Package ‘huge’

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Description Provides a general framework for high-dimensional undirected graph estimation. It integrates data preprocessing, neighborhood screening, graph estimation, and model selection techniques into a pipeline. In preprocessing stage, the nonparanormal(npn) transformation is applied to help relax the normality assumption. In the graph estimation stage, the graph structure is estimated by Meinshausen-Buhlmann graph estimation or the graphical lasso, and both methods can be further accelerated by the lossy screening rule preselecting the neighborhood of each variable by correlation thresholding. We target on high-dimensional data analysis usually d >> n, and the computation is memory-optimized using the sparse matrix output. We also provide a computationally efficient approach, correlation thresholding graph estimation. Three regularization/thresholding parameter selection methods are included in this package: (1)stability approach for regularization selection (2) rotation information criterion (3) extended Bayesian information criterion which is only available for the graphical lasso.
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huge-package

High-Dimensional Undirected Graph Estimation

Description

A package for high-dimensional undirected graph estimation

Details

Package: huge
Type: Package
Version: 1.2.7
Date: 2015-09-14
License: GPL-2
LazyLoad: yes
The package "huge" provides 8 main functions:
(1) the data generator creates random samples from multivariate normal distributions with different graph structures. Please refer to huge.generator.
(2) the nonparanormal (npn) transformation helps relax the normality assumption. Please refer to huge.npn.
(3) The correlation thresholding graph estimation. Please refer to huge.
(4) The Meinshausen-Buhlmann graph estimation. Please refer to huge.
(5) The graphical Lasso algorithm using lossless screening rule. Please refer and huge.

**Both (4) and (5) can be further accelerated by the lossy screening rule preselecting the neighborhood of each node via thresholding sample correlation.

(6) The model selection using the stability approach to regularization selection. Please refer to huge.select.
(7) The model selection using the rotation information criterion. Please refer to huge.select.
(8) The model selection using the extended Bayesian information criterion. Please refer to huge.select.

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References
High-dimensional undirected graph estimation

Description

The main function for high-dimensional undirected graph estimation. Three graph estimation methods, including (1) Meinshausen-Buhlmann graph estimation (mb) (2) graphical lasso (glasso) (3) correlation thresholding graph estimation (ct) and (4) tuning-insensitive graph estimation (tiger), are available for data analysis.

Usage

huge(
  x,
  lambda = NULL,
  nlambda = NULL,
  lambda.min.ratio = NULL,
  method = "mb",
  scr = NULL,
  scr.num = NULL,
  cov.output = FALSE,
  sym = "or",
  verbose = TRUE
)

Arguments

x

There are 2 options: (1) x is an n by d data matrix (2) a d by d sample covariance matrix. The program automatically identifies the input matrix by checking the symmetry. (n is the sample size and d is the dimension).

lambda

A sequence of decreasing positive numbers to control the regularization when method = "mb", "glasso" or "tiger", or the thresholding in method = "ct". Typical usage is to leave the input lambda = NULL and have the program compute its own lambda sequence based on nlambda and lambda.min.ratio. Users can also specify a sequence to override this. When method = "mb", "glasso" or "tiger", use with care - it is better to supply a decreasing sequence values than a single (small) value.

nlambda

The number of regularization/thresholding parameters. The default value is 30 for method = "ct" and 10 for method = "mb", "glasso" or "tiger".

lambda.min.ratio

If method = "mb", "glasso" or "tiger", it is the smallest value for lambda, as a fraction of the upperbound (MAX) of the regularization/thresholding parameter which makes all estimates equal to 0. The program can automatically generate lambda as a sequence of length = nlambda starting from MAX to
lambda.min.ratio*MAX in log scale. If method = "ct", it is the largest sparsity level for estimated graphs. The program can automatically generate lambda as a sequence of length = nlambda, which makes the sparsity level of the graph path increases from 0 to lambda.min.ratio evenly. The default value is 0.1 when method = "mb", "glasso" or "tiger", and 0.05 method = "ct".

method
Graph estimation methods with 4 options: "mb", "ct", "glasso" and "tiger". The default value is "mb".

scr
If scr = TRUE, the lossy screening rule is applied to preselect the neighborhood before the graph estimation. The default value is FALSE. NOT applicable when method = "ct", "mb", or "tiger".

scr.num
The neighborhood size after the lossy screening rule (the number of remaining neighbors per node). ONLY applicable when scr = TRUE. The default value is n-1. An alternative value is n/log(n). ONLY applicable when scr = TRUE and method = "mb".

cov.output
If cov.output = TRUE, the output will include a path of estimated covariance matrices. ONLY applicable when method = "glasso". Since the estimated covariance matrices are generally not sparse, please use it with care, or it may take much memory under high-dimensional setting. The default value is FALSE.

sym
Symmetrize the output graphs. If sym = "and", the edge between node i and node j is selected ONLY when both node i and node j are selected as neighbors for each other. If sym = "or", the edge is selected when either node i or node j is selected as the neighbor for each other. The default value is "or". ONLY applicable when method = "mb" or "tiger".

verbose
If verbose = FALSE, tracing information printing is disabled. The default value is TRUE.

Details
The graph structure is estimated by Meinshausen-Buhlmann graph estimation or the graphical lasso, and both methods can be further accelerated via the lossy screening rule by preselecting the neighborhood of each variable by correlation thresholding. We target on high-dimensional data analysis usually d » n, and the computation is memory-optimized using the sparse matrix output. We also provide a highly computationally efficient approaches correlation thresholding graph estimation.

Value
An object with S3 class "huge" is returned:

data
The n by d data matrix or d by d sample covariance matrix from the input

cov.input
An indicator of the sample covariance.

ind.mat
The scr.num by k matrix with each column corresponding to a variable in ind.group and contains the indices of the remaining neighbors after the GSS. ONLY applicable when scr = TRUE and approx = FALSE

lambda
The sequence of regularization parameters used in mb or thresholding parameters in ct.

sym
The sym from the input. ONLY applicable when method = "mb" or "tiger".
The function `huge` estimates the graph path. For more information about the optimal graph selection, please refer to `huge.select`.

### Note

This function ONLY estimates the graph path. For more information about the optimal graph selection, please refer to `huge.select`.

### See Also

`huge.generator`, `huge.select`, `huge.plot`, `huge.roc`, and `huge-package`.

### Examples

```r
# generate data
L = huge.generator(n = 50, d = 12, graph = "hub", g = 4)

# graph path estimation using mb
out1 = huge(L$data)
out1
plot(out1)  # Not aligned
plot(out1, align = TRUE)  # Aligned
huge.plot(out1$path[[3]])

# graph path estimation using the sample covariance matrix as the input.
# out1 = huge(cor(L$data), method = "glasso")
# out1
# plot(out1)  # Not aligned
# plot(out1, align = TRUE)  # Aligned
# huge.plot(out1$path[[3]])
```
huge.ct

# graph path estimation using ct
# out2 = huge(L$data, method = "ct")
# out2
# plot(out2)

# graph path estimation using glasso
# out3 = huge(L$data, method = "glasso")
# out3
# plot(out3)

# graph path estimation using tiger
# out4 = huge(L$data, method = "tiger")
# out4
# plot(out4)

---

**huge.ct**  
*Graph estimation via correlation thresholding (ct)*

**Description**

See more details in **huge**

**Usage**

```r
huge.ct(  
x,  
nlambda = NULL,  
lambda.min.ratio = NULL,  
lambda = NULL,  
verbose = TRUE
)
```

**Arguments**

- `x`  
  There are 2 options: (1) `x` is an `n` by `d` data matrix (2) a `d` by `d` sample covariance matrix. The program automatically identifies the input matrix by checking the symmetry. (`n` is the sample size and `d` is the dimension).

- `nnlambda`  
  The number of regularization/thresholding parameters. The default value is 30 for method = "ct" and 10 for method = "mb", "glasso" or "tiger".

- `lambda.min.ratio`  
  If method = "mb", "glasso" or "tiger", it is the smallest value for `lambda`, as a fraction of the upperbound (MAX) of the regularization/thresholding parameter which makes all estimates equal to 0. The program can automatically generate `lambda` as a sequence of length = `nnlambda` starting from `MAX` to `lambda.min.ratio*MAX` in log scale. If method = "ct", it is the largest sparsity level for estimated graphs. The program can automatically generate `lambda` as a sequence of length = `nnlambda`, which makes the sparsity level of the graph path
increases from 0 to lambda.min.ratio evenly. The default value is 0.1 when method = "mb", "glasso" or "tiger", and 0.05 method = "ct".

lambda
A sequence of decreasing positive numbers to control the regularization when method = "mb", "glasso" or "tiger", or the thresholding in method = "ct". Typical usage is to leave the input lambda = NULL and have the program compute its own lambda sequence based on nlambda and lambda.min.ratio. Users can also specify a sequence to override this. When method = "mb", "glasso" or "tiger", use with care - it is better to supply a decreasing sequence values than a single (small) value.

verbose
If verbose = FALSE, tracing information printing is disabled. The default value is TRUE.

See Also
huge, and huge-package.

huge.generator  Data generator

Description
Implements the data generation from multivariate normal distributions with different graph structures, including "random", "hub", "cluster", "band" and "scale-free".

Usage
huge.generator(
  n = 200,
  d = 50,
  graph = "random",
  v = NULL,
  u = NULL,
  g = NULL,
  prob = NULL,
  vis = FALSE,
  verbose = TRUE
)

Arguments
n  The number of observations (sample size). The default value is 200.
d  The number of variables (dimension). The default value is 50.
graph  The graph structure with 4 options: "random", "hub", "cluster", "band" and "scale-free".
v  The off-diagonal elements of the precision matrix, controlling the magnitude of partial correlations with u. The default value is 0.3.
A positive number being added to the diagonal elements of the precision matrix, to control the magnitude of partial correlations. The default value is 0.1.

For "cluster" or "hub" graph, g is the number of hubs or clusters in the graph. The default value is about d/20 if d >= 40 and 2 if d < 40. For "band" graph, g is the bandwidth and the default value is 1. NOT applicable to "random" graph.

For "random" graph, it is the probability that a pair of nodes has an edge. The default value is 3/d. For "cluster" graph, it is the probability that a pair of nodes has an edge in each cluster. The default value is 6*g/d if d/g <= 30 and 0.3 if d/g > 30. NOT applicable to "hub" or "band" graphs.

Visualize the adjacency matrix of the true graph structure, the graph pattern, the covariance matrix and the empirical covariance matrix. The default value is FALSE.

If verbose = FALSE, tracing information printing is disabled. The default value is TRUE.

Given the adjacency matrix theta, the graph patterns are generated as below:

(I) "random": Each pair of off-diagonal elements are randomly set theta[i,j]=theta[j,i]=1 for i!=j with probability prob, and 0 otherwise. It results in about d*(d-1)*prob/2 edges in the graph.

(II) "hub": The row/columns are evenly partitioned into g disjoint groups. Each group is associated with a "center" row i in that group. Each pair of off-diagonal elements are set theta[i,j]=theta[j,i]=1 for i!=j if j also belongs to the same group as i and 0 otherwise. It results in d - g edges in the graph.

(III) "cluster": The row/columns are evenly partitioned into g disjoint groups. Each pair of off-diagonal elements are set theta[i,j]=theta[j,i]=1 for i!=j with the probability prob if both i and j belong to the same group, and 0 otherwise. It results in about g*(d/g)*(d/g-1)*prob/2 edges in the graph.

(IV) "band": The off-diagonal elements are set to be theta[i,j]=1 if 1<=|i-j|<=g and 0 otherwise. It results in (2d-1-g)*g/2 edges in the graph.

(V) "scale-free": The graph is generated using B-A algorithm. The initial graph has two connected nodes and each new node is connected to only one node in the existing graph with the probability proportional to the degree of the each node in the existing graph. It results in d edges in the graph.

The adjacency matrix theta has all diagonal elements equal to 0. To obtain a positive definite precision matrix, the smallest eigenvalue of theta*theta (denoted by e) is computed. Then we set the precision matrix equal to theta*theta+e*(|e|+0.1+u)I. The covariance matrix is then computed to generate multivariate normal data.

Value

An object with S3 class "sim" is returned:
data: The \( n \) by \( d \) matrix for the generated data

\( \sigma \): The covariance matrix for the generated data

\( \Omega \): The precision matrix for the generated data

\( \Sigma^{\text{emp}} \): The empirical covariance matrix for the generated data

\( \Theta \): The adjacency matrix of true graph structure (in sparse matrix representation) for the generated data

See Also

`huge` and `huge-package`

Examples

```r
## band graph with bandwidth 3
L = huge.generator(graph = "band", g = 3)
plot(L)

## random sparse graph
L = huge.generator(vis = TRUE)

## random dense graph
L = huge.generator(prob = 0.5, vis = TRUE)

## hub graph with 6 hubs
L = huge.generator(graph = "hub", g = 6, vis = TRUE)

## hub graph with 8 clusters
L = huge.generator(graph = "cluster", g = 8, vis = TRUE)

## scale-free graphs
L = huge.generator(graph = "scale-free", vis = TRUE)
```

---

### huge.glasso

The graphical lasso (glasso) using sparse matrix output

**Description**

See more details in `huge`

**Usage**

```r
huge.glasso(
  x,
  lambda = NULL,
  lambda.min.ratio = NULL,
  nlambda = NULL,
  scr = NULL,
  cov.output = FALSE,
  verbose = TRUE
)
```
**Arguments**

- **x**: There are 2 options: (1) \( x \) is an \( n \times d \) data matrix (2) a \( d \) by \( d \) sample covariance matrix. The program automatically identifies the input matrix by checking the symmetry. (\( n \) is the sample size and \( d \) is the dimension).

- **lambda**: A sequence of decreasing positive numbers to control the regularization when method = "mb", "glasso" or "tiger", or the thresholding in method = "ct". Typical usage is to leave the input lambda = NULL and have the program compute its own lambda sequence based on nlambda and lambda.min.ratio. Users can also specify a sequence to override this. When method = "mb", "glasso" or "tiger", use with care - it is better to supply a decreasing sequence values than a single (small) value.

- **lambda.min.ratio**: If method = "mb", "glasso" or "tiger", it is the smallest value for lambda, as a fraction of the upperbound (MAX) of the regularization/thresholding parameter which makes all estimates equal to 0. The program can automatically generate lambda as a sequence of length = nlambda starting from MAX to lambda.min.ratio*MAX in log scale. If method = "ct", it is the largest sparsity level for estimated graphs. The program can automatically generate lambda as a sequence of length = nlambda, which makes the sparsity level of the graph path increases from 0 to lambda.min.ratio evenly. The default value is 0.1 when method = "mb", "glasso" or "tiger", and 0.05 method = "ct".

- **nlambda**: The number of regularization/thresholding parameters. The default value is 30 for method = "ct" and 10 for method = "mb", "glasso" or "tiger".

- **scr**: If scr = TRUE, the lossy screening rule is applied to preselect the neighborhood before the graph estimation. The default value is FALSE. NOT applicable when method = "ct", "mb", "glasso" or "tiger".

- **cov.output**: If cov.output = TRUE, the output will include a path of estimated covariance matrices. ONLY applicable when method = "glasso". Since the estimated covariance matrices are generally not sparse, please use it with care, or it may take much memory under high-dimensional setting. The default value is FALSE.

- **verbose**: If verbose = FALSE, tracing information printing is disabled. The default value is TRUE.

**See Also**

huge, and huge-package.

---

**huge.inference**  
**Graph inference**

**Description**

Implements the inference for high dimensional graphical models, including Gaussian and Nonparamnormal graphical models We consider the problems of testing the presence of a single edge and the hypothesis is that the edge is absent.
Usage

huge.inference(data, T, adj, alpha = 0.05, type = "Gaussian", method = "score")

Arguments

data: The input n by d data matrix (n is the sample size and d is the dimension).
T: The estimated inverse of correlation matrix of the data.
adj: The adjacency matrix corresponding to the graph.
alpha: The significance level of hypothesis. The default value is 0.05.
type: The type of input data. There are 2 options: "Gaussian" and "Nonparanormal". The default value is "Gaussian".
method: When using nonparanormal graphical model. Test method with 2 options: "score" and "wald". The default value is "score".

Details

For Nonparanormal graphical model we provide Score test method and Wald Test. However it is really slow for inferencing on Nonparanormal model, especially for large data.

Value

An object is returned:
data: The n by d data matrix from the input.
p: The d by d p-value matrix of hypothesis.
error: The type I error of hypothesis at alpha significance level.

References

1. Q Gu, Y Cao, Y Ning, H Liu. Local and global inference for high dimensional nonparanormal graphical models.

See Also

huge, and huge-package.

Examples

#generate data
L = huge.generator(n = 50, d = 12, graph = "hub", g = 4)

#graph path estimation using glasso
est = huge(L$data, method = "glasso")

#inference of Gaussian graphical model at 0.05 significance level
T = tail(est$icov, 1)[[1]]
out1 = huge.inference(L$data, T, L$theta)

# inference of Nonparanormal graphical model using score test at 0.05 significance level
T = tail(est$icov, 1)[[1]]
out2 = huge.inference(L$data, T, L$theta, type = "Nonparanormal")

# inference of Nonparanormal graphical model using wald test at 0.05 significance level
T = tail(est$icov, 1)[[1]]
out3 = huge.inference(L$data, T, L$theta, type = "Nonparanormal", method = "wald")

# inference of Nonparanormal graphical model using wald test at 0.1 significance level
T = tail(est$icov, 1)[[1]]
out4 = huge.inference(L$data, T, L$theta, 0.1, type = "Nonparanormal", method = "wald")

---

huge.mb  Meinshausen & Buhlmann graph estimation

Description

See more details in huge

Usage

huge.mb(

  x,
  lambda = NULL,
  nlambda = NULL,
  lambda.min.ratio = NULL,
  scr = NULL,
  scr.num = NULL,
  idx.mat = NULL,
  sym = "or",
  verbose = TRUE
)

Arguments

x  There are 2 options: (1) x is an n by d data matrix (2) a d by d sample covariance matrix. The program automatically identifies the input matrix by checking the symmetry. (n is the sample size and d is the dimension).

lambda  A sequence of decreasing positive numbers to control the regularization when method = "mb", "glasso" or "tiger", or the thresholding in method = "ct". Typical usage is to leave the input lambda = NULL and have the program compute its own lambda sequence based on nlambda and lambda.min.ratio. Users can also specify a sequence to override this. When method = "mb", "glasso" or "tiger", use with care - it is better to supply a decreasing sequence values than a single (small) value.
nlambda
The number of regularization/thresholding parameters. The default value is 30 for method = "ct" and 10 for method = "mb", "glasso" or "tiger".

lambda.min.ratio
If method = "mb", "glasso" or "tiger", it is the smallest value for lambda, as a fraction of the upperbound (MAX) of the regularization/thresholding parameter which makes all estimates equal to 0. The program can automatically generate lambda as a sequence of length = nlambda starting from MAX to lambda.min.ratio*MAX in log scale. If method = "ct", it is the largest sparsity level for estimated graphs. The program can automatically generate lambda as a sequence of length = nlambda, which makes the sparsity level of the graph path increases from 0 to lambda.min.ratio evenly. The default value is 0.1 when method = "mb", "glasso" or "tiger", and 0.05 method = "ct".

scr
If scr = TRUE, the lossy screening rule is applied to preselect the neighborhood before the graph estimation. The default value is FALSE. NOT applicable when method = "ct", "mb", or "tiger".

scr.num
The neighborhood size after the lossy screening rule (the number of remaining neighbors per node). ONLY applicable when scr = TRUE. The default value is n-1. An alternative value is n/log(n). ONLY applicable when scr = TRUE and method = "mb".

idx.mat
Index matrix for screening.

sym
Symmetrize the output graphs. If sym = "and", the edge between node i and node j is selected ONLY when both node i and node j are selected as neighbors for each other. If sym = "or", the edge is selected when either node i or node j is selected as the neighbor for each other. The default value is "or". ONLY applicable when method = "mb" or "tiger".

verbose
If verbose = FALSE, tracing information printing is disabled. The default value is TRUE.

See Also
huge, and huge-package.
Arguments

- **x**: The \( n \) by \( d \) data matrix representing \( n \) observations in \( d \) dimensions.

- **npn.func**: The transformation function used in the npn transformation. If npn.func = "truncation", the truncated ECDF is applied. If npn.func = "shrinkage", the shrunkened ECDF is applied. The default is "shrinkage". If npn.func = "skeptic", the nonparanormal skeptic is applied.

- **npn.thresh**: The truncation threshold used in nonparanormal transformation, ONLY applicable when npn.func = "truncation". The default value is \( 1/(4*{(n}^{0.25})*\sqrt{\pi*\log(n)}) \).

- **verbose**: If verbose = FALSE, tracing information printing is disabled. The default value is TRUE.

Details

The nonparanormal extends Gaussian graphical models to semiparametric Gaussian copula models. Motivated by sparse additive models, the nonparanormal method estimates the Gaussian copula by marginally transforming the variables using smooth functions. Computationally, the estimation of a nonparanormal transformation is very efficient and only requires one pass of the data matrix.

Value

- **data**: A \( d \) by \( d \) nonparanormal correlation matrix if npn.func = "skeptic", and \( A \) \( n \) by \( d \) data matrix representing \( n \) observations in \( d \) transformed dimensions otherwise.

See Also

huge and huge-package.

Examples

```r
# generate nonparanormal data
L = huge.generator(graph = "cluster", g = 5)
L$data = L$data^5

# transform the data using the shrunken ECDF
Q = huge.npn(L$data)

# transform the non-Gaussian data using the truncated ECDF
Q = huge.npn(L$data, npn.func = "truncation")

# transform the non-Gaussian data using the truncated ECDF
Q = huge.npn(L$data, npn.func = "skeptic")
```
**huge.plot**  
*Graph visualization*

**Description**

Implements the graph visualization using adjacency matrix. It can automatic organize 2D embedding layout.

**Usage**

```r
huge.plot(
  G,
  epsflag = FALSE,
  graph.name = "default",
  cur.num = 1,
  location = NULL
)
```

**Arguments**

- **G**: The adjacency matrix corresponding to the graph.
- **epsflag**: If `epsflag = TRUE`, save the plot as an eps file in the target directory. The default value is `FALSE`.
- **graph.name**: The name of the output eps files. The default value is "default".
- **cur.num**: The number of plots saved as eps files. Only applicable when `epsflag = TRUE`. The default value is 1.
- **location**: Target directory. The default value is the current working directory.

**Details**

The user can change `cur.num` to plot several figures and select the best one. The implementation is based on the popular package "igraph".

**See Also**

`huge` and `huge-package`.

**Examples**

```r
## visualize the hub graph
L = huge.generator(graph = "hub")
huge.plot(L$theta)

## visualize the band graph
L = huge.generator(graph = "band", g=5)
huge.plot(L$theta)
```
## visualize the cluster graph
L = huge.generator(graph = "cluster")
huge.plot(L$theta)

## plot 5 graphs and save the plots as eps files in the tempdir()
huge.plot(L$theta, epsflag = TRUE, cur.num = 5, location = tempdir())

---

**huge.roc**

### Draw ROC Curve for a graph path

**Description**

Draws ROC curve for a graph path according to the true graph structure.

**Usage**

```r
huge.roc(path, theta, verbose = TRUE)
```

**Arguments**

- `path`: A graph path.
- `theta`: The true graph structure.
- `verbose`:
  - If `verbose = FALSE`, tracing information printing is disabled. The default value is `TRUE`.

**Details**

To avoid the horizontal oscillation, false positive rates is automatically sorted in the ascent order and true positive rates also follow the same order.

**Value**

An object with S3 class "roc" is returned:

- `F1`: The F1 scores along the graph path.
- `tp`: The true positive rates along the graph path.
- `fp`: The false positive rates along the graph path.
- `AUC`: Area under the ROC curve

**Note**

For a lasso regression, the number of nonzero coefficients is at most n-1. If d>>n, even when regularization parameter is very small, the estimated graph may still be sparse. In this case, the AUC may not be a good choice to evaluate the performance.

**See Also**

`huge` and `huge-package`.
Examples

```r
#generate data
L = huge.generator(d = 200, graph = "cluster", prob = 0.3)
out1 = huge(L$data)

#draw ROC curve
Z1 = huge.roc(out1$path,L$theta)

#Maximum F1 score
max(Z1$F1)
```

huge.select

Model selection for high-dimensional undirected graph estimation

Description

Implements the regularization parameter selection for high dimensional undirected graph estimation. The optional approaches are rotation information criterion (ric), stability approach to regularization selection (stars) and extended Bayesian information criterion (ebic).

Usage

```r
huge.select(
  est,
  criterion = NULL,
  ebic.gamma = 0.5,
  stars.thresh = 0.1,
  stars.subsample.ratio = NULL,
  rep.num = 20,
  verbose = TRUE
)
```

Arguments

- `est` : An object with S3 class "huge".
- `criterion` : Model selection criterion. "ric" and "stars" are available for all 3 graph estimation methods. ebic is only applicable when est$method = "glasso" in huge(). The default value is "ric".
- `ebic.gamma` : The tuning parameter for ebic. The default value is 0.5. Only applicable when est$method = "glasso" and criterion = "ebic".
- `stars.thresh` : The variability threshold in stars. The default value is 0.1. An alternative value is 0.05. Only applicable when criterion = "stars".
- `stars.subsample.ratio` : The subsampling ratio. The default value is \( 10 \times \sqrt{n}/n \) when \( n>144 \) and 0.8 when \( n\leq 144 \), where \( n \) is the sample size. Only applicable when criterion = "stars".
**Details**

Stability approach to regularization selection (stars) is a natural way to select optimal regularization parameter for all three estimation methods. It selects the optimal graph by variability of subsamplings and tends to overselect edges in Gaussian graphical models. Besides selecting the regularization parameters, stars can also provide an additional estimated graph by merging the corresponding subsampled graphs using the frequency counts. The subsampling procedure in stars may NOT be very efficient, we also provide the recent developed highly efficient, rotation information criterion approach (ric). Instead of tuning over a grid by cross-validation or subsampling, we directly estimate the optimal regularization parameter based on random Rotations. However, ric usually has very good empirical performances but suffers from underselections sometimes. Therefore, we suggest if user are sensitive of false negative rates, they should either consider increasing \( r.num \) or applying the stars to model selection. Extended Bayesian information criterion (ebic) is another competitive approach, but the ebic.gamma can only be tuned by experience.

**Value**

An object with S3 class "select" is returned:

- **refit**: The optimal graph selected from the graph path.
- **opt.icov**: The optimal precision matrix from the path only applicable when method = "glasso".
- **opt.cov**: The optimal covariance matrix from the path only applicable when method = "glasso" and est$cov is available.
- **merge**: The graph path estimated by merging the subsampling paths. Only applicable when the input criterion = "stars".
- **variability**: The variability along the subsampling paths. Only applicable when the input criterion = "stars".
- **ebic.scores**: Extended BIC scores for regularization parameter selection. Only applicable when criterion = "ebic".
- **opt.index**: The index of the selected regularization parameter. NOT applicable when the input criterion = "ric".
- **opt.lambda**: The selected regularization/thresholding parameter.
- **opt.sparsity**: The sparsity level of "refit".

and anything else included in the input est

**Note**

The model selection is NOT available when the data input is the sample covariance matrix.
huge.tiger

Tuning-insensitive graph estimation

See Also

huge and huge-package.

Examples

```r
#generate data
L = huge.generator(d = 20, graph="hub")
out.mb = huge(L$data)
out.ct = huge(L$data, method = "ct")
out.glasso = huge(L$data, method = "glasso")

#model selection using ric
out.select = huge.select(out.mb)
plot(out.select)

#model selection using stars
#out.select = huge.select(out.ct, criterion = "stars", stars.thresh = 0.05, rep.num=10)
#plot(out.select)

#model selection using ebic
out.select = huge.select(out.glasso, criterion = "ebic")
plot(out.select)
```

Description

See more details in huge

Usage

```r
huge.tiger(
  x,
  lambda = NULL,
  nlambda = NULL,
  lambda.min.ratio = NULL,
  sym = "or",
  verbose = TRUE
)
```

Arguments

- `x` There are 2 options: (1) `x` is an \( n \times d \) data matrix (2) a \( d \times d \) sample covariance matrix. The program automatically identifies the input matrix by checking the symmetry. (\( n \) is the sample size and \( d \) is the dimension).
lambda A sequence of decreasing positive numbers to control the regularization when method = "mb", "glasso" or "tiger", or the thresholding in method = "ct". Typical usage is to leave the input lambda = NULL and have the program compute its own lambda sequence based on nlambda and lambda.min.ratio. Users can also specify a sequence to override this. When method = "mb", "glasso" or "tiger", use with care - it is better to supply a decreasing sequence values than a single (small) value.
nlambda The number of regularization/thresholding parameters. The default value is 30 for method = "ct" and 10 for method = "mb", "glasso" or "tiger".
lambda.min.ratio If method = "mb", "glasso" or "tiger", it is the smallest value for lambda, as a fraction of the upperbound (MAX) of the regularization/thresholding parameter which makes all estimates equal to 0. The program can automatically generate lambda as a sequence of length = nlambda starting from MAX to lambda.min.ratio*MAX in log scale. If method = "ct", it is the largest sparsity level for estimated graphs. The program can automatically generate lambda as a sequence of length = nlambda, which makes the sparsity level of the graph path increases from 0 to lambda.min.ratio evenly. The default value is 0.1 when method = "mb", "glasso" or "tiger", and 0.05 method = "ct".
sym Symmetrize the output graphs. If sym = "and", the edge between node i and node j is selected ONLY when both node i and node j are selected as neighbors for each other. If sym = "or", the edge is selected when either node i or node j is selected as the neighbor for each other. The default value is "or". ONLY applicable when method = "mb" or "tiger".
verbose If verbose = FALSE, tracing information printing is disabled. The default value is TRUE.

See Also

huge, and huge-package.

plot.huge Plot function for S3 class "huge"

Description

Plot sparsity level information and 3 typical sparse graphs from the graph path.

Usage

## S3 method for class 'huge'
plot(x, align = FALSE, ...)

Arguments

x An object with S3 class "huge"
align If align = FALSE, 3 plotted graphs are aligned
... System reserved (No specific usage)
plot.roc

Description

Plot the ROC curve for an object with S3 class "roc".

Usage

```r
## S3 method for class 'roc'
plot(x, ...)  
```

Arguments

- `x`: An object with S3 class "roc"
- `...`: System reserved (No specific usage)

See Also

- `huge.roc`

plot.select

Description

Plot the optimal graph by model selection.

Usage

```r
## S3 method for class 'select'
plot(x, ...)  
```

Arguments

- `x`: An object with S3 class "select"
- `...`: System reserved (No specific usage)

See Also

- `huge.select`
**plot.sim**

*Plot function for S3 class "sim"*

**Description**

Visualize the covariance matrix, the empirical covariance matrix, the adjacency matrix and the graph pattern of the true graph structure.

**Usage**

```r
## S3 method for class 'sim'
plot(x, ...)
```

**Arguments**

- `x` An object with S3 class "sim"
- `...` System reserved (No specific usage)

**See Also**

huge.generator and huge

---

**print.huge**

*Print function for S3 class "huge"*

**Description**

Print the information about the model usage, the graph path length, graph dimension, sparsity level.

**Usage**

```r
## S3 method for class 'huge'
print(x, ...)
```

**Arguments**

- `x` An object with S3 class "huge"
- `...` System reserved (No specific usage)

**See Also**

huge
print.roc

Print function for S3 class "roc"

Description
Print the information about true positive rates, false positive rates, the area under curve and maximum F1 score.

Usage
## S3 method for class 'roc'
print(x, ...)

Arguments
x An object with S3 class "roc".
... System reserved (No specific usage)

See Also
huge.roc

print.select

Print function for S3 class "select"

Description
Print the information about the model usage, graph dimension, model selection criterion, sparsity level of the optimal graph.

Usage
## S3 method for class 'select'
print(x, ...)

Arguments
x An object with S3 class "select".
... System reserved (No specific usage)

See Also
huge.select
**print.sim**

*Print function for S3 class "sim"

**Description**

Print the information about the sample size, the dimension, the pattern and sparsity of the true graph structure.

**Usage**

```r
## S3 method for class 'sim'
print(x, ...)
```

**Arguments**

- `x`: An object with S3 class "sim".
- `...`: System reserved (No specific usage)

**See Also**

`huge.generator`

---

**stockdata**

*Stock price of S&P 500 companies from 2003 to 2008*

**Description**

This data set consists of stock price and company information.

**Usage**

```r
data(stockdata)
```

**Format**

The format is a list containing contains two matrices. 1. data - 1258x452, represents the 452 stocks' close prices for 1258 trading days. 2. info - 452x3: The 1st column: the query symbol for each company. The 2nd column: the category for each company. The 3rd column: the full name of each company.

**Details**

This data set can be used to perform high-dimensional graph estimation to analyze the relationships between S&P 500 companies.
Source

It was publicly available at finance.yahoo, which is now out of date

Examples

data(stockdata)
image(stockdata$data)
stockdata$info
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