Package ‘BDgraph’

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Description A general framework to perform Bayesian structure learning in undirected graphical models. The main target is high-dimensional data analysis wherein either continuous or discrete variables.
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**Description**

The R package **BDgraph** provides statistical tools for Bayesian structure learning in undirected graphical models based on birth-death MCMC method. It implements the recent improvements in the Bayesian literature, including Mohammadi and Wit (2015) and Mohammadi et al. (2015).

**Details**

The package includes 10 main functions:

- `bdgraph`: birth-death MCMC sampling algorithm for graphical models
- `bdgraph.sim`: Synthetic graph data generator
- `bdgraph.npt`: Nonparametric transfer
- `compare`: Comparing the result
- `phat`: Posterior link probabilities
- `plotcoda`: Convergence plot
- `plotroc`: ROC plot
- `rgwish`: Sampling from G-Wishart distribution
- `select`: Selecting the best graph
- `traceplot`: Trace plot of graph size

**Author(s)**

Abdolreza Mohammadi (<a.mohammadi@rug.nl>) and Ernst Wit
bdgraph

Description

The main function of the BDgraph package. The function consists of two sampling algorithm for model determination in undirected graphical models based on birth-death MCMC method.

Usage

bdgraph( data, n = NULL, method = "ggm", iter = 5000, burnin = iter / 2, b = 3, D = NULL, Gstart = "empty" )

Arguments

data It could be a \((n \times p)\) matrix or a data.frame of data or a covariance matrix as \(S = X'X\) which \(X\) is the data matrix. It also could be an object of class "simulate", from function bdgraph.sim.
n The number of observations. It is needed if the "data" is a covariance matrix.
method A character with two options "ggm" (default) and "gcgm". Option "ggm" is for Gaussian graphical models based on Gaussianity assumption. Option "gcgm" is for Gaussian copula graphical models for the data that not follow Gaussianity assumption (e.g. continuous non-Gaussian, discrete, or mixed dataset).
iter The number of iteration for the sampling algorithm.
burnin The number of burn-in iteration for the sampling algorithm.
b The degree of freedom for G-Wishart distribution, \(W_G(b, D)\), which is a prior distribution of the precision matrix. The default is 3.
D The positive definite matrix for G-Wishart distribution, \(W_G(b, D)\). The default is an identity matrix.
Gstart It corresponds to a starting point for graph. It can be "full" (default), "empty", or an object with S3 class "bdgraph". Option "full" means the initial graph is a full graph and "empty" means a empty graph. Gstart also could be an object with S3 class "bdgraph"; With this option we could run the sampling algorithm from last objects of previous run (see examples).

References


Value

An object with S3 class "bdgraph" is returned:

- `sampleGraphs`: A vector which includes the adjacency matrices for all iterations after burn-in.
- `graphWeights`: A vector which includes the waiting times for all iterations after burn-in.
- `allGraphs`: A vector which includes the adjacency matrices for all iterations (includes burn-in iteration). It is needed for monitoring the convergence of the BD-MCMC algorithm.
- `allWeights`: A vector which includes the waiting times for all iterations (includes burn-in iteration). It is needed for monitoring the convergence of the BD-MCMC algorithm.
- `Khat`: Estimation for precision matrix which is a mean of all samples from precision matrices.

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


See Also

`bdgraphNsim`, `summaryNdgraph`, and `compare`

Examples

```r
# Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 20, p = 6, size = 7, vis = TRUE )

output <- bdgraph( data = data.sim, iter = 1000 )

summary(output)

# To compare our result with true graph
compare( data = data.sim, output, colnames = c("True graph", "BDgraph") )

output2 <- bdgraph( data = data.sim, iter = 5000, Gstart = output )

compare( data = data.sim, output, output2, colnames = c("True graph", "First run", "Second run") )
```
bdgraph.npn

# generating mixed data from a 'scale-free' graph
data.sim <- bdgraph.sim( n = 100, p = 6, type = "mixed", graph = "scale-free", vis = TRUE )

output <- bdgraph( data = data.sim, method = "gcgm", iter = 10000 )

summary( output )

compare( data.sim, output )

## End(Not run)

bdgraph.npn  Nonparametric transfer

Description

This function transfers non-Gaussian data to Gaussian.

Usage

bdgraph.npn( data, npn = "shrinkage", npn.thresh = NULL )

Arguments

data  It could be a \((n \times p)\) matrix or a data.frame corresponding to the data.

npn  A character with three options "shrinkage" (default), "truncation", and "skeptic". Option "shrinkage" is for the shrunken transformation, option "truncation" is for the truncated transformation and option "skeptic" is for the non-paranormal skeptic transformation. For more details see references.

npn.thresh  The truncation threshold; it is only for the truncated transformation (when npn = "truncation"). The default value is \(1/(4n^{1/4}\sqrt{\pi \log(n)})\).

Value

data  A \((n \times p)\) matrix of transferred data, if npn = "shrinkage" or "truncation", and a non-paranormal correlation \((p \times p)\) matrix, if npn = "skeptic".

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


bdgraph.sim

Synthetic graph data generator

Description

This function implements a synthetic graph data generation for multivariate distributions with different types of underlying graph structures, including "random", "cluster", "scale-free", "hub", "fixed", and "circle". Based on the underlying graph structure, it generates four different types of datasets, including multivariate Gaussian, non-Gaussian, discrete, or mixed data.

Usage

bdgraph.sim( n = 2, p = 10, graph = "random", size = NULL, prob = 0.2, class = NULL, type = "Gaussian", cut = 4, b = 3, D = diag(p), K = NULL, sigma = NULL, mean = 0, vis = FALSE )

Arguments

n
The number of samples required. The default value is 2.

p
The number of variables (nodes). The default value is 10.

graph
The graph structure with option "random" (as a default), "cluster", "scale-free", "hub", "fixed", and "circle". It also could be an adjacency matrix corresponding to a graph structure (an upper triangular matrix in which \( g_{ij} = 1 \) if there is a link between notes \( i \) and \( j \), otherwise \( g_{ij} = 0 \)).

size
The number of links in the true graph (graph size).
For a "random" graph, it is the probability that a pair of nodes has a link. The default value is 0.2.

Number of classes for option "cluster".

Type of data with four options "Gaussian" (as a default), "non-Gaussian", "discrete", and "mixed". For option "Gaussian", data are generated from multivariate normal distribution. For option "non-Gaussian", data are transferred multivariate normal distribution to continuous multivariate non-Gaussian distribution. For option "discrete", data are transferred from multivariate normal distribution to discrete multivariate distribution. For option "mixed", data are transferred from multivariate normal distribution to mixture of 'count', 'ordinal', 'non-Gaussian', 'binary' and 'Gaussian', respectively.

Number of categories for simulating discrete data (type = "discrete"). The default value is 4.

The degree of freedom for G-Wishart distribution, \( W_G(b, D) \). The default is 3.

The positive definite \((p\times p)\) "scale" matrix for G-Wishart distribution, \( W_G(b, D) \). The default is an identity matrix.

A positive-definite symmetric matrix specifying the precision matrix. It is for option graph = "fixed".

A positive-definite symmetric matrix specifying the covariance matrix. It is for option graph = "fixed".

A vector specifying the mean of the variables. The default value is a zero vector.

Visualize the true graph pattern. The default value is FALSE.

An object with S3 class "simulate" is returned:

Generated data as a \( n \times p \) matrix.

The covariance matrix of the generated data.

The precision matrix of the generated data.

The adjacency matrix corresponding to the true graph structure.

Abdolreza Mohammadi and Ernst Wit


See Also

bdgraph

Examples

## Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 50, p = 10, prob = 0.3, vis = TRUE )
print(data.sim)

# generating multivariate normal data from a 'hub' graph
data.sim <- bdgraph.sim( n = 3, p = 6, graph = "hub", vis = FALSE )
data.sim $ data

# generating mixed data from a 'hub' graph
data.sim <- bdgraph.sim( n = 10, p = 8, graph = "hub", type = "mixed" )
data.sim $ data

## End(Not run)

---

**CellSignal**

*A flow cytometry dataset*

Description

This dataset contains flow cytometry of 11 proteins measured on 11672 red blood cells.

Usage

data(CellSignal)

Format

The format is a list of 11672 rows (number of cells) and 11 column (number of proteins).

Source

Data are publicly available at http://www.sciencemag.org/content/308/5721/523/suppl/DC1

Examples

data( CellSignal )
head( CellSignal )
boxplot( CellSignal )
Description

With this function, we can check the performance of our method and compare it with other alternative approaches.

Usage

```r
compare( G, est, est2 = NULL, est3 = NULL, colnames = NULL, vis = FALSE )
```

Arguments

- **G**: The adjacency matrix corresponding to the true graph in which $g_{ij} = 1$ if there is a link between notes $i$ and $j$, otherwise $g_{ij} = 0$. It also can be an object with S3 class "simulate" from function `bdgraph.sim`.
- **est**: An adjacency matrix corresponding to an estimated graph. It also can be an object with S3 class "bdgraph" from function `bdgraph` or "select" (from `huge` package).
- **est2**: An adjacency matrix corresponding to an estimated graph. It also can be an object with S3 class "bdgraph" from function `bdgraph` or "select" (from `huge` package).
- **est3**: An adjacency matrix corresponding to an estimated graph. It also can be an object with S3 class "bdgraph" from function `bdgraph` or "select" (from `huge` package).
- **colnames**: A character vector giving the column names for the result table.
- **vis**: Logical: if TRUE you will see a plot result. The default is FALSE.

Value

- **True positive**: The number of correctly estimated links.
- **True negative**: The number of true non-existing links which is correctly estimated.
- **False positive**: The number of links which they are not in the true graph, but are incorrectly estimated.
- **False negative**: The number of links which they are in the true graph, but are not estimated.
- **Accuracy**: the number of true results (both true positives and true negatives) divided by the total number of true and false results.
- **Balanced F-score**: A weighted average of the "positive predictive" and "true positive rate". F-score value reaches its best value at 1 and worst score at 0.
- **Positive predictive**: The number of correctly estimated links divided by the total number of links in the estimated graph.
True positive rate
The number of correctly estimated links divided by the total number of links in the true graph.

False positive rate
The false positive value divided by the total number of links in the true graph.

Author(s)
Abdolreza Mohammadi, Antonio Abbruzzo, Ivan Vujacic, and Ernst Wit

References


See Also
bdgraph and select

Examples
```r
## Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 50, p = 6, size = 7, vis = TRUE )

# running sampling algorithm
output <- bdgraph( data = data.sim, iter = 10000 )
# comparing the result
compare( data.sim, output, colnames = c("true", "BDgraph"), vis = TRUE )

# estimate the true graph by 'huge' package
require( huge )
huge.g <- huge( data.sim $ data, method = "mb" )
huge.g <- huge.select( huge.g )

# comparing the result
compare( data.sim, output, huge.g, colnames = c("true", "BDgraph", "huge"), vis = TRUE )

## End(Not run)
```
geneExpression

**Human gene expression dataset**

**Description**
This data set contains human gene expression of 100 transcripts (with unique Illumina TargetID) measured on 60 unrelated individuals.

**Usage**
```r
data(geneExpression)
```

**Format**
The format is a matrix with 60 rows (number of individuals) and 100 column (number of transcripts).

**Source**
The genotypes of those 60 unrelated individuals are available from the Sanger Institute website at ftp://ftp.sanger.ac.uk/pub/genevar

**Examples**
```r
data( geneExpression )
dim( geneExpression )
head( geneExpression )
boxplot( geneExpression )
```

---

**phat**

**Posterior link probabilities**

**Description**
Provides the posterior link probabilities for all possible links in the graph.

**Usage**
```r
phat( output, round = 3 )
```

**Arguments**
- **output**: An object of S3 class "bdgraph", from function `bdgraph`.
- **round**: A value for rounding all probabilities to the specified number of decimal places (default is 3).
plot.bdgraph

Value

phat Upper triangular matrix which corresponds the posterior probabilities for all possible links.

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


See Also

bdgraph and bdgraph.sim

Examples

## Not run:
# generating multivariate normal data from a 'circle' graph
data.sim <- bdgraph.sim( n = 70, p = 6, graph = "circle", vis = TRUE )

output <- bdgraph( data = data.sim, iter = 10000 )

phat( output, round = 2 )

## End(Not run)

---

plot.bdgraph \hspace{1cm} \textit{Plot function for S3 class "bdgraph"}

Description

Visualize pattern of the graphs with the highest posterior probabilities.

Usage

## S3 method for class 'bdgraph'
plot( x, g = 1, layout = layout.circle, ... )
plot.simulate

Arguments

- `x`: An object of S3 class "bdgraph", from function `bdgraph`.
- `g`: The number of graphs with highest probabilities (default is 1).
- `layout`: The vertex placement algorithm which is according to `igraph` package. The default is "layout.circle".
- ... System reserved (no specific usage).

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


See Also

`bdgraph`

Examples

```r
## Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 50, p = 6, vis = TRUE )

output <- bdgraph( data = data.sim )
plot(output)
plot(output, g = 4 )
## End(Not run)
```

Description

Visualize structure of the true graph.
Usage

### S3 method for class 'simulate'

```r
plot(x, main = NULL, layout = layout.circle, ...)
```

Arguments

- **x**: An object of S3 class "simulate", from function `bdgraph.sim`.
- **main**: Graphical parameter (see plot).
- **layout**: The vertex placement algorithm which is according to `igraph` package. The default is "layout.circle".
- **...**: System reserved (no specific usage).

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


See Also

`bdgraph`

Examples

```r
## Not run:
# generating synthetic multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim(n = 10, p = 15)

plot(data.sim)

## End(Not run)
```
Description
Displays a plot which provides the cumulative occupancy fractions of all possible links in the graph. The plot can be used for monitoring the convergence of the BD-MCMC sampling algorithm.

Usage
plotcoda( output, thin = NULL, main = NULL, links = TRUE, ... )

Arguments
output An object of S3 class "bdgraph", from function bdgraph.
thin An option for getting fast result for a cumulative plot according to part of the iteration.
main Graphical parameter (see plot).
links Logical: if TRUE and number of variables (p) is more that 15, you will see a plot result for 100 selected links. The default is TRUE.
... System reserved (no specific usage).

Details
Note that a spending time for this function depends on the number of nodes. It should be slow for the high-dimensional graphs. For fast faster, you can choose bigger value than other alternatives for the ‘thin’ option.

Author(s)
Abdolreza Mohammadi and Ernst Wit

References

See Also
bdgraph
Examples

```r
## Not run:
# generating multivariate normal data from a 'circle' graph
data.sim <- bdgraph.sim( n = 50, p = 6, graph = "circle", vis = TRUE )

output <- bdgraph( data = data.sim )
plotcoda( output )
## End(Not run)
```

plotroc  

ROC plot

Description

Draws the ROC curve according to the true graph structure for the object of S3 class "bdgraph", from function `bdgraph`.

Usage

```r
plotroc( G, prob, prob2 = NULL, cut = 20, smooth = FALSE )
```

Arguments

- **G**: The adjacency matrix corresponding to the true graph structure in which $g_{ij} = 1$ if there is a link between notes $i$ and $j$, otherwise $g_{ij} = 0$. It also can be an object of S3 class "simulate", from function `bdgraph.sim`.
- **prob**: Upper triangular matrix which shows the stimated posterior probabilities for all possible links. It also can be an object of S3 class "bdgraph", from function `bdgraph`.
- **prob2**: This option is for comparing two different estimations. Upper triangular matrix which shows the stimated posterior inclusion probabilities for all possible links. It also can be an object of S3 class "bdgraph", from function `bdgraph`.
- **cut**: Number of cut points. The default value is 20.
- **smooth**: Logical: for smoothing the ROC curve. The default is FALSE.

Author(s)

Abdolreza Mohammadi and Ernst Wit
print.bdgraph

References


See Also

bdgraph and compare

Examples

```r
## Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 50, p = 6, size = 7, vis = TRUE )

# running sampling algorithm
output <- bdgraph( data = data.sim, iter = 10000 )
# comparing the result
plotroc( data.sim, output )

# To compare the result based on CGMs approach
output2 <- bdgraph( data = data.sim, method = "gcgm", iter = 10000 )
# comparing the results
plotroc( data.sim, output, output2 )
legend( "bottomright", c("Gaussian", "Copula"), lty = c(1,2), col = c(1, 4))

## End(Not run)
```

print.bdgraph

*Print function for S3 class "bdgraph"

Description

Print the information about the best graph which is the graph with the highest posterior probability. It provides adjacency matrix, size and posterior probability of the best graph.

Usage

```
## S3 method for class 'bdgraph'
print( x, round = 3, Khat = FALSE, phat = FALSE, ... )
```
print.bdgraph

Arguments

x  An object of S3 class "bdgraph", from function bdgraph.

round  A value to round the probabilities to the specified number of decimal places (default is 3).

Khat  Logical: if TRUE you will see the estimation of the precision matrix. The default is FALSE.

phat  Logical: if TRUE you will see the posterior link probabilities. The default is FALSE.

...  System reserved (no specific usage).

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


See Also

bdgraph

Examples

## Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 50, p = 6, vis = TRUE )

output <- bdgraph( data = data.sim )

print( output )

print( output, Khat = TRUE, phat = TRUE )

## End(Not run)
print.simulate

Print function for S3 class "simulate"

Description

Print the information about the type of data, the sample size, the graph type, the number of nodes, number of links and sparsity of the true graph.

Usage

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

Arguments

- `x` - An object of S3 class "simulate", from function `bdgraph.sim`.
- `...` - System reserved (no specific usage).

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


See Also

`bdgraph.sim`

Examples

```r
## Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 20, p = 10, vis = TRUE )

print( data.sim )

## End(Not run)
```
Posterior probabilities of the graphs

Description

Provides the posterior probabilities for the 'g' most likely graphs or a specific graph, 'G'.

Usage

prob(output, g = 4, G = NULL)

Arguments

output
An object of S3 class "bdgraph", from function bdgraph.
g
The number of graphs with the highest posterior probabilities to be shown (default is 4). This option is ignored if 'G' is specified.
G
Adjacency matrix corresponding to a graph structure. It is an upper triangular matrix in which \( g_{ij} = 1 \) if there is a link between notes \( i \) and \( j \), otherwise \( g_{ij} = 0 \). It also can be an object of S3 class "simulate", from function bdgraph.sim.

Value

best.G
The graphs with the highest posterior probabilities.
prob.G
A vector of the posterior probabilities of the graphs corresponding to 'best.G'.

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


See Also

bdgraph
Examples

```r
## Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 50, p = 6, size = 6, vis = TRUE )

output <- bdgraph( data = data.sim )

# Estimated posterior probability of the true graph
prob( output, G = data.sim )

# Estimated posterior probability of the first and second graphs with highest probabilities
prob( output, g = 2 )

## End(Not run)
```

---

**rgwish**  
*Sampling from G-Wishart distribution*

**Description**

Generate random matrices, distributed according to the G-Wishart distribution with parameters $b$ and $D$, $W_G(b, D)$.

**Usage**

```r
rgwish( n = 1, G = NULL, b = 3, D = NULL )
```

**Arguments**

- `n` The number of samples required. The default value is 1.
- `G` Adjacency matrix corresponding to the graph structure. It is an upper triangular matrix in which $g_{ij} = 1$ if there is a link between notes $i$ and $j$, otherwise $g_{ij} = 0$.
- `b` The degree of freedom for G-Wishart distribution, $W_G(b, D)$. The default value is 3.
- `D` The positive definite ($p \times p$) "scale" matrix for G-Wishart distribution, $W_G(b, D)$. The default is an identity matrix.

**Details**

Sampling from G-Wishart distribution, $K \sim W_G(b, D)$, with density:

$$Pr(K) \propto |K|^{(b-2)/2} \exp \left\{ -\frac{1}{2} \text{trace}(K \times D) \right\},$$

which $b > 2$ is the degree of freedom and $D$ is a symmetric positive definite matrix.
Value

A numeric array, say A, of dimension \((p \times p \times n)\), where each \(A_{[i,j]}\) is a positive definite matrix, a realization of the G-Wishart distribution, \(W_G(b, D)\).

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


Examples

```r
# Not run:
G <- toeplitz( c( 0, 1, rep( 0, 3 ) ) )
G # graph with 5 nodes and 4 links

sample <- rgwish( n = 3, G = G, b = 3, D = diag(5) )
sample

# End(Not run)
```

---

**rwish**

*Sampling from Wishart distribution*

**Description**

Generate random matrices, distributed according to the Wishart distribution with parameters \(b\) and \(D\), \(W(b, D)\).

**Usage**

```r
rwish( n = 1, p = 2, b = 3, D = diag(p) )
```
**Arguments**

- **n**: The number of samples required. The default value is 1.
- **p**: The number of variables (nodes). The default value is 2.
- **b**: The degree of freedom for Wishart distribution, \(W(b, D)\). The default value is 3.
- **D**: The positive definite \((p \times p)\) "scale" matrix for Wishart distribution, \(W(b, D)\). The default is an identity matrix.

**Details**

Sampling from Wishart distribution, \(K \sim W(b, D)\), with density:

\[
Pr(K) \propto |K|^{(b-2)/2} \exp\left\{ -\frac{1}{2} \text{trace}(K \times D) \right\},
\]

which \(b > 2\) is the degree of freedom and \(D\) is a symmetric positive definite matrix.

**Value**

A numeric array, say \(A\), of dimension \((p \times p \times n)\), where each \(A[\ , \ , i]\) is a positive definite matrix, a realization of the Wishart distribution \(W(b, D)\).

**Author(s)**

Abdolreza Mohammadi and Ernst Wit

**References**


**Examples**

```r
## Not run:
sample <- rwish(n = 3, p = 5, b = 3, D = diag(p))
sample

## End(Not run)
```
select

Selecting the best graph

Description

Provides the graphs with the highest posterior probabilities. For more specific selection of graphs consult the 'prob' function.

Usage

select( output, cut = NULL, vis = FALSE )

Arguments

output An object of S3 class "bdgraph", from function bdgraph.
cut Threshold for including the links in the selected graph based on the posterior probabilities of the links; See the examples.
vis Logical: if TRUE you will see the plot of best graph. The default is FALSE.

Value

G Adjacency matrix corresponding to the selected graph.

Author(s)

Abdolreza Mohammadi and Ernst Wit

References


See Also

bdgraph
### Examples

```r
### Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 50, p = 6, size = 7, vis = TRUE )

output <- bdgraph( data = data.sim )
select( output )
select( output, cut = 0.5, vis = TRUE )

### End(Not run)
```

---

**summary.bdgraph**  
*Summary function for S3 class "bdgraph"*

---

**Description**

This function provides a summary of the result from BD-MCMC sampling algorithm.

**Usage**

```r
## S3 method for class 'bdgraph'
summary( object, vis = TRUE, ... )
```

**Arguments**

- `object`: An object of S3 class "bdgraph", from function `bdgraph`.
- `vis`: Logical: if TRUE (default) you will see the plot result.
- `...`: System reserved (no specific usage).

**Value**

- `best.graph`: The adjacency matrix corresponding to the selected graph which has the highest posterior probability.
- `phat`: Upper triangular matrix corresponding to the posterior probabilities of all possible links.
- `Khat`: The estimated precision matrix.

**Author(s)**

Abdolreza Mohammadi and Ernst Wit
References


See Also

bdgraph

Examples

```r
## Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 50, p = 6, vis = TRUE )

output <- bdgraph( data = data.sim )

summary(output)

summary( output, vis = FALSE )

## End(Not run)
```

surveyData  

*Labor force survey data*

Description

The survey data concerns 1002 males in the U.S labor force, described by Hoff (2007). The seven observed variables which have been measured on various scales are as follow: the income (income), degree (degree), the number of children (children), parents income (pincome), parents degree (pdegree), number of parents children (pchildren), and age (age).

Usage

```r
data(surveyData)
```

Format

The format is a matrix with 1002 rows (number of individuals) and 7 column (number of variables).
References


Examples

```r
data( surveyData )
dim( surveyData )
head( surveyData )
boxplot( surveyData )
```

---

**traceplot**

*Trace plot of graph size*

Description

Trace plot for graph size for the objects of S3 class "bdgraph", from function **bdgraph**. It is a tool for monitoring the convergence of the BD-MCMC sampling algorithm.

Usage

```r
traceplot( output, acf = FALSE, pacf = FALSE, main = NULL, ... )
```

Arguments

- `output`: An object of S3 class "bdgraph", from function `bdgraph`.
- `acf`: Logical: if TRUE you will see the plot of autocorrelation functions for graph size. The default is FALSE.
- `pacf`: Logical: if TRUE you will see the plot of partial autocorrelations for graph size. The default is FALSE.
- `main`: Graphical parameter (see plot).
- `...`: System reserved (no specific usage).

Author(s)

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References


See Also

bdgraph

Examples

## Not run:
# generating multivariate normal data from a 'random' graph
data.sim <- bdgraph.sim( n = 50, p = 6, size = 7, vis = TRUE )

output <- bdgraph( data = data.sim, iter = 10000 )

traceplot(output)

traceplot( output, acf = TRUE, pacf = TRUE )

## End(Not run)
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