

Package ‘mniw’

October 13, 2022

Type Package

Title The Matrix-Normal Inverse-Wishart Distribution

Version 1.0.1

Date 2022-08-11

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/mlsy/mniw/>

BugReports <https://github.com/mlsy/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 7.2.1

VignetteBuilder knitr

NeedsCompilation yes

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Repository CRAN

Date/Publication 2022-08-22 16:30:05 UTC

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

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See Also

Useful links:

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

crossprodV	<i>Matrix cross-product.</i>
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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>
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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 (%).

Srg Surgery related problem rate (%).

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	<i>The Matrix-Normal distribution.</i>
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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

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

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.
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.

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](#).

Value

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

MNIW	<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

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 x q matrix.
mu	Mean vector(s). Either a vector of length q or an n x q matrix. If missing defaults to a vector of zeros.
Sigma	Covariance matrix or matrices. Either a q x q matrix or a q x q x 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 x 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 x q matrix. In the latter case each row is a different vector.
V	Observation variances. Either a matrix of size q x q or a q x q x n array.

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

`nsamples` number of posterior samples to draw.

`Y` N x q matrix of responses.

`V` Either a q x q variance matrix or an q x q x N array of such matrices.

`X` N x p matrix of covariates.

`prior` parameters of the prior MNIW distribution on the hyperparameters (see **Details**).

`init` (optional) list with elements `Beta`, `Sigma`, and `Mu` providing the initial values for these. Default values are `Beta = matrix(0, p, q)`, `Sigma = diag(q)`, and `Mu = Y`.

`burn` integer number of burn-in samples, or fraction of `nsamples` to prepend as burn-in.

`updateHyp, storeHyp` logical. Whether or not to update/store the hyperparameter draws.

`updateRX, storeRX` logical. Whether or not to update/store the random-effects draws.

Details

The RxNormLM model is given by

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

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

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

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

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))))
```

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