

The mvtnorm Package

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Title Multivariate Normal and T Distribution

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Description Computes multivariate normal and t probabilities, quantiles and densities.

Imports stats

Depends R(>= 1.9.0)

License GPL

R topics documented:

| | |
|----------------------------|-----------|
| Mvnorm | 1 |
| Mvt | 2 |
| mvtnorm-internal | 3 |
| pmvnorm | 3 |
| pmvt | 5 |
| qmvnorm | 7 |
| qmvt | 9 |
| Index | 10 |

Mvnorm *The Multivariate Normal Distribution*

Description

These functions provide information about the multivariate normal distribution with mean equal to mean and covariance matrix `sigma`. `dmvnorm` gives the density and `rmvnorm` generates random deviates.

Usage

```
dmvnorm(x, mean, sigma, log=FALSE)
rmvnorm(n, mean, sigma)
```

Arguments

| | |
|-------|--|
| x | Vector or matrix of quantiles. If x is a matrix, each row is taken to be a quantile. |
| n | Number of observations. |
| mean | Mean vector, default is <code>rep(0, length = ncol(x))</code> . |
| sigma | Covariance matrix, default is <code>diag(ncol(x))</code> . |
| log | Logical; if TRUE, densities d are given as <code>log(d)</code> . |

Author(s)

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See Also

[pmvnorm](#), [rnorm](#), [qmvnorm](#)

Examples

```
dmvnorm(x=c(0,0))
dmvnorm(x=c(0,0), mean=c(1,1))
x <- rmvnorm(n=100, mean=c(1,1))
plot(x)
```

Mvt

The Multivariate t Distribution

Description

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

Usage

```
rmvt(n, sigma = diag(2), df = 1)
dmvt(x, delta, sigma, df = 1, log = 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. |
| sigma | Covariance matrix, default is <code>diag(ncol(x))</code> . |
| df | degree of freedom as integer. |
| log | Logical; if TRUE, densities d are given as <code>log(d)</code> . |

See Also

[pmvt](#) and [qmvmt](#)

Examples

```
dmvt(x=c(0,0), sigma = diag(2))
x <- rmvt(n=100, sigma = diag(2), df = 3)
plot(x)
```

mvtnorm-internal *Internal mvtnorm function*

Description

Internal mvtnorm functions.

Usage

```
mvt(lower, upper, df, corr, delta, maxpts = 25000, abseps = 0.001,
     releps = 0)
```

Details

This functions are not to be called by the user.

pmvnorm *Multivariate Normal Distribution*

Description

Computes the distribution function of the multivariate normal distribution for arbitrary limits and correlation matrices based on algorithms by Genz and Bretz.

Usage

```
pmvnorm(lower=-Inf, upper=Inf, mean=rep(0, length(lower)),
         corr=NULL, sigma=NULL, maxpts = 25000, abseps = 0.001,
         releps = 0)
```

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. Either <code>corr</code> or <code>sigma</code> can be specified. If <code>sigma</code> is given, the problem is standardized. If neither <code>corr</code> nor <code>sigma</code> is given, the identity matrix is used for <code>sigma</code> . |
| maxpts | maximum number of function values as integer. |
| abseps | absolute error tolerance as double. |
| releps | relative error tolerance as double. |

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 methodology is described in Genz (1992, 1993).

Note 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](#).

Multivariate normal density and random numbers are available using [dmvnorm](#) and [rmvnorm](#).

Value

The evaluated distribution function is returned with attributes

| | |
|-------|------------------------------|
| error | estimated absolute error and |
| msg | status messages. |

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

See Also

[qmvnorm](#)

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, maxpts = 25000, abseps = 0.001,
      releps = 0)

```

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. |
| df | degree of freedom as integer. |
| 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. If neither <code>corr</code> nor <code>sigma</code> is given, the identity matrix is used for <code>sigma</code> . |
| maxpts | maximum number of function values as integer. |
| abseps | absolute error tolerance as double. |
| releps | relative error tolerance as double. |

Details

This program 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 is described in Genz and Bretz (1999, 2002).

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

$$I = K \int s^{df-1} \exp(-s^2/2) \Phi(s \cdot lower/\sqrt{df} - delta, s \cdot upper/\sqrt{df} - delta) ds$$

where $\Phi(a, b) = K' \int_a^b \exp(-x'Ax/2) dx$ is the multivariate normal distribution, $K' = 1/\sqrt{\det(A)(2\pi)^m}$ and $K = 2^{1-df/2}/\text{Gamma}(df/2)$ are constants and the (single) integral of I goes from 0 to `+Inf`.

Note that both `-Inf` and `+Inf` may be specified in the lower and upper integral limits in order to compute one-sided probabilities. Randomized quasi-Monte Carlo methods are used for the computations.

Univariate problems are passed to `pt`.

Further information can be obtained from the quoted articles, which can be downloaded (together with additional material and additional codes) from the websites <http://www.bioinf.uni-hannover.de/~bretz/> and <http://www.sci.wsu.edu/math/faculty/genz/homepage>.

If `df = 0`, normal probabilities are returned.

Value

The evaluated distribution function is returned with attributes

| | |
|--------------------|------------------------------|
| <code>error</code> | estimated absolute error and |
| <code>msg</code> | status messages. |

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.

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)
### covariance matrix
cv <- C %*% V %*% t(C)
### correlation matrix
dv <- t(1/sqrt(diag(cv)))
cr <- cv * (t(dv) %*% dv)
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
}

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=rep(300,5),
          corr=diag(5))

a
b

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

# correlation and covariance 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 an inversion of the algorithms by Genz and Bretz.

Usage

```

qmvnorm(p, interval = c(-10, 10), tail = c("lower.tail", "upper.tail", "both.tails"),
        mean = 0, corr = NULL, sigma = NULL, maxpts = 25000, abseps = 0.001,
        releps = 0, ...)

```

Arguments

| | |
|----------|---|
| p | probability. |
| interval | a vector containing the end-points of the interval to be searched by uniroot . |
| 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 $P[-x \leq X \leq x] = p$. |
| mean | the mean vector of length n . |
| 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. If neither <code>corr</code> nor <code>sigma</code> is given, the identity matrix is used for <code>sigma</code> . |
| maxpts | maximum number of function values as integer. |
| abseps | absolute integration error tolerance as double. |
| releps | relative integration error tolerance as double. |
| ... | additional parameters to be passed to uniroot . |

Details

Only equicoordinate quantiles are computed, i.e., the quantiles in each dimension coincide. Currently, the distribution function is inverted by using the [uniroot](#) function which may result in limited accuracy of the quantiles.

Value

A list with four components: `quantile` and `f.quantile` give the location of the quantile and the value of the function evaluated at that point. `iter` and `estim.prec` give the number of iterations used and an approximate estimated precision from [uniroot](#).

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 an inversion of the algorithms by Genz and Bretz.

Usage

```
qmvT(p, interval = c(-10, 10), tail = c("lower.tail", "upper.tail", "both.tails"),
      df = 1, delta = 0, corr = NULL, sigma = NULL, maxpts = 25000,
      abseps = 0.001, releps = 0, ...)
```

Arguments

| | |
|----------|---|
| p | probability. |
| interval | a vector containing the end-points of the interval to be searched by uniroot . |
| 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 . |
| df | degree of freedom as integer. |
| 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. If neither <code>corr</code> nor <code>sigma</code> is given, the identity matrix is used for <code>sigma</code> . |
| maxpts | maximum number of function values as integer. |
| abseps | absolute integration error tolerance as double. |
| releps | relative integration error tolerance as double. |
| ... | additional parameters to be passed to uniroot . |

Details

Only equicoordinate quantiles are computed, i.e., the quantiles in each dimension coincide. Currently, the distribution function is inverted by using the [uniroot](#) function which may result in limited accuracy of the quantiles.

Value

A list with four components: `quantile` and `f.quantile` give the location of the quantile and the value of the function evaluated at that point. `iter` and `estim.prec` give the number of iterations used and an approximate estimated precision from [uniroot](#).

See Also

[pmvnorm](#), [qmt](#)

Examples

```
qmt(0.95, df = 16, tail = "both")
```

Index

*Topic **distribution**

Mvnorm, 1

Mvt, 2

pmvnorm, 3

pmvt, 5

qmvnorm, 7

qmvt, 9

*Topic **internal**

mvtnorm-internal, 3

*Topic **multivariate**

Mvnorm, 1

Mvt, 2

dmvnorm, 4

dmvnorm (*Mvnorm*), 1

dmvt (*Mvt*), 2

Mvnorm, 1

Mvt, 2

mvt (*mvtnorm-internal*), 3

mvtnorm-internal, 3

pmvnorm, 2, 3, 8, 9

pmvt, 2, 4, 5

pnorm, 4

pt, 6

qmvnorm, 2, 4, 7

qmvt, 2, 6, 8, 9, 9

rmvnorm, 4

rmvnorm (*Mvnorm*), 1

rmvt (*Mvt*), 2

rnorm, 2

uniroot, 8, 9