

Package ‘matrixNormal’

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Description Computes densities, probabilities, and random deviates of the Matrix Normal (Pocuca et al. (2019) <[doi:10.48550/arXiv.1910.02859](https://doi.org/10.48550/arXiv.1910.02859)>). Also includes simple but useful matrix functions. See the vignette for more information.

License GPL-3

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is.symmetric.matrix *Is a matrix symmetric or positive-definite?*

Description

Determines 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, a matrix is symmetric if the difference between the matrix and its transpose is between -tol and tol.

Details

A tolerance is added to indicate if a matrix A is approximately symmetric. If A is not symmetric, a message and first few rows of the matrix is printed. If A has any missing values, NA is returned.

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

Note

Functions are adapted from Frederick Novomestky's **matrixcalc** package in order to implement the `rmatnorm` function. The following changes are made:

- 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. This is 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. The functions are same.
# 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

Computes the density (`dmatnorm`), calculates the cumulative distribution function (CDF, `pmatnorm`), and generates 1 random number (`rmatnorm`) from the matrix normal:

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

.

Usage

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

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

```
rmatnorm(s = 1, M, U, V, tol = .Machine$double.eps^0.5, method = "chol")
```

Arguments

- | | |
|---|---|
| A | The numeric $n \times p$ matrix that follows the matrix-normal. Value used to calculate the density. |
| M | The mean $n \times p$ matrix that is numeric and real. Must contain non-missing values. Parameter of matrix Normal. |

U	The individual scale $n \times n$ real positive-definite matrix (rows). Must contain non-missing values. Parameter of matrix Normal.
V	The parameter scale $p \times p$ real positive-definite matrix (columns). Must contain non-missing values. Parameter of matrix Normal.
tol	A numeric tolerance level used to check if a matrix is symmetric. That is, a matrix is symmetric if the difference between the matrix and its transpose is between $-tol$ and tol .
log	Logical; if TRUE, the logarithm of the density is returned.
Lower	The $n \times p$ matrix of lower limits for CDF.
Upper	The $n \times p$ matrix of upper limits for CDF.
keepAttr	logical indicating if attributes such as <code>error</code> and <code>msg</code> should be attached to the return value. The default, TRUE is back compatible.
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).
s	The number of observations desired to simulate from the matrix normal. Defaults to 1. Currently has no effect but acts as a placeholder in future releases.
method	String specifying the matrix decomposition used to determine the matrix root of the Kronecker product of U and V in <code>rmatnorm</code> . Possible methods are eigenvalue decomposition ("eigen"), singular value decomposition ("svd"), and Cholesky decomposition ("chol"). The Cholesky (the default) is typically fastest, but not by much though. Passed to <code>**mvtnorm**::rmvnorm</code> .

Details

These functions rely heavily on this following property of matrix normal distribution. Let `koch()` refer to the Kronecker product of a matrix. For a $n \times p$ matrix A , if

$$A \sim \text{MatNorm}(M, U, V),$$

then

$$\text{vec}(A) \sim \text{MVN}_{np}(M, \text{Sigma} = \text{koch}(V, U)).$$

Thus, the probability of $\text{Lower} < A < \text{Upper}$ in the matrix normal can be found by using the CDF of `vec(A)`, which is given by `pmvnorm` function in `mvtnorm`. See [algorithms](#) and [pmvnorm](#) for more information.

Also, we can simulate a random matrix A from a matrix normal by sampling `vec(A)` from `rmvnorm` function in `mvtnorm`. This matrix A takes the rownames from U and the colnames from V .

Calculating Matrix Normal Probabilities

From the `mvtnorm` package, three algorithms are available for evaluating normal probabilities:

- The default is the randomized Quasi-Monte-Carlo procedure by Genz (1992, 1993) and Genz and Bretz (2002) applicable to arbitrary covariance structures and dimensions up to 1000.

- For smaller dimensions (up to 20) and non-singular covariance matrices, the algorithm by Miwa et al. (2003) can be used as well.
- For two- and three-dimensional problems and semi-infinite integration region, TVPACK implements an interface to the methods described by Genz (2004).

The . . . arguments define the hyper-parameters for GenzBertz algorithm:

maxpts maximum number of function values as integer. The internal FORTRAN code always uses a minimum number depending on the dimension. Default 25000.

abseps absolute error tolerance.

releps relative error tolerance as double.

Note

Ideally, both scale matrices are positive-definite. If they do not appear to be symmetric, the tolerance should be increased. Since symmetry is checked, the ‘checkSymmetry’ arguments in ‘mvt-norm::rmvnorm()’ are set to FALSE.

References

Pocuca, N., Gallagher, M.P., Clark, K.M., & McNicholas, P.D. (2019). Assessing and Visualizing Matrix Variate Normality. Methodology. <<https://arxiv.org/abs/1910.02859>>

Gupta, A. K. and D. K. Nagar (1999). Matrix Variate Distributions. Boca Raton: Chapman & Hall/CRC Press.

Examples

```
# Data Used
# if( !requireNamespace("datasets", quietly = TRUE)) { install.packages("datasets")} #part of baseR.
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, 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(1, M, U, V)

# M has a different sample size than U; will return an error.
## Not run:
M <- cbind(rnorm(4, 435, 296), rnorm(4, 27, 11))
rmatnorm(M, U, V)

## End(Not run)
```

special.matrix

Generating Special Matrices

Description

Creates an Identity Matrix I and a Matrix of Ones J .

- $I()$: Creates 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 . Names of rows and columns (`dimnames`) are included.
- $J()$: Creates a matrix of ones with any number of rows and columns. Names of rows and columns (`dimnames`) are included.

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.

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

Matrix Trace

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))
```

vec *Stacks a Matrix using matrix operator "vec"*

Description

Returns a column vector that stacks the columns of *A*, a *m* x *n* matrix.

Usage

```
vec(A, use.Names = TRUE)
```

Arguments

<i>A</i>	A matrix with <i>m</i> rows and <i>n</i> columns.
<i>use.Names</i>	Logical. If TRUE, the names of <i>A</i> are taken to be names of the stacked matrix. Default: TRUE.

Value

A vector with *mn* elements.

Note

1. Unlike other 'vec()' functions on CRAN, `matrixNormal` version inherits names from matrices to their vectorized forms.
2. `vec()` was adapted from Frederick Novomestky's **matrixcalc**. This function is edited so that it can take dimension names and return the matrix as a vector.
3. These functions were used as accessories for other `matrixNormal` functions.

References

Magnus, J. R. and H. Neudecker (1999). *Matrix Differential Calculus with Applications in Statistics and Econometrics*. Second Edition, John Wiley, ed.

See Also

Other matrix: [special.matrix](#), [tr\(\)](#)

Examples

```
M <- matrix(c(4, 5, 6, 7, 8, 9), nrow = 3)
M
vec(M)
if (!requireNamespace("matrixcalc", quietly = TRUE)) {
# Compare vec from \pkg{matrixcalc} and new function.
matrixcalc::vec(M)
# The names are rownames(M):colnames(M) in that order.
# Very similar to matrixcalc but dimension names are different.
```

```

} else {
  message("you need to install the package matrixcalc to compare this example.")
}

```

vech *Half-Vectorization of a matrix*

Description

Stacks elements of the lower triangle of a numeric symmetric matrix A .

Usage

```
vech(A, use.Names = TRUE, tol = .Machine$double.eps^0.5)
```

Arguments

<code>A</code>	A matrix with m rows and n columns.
<code>use.Names</code>	Logical. If TRUE, the names of A are taken to be names of the stacked matrix. Default: TRUE.
<code>tol</code>	A numeric tolerance level used to check if a matrix is symmetric. That is, a matrix is symmetric if the difference between the matrix and its transpose is between $-tol$ and tol .

Details

For a symmetric matrix A , the vectorization of A contains more information than necessary. The half-vectorization, denoted `vech()`, of a symmetric square n by n matrix A is the vectorization of the lower triangular portion.

Value

A vector with $n(n+1)/2$ elements.

Note

Unlike other `vech()` functions available on CRAN, `matrixNormal` version may inherit names from matrices to their vectorized forms.

Examples

```

x <- matrix(c(1, 2, 2, 4),
  nrow = 2, byrow = TRUE,
  dimnames = list(1:2, c("Sex", "Smoker")))
)
print(x)

# Example 1

```

```
vech(x)
# If you just want the vectorized form
vech(x, use.Names = FALSE)

# Example 2: If one has NA's
x[1, 2] <- x[2, 1] <- NA
vech(x)
```

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