Package ‘sparseMVN’

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Type Package

Title Multivariate Normal Functions for Sparse Covariance and Precision Matrices.

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Description Computes multivariate normal (MVN) densities, and samples from MVN distributions, when the covariance or precision matrix is sparse.

License MPL (>= 2.0)

Depends Matrix (>= 1.1.4), R (>= 3.1.2)

Suggests mvtnorm, plyr, knitr, testthat

VignetteBuilder knitr

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NeedsCompilation no

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sparseMVN-package  
Multivariate normal functions for sparse covariate and precision matrices.

Description

Multivariate normal functions for sparse covariate and precision matrices.

Details

Computes multivariate normal (MVN) densities, and samples from MVN distributions, when either the covariance or precision matrix is stored as a sparse Matrix (a dsCMatrix object, as defined in the Matrix package. The user can provide the precision matrix directly, rather than convert it to a covariance via matrix inversion.

rmvn.sparse  
Multivariate normal functions with sparse covariance/precision matrix.

Description

Efficient sampling and density calculation from a multivariate normal, when the covariance or precision matrix is sparse. These functions are designed for MVN samples of very large dimension.

Usage

rmvn.sparse(n, mu, CH, prec = TRUE)
dmvn.sparse(x, mu, CH, prec = TRUE)

Arguments

n  
number of samples

mu  
mean (numeric vector)

CH  
An object of class dCHMsimpl or dCHMsuper that represents the Cholesky factorization of either the precision (default) or covariance matrix. See details.

prec  
If TRUE, CH is the Cholesky decomposition of the precision matrix. If false, it is the decomposition for the covariance matrix.

x  
numeric matrix, where each row is an MVN sample.
**rmvn.sparse**

**Details**

These functions use sparse matrix operations to sample from, or compute the log density of, a multivariate normal distribution. The user must compute the Cholesky decomposition first, using the Cholesky function in the Matrix package. This function operates on a sparse symmetric matrix, and returns an object of class `dCHMsimpl` or `dCHMsuper` (this depends on the algorithm that was used for the decomposition). This object contains information about any fill-reducing permutations that were used to preserve sparsity. The `rmvn.sparse` and `dmvn.sparse` functions use this permutation information, even if pivoting was turned off.

**Examples**

```r
require(Matrix)

m <- 20
p <- 2
k <- 4

## build sample sparse covariance matrix
Q1 <- tril(kronecker(Matrix(seq(0.1, p*2, length=p*p), p, p), diag(m)))
Q2 <- cBind(Q1, Matrix(0, m*p, k))
Q3 <- rBind(Q2, cBind(Matrix(rnorm(k*m*p), k, m*p), Diagonal(k)))
V <- tcrossprod(Q3)
CH <- Cholesky(V)

x <- rmvn.sparse(10, rep(0, p*p+k), CH, FALSE)
## print(x)

y <- dmvn.sparse(x[1,], rep(0, p*m+k), CH, FALSE)
## print(y)
```
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