

# Package ‘BCDAG’

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**Title** Bayesian Structure and Causal Learning of Gaussian Directed Graphs

**Version** 1.1.3

**Description** A collection of functions for structure learning of causal networks and estimation of joint causal effects from observational Gaussian data. Main algorithm consists of a Markov chain Monte Carlo scheme for posterior inference of causal structures, parameters and causal effects between variables.

References:

F. Castelletti and A. Mascaro (2021) <[doi:10.1007/s10260-021-00579-1](https://doi.org/10.1007/s10260-021-00579-1)>.

F. Castelletti and A. Mascaro (2022) <[doi:10.48550/arXiv.2201.12003](https://doi.org/10.48550/arXiv.2201.12003)>.

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as_graphNEL	<i>Transform adjacency matrix into graphNEL object</i>
-------------	--

---

### Description

Function to transform an adjacency matrix into a graphNEL object.

### Usage

```
as_graphNEL(DAG)
```

### Arguments

DAG	Adjacency matrix of a DAG
-----	---------------------------

### Value

A graphNEL object

### Examples

```
# Randomly generate DAG
q <- 4; w = 0.2
set.seed(123)
DAG <- rDAG(q,w)
as_graphNEL(DAG)
```

---

causaleffect	<i>Compute causal effects between variables</i>
--------------	---

---

### Description

This function computes the total joint causal effect on variable response consequent to an intervention on variables targets for a given a DAG structure and parameters (D,L)

### Usage

```
causaleffect(targets, response, L, D)
```

### Arguments

targets	numerical vector with labels of target nodes
response	numerical label of response variable
L	$(q, q)$ matrix of regression-coefficient parameters
D	$(q, q)$ diagonal matrix of conditional-variance parameters

### Details

We assume that the joint distribution of random variables  $X_1, \dots, X_q$  is zero-mean Gaussian with covariance matrix Markov w.r.t. a Directed Acyclic Graph (DAG). In addition, the allied Structural Equation Model (SEM) representation of a Gaussian DAG-model allows to express the covariance matrix as a function of the (Cholesky) parameters (D,L), collecting the conditional variances and regression coefficients of the SEM.

The total causal effect on a given variable of interest (response) consequent to a joint intervention on a set of variables (targets) is defined according to Pearl's do-calculus theory and under the Gaussian assumption can be expressed as a function of parameters (D,L).

### Value

The joint total causal effect, represented as a vector of same length of targets

### Author(s)

Federico Castelletti and Alessandro Mascaro

### References

- J. Pearl (2000). *Causality: Models, Reasoning, and Inference*. Cambridge University Press, Cambridge.
- F. Castelletti and A. Mascaro (2021). Structural learning and estimation of joint causal effects among network-dependent variables. *Statistical Methods and Applications*, Advance publication.
- P. Nandy, M.H. Maathuis and T. Richardson (2017). Estimating the effect of joint interventions from observational data in sparse high-dimensional settings. *Annals of Statistics* 45(2), 647-674.

**Examples**

```
# Randomly generate a DAG and the DAG-parameters
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
# Total causal effect on node 1 of an intervention on {5,6}
causaleffect(targets = c(6,7), response = 1, L = L, D = D)
# Total causal effect on node 1 of an intervention on {5,7}
causaleffect(targets = c(5,7), response = 1, L = L, D = D)
```

---

 confint.bcdagCE

*Credible Intervals for bcdagCE Object*


---

**Description**

Computes credible (not confidence!) intervals for one or more target variables from objects of class bcdagCE.

**Usage**

```
## S3 method for class 'bcdagCE'
confint(object, parm = "all", level = 0.95, ...)
```

**Arguments**

object	a bcdagCE object from which credible intervals are computed.
parm	an integer vector indexing the target variables for which credible intervals are computed. If missing, all variables are considered.
level	the credible level required.
...	additional arguments.

**Value**

A matrix with columns giving lower and upper credible limits for each variable.

**Examples**

```
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
```

```

n = 200
# Generate observations from a Gaussian DAG-model
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)
# Run the MCMC (set S = 5000 and burn = 1000 for better results)
out_mcmc = learn_DAG(S = 5000, burn = 1000, a = q, U = diag(1,q)/n, data = X, w = w,
                    fast = TRUE, save.memory = FALSE, verbose = FALSE)
out_ce <- get_causaleffect(out_mcmc, targets = c(4,6), response = 1)
confint(out_ce, c(4,6), 0.95)

```

---

<code>get_causaleffect</code>	<i>Estimate total causal effects from the MCMC output</i>
-------------------------------	---

---

## Description

This function provides causal effect estimates from the output of `learn_DAG`

## Usage

```
get_causaleffect(learnDAG_output, targets, response, verbose = TRUE)
```

## Arguments

<code>learnDAG_output</code>	object of class <code>bcdag</code>
<code>targets</code>	numerical $(p, 1)$ vector with labels of target nodes
<code>response</code>	numerical label of response variable
<code>verbose</code>	if TRUE, progress bar of MCMC sampling is displayed

## Details

Output of `learn_dag` function consists of  $S$  draws from the joint posterior of DAGs and DAG-parameters in a zero-mean Gaussian DAG-model; see the documentation of `learn_DAG` for more details.

The total causal effect on a given variable of interest (`response`) consequent to a joint intervention on a set of variables (`targets`) is defined according to Pearl's do-calculus theory and under the Gaussian assumption can be expressed as a function of parameters  $(D, L)$ , representing a (Cholesky) reparameterization of the covariance matrix.

Specifically, to each intervened variable a causal effect coefficient is associated and the posterior distribution of the latter can be recovered from posterior draws of the DAG parameters returned by `learn_DAG`. For each coefficient a sample of size  $S$  from its posterior is available. If required, the only Bayesian Model Average (BMA) estimate (obtained as the sample mean of the  $S$  draws) can be returned by setting `BMA = TRUE`.

Notice that, whenever implemented with `collapse = FALSE`, `learn_DAG` returns the marginal posterior distribution of DAGs only. In this case, `get_causaleffect` preliminarily performs posterior inference of DAG parameters by drawing samples from the posterior of  $(D, L)$ .

Print, summary and plot methods are available for this function. `print` returns the values of the prior hyperparameters used in the `learnDAG` function. `summary` returns, for each causal effect parameter, the marginal posterior mean and quantiles for different  $\alpha$  levels, and posterior probabilities of negative, null and positive causal effects. `plot` provides graphical summaries (boxplot and histogram of the distribution) for the posterior of each causal effect parameter.

### Value

An S3 object of class `bcdagCE` containing  $S$  draws from the joint posterior distribution of the  $p$  causal effect coefficients, organized into an  $(S, p)$  matrix, posterior means and credible intervals (under different  $(1-\alpha)$  levels) for each causal effect coefficient, and marginal posterior probabilities of positive, null and negative causal effects.

### Author(s)

Federico Castelletti and Alessandro Mascaro

### References

- J. Pearl (2000). *Causality: Models, Reasoning, and Inference*. Cambridge University Press, Cambridge.
- F. Castelletti and A. Mascaro (2021) Structural learning and estimation of joint causal effects among network-dependent variables. *Statistical Methods and Applications*, Advance publication.
- P. Nandy, M.H. Maathuis and T. Richardson (2017). Estimating the effect of joint interventions from observational data in sparse high-dimensional settings. *Annals of Statistics* 45(2), 647-674.

### Examples

```
# Randomly generate a DAG and the DAG-parameters
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
n = 200
# Generate observations from a Gaussian DAG-model
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)
# Run the MCMC (set S = 5000 and burn = 1000 for better results)
out_mcmc = learn_DAG(S = 5000, burn = 1000, a = q, U = diag(1,q)/n, data = X, w = w,
                    fast = TRUE, save.memory = FALSE)
head(out_mcmc$Graphs)
head(out_mcmc$L)
head(out_mcmc$D)
# Compute the BMA estimate of coefficients representing
# the causal effect on node 1 of an intervention on {3,4}
out_causal = get_causaleffect(learnDAG_output = out_mcmc, targets = c(3,4), response = 1)$post_mean

# Methods
print(out_causal)
```

```
summary(out_causal)
plot(out_causal)
```

---

get\_diagnostics      *MCMC diagnostics*

---

## Description

This function provides diagnostics of convergence for the MCMC output of learn\_DAG function.

## Usage

```
get_diagnostics(learnDAG_output, ask = TRUE, nodes = integer(0))
```

## Arguments

learnDAG_output	object of class bcdag
ask	Boolean argument passed to par() for visualization;
nodes	Numerical vector indicating those nodes for which we want to compute the posterior probability of edge inclusion;

## Details

Function learn\_DAG implements a Markov Chain Monte Carlo (MCMC) algorithm for structure learning and posterior inference of Gaussian DAGs. Output of the algorithm is a collection of  $S$  DAG structures (represented as  $(q, q)$  adjacency matrices) and DAG parameters  $(D, L)$  approximately drawn from the joint posterior. In addition, if learn\_DAG is implemented with collapse = TRUE, the only approximate marginal posterior of DAGs (represented by the collection of  $S$  DAG structures) is returned; see the documentation of learn\_DAG for more details.

Diagnostics of convergence for the MCMC output are conducted by monitoring across MCMC iterations: (1) the number of edges in the DAGs; (2) the posterior probability of edge inclusion for each possible edge  $u- > v$ . With regard to (1), a traceplot of the number of edges in the DAGs visited by the MCMC chain at each step  $s = 1, \dots, S$  is first provided as the output of the function. The absence of trends in the plot can provide information on a genuine convergence of the MCMC chain. In addition, the traceplot of the average number of edges in the DAGs visited up to time  $s$ , for  $s = 1, \dots, S$ , is also returned. The convergence of the curve around a "stable" average size generally suggests good convergence of the algorithm. With regard to (2), for each edge  $u- > v$ , the posterior probability at time  $s$ , for  $s = 1, \dots, S$ , can be estimated as the proportion of DAGs visited by the MCMC up to time  $s$  which contain the directed edge  $u- > v$ . Output is organized in  $q$  plots (one for each node  $v = 1, \dots, q$ ), each summarizing the posterior probabilities of edges  $u- > v$ ,  $u = 1, \dots, q$ . If the number of nodes is larger than 30 the traceplot of a random sample of 30 nodes is returned.

## Value

A collection of plots summarizing the behavior of the number of edges and the posterior probabilities of edge inclusion computed from the MCMC output.

**Author(s)**

Federico Castelletti and Alessandro Mascaro

**References**

F. Castelletti and A. Mascaro (2021). Structural learning and estimation of joint causal effects among network-dependent variables. *Statistical Methods and Applications*, Advance publication.

F. Castelletti (2020). Bayesian model selection of Gaussian Directed Acyclic Graph structures. *International Statistical Review* 88 752-775.

**Examples**

```
# Randomly generate a DAG and the DAG-parameters
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
n = 200
# Generate observations from a Gaussian DAG-model
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)
# Run the MCMC for posterior inference of DAGs only (collapse = TRUE)
out_mcmc = learn_DAG(S = 5000, burn = 1000, a = q, U = diag(1,q)/n, data = X, w = 0.1,
                    fast = TRUE, save.memory = FALSE, collapse = TRUE)

# Produce diagnostic plots
get_diagnostics(out_mcmc)
```

---

get\_edgeprobs

*Compute posterior probabilities of edge inclusion from the MCMC output*

---

**Description**

This function computes the posterior probability of inclusion for each edge  $u \rightarrow v$  given the MCMC output of learn\_DAG;

**Usage**

```
get_edgeprobs(learnDAG_output)
```

**Arguments**

learnDAG\_output  
object of class bcdag

**Details**

Output of learn\_dag function consists of  $S$  draws from the joint posterior of DAGs and DAG-parameters in a zero-mean Gaussian DAG-model; see the documentation of learn\_DAG for more details.

The posterior probability of inclusion of  $u \rightarrow v$  is estimated as the frequency of DAGs visited by the MCMC which contain the directed edge  $u \rightarrow v$ . Posterior probabilities are collected in a  $(q, q)$  matrix with  $(u, v)$ -element representing the estimated posterior probability of edge  $u \rightarrow v$ .

**Value**

A  $(q, q)$  matrix with posterior probabilities of edge inclusion

**Author(s)**

Federico Castelletti and Alessandro Mascaro

**References**

F. Castelletti and A. Mascaro (2021). Structural learning and estimation of joint causal effects among network-dependent variables. *Statistical Methods and Applications*, Advance publication.

**Examples**

```
# Randomly generate a DAG and the DAG-parameters
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
# Generate observations from a Gaussian DAG-model
n = 200
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)
# Run the MCMC (Set S = 5000 and burn = 1000 for better results)
out_mcmc = learn_DAG(S = 5000, burn = 1000, a = q, U = diag(1,q)/n, data = X, w = 0.1,
                    fast = TRUE, save.memory = FALSE)
# Compute posterior probabilities of edge inclusion
get_edgeprobs(out_mcmc)
```

---

get\_MAPdag

*Compute the maximum a posteriori DAG model from the MCMC output*

---

**Description**

This function computes the maximum a posteriori DAG model estimate (MAP) from the MCMC output of learn\_DAG

**Usage**

```
get_MAPdag(learnDAG_output)
```

**Arguments**

```
learnDAG_output
      object of class bcdag
```

**Details**

Output of `learn_dag` function consists of  $S$  draws from the joint posterior of DAGs and DAG-parameters in a zero-mean Gaussian DAG-model; see the documentation of `learn_DAG` for more details.

The Maximum A Posteriori (MAP) model estimate is defined as the DAG visited by the MCMC with the highest associated posterior probability. Each DAG posterior probability is estimated as the frequency of visits of the DAG in the MCMC chain. The MAP estimate is represented through its  $(q, q)$  adjacency matrix, with  $(u, v)$ -element equal to one whenever the MAP contains  $u \rightarrow v$ , zero otherwise.

**Value**

The  $(q, q)$  adjacency matrix of the maximum a posteriori DAG model

**Author(s)**

Federico Castelletti and Alessandro Mascaro

**References**

F. Castelletti and A. Mascaro (2021). Structural learning and estimation of joint causal effects among network-dependent variables. *Statistical Methods and Applications*, Advance publication.

G. Garcia-Donato and M.A. Martinez-Beneito (2013). On sampling strategies in Bayesian variable selection problems with large model spaces. *Journal of the American Statistical Association* 108 340-352.

**Examples**

```
# Randomly generate a DAG and the DAG-parameters
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
# Generate observations from a Gaussian DAG-model
n = 200
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)
# Run the MCMC (Set S = 5000 and burn = 1000 for better results)
out_mcmc = learn_DAG(S = 500, burn = 100, a = q, U = diag(1,q)/n, data = X, w = 0.1,
```

```
                                fast = TRUE, save.memory = FALSE)
# Produce the MAP DAG estimate
get_MAPdag(out_mcmc)
```

---

`get_MPMdag`*Compute the median probability DAG model from the MCMC output*

---

### Description

This function computes the Median Probability DAG Model estimate (MPM) from the MCMC output of `learn_DAG`

### Usage

```
get_MPMdag(learnDAG_output)
```

### Arguments

`learnDAG_output`  
object of class `bcdag`

### Details

Output of `learn_dag` function consists of  $S$  draws from the joint posterior of DAGs and DAG-parameters in a zero-mean Gaussian DAG-model; see the documentation of `learn_DAG` for more details.

The Median Probability DAG Model estimate (MPM) is obtained by including all edges whose posterior probability exceeds 0.5. The posterior probability of inclusion of  $u- > v$  is estimated as the frequency of DAGs visited by the MCMC which contain the directed edge  $u- > v$ ; see also function `get_edgeprobs` and the corresponding documentation.

### Value

The  $(q, q)$  adjacency matrix of the median probability DAG model

### Author(s)

Federico Castelletti and Alessandro Mascaro

### References

F. Castelletti and A. Mascaro (2021). Structural learning and estimation of joint causal effects among network-dependent variables. *Statistical Methods and Applications*, Advance publication

M.M. Barbieri and J.O. Berger (2004). Optimal predictive model selection. *The Annals of Statistics* 32 870-897

**Examples**

```

# Randomly generate a DAG and the DAG-parameters
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
# Generate observations from a Gaussian DAG-model
n = 200
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)
# Run the MCMC (Set S = 5000 and burn = 1000 for better results)
out_mcmc = learn_DAG(S = 5000, burn = 1000, a = q, U = diag(1,q)/n, data = X, w = 0.1,
                    fast = TRUE, save.memory = FALSE)
# Produce the MPM DAG estimate
get_MPMdag(out_mcmc)

```

---

get\_neighboringDAGs     *Enumerate all neighbors of a DAG*

---

**Description**

This function takes any DAG with  $q$  nodes as input and returns all the neighboring DAGs, i.e. all those DAGs that can be reached by the addition, removal or reversal of an edge.

**Usage**

```
get_neighboringDAGs(DAG)
```

**Arguments**

DAG                      Adjacency matrix of a DAG

**Value**

The  $(q, q, K)$  array containing all neighboring DAGs, with  $K$  being the total number of neighbors

**Examples**

```

# Randomly generate a DAG
q <- 4; w <- 0.2
set.seed(123)
DAG <- rDAG(q,w)
# Get neighbors
neighbors <- get_neighboringDAGs(DAG)
neighbors

```

learn\_DAG

*MCMC scheme for Gaussian DAG posterior inference***Description**

This function implements a Markov Chain Monte Carlo (MCMC) algorithm for structure learning of Gaussian DAGs and posterior inference of DAG model parameters

**Usage**

```
learn_DAG(
  S,
  burn,
  data,
  a,
  U,
  w,
  fast = FALSE,
  save.memory = FALSE,
  collapse = FALSE,
  verbose = TRUE
)
```

**Arguments**

S	integer final number of MCMC draws from the posterior of DAGs and parameters
burn	integer initial number of burn-in iterations, needed by the MCMC chain to reach its stationary distribution and not included in the final output
data	$(n, q)$ data matrix
a	common shape hyperparameter of the compatible DAG-Wishart prior, $a > q - 1$
U	position hyperparameter of the compatible DAG-Wishart prior, a $(q, q)$ s.p.d. matrix
w	edge inclusion probability hyperparameter of the DAG prior in $[0, 1]$
fast	boolean, if TRUE an approximate proposal for the MCMC moves is implemented
save.memory	boolean, if TRUE MCMC draws are stored as strings, instead of arrays
collapse	boolean, if TRUE only structure learning of DAGs is performed
verbose	If TRUE, progress bars are displayed

**Details**

Consider a collection of random variables  $X_1, \dots, X_q$  whose distribution is zero-mean multivariate Gaussian with covariance matrix Markov w.r.t. a Directed Acyclic Graph (DAG). Assuming the underlying DAG is unknown (model uncertainty), a Bayesian method for posterior inference on the

joint space of DAG structures and parameters can be implemented. The proposed method assigns a prior on each DAG structure through independent Bernoulli distributions,  $Ber(w)$ , on the 0-1 elements of the DAG adjacency matrix. Conditionally on a given DAG, a prior on DAG parameters  $(D, L)$  (representing a Cholesky-type reparameterization of the covariance matrix) is assigned through a compatible DAG-Wishart prior; see also function `rDAGWishart` for more details.

Posterior inference on the joint space of DAGs and DAG parameters is carried out through a Partial Analytic Structure (PAS) algorithm. Two steps are iteratively performed for  $s = 1, 2, \dots$ : (1) update of the DAG through a Metropolis Hastings (MH) scheme; (2) sampling from the posterior distribution of the (updated DAG) parameters. In step (1) the update of the (current) DAG is performed by drawing a new (direct successor) DAG from a suitable proposal distribution. The proposed DAG is obtained by applying a local move (insertion, deletion or edge reversal) to the current DAG and is accepted with probability given by the MH acceptance rate. The latter requires to evaluate the proposal distribution at both the current and proposed DAGs, which in turn involves the enumeration of all DAGs that can be obtained from local moves from respectively the current and proposed DAG. Because the ratio of the two proposals is approximately equal to one, and the approximation becomes as precise as  $q$  grows, a faster strategy implementing such an approximation is provided with `fast = TRUE`. The latter choice is especially recommended for moderate-to-large number of nodes  $q$ .

Output of the algorithm is a collection of  $S$  DAG structures (represented as  $(q, q)$  adjacency matrices) and DAG parameters  $(D, L)$  approximately drawn from the joint posterior. The various outputs are organized in  $(q, q, S)$  arrays; see also the example below. If the target is DAG learning only, a collapsed sampler implementing the only step (1) of the MCMC scheme can be obtained by setting `collapse = TRUE`. In this case, the algorithm outputs a collection of  $S$  DAG structures only. See also functions `get_edgeprobs`, `get_MAPdag`, `get_MPMdag` for posterior summaries of the MCMC output.

`Print`, `summary` and `plot` methods are available for this function. `print` provides information about the MCMC output and the values of the input prior hyperparameters. `summary` returns, besides the previous information, a  $(q, q)$  matrix collecting the marginal posterior probabilities of edge inclusion. `plot` returns the estimated Median Probability DAG Model (MPM), a  $(q, q)$  heat map with estimated marginal posterior probabilities of edge inclusion, and a barplot summarizing the distribution of the size of DAGs visited by the MCMC.

### Value

An S3 object of class `bcdag`, with a `type` attribute describing the chosen output format:

- "complete" (`collapse = FALSE`, `save.memory = FALSE`):  $S$  draws of DAGs and parameters  $(D, L)$ , stored in three  $(q, q, S)$  arrays;
- "compressed" (`collapse = FALSE`, `save.memory = TRUE`):  $S$  draws of DAGs and parameters  $(D, L)$ , stored as character vectors;
- "collapsed" (`collapse = TRUE`, `save.memory = FALSE`):  $S$  draws of DAGs, stored in a  $(q, q, S)$  array;
- "compressed and collapsed" (`collapse = TRUE`, `save.memory = TRUE`):  $S$  draws of DAGs, stored as a character vector;

### Author(s)

Federico Castelletti and Alessandro Mascaro

## References

- F. Castelletti and A. Mascaro (2021). Structural learning and estimation of joint causal effects among network-dependent variables. *Statistical Methods and Applications*, Advance publication.
- F. Castelletti and A. Mascaro (2022). BCDAG: An R package for Bayesian structural and Causal learning of Gaussian DAGs. *arXiv pre-print*, url: <https://arxiv.org/abs/2201.12003>
- F. Castelletti (2020). Bayesian model selection of Gaussian Directed Acyclic Graph structures. *International Statistical Review* 88 752-775.

## Examples

```
# Randomly generate a DAG and the DAG-parameters
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
# Generate observations from a Gaussian DAG-model
n = 200
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)

## Set S = 5000 and burn = 1000 for better results

# [1] Run the MCMC for posterior inference of DAGs and parameters (collapse = FALSE)
out_mcmc = learn_DAG(S = 50, burn = 10, a = q, U = diag(1,q)/n, data = X, w = 0.1,
                    fast = FALSE, save.memory = FALSE, collapse = FALSE)
# [2] Run the MCMC for posterior inference of DAGs only (collapse = TRUE)
out_mcmc_collapse = learn_DAG(S = 50, burn = 10, a = q, U = diag(1,q)/n, data = X, w = 0.1,
                              fast = FALSE, save.memory = FALSE, collapse = TRUE)
# [3] Run the MCMC for posterior inference of DAGs only with approximate proposal
# distribution (fast = TRUE)
# out_mcmc_collapse_fast = learn_DAG(S = 50, burn = 10, a = q, U = diag(1,q)/n, data = X, w = 0.1,
#                                 fast = FALSE, save.memory = FALSE, collapse = TRUE)
# Compute posterior probabilities of edge inclusion and Median Probability DAG Model
# from the MCMC outputs [2] and [3]
get_edgeprobs(out_mcmc_collapse)
# get_edgeprobs(out_mcmc_collapse_fast)
get_MPMdag(out_mcmc_collapse)
# get_MPMdag(out_mcmc_collapse_fast)

# Methods
print(out_mcmc)
summary(out_mcmc)
plot(out_mcmc)
```

---

leukemia

*Protein levels for 68 diagnosed AML patients of subtype M2*

---

### Description

A dataset containing the protein expression levels of 18 proteins for 68 AML patients of subtype M2 (according to French-American-British (FAB) classification system). The 18 proteins selected are known to be involved in apoptosis and cell cycle regulation according to the KEGG database (Kanehisa et al. 2012). This is a subset of the dataset presented in Kornblau et al. (2009).

### Usage

leukemia

### Format

A data frame with 68 rows and 18 variables:

**AKT** AKT protein, expression level

**AKT,p308** AKT,p308 protein, expression level

**AKT,p473** AKT,p473 protein, expression level

**BAD** BAD protein, expression level

**BAD,p112** BAD,p112 protein, expression level

**BAD,p136** BAD,p136 protein, expression level

**BAD,p155** BAD,p155 protein, expression level

**BAX** BAX protein, expression level

**BCL2** BCL2 protein, expression level

**BCLXL** BCLXL protein, expression level

**CCND1** CCND1 protein, expression level

**GSK3** GSK3 protein, expression level

**GSK3,p** GSK3.p protein, expression level

**MYC** MYC protein, expression level

**PTEN** PTEN protein, expression level

**PTEN,p** PTEN.p protein, expression level

**TP53** TP53 protein, expression level

**XIAP** XIAP protein, expression level ...

### Source

<http://bioinformatics.mdanderson.org/Supplements/Kornblau-AML-RPPA/aml-rppa.xls>

## References

Kornblau, S. M., Tibes, R., Qiu, Y. H., Chen, W., Kantarjian, H. M., Andreeff, M., ... & Mills, G. B. (2009). Functional proteomic profiling of AML predicts response and survival. *Blood, The Journal of the American Society of Hematology*, 113(1), 154-164.

Kanehisa, M., Goto, S., Sato, Y., Furumichi, M., & Tanabe, M. (2012). KEGG for integration and interpretation of large-scale molecular data sets. *Nucleic acids research*, 40(D1), D109-D114.

---

plot.bcdag	<i>bcdag object plot</i>
------------	--------------------------

---

## Description

This method returns summary plots of the output of learn\_DAG().

## Usage

```
## S3 method for class 'bcdag'
plot(x, ..., ask = TRUE)
```

## Arguments

x	a bcdag object for which a plot is desired
...	additional arguments affecting the summary produced
ask	Boolean argument passed to par() for visualization;

## Value

Plot of the Median Probability DAG, a heatmap of the probabilities of edge inclusion and an histogram of the sizes of graphs visited by learn\_DAG().

## Examples

```
n <- 1000
q <- 4
DAG <- matrix(c(0,1,1,0,0,0,0,0,0,0,0,0,0,1,1,0), nrow = q)

L <- DAG
L[L != 0] <- runif(q, 0.2, 1)
diag(L) <- c(1,1,1,1)
D <- diag(1, q)
Sigma <- t(solve(L))%*%D%*%solve(L)

a <- 6
g <- 1/1000
U <- g*diag(1,q)
w = 0.2
```

```

set.seed(1)
X <- mvtnorm::rmvnorm(n, sigma = Sigma)

out <- learn_DAG(1000, 0, X, a, U, w, fast = TRUE, collapse = TRUE, save.memory = FALSE)
plot(out)

```

---

plot.bcdagCE                    *bcdagCE object plot*

---

### Description

This method returns summary plots of the output of `get_causaleffect()`.

### Usage

```

## S3 method for class 'bcdagCE'
plot(x, ..., which_ce = integer(0))

```

### Arguments

<code>x</code>	a <code>bcdagCE</code> object for which a plot is desired
<code>...</code>	additional arguments affecting the summary produced
<code>which_ce</code>	specifies the list of nodes for which you intend to generate a boxplot and a histogram

### Value

Boxplot and histogram of the posterior distribution of the causal effects computed using `get_causaleffect()`.

### Examples

```

q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
n = 200
# Generate observations from a Gaussian DAG-model
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)
# Run the MCMC (set S = 5000 and burn = 1000 for better results)
out_mcmc = learn_DAG(S = 500, burn = 100, a = q, U = diag(1,q)/n, data = X, w = w,
                    fast = TRUE, save.memory = FALSE, verbose = FALSE)
out_ce <- get_causaleffect(out_mcmc, targets = c(4,6), response = 1)
plot(out_ce)

```

---

```
print.bcdag          bcdag object print
```

---

### Description

This method returns a summary of the input given to `learn_DAG()` to produce the `bcdag` object.

### Usage

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

### Arguments

```
x          a bcdag object for which a summary is desired
...        additional arguments affecting the summary produced
```

### Value

A printed message listing the inputs given to `learn_DAG`.

### Examples

```
n <- 1000
q <- 4
DAG <- matrix(c(0,1,1,0,0,0,0,0,0,0,0,0,0,1,1,0), nrow = q)

L <- DAG
L[L != 0] <- runif(q, 0.2, 1)
diag(L) <- c(1,1,1,1)
D <- diag(1, q)
Sigma <- t(solve(L))%*%D%*%solve(L)

a <- 6
g <- 1/1000
U <- g*diag(1,q)
w = 0.2

set.seed(1)
X <- mvtnorm::rmvnorm(n, sigma = Sigma)

out <- learn_DAG(1000, 0, X, a, U, w, fast = TRUE, collapse = TRUE, save.memory = FALSE)
print(out)
```

---

print.bcdagCE	<i>bcdagCE object print</i>
---------------	-----------------------------

---

### Description

This method returns a summary of the inputs given to `learn_DAG()` and `get_causaleffect()` to obtain the `bcdagCE` object.

### Usage

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

### Arguments

x	a <code>bcdagCE</code> object for which a summary is desired
...	additional arguments affecting the summary produced

### Value

A printed message listing the inputs given to `learn_DAG` and `get_causaleffect`.

### Examples

```
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
n = 200
# Generate observations from a Gaussian DAG-model
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)
# Run the MCMC (set S = 5000 and burn = 1000 for better results)
out_mcmc = learn_DAG(S = 5000, burn = 1000, a = q, U = diag(1,q)/n, data = X, w = w,
                    fast = TRUE, save.memory = FALSE, verbose = FALSE)
out_ce <- get_causaleffect(out_mcmc, targets = c(4,6), response = 1)
print(out_ce)
```

---

rDAG

*Generate a Directed Acyclic Graph (DAG) randomly*


---

**Description**

This function randomly generates a Directed Acyclic Graph (DAG) with  $q$  nodes and probability of edge inclusion  $w$ .

**Usage**

```
rDAG(q, w)
```

**Arguments**

$q$	number of nodes
$w$	probability of edge inclusion in $[0, 1]$

**Details**

The  $0-1$  adjacency matrix of the DAG is generated by drawing each element in the lower triangular part in  $0, 1$  with probability  $1-w, w$ . Accordingly, the DAG has lower-triangular adjacency matrix and nodes are numerically labeled according to a topological ordering implying  $u > v$  whenever  $u-v$ .

**Value**

DAG ( $q, q$ ) adjacency matrix of the generated DAG

**Examples**

```
# Randomly generate a DAG on q = 8 nodes with probability of edge inclusion w = 0.2
q = 8
w = 0.2
set.seed(123)
rDAG(q = q, w = w)
```

---

rDAGWishart

*Random samples from a compatible DAG-Wishart distribution*


---

**Description**

This function implements a direct sampling from a compatible DAG-Wishart distribution with parameters  $a$  and  $U$ .

**Usage**

```
rDAGWishart(n, DAG, a, U)
```

**Arguments**

n	number of samples
DAG	$(q, q)$ adjacency matrix of the DAG
a	common shape hyperparameter of the compatible DAG-Wishart, $a > q - 1$
U	position hyperparameter of the compatible DAG-Wishart, a $(q, q)$ s.p.d. matrix

**Details**

Assume the joint distribution of random variables  $X_1, \dots, X_q$  is zero-mean Gaussian with covariance matrix Markov w.r.t. a Directed Acyclic Graph (DAG). The allied Structural Equation Model (SEM) representation of a Gaussian DAG-model allows to express the covariance matrix as a function of the (Cholesky) parameters  $(D, L)$ , collecting the regression coefficients and conditional variances of the SEM.

The DAG-Wishart distribution (Cao et. al, 2019) with shape hyperparameter  $a = (a_1, \dots, a_q)$  and position hyperparameter  $U$  (a s.p.d.  $(q, q)$  matrix) provides a conjugate prior for parameters  $(D, L)$ . In addition, to guarantee compatibility among Markov equivalent DAGs (same marginal likelihood), the default choice (here implemented)  $a_j = a + |pa(j)| - q + 1$  ( $a > q - 1$ ), with  $|pa(j)|$  the number of parents of node  $j$  in the DAG, was introduced by Peluso and Consonni (2020).

**Value**

A list of two elements: a  $(q, q, n)$  array collecting  $n$  sampled matrices  $L$  and a  $(q, q, n)$  array collecting  $n$  sampled matrices  $D$

**Author(s)**

Federico Castelletti and Alessandro Mascaro

**References**

F. Castelletti and A. Mascaro (2021). Structural learning and estimation of joint causal effects among network-dependent variables. *Statistical Methods and Applications*, Advance publication.

X. Cao, K. Khare and M. Ghosh (2019). Posterior graph selection and estimation consistency for high-dimensional Bayesian DAG models. *The Annals of Statistics* 47 319-348.

S. Peluso and G. Consonni (2020). Compatible priors for model selection of high-dimensional Gaussian DAGs. *Electronic Journal of Statistics* 14(2) 4110 - 4132.

**Examples**

```
# Randomly generate a DAG on q = 8 nodes with probability of edge inclusion w = 0.2
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
```

```
# Draw from a compatible DAG-Wishart distribution with parameters a = q and U = diag(1,q)
outDL = rDAGWishart(n = 5, DAG = DAG, a = q, U = diag(1, q))
outDL
```

---

summary.bcdag                    *bcdag object summaries*

---

## Description

This method produces summaries of the input and output of the function learn\_DAG().

## Usage

```
## S3 method for class 'bcdag'
summary(object, ...)
```

## Arguments

object                    a bcdag object for which a summary is desired  
 ...                      additional arguments affecting the summary produced

## Value

A printed message listing the inputs given to learn\_DAG and the estimated posterior probabilities of edge inclusion.

## Examples

```
n <- 1000
q <- 4
DAG <- matrix(c(0,1,1,0,0,0,0,0,0,0,0,0,0,1,1,0), nrow = q)

L <- DAG
L[L != 0] <- runif(q, 0.2, 1)
diag(L) <- c(1,1,1,1)
D <- diag(1, q)
Sigma <- t(solve(L))%*%D%*%solve(L)

a <- 6
g <- 1/1000
U <- g*diag(1,q)
w = 0.2

set.seed(1)
X <- mvtnorm::rmvnorm(n, sigma = Sigma)

out <- learn_DAG(1000, 0, X, a, U, w, fast = TRUE, collapse = TRUE, save.memory = FALSE)
summary(out)
```

---

summary.bcdagCE      *bcdagCE object summary*

---

### Description

This method produces summaries of the input and output of the function `get_causaleffect()`.

### Usage

```
## S3 method for class 'bcdagCE'
summary(object, ...)
```

### Arguments

<code>object</code>	a <code>bcdagCE</code> object for which a summary is desired
<code>...</code>	additional arguments affecting the summary produced

### Value

A printed message listing the inputs given to `learn_DAG()` and `get_causaleffect()` and summary statistics of the posterior distribution.

### Examples

```
q = 8
w = 0.2
set.seed(123)
DAG = rDAG(q = q, w = w)
outDL = rDAGWishart(n = 1, DAG = DAG, a = q, U = diag(1, q))
L = outDL$L; D = outDL$D
Sigma = solve(t(L))%*%D%*%solve(L)
n = 200
# Generate observations from a Gaussian DAG-model
X = mvtnorm::rmvnorm(n = n, sigma = Sigma)
# Run the MCMC (set S = 5000 and burn = 1000 for better results)
out_mcmc = learn_DAG(S = 500, burn = 100, a = q, U = diag(1,q)/n, data = X, w = w,
                    fast = TRUE, save.memory = FALSE, verbose = FALSE)
out_ce <- get_causaleffect(out_mcmc, targets = c(4,6), response = 1)
# summary(out_ce)
```

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