

Package ‘sparseMVN’

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Type Package

Title Multivariate normal functions for sparse covariate 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 (>= 1.1.0), R (>= 3.0.2)

Suggests mvtnorm, reshape2, plyr

NeedsCompilation no

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

Description

Computes multivariate normal (MVN) densities, and samples from MVN distributions, for sparse covariance and precision matrices. This package uses the sparse matrix classes and algorithms in the Matrix package for computational efficiency.

Details

Package: sparseMVN
Type: Package
Version: 0.1-0
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LazyLoad: yes

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mvn.sparse *Sampling and log density functions for multivariate normal distribution, given a sparse covariance or 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

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

Arguments

x	numeric matrix, where each row is an mvn sample.
n	number of draws
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.

Details

This function uses 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.

Value

For rmvn.sparse, a base R matrix with n rows, with each draw in each row. The number of columns is equal to the length of mu.

For dmvn.sparse, a vector with a length equal to the number of rows of x, containing the MVN log densities evaluated at each row of x.

Examples

```
if (require(Matrix)) {
  m <- 50
  p <- 2
  k <- 6

  ## build sample covariance matrix
  Q1 <- tril(kronecker(Matrix(seq(0.1,p,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)

  ## assume mean at origin

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

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

}

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