Package ‘mvtnorm’

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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, 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


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**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**

```r
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)
```

**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)`.
- `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.

Author(s)
Friedrich Leisch and Fabian Scheipl

See Also
pmvnorm, rnorm, qmvnorm

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)

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

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. dmvnorm gives the density and rmvnt generates random deviates.

Usage
rmvnt(n, sigma = diag(2), df = 1, delta = rep(0, nrow(sigma)),
    type = c("shifted", "Kshirsagar"), ...)
dmvnt(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. 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 \( X \) denotes a random vector following a \( t \) distribution with location vector \( 0 \) and scale matrix \( \Sigma \) (written \( X \sim t_\nu(0, \Sigma) \)), the scale matrix (the argument sigma) is not equal to the covariance matrix \( Cov(X) \) of \( X \). If the degrees of freedom \( \nu \) (the argument df) is larger than 2, then \( Cov(X) = \Sigma \nu / (\nu - 2) \). Furthermore, in this case the correlation matrix \( Cor(X) \) 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 \( df = 1\inf \) 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


See Also

`pmvt()` and `qmvt()`

Examples

```r
## 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, ...)

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. 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.
...          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, 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.

Value

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

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

http://www.sci.wsu.edu/math/faculty/genz/homepage

References


See Also

qmvnorm

Examples

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

corr[upper.tri(corr)] <- 0.5

def prob <- pmvnorm(lower, upper, mean, corr)
print(prob)

cf 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
def 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 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, ...)
```

**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. 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. 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.

... 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

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

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) $\delta$ and degrees of freedom $\nu$ the following integral is evaluated:

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

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).
pmvt

Source

http://www.sci.wsu.edu/math/faculty/genz/homepage

References


See Also

qmvt

Examples

```r
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(1,1,0,0,-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 %*% 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
}
### uniroot for this simple problem
round(uniroot(myfct, lower=1, upper=5, alpha=0.95)$root, 3)
# compare pmv and pmvnorm for large df:

a <- pmvnorm(lower=-Inf, upper=1, mean=rep(0, 5), corr=diag(5))
b <- pmv(lower=-Inf, upper=1, df=300, corr=diag(5))
a
b
stopifnot(round(a, 2) == round(b, 2))
# correlation and scale matrix

a <- pmv(lower=-Inf, upper=2, delta=rep(0, 5), df=3,
         sigma = diag(5)*2)
b <- pmv(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 <- pmv(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, ...)

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. 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.

... 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.

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


See Also

pmvnorm, qmvtnorm
Examples
qmvmnorm(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"), pto1 = 0.001, maxiter = 500, trace = FALSE, ...)

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 \( df = \infty \).
- **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 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. type = "Kshirsagar" corresponds to formula (1.4) in Genz and Bretz (2009) (see also Chapter 5.1 in Kotz and Nadarajah (2004)) and type = "shifted" 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 \([p-\text{ptol}, p+\text{ptol}]\). maxiter is the maximum number of iterations for the root finding algorithm. trace prints the iterations of the root finder.

Details

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

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


See Also

pmvnorm, qmvnorm

Examples

```r
## 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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