1). J will make a n x m J matrix, given the number of rows, n, and number of columns, m. Names of rows and columns (dimnames) are included.

See Also

Other matrix: [tr](#), [vec](#)

Examples

```
#To create an identity matrix of order 12
I(12)
#To make a matrix of 6 rows and 10 columns of all ones
J(6,10)
#To make a matrix of unity, dimensions 6 x 6 .
J(6)
```

tr	<i>Matrix Trace</i>
----	---------------------

Description

Computes the trace of a square numeric matrix A.

Usage

```
tr(A)
```

Arguments

A Square matrix.

Note

If the argument is not a square numeric matrix, the function presents an error and terminates.

See Also

Other matrix: [special.matrix](#), [vec](#)

Examples

```
A <- matrix( seq( 1, 16, 1 ), nrow=4, byrow=TRUE )
A
tr( A )
tr( I(3) )
```


Index

- *Topic **distribution**
 - matrixNormal_Distribution, 4
 - vec, 8
- *Topic **identity**
 - special.matrix, 6
- *Topic **matrixNormal**
 - matrixNormal_Distribution, 4
- *Topic **matrix**
 - is.symmetric.matrix, 2
 - special.matrix, 6
 - tr, 7
 - vec, 8
- *Topic **ones**
 - special.matrix, 6

algorithms, 5

dmatnorm (matrixNormal_Distribution), 4

GenzBretz, 4

I (special.matrix), 6

is.positive.definite

- (is.symmetric.matrix), 2

is.positive.semi.definite

- (is.symmetric.matrix), 2

is.square.matrix (is.symmetric.matrix),
2

is.symmetric.matrix, 2

J (special.matrix), 6

matrixNormal_Distribution, 4

Miwa, 4

pmatnorm (matrixNormal_Distribution), 4

pmvnorm, 5

rmatnorm (matrixNormal_Distribution), 4

rmvnorm, 5

special.matrix, 6, 7, 8

tr, 6, 7, 8

TVPACK, 4

vec, 6, 7, 8