

# Package: mvtnorm (via r-universe)

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**Title** Multivariate Normal and t Distributions

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**Description** Computes multivariate normal and t probabilities, quantiles, random deviates, and densities. Log-likelihoods for multivariate Gaussian models and Gaussian copulae parameterised by Cholesky factors of covariance or precision matrices are implemented for interval-censored and exact data, or a mix thereof. Score functions for these log-likelihoods are available. A class representing multiple lower triangular matrices and corresponding methods are part of this package.

**Imports** stats

**Depends** R(>= 3.5.0)

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**License** GPL-2

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**NeedsCompilation** yes

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mvtnorm-package	<i>Multivariate Normal and t Distributions</i>
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## Description

Computes multivariate normal and t probabilities, quantiles, random deviates, and densities. Log-likelihoods for multivariate Gaussian models and Gaussian copulae parameterised by Cholesky factors of covariance or precision matrices are implemented for interval-censored and exact data, or a mix thereof. Score functions for these log-likelihoods are available. A class representing multiple lower triangular matrices and corresponding methods are part of this package.

## Details

Package **mvtnorm** provides functionality for dealing with multivariate normal and t-distributions. The package interfaces FORTRAN and C code for evaluating multivariate normal probabilities written by Alan Genz and Tetsuhisa Miwa. Functions `pmvnorm`, `pmvt`, `qmvnorm`, and `qmvt` return normal and t probabilities or corresponding quantiles computed by these original implementations. Users interested in the computation of such probabilities or quantiles, for example for multiple testing purposes, should use this functionality.

When the multivariate normal log-likelihood function, defined by the log-probability in the discrete or interval-censored case or by the log-density for exact real observations, or a mix thereof, shall be computed, functions `lpmvnorm`, `ldmvnorm`, and `ldpmvnorm` are better suited. They rely on an independent implementation of Genz' algorithm (for log-probabilities), can be customised (different quasi-Monte Carlo schemes), and are a bit faster. Most importantly, the corresponding score functions are available through functions `slpmvnorm`, `sldmvnorm`, or `sldpmvnorm`, which help to speed-up parameter estimation considerably. Users interested in this functionality should consult the `lpmvnorm_src` package vignette.

## See Also

`vignette("lpmvnorm_src", package = "mvtnorm")`

**Description**

Choose between three algorithms for evaluating normal (and t-) distributions and define hyper parameters.

**Usage**

```
GenzBretz(maxpts = 25000, abseps = 0.001, releps = 0)
Miwa(steps = 128, checkCorr = TRUE, maxval = 1e3)
TVPACK(abseps = 1e-6)
```

**Arguments**

maxpts	maximum number of function values as integer. The internal FORTRAN code always uses a minimum number depending on the dimension. (for example 752 for three-dimensional problems).
abseps	absolute error tolerance; for TVPACK only used for dimension 3.
releps	relative error tolerance as double.
steps	number of grid points to be evaluated; cannot be larger than 4097.
checkCorr	logical indicating if a check for singularity of the correlation matrix should be performed (once per function call to <code>pmvt()</code> or <code>pmvnorm()</code> ).
maxval	replacement for <code>Inf</code> when non-orthant probabilities involving <code>Inf</code> shall be computed.

**Details**

There are three algorithms available for evaluating normal (and two algorithms for t-) 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 normal probabilities, smaller dimensions (up to 20) and non-singular covariance matrices, the algorithm by Miwa et al. (2003) can be used as well. This algorithm can compute orthant probabilities (lower being `-Inf` or upper equal to `Inf`). Non-orthant probabilities are computed from the corresponding orthant probabilities, however, infinite limits are replaced by `maxval` along with a warning.

For two- and three-dimensional problems and semi-infinite integration region, TVPACK implements an interface to the methods described by Genz (2004).

**Value**

An object of class "GenzBretz", "Miwa", or "TVPACK" defining hyper parameters.

## References

- Genz, A. (1992). Numerical computation of multivariate normal probabilities. *Journal of Computational and Graphical Statistics*, **1**, 141–150.
- Genz, A. (1993). Comparison of methods for the computation of multivariate normal probabilities. *Computing Science and Statistics*, **25**, 400–405.
- Genz, A. and Bretz, F. (2002). Methods for the computation of multivariate t-probabilities. *Journal of Computational and Graphical Statistics*, **11**, 950–971.
- Genz, A. (2004). Numerical computation of rectangular bivariate and trivariate normal and t-probabilities, *Statistics and Computing*, **14**, 251–260.
- Genz, A. and Bretz, F. (2009), *Computation of Multivariate Normal and t Probabilities*. Lecture Notes in Statistics, Vol. 195. Springer-Verlag, Heidelberg.
- Miwa, A., Hayter J. and Kuriki, S. (2003). The evaluation of general non-centred orthant probabilities. *Journal of the Royal Statistical Society, Ser. B*, **65**, 223–234.
- Mi, X., Miwa, T. and Hothorn, T. (2009). mvtnorm: New numerical algorithm for multivariate normal probabilities. *The R Journal* **1**(1): 37–39. [https://journal.r-project.org/archive/2009-1/RJournal\\_2009-1\\_Mi+et+al.pdf](https://journal.r-project.org/archive/2009-1/RJournal_2009-1_Mi+et+al.pdf)

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interface	<i>(Experimental) User Interface to Multiple Multivariate Normal Distributions</i>
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## Description

A (still experimental) simple user interface for computing on multiple multivariate normal distributions.

## Usage

```
mvnorm(mean, chol, invchol)
## S3 method for class 'mvnorm'
aperm(a, perm, ...)
margDist(object, which, ...)
## S3 method for class 'mvnorm'
margDist(object, which, ...)
condDist(object, which_given, given, ...)
## S3 method for class 'mvnorm'
condDist(object, which_given, given, ...)
## S3 method for class 'mvnorm'
simulate(object, nsim = dim(object$scale)[1L], seed = NULL,
          standardize = FALSE, as.data.frame = FALSE, ...)
## S3 method for class 'mvnorm'
logLik(object, obs, lower, upper, standardize = FALSE, ...)
## S3 method for class 'mvnorm'
llgrad(object, obs, lower, upper, standardize = FALSE, ...)
```

**Arguments**

<code>chol</code>	either an <code>ltMatrices</code> object specifying (multiple) Cholesky factors of the covariance matrix or one single numeric lower triangular square matrix.
<code>invchol</code>	either an <code>ltMatrices</code> object specifying (multiple) inverse Cholesky factors of the covariance matrix or one single numeric lower triangular square matrix.
<code>a, object</code>	objects of class <code>mvnorm</code> .
<code>perm</code>	a permutation of the covariance matrix corresponding to <code>a</code> .
<code>which</code>	names or indices of elements whose marginal distribution is of interest.
<code>which_given</code>	names or indices of elements to condition on.
<code>given</code>	matrix of realisations to condition on (number of rows is equal to <code>length(which)</code> ), the number of columns corresponds to the number of matrices in <code>chol</code> or <code>invchol</code> .
<code>lower</code>	matrix of lower limits (one column for each observation, $J$ rows).
<code>upper</code>	matrix of upper limits (one column for each observation, $J$ rows).
<code>obs</code>	matrix of exact observations (one column for each observation, $J$ rows).
<code>mean</code>	matrix of means (one column for each observation, length is recycled to length of <code>obs</code> , <code>lower</code> and <code>upper</code> ).
<code>seed</code>	an object specifying if and how the random number generator should be initialized, see <a href="#">simulate</a> .
<code>standardize</code>	logical, should the Cholesky factor (or its inverse) undergo standardization (ensuring the covariance matrix is a correlation matrix) before computing the likelihood.
<code>nsim</code>	number of samples to draw.
<code>as.data.frame</code>	logical, convert the $J \times N$ matrix result to a classical $N \times J$ data frame.
<code>...</code>	Additional arguments to <code>ldpmvnorm</code> and <code>sldpmvnorm</code>

**Details**

The constructor `mvnorm` can be used to specify (multiple) multivariate normal distributions. `margDist` derives marginal and `condDist` conditional distributions from such objects. A `simulate` method exists for drawn samples from multivariate normals.

The continuous (data in `obs`), discrete (intervals in `lower` and `upper`), and mixed continuous-discrete log-likelihood is implemented in `logLik`. The corresponding gradients with respect to all model parameters and with respect to the data arguments is available from `llgrad`.

Rationals and examples are given in Chapter 7 of the package vignette linked to below.

**Value**

`mvnorm`, `margDist`, and `condDist` return objects of class `mvnorm`. `logLik` returns the log-likelihood and `llgrad` a list with gradients.

**See Also**

`vignette("lmvnorm_src", package = "mvtnorm")`

lpmvnorm

*Multivariate Normal Log-likelihood and Score Functions***Description**

Computes the log-likelihood (contributions) of multiple exact or interval-censored observations (or a mix thereof) from multivariate normal distributions and evaluates corresponding score functions.

**Usage**

```
lpmvnorm(lower, upper, mean = 0, center = NULL, chol, invchol, logLik = TRUE,
          M = NULL, w = NULL, seed = NULL, tol = .Machine$double.eps, fast = FALSE)
slpmvnorm(lower, upper, mean = 0, center = NULL, chol, invchol, logLik = TRUE,
           M = NULL, w = NULL, seed = NULL, tol = .Machine$double.eps, fast = FALSE)
ldmvnorm(obs, mean = 0, chol, invchol, logLik = TRUE)
sldmvnorm(obs, mean = 0, chol, invchol, logLik = TRUE)
ldpmvnorm(obs, lower, upper, mean = 0, chol, invchol, logLik = TRUE, ...)
sldpmvnorm(obs, lower, upper, mean = 0, chol, invchol, logLik = TRUE, ...)
```

**Arguments**

lower	matrix of lower limits (one column for each observation, $J$ rows).
upper	matrix of upper limits (one column for each observation, $J$ rows).
obs	matrix of exact observations (one column for each observation, $J$ rows).
mean	matrix of means (one column for each observation, length is recycled to length of obs, lower and upper).
center	matrix of negative rescaled means (one column for each observation, length is recycled to length of lower and upper) as returned by <code>cond_mvnorm(..., center = TRUE)</code> .
chol	Cholesky factors of covariance matrices as <code>ltMatrices</code> object, length is recycled to length of obs, lower and upper.
invchol	Cholesky factors of precision matrices as <code>ltMatrices</code> object, length is recycled to length of lower and upper. Either chol or invchol must be given.
logLik	logical, if TRUE, the log-likelihood is returned, otherwise the individual contributions to the sum are returned.
M	number of iterations, early stopping based on estimated errors is NOT implemented.
w	an optional matrix of weights with $J - 1$ rows. This allows to replace the default Monte-Carlo procedure (Genz, 1992) with a quasi-Monte-Carlo approach (Genz & Bretz, 2002). Note that the same weights for evaluating the multivariate normal probability are used for all observations when <code>ncol(w) == M</code> is specified. If <code>ncol(w) == ncol(lower) * M</code> , each likelihood contribution is evaluated on the corresponding sub-matrix. If w is NULL, different uniform numbers are drawn for each observation.

seed	an object specifying if and how the random number generator should be initialized, see <a href="#">simulate</a> . Only applied when w is NULL.
tol	tolerance limit, values smaller than tol are interpreted as zero.
fast	logical, if TRUE, a faster but less accurate version of pnorm is used internally.
...	additional arguments to lpmvnorm.

## Details

Evaluates the multivariate normal log-likelihood defined by means and chol over boxes defined by lower and upper or for exact observations obs.

Monte-Carlo (Genz, 1992, the default) and quasi-Monte-Carlo (Genz & Bretz, 2002) integration is implemented, the latter with weights obtained, for example, from packages **qrng** or **randtoolbox**. It is the responsibility of the user to ensure a meaningful lattice is used. In case of doubt, use plain Monte-Carlo (w = NULL) or [pmvnorm](#).

s1pmvnorm computes both the individual log-likelihood contributions and the corresponding score matrix (of dimension  $J \times (J + 1)/2 \times N$ ) if chol contains diagonal elements. Otherwise, the dimension is  $J \times (J - 1)/2 \times N$ . The scores for exact or mixed exact-interval observations are computed by sldmvnorm and sldpmvnorm, respectively.

More details can be found in the lmvnorm\_src package vignette.

## Value

The log-likelihood (logLik = TRUE) or the individual contributions to the log-likelihood. s1pmvnorm, sldmvnorm, and sldpmvnorm return the score matrices and, optionally (logLik = TRUE), the individual log-likelihood contributions as well as scores for obs, lower, upper, and mean.

## References

- Genz, A. (1992). Numerical computation of multivariate normal probabilities. *Journal of Computational and Graphical Statistics*, **1**, 141–150.
- Genz, A. and Bretz, F. (2002), Methods for the computation of multivariate t-probabilities. *Journal of Computational and Graphical Statistics*, **11**, 950–971.

## See Also

[dmvnorm](#), vignette("lmvnorm\_src", package = "mvtnorm")

## Examples

```
### five observations
N <- 5L
### dimension
J <- 4L

### lower and upper bounds, ie interval-censoring
lwr <- matrix(-runif(N * J), nrow = J)
upr <- matrix(runif(N * J), nrow = J)
```

```

### Cholesky factor
(C <- ltMatrices(runif(J * (J + 1) / 2), diag = TRUE))
### corresponding covariance matrix
(S <- as.array(Tcrossprod(C))[, , 1])

### plain Monte-Carlo (Genz, 1992)
w <- NULL
M <- 25000
### quasi-Monte-Carlo (Genz & Bretz, 2002, but with different weights)
if (require("qrng")) w <- t(ghalton(M * N, J - 1))

### log-likelihood
lpmvnorm(lower = lwr, upper = upr, chol = C, w = w, M = M)

### compare with pmvnorm
exp(lpmvnorm(lower = lwr, upper = upr, chol = C, logLik = FALSE, w = w, M = M))
sapply(1:N, function(i) pmvnorm(lower = lwr[,i], upper = upr[,i], sigma = S))

### log-lik contributions and score matrix
slpmvnorm(lower = lwr, upper = upr, chol = C, w = w, M = M, logLik = TRUE)

```

---

ltMatrices

*Multiple Lower Triangular or Symmetric Matrices*


---

## Description

A class representing multiple lower triangular or symmetric matrices and some methods.

## Usage

```

ltMatrices(object, diag = FALSE, byrow = FALSE, names = TRUE)
syMatrices(object, diag = FALSE, byrow = FALSE, names = TRUE)
## S3 method for class 'ltMatrices'
as.array(x, symmetric = FALSE, ...)
## S3 method for class 'syMatrices'
as.array(x, ...)
## S3 method for class 'ltMatrices'
diagonals(x, ...)
## S3 method for class 'syMatrices'
diagonals(x, ...)
## S3 method for class 'matrix'
diagonals(x, ...)
## S3 method for class 'integer'
diagonals(x, ...)
diagonals(x) <- value
## S3 replacement method for class 'ltMatrices'
diagonals(x) <- value
## S3 replacement method for class 'syMatrices'

```



```

diagonals(x) <- value
## S3 method for class 'ltMatrices'
solve(a, b, transpose = FALSE, ...)
## S3 method for class 'syMatrices'
chol(x, ...)
## S3 method for class 'chol'
aperm(a, perm, ...)
## S3 method for class 'invchol'
aperm(a, perm, ...)
## S3 method for class 'ltMatrices'
aperm(a, perm, ...)
## S3 method for class 'syMatrices'
aperm(a, perm, ...)
deperma(chol = solve(invchol), permuted_chol = solve(permuted_invchol),
        invchol, permuted_invchol, perm, score_schol)
## S3 method for class 'ltMatrices'
Mult(x, y, transpose = FALSE, ...)
## S3 method for class 'syMatrices'
Mult(x, y, ...)
Tcrossprod(x, diag_only = FALSE)
Crossprod(x, diag_only = FALSE)
logdet(x)
Lower_tri(x, diag = FALSE, byrow = attr(x, "byrow"))
is.ltMatrices(x)
is.syMatrices(x)
as.ltMatrices(x)
## S3 method for class 'ltMatrices'
as.ltMatrices(x)
## S3 method for class 'syMatrices'
as.ltMatrices(x)
as.syMatrices(x)
is.chol(x)
is.invchol(x)
as.chol(x)
as.invchol(x)
chol2cov(x)
invchol2chol(x)
chol2invchol(x)
invchol2cov(x)
invchol2pre(x)
chol2pre(x)
Dchol(x, D = 1 / sqrt(Tcrossprod(x, diag_only = TRUE)))
invcholD(x, D = sqrt(Tcrossprod(solve(x), diag_only = TRUE)))
chol2cor(x)
invchol2cor(x)
chol2pc(x)
invchol2pc(x)
vectrick(C, S, A, transpose = c(TRUE, TRUE))

```

```

standardize(chol, invchol)
destandardize(chol = solve(invchol), invchol, score_schol)
as.ltMatrices(x)

```

### Arguments

object	a matrix representing the lower triangular elements of $N$ lower triangular matrix, each of dimension $J \times J$ . Dimensions of object depend on diag: With diagonal elements, object is a $J(J + 1)/2 \times N$ matrix, otherwise, the number of rows is $J(J - 1)/2$ .
diag	logical, object contains diagonal elements if TRUE, otherwise unit diagonal elements are assumed.
byrow	logical, object represents matrices in row-major order if TRUE or, otherwise, in column-major order.
names	logical or character vector of length $J$ .
symmetric	logical, object is interpreted as a symmetric matrix if TRUE.
diag_only	logical, compute diagonal elements of crossproduct only if TRUE.
x, chol, invchol, permuted_chol, permuted_invchol	object of class ltMatrices or syMatrices (for chol).
value	a matrix of diagonal elements to be assigned (of dimension $J \times N$ ).
a	object of class ltMatrices.
perm	a permutation of the covariance matrix corresponding to a.
D	a matrix (of dimension $J \times N$ ) of diagonal elements to be multiplied with.
y	matrix with $J$ rows.
b	matrix with $J$ rows.
C	an object of class ltMatrices.
S	an object of class ltMatrices or a matrix with $J^2$ rows representing multiple $J \times J$ matrices (columns of vec operators).
A	an object of class ltMatrices.
transpose	a logical of length two indicating if A or B shall be transposed in vectrick. For solve, this argument being true computes solve(t(a), b) (in absence of a t() method for ltMatrices objects).
score_schol	score matrix for a standardized chol object.
...	additional arguments, currently ignored.

### Details

ltMatrices interprets a matrix as lower triangular elements of multiple lower triangular matrices. The corresponding class can be used to store such matrices efficiently. Matrix multiplications, solutions to linear systems, explicit inverses, and crossproducts can be computed based on such objects. Details can be found in the lmvnorm\_src package vignette.

syMatrices only store the lower triangular parts of multiple symmetric matrices.

**Value**

The constructor `ltMatrices` returns objects of class `ltMatrices` with corresponding methods. The constructor `syMatrices` returns objects of class `syMatrices` with a reduced set of methods.

**See Also**

`vignette("lmvnorm_src", package = "mvtnorm")`

**Examples**

```
J <- 4L
N <- 2L
dm <- paste0("d", 1:J)
xm <- paste0("x", 1:N)
(C <- ltMatrices(matrix(runif(N * J * (J + 1) / 2),
                      ncol = N, dimnames = list(NULL, xm)),
                 diag = TRUE, names = dm))

## dimensions and names
dim(C)
dimnames(C)
names(C)

## subset
C[,2:3]

## multiplication
y <- matrix(runif(N * J), nrow = J)
Mult(C, y)

## solve
solve(C)
solve(C, y)

## tcrossprod
Tcrossprod(C)

## convert to matrix
as.array(solve(C[1,]))[, ,1]
```

**Description**

Computes means and Cholesky factors of covariance or precision matrices of multiple multivariate normal distributions.

**Usage**

```
marg_mvnorm(chol, invchol, which = 1L)
cond_mvnorm(chol, invchol, which_given = 1L, given, center = FALSE)
```

**Arguments**

chol	Cholesky factors of covariance matrices as <code>ltMatrices</code> object, length is recycled to length of lower and upper.
invchol	Cholesky factors of precision matrices as <code>ltMatrices</code> object, length is recycled to length of lower and upper. Either chol or invchol must be given.
which	names or indices of elements those marginal distribution is of interest.
which_given	names or indices of elements to condition on.
given	matrix of realisations to condition on (number of rows is equal to length(which), the number of columns corresponds to the number of matrices in chol or invchol).
center	logical, if TRUE, the negative rescaled conditional mean is returned (such that it can be specified as center argument to <code>slp_mvnorm</code> ). By default, the conditional mean is returned.

**Details**

Derives parameters of the requested marginal or conditional distributions, defined by chol (Cholesky factor of covariance) or invchol (Cholesky factor of precision matrix) and, for conditional distributions, the mean.

More details can be found in the `lmvnorm_src` package vignette.

**Value**

A named list.

**See Also**

```
vignette("lmvnorm_src", package = "mvtnorm")
```

---

Mvnorm

*Multivariate Normal Density and Random Deviates*


---

**Description**

These functions provide the density function and a random number generator for the multivariate normal distribution with mean equal to mean and covariance matrix sigma.

**Usage**

```
dmvnorm(x, mean = rep(0, p), sigma = diag(p), log = FALSE, checkSymmetry = TRUE)
rmvnorm(n, mean = rep(0, nrow(sigma)), sigma = diag(length(mean)),
  method=c("eigen", "svd", "chol"), pre0.9_9994 = FALSE,
  checkSymmetry = TRUE, rnorm = stats::rnorm)
```

**Arguments**

<code>x</code>	vector or matrix of quantiles. When <code>x</code> is a matrix, each row is taken to be a quantile and columns correspond to the number of dimensions, <code>p</code> .
<code>n</code>	number of observations.
<code>mean</code>	mean vector, default is <code>rep(0, length = ncol(x))</code> . In <code>ldmvnorm</code> or <code>sldmvnorm</code> , <code>mean</code> is a matrix with observation-specific means arranged in columns.
<code>sigma</code>	covariance matrix, default is <code>diag(ncol(x))</code> .
<code>log</code>	logical; if TRUE, densities <code>d</code> are given as <code>log(d)</code> .
<code>method</code>	string specifying the matrix decomposition used to determine the matrix root of <code>sigma</code> . Possible methods are eigenvalue decomposition (" <code>eigen</code> ", default), singular value decomposition (" <code>svd</code> "), and Cholesky decomposition (" <code>chol</code> "). The Cholesky is typically fastest, not by much though.
<code>pre0.9_9994</code>	logical; if FALSE, the output produced in <code>mvtnorm</code> versions up to 0.9-9993 is reproduced. In 0.9-9994, the output is organized such that <code>rmvnorm(10, ...)</code> has the same first ten rows as <code>rmvnorm(100, ...)</code> when called with the same seed.
<code>checkSymmetry</code>	logical; if FALSE, skip checking whether the covariance matrix is symmetric or not. This will speed up the computation but may cause unexpected outputs when ill-behaved <code>sigma</code> is provided. The default value is TRUE.
<code>rnorm</code>	a function with the same interface as <code>rnorm</code> . This allows switching to other generators of standard normal variables.

**Details**

`dmvnorm` computes the density function of the multivariate normal specified by `mean` and the covariance matrix `sigma`.

`rmvnorm` generates multivariate normal variables.

**See Also**

[pmvnorm](#), [rnorm](#), [qmvnorm](#), `vignette("ldmvnorm_src", package = "mvtnorm")`

**Examples**

```
dmvnorm(x=c(0,0))
dmvnorm(x=c(0,0), mean=c(1,1))

sigma <- matrix(c(4,2,2,3), ncol=2)
x <- rmvnorm(n=500, mean=c(1,2), sigma=sigma)
colMeans(x)
var(x)
dS <- dmvnorm(x, sigma = sigma)

### alternative interface
C <- t(chol(sigma))
(C <- ltMatrices(C[lower.tri(C, diag = TRUE)], diag = TRUE))
dC <- exp(ldmvnorm(obs = t(x), chol = C, logLik = FALSE))
```

```

all.equal(dS, dC)

x <- rmvnorm(n=500, mean=c(1,2), sigma=sigma, method="chol")
colMeans(x)
var(x)

plot(x)

```

Mvt

*The Multivariate t Distribution***Description**

These functions provide information about the multivariate  $t$  distribution with non-centrality parameter (or mode)  $\delta$ , scale matrix  $\sigma$  and degrees of freedom  $df$ . `dmvt` gives the density and `rmvt` generates random deviates.

**Usage**

```

rmvt(n, sigma = diag(2), df = 1, delta = rep(0, nrow(sigma)),
     type = c("shifted", "Kshirsagar"), ...)
dmvt(x, delta = rep(0, p), sigma = diag(p), df = 1, log = TRUE,
     type = "shifted", checkSymmetry = TRUE)

```

**Arguments**

<code>x</code>	vector or matrix of quantiles. If <code>x</code> is a matrix, each row is taken to be a quantile.
<code>n</code>	number of observations.
<code>delta</code>	the vector of noncentrality parameters of length <code>n</code> , for <code>type = "shifted"</code> <code>delta</code> specifies the mode.
<code>sigma</code>	scale matrix, defaults to <code>diag(ncol(x))</code> .
<code>df</code>	degrees of freedom. <code>df = 0</code> or <code>df = Inf</code> corresponds to the multivariate normal distribution.
<code>log</code>	<b>logical</b> indicating whether densities $d$ are given as $\log(d)$ .
<code>type</code>	type of the noncentral multivariate $t$ distribution. <code>type = "Kshirsagar"</code> corresponds to formula (1.4) in Genz and Bretz (2009) (see also Chapter 5.1 in Kotz and Nadarajah (2004)). This is the noncentral $t$ -distribution needed for calculating the power of multiple contrast tests under a normality assumption. <code>type = "shifted"</code> corresponds to the formula right before formula (1.4) in Genz and Bretz (2009) (see also formula (1.1) in Kotz and Nadarajah (2004)). It is a location shifted version of the central $t$ -distribution. This noncentral multivariate $t$ distribution appears for example as the Bayesian posterior distribution for the regression coefficients in a linear regression. In the central case both types coincide. Note that the defaults differ from the default in <code>pmvt()</code> (for reasons of backward compatibility).

checkSymmetry logical; if FALSE, skip checking whether the covariance matrix is symmetric or not. This will speed up the computation but may cause unexpected outputs when ill-behaved sigma is provided. The default value is TRUE.

... additional arguments to `rmvnorm()`, for example method.

## Details

If  $\mathbf{X}$  denotes a random vector following a  $t$  distribution with location vector  $\mathbf{0}$  and scale matrix  $\Sigma$  (written  $X \sim t_\nu(\mathbf{0}, \Sigma)$ ), the scale matrix (the argument `sigma`) is not equal to the covariance matrix  $Cov(\mathbf{X})$  of  $\mathbf{X}$ . If the degrees of freedom  $\nu$  (the argument `df`) is larger than 2, then  $Cov(\mathbf{X}) = \Sigma\nu/(\nu - 2)$ . Furthermore, in this case the correlation matrix  $Cor(\mathbf{X})$  equals the correlation matrix corresponding to the scale matrix  $\Sigma$  (which can be computed with `cov2cor()`). Note that the scale matrix is sometimes referred to as “dispersion matrix”; see McNeil, Frey, Embrechts (2005, p. 74). For type = “shifted” the density

$$c(1 + (x - \delta)'S^{-1}(x - \delta)/\nu)^{-(\nu+m)/2}$$

is implemented, where

$$c = \Gamma((\nu + m)/2)/((\pi\nu)^{m/2}\Gamma(\nu/2)|S|^{1/2}),$$

$S$  is a positive definite symmetric matrix (the matrix `sigma` above),  $\delta$  is the non-centrality vector and  $\nu$  are the degrees of freedom.

`df=0` historically leads to the multivariate normal distribution. From a mathematical point of view, rather `df=Inf` corresponds to the multivariate normal distribution. This is (now) also allowed for `rmvt()` and `dmvt()`.

Note that `dmvt()` has default `log = TRUE`, whereas `dmvnorm()` has default `log = FALSE`.

## References

McNeil, A. J., Frey, R., and Embrechts, P. (2005). *Quantitative Risk Management: Concepts, Techniques, Tools*. Princeton University Press.

## See Also

`pmvt()` and `qmvmt()`

## Examples

```
## basic evaluation
dmvt(x = c(0,0), sigma = diag(2))

## check behavior for df=0 and df=Inf
x <- c(1.23, 4.56)
mu <- 1:2
Sigma <- diag(2)
x0 <- dmvt(x, delta = mu, sigma = Sigma, df = 0) # default log = TRUE!
x8 <- dmvt(x, delta = mu, sigma = Sigma, df = Inf) # default log = TRUE!
xn <- dmvnorm(x, mean = mu, sigma = Sigma, log = TRUE)
stopifnot(identical(x0, x8), identical(x0, xn))
```

```

## X ~ t_3(0, diag(2))
x <- rmvt(100, sigma = diag(2), df = 3) # t_3(0, diag(2)) sample
plot(x)

## X ~ t_3(mu, Sigma)
n <- 1000
mu <- 1:2
Sigma <- matrix(c(4, 2, 2, 3), ncol=2)
set.seed(271)
x <- rep(mu, each=n) + rmvt(n, sigma=Sigma, df=3)
plot(x)

## Note that the call rmvt(n, mean=mu, sigma=Sigma, df=3) does *not*
## give a valid sample from t_3(mu, Sigma)! [and thus throws an error]
try(rmvt(n, mean=mu, sigma=Sigma, df=3))

## df=Inf correctly samples from a multivariate normal distribution
set.seed(271)
x <- rep(mu, each=n) + rmvt(n, sigma=Sigma, df=Inf)
set.seed(271)
x. <- rmvnorm(n, mean=mu, sigma=Sigma)
stopifnot(identical(x, x.))

```

---

pmvnorm

---

*Multivariate Normal Distribution*


---

## Description

Computes the distribution function of the multivariate normal distribution for arbitrary limits and correlation matrices.

## Usage

```

pmvnorm(lower=-Inf, upper=Inf, mean=rep(0, length(lower)),
        corr=NULL, sigma=NULL, algorithm = GenzBretz(), keepAttr=TRUE,
        seed = NULL, ...)

```

## Arguments

lower	the vector of lower limits of length n.
upper	the vector of upper limits of length n.
mean	the mean vector of length n.
corr	the correlation matrix of dimension n.
sigma	the covariance matrix of dimension n less than 1000. Either corr or sigma can be specified. If sigma is given, the problem is standardized internally. If corr is given, it is assumed that appropriate standardization was performed by the user. If neither corr nor sigma is given, the identity matrix is used for sigma.



algorithm	an object of class <a href="#">GenzBretz</a> , <a href="#">Miwa</a> or <a href="#">TVPACK</a> specifying both the algorithm to be used as well as the associated hyper parameters.
keepAttr	<a href="#">logical</a> indicating if <a href="#">attributes</a> such as <code>error</code> and <code>msg</code> should be attached to the return value. The default, <code>TRUE</code> is back compatible.
seed	an object specifying if and how the random number generator should be initialized, see <a href="#">simulate</a> .
...	additional parameters (currently given to <a href="#">GenzBretz</a> for backward compatibility issues).

## Details

This program involves the computation of multivariate normal probabilities with arbitrary correlation matrices. It involves both the computation of singular and nonsingular probabilities. The implemented methodology is described in Genz (1992, 1993) (for algorithm [GenzBretz](#)), in Miwa et al. (2003) for algorithm [Miwa](#) (useful up to dimension 20) and Genz (2004) for the [TVPACK](#) algorithm (which covers 2- and 3-dimensional problems for semi-infinite integration regions).

Note the default algorithm [GenzBretz](#) is randomized and hence slightly depends on `.Random.seed` and that both `-Inf` and `+Inf` may be specified in lower and upper. For more details see [pmvt](#).

The multivariate normal case is treated as a special case of [pmvt](#) with `df=0` and univariate problems are passed to [pnorm](#).

The multivariate normal density and random deviates are available using [dmvnorm](#) and [rmvnorm](#).

[pmvnorm](#) is based on original implementations by Alan Genz, Frank Bretz, and Tetsuhisa Miwa developed for computing accurate approximations to the normal integral. Users interested in computing log-likelihoods involving such normal probabilities should consider function [lpmvnorm](#), which is more flexible and efficient for this task and comes with the ability to evaluate score functions.

## Value

The evaluated distribution function is returned, if `keepAttr` is true, with attributes

<code>error</code>	estimated absolute error
<code>msg</code>	status message(s).
<code>algorithm</code>	a <a href="#">character</a> string with <code>class(algorithm)</code> .

## References

- Genz, A. (1992). Numerical computation of multivariate normal probabilities. *Journal of Computational and Graphical Statistics*, **1**, 141–150.
- Genz, A. (1993). Comparison of methods for the computation of multivariate normal probabilities. *Computing Science and Statistics*, **25**, 400–405.
- Genz, A. (2004). Numerical computation of rectangular bivariate and trivariate normal and t-probabilities, *Statistics and Computing*, **14**, 251–260.
- Genz, A. and Bretz, F. (2009), *Computation of Multivariate Normal and t Probabilities*. Lecture Notes in Statistics, Vol. 195. Springer-Verlag, Heidelberg.
- Miwa, T., Hayter J. and Kuriki, S. (2003). The evaluation of general non-centred orthant probabilities. *Journal of the Royal Statistical Society, Ser. B*, **65**, 223–234.

**See Also**

[qmvnorm](#) for quantiles and [lpmvnorm](#) for log-likelihoods.

**Examples**

```
n <- 5
mean <- rep(0, 5)
lower <- rep(-1, 5)
upper <- rep(3, 5)
corr <- diag(5)
corr[lower.tri(corr)] <- 0.5
corr[upper.tri(corr)] <- 0.5
prob <- pmvnorm(lower, upper, mean, corr)
print(prob)

stopifnot(pmvnorm(lower=-Inf, upper=3, mean=0, sigma=1) == pnorm(3))

a <- pmvnorm(lower=-Inf, upper=c(.3, .5), mean=c(2, 4), diag(2))

stopifnot(round(a, 16) == round(prod(pnorm(c(.3, .5), c(2, 4))), 16))

a <- pmvnorm(lower=-Inf, upper=c(.3, .5, 1), mean=c(2, 4, 1), diag(3))

stopifnot(round(a, 16) == round(prod(pnorm(c(.3, .5, 1), c(2, 4, 1))), 16))

# Example from R News paper (original by Genz, 1992):

m <- 3
sigma <- diag(3)
sigma[2,1] <- 3/5
sigma[3,1] <- 1/3
sigma[3,2] <- 11/15
pmvnorm(lower=rep(-Inf, m), upper=c(1,4,2), mean=rep(0, m), corr=sigma)

# Correlation and Covariance

a <- pmvnorm(lower=-Inf, upper=c(2,2), sigma = diag(2)*2)
b <- pmvnorm(lower=-Inf, upper=c(2,2)/sqrt(2), corr=diag(2))
stopifnot(all.equal(round(a,5) , round(b, 5)))
```

**Description**

Computes the the distribution function of the multivariate t distribution for arbitrary limits, degrees of freedom and correlation matrices based on algorithms by Genz and Bretz.

**Usage**

```
pmvt(lower=-Inf, upper=Inf, delta=rep(0, length(lower)),
      df=1, corr=NULL, sigma=NULL, algorithm = GenzBretz(),
      type = c("Kshirsagar", "shifted"), keepAttr=TRUE, seed = NULL, ...)
```

**Arguments**

lower	the vector of lower limits of length n.
upper	the vector of upper limits of length n.
delta	the vector of noncentrality parameters of length n, for type = "shifted" delta specifies the mode.
df	degree of freedom as integer. Normal probabilities are computed for df=0.
corr	the correlation matrix of dimension n.
sigma	the scale matrix of dimension n. Either corr or sigma can be specified. If sigma is given, the problem is standardized internally. If corr is given, it is assumed that appropriate standardization was performed by the user. If neither corr nor sigma is given, the identity matrix is used for sigma.
algorithm	an object of class <a href="#">GenzBretz</a> or <a href="#">TVPACK</a> defining the hyper parameters of this algorithm.
type	type of the noncentral multivariate t distribution to be computed. The choice type = "Kshirsagar" corresponds to formula (1.4) in Genz and Bretz (2009) (see also Chapter 5.1 in Kotz and Nadarajah (2004)). This is the noncentral t-distribution needed for calculating the power of multiple contrast tests under a normality assumption. type = "shifted" corresponds to the formula right before formula (1.4) in Genz and Bretz (2009) (see also formula (1.1) in Kotz and Nadarajah (2004)). It is a location shifted version of the central t-distribution. This noncentral multivariate t distribution appears for example as the Bayesian posterior distribution for the regression coefficients in a linear regression. In the central case both types coincide.
keepAttr	<a href="#">logical</a> indicating if <a href="#">attributes</a> such as error and msg should be attached to the return value. The default, TRUE is back compatible.
seed	an object specifying if and how the random number generator should be initialized, see <a href="#">simulate</a> .
...	additional parameters (currently given to GenzBretz for backward compatibility issues).

**Details**

This function involves the computation of central and noncentral multivariate t-probabilities with arbitrary correlation matrices. It involves both the computation of singular and nonsingular probabilities. The methodology (for default `algorithm = GenzBretz()`) is based on randomized quasi Monte Carlo methods and described in Genz and Bretz (1999, 2002).

Because of the randomization, the result for this algorithm (slightly) depends on `.Random.seed`.

For 2- and 3-dimensional problems one can also use the [TVPACK](#) routines described by Genz (2004), which only handles semi-infinite integration regions (and for type = "Kshirsagar" only central problems).

For type = "Kshirsagar" and a given correlation matrix `corr`, for short  $A$ , say, (which has to be positive semi-definite) and degrees of freedom  $\nu$  the following values are numerically evaluated

$$I = 2^{1-\nu/2}/\Gamma(\nu/2) \int_0^\infty s^{\nu-1} \exp(-s^2/2) \Phi(s \cdot \text{lower}/\sqrt{\nu} - \delta, s \cdot \text{upper}/\sqrt{\nu} - \delta) ds$$

where

$$\Phi(a, b) = (\det(A)(2\pi)^m)^{-1/2} \int_a^b \exp(-x'Ax/2) dx$$

is the multivariate normal distribution and  $m$  is the number of rows of  $A$ .

For type = "shifted", a positive definite symmetric matrix  $S$  (which might be the correlation or the scale matrix), mode (vector)  $\delta$  and degrees of freedom  $\nu$  the following integral is evaluated:

$$c \int_{\text{lower}_1}^{\text{upper}_1} \dots \int_{\text{lower}_m}^{\text{upper}_m} (1 + (x - \delta)'S^{-1}(x - \delta)/\nu)^{-(\nu+m)/2} dx_1 \dots dx_m,$$

where

$$c = \Gamma((\nu + m)/2)/((\pi\nu)^{m/2}\Gamma(\nu/2)|S|^{1/2}),$$

and  $m$  is the number of rows of  $S$ .

Note that both `-Inf` and `+Inf` may be specified in the lower and upper integral limits in order to compute one-sided probabilities.

Univariate problems are passed to `pt`. If `df = 0`, normal probabilities are returned.

## Value

The evaluated distribution function is returned, if `keepAttr` is true, with attributes

<code>error</code>	estimated absolute error and
<code>msg</code>	status message (a <code>character</code> string).
<code>algorithm</code>	a <code>character</code> string with <code>class(algorithm)</code> .

## References

- Genz, A. and Bretz, F. (1999), Numerical computation of multivariate t-probabilities with application to power calculation of multiple contrasts. *Journal of Statistical Computation and Simulation*, **63**, 361–378.
- Genz, A. and Bretz, F. (2002), Methods for the computation of multivariate t-probabilities. *Journal of Computational and Graphical Statistics*, **11**, 950–971.
- Genz, A. (2004), Numerical computation of rectangular bivariate and trivariate normal and t-probabilities, *Statistics and Computing*, **14**, 251–260.
- Genz, A. and Bretz, F. (2009), *Computation of Multivariate Normal and t Probabilities*. Lecture Notes in Statistics, Vol. 195. Springer-Verlag, Heidelberg.

S. Kotz and S. Nadarajah (2004), *Multivariate t Distributions and Their Applications*. Cambridge University Press. Cambridge.

Edwards D. and Berry, Jack J. (1987), The efficiency of simulation-based multiple comparisons. *Biometrics*, **43**, 913–928.

### See Also

[qmv](#)

### Examples

```
n <- 5
lower <- -1
upper <- 3
df <- 4
corr <- diag(5)
corr[lower.tri(corr)] <- 0.5
delta <- rep(0, 5)
prob <- pmvt(lower=lower, upper=upper, delta=delta, df=df, corr=corr)
print(prob)
```

```
pmvt(lower=-Inf, upper=3, df = 3, sigma = 1) == pt(3, 3)
```

```
# Example from R News paper (original by Edwards and Berry, 1987)
```

```
n <- c(26, 24, 20, 33, 32)
V <- diag(1/n)
df <- 130
C <- c(1,1,1,0,0,-1,0,0,1,0,0,-1,0,0,1,0,0,0,-1,-1,0,0,-1,0,0)
C <- matrix(C, ncol=5)
### scale matrix
cv <- C %%% tcrossprod(V, C)
### correlation matrix
cr <- cov2cor(cv)
delta <- rep(0,5)
```

```
myfct <- function(q, alpha) {
  lower <- rep(-q, ncol(cv))
  upper <- rep(q, ncol(cv))
  pmvt(lower=lower, upper=upper, delta=delta, df=df,
        corr=cr, abseps=0.0001) - alpha
}
```

```
### uniroot for this simple problem
round(uniroot(myfct, lower=1, upper=5, alpha=0.95)$root, 3)
```

```
# compare pmvt and pmvnorm for large df:
```

```
a <- pmvnorm(lower=-Inf, upper=1, mean=rep(0, 5), corr=diag(5))
b <- pmvt(lower=-Inf, upper=1, delta=rep(0, 5), df=300,
          corr=diag(5))
a
```

```

b
stopifnot(round(a, 2) == round(b, 2))

# correlation and scale matrix

a <- pmvt(lower=-Inf, upper=2, delta=rep(0,5), df=3,
          sigma = diag(5)*2)
b <- pmvt(lower=-Inf, upper=2/sqrt(2), delta=rep(0,5),
          df=3, corr=diag(5))
attributes(a) <- NULL
attributes(b) <- NULL
a
b
stopifnot(all.equal(round(a,3) , round(b, 3)))

a <- pmvt(0, 1,df=10)
attributes(a) <- NULL
b <- pt(1, df=10) - pt(0, df=10)
stopifnot(all.equal(round(a,10) , round(b, 10)))

```

---

qmvnorm

*Quantiles of the Multivariate Normal Distribution*


---

### Description

Computes the equicoordinate quantile function of the multivariate normal distribution for arbitrary correlation matrices based on inversion of `pmvnorm`, using a stochastic root finding algorithm described in Bornkamp (2018).

### Usage

```

qmvnorm(p, interval = NULL, tail = c("lower.tail", "upper.tail", "both.tails"),
        mean = 0, corr = NULL, sigma = NULL, algorithm = GenzBretz(),
        ptol = 0.001, maxiter = 500, trace = FALSE, seed = NULL, ...)

```

### Arguments

<code>p</code>	probability.
<code>interval</code>	optional, a vector containing the end-points of the interval to be searched. Does not need to contain the true quantile, just used as starting values by the root-finder. If equal to <code>NULL</code> a guess is used.
<code>tail</code>	specifies which quantiles should be computed. <code>lower.tail</code> gives the quantile $x$ for which $P[X \leq x] = p$ , <code>upper.tail</code> gives $x$ with $P[X > x] = p$ and <code>both.tails</code> leads to $x$ with $P[-x \leq X \leq x] = p$ .
<code>mean</code>	the mean vector of length <code>n</code> .
<code>corr</code>	the correlation matrix of dimension <code>n</code> .

sigma	the covariance matrix of dimension $n$ . Either <code>corr</code> or <code>sigma</code> can be specified. If <code>sigma</code> is given, the problem is standardized internally. If <code>corr</code> is given, it is assumed that appropriate standardization was performed by the user. If neither <code>corr</code> nor <code>sigma</code> is given, the identity matrix is used for <code>sigma</code> .
algorithm	an object of class <a href="#">GenzBretz</a> , <a href="#">Miwa</a> or <a href="#">TVPACK</a> specifying both the algorithm to be used as well as the associated hyper parameters.
ptol, maxiter, trace	Parameters passed to the stochastic root-finding algorithm. Iteration stops when the 95% confidence interval for the predicted quantile is inside $[p-ptol, p+ptol]$ . <code>maxiter</code> is the maximum number of iterations for the root finding algorithm. <code>trace</code> prints the iterations of the root finder.
seed	an object specifying if and how the random number generator should be initialized, see <a href="#">simulate</a> .
...	additional parameters to be passed to <a href="#">GenzBretz</a> .

### Details

Only equicoordinate quantiles are computed, i.e., the quantiles in each dimension coincide. The result is seed dependent.

### Value

A list with two components: `quantile` and `f.quantile` give the location of the quantile and the difference between the distribution function evaluated at the quantile and  $p$ .

### References

Bornkamp, B. (2018). Calculating quantiles of noisy distribution functions using local linear regressions. *Computational Statistics*, **33**, 487–501.

### See Also

[pmvnorm](#), [qmv<sub>t</sub>](#)

### Examples

```
qmvnorm(0.95, sigma = diag(2), tail = "both")
```

---

qmv<sub>t</sub>
*Quantiles of the Multivariate t Distribution*


---

### Description

Computes the equicoordinate quantile function of the multivariate  $t$  distribution for arbitrary correlation matrices based on inversion of [pmv<sub>t</sub>](#), using a stochastic root finding algorithm described in Bornkamp (2018).

**Usage**

```
qmvt(p, interval = NULL, tail = c("lower.tail", "upper.tail", "both.tails"),
     df = 1, delta = 0, corr = NULL, sigma = NULL, algorithm = GenzBretz(),
     type = c("Kshirsagar", "shifted"), ptol = 0.001, maxiter = 500,
     trace = FALSE, seed = NULL, ...)
```

**Arguments**

p	probability.
interval	optional, a vector containing the end-points of the interval to be searched. Does not need to contain the true quantile, just used as starting values by the root-finder. If equal to NULL a guess is used.
tail	specifies which quantiles should be computed. <code>lower.tail</code> gives the quantile $x$ for which $P[X \leq x] = p$ , <code>upper.tail</code> gives $x$ with $P[X > x] = p$ and <code>both.tails</code> leads to $x$ with $P[-x \leq X \leq x] = p$ .
delta	the vector of noncentrality parameters of length $n$ , for <code>type = "shifted"</code> delta specifies the mode.
df	degree of freedom as integer. Normal quantiles are computed for $df = 0$ or $df = \text{Inf}$ .
corr	the correlation matrix of dimension $n$ .
sigma	the covariance matrix of dimension $n$ . Either <code>corr</code> or <code>sigma</code> can be specified. If <code>sigma</code> is given, the problem is standardized internally. If <code>corr</code> is given, it is assumed that appropriate standardization was performed by the user. If neither <code>corr</code> nor <code>sigma</code> is given, the identity matrix in the univariate case (so <code>corr = 1</code> ) is used for <code>corr</code> .
algorithm	an object of class <a href="#">GenzBretz</a> or <a href="#">TVPACK</a> defining the hyper parameters of this algorithm.
type	type of the noncentral multivariate t distribution to be computed. The choice <code>type = "Kshirsagar"</code> corresponds to formula (1.4) in Genz and Bretz (2009) (see also Chapter 5.1 in Kotz and Nadarajah (2004)) and <code>type = "shifted"</code> corresponds to the formula before formula (1.4) in Genz and Bretz (2009) (see also formula (1.1) in Kotz and Nadarajah (2004)).
ptol, maxiter, trace	Parameters passed to the stochastic root-finding algorithm. Iteration stops when the 95% confidence interval for the predicted quantile is inside $[p-\text{ptol}, p+\text{ptol}]$ . <code>maxiter</code> is the maximum number of iterations for the root finding algorithm. <code>trace</code> prints the iterations of the root finder.
seed	an object specifying if and how the random number generator should be initialized, see <a href="#">simulate</a> .
...	additional parameters to be passed to <a href="#">GenzBretz</a> .

**Details**

Only equicoordinate quantiles are computed, i.e., the quantiles in each dimension coincide. The result is seed dependent.



**Value**

A list with two components: `quantile` and `f.quantile` give the location of the quantile and the difference between the distribution function evaluated at the quantile and `p`.

**References**

Bornkamp, B. (2018). Calculating quantiles of noisy distribution functions using local linear regressions. *Computational Statistics*, **33**, 487–501.

**See Also**

[p<sub>m</sub>vnorm](#), [q<sub>m</sub>vnorm](#)

**Examples**

```
## basic evaluation
qmvt(0.95, df = 16, tail = "both")

## check behavior for df=0 and df=Inf
Sigma <- diag(2)
set.seed(29)
q0 <- qmvt(0.95, sigma = Sigma, df = 0, tail = "both")$quantile
set.seed(29)
q8 <- qmvt(0.95, sigma = Sigma, df = Inf, tail = "both")$quantile
set.seed(29)
qn <- qmvnorm(0.95, sigma = Sigma, tail = "both")$quantile
stopifnot(identical(q0, q8),
           isTRUE(all.equal(q0, qn, tol = (.Machine$double.eps)^(1/3))))

## if neither sigma nor corr are provided, corr = 1 is used internally
df <- 0
set.seed(29)
qt95 <- qmvt(0.95, df = df, tail = "both")$quantile
set.seed(29)
qt95.c <- qmvt(0.95, df = df, corr = 1, tail = "both")$quantile
set.seed(29)
qt95.s <- qmvt(0.95, df = df, sigma = 1, tail = "both")$quantile
stopifnot(identical(qt95, qt95.c),
           identical(qt95, qt95.s))

df <- 4
set.seed(29)
qt95 <- qmvt(0.95, df = df, tail = "both")$quantile
set.seed(29)
qt95.c <- qmvt(0.95, df = df, corr = 1, tail = "both")$quantile
set.seed(29)
qt95.s <- qmvt(0.95, df = df, sigma = 1, tail = "both")$quantile
stopifnot(identical(qt95, qt95.c),
           identical(qt95, qt95.s))
```

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