The mvtnorm Package

August 23, 2006

Title Multivariate Normal and T Distribution

Version 0.7-3

Date $Date: 2006/08/23 08:48:24 $

Author Alan Genz <AlanGenz@wsu.edu>, Frank Bretz <frank.bretz@pharma.novartis.com>, R port by Torsten Hothorn <Torsten.Hothorn@rzmail.uni-erlangen.de>

Maintainer Torsten Hothorn <Torsten.Hothorn@rzmail.uni-erlangen.de>

Description computes the multivariate normal and t distribution

Depends R(>= 1.9.0)

License GPL

R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mvnorm</td>
<td>1</td>
</tr>
<tr>
<td>mvtnorm-internal</td>
<td>2</td>
</tr>
<tr>
<td>pmvnorm</td>
<td>3</td>
</tr>
<tr>
<td>pmvt</td>
<td>4</td>
</tr>
<tr>
<td>qmvnorm</td>
<td>7</td>
</tr>
<tr>
<td>qmv</td>
<td>8</td>
</tr>
</tbody>
</table>

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 `rep(0, length = ncol(x))`.
- **sigma**: Covariance matrix, default is `diag(ncol(x))`.
- **log**: Logical; if TRUE, densities d are given as log(d).

Author(s)

Friedrich Leisch <Friedrich.Leisch@ci.tuwien.ac.at>

See Also

`pmvnorm`, `rnorm`, `qmvnorm`

Examples

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

Description

Internal mvtnorm functions.

Usage

```r
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**

```r
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 corr or sigma can be specified. If sigma is given, the problem is standardized. If neither corr nor sigma is given, the identity matrix is used for sigma.
- `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.

**Author(s)**

Fortran Code by Alan Genz <AlanGenz@wsu.edu> and Frank Bretz <frank.bretz@pharma.novartis.com>,  
R port by Torsten Hothorn <Torsten.Hothorn@rzmail.uni-erlangen.de>
References


See Also

`qmvnorm`

Examples

```r
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=rep(c(.3,.5),2),mean=rep(c(2,4),2))
stopifnot(round(a,16) == round(prod(pnorm(c(.3,.5),c(2,4))),16))
a <- pmvnorm(lower=-Inf, upper=rep(c(.3,.5,1),3),mean=rep(c(2,4,1),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=rep(c(1,4,2), m), 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*
pmvt

Description

Computes 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)
rmvt(n, sigma=diag(2), df=1)

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

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

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

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 \( K = 2^{1-d_f/2}/\Gamma(d_f/2) \) 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.

rmvt is a wrapper to rmvnorm for random number generation.

If df = 0, normal probabilities are returned.
Value

The evaluated distribution function is returned with attributes

- `error`: estimated absolute error
- `msg`: status messages.

Author(s)

Fortran Code by Alan Genz <AlanGenz@wsu.edu> and Frank Bretz <frank.bretz@pharma.novartis.com>, R port by Torsten Hothorn <Torsten.Hothorn@rzmail.uni-erlangen.de>

References


See Also

- `qmvt`

Examples

```r
n <- 5
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)

```r
n <- c(26, 24, 20, 33, 32)
V <- diag(1/n)
df <- 130
C <- c(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(unroot(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 <- pmvnorm(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)))

rmvt(10, sigma=diag(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.tail"), 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. `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. If neither `corr` nor `sigma` is given, the identity matrix is used for `sigma`.
- **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

```r
qmvt(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

```r
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): probability.
- **interval** (vector containing the end-points of the interval to be searched by `uniroot`).
- **tail** (vector containing the end-points of the interval to be searched by `uniroot`.
- **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** (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 **corr** or **sigma** can be specified. If **sigma** is given, the problem is standardized. If neither **corr** nor **sigma** is given, the identity matrix is used for **sigma**.
- **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

```r
qmvt(0.95, df = 16, tail = "both")
```
Index

*Topic distribution
   Mvnorm, 1
   pmvnorm, 2
   pmvt, 4
   qmvnorm, 7
   qmvt, 8
*Topic internal
   mvtnorm-internal, 2
*Topic multivariate
   Mvnorm, 1
dmvnorm, 3
dmvnorm (Mvnorm), 1
Mvnorm, 1
mvt (mvtnorm-internal), 2
mvtnorm-internal, 2
   pmvnorm, 2, 2, 8, 9
   pmvt, 3, 4
   pnorm, 3
   pt, 5
   qmvnorm, 2, 3, 7
   qmvt, 6, 8, 8, 9
rmvnorm, 3, 5
rmvnorm (Mvnorm), 1
rmvt (pmvt), 4
rnorm, 2
uniroot, 7–9