Package ‘GGMridge’

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Title Gaussian Graphical Models Using Ridge Penalty Followed by Thresholding and Reestimation

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Description Estimation of partial correlation matrix using ridge penalty followed by thresholding and reestimation. Under multivariate Gaussian assumption, the matrix constitutes an Gaussian graphical model (GGM).

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**Description**

Estimation of partial correlation matrix using ridge penalty followed by thresholding and reestimation. Under multivariate Gaussian assumption, the matrix constitutes an Gaussian graphical model (GGM).

**Details**

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- **Type:** Package
- **Version:** 1.2
- **Date:** 2022-06-05
- **License:** GPL-2

**Author(s)**

Min Jin Ha and Shanon T. Holloway

**References**


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**EM.mixture**

*Estimation of the mixture distribution using EM algorithm*

**Description**

Estimation of the parameters, null proportion, and degrees of freedom of the exact null density in the mixture distribution.

**Usage**

```
EM.mixture(p, eta0, df, tol)
```
**getEfronp**

**Arguments**

- `p` A numeric vector representing partial correlation coefficients.
- `eta0` An initial value for the null proportion; 1-`eta0` is the non-null proportion.
- `df` An initial value for the degrees of freedom of the exact null density.
- `tol` The tolerance level for convergence.

**Value**

- `df` Estimated degrees of freedom of the null density.
- `eta0` Estimated null proportion.
- `iter` The number of iterations required to reach convergence.

**Author(s)**

Min Jin Ha

**References**


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**getEfronp**

*Estimation of empirical null distribution.*

**Description**

Estimation of empirical null distribution using Efron’s central matching.

**Usage**

```r
getEfronp(z, bins = 120L, maxQ = 9, pct = 0.0, pct0 = 0.25,
cc = 1.2, plotIt = FALSE)
```

**Arguments**

- `z` A numeric vector of z values following the theoretical normal null distribution.
- `bins` The number of intervals for density estimation of the marginal density of z.
- `maxQ` The maximum degree of the polynomial to be considered for density estimation of the marginal density of z.
- `pct` Low and top (pct*100) to estimate f(z).
- `pct0` Low and top (pct0*100) excluded to estimate f0(z).
- `cc` The central parts (mu - sigma*cc, mu + sigma*cc) of the empirical distribution z are used for an estimate of the null proportion (eta).
- `plotIt` TRUE if density plot is to be produced.
The corrected z values to follow empirically standard normal distribution.

The corrected p values using the correct z values.

The chosen degree of polynomial for the estimated marginal density.

The location parameter for the normal null distribution.

The scale parameter for the normal null distribution.

The estimated null proportion.

Author(s)

Min Jin Ha

References


Examples

```r
p <- 100 # number of variables
n <- 50 # sample size

# Simulate data
simulation <- simulateData(G = p, etaA = 0.02, n = n, r = 1)
data <- simulation$data[[1]]
stddata <- scale(x = data, center = TRUE, scale = TRUE)

# estimate ridge parameter
lambda.array <- seq(from = 0.1, to = 20, by = 0.1) * (n - 1.0)
fit <- lambda.cv(x = stddata, lambda = lambda.array, fold = 10L)
lambda <- fit$lambda[which.min(fit$spe)] / (n - 1.0)

# calculate partial correlation
# using ridge inverse
w.upper <- which(upper.tri(diag(p)))
partial <- solve(lambda * diag(p) + cor(data))
partial <- (-scaledMat(x = partial))[w.upper]
```
ksStat

The Kolmogorov-Smirnov Statistic for p-Values

Description
Calculates the Kolmogorov-Smirnov statistic for p-values

Usage
ksStat(p)

Arguments
p
A numeric vector with p-values.

Value
Kolmogorov-Smirnov statistic

Author(s)
Min Jin Ha

Examples
p <- runif(100)
ksStat(p = p)
ks.test(p, y = "punif") # compare with ks.test

lambda.cv

Choose the Tuning Parameter of the Ridge Inverse

Description
Choose the tuning parameter of the ridge inverse by minimizing cross validation estimates of the total prediction errors of the p separate ridge regressions.

Usage
lambda.cv(x, lambda, fold)
Arguments

- **x**: An n by p data matrix.
- **lambda**: A numeric vector of candidate tuning parameters.
- **fold**: fold-cross validation is performed.

Value

- **lambda**: The selected tuning parameter, which minimizes the total prediction errors.
- **spe**: The total prediction error for all the candidate lambda values.

Author(s)

Min Jin Ha

References


Examples

```r
p <- 100  # number of variables
n <- 50   # sample size

# Simulate data
simulation <- simulateData(G = p, etaA = 0.02, n = n, r = 1)
data <- simulation$data[[1L]]
stddata <- scale(x = data, center = TRUE, scale = TRUE)

# estimate ridge parameter
lambda.array <- seq(from = 0.1, to = 20, by = 0.1) * (n - 1.0)
fit <- lambda.cv(x = stddata, lambda = lambda.array, fold = 10L)
lambda <- fit$lambda[which.min(fit$spe)] / (n - 1.0)

# calculate partial correlation
# using ridge inverse
partial <- solve(lambda*diag(p) + cor(data))
partial <- -scaledMat(x = partial)
```
Choose the Tuning Parameter of the Ridge Inverse and Thresholding Level of the Empirical p-Values

Description

Choose the tuning parameter of the ridge inverse and p-value cutoff by minimizing cross validation estimates of the total prediction errors of the p separate ridge regressions.

Usage

lambda.pcut.cv(x, lambda, pcut, fold = 10L)

Arguments

x n by p data matrix.
lambda A vector of candidate tuning parameters.
pcut A vector of candidate cutoffs of pvalues.
fold fold-cross validation is performed.

Value

The total prediction errors for all lambda (row-wise) and pcut (column-wise)

Author(s)

Min Jin Ha

References


Examples

p <- 100 # number of variables
n <- 50 # sample size

# Simulate data
simulation <- simulateData(G = p, etaA = 0.02, n = n, r = 1)
data <- simulation$data[[1L]]
stddata <- scale(x = data, center = TRUE, scale = TRUE)

# Selection of a lambda and a p-value cutoff
lambda.pcut.cv1

Choose the Tuning Parameter of the Ridge Inverse and Thresholding Level of the Empirical p-Values.

Description

Calculate total prediction error for test data after fitting partial correlations from train data for all values of lambda and pcut.

Usage

lambda.pcut.cv1(train, test, lambda, pcut)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>train</td>
<td>An n x p data matrix from which the model is fitted.</td>
</tr>
<tr>
<td>test</td>
<td>An m x p data matrix from which the model is evaluated.</td>
</tr>
<tr>
<td>lambda</td>
<td>A vector of candidate tuning parameters.</td>
</tr>
<tr>
<td>pcut</td>
<td>A vector of candidate cutoffs of pvalues.</td>
</tr>
</tbody>
</table>

Value

Total prediction error for all the candidate lambda and pvalue cutoff values.

Author(s)

Min Jin Ha

References

Examples

```r
p <- 100 # number of variables
n <- 50 # sample size

# Simulate data
simulation <- simulateData(G = p, etaA = 0.02, n = n, r = 1)
data <- simulation$data[[1L]]

# Split into train/test sets
train <- data[-testindex,,drop = FALSE]
stdTrain <- scale(x = train, center = TRUE, scale = TRUE)

# Calculate total prediction
# errors for all candidate
# lambda and p-value cutoffs
lambda.array <- seq(from = 0.1, to = 5, length = 10) * (n - 1.0)
pcut.array <- seq(from = 0.01, to = 0.05, by = 0.01)
tpe <- lambda.pcut.cv1(train = stdTrain,
                       test = stdTest,
                       lambda = lambda.array,
                       pcut = pcut.array)
```

---

**lambda.TargetD**

*Shrinkage Estimation of a Covariance Matrix Toward an Identity Matrix*

**Description**

Estimation of a weighted average of a sample covariance (correlation) matrix and an identity matrix.

**Usage**

```r
lambda.TargetD(x)
```

**Arguments**

- `x`: Centered data for covariance shrinkage and standardized data for correlation shrinkage.
Details

An analytical approach to the estimate ridge parameter.

Value

The estimates of shrinkage intensity.

Author(s)

Min Jin Ha

References


Examples

```
# Simulate data
simulation <- simulateData(G = 100, etaA = 0.02, n = 50, r = 10)
dat <- simulation$data[[1L]]
stddat <- scale(x = dat, center = TRUE, scale = TRUE)

shrinkage.lambda <- lambda.TargetD(x = stddat)

# the ridge parameter
ridge.lambda <- shrinkage.lambda / (1.0 - shrinkage.lambda)

# partial correlation matrix
partial <- -scaledMat(x = partial)
```
Usage

ne.lambda.cv(y, x, lambda, fold)

Arguments

y Length n response vector.

x n x p matrix for covariates with p variables and n sample size.

lambda A numeric vector for candidate tuning parameters for a ridge regression.

fold fold-cross validation used to choose the tuning parameter.

Value

lambda The selected tuning parameter, which minimizes the prediction error.

spe The prediction error for all of the candidate lambda values.

Author(s)

Min Jin Ha

References


Examples

```r
p <- 100 # number of variables
n <- 50 # sample size

# Simulate data
sim <- simulateData(G = p, etaA = 0.02, n = n, r = 1)
data <- sim$data[,1]
std <- scale(x = data, center = TRUE, scale = TRUE)

X <- std[,,-1]
y <- std[,1]

fit.lambda <- ne.lambda.cv(y = y, x = X, lambda = seq(from = 0.01, to = 1, by = 0.1), fold = 10)
lambda <- fit.lambda$lambda[which.min(fit.lambda$spe)]
```
Estimation of Partial Correlation Matrix Using \( p \) Separate Ridge Regressions.

**Description**

The partial correlation matrix is estimated by \( p \) separate ridge regressions with the parameters selected by cross validation.

**Usage**

```r
R.separate.ridge(x, fold, lambda, verbose = FALSE)
```

**Arguments**

- **x**: \( n \times p \) data matrix; \( n \) is the \# of samples and \( p \) is the \# of variables.
- **fold**: Ridge parameters are selected by fold-cross validations separately for each regression.
- **lambda**: The candidate ridge parameters for all \( p \) ridge regressions.
- **verbose**: TRUE/FALSE; if TRUE, print the procedure.

**Value**

- **R**: The partial correlation matrix.
- **lambda.sel**: The selected tuning parameters for \( p \) ridge regressions.

**Author(s)**

Min Jin Ha

**References**


**Examples**

```r
p <- 100 # number of variables
n <- 50 # sample size

# Simulate data
simulation <- simulateData(G = p, etaA = 0.02, n = n, r = 1)
data <- simulation$data[[1L]]
stddata <- scale(x = data, center = TRUE, scale = FALSE)
```
# estimate ridge parameter

w.upper <- which(upper.tri(diag(p)))

lambda.array <- seq(from = 0.1, to = 20, by=0.1) * (n-1.0)
partial.sep <- R.separate.ridge(x = stddata, lambda = lambda.array, fold = 5L, verbose = TRUE)$R[w.upper]

---

**scaledMat**  
*Scale a square matrix*

**Description**

Scale a square matrix to have unit diagonal elements.

**Usage**

```r
scaledMat(x)
```

**Arguments**

- `x`: A square matrix with positive diagonal elements

**Value**

Scaled matrix of `x`

**Author(s)**

Min Jin Ha

**Examples**

```r
# Simulate data
simulation <- simulateData(G = 100, etaA = 0.02, n = 50, r = 10)
dat <- simulation$data[[1L]]
correlation <- scaledMat(x = cov(dat))
```
simulateData

Generate Simulation Data from a Random Network.

Description
Generate a random network where both the network structure and the partial correlation coefficients are random. The data matrices are generated from multivariate normal distribution with the covariance matrix corresponding to the network.

Usage
simulateData(G, etaA, n, r, dist = "mvnorm")

Arguments
- `G` The number of variables (vertices)
- `etaA` The proportion of non-null edges among all the G(G-1)/2 edges.
- `n` The sample size.
- `r` The number of replicated G by N data matrices.
- `dist` A function which indicates the distribution of sample. "mvnorm" is multivariate normal distribution and "mvt" is multivariate t distribution with df=2. The default is set by "mvnorm".

Value
- `data` a list, each element containing an n X G matrix of simulated data.
- `true.partialcor` The partial correlation matrix which the datasets are generated from.
- `truecor.scaled` The covariance matrix calculated from the partial correlation matrix.
- `sig.node` The indices of nonzero upper triangle elements of partial correlation matrix.

Author(s)
Min Jin Ha

References

Examples
simulation <- simulateData(G = 100, etaA = 0.02, n = 50, r = 10)
structuredEstimate

Estimation of Partial Correlation Matrix Given Zero Structure.

Description

Estimation of nonzero entries of the partial correlation matrix given zero structure.

Usage

structuredEstimate(x, E)

Arguments

x
n by p data matrix with the number of variables p and sample size n.
E
The row and column indices of zero entries of the partial correlation matrix.

Value

R
The partial correlation matrix.
K
The inverse covariance matrix.
RSS
The residual sum of squares.

Author(s)

Min Jin Ha

References


Examples

p <- 100 # number of variables
n <- 50 # sample size

# Simulate data
simulation <- simulateData(G = p, etaA = 0.02, n = n, r = 1)
data <- simulation$data[[1L]]
stddata <- scale(x = data, center = TRUE, scale = TRUE)

# estimate ridge parameter
lambda.array <- seq(from = 0.1, to = 20, by = 0.1) * (n-1.0)
fit <- lambda.cv(x = stddata, lambda = lambda.array, fold = 10L)
transFisher <- fit$lambda[which.min(fit$spe)]/(n-1)

# calculate partial correlation
# using ridge inverse
w.upper <- which(upper.tri(diag(p)))

partial <- solve(lambda * diag(p) + cor(data))

# get p-values from empirical
# null distribution
efron.fit <- getEfronp(z = transFisher(x = partial),
                       bins = 50L,
                       maxQ = 13)

# estimate the edge set of
# partial correlation graph with
# FDR control at level 0.01
w.array <- which(upper.tri(diag(p)), arr.ind=TRUE)
th <- 0.01
wsig <- which(p.adjust(efron.fit$correctp, method="BH") < th)
E <- w.array[wsig,]
dim(E)

# structured estimation
fit <- structuredEstimate(x = stddata, E = E)

transFisher

Fisher’s Z-Transformation

Description
Fisher’s Z-transformation of (partial) correlation.

Usage
transFisher(x)

Arguments

x A vector having entries between -1 and 1.
transFisher

Value

Fisher’s Z-transformed values

Author(s)

Min Jin Ha

Examples

###############################
# Simulate data
###############################
simulation <- simulateData(G = 100, etaA = 0.02, n = 50, r = 1)
dat <- simulation$data[[1L]]
stddat <- scale(x = dat, center = TRUE, scale = TRUE)

shrinkage.lambda <- lambda.TargetD(x = stddat)

###############################
# the ridge parameter
###############################
ridge.lambda <- shrinkage.lambda / (1.0 - shrinkage.lambda)

###############################
# partial correlation matrix
###############################
partial <- solve(cor(dat) + ridge.lambda * diag(ncol(dat)))
partial <- -scaledMat(x = partial)

###############################
# Fisher’s Z transformation of
# upper diagonal of the partial
# correlation matrix
###############################
w.upper <- which(upper.tri(diag(nrow(dat))))
psi <- transFisher(x = partial[w.upper])
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