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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.

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`mvtnorm-package` *Multivariate Normal and t Distributions*

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 `lmvnorm_src` package vignette.

See Also

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

`algorithms` *Choice of Algorithm and Hyper Parameters*

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 `pmvt()` or `pmvnorm()`).
`maxval`	replacement for `Inf` when non-orthant probabilities involving `Inf` 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); Genz (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, Hayter, and Kuriki (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**(2), 141–149. doi:10.1080/10618600.1992.10477010.

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**(3), 251–260. doi:10.1023/B:STCO.0000035304.20635.31.

Genz A, Bretz F (2002). "Methods for the Computation of Multivariate t Probabilities." *Journal of Computational and Graphical Statistics*, **11**(4), 950–971. doi:10.1198/106186002394.

Miwa T, Hayter AJ, Kuriki S (2003). "The Evaluation of General Non-centred Orthant Probabilities." *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, **65**(1), 223–234. doi:10.1111/14679868.00382.

`interface` *User Interface to Multiple Multivariate Normal Distributions*

Description

A simple user interface for computing on multiple multivariate normal distributions.

Usage

```
mvnorm(mean, invcholmean, 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

`chol`	either an `ltMatrices` object specifying (multiple) Cholesky factors of the covariance matrix or one single numeric lower triangular square matrix.
`invchol`	either an `ltMatrices` object specifying (multiple) inverse Cholesky factors of the covariance matrix or one single numeric lower triangular square matrix.

a, object	objects of class mvnorm.
perm	a permutation of the covariance matrix corresponding to a.
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.
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).
invcholmean	matrix of scaled means, that is, invchol %*% mean, one column for each observation, length is recycled to length of obs, lower and upper.
seed	an object specifying if and how the random number generator should be initialized, see simulate.
standardize	logical, should the Cholesky factor (or its inverse) undergo standardization (ensuring the covariance matrix is a correlation matrix) before computing the likelihood.
nsim	number of samples to draw.
as.data.frame	logical, convert the $J x N$ matrix result to a classical $N x J$ data frame.
...	Additional arguments to ldpmvnorm and sldpmvnorm

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, invcholmean, center = NULL, chol, invchol, logLik = TRUE,
        M = NULL, w = NULL, seed = NULL, tol = .Machine$double.eps, fast = FALSE)
slpmvnorm(lower, upper, mean, invcholmean, center = NULL, chol, invchol, logLik = TRUE,
         M = NULL, w = NULL, seed = NULL, tol = .Machine$double.eps, fast = FALSE)
ldmvnorm(obs, mean, invcholmean, chol, invchol, logLik = TRUE)
sldmvnorm(obs, mean, invcholmean, chol, invchol, logLik = TRUE)
ldpmvnorm(obs, lower, upper, mean, invcholmean, chol, invchol, logLik = TRUE, ...)
sldpmvnorm(obs, lower, upper, mean, invcholmean, 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).
invcholmean	matrix of means left-multiplied with inverse Cholesky factor (invchol %*% mean, 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 cond_mvnorm(..., center = TRUE)..
chol	Cholesky factors of covariance matrices as ltMatrices object, length is recylced to length of obs, lower and upper.
invchol	Cholesky factors of precision matrices as ltMatrices object, length is recylced 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 and Bretz 2002). Note that the same weights for evaluating the multivariate normal probability are used for all observations when ncol(w) == M is specified.

	If `ncol(w) == ncol(lower) * M`, 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 `simulate`. 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 and 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`.

`slpmvnorm` 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. `slpmvnorm`, `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**(2), 141–149. doi:10.1080/10618600.1992.10477010.

Genz A, Bretz F (2002). "Methods for the Computation of Multivariate t Probabilities." *Journal of Computational and Graphical Statistics*, **11**(4), 950–971. doi:10.1198/106186002394.

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)
```

`lpRR` *Multivariate Normal Log-likelihood and Score Functions for Reduced Rank Covariances*

Description

Computes the log-likelihood (contributions) of interval-censored observations from multivariate normal distributions with reduced rank structure and evaluates corresponding score functions.

Usage

```
lpRR(lower, upper, mean = 0, B, D = rep(1, nrow(B)),
     Z, weights = 1 / ncol(Z), log.p = TRUE)
slpRR(lower, upper, mean = 0, B, D = rep(1, nrow(B)),
      Z, weights = 1 / ncol(Z), log.p = TRUE)
```

Arguments

`lower`	vector of lower limits (one element for each dimension, J elements).
`upper`	vector of upper limits (one element for each dimension, J elements).
`mean`	vector of means (one element for each dimension, length is recycled to length of `lower` and `upper`).
`B`	matrix of dimension $J \times K$.

D	vector of J diagonal elements.
Z	matrix of standard normal random variables, with K nrows.
weights	optional weights.
log.p	logical. By default, log-probabilities are returned.

Details

Evaluates the multivariate normal log-likelihood defined by mean, B and D when the covariance is $\Sigma = BB^\top + D$ over boxes defined by lower and upper. Details are given in Genz and Bretz (2009), Chapter 2.3.1.

slpRR computes the corresponding score functions with respect to lower, upper, mean, B and D.

More details can be found in the lmvnorm_src package vignette.

Value

The log-likelihood (log.p = TRUE) or corresponding probability. slpRR return the scores.

References

Genz A, Bretz F (2009). *Computation of Multivariate Normal and t Probabilities*, series Lecture Notes in Statistics. Springer-Verlag, Heidelberg, Germany. ISBN 978-3-642-01688-2.

See Also

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

Examples

```
J <- 6
K <- 3
B <- matrix(rnorm(J * K), nrow = J)
D <- runif(J)
S <- tcrossprod(B) + diag(D)
a <- -(2 + runif(J))
b <- 2 + runif(J)
M <- 1e4
Z <- matrix(rnorm(K * M), nrow = K)
## log-likelihood
lpRR(lower = a, upper = b, B = B, D = D, Z = Z)
## score wrt all arguments
slpRR(lower = a, upper = b, B = B, D = D, Z = Z)
```

`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)
## S3 method for class 'ltMatrices'
tcrossprod(x, y = NULL, ...)
## S3 method for class 'syMatrices'
tcrossprod(x, y = NULL, ...)
## S3 method for class 'ltMatrices'
crossprod(x, y = NULL, ...)
## S3 method for class 'syMatrices'
crossprod(x, y = NULL, ...)
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)
cov2invchol(x)
cov2chol(x)
invchol(x, ...)
## S3 method for class 'syMatrices'
invchol(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 triagular 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 or J^2 rows, interpreted as matrix of vectors or matrix of vectorised quadratic matrices.
`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 JxJ 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, explicite 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)
C

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

## tcrossprod
Tcrossprod(C)
tcrossprod(C)

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

---

margcond *Marginal and Conditional Multivariate Normal Distributions*

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 ltMatrices object, length is recylced to length of lower and upper.
invchol	Cholesky factors of precision matrices as ltMatrices object, length is recylced 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 slpmvnorm). 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

x	vector or matrix of quantiles. When x is a matrix, each row is taken to be a quantile and columns correspond to the number of dimensions, p.
n	number of observations.
mean	mean vector, default is rep(0, length = ncol(x)). In ldmvnorm or sldmvnorm, mean is a matrix with observation-specific means arranged in columns.
sigma	covariance matrix, default is diag(ncol(x)).
log	logical; if TRUE, densities d are given as log(d).
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.
pre0.9_9994	logical; if FALSE, the output produced in mvtnorm versions up to 0.9-9993 is reproduced. In 0.9-9994, the output is organized such that rmvnorm(10,...) has the same first ten rows as rmvnorm(100, ...) when called with the same seed.
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.
rnorm	a function with the same interface as rnorm. 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("lmvnorm_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

`x`	vector or matrix of quantiles. If `x` is a matrix, each row is taken to be a quantile.
`n`	number of observations.
`delta`	the vector of noncentrality parameters of length `n`, for `type = "shifted"` delta specifies the mode.
`sigma`	scale matrix, defaults to `diag(ncol(x))`.
`df`	degrees of freedom. `df = 0` or `df = Inf` corresponds to the multivariate normal distribution.
`log`	`logical` indicating whether densities d are given as $\log(d)$.
`type`	type of the noncentral multivariate t distribution. 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. Note that the defaults differ from the default in `pmvt()` (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 $\boldsymbol{X}$ denotes a random vector following a t distribution with location vector $\mathbf{0}$ and scale matrix Σ (written $X \sim t_\nu(\mathbf{0}, \Sigma)$), the scale matrix (the argument sigma) is not equal to the covariance matrix $Cov(\boldsymbol{X})$ of $\boldsymbol{X}$. If the degrees of freedom ν (the argument df) is larger than 2, then $Cov(\boldsymbol{X}) = \Sigma\nu/(\nu-2)$. Furthermore, in this case the correlation matrix $Cor(\boldsymbol{X})$ equals the correlation matrix corresponding to the scale matrix Σ (which can be computed with cov2cor()). Note that the scale matrix is sometimes referred to as "dispersion matrix"; see McNeil, Frey, and 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), δ is the non-centrality vector and ν 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

Genz A, Bretz F (2009). *Computation of Multivariate Normal and t Probabilities*, series Lecture Notes in Statistics. Springer-Verlag, Heidelberg, Germany. ISBN 978-3-642-01688-2.

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

McNeil AJ, Frey R, Embrechts P (2005). *Quantitative Risk Management: Concepts, Techniques, Tools*. Princeton University Press, Princeton, New Jersey, U.S.A.

See Also

pmvt() and qmvt()

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 GenzBretz, Miwa or TVPACK specifying both the algorithm to be used as well as the associated hyper parameters.
keepAttr	logical indicating if attributes 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 simulate.
...	additional parameters (currently given to GenzBretz 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) and Genz (1993) for algorithm GenzBretz, in Miwa, Hayter, and Kuriki (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.

An overview is available from Genz and Bretz (2009).

Value

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

error	estimated absolute error
msg	status message(s).
algorithm	a character string with class(algorithm).

References

Genz A (1992). "Numerical Computation of Multivariate Normal Probabilities." *Journal of Computational and Graphical Statistics*, **1**(2), 141–149. doi:10.1080/10618600.1992.10477010.

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**(3), 251–260. doi:10.1023/B:STCO.0000035304.20635.31.

Genz A, Bretz F (2009). *Computation of Multivariate Normal and t Probabilities*, series Lecture Notes in Statistics. Springer-Verlag, Heidelberg, Germany. ISBN 978-3-642-01688-2.

Miwa T, Hayter AJ, Kuriki S (2003). "The Evaluation of General Non-centred Orthant Probabilities." *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, **65**(1), 223–234. doi:10.1111/14679868.00382.

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)))
```

pmvt *Multivariate t Distribution*

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 GenzBretz or TVPACK 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	logical indicating if attributes 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 simulate.
...	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); Genz and Bretz (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 ν the following values are numerically evaluated

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

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) δ and degrees of freedom ν the following integral is evaluated:

$$c \int_{lower_1}^{upper_1} ... \int_{lower_m}^{upper_m} (1 + (x - \delta)' S^{-1} (x - \delta)/\nu)^{-(\nu+m)/2}\, dx_1 ... dx_m,$$

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

`error`	estimated absolute error and
`msg`	status message (a `character` string).
`algorithm`	a `character` string with `class(algorithm)`.

References

Genz A (2004). "Numerical Computation of Rectangular Bivariate and Trivariate Normal and t Probabilities." *Statistics and Computing*, **14**(3), 251–260. doi:10.1023/B:STCO.0000035304.20635.31.

Genz A, Bretz F (2009). *Computation of Multivariate Normal and t Probabilities*, series Lecture Notes in Statistics. Springer-Verlag, Heidelberg, Germany. ISBN 978-3-642-01688-2.

Genz A, Bretz F (1999). "Numerical Computation of Multivariate t-probabilities with Application to Power Calculation of Multiple Contrasts." *Journal of Statistical Computation and Simulation*, **63**(4), 103–117. doi:10.1080/00949659908811962.

Genz A, Bretz F (2002). "Methods for the Computation of Multivariate t Probabilities." *Journal of Computational and Graphical Statistics*, **11**(4), 950–971. doi:10.1198/106186002394.

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

See Also

qmvt

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

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. `lower.tail` gives the quantile x for which $P[X \leq x] = p$, `upper.tail` gives x with $P[X > x] = p$ and `both.tails` leads to x with $P[-x \leq X \leq x] = p$.
mean	the mean vector of length n.
corr	the correlation matrix of dimension n.
sigma	the covariance 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 `GenzBretz`, `Miwa` or `TVPACK` 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]. `maxiter` is the maximum number of iterations for the root finding algorithm. `trace` prints the iterations of the root finder.
seed	an object specifying if and how the random number generator should be initialized, see `simulate`.
...	additional parameters to be passed to `GenzBretz`.

Details

Only equicoordinate quantiles are computed, i.e., the quantiles in each dimension coincide. The result is seed dependend. The concept is explained in Bornkamp (2018).

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**(1), 487–501. doi:10.1007/s0018001707360.

See Also

`pmvnorm`, `qmvt`

Examples

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

qmvt *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 pmvt, 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. lower.tail gives the quantile x for which $P[X \leq x] = p$, upper.tail gives x with $P[X > x] = p$ and both.tails leads to x with $P[-x \leq X \leq x] = p$.
delta	the vector of noncentrality parameters of length n, for type = "shifted" delta specifies the mode.
df	degree of freedom as integer. Normal quantiles are computed for df = 0 or df = Inf.
corr	the correlation matrix of dimension n.
sigma	the covariance 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 in the univariate case (so corr = 1) is used for corr.
algorithm	an object of class GenzBretz or TVPACK 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).

`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]. `maxiter` is the maximum number of iterations for the root finding algorithm. `trace` prints the iterations of the root finder.

`seed`
: an object specifying if and how the random number generator should be initialized, see `simulate`.

`...`
: additional parameters to be passed to `GenzBretz`.

Details

Only equicoordinate quantiles are computed, i.e., the quantiles in each dimension coincide. The result is seed dependend. The concept is explained in Bornkamp (2018).

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**(1), 487–501. doi:10.1007/s0018001707360.

Genz A, Bretz F (2009). *Computation of Multivariate Normal and t Probabilities*, series Lecture Notes in Statistics. Springer-Verlag, Heidelberg, Germany. ISBN 978-3-642-01688-2.

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

See Also

`pmvnorm`, `qmvnorm`

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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