

Package ‘PCBN’

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Title Inference of Pair-Copula Bayesian Networks

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Description Creates, fits and samples Pair-Copula Bayesian networks (PCBN) under some restrictions on the underlying Directed Acyclic Graph (DAG), that is, no active cycles nor interfering v-structures, following Derumigny, Horsman and Kurowicka (2025) <[doi:10.48550/arXiv.2510.03518](https://doi.org/10.48550/arXiv.2510.03518)>.

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Suggests knitr, rmarkdown, testthat (>= 3.0.0), data.tree, Rgraphviz

URL <https://github.com/AlexisDerumigny/PCBN>

BugReports <https://github.com/AlexisDerumigny/PCBN/issues>

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active_cycles	<i>Checks if a graph contains active cycles</i>
---------------	---

Description

Checks if a graph contains active cycles

Usage

```
active_cycles(DAG, early.stopping = FALSE)
```

```
has_active_cycles(DAG)
```

```
plot_active_cycles(DAG, active_cycles_list = NULL)
```

Arguments

DAG Directed Acyclic

early_stopping if TRUE, stop at the first active cycle that is found.

active_cycles_list a list of active cycles as given by active_cycles. If this is NULL, the function active_cycles is run on DAG to find the active cycles to be displayed.

Value

active_cycles returns a list containing the active cycles. Each active cycle is a character vector of the name of the nodes involved in the active cycle. The first element of this vector is the converging node of the active cycle.

has_active_cycles returns TRUE if at least 1 active cycle is found. Otherwise, it returns FALSE.

plot_active_cycles is called for its side-effects only. It plots the active cycles if any, and else prints a message.

See Also

the helper functions [path_hasConvergingConnections](#), [path_hasChords](#) that are used to find the active cycles.

[is_restrictedDAG](#) to check also whether the DAG contains interfering v-structures.

Examples

```
DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
```

```
active_cycles(DAG) # no active cycle
```

```
DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U2')
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
```

```
active_cycles(DAG) # 1 active cycle
```

```
DAG = create_empty_DAG(5)
DAG = bnlearn::set.arc(DAG, 'U1', 'U2')
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U5')
DAG = bnlearn::set.arc(DAG, 'U3', 'U5')
```

```

active_cycles(DAG) # 2 active cycles
active_cycles(DAG, early.stopping = TRUE) # The first active cycle

# Plotting the active cycles
plot_active_cycles(DAG)
# which is the same as
plot_active_cycles(DAG, active_cycles_list = active_cycles(DAG))

# We now fix the active cycles by adding the some arcs.
fixedDAG = fix_active_cycles(DAG)
# We can see that no active cycles is plotted anymore
plot_active_cycles(fixedDAG)
has_active_cycles(fixedDAG)
# This is because two edges have been added, as can be seen on:
plot(fixedDAG)

```

B_sets_are_increasing Checks if the B-sets for a particular node form an increasing sequence.

Description

Checks if the B-sets for a particular node form an increasing sequence.

Usage

```
B_sets_are_increasing(B_sets)
```

Arguments

B_sets a boolean matrix with $(2 + \text{length}(\text{children}))$ columns and $\text{length}(\text{parents})$ rows. They are assumed to be sorted in increasing order of row sums, i.e. by increasing order of set cardinality. Typically, this will be the output of `find_B_sets_v`.

Value

TRUE if the B-sets form an ordered sequence, otherwise returns FALSE.

Examples

```

B_sets = matrix(c(FALSE, FALSE, FALSE, FALSE,
                  TRUE , FALSE, FALSE, FALSE,
                  TRUE , TRUE , FALSE, FALSE,
                  TRUE , TRUE , TRUE , TRUE),
               nrow = 4, byrow = TRUE)

```

```
B_sets_are_increasing(B_sets)
```

```
B_sets = matrix(c(FALSE, FALSE, FALSE, FALSE,
```

```

TRUE , FALSE, TRUE , FALSE,
TRUE , TRUE , FALSE, FALSE,
TRUE , TRUE , TRUE , TRUE),
nrow = 4, byrow = TRUE)

```

```
B_sets_are_increasing(B_sets)
```

B_sets_cut_increments *Find the decomposition of B-sets*

Description

Find the decomposition of B-sets

Usage

```
B_sets_cut_increments(B_sets)
```

Arguments

B_sets matrix of B-sets, assumed to be increasing. This means [find_interfering_v_from_B_sets](#) should return NULL on this matrix. This can be the output of [find_B_sets_v](#) or of [B_sets_make_unique](#).

Value

a list of vectors of characters. Each element of the list corresponds to one $\Delta Bset = Bset[i] Bset[i-1]$.

Examples

```

B_sets = matrix(c(FALSE, FALSE, FALSE, FALSE,
TRUE , FALSE, FALSE, FALSE,
TRUE , TRUE , FALSE, FALSE,
TRUE , TRUE , TRUE , TRUE),
nrow = 4, byrow = TRUE)

```

```
colnames(B_sets) <- c("U1", "U2", "U3", "U4")
```

```
B_sets_cut_increments(B_sets)
```

`B_sets_make_unique` *Compress a given collection of B-sets*

Description

Compress a given collection of B-sets

Usage

```
B_sets_make_unique(B_sets)
```

Arguments

`B_sets` a boolean matrix with $(2 + \text{length}(\text{children}))$ columns and $\text{length}(\text{parents})$ rows. They are assumed to be sorted in increasing order of row sums, i.e. by increasing order of set cardinality. Typically, this will be the output of `find_B_sets_v` for some node `v`.

Value

a 'data.frame' made of the unique rows of 'B_sets'. An additional column 'nodes' is added at the start. It contains all the children of `v` corresponding to this B-set.

Examples

```
DAG = create_empty_DAG(5)
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
DAG = bnlearn::set.arc(DAG, 'U4', 'U5')
B_sets = find_B_sets_v(DAG, v = 'U4')

B_sets_make_unique(B_sets)
```

`complete_and_check_orders`

Complete an order and check whether these are valid orders on parents sets

Description

Complete an order and check whether these are valid orders on parents sets

Usage

```
complete_and_check_orders(DAG, order_hash)
```

Arguments

DAG the DAG
 order_hash the hashmaps of orders

Value

NULL. This function has only side-effects, and modifies order_hash. It stops if the orders are not valid orders on the parents sets.

Examples

```
DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')

order_hash = r2r::hashmap()
try({complete_and_check_orders(DAG, order_hash)})
# Error because the order of the parents on "U3" should be specified.

order_hash[['U3']] = c("U1", "U2")
complete_and_check_orders(DAG, order_hash)
r2r::keys(order_hash)
# We obtain "U3" and "U4" because they both have parents
```

compute_sample_margin *Computes a conditional margin during sampling*

Description

Computes a conditional margin during sampling

Usage

```
compute_sample_margin(
  object,
  data,
  v,
  cond_set,
  check_PCBN = TRUE,
  verbose = 1
)
```



```
identical(data[, "U1"], u_1_given2)
```

```
create_empty_DAG      Create empty DAG
```

Description

This function creates a directed graph with a total of ‘N_nodes’ nodes and no arcs. The nodes are named ‘U1’, ‘U2’, etc.

Usage

```
create_empty_DAG(N_nodes)
```

Arguments

N_nodes An integer equal to the number of nodes

Value

A bnlearn graph object with ‘N_nodes’ nodes and no arcs

See Also

[bnlearn::empty.graph()] which this function wraps.

Examples

```
create_empty_DAG(6)
create_empty_DAG(10)
```

```
DAG_to_restrictedDAG  Turns a general graph into a restricted graph.
```

Description

Turns a general graph into a restricted graph.

Usage

```
DAG_to_restrictedDAG(DAG)

fix_active_cycles(DAG, active_cycles_list = NULL)

fix_interfering_vstructs(DAG, all_B_sets = NULL)
```

Arguments

DAG a directed acyclic graph object, of class bn.
 active_cycles_list, all_B_sets
 respective outputs of the functions [active_cycles](#) and [find_B_sets](#). If they are NULL, the respective function is called to compute them.

Value

Restricted DAG.

See Also

[is_restrictedDAG](#) to check whether a given DAG is restricted.

Examples

```
# DAG with an active cycle at node 5
DAG = create_empty_DAG(5)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U1', 'U2')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U5')
DAG = bnlearn::set.arc(DAG, 'U4', 'U5')

# Fixed graph has extra arcs 1 -> 5, 2 -> 5
fixed_DAG = DAG_to_restrictedDAG(DAG)

# DAG with an interfering v-structures node 3
DAG = create_empty_DAG(5)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U5')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U5')

# Fixed graph has extra arc 1 -> 5
fixed_DAG = DAG_to_restrictedDAG(DAG)
```

default_envir

Fits the copula joining w and v given cond_set abiding by the conditional independencies of the graph

Description

Fits the copula joining w and v given cond_set abiding by the conditional independencies of the graph

Usage

```
default_envir()
```

```
BiCopCondFit(
  data,
  DAG,
  v,
  w,
  cond_set,
  familyset,
  order_hash,
  e,
  verbose = 1,
  method
)
```

```
ComputeCondMargin(
  data,
  DAG,
  v,
  cond_set,
  familyset,
  order_hash,
  e,
  verbose = 1,
  method = method
)
```

Arguments

data	data frame
DAG	Directed Acyclic Graph
v, w	nodes of the graph
cond_set	vector of nodes of DAG. They should all be parents of v. They should be ordered from the smallest to the biggest.
familyset	vector of copula families
order_hash	hashmap of parental orders
e	environment containing all the hashmaps
verbose	if 0, don't print anything. If verbose >= 1, print information about the fitting procedure.
method	indicates the estimation method ("mle" for maximum likelihood estimation or "itau" of inversion of Kendall's tau)

Value

default_envir returns an environment to be passed to BiCopCondFit or to ComputeCondMargin.

BiCopCondFit returns the fitted copula object of v, w given `cond_set`. ComputeCondMargin returns the fitted conditional margins of v given `cond_set`.

Both functions store all intermediary results in `e` to save computation time.

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

fam = matrix(c(0, 0, 1,
              0, 0, 1,
              0, 0, 0), byrow = TRUE, ncol = 3)

tau = 0.2 * fam

my_PCBN = new_PCBN(
  DAG, order_hash,
  copula_mat = list(tau = tau, fam = fam))

mydata = PCBN_sim(my_PCBN, N = 5)
e = default_envir()
ls(e)
C_13 = BiCopCondFit(data = mydata, DAG = DAG, v = "U1", w = "U3",
  cond_set = c(), familyset = 1, order_hash = order_hash,
  e = e, method = "mle")

C_23_1 = BiCopCondFit(data = mydata, DAG = DAG, v = "U2", w = "U3",
  cond_set = "U1", familyset = 1, order_hash = order_hash,
  e = e, method = "itau")

U_2_13 = ComputeCondMargin(data = mydata, DAG = DAG,
  v = "U2", cond_set = c("U1", "U3"),
  familyset = 1, order_hash = order_hash, e = e,
  method = "mle")
```

dsep_set

D-separation of two nodes given a set in a DAG

Description

D-separation of two nodes given a set in a DAG

Usage

```
dsep_set(DAG, X, Y, Z = NULL)
```

Arguments

DAG	Directed Acyclic Graph
X	node
Y	node
Z	set

Value

TRUE if the sets are d-separated and FALSE if not

Examples

```
DAG = create_empty_DAG(5)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')

dsep_set(DAG, 'U1', 'U5')
```

extend_orders	<i>Fills in all possible orders for the next node for each possible order</i>
---------------	---

Description

Fills in all possible orders for the next node for each possible order

Usage

```
extend_orders(DAG, all_orders, node)
```

Arguments

DAG	Directed Acyclic Graph
all_orders	list of orders
node	node

Value

list of order hashmaps

Examples

```

DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')

# Start with empty order
order_hash = r2r::hashmap()

all_orders_3 = find_all_orders_v(DAG, v = "U3", order_hash = order_hash)
print(all_orders_3)

# Two possible choices for node 3, let's use the first
order_hash[['U3']] = all_orders_3[[1]]

extended_orders = extend_orders(DAG, list(order_hash), node = 'U4')
length(extended_orders)
# We can extend this order in 4 ways:
for (i in 1:length(extended_orders)){
  print(extended_orders[[i]][['U4']])
}
# We never pick U2 and U3 first, because their copula is not specified

```

find_all_orders

Finds all possible copula assignments given a DAG

Description

Finds all possible copula assignments given a DAG

Usage

```
find_all_orders(DAG)
```

Arguments

DAG Directed Acyclic Graph

Value

a list of hashmaps containing the possible orders

Examples

```

DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
all_orders = find_all_orders(DAG)
length(all_orders)
# 8 orders
for (i in 1:length(all_orders)){
  cat("Order ", i, ": \n")
  cat("U3:", all_orders[[i]][['U3']], "\n")
  cat(" ; U4:", all_orders[[i]][['U4']], "\n")
}

```

find_all_orders_v *Finds all possible orders of node v given previous copula assignments*

Description

Finds all possible orders of node v given previous copula assignments

Usage

```
find_all_orders_v(DAG, v, order_hash)
```

Arguments

DAG	Directed Acyclic Graph
v	node
order_hash	hashmap of orders

Value

list of vectors containing all possible orders for v

Examples

```

DAG = create_empty_DAG(5)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
DAG = bnlearn::set.arc(DAG, 'U1', 'U5')
DAG = bnlearn::set.arc(DAG, 'U2', 'U5')

```

```

DAG = bnlearn::set.arc(DAG, 'U3', 'U5')
DAG = bnlearn::set.arc(DAG, 'U4', 'U5')

# Start with empty order
order_hash = r2r::hashmap()

all_orders_3 = find_all_orders_v(DAG, v = "U3", order_hash = order_hash)
print(all_orders_3)

# Two possible choices for node 3, let's use the first
order_hash[['U3']] = all_orders_3[[1]]

all_orders_4 = find_all_orders_v(DAG, v = "U4", order_hash = order_hash)
print(all_orders_4)

# Four possible choices for node 4, let's use the third
order_hash[['U4']] = all_orders_4[[3]]

all_orders_5 = find_all_orders_v(DAG, v = "U5", order_hash = order_hash)
print(all_orders_5)

# Eight possible orders for node 5; let's use the fourth
order_hash[['U5']] = all_orders_5[[4]]

```

find_B_sets

Find all the B-sets of a given DAG

Description

Find all the B-sets of a given DAG

Find the B sets for a given node v

Usage

```
find_B_sets(DAG)
```

```
find_B_sets_v(DAG, v)
```

Arguments

DAG A bnlearn graph object

v node at which we want to find the B-sets

Value

find_B_sets returns a list with three elements

- B_sets list of B-sets matrices for each node;
- has_interfering_vstrucs a boolean specifying if the graph contains interfering v-structures or not;
- nodes_with_inter_vs a list containing nodes forming the interfering v-structures.

find_B_sets_v returns a boolean matrix with $(2 + \text{length}(\text{children}))$ columns and $\text{length}(\text{parents})$ rows. This is also true if $\text{length}(\text{parents}) == 0$ and $\text{length}(\text{parents}) == 1$.

Examples

```
DAG = create_empty_DAG(6)
DAG = bnlearn::set.arc(DAG, 'U1', 'U5')
DAG = bnlearn::set.arc(DAG, 'U2', 'U5')
DAG = bnlearn::set.arc(DAG, 'U3', 'U5')
DAG = bnlearn::set.arc(DAG, 'U4', 'U5')
```

```
DAG = bnlearn::set.arc(DAG, 'U1', 'U6')
DAG = bnlearn::set.arc(DAG, 'U2', 'U6')
DAG = bnlearn::set.arc(DAG, 'U5', 'U6')
```

```
find_B_sets_v(DAG, v = 'U5')
B_sets = find_B_sets(DAG)
B_sets$B_sets
```

find_cond_copula_specified

Find among parents of a node, the one that has a conditional copula specified

Description

Find among parents of a node, the one that has a conditional copula specified

Usage

```
find_cond_copula_specified(DAG, order_hash, v, cond)
```

Arguments

DAG	Directed Acyclic Graph object corresponding to the model
order_hash	hashmap of orders of the parental sets
v	node in DAG
cond	vector of nodes in DAG. This must not be empty. It is assumed that conditionally independent nodes have already been removed by the function remove_CondInd . It is assumed to have been already sorted.

Value

a list with

- a node w such that the conditional copula $C_{w,v|cond[-v]}$ has been specified in the model.
If no such node can be found, an error message is raised.
- the set `cond[-v]`

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

find_cond_copula_specified(DAG = DAG, order_hash = order_hash,
                           v = "U3", cond = c("U1"))
# returns "U1" because the copula  $c_{\{1,3\}}$  is known

find_cond_copula_specified(DAG = DAG, order_hash = order_hash,
                           v = "U3", cond = c("U1", "U2"))
# returns "U2" because the copula  $c_{\{2,3|1\}}$  is known
```

```
find_interfering_v_from_B_sets
```

Find all interfering v-structures for a given collection of B-sets

Description

Find all interfering v-structures for a given collection of B-sets

Usage

```
find_interfering_v_from_B_sets(B_sets)
```

Arguments

B_sets a boolean matrix with $(2 + \text{length}(\text{children}))$ columns and $\text{length}(\text{parents})$ rows. They are assumed to be sorted in increasing order of row sums, i.e. by increasing order of set cardinality. Typically, this will be the output of `find_B_sets_v` for some node v .

Value

NULL if there is no interfering v-structures. Else, it returns a data.frame with 4 columns

- A: a list of children of v
- B: a list of children of v, disjoint from A
- parents.A.but.not.parents.B: a list of common parents of nodes of A, that are not parents of nodes of B
- parents.B.but.not.parents.A: a list of common parents of nodes of B, that are not parents of nodes of A

Each line correspond to 1 interfering v-structure.

Examples

```
DAG = create_empty_DAG(7)
DAG = bnlearn::set.arc(DAG, 'U1', 'U5')
DAG = bnlearn::set.arc(DAG, 'U2', 'U5')
DAG = bnlearn::set.arc(DAG, 'U3', 'U5')
DAG = bnlearn::set.arc(DAG, 'U4', 'U5')

DAG = bnlearn::set.arc(DAG, 'U1', 'U6')
DAG = bnlearn::set.arc(DAG, 'U5', 'U6')
DAG = bnlearn::set.arc(DAG, 'U2', 'U7')
DAG = bnlearn::set.arc(DAG, 'U5', 'U7')

B_sets = find_B_sets_v(DAG, v = 'U5')
find_interfering_v_from_B_sets(B_sets)

# Adding the missing arc
DAG = bnlearn::set.arc(DAG, 'U1', 'U7')
# Now no interfering v-structure
B_sets = find_B_sets_v(DAG, v = 'U5')
find_interfering_v_from_B_sets(B_sets)
```

fit_copulas

Fit the copulas of a PCBN given data

Description

Fit the copulas of a PCBN given data

Fit all possible orders given a DAG

Usage

```

fit_copulas(
  data,
  DAG,
  order_hash,
  familyset = c(1, 3, 4, 5, 6),
  familyMatrix = NULL,
  e,
  verbose = 1,
  method = "mle"
)

fit_all_orders(
  data,
  DAG,
  familyset = c(1, 3, 4, 5, 6),
  e,
  score_metric = "BIC",
  verbose = 1
)

```

Arguments

data	data frame
DAG	Directed Acyclic Graph
order_hash	hashmap of parental orders
familyset	vector of copula families
familyMatrix	matrix of families, with named rows and columns. This should be used if the copula families are known/fixed. This overrides familyset.
e	environment containing all the hashmaps
verbose	if 0, don't print anything. If verbose >= 1, print information about the simulation procedure.
method	indicates the estimation method ("mle" for maximum likelihood estimation or "itau" of inversion of Kendall's tau).
score_metric	name of the metric used to choose the best order. Possible choices are logLik, AIC and BIC.

Value

fit_copulas returns the fitted PCBN, with an additional element called `metrics` which is a named vector of length 3 with names `c("logLik", "BIC", "AIC")`, where $AIC = -2 * \logLik + 2 * nparameters$ and $BIC = -2 * \logLik + \log(n) * nparameters$, for a sample size n and $nparameters$ is the number of parameters.

fit_all_orders returns a list containing:

- `best_fit` the PCBN which is the best according to the metric `score_metric`.

- `fitted_list` the list of all fitted PCBNs.
- `metrics` the matrix of metrics (logLik, BIC, AIC). Each row `i` of this matrix corresponds to a PCBN with a different set of parents' orderings, and corresponds to element `i` of `fitted_list`.

See Also

[BiCopCondFit](#) which this function wraps.

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

fam = matrix(c(0, 0, 1,
              0, 0, 1,
              0, 0, 0), byrow = TRUE, ncol = 3)

tau = 0.2 * fam

my_PCBN = new_PCBN(
  DAG, order_hash,
  copula_mat = list(tau = tau, fam = fam))

mydata = PCBN_sim(my_PCBN, N = 5)
e = default_envir()

result = fit_copulas(data = mydata, DAG = DAG,
                    order_hash = order_hash,
                    familyset = 1, e = e)

result_all_orders = fit_all_orders(data = mydata, DAG = DAG,
                                  familyset = 1, e = e)

# The two fitted PCBNs are:
print(result_all_orders$fitted_list[[1]])
print(result_all_orders$fitted_list[[2]])
# and the metrics matrix is:
print(result_all_orders$metrics)

# The PCBN corresponding to the true order U1 < U2 is usually better
# than the second one. This Will be more clear with a bigger sample size.
```

has_interfering_vstrucs

Checks if graph has interfering v-structures

Description

Checks if graph has interfering v-structures

Usage

```
has_interfering_vstrucs(DAG, verbose = 0)
```

Arguments

DAG	Directed Acyclic Graph
verbose	if verbose is 0, do not print anything. If verbose is positive, print the name of the first node at which the interfering v-structure is found.

Value

TRUE if graph contains (at least) an interfering v-structure, and FALSE if it does not contain any interfering v-structure.

Examples

```
DAG = create_empty_DAG(5)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U5')
DAG = bnlearn::set.arc(DAG, 'U3', 'U5')

# There is one interfering v-structure
has_interfering_vstrucs(DAG, verbose = 1)

DAG = bnlearn::set.arc(DAG, 'U1', 'U5')
# Now no interfering v-structure
has_interfering_vstrucs(DAG)
```

 is_cond_copula_specified

Checks if a given (conditional) copula has already been specified

Description

Checks if a given (conditional) copula has already been specified

Usage

```
is_cond_copula_specified(DAG, order_hash, w, v, cond)
```

Arguments

DAG	Directed Acyclic Graph object corresponding to the model
order_hash	hashmap of orders of the parental sets
w	node in DAG
v	node in DAG
cond	vector of nodes in DAG. It is assumed to have been already sorted.

Value

TRUE if the conditional copula $C_{w,v|cond}$ has been specified in the model

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

is_cond_copula_specified(DAG = DAG, order_hash = order_hash,
  w = "U1", v = "U3", cond = c())
# returns TRUE because the copula  $c_{\{1,3\}}$  is known

is_cond_copula_specified(DAG = DAG, order_hash = order_hash,
  w = "U2", v = "U3", cond = c())
# returns FALSE because the copula  $c_{\{2,3\}}$  is not known

is_cond_copula_specified(DAG = DAG, order_hash = order_hash,
  w = "U2", v = "U3", cond = c("U1"))
# returns TRUE because the copula  $c_{\{2,3 | 1\}}$  is known
```

 is_order_abiding_Bsets

Check whether a certain order abides by the B-sets

Description

Check whether a certain order abides by the B-sets

Usage

```
is_order_abiding_Bsets(DAG, order_hash)
```

```
is_order_abiding_Bsets_v(B_sets, orderParents)
```

Arguments

DAG	the considered DAG
order_hash	the hashmaps of parents ordering
B_sets	matrix of B-sets, assumed to be increasing. This can be the output of find_B_sets_v or of B_sets_make_unique .
orderParents	a vector of characters, interpreted as the ordered parents

Value

It returns 'TRUE' if the order abides by the B-sets, and 'FALSE' else.

Examples

```
DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")
order_hash[['U4']] = c("U1", "U3")
is_order_abiding_Bsets(DAG, order_hash)
order_hash[['U3']] = c("U2", "U1")
is_order_abiding_Bsets(DAG, order_hash)
```

is_restrictedDAG	<i>Does a DAG satisfy the restrictions of no active cycle and no interfering v-structures</i>
------------------	---

Description

This functions checks whether the DAG is restricted, i.e. whether it has no active cycles nor any interfering v-structures.

Usage

```
is_restrictedDAG(DAG, verbose = 2, check_both = TRUE)
```

Arguments

DAG	the DAG object
verbose	if verbose is 2, details are printed. If verbose is 1, details are printed only if an active cycle or an interfering v-structure is found. If verbose is 0 the function does not print anything and only returns TRUE or FALSE.
check_both	if TRUE, both v-structures and active cycles are checked anyway. If FALSE, the function stops early if it already found any v-structures.

Value

TRUE if the PCBN satisfies both restrictions. FALSE if at least one of the restrictions is not satisfies.

See Also

[DAG_to_restrictedDAG](#) for one way of making the DAG to be restricted if it is not the case.

[active_cycles](#) to find all active cycles. [has_interfering_vstrucs](#) to check only for interfering v-structures.

Examples

```
DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U2')
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')

is_restrictedDAG(DAG) # 1 active cycle
```

logLik.PCBN

Log-likelihood of a PCBN object

Description

This function computes the log-likelihood of the PCBN model given a dataset of i.i.d. observations uniformly (or approximatively uniformly) distributed on $[0, 1]$. This is the same as the logarithm of the density of the PCBN at the observations.

Usage

```
## S3 method for class 'PCBN'
logLik(object, data_uniform, ...)
```

Arguments

object	the PCBN object
data_uniform	the dataset for which the log-likelihood is computed. It must have already been standardized to uniform margins.
...	other arguments, ignored for the moment

Value

the log-likelihood of the PCBN model for the given dataset

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

fam = matrix(c(0, 0, 1,
              0, 0, 1,
              0, 0, 0), byrow = TRUE, ncol = 3)
tau = 0.2 * fam

my_PCBN = new_PCBN(
  DAG, order_hash,
  copula_mat = list(tau = tau, fam = fam))

mydata = PCBN_sim(my_PCBN, N = 10)

logLik(my_PCBN, mydata)
```

new_PCBN	<i>Initializes PCBN class</i>
----------	-------------------------------

Description

Initializes PCBN class

Usage

```
new_PCBN(DAG, order_hash, copula_mat, verbose = 0)
```

Arguments

DAG	the corresponding DAG (a 'bn' object)
order_hash	a hashmap of character vectors Each character vector corresponds to the order of the parents for the given node.
copula_mat	a list with at least two components: <ul style="list-style-type: none"> • fam the matrix of families • tau the matrix of Kendall's tau They both should be matrices of size $d * d$, where d is the number of nodes in the graph DAG.
verbose	If 0, no message is printed. If 1 (recommended), information is printed during the checking of the PCBN.

Value

the new PCBN

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

fam = matrix(c(0, 0, 1,
              0, 0, 1,
              0, 0, 0), byrow = TRUE, ncol = 3)
tau = 0.2 * fam

my_PCBN = new_PCBN(
  DAG, order_hash,
  copula_mat = list(tau = tau, fam = fam))
```

path_hasConvergingConnections

Checks a path for converging connections and chords.

Description

Checks a path for converging connections and chords.

Usage

```
path_hasConvergingConnections(DAG, path)
```

```
path_hasChords(DAG, path)
```

Arguments

DAG	Directed Acyclic Graph.
path	character vector of nodes in the DAG forming a trail.

Value

path_hasConvergingConnections returns TRUE if the path contains a converging connection.

path_hasChords returns TRUE if the path contains a chord.

See Also

[active_cycles](#) which uses these two functions.

Examples

```
DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U2')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')
path_hasConvergingConnections(DAG, c('U1', 'U2', 'U3', 'U4')) # FALSE
path_hasChords(DAG, c('U1', 'U2', 'U3', 'U4')) # FALSE
```

```
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
path_hasConvergingConnections(DAG, c('U1', 'U2', 'U3', 'U4')) # FALSE
path_hasChords(DAG, c('U1', 'U2', 'U3', 'U4')) # TRUE: has a chord
```

```
DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U2')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U4', 'U3')
path_hasConvergingConnections(DAG, c('U1', 'U2', 'U3', 'U4'))
# TRUE: has a converging connection
path_hasChords(DAG, c('U1', 'U2', 'U3', 'U4')) # FALSE
```

Description

This function computes the Probability Density Function of a PCBN model.

Usage

```
PCBN_PDF(PCBN, newdata)
```

Arguments

PCBN	PCBN object
newdata	new data on which the PDF should be computed

Details

This is a wrapper to [logLik.PCBN](#).

Value

the probability density at newdata.

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

fam = matrix(c(0, 0, 1,
              0, 0, 1,
              0, 0, 0), byrow = TRUE, ncol = 3)
tau = 0.2 * fam

my_PCBN = new_PCBN(
  DAG, order_hash,
  copula_mat = list(tau = tau, fam = fam))

mydata = PCBN_sim(my_PCBN, N = 10)

PCBN_PDF(my_PCBN, mydata)
```

PCBN_sim

*Simulate data from a specified PCBN***Description**

Simulate data from a specified PCBN

Usage

```
PCBN_sim(object, N, check_PCBN = TRUE, verbose = 1)
```

Arguments

object	PCBN object to simulate from. This does not work if the PCBN does not abide by the B-sets. And in general, it does not work if the PCBN is outside of the class of restricted PCBNS.
N	sample size
check_PCBN	check whether the given PCBN satisfies the restrictions. If this is set to FALSE, no checking is performed. This means that the error due to the a non-restricted PCBN object (if this is the case) will occur later in the computations (and may not be so clear - typically it is because of failing to find a given conditional copula). Nevertheless, even with 'check_PCBN = TRUE' it could be that some error happen later if the parental orderings are not compatible with each other.
verbose	if 0, don't print anything. If verbose >= 1, print information about the simulation procedure.

Value

a data frame of N samples

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

fam = matrix(c(0, 0, 1,
              0, 0, 1,
              0, 0, 0), byrow = TRUE, ncol = 3)

tau = 0.2 * fam

my_PCBN = new_PCBN(
  DAG, order_hash,
  copula_mat = list(tau = tau, fam = fam))
```

```
mydata = PCBN_sim(my_PCBN, N = 5)
```

plot.PCBN	<i>Print and plot PCBN objects</i>
-----------	------------------------------------

Description

Print and plot PCBN objects

Usage

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

## S3 method for class 'PCBN'
print(x, print.orders = "non-empty", ...)
```

Arguments

<code>x</code>	PCBN object
<code>...</code>	other arguments, unused
<code>print.orders</code>	if "all", print all orders. If "non-empty", this only prints the non-empty ones.

Value

No return value, both functions are called for side effects only.

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

fam = matrix(c(0, 0, 1,
              0, 0, 1,
              0, 0, 0), byrow = TRUE, ncol = 3)
tau = 0.2 * fam

my_PCBN = new_PCBN(
  DAG, order_hash,
  copula_mat = list(tau = tau, fam = fam))
print(my_PCBN)
plot(my_PCBN)
```

possible_candidates *Possible candidates to be added to a partial order*

Description

When given a partial order of a PCBN, one can complete it by adding one of the parents' node to the partial order. Some nodes can be added; they are then called "possible candidates".

Usage

```
possible_candidates(DAG, v, order_v, order_hash, B_minus_0)
```

```
possible_candidate_incoming_arc(DAG, w, v, order_v, order_hash)
```

```
possible_candidate_outgoing_arc(DAG, w, v, order_v, order_hash)
```

Arguments

DAG	Directed Acyclic Graph.
order_v	partial order for node v.
order_hash	hashmap of parental orders
B_minus_0	this is the current B-set, without the elements of order_v, i.e. this is the set of elements that could be considered possible candidates.
w, v	nodes in DAG. w is assumed to be a parent of v.

Details

possible_candidate_incoming_arc returns a node o such w is a parent of o, and w can be used as an incoming arc to v by the node o. If no such o can be found, w cannot be used as a potential candidate for the order of v by incoming arc. Then, the function possible_candidate_incoming_arc returns NULL.

In the same way, possible_candidate_outgoing_arc returns a node o such o is a parent of w, and w can be used as an outgoing arc to v by the node o.

Value

possible_candidates returns a vector of possible candidates, potentially empty. Both possible_candidate_incoming_arc and possible_candidate_outgoing_arc return either a node o, or NULL if they could not find such a node.

See Also

[dsep_set](#) for checking whether two sets of nodes are d-separated by another set. [find_B_sets](#) to find the B-sets.

Examples

```

DAG = create_empty_DAG(4)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')
DAG = bnlearn::set.arc(DAG, 'U1', 'U4')
DAG = bnlearn::set.arc(DAG, 'U2', 'U4')
DAG = bnlearn::set.arc(DAG, 'U3', 'U4')

order_hash = r2r::hashmap()
order_hash[['U3']] = c("U1", "U2")

# Node of interest
v = "U4"

# If we start by 1, then the arc 1 -> 3 cannot be used as an incoming arc
# (it is actually an outgoing arc)
possible_candidate_incoming_arc(
  DAG = DAG, w = "U3", v = v, order_v = c("U1"), order_hash = order_hash)
possible_candidate_outgoing_arc(
  DAG = DAG, w = "U3", v = v, order_v = c("U1"), order_hash = order_hash)
possible_candidates(
  DAG = DAG, v = v, order_v = c("U1"), order_hash = order_hash, B_minus_0 = "U2")

```

remove_CondInd	<i>Remove elements from a conditioning set by using conditional independence</i>
----------------	--

Description

Remove elements from a conditioning set by using conditional independence

Usage

```
remove_CondInd(DAG, node, cond_set)
```

Arguments

DAG	Directed Acyclic Graph
node	node
cond_set	vector of nodes in conditioning set

Value

a vector containing the nodes that cannot be removed from the conditioning set.

Examples

```
DAG = create_empty_DAG(3)
DAG = bnlearn::set.arc(DAG, 'U1', 'U3')
DAG = bnlearn::set.arc(DAG, 'U2', 'U3')

remove_CondInd(DAG = DAG, node = "U1", cond_set = c("U2"))
remove_CondInd(DAG = DAG, node = "U3", cond_set = c("U1"))
```

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