

Package: ksm (via r-universe)

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Type Package

Title Kernel Density Estimation for Random Symmetric Positive Definite Matrices

Version 1.1

Description Kernel smoothing for Wishart random matrices described in Daayeb, Khardani and Ouimet (2025) [doi:10.48550/arXiv.2506.08816](https://doi.org/10.48550/arXiv.2506.08816), Gaussian and log-Gaussian models using least square or likelihood cross validation criteria for optimal bandwidth selection.

BugReports <https://github.com/lbelzile/ksm/issues>

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bandwidth_optim	<i>Bandwidth optimization for symmetric matrix kernels</i>
-----------------	--

Description

Given a sample of positive definite matrices, perform numerical maximization of the h-block least square (lscv) or leave-one-out likelihood (lcv) cross-validation criteria using a root search.

Usage

```
bandwidth_optim(
  x,
  criterion = c("lscv", "lcv"),
  kernel = c("Wishart", "smlnorm", "smnorm"),
  tol = 1e-04,
```

```

    h = 1L,
    bounds = c(1e-04, 10)
  )

```

Arguments

x	sample of symmetric matrix observations from which to build the kernel density kernel
criterion	optimization criterion, one of lscv for least square cross-validation at lag h or lcv for leave-one-out cross-validation.
kernel	string, one of Wishart, smlnorm (log-Gaussian) or smnorm (Gaussian).
tol	double, tolerance of optimization (root search)
h	lag step for consideration of observations, for the case criterion=lscv
bounds	vector of length 2 containing the bounds for the search

Value

double, the optimal bandwidth up to tol

Examples

```

x <- simu_rdens(n = 100, model = 3, d = 3)
bandwidth_optim(x = x,
  criterion = "lscv",
  kernel = "Wishart",
  h = 2L)

```

dinvWishart	<i>Density of inverse Wishart random matrix</i>
-------------	---

Description

Density of inverse Wishart random matrix

Usage

```
dinvWishart(x, df, S, log = FALSE)
```

Arguments

x	array of dimension d by d by n
df	degrees of freedom
S	symmetric positive definite matrix of dimension d by d
log	logical; if TRUE, returns the log density

Value

a vector of length n containing the log-density of the inverse Wishart.

`dmbeta2` *Matrix beta type II density function*

Description

Given a random matrix x , compute the density for arguments `shape1` and `shape2`

Usage

```
dmbeta2(x, shape1, shape2, log = TRUE)
```

Arguments

`x` cube of dimension d by d by n containing the random matrix samples
`shape1` positive shape parameter, strictly larger than $(d - 1)/2$.
`shape2` positive shape parameter, strictly larger than $(d - 1)/2$.
`log` [logical] if TRUE (default), returns the log density.

Value

a vector of length n

`dsmlnorm` *Symmetric matrix-variate lognormal density*

Description

Density of the lognormal matrix-variate density, defined through the matrix logarithm, with the Jacobian resulting from the transformation

Usage

```
dsmlnorm(x, b, M, log = TRUE)
```

Arguments

`x` [cube] array of dimension d by d by n
`b` [numeric] scale parameter, strictly positive
`M` [matrix] location matrix, positive definite
`log` [logical] if TRUE (default), returns the log density

Value

a vector of length n

dsmnorm	<i>Symmetric matrix-variate normal density</i>
---------	--

Description

Symmetric matrix-variate normal density

Usage

```
dsmnorm(x, b, M, log = TRUE)
```

Arguments

x	[cube] array of dimension d by d by n
b	[numeric] scale parameter, strictly positive
M	[matrix] location matrix, positive definite
log	[logical] if TRUE (default), returns the log density

Value

a vector of length n

dWishart	<i>Density of Wishart random matrix</i>
----------	---

Description

Density of Wishart random matrix

Usage

```
dWishart(x, df, S, log = FALSE)
```

Arguments

x	array of dimension d by d by n
df	degrees of freedom
S	symmetric positive definite matrix of dimension d by d
log	logical; if TRUE, returns the log density

Value

a vector of length n containing the log-density of the Wishart.

integrate_spd

Integration with respect to symmetric positive definite matrices

Description

Given a function f defined over the space of symmetric positive definite matrices, compute an integral via numerical integration using the routine [cubintegrate](#).

Usage

```
integrate_spd(
  f,
  dim,
  tol = 0.001,
  lb = 1e-08,
  ub = Inf,
  neval = 1000000L,
  method = c("suave", "hcubature"),
  ...
)
```

Arguments

<code>f</code>	function to evaluate that takes as arguments array of size <code>dim</code> by <code>dim</code> by 1.
<code>dim</code>	dimension of integral, only two or three dimensions are supported
<code>tol</code>	double for tolerance of numerical integral
<code>lb</code>	lower bound for integration range of eigenvalues
<code>ub</code>	upper bound for integration range of eigenvalues
<code>neval</code>	maximum number of evaluations
<code>method</code>	string indicating the method from cubature
<code>...</code>	additional arguments for the function <code>f</code>

Value

list returned by the integration routine. See the documentation of [cubintegrate](#) for more details.

Examples

```
integrate_spd(
  dim = 2L,
  neval = 1e4L,
  f = function(x, S){
    dWishart(x, df = 10, S = S, log = FALSE)},
  S = diag(2))
```

kdens_smlnorm	<i>Symmetric matrix log-normal kernel density</i>
---------------	---

Description

Given a sample of m points xs from an original sample and a set of n new sample matrices x at which to evaluate the symmetric matrix normal log kernel, return the density with bandwidth parameter b .

Usage

```
kdens_smlnorm(x, xs, b, log = TRUE)
```

Arguments

x	cube of size d by d by n of points at which to evaluate the density
xs	cube of size d by d by m of sample matrices which are used to construct the kernel
b	positive double giving the bandwidth parameter
log	bool; if TRUE, return the log density

Value

a vector of length n containing the (log) density of the sample x

kdens_smnorm	<i>Symmetric matrix normal kernel density</i>
--------------	---

Description

Given a sample of m points xs from an original sample and a set of n new sample matrices x at which to evaluate the symmetric matrix normal kernel, return the density with bandwidth parameter b . Note that this kernel suffers from boundary spillover.

Usage

```
kdens_smnorm(x, xs, b, log = TRUE)
```

Arguments

x	cube of size d by d by n of points at which to evaluate the density
xs	cube of size d by d by m of sample matrices which are used to construct the kernel
b	positive double giving the bandwidth parameter
log	bool; if TRUE, return the log density

Value

a vector of length n containing the (log) density of the sample x

kdens_symmat	<i>Kernel density estimators for symmetric matrices</i>
--------------	---

Description

Given a sample of m points xs from an original sample and a set of n new sample symmetric positive definite matrices x at which to evaluate the kernel, return the density with bandwidth parameter b.

Usage

```
kdens_symmat(x, xs, kernel = "Wishart", b = 1, log = TRUE)
```

Arguments

x	cube of size d by d by n of points at which to evaluate the density
xs	cube of size d by d by m of sample matrices which are used to construct the kernel
kernel	string, one of Wishart, smnorm or smlnorm.
b	positive double giving the bandwidth parameter
log	bool; if TRUE, return the log density

Value

a vector of length n containing the (log) density of the sample x

kdens_Wishart	<i>Wishart kernel density</i>
---------------	-------------------------------

Description

Given a sample of m points xs from an original sample and a set of n new sample matrices x at which to evaluate the Wishart kernel, return the density with bandwidth parameter b.

Usage

```
kdens_Wishart(x, xs, b, log = TRUE)
```

Arguments

x	cube of size d by d by n of points at which to evaluate the density
xs	cube of size d by d by m of sample matrices which are used to construct the kernel
b	positive double giving the bandwidth parameter
log	bool; if TRUE, return the log density

Value

a vector of length n containing the (log) density of the sample x

lcv_kdens_symmat	<i>Likelihood cross-validation for symmetric positive definite matrix kernels</i>
------------------	---

Description

Given a cube of sample observations (consisting of random symmetric positive definite matrices), and a vector of candidate bandwidth parameters b, compute the leave-one-out likelihood cross-validation criterion and return the bandwidth among the choices that maximizes the criterion.

Usage

```
lcv_kdens_symmat(x, b, h = 1L, kernel = "Wishart")
```

Arguments

x	array of dimension d by d by n
b	vector of candidate bandwidth, strictly positive
h	integer for the lag vector for determining which observation to exclude, any data point in a radius of h
kernel	string indicating the kernel, one of Wishart, smlnorm or smnorm.

Value

a list with arguments

- lcv vector of likelihood cross validation criterion
- b vector of candidate bandwidth
- h lag for leave-one-out
- bandwidth optimal bandwidth among candidates
- kernel string indicating the choice of kernel function

lcv_kern_smlnorm	<i>Likelihood cross validation criterion for symmetric matrix lognormal kernel</i>
------------------	--

Description

Given a cube x and a bandwidth b , compute the leave-one-out cross validation criterion by taking out a slice and evaluating the kernel at the holdout value, excluding points that are at distance at least $h-1$ apart.

Usage

```
lcv_kern_smlnorm(x, b, h = 1L)
```

Arguments

x	[cube] array of dimension d by d by n
b	[numeric] scale parameter, strictly positive
h	integer lag for excluding observations

Value

the value of the log objective function

lcv_kern_smnorm	<i>Likelihood cross validation criterion for symmetric matrix normal kernel</i>
-----------------	---

Description

Given a cube x and a bandwidth b , compute the leave-one-out cross validation criterion by taking out a slice and evaluating the kernel at the holdout values, excluding points that are at distance at least $h-1$ apart.

Usage

```
lcv_kern_smnorm(x, b, h = 1L)
```

Arguments

x	[cube] array of dimension d by d by n
b	[numeric] scale parameter, strictly positive
h	integer lag for excluding observations

Value

the value of the log objective function

lcv_kern_Wishart	<i>Likelihood cross validation criterion for Wishart kernel</i>
------------------	---

Description

Given a cube x and a bandwidth b , compute the leave-one-out cross validation criterion by taking out a slice and evaluating the kernel at the holdout value, excluding points that are at distance at least $h-1$ apart.

Usage

```
lcv_kern_Wishart(x, b, h = 1)
```

Arguments

x	[cube] array of dimension d by d by n
b	[numeric] scale parameter, strictly positive
h	integer lag for excluding observations

Value

the value of the log objective function

lscv_kdens_symmat	<i>Least square cross-validation for symmetric positive definite matrix kernels</i>
-------------------	---

Description

Given a cube of sample observations (consisting of random symmetric positive definite matrices), and a vector of candidate bandwidth parameters b , compute the least square likelihood cross-validation criterion and return the bandwidth among the choices that minimizes the criterion.

Usage

```
lscv_kdens_symmat(x, b, h = 1L, kernel = "Wishart")
```

Arguments

x	array of dimension d by d by n
b	vector of candidate bandwidth, strictly positive
h	integer for the lag vector for determining which observation to exclude, any data point in a radius of h
kernel	string indicating the kernel, one of <code>Wishart</code> , <code>smnorm</code> or <code>smlnorm</code> .

Value

a list with arguments

- lscv vector of likelihood cross validation criterion
- b vector of candidate bandwidth
- h lag for leave-one-out
- bandwidth optimal bandwidth among candidates
- kernel string indicating the choice of kernel function

lscv_kern_smlnorm	<i>Least square cross validation criterion for log symmetric matrix normal kernel</i>
-------------------	---

Description

Finite sample h-block leave-one-out approximation to the least square criterion, omitting constant term. Only pairs that are $|i - j| \leq h$ apart are considered.

Usage

```
lscv_kern_smlnorm(x, b, h = 1L)
```

Arguments

x	[cube] array of dimension d by d by n
b	[numeric] scale parameter, strictly positive
h	[int] integer indicating the separation lag

Value

a double containing the log of the least square cross validation criterion

lscv_kern_smnorm	<i>Least square cross validation criterion for matrix normal kernel</i>
------------------	---

Description

Finite sample h-block leave-one-out approximation to the least square criterion, omitting constant term. Only pairs that are $|i - j| \leq h$ apart are considered.

Usage

```
lscv_kern_smnorm(x, b, h = 1L)
```

Arguments

x	[cube] array of dimension d by d by n
b	[numeric] scale parameter, strictly positive
h	[int] integer indicating the separation lag

Value

a double containing the log of the least square cross validation criterion

lscv_kern_Wishart	<i>Least square cross validation criterion for Wishart kernel</i>
-------------------	---

Description

Finite sample h-block leave-one-out approximation to the least square criterion, omitting constant term.

Usage

```
lscv_kern_Wishart(x, b, h = 1L)
```

Arguments

x	[cube] array of dimension d by d by n
b	[numeric] scale parameter, strictly positive
h	separation vector; only pairs that are $ i - j \leq h$ apart are considered

Value

a double containing the a vector of length two containing the log of the summands

mgamma	<i>Multivariate gamma function</i>
--------	------------------------------------

Description

Given a vector of points x and an order p, compute the multivariate gamma function. The function is defined as

$$\gamma_p(x) = \pi^{p(p-1)/4} \prod_{i=1}^p \Gamma\{x + (1 - i)/2\}.$$

Usage

```
mgamma(x, p, log = FALSE)
```

Arguments

x [vector] of points at which to evaluate the function
p [int] dimension of the multivariate gamma function, strictly positive.
log [logical] if TRUE, returns the log multivariate gamma function.

Value

a matrix with one column of the same length as x

realvar	<i>Realized variance of Amazon and SPY</i>
---------	--

Description

Intraday realized covariances of the returns between the Amazon stock (`rvarAMZN`) and the SPDR S&P 500 ETF (`rvarSPY`) using five minutes data, for the period of September 13th, 2023 to September 12, 2024.

Usage

```
realvar
```

Format

A 2 by 2 by 250 array

Source

Anne MacKay

Examples

```
data(realvar, package = "ksm")  
bopt <- bandwidth_optim(  
  x = realvar,  
  criterion = "lscv",  
  kernel = "Wishart",  
  h = 4L  
)
```

 Riccati

Solver for Riccati equation

Description

Given two matrices M and S , solve Riccati equation by iterative updating to find the solution R , where the latter satisfies

$$R = MRM^T + S$$

until convergence (i.e., when the Frobenius norm is less than `tol`, or the maximum number of iterations `maxiter` is reached).

Usage

```
Riccati(M, S, tol = 1e-08, maxiter = 10000L)
```

Arguments

<code>M</code>	matrix
<code>S</code>	matrix
<code>tol</code>	double for tolerance
<code>maxiter</code>	integer, the maximum number of iterations

Value

a list containing

- solution matrix solution to Riccati's equation
- error numerical error
- niter number of iteration
- convergence bool indicating convergence (TRUE) if `niter < maxiter`

 rinvWishart

Random matrix generation from the inverse Wishart distribution

Description

Random matrix generation from the inverse Wishart distribution

Usage

```
rinvWishart(n, df, S)
```

Arguments

n	[integer] sample size
df	[double] degrees of freedom, positive
S	[matrix] a d by d positive definite scale matrix

Value

an array of dimension d by d by n containing the samples

rmbeta2	<i>Random matrix generation from matrix beta type II distribution</i>
---------	---

Description

This function only supports the case of diagonal matrices

Usage

```
rmbeta2(n, d, shape1, shape2)
```

Arguments

n	sample size
d	dimension of the matrix
shape1	positive shape parameter, strictly larger than $(d - 1)/2$.
shape2	positive shape parameter, strictly larger than $(d - 1)/2$.

Value

a cube of dimension d by d by n

rmnorm	<i>Random vector generation from the multivariate normal distribution</i>
--------	---

Description

Sampler derived using the eigendecomposition of the covariance matrix vcov.

Usage

```
rmnorm(n, mean, vcov)
```

Arguments

n	sample size
mean	mean vector of length d
vcov	a square positive definite covariance matrix, of the same dimension as mean.

Value

an n by d matrix of samples

Examples

```
rmnorm(n = 10, mean = c(0, 2), vcov = diag(2))
```

rWAR	<i>Random matrix generation from first-order autoregressive Wishart process</i>
------	---

Description

Given a matrix of coefficients M and a covariance matrix Σ , simulate n random matrices from a first-order autoregressive Wishart process by simulating from cross-products of vector autoregressions

Usage

```
rWAR(n, M, Sigma, K = NULL, order = 1L, burnin = 25L)
```

Arguments

n	sample size
M	matrix of autoregressive coefficients
Sigma	covariance matrix
K	integer, degrees of freedom
order	order of autoregressive process, only 1 is supported at current.
burnin	number of iterations discarded

Value

an array of size d by d by n containing the samples

References

C. Gouriéroux, J. Jasiak, and R. Sufana (2009). The Wishart Autoregressive process of multivariate stochastic volatility, *Journal of Econometrics*, 150(2), 167-181, <doi:10.1016/j.jeconom.2008.12.016>.

Examples

```
M <- matrix(c(0.3, -0.3, -0.3, 0.3), nrow = 2)
Sigma <- matrix(c(1, 0.5, 0.5, 1), nrow = 2)
rWAR(n = 10, M = M, Sigma = Sigma, K = 5)
```

rWishart

Random matrix generation from Wishart distribution

Description

Random matrix generation from Wishart distribution

Usage

```
rWishart(n, df, S)
```

Arguments

n [integer] sample size
df [double] degrees of freedom, positive
S [matrix] a d by d positive definite scale matrix

Value

an array of dimension d by d by n containing the samples

symmetrize

Symmetrize matrix

Description

Given an input matrix, symmetrize by taking average of lower and upper triangular components as $A + A^T$.

Usage

```
symmetrize(A)
```

Arguments

A square matrix

Value

symmetrized version of A

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