

# The mnormt Package

March 18, 2007

**Version** 1.2-1

**Date** 2007-03-16

**Title** The multivariate normal and t distributions

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**Depends** R (>= 2.2.0)

**Description** This package provides functions for computing the density and the distribution function of, and for generating random vectors from the multivariate normal and multivariate t distributions. It provides functions similar in scope to those of the package 'mvtnorm', but with some differences; one of these is that probabilities are computed via a non-Monte Carlo method.

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**URL** <http://azzalini.stat.unipd.it/SW/Pkg-mnormt>

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dmnorm	<i>Multivariate normal distribution</i>
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## Description

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

**Usage**

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

**Arguments**

<code>x</code>	for <code>dmnorm</code> , this is either a vector of length <code>d</code> or a matrix with <code>d</code> columns, where <code>d=ncol(varcov)</code> , giving the coordinates of the point(s) where the density must be evaluated; for <code>pmnorm</code> , only a vector of length <code>d</code> is allowed, and <code>d</code> cannot exceed 20
<code>mean</code>	a numeric vector representing the expected value of the distribution; it must be of length <code>d</code> , as defined above
<code>varcov</code>	a 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>log</code>	a logical value; if <code>TRUE</code> , the logarithm of the density is computed
<code>...</code>	parameters passed to <code>sadmvn</code> , among <code>maxpts</code> , <code>absrel</code> , <code>releps</code>
<code>n</code>	the number of random numbers 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: <code>0</code> )

**Details**

Function `sadmvn` is an interface to a Fortran-77 routine with the same name written by Alan Genz, and available from his web page; this makes uses of some auxiliary functions whose authors are documented in the Fortran code. The routine uses an adaptive integration method.

**Value**

`dmnorm` returns a vector of density values (possibly log-transformed); `pmnorm` and `sadmvn` return a single probability with attributes giving details on the achieved accuracy; `rmnorm` returns a matrix of `n` rows of random vectors

**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 an 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. Porting 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/mvn.f>

**See Also**

[dnorm](#), [dmt](#)

**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)
f <- dnorm(cbind(x,y,z), mu, Sigma)
p1 <- pmnorm(c(2,11,3), mu, Sigma)
p2 <- pmnorm(c(2,11,3), mu, Sigma, maxpts=10000, abseps=1e-10)
x <- rmnorm(10, mu, Sigma)
p <- sadmvn(lower=c(2,11,3), upper=rep(Inf,3), mu, Sigma) # upper tail
#
p1 <- pnorm(0, 1, 2)
p2 <- pmnorm(0, 1, 2^2)
```

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dmt

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*Multivariate t distribution*


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**Description**

The probability density function, the distribution function and random number generation for the multivariate t probability distribution

**Usage**

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

**Arguments**

<code>x</code>	for <code>dmt</code> , this is either a vector of length <code>d</code> or a matrix with <code>d</code> columns, where $d = \text{ncol}(S)$ , giving the coordinates of the point(s) where the density must be evaluated; for <code>pmt</code> , only a vector of length <code>d</code> is allowed, and <code>d</code> cannot exceed 20
<code>mean</code>	a numeric vector representing the location parameter of the distribution (equal to the expected value when $df > 1$ ); it must be of length <code>d</code> , as defined above
<code>S</code>	a positive definite matrix representing the scale matrix of the distribution, such that $S * df / (df - 2)$ is the variance-covariance matrix when $df > 2$ ; a vector of length 1 is also allowed (in this case, $d = 1$ is set)
<code>df</code>	degrees of freedom; it must be a positive integer for <code>pmt</code> and <code>sadmvt</code> , otherwise a positive number; if <code>df = Inf</code> (default value), the corresponding <code>*mnorm</code> function is called
<code>log</code>	a logical value; if <code>TRUE</code> , the logarithm of the density is computed
<code>...</code>	parameters passed to <code>sadmvt</code> , among <code>maxpts</code> , <code>absrel</code> , <code>releps</code>
<code>n</code>	the number of random numbers 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: $2000 * d$ )
<code>abseps</code>	absolute error tolerance (default value: $1e-6$ )
<code>releps</code>	relative error tolerance (default value: 0)

**Details**

Function `sadmvt` is an interface to a Fortran-77 routine with the same name written by Alan Genz, and available from his web page; this makes uses of some auxiliary functions whose authors are documented in the Fortran code. The routine uses an adaptive integration method.

**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; `rmt` returns a matrix of `n` rows of random vectors

**Note**

The attributes `error` and `status` of the probability returned by `pmt` and `sadmvt` indicate whether the function had a normal termination, achieving the required accuracy. If this is not the case, re-run the function with an 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. Porting to R and additional R code by Adelchi Azzalini

**References**

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

**See Also**

[dt](#), [dmnorm](#)

**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
```

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