

# Package ‘mnormt’

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**Title** The Multivariate Normal and t Distributions

**Author** Fortran code by Alan Genz and other people referred to in the code,  
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**Depends** R (>= 2.2.0)

**Description** Functions are provided for computing the density and the  
distribution function of multivariate normal and “t” random variables,  
and for generating random vectors sampled from these distributions.  
Probabilities are computed via non-Monte Carlo methods; different routines  
are used in the case d=1, d=2, d>2, if d denotes the number of dimensions.

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mnormt-package

The 'mnormt' package: summary information

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## Description

This package provides functions for computing the density and the distribution function of multivariate normal and multivariate Student's  $t$  variates and for generating random vectors sampled from these distributions.

## Details

Probabilities are computed via a non-Monte Carlo method. Different routines are used in the three cases  $d=1$ ,  $d=2$ ,  $d>2$ , if  $d$  denotes the number of dimensions.

## Licence

This package and its documentation are usable under the terms of the "GNU General Public License" version 3 or version 2, as you prefer; a copy of them is available from <https://www.R-project.org/Licenses/>.

## Author(s)

Adelchi Azzalini (R code and package creation) and Alan Genz (Fortran code, see references below; this incorporates routines of other authors)

## References

Genz, A. (1992). Numerical Computation of Multivariate Normal Probabilities. *J. Computational and Graphical Statist.*, **1**, 141-149.

Genz, A. (1993). Comparison of methods for the computation of multivariate normal probabilities. *Computing Science and Statistics*, **25**, 400-405.

Genz, A.: Fortran code available at <http://www.math.wsu.edu/math/faculty/genz/software/fort77/mvn.f>

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dmnorm

Multivariate normal distribution

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## Description

The probability density function, the distribution function and random number generation for the multivariate normal (Gaussian) distribution

**Usage**

```
dmnorm(x, mean = rep(0, d), varcov, log = FALSE)
pmnorm(x, mean = rep(0, d), varcov, ...)
rmnorm(n = 1, mean = rep(0, d), varcov, sqrt=NULL)
sadmvn(lower, upper, mean, varcov, maxpts = 2000*d, abseps = 1e-06, releps = 0)
```

**Arguments**

<code>x</code>	either a vector of length <code>d</code> or a matrix with <code>d</code> columns, where <code>d=ncol(varcov)</code> , representing the coordinates of the point(s) where the density must be evaluated; for <code>pmnorm</code> , <code>d</code> cannot exceed 20.
<code>mean</code>	either a vector of length <code>d</code> , representing the mean value, or (except for <code>rmnorm</code> ) a matrix whose rows represent different mean vectors; in the matrix case, only allowed for <code>dmnorm</code> and <code>pmnorm</code> , its dimensions must match those of <code>x</code> .
<code>varcov</code>	a symmetric positive-definite matrix representing the variance-covariance matrix of the distribution; a vector of length 1 is also allowed (in this case, <code>d=1</code> is set).
<code>sqrt</code>	if not NULL (default value is NULL), a square root of the intended <code>varcov</code> matrix; see ‘Details’ for a full description.
<code>log</code>	a logical value (default value is FALSE); if TRUE, the logarithm of the density is computed.
<code>...</code>	parameters passed to <code>sadmvn</code> , among <code>maxpts</code> , <code>abseps</code> , <code>releps</code> .
<code>n</code>	the number of random vectors to be generated.
<code>lower</code>	a numeric vector of lower integration limits of the density function; must be of maximal length 20; <code>+Inf</code> and <code>-Inf</code> entries are allowed.
<code>upper</code>	a numeric vector of upper integration limits of the density function; must be of maximal length 20; <code>+Inf</code> and <code>-Inf</code> entries are allowed.
<code>maxpts</code>	the maximum number of function evaluations (default value: <code>2000*d</code> ).
<code>abseps</code>	absolute error tolerance (default value: <code>1e-6</code> ).
<code>releps</code>	relative error tolerance (default value: 0).

**Details**

The function `pmnorm` works by making a suitable call to `sadmvn` if `d>2`, or to `biv.nt.prob` if `d=2`, or to `pnorm` if `d=1`. Function `sadmvn` is an interface to a Fortran-77 routine with the same name written by Alan Genz, available from his web page, which works using an adaptive integration method. This Fortran-77 routine makes use of some auxiliary functions whose authors are documented in the code.

If `sqrt=NULL` (default value), the working of `rmnorm` involves computation of a square root of `varcov` via the Cholesky decomposition. If a non-NULL value of `sqrt` is supplied, it is assumed that it represents a matrix,  $R$  say, such that  $R'R$  represents the required variance-covariance matrix of the distribution; in this case, the argument `varcov` is ignored. This mechanism is intended primarily for use in a sequence of calls to `rmnorm`, all sampling from a distribution with fixed variance matrix; a suitable matrix `sqrt` can then be computed only once beforehand, avoiding that the same operation is repeated multiple times along the sequence of calls; see the examples below. Another use of

`sqrt` is to supply a different form of square root of the variance-covariance matrix, in place of the Cholesky factor.

For efficiency reasons, `rmnorm` does not perform checks on the supplied arguments.

If, after setting the same seed value to `set.seed`, two calls to `rmnorm` are made with the same arguments except that one generates `n1` vectors and the other `n2` vectors, with `n1 < n2`, then the `n1` vectors of the first call coincide with the initial `n2` vectors of the second call.

### Value

`dmnorm` returns a vector of density values (possibly log-transformed); `pmnorm` returns a vector of probabilities, possibly with attributes on the accuracy in case `x` is a vector; `sadmvn` return a single probability with attributes giving details on the achieved accuracy; `rmnorm` returns a matrix of `n` rows of random vectors or a vector in case `n=1`.

### Note

The attributes `error` and `status` of the probability returned by `pmnorm` and `sadmvn` indicate whether the function had a normal termination, achieving the required accuracy. If this is not the case, re-run the function with a higher value of `maxpts`

### Author(s)

Fortran code of `SADMVN` and most auxiliary functions by Alan Genz, some additional auxiliary functions by people referred to within his program. Interface to `R` and additional `R` code by Adelchi Azzalini

### References

Genz, A. (1992). Numerical Computation of multivariate normal probabilities. *J. Computational and Graphical Statist.*, **1**, 141-149.

Genz, A. (1993). Comparison of methods for the computation of multivariate normal probabilities. *Computing Science and Statistics*, **25**, 400-405.

Genz, A.: Fortran code available at <http://www.math.wsu.edu/math/faculty/genz/software/fort77/mvn.f>

### See Also

`dnorm`, `dmt`, `biv.nt.prob`

### Examples

```
x <- seq(-2, 4, length=21)
y <- cos(2*x) + 10
z <- x + sin(3*y)
mu <- c(1,12,2)
Sigma <- matrix(c(1,2,0,2,5,0.5,0,0.5,3), 3, 3)
f <- dmnorm(cbind(x,y,z), mu, Sigma)
f0 <- dmnorm(mu, mu, Sigma)
p1 <- pmnorm(c(2,11,3), mu, Sigma)
```

```

p2 <- pmnorm(c(2,11,3), mu, Sigma, maxpts=10000, abseps=1e-10)
p <- pmnorm(cbind(x,y,z), mu, Sigma)
#
set.seed(123)
x1 <- rmnorm(5, mu, Sigma)
set.seed(123)
x2 <- rmnorm(5, mu, sqrt=chol(Sigma)) # x1=x2
eig <- eigen(Sigma, symmetric = TRUE)
R <- t(eig$vectors %*% diag(sqrt(eig$values)))
for(i in 1:50) x <- rmnorm(5, mu, sqrt=R)
#
p <- sadmvn(lower=c(2,11,3), upper=rep(Inf,3), mu, Sigma) # upper tail
#
p0 <- pmnorm(c(2,11), mu[1:2], Sigma[1:2,1:2])
p1 <- biv.nt.prob(0, lower=rep(-Inf,2), upper=c(2, 11), mu[1:2], Sigma[1:2,1:2])
p2 <- sadmvn(lower=rep(-Inf,2), upper=c(2, 11), mu[1:2], Sigma[1:2,1:2])
c(p0, p1, p2, p0-p1, p0-p2)
#
p1 <- pnorm(0, 1, 3)
p2 <- pmnorm(0, 1, 3^2)

```

dmt

*Multivariate t distribution*

## Description

The probability density function, the distribution function and random number generation for the multivariate Student's *t* distribution

## Usage

```

dmt(x, mean = rep(0, d), S, df=Inf, log = FALSE)
pmt(x, mean = rep(0, d), S, df=Inf, ...)
rmt(n = 1, mean = rep(0, d), S, df=Inf, sqrt=NULL)
sadmvt(df, lower, upper, mean, S, maxpts = 2000*d, abseps = 1e-06, releps = 0)
biv.nt.prob(df, lower, upper, mean, S)

```

## Arguments

- |      |  |
|------|--|
| x    | either a vector of length d or a matrix with d columns, where d=ncol(S), giving the coordinates of the point(s) where the density must be evaluated; for pmt, d cannot exceed 20.  |
| mean | either a vector of length d, representing the location parameter (equal to the mean vector when df>1) or a matrix whose rows represent different mean vectors (except for rmt); in the matrix case, its dimensions must match those of x.    |
| S    | a symmetric positive-definite matrix representing the scale matrix of the distribution, such that $S \cdot df / (df - 2)$ is the variance-covariance matrix when $df > 2$ ; a vector of length 1 is also allowed (in this case, d=1 is set). |

df	degrees of freedom; it must be a positive integer for pmt, sadmvt and biv.nt.prob, otherwise a positive number. If df=Inf (default value), the corresponding *mnorm function is called, unless d=2; in this case biv.nt.prob is used. If biv.nt.prob is called with df=Inf, it returns the probability of a rectangle assigned by a bivariate normal distribution.
log	a logical value(default value is FALSE); if TRUE, the logarithm of the density is computed.
sqrt	if not NULL (default value is NULL), a square root of the intended scale matrix S; see ‘Details’ for a full description.
...	parameters passed to sadmvt, among maxpts, absrel, releps.
n	the number of random vectors to be generated
lower	a numeric vector of lower integration limits of the density function; must be of maximal length 20; +Inf and -Inf entries are allowed.
upper	a numeric vector of upper integration limits of the density function; must be of maximal length 20; +Inf and -Inf entries are allowed
maxpts	the maximum number of function evaluations (default value: 2000*d)
abseps	absolute error tolerance (default value: 1e-6).
releps	relative error tolerance (default value: 0).

## Details

The functions sadmvt and biv.nt.prob are interfaces to Fortran-77 routines by Alan Genz, and available from his web page; they makes uses of some auxiliary functions whose authors are documented in the Fortran code. The routine sadmvt uses an adaptive integration method. The routine biv.nt.prob is specific for the bivariate case; if df<1 or df=Inf, it computes the bivariate normal distribution function using a non-iterative method described in a reference given below. If pmt is called with d>2, this is converted into a suitable call to sadmvt; if d=2, a call to biv.nt.prob is used; if d=1, then pt is used.

If sqrt=NULL (default value), the working of rmt involves computation of a square root of S via the Cholesky decomposition. If a non-NULL value of sqrt is supplied, it is assumed that it represents a square root of the scale matrix, otherwise represented by S, whose value is ignored in this case. This mechanism is intended primarily for use in a sequence of calls to rmt, all sampling from a distribution with fixed scale matrix; a suitable matrix sqrt can then be computed only once beforehand, avoiding that the same operation is repeated multiple times along the sequence of calls. For examples of use of this argument, see those in the documentation of [rmnorm](#). Another use of sqrt is to supply a different form of square root of the scale matrix, in place of the Cholesky factor.

For efficiency reasons, rmt does not perform checks on the supplied arguments.

## Value

dmt returns a vector of density values (possibly log-transformed); pmt and sadmvt return a single probability with attributes giving details on the achieved accuracy, provided x of pmnorm is a vector; rmt returns a matrix of n rows of random vectors

**Note**

The attributes `error` and `status` of the probability returned by `sadmvt` and by `pmt` (the latter only if `x` is a vector and `d>2`) indicate whether the function had a normal termination, achieving the required accuracy. If this is not the case, re-run the function with a higher value of `maxpts`.

**Author(s)**

Fortran code of `SADMVT` and most auxiliary functions by Alan Genz, some additional auxiliary functions by people referred to within his program; interface to R and additional R code by Adelchi Azzalini.

**References**

Genz, A.: Fortran code in files `mvt.f` and `mvtldstpack.f` available at <http://www.math.wsu.edu/math/faculty/genz/software/>

Dunnnett, C.W. and Sobel, M. (1954). A bivariate generalization of Student's *t*-distribution with tables for certain special cases. *Biometrika* 41, 153–169.

**See Also**

`dt`, `rmnorm` for use of argument `sqrt`

**Examples**

```
x <- seq(-2,4,length=21)
y <- 2*x+10
z <- x*cos(y)
mu <- c(1,12,2)
Sigma <- matrix(c(1,2,0,2,5,0.5,0,0.5,3), 3, 3)
df <- 4
f <- dmt(cbind(x,y,z), mu, Sigma,df)
p1 <- pmt(c(2,11,3), mu, Sigma, df)
p2 <- pmt(c(2,11,3), mu, Sigma, df, maxpts=10000, abseps=1e-8)
x <- rmt(10, mu, Sigma, df)
p <- sadmvt(df, lower=c(2,11,3), upper=rep(Inf,3), mu, Sigma) # upper tail
#
p0 <- pmt(c(2,11), mu[1:2], Sigma[1:2,1:2], df=5)
p1 <- biv.nt.prob(5, lower=rep(-Inf,2), upper=c(2, 11), mu[1:2], Sigma[1:2,1:2])
p2 <- sadmvt(5, lower=rep(-Inf,2), upper=c(2, 11), mu[1:2], Sigma[1:2,1:2])
c(p0, p1, p2, p0-p1, p0-p2)
```

**Description**

The inverse of a symmetric positive-definite matrix and its log-determinant

**Usage**

```
pd.solve(x, silent = FALSE, log.det=FALSE)
```

**Arguments**

x	a symmetric positive-definite matrix.
silent	a logical value which indicates the action to take in case of an error. If <code>silent==TRUE</code> and an error occurs, the function silently returns a NULL value; if <code>silent==FALSE</code> (default), an error generates a stop with an error message.
log.det	a logical value to indicate whether the log-determinant of x is required (default is FALSE).

**Details**

The function checks that x is a symmetric positive-definite matrix. If an error is detected, an action is taken which depends on the value of the argument `silent`.

**Value**

the inverse matrix of x; if `log.det=TRUE`, this inverse has an attribute which contains the logarithm of the determinant of x.

**Author(s)**

Adelchi Azzalini

**Examples**

```
x <- toeplitz(rev(1:4))
x.inv <- pd.solve(x)
print(x.inv %*% x)
x.inv <- pd.solve(x, log.det=TRUE)
logDet <- attr(x.inv, "log.det")
print(abs(logDet - determinant(x, logarithm=TRUE)$modulus))
```



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