

Package: mniw (via r-universe)

October 31, 2024

Type Package

Title The Matrix-Normal Inverse-Wishart Distribution

Version 1.0.2

Date 2024-09-19

Description Density evaluation and random number generation for the Matrix-Normal Inverse-Wishart (MNIW) distribution, as well as the the Matrix-Normal, Matrix-T, Wishart, and Inverse-Wishart distributions. Core calculations are implemented in a portable (header-only) C++ library, with matrix manipulations using the 'Eigen' library for linear algebra. Also provided is a Gibbs sampler for Bayesian inference on a random-effects model with multivariate normal observations.

URL <https://github.com/mlysy/mniw/>, <https://mlysy.github.io/mniw/>

BugReports <https://github.com/mlysy/mniw/issues>

License GPL-3

Depends R (>= 2.10)

Imports Rcpp (>= 0.11.6)

LinkingTo Rcpp, RcppEigen

LazyData true

Suggests testthat, knitr, rmarkdown

Encoding UTF-8

RoxygenNote 7.3.2

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

Repository <https://mlysy.r-universe.dev>

RemoteUrl <https://github.com/mlysy/mniw>

RemoteRef HEAD

RemoteSha ef05408960e06308037ea9fcd1c5e54aefba6e3

Contents

mniw-package	2
crossprodV	3
Hospitals	3
MatrixNormal-dist	4
MatrixT-dist	5
MNIW-dist	6
MultiNormal-dist	7
rRxNorm	8
RxNormLM	9
Wishart-dist	13
Index	16

mniw-package	<i>Tools for the Matrix-Normal Inverse-Wishart distribution.</i>
--------------	--

Description

Density evaluation and random number generation for the Matrix-Normal Inverse-Wishart (MNIW) distribution, as well as its constituent distributions, i.e., the Matrix-Normal, Matrix-T, Wishart, and Inverse-Wishart distributions.

Details

The Matrix-Normal Inverse-Wishart (MNIW) distribution $(\mathbf{X}, \mathbf{V}) \sim \text{MNIW}(\mathbf{\Lambda}, \mathbf{\Sigma}, \mathbf{\Psi}, \nu)$ on random matrices $\mathbf{X}_{p \times q}$ and symmetric positive-definite $\mathbf{V}_{q \times q}$ is defined as

$$\begin{aligned} \mathbf{V} &\sim \text{Inverse-Wishart}(\mathbf{\Psi}, \nu) \\ \mathbf{X} \mid \mathbf{V} &\sim \text{Matrix-Normal}(\mathbf{\Lambda}, \mathbf{\Sigma}, \mathbf{V}), \end{aligned}$$

where the Matrix-Normal distribution is defined as the multivariate normal

$$\text{vec}(\mathbf{X}) \sim \mathcal{N}(\text{vec}(\mathbf{\Lambda}), \mathbf{V} \otimes \mathbf{\Sigma}),$$

where $\text{vec}(\mathbf{X})$ is a vector stacking the columns of \mathbf{X} , and $\mathbf{V} \otimes \mathbf{\Sigma}$ denotes the Kronecker product.

Author(s)

Maintainer: Martin Lysy <mlysy@uwaterloo.ca>

Authors:

- Bryan Yates

See Also

Useful links:

- <https://github.com/mlysy/mniw/>
- <https://mlysy.github.io/mniw/>
- Report bugs at <https://github.com/mlysy/mniw/issues>

crossprodV	<i>Matrix cross-product.</i>
------------	------------------------------

Description

Vectorized matrix cross-products $t(X) V Y$ or $t(X) V^{-1} Y$.

Usage

```
crossprodV(X, Y = NULL, V, inverse = FALSE)
```

Arguments

X	A matrix of size $p \times q$, or an array of size $p \times q \times n$.
Y	A matrix of size $p \times r$, or an array of size $p \times r \times n$. If missing defaults to $Y = X$.
V	A matrix of size $p \times p$, or an array of size $p \times p \times n$.
inverse	Logical; whether or not the inner product should be calculated with V or V^{-1} .

Value

An array of size $q \times r \times n$.

Examples

```
# problem dimensions
p <- 4
q <- 2
r <- 3
n <- 5
X <- array(rnorm(p*q*n), dim = c(p, q, n)) # vectorized
Y <- array(rnorm(p*r*n), dim = c(p, r, n)) # vectorized
V <- crossprod(matrix(rnorm(p*p), p, p)) # not vectorized (but positive definite)
crossprodV(X = X, V = V) # self cross-product
# cross-product with inverse matrix weight
crossprodV(X = X, V = V, Y = Y, inverse = TRUE)
```

Hospitals	<i>Hospital profiling data.</i>
-----------	---------------------------------

Description

Information on patient-reported problem rates for 27 teaching hospitals and private academic health centers in the United States.

Usage

Hospitals

Format

A data frame with 27 rows (one for each hospital) and 4 variables:

NSrg Non-surgery related problem rate (percent).

Srg Surgery related problem rate (percent).

Severity Average health index for surveyed patients.

Size Number of patients surveyed.

References

Everson, P.J. and Morris, C.N. "Inference for multivariate normal hierarchical models." *Journal of the Royal Statistical Society, Series B* 62:2 (2000): 399-412.

MatrixNormal-dist *The Matrix-Normal distribution.*

Description

Density and random sampling for the Matrix-Normal distribution.

Usage

dmNorm(X, Lambda, SigmaR, SigmaC, log = FALSE)

rMNorm(n, Lambda, SigmaR, SigmaC)

Arguments

X	Argument to the density function. Either a $p \times q$ matrix or a $p \times q \times n$ array.
Lambda	Mean parameter. Either a $p \times q$ matrix or a $p \times q \times n$ array.
SigmaR	Between-row covariance matrix. Either a $p \times p$ matrix or a $p \times p \times n$ array.
SigmaC	Between-column covariance matrix Either a $q \times q$ matrix or a $q \times q \times n$ array.
log	Logical; whether or not to compute the log-density.
n	Integer number of random samples to generate.

Details

The Matrix-Normal distribution $\mathbf{X} \sim \text{Matrix-Normal}(\mathbf{\Lambda}, \mathbf{\Sigma}_R, \mathbf{\Sigma}_C)$ on the random matrix $\mathbf{X}_{p \times q}$ is defined as

$$\text{vec}(\mathbf{X}) \sim \mathcal{N}(\text{vec}(\mathbf{\Lambda}), \mathbf{\Sigma}_C \otimes \mathbf{\Sigma}_R),$$

where $\text{vec}(\mathbf{X})$ is a vector stacking the columns of \mathbf{X} , and $\mathbf{\Sigma}_C \otimes \mathbf{\Sigma}_R$ denotes the Kronecker product.

Value

A vector length n for density evaluation, or an array of size $p \times q \times n$ for random sampling.

Examples

```
# problem dimensions
p <- 4
q <- 2
n <- 10 # number of observations
# parameter values
Lambda <- matrix(rnorm(p*q),p,q) # mean matrix
# row-wise variance matrix (positive definite)
SigmaR <- crossprod(matrix(rnorm(p*p), p, p))
SigmaC <- rwish(n, Psi = diag(q), nu = q + 1) # column-wise variance (vectorized)

# random sample
X <- rMNorm(n, Lambda = Lambda, SigmaR = SigmaR, SigmaC = SigmaC)

# log-density at each sampled value
dMNorm(X, Lambda = Lambda, SigmaR = SigmaR, SigmaC = SigmaC, log = TRUE)
```

MatrixT-dist

The Matrix-t distribution.

Description

Density and sampling for the Matrix-t distribution.

Usage

```
dMT(X, Lambda, SigmaR, SigmaC, nu, log = FALSE)
```

```
rMT(n, Lambda, SigmaR, SigmaC, nu)
```

Arguments

<code>X</code>	Argument to the density function. Either a $p \times q$ matrix or a $p \times q \times n$ array.
<code>Lambda</code>	Mean parameter. Either a $p \times q$ matrix or a $p \times q \times n$ array.
<code>SigmaR</code>	Between-row covariance matrix. Either a $p \times p$ matrix or a $p \times p \times n$ array.
<code>SigmaC</code>	Between-column covariance matrix. Either a $q \times q$ matrix or a $q \times q \times n$ array.
<code>nu</code>	Degrees-of-freedom parameter. A scalar or vector of length n .
<code>log</code>	Logical; whether or not to compute the log-density.
<code>n</code>	Integer number of random samples to generate.

Details

The Matrix-T distribution $\mathbf{X} \sim \text{Matrix-T}(\mathbf{\Lambda}, \mathbf{\Sigma}, \mathbf{\Psi}, \nu)$ on a random matrix $\mathbf{X}_{p \times q}$ is the marginal distribution of \mathbf{X} in $(\mathbf{X}, \mathbf{V}) \sim \text{MNIW}(\mathbf{\Lambda}, \mathbf{\Sigma}, \mathbf{\Psi}, \nu)$, where the Matrix-Normal Inverse-Wishart (MNIW) distribution is defined in [MNIW-dist](#).

Value

A vector length n for density evaluation, or an array of size p x q x n for random sampling.

MNIW-dist	<i>Generate samples from the Matrix-Normal Inverse-Wishart distribution.</i>
-----------	--

Description

Generate samples from the Matrix-Normal Inverse-Wishart distribution.

Usage

```
rMNIW(n, Lambda, Sigma, Psi, nu, prec = FALSE)
```

```
rmniw(n, Lambda, Omega, Psi, nu)
```

Arguments

n	number of samples.
Lambda	A mean matrix of size p x q or an array of size p x q x n. Defaults to matrix of zeros when missing.
Sigma	A row-wise variance or precision matrix of size p x p, or an array of size p x p x n. Defaults to the identity matrix when missing.
Psi	A scale matrix of size q x q, or an array of size q x q x n. Defaults to identity matrix when missing.
nu	Scalar degrees-of-freedom parameter.
prec	Logical; whether or not Sigma is on the variance or precision scale.
Omega	A between-row precision matrix of size p x p, or an array of size p x p x n. Defaults to the identity matrix when missing.

Details

The Matrix-Normal Inverse-Wishart (MNIW) distribution $(\mathbf{X}, \mathbf{V}) \sim \text{MNIW}(\mathbf{\Lambda}, \mathbf{\Sigma}, \mathbf{\Psi}, \nu)$ on random matrices $\mathbf{X}_{p \times q}$ and symmetric positive-definite $\mathbf{V}_{q \times q}$ is defined as

$$\begin{aligned} \mathbf{V} &\sim \text{Inverse-Wishart}(\mathbf{\Psi}, \nu) \\ \mathbf{X} \mid \mathbf{V} &\sim \text{Matrix-Normal}(\mathbf{\Lambda}, \mathbf{\Sigma}, \mathbf{V}), \end{aligned}$$

where the Matrix-Normal distribution is defined as the multivariate normal

$$\text{vec}(\mathbf{X}) \sim \mathcal{N}(\text{vec}(\mathbf{\Lambda}), \mathbf{V} \otimes \mathbf{\Sigma}),$$

where $\text{vec}(\mathbf{X})$ is a vector stacking the columns of \mathbf{X} , and $\mathbf{V} \otimes \mathbf{\Sigma}$ denotes the Kronecker product.

`rmniw()` is a convenience wrapper to `rMNIW(Sigma = Omega, prec = TRUE)`, for the common situation in Bayesian inference with conjugate priors when between-row variances are naturally parametrized on the precision scale.

Value

A list with elements:

`X` Array of size $p \times q \times n$ random samples from the Matrix-Normal component (see Details).

`V` Array of size $q \times q \times n$ of random samples from the Inverse-Wishart component.

Examples

```
# problem dimensions
p <- 2
q <- 3
n <- 10 # number of samples
# parameter specification
Lambda <- matrix(rnorm(p*q),p,q) # single argument
Sigma <- rwish(n, Psi = diag(p), nu = p + rexp(1)) # vectorized argument
Psi <- rwish(n = 1, Psi = diag(q), nu = q + rexp(1)) # single argument
nu <- q + rexp(1)
# simulate n draws
rMNIW(n, Lambda = Lambda, Sigma = Sigma, Psi = Psi, nu = nu)
```

MultiNormal-dist

The Multivariate Normal distribution.

Description

Density and random sampling for the Multivariate Normal distribution.

Usage

```
dmNorm(x, mu, Sigma, log = FALSE)
```

```
rmNorm(n, mu, Sigma)
```

Arguments

x	Argument to the density function. A vector of length q or an $n \times q$ matrix.
mu	Mean vector(s). Either a vector of length q or an $n \times q$ matrix. If missing defaults to a vector of zeros.
Sigma	Covariance matrix or matrices. Either a $q \times q$ matrix or a $q \times q \times n$ array. If missing defaults to the identity matrix.
log	Logical; whether or not to compute the log-density.
n	Integer number of random samples to generate.

Value

A vector for densities, or a $n \times q$ matrix for random sampling.

Examples

```
# Parameter specification
q <- 4 # number of dimensions
mu <- 1:q # mean vector
V <- toeplitz(exp(-seq(1:q))) # variance matrix

# Random sample
n <- 100
X <- rmNorm(n, mu, V)

# Calculate log density for each sampled vector
dmNorm(X, mu, V, log = TRUE)
```

rRxNorm	<i>Conditional sampling for Multivariate-Normal Random-Effects model.</i>
---------	---

Description

Sample from the conditional parameter distribution given the data and hyperparameters of the Multivariate-Normal Random-Effects (mNormRE) model (see **Details**).

Usage

```
rRxNorm(n, x, V, lambda, Sigma)
```

Arguments

n	Integer number of random samples to generate.
x	Data observations. Either a vector of length q or a $n \times q$ matrix. In the latter case each row is a different vector.
V	Observation variances. Either a matrix of size $q \times q$ or a $q \times q \times n$ array.

lambda	Prior means. Either a vector of length q or an n × q matrix. In the latter case each row is a different mean. Defaults to zeros.
Sigma	Prior variances. Either a matrix of size q × q or a q × q × n array. Defaults to identity matrix.

Details

Consider the hierarchical multivariate normal model

$$\begin{aligned} \boldsymbol{\mu} &\sim \mathcal{N}(\boldsymbol{\lambda}, \boldsymbol{\Sigma}) \\ \boldsymbol{x} \mid \boldsymbol{\mu} &\sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{V}). \end{aligned}$$

The Multivariate-Normal Random-Effects model $\boldsymbol{\mu} \sim \text{RxNorm}(\boldsymbol{x}, \boldsymbol{V}, \boldsymbol{\lambda}, \boldsymbol{\Sigma})$ on the random vector $\boldsymbol{\mu}_q$ is defined as the posterior distribution $p(\boldsymbol{\mu} \mid \boldsymbol{x}, \boldsymbol{\lambda}, \boldsymbol{\Sigma})$. This distribution is multivariate normal; for the mathematical specification of its parameters please see vignette("mniw-distributions", package = "mniw").

Examples

```
# data specification
q <- 5
y <- rnorm(q)
V <- rwish(1, diag(q), q+1)
# prior specification
lambda <- rep(0,q)
A <- diag(q)
n <- 10
# random sampling
rRxNorm(n, y, V, lambda, A)
```

RxNormLM

Bayesian inference for a random-effects regression model.

Description

Gibbs sampler for posterior distribution of parameters and hyperparameters of a multivariate normal random-effects linear regression model called RxNormLM (see Details).

Usage

```
RxNormLM(
  nsamples,
  Y,
  V,
  X,
  prior = NULL,
  init,
  burn,
  updateHyp = TRUE,
```

```

storeHyp = TRUE,
updateRX = TRUE,
storeRX = FALSE
)

```

Arguments

<code>nsamples</code>	number of posterior samples to draw.
<code>Y</code>	$N \times q$ matrix of responses.
<code>V</code>	Either a $q \times q$ variance matrix or an $q \times q \times N$ array of such matrices.
<code>X</code>	$N \times p$ matrix of covariates.
<code>prior</code>	parameters of the prior MNIW distribution on the hyperparameters (see Details).
<code>init</code>	(optional) list with elements <code>Beta</code> , <code>Sigma</code> , and <code>Mu</code> providing the initial values for these. Default values are <code>Beta = matrix(0, p, q)</code> , <code>Sigma = diag(q)</code> , and <code>Mu = Y</code> .
<code>burn</code>	integer number of burn-in samples, or fraction of <code>nsamples</code> to prepend as burn-in.
<code>updateHyp, storeHyp</code>	logical. Whether or not to update/store the hyperparameter draws.
<code>updateRX, storeRX</code>	logical. Whether or not to update/store the random-effects draws.

Details

The RxNormLM model is given by

$$y_i \mid \mu_i \sim_i idN(\mu_i, V_i)$$

$$\mu_i \mid \beta, \Sigma \sim_i sim_i ndN(x_i' \beta, \Sigma)$$

$$\beta, \Sigma \sim MNIW(\Lambda, \Omega^{-1}, \Psi, \nu),$$

where y_i and μ_i are response and random-effects vectors of length q , x_i are covariate vectors of length p , and (β, Σ) are hyperparameter matrices of size $p \times q$ and $q \times q$.

The MNIW prior distribution is given by a list with elements `Lambda`, `Omega`, `Psi`, and `nu`. If any of these is `NULL` or missing, the default value is 0. Note that `Omega == 0` gives a Lebesgue prior to β .

Value

A list with (potential) elements:

`Beta` An $p \times q \times nsamples$ array of regression coefficient iterations (if `storeHyp == TRUE`)

`Sigma` An $q \times q \times nsamples$ array of regression variance matrices (if `storeHyp == TRUE`)

`Mu` An $n \times q \times nsamples$ array of random effects (if `storeRX == TRUE`)

Examples

```

# problem dimensions
n <- sample(10:20,1) # number of observations
p <- sample(1:4,1) # number of covariates
q <- sample(1:4,1) # number of responses

# hyperparameters
Lambda <- rMNorm(1, Lambda = matrix(0, p, q))
Omega <- crossprod(rMNorm(1, Lambda = matrix(0, p, p)))
Psi <- crossprod(rMNorm(1, Lambda = matrix(0, q, q)))
nu <- rexp(1) + (q+1)
prior <- list(Lambda = Lambda, Omega = Omega, Psi = Psi, nu = nu)

# random-effects parameters
BSig <- rmniw(1, Lambda = Lambda, Omega = Omega, Psi = Psi, nu = nu)
Beta <- BSig$X
Sigma <- BSig$V

# design matrix
X <- rMNorm(1, matrix(0, n, p))

# random-effects themselves
Mu <- rmNorm(n, X %*% Beta, Sigma)

# generate response data
V <- rwish(n, Psi = diag(q), nu = q+1) # error variances
Y <- rmNorm(n, mu = Mu, Sigma = V) # responses

# visual checks for each component of Gibbs sampler

# sample from p(Mu | Beta, Sigma, Y)
nsamples <- 1e5
out <- RxNormLM(nsamples,
  Y = Y, V = V, X = X,
  prior = prior,
  init = list(Beta = Beta, Sigma = Sigma, Mu = Mu),
  burn = floor(nsamples/10),
  updateHyp = FALSE,
  storeHyp = FALSE,
  updateRX = TRUE,
  storeRX = TRUE)

# conditional distribution is RxNorm:
iObs <- sample(n, 1) # pick an observation at random
# calculate the RxNorm parameters
G <- Sigma %*% solve(V[, ,iObs] + Sigma)
xB <- c(X[iObs, ,drop=FALSE] %*% Beta)
muRx <- G %*% (Y[iObs,] - xB) + xB
SigmaRx <- G %*% V[, ,iObs]

# a' * mu_i is univariate normal with known mean and variance:
a <- rnorm(q) # arbitrary vector

```

```

amui <- crossprod(a, out$Mu[iObs,,]) # a' * mu_i

hist(amui, breaks = 100, freq = FALSE,
     xlab = "", main = expression("Histogram of "*a^T*mu[i]))
curve(dnorm(x, mean = sum(a * muRx),
           sd = sqrt(crossprod(a, SigmaRx %**% a)[1])),
      add = TRUE, col = "red")
legend("topright",
      legend = c("Observed", "Expected"),
      lwd = c(NA, 2), pch = c(22, NA), seg.len = 1.5,
      col = c("black", "red"), bg = c("white", NA))

# sample from p(Beta, Sigma | Mu, Y)
nsamples <- 1e5
out <- RxNormLM(nsamples,
                Y = Y, V = V, X = X,
                prior = prior,
                init = list(Beta = Beta, Sigma = Sigma, Mu = Mu),
                burn = floor(nsamples/10),
                updateHyp = TRUE,
                storeHyp = TRUE,
                updateRX = FALSE,
                storeRX = FALSE)

# conditional distribution is MNIW:
# calculate the MNIW parameters
OmegaHat <- crossprod(X) + Omega
LambdaHat <- solve(OmegaHat, crossprod(X, Mu) + Omega %**% Lambda)
PsiHat <- Psi + crossprod(Mu) + crossprod(Lambda, Omega %**% Lambda)
PsiHat <- PsiHat - crossprod(LambdaHat, OmegaHat %**% LambdaHat)
nuHat <- nu + n

# a' Sigma^{-1} a is chi^2 with known parameters:
a <- rnorm(q)
aSiga <- drop(crossprodV(a, V = out$Sigma, inverse = TRUE))
sigX <- crossprod(a, solve(PsiHat, a))[1]
hist(aSiga, breaks = 100, freq = FALSE,
     xlab = "", main = expression("Histogram of "*a^T*Sigma^{-1}*a))
curve(dchisq(x/sigX, df = nuHat)/sigX, add = TRUE, col = "red")
legend("topright",
      legend = c("Observed", "Expected"),
      lwd = c(NA, 2), pch = c(22, NA), seg.len = 1.5,
      col = c("black", "red"), bg = c("white", NA))

# a' Beta b is student-t with known parameters:
a <- rnorm(p)
b <- rnorm(q)
# vectorized calculations
aBetab <- crossprodV(X = aperm(out$Beta, c(2,1,3)),
                    Y = b, V = diag(q)) # Beta b

```

```

aBetaB <- drop(crossprodV(X = a, Y = aBetaB, V = diag(p))) # a' Beta b
# student-t parameters
muT <- crossprod(a, LambdaHat %*% b)[1]
nuT <- nuHat-q+1
sigmaT <- crossprodV(a, V = OmegaHat, inverse = TRUE)[1]
sigmaT <- sigmaT * crossprodV(b, V = PsiHat)[1]
sigmaT <- sqrt(sigmaT / nuT)

hist(aBetaB, breaks = 100, freq = FALSE,
     xlab = "", main = expression("Histogram of "a^T*Beta*a))
curve(dt((x-muT)/sigmaT, df = nuT)/sigmaT, add = TRUE, col = "red")
legend("topright",
     legend = c("Observed", "Expected"),
     lwd = c(NA, 2), pch = c(22, NA), seg.len = 1.5,
     col = c("black", "red"), bg = c("white", NA))

```

Wishart-dist

Wishart and Inverse-Wishart distributions.

Description

Densities and random sampling for the Wishart and Inverse-Wishart distributions.

Usage

```

dwish(X, Psi, nu, log = FALSE)

rwish(n, Psi, nu)

diwish(X, Psi, nu, log = FALSE)

riwish(n, Psi, nu)

dwishart(X, Psi, nu, inverse = FALSE, log = FALSE)

rwishart(n, Psi, nu, inverse = FALSE)

```

Arguments

X	Argument to the density function. Either a $q \times q$ matrix or a $q \times q \times n$ array.
Psi	Scale parameter. Either a $q \times q$ matrix or a $q \times q \times n$ array.
nu	Degrees-of-freedom parameter. A scalar or vector of length n.
log	Logical; whether or not to compute the log-density.
n	Integer number of random samples to generate.
inverse	Logical; whether or not to use the Inverse-Wishart distribution.

Details

The Wishart distribution $\mathbf{X} \sim \text{Wishart}(\Psi, \nu)$ on a symmetric positive-definite random matrix \mathbf{X} of size $q \times q$ has PDF

$$f(\mathbf{X} \mid \Psi, \nu) = \frac{|\mathbf{X}|^{(\nu-q-1)/2} \exp\{-\text{tr}(\Psi^{-1}\mathbf{X})/2\}}{2^{q\nu/2} |\Psi|^{\nu/2} \Gamma_q(\nu/2)},$$

where $\Gamma_q(\alpha)$ is the multivariate gamma function,

$$\Gamma_q(\alpha) = \pi^{q(q-1)/4} \prod_{i=1}^q \Gamma(\alpha + (1-i)/2).$$

The Inverse-Wishart distribution $\mathbf{X} \sim \text{Inverse-Wishart}(\Psi, \nu)$ is defined as $\mathbf{X}^{-1} \sim \text{Wishart}(\Psi^{-1}, \nu)$. `dwish()` and `diwish()` are convenience wrappers for `dwishart()`, and similarly `rwish()` and `riwish()` are wrappers for `rwishart()`.

Value

A vector length `n` for density evaluation, or an array of size `q x q x n` for random sampling.

Examples

```
# Random sampling

n <- 1e5
q <- 3
Psi1 <- crossprod(matrix(rnorm(q^2),q,q))
nu <- q + runif(1, 0, 5)

X1 <- rwish(n,Psi1,nu) # Wishart

# plot it
plot_fun <- function(X) {
  q <- dim(X)[1]
  par(mfrow = c(q,q))
  for(ii in 1:q) {
    for(jj in 1:q) {
      hist(X[ii,jj,], breaks = 100, freq = FALSE,
           xlab = "", main = parse(text = paste0("X[", ii, jj, "]")))
    }
  }
}

plot_fun(X1)

# "vectorized" scale parameter
Psi2 <- 5 * Psi1
vPsi <- array(c(Psi1, Psi2), dim = c(q, q, n))
X2 <- rwish(n, Psi = vPsi, nu = nu)
plot_fun(X2)
```

```
# Inverse-Wishart
X3 <- riwish(n, Psi2, nu)
plot_fun(X3)

# log-density calculation for sampled values
par(mfrow = c(1,1))
hist(dwish(X2, vPsi, nu, log = TRUE),
     breaks = 100, freq = FALSE, xlab = "",
     main = expression("log-p"*(X[2]*" | "list(Psi,nu))))
```

Index

* datasets

Hospitals, 3

crossprodV, 3

diwish (Wishart-dist), 13

dMNorm (MatrixNormal-dist), 4

dmNorm (MultiNormal-dist), 7

dMT (MatrixT-dist), 5

dwish (Wishart-dist), 13

dwishart (Wishart-dist), 13

Hospitals, 3

MatrixNormal (MatrixNormal-dist), 4

MatrixNormal-dist, 4

MatrixT (MatrixT-dist), 5

MatrixT-dist, 5

MNIW (MNIW-dist), 6

mniw (mniw-package), 2

MNIW-dist, 6, 6

mniw-package, 2

MultiNormal (MultiNormal-dist), 7

MultiNormal-dist, 7

riwish (Wishart-dist), 13

rMNIW (MNIW-dist), 6

rmniw (MNIW-dist), 6

rMNorm (MatrixNormal-dist), 4

rmNorm (MultiNormal-dist), 7

rMT (MatrixT-dist), 5

rRxNorm, 8

rwish (Wishart-dist), 13

rwishart (Wishart-dist), 13

RxNormLM, 9

Wishart (Wishart-dist), 13

Wishart-dist, 13