Package ‘bnlearn’

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Title Bayesian Network Structure Learning, Parameter Learning and Inference
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Author Marco Scutari [aut, cre], Robert Ness [ctb]
Maintainer Marco Scutari <marco.scutari@gmail.com>
Description Bayesian network structure learning, parameter learning and inference.
   This package implements constraint-based (PC, GS, IAMB, Inter-IAMB, Fast-IAMB, MMPC, Hiton-PC, HPC), pairwise (ARACNE and Chow-Liu), score-based (Hill-Climbing and Tabu Search) and hybrid (MMHC, RSMAX2, H2PC) structure learning algorithms for discrete, Gaussian and conditional Gaussian networks, along with many score functions and conditional independence tests.
   The Naive Bayes and the Tree-Augmented Naive Bayes (TAN) classifiers are also implemented.
   Some utility functions (model comparison and manipulation, random data generation, arc orientation testing, simple and advanced plots) are included, as well as support for parameter estimation (maximum likelihood and Bayesian) and inference, conditional probability queries, cross-validation, bootstrap and model averaging.
   Development snapshots with the latest bugfixes are available from <http://www.bnlearn.com>.
URL http://www.bnlearn.com/
License GPL (>= 2)
LazyData yes

R topics documented:

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bnlearn-package

Bayesian network structure learning, parameter learning and inference

Description

Bayesian network structure learning (via constraint-based, score-based and hybrid algorithms), parameter learning (via ML and Bayesian estimators) and inference (via approximate inference algorithms).

Details

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bnlearn implements key algorithms covering all stages of Bayesian network modelling: data preprocessing, structure learning combining data and expert/prior knowledge, parameter learning, and inference (including causal inference via do-calculus). bnlearn aims to be a one-stop shop for Bayesian networks in R, providing the tools needed for learning and working with discrete Bayesian networks, Gaussian Bayesian networks and conditional linear Gaussian Bayesian networks on real-world data. Incomplete data with missing values are also supported. Furthermore the modular nature of bnlearn makes it easy to use it for simulation studies.

Implemented structure learning algorithms include:

- *Constraint-based algorithms*, which use conditional independence tests to learn conditional independence constraints from data. The constraints in turn are used to learn the structure of
the Bayesian network under the assumption that conditional independence implies graphical separation (so, two variables that are independent cannot be connected by an arc).

- **Score-based algorithms**, which are general-purpose optimization algorithms that rank network structures with respect to a goodness-of-fit score.

- **Hybrid algorithms** combine aspects of both constraint-based and score-based algorithms, as they use conditional independence tests (usually to reduce the search space) and network scores (to find the optimal network in the reduced space) at the same time.

For more details about structure learning algorithms see [structure learning](#); available conditional independence tests are described in [independence tests](#) and available network scores are described in [network scores](#). Specialized algorithms to learn the structure of Bayesian network classifiers are described in [network classifiers](#). All algorithms support the use of whitelists and blacklists to include and exclude arcs from the networks (see [whitelists and blacklists](#)); and many have parallel implementation built on the **parallel** package. Bayesian network scores support the use of graphical priors.

Parameter learning approaches include both frequentist and Bayesian estimators. Inference is implemented using approximate algorithms via particle filters approaches such as likelihood weighting, and covers conditional probability queries, prediction and imputation.

Additional facilities include support for bootstrap and cross-validation; advanced plotting capabilities implemented on top of **Rgraphviz** and **lattice**; model averaging; random graphs and random samples generation; import/export functions to integrate **bnlearn** with software such as Hugin and GeNle; an associated Bayesian network repository of golden-standard networks at [http://www.bnlearn.com/repository](http://www.bnlearn.com/repository).

Use `citation("bnlearn")` to find out how to cite **bnlearn** in publications and other materials; and visit [http://www.bnlearn.com](http://www.bnlearn.com) for more examples and code from publications using **bnlearn**.

### Author(s)

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### References

**reference books:**  

**from the author:**  

Examples

```r
## the workflow of Bayesian network modelling in bnlearn:
# choose the data set to work on...
data(learning.test)
# ... choose an algorithm and learn the structure of the network from the data...
et = hc(learning.test)
# ... plot it...
## Not run: graphviz.plot(net)
# ... learn the parameters of the network...
bn = bn.fit(net, learning.test)
# ... explore the network with a classic bar chart...
## Not run: graphviz.chart(bn)
# ... and perform inference to answer any question that interests you!
cpquery(bn, event = (A == "a"), evidence = (C == "a"))
```

**alarm**

ALARM monitoring system (synthetic) data set

**Description**

The ALARM ("A Logical Alarm Reduction Mechanism") is a Bayesian network designed to provide an alarm message system for patient monitoring.

**Usage**

data(alarm)

**Format**

The alarm data set contains the following 37 variables:

- CVP (central venous pressure): a three-level factor with levels LOW, NORMAL and HIGH.
- PCWP (pulmonary capillary wedge pressure): a three-level factor with levels LOW, NORMAL and HIGH.
- HIST (history): a two-level factor with levels TRUE and FALSE.
- TPR (total peripheral resistance): a three-level factor with levels LOW, NORMAL and HIGH.
- BP (blood pressure): a three-level factor with levels LOW, NORMAL and HIGH.
- CO (cardiac output): a three-level factor with levels LOW, NORMAL and HIGH.
- HRBP (heart rate / blood pressure): a three-level factor with levels LOW, NORMAL and HIGH.
• HREK (heart rate measured by an EKG monitor): a three-level factor with levels LOW, NORMAL and HIGH.
• HRSA (heart rate/oxygen saturation): a three-level factor with levels LOW, NORMAL and HIGH.
• PAP (pulmonary artery pressure): a three-level factor with levels LOW, NORMAL and HIGH.
• SAO2 (arterial oxygen saturation): a three-level factor with levels LOW, NORMAL and HIGH.
• FI02 (fraction of inspired oxygen): a two-level factor with levels LOW and NORMAL.
• PRSS (breathing pressure): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
• ECO2 (expelled CO2): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
• MINV (minimum volume): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
• MVS (minimum volume set): a three-level factor with levels LOW, NORMAL and HIGH.
• HYP (hypovolemia): a two-level factor with levels TRUE and FALSE.
• LVF (left ventricular failure): a two-level factor with levels TRUE and FALSE.
• APL (anaphylaxis): a two-level factor with levels TRUE and FALSE.
• ANES (insufficient anesthesia/analgesia): a two-level factor with levels TRUE and FALSE.
• PMB (pulmonary embolus): a two-level factor with levels TRUE and FALSE.
• INT (intubation): a three-level factor with levels NORMAL, ESOPHAGEAL and ONESIDED.
• KINK (kinked tube): a two-level factor with levels TRUE and FALSE.
• DISC (disconnection): a two-level factor with levels TRUE and FALSE.
• LVV (left ventricular end-diastolic volume): a three-level factor with levels LOW, NORMAL and HIGH.
• STKV (stroke volume): a three-level factor with levels LOW, NORMAL and HIGH.
• CCHL (catecholamine): a two-level factor with levels NORMAL and HIGH.
• ERLO (error low output): a two-level factor with levels TRUE and FALSE.
• HR (heart rate): a three-level factor with levels LOW, NORMAL and HIGH.
• ERCA (electrocauter): a two-level factor with levels TRUE and FALSE.
• SHNT (shunt): a two-level factor with levels NORMAL and HIGH.
• PVS (pulmonary venous oxygen saturation): a three-level factor with levels LOW, NORMAL and HIGH.
• CO2 (arterial CO2): a three-level factor with levels LOW, NORMAL and HIGH.
• VALV (pulmonary alveoli ventilation): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
• VLANG (lung ventilation): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
• VTUB (ventilation tube): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
• VMCH (ventilation machine): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
alpha.star

Estimate the optimal imaginary sample size for BDe(u)

Description

Estimate the optimal value of the imaginary sample size for the BDe score, assuming a uniform prior and given a network structure and a data set.

Usage

alpha.star(x, data, debug = FALSE)

Arguments

x an object of class bn (for bn.fit and custom.fit) or an object of class bn.fit (for bn.net).

data a data frame containing the variables in the model.

d debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Value

alpha.star() returns a positive number, the estimated optimal imaginary sample size value.
Author(s)

Marco Scutari

References


Examples

data(learning.test)
dag <- hc(learning.test, score = "bic")

for (i in 1:3) {

  a <- alpha.star(dag, learning.test)
dag <- hc(learning.test, score = "bde", iss = a)
}

arc operations

Drop, add or set the direction of an arc or an edge

Description

Drop, add or set the direction of a directed or undirected arc (also known as edge).

Usage

# arc operations.
set.arc(x, from, to, check.cycles = TRUE, check.illegal = TRUE, debug = FALSE)
drop.arc(x, from, to, debug = FALSE)
reverse.arc(x, from, to, check.cycles = TRUE, check.illegal = TRUE, debug = FALSE)

# edge (i.e. undirected arc) operations
set.edge(x, from, to, check.cycles = TRUE, check.illegal = TRUE, debug = FALSE)
drop.edge(x, from, to, debug = FALSE)

Arguments

x an object of class bn.
from a character string, the label of a node.
to a character string, the label of another node.
check.cycles a boolean value. If TRUE the graph is tested for acyclicity; otherwise the graph is returned anyway.
check.illegal

check.illegal is a boolean value. If TRUE arcs that break the parametric assumptions of x, such as those from continuous to discrete nodes in conditional Gaussian networks, cause an error.

dataCheck

dataCheck is a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

The set.arc() function operates in the following way:

- if there is no arc between from and to, the arc from → to is added.
- if there is an undirected arc between from and to, its direction is set to from → to.
- if the arc to → from is present, it is reversed.
- if the arc from → to is present, no action is taken.

The drop.arc() function operates in the following way:

- if there is no arc between from and to, no action is taken.
- if there is a directed or an undirected arc between from and to, it is dropped regardless of its direction.

The reverse.arc() function operates in the following way:

- if there is no arc between from and to, it returns an error.
- if there is an undirected arc between from and to, it returns an error.
- if the arc to → from is present, it is reversed.
- if the arc from → to is present, it is reversed.

The set.edge() function operates in the following way:

- if there is no arc between from and to, the undirected arc from - to is added.
- if there is an undirected arc between from and to, no action is taken.
- if either the arc from → to or the arc to → from are present, they are replaced with the undirected arc from - to.

The drop.edge() function operates in the following way:

- if there is no undirected arc between from and to, no action is taken.
- if there is an undirected arc between from and to, it is removed.
- if there is a directed arc between from and to, no action is taken.

Value

All functions return invisibly an updated copy of x.

Author(s)

Marco Scutari


**Examples**

```r
data(learning.test)
res <- gs(learning.test)

### use debug = TRUE to get more information.
set.arc(res, "A", "B")
drop.arc(res, "A", "B")
drop.edge(res, "A", "B")
reverse.arc(res, "A", "D")
```

---

**arc.strength**

**Measure arc strength**

**Description**

Measure the strength of the probabilistic relationships expressed by the arcs of a Bayesian network, and use model averaging to build a network containing only the significant arcs.

**Usage**

- `arc.strength(x, data, criterion = NULL, ..., debug = FALSE)`
- `boot.strength(data, cluster = NULL, R = 200, m = nrow(data), algorithm, algorithm.args = list(), cpdag = TRUE, debug = FALSE)`
- `custom.strength(networks, nodes, weights = NULL, cpdag = TRUE, debug = FALSE)`
- `bf.strength(x, data, score, ..., debug = FALSE)`
- `mean(x, ..., weights = NULL)`
- `averaged.network(strength, nodes, threshold)`

**Arguments**

- `x` an object of class `bn.strength` (for `mean()`) or of class `bn` (for all other functions).
- `networks` a list, containing either object of class `bn` or arc sets (matrices or data frames with two columns, optionally labeled "from" and "to"); or an object of class `bn.kcv` or `bn.kcv.list` from `bn.cv()`.
- `data` a data frame containing the data the Bayesian network was learned from (for `arc.strength()`) or that will be used to compute the arc strengths (for `boot.strength()` and `bf.strength()`).
arc.strength

cluster an optional cluster object from package parallel.
strength an object of class bn.strength, see below.
threshold a numeric value, the minimum strength required for an arc to be included in the averaged network. The default value is the threshold attribute of the strength argument.
node a vector of character strings, the labels of the nodes in the network. In averaged.network, it defaults to the set of the unique node labels in the strength argument.
criterion, score a character string. For arc.strength(), the label of a score function or an independence test; see network scores for details. For bf.strength(), the label of the score used to compute the Bayes factors; see BF for details.
R a positive integer, the number of bootstrap replicates.
m a positive integer, the size of each bootstrap replicate.
weights a vector of non-negative numbers, to be used as weights when averaging arc strengths (in mean()) or network structures (in custom.strength()) to compute strength coefficients. If NULL, weights are assumed to be uniform.
cpdag a boolean value. If TRUE, the (PDAG of) the equivalence class is used instead of the network structure itself. It should make it easier to identify score-equivalent arcs.
algorithm a character string, the structure learning algorithm to be applied to the bootstrap replicates. See structure learning and the documentation of each algorithm for details.
algorithm.args a list of extra arguments to be passed to the learning algorithm.
... in arc.strength(), the additional tuning parameters for the network score (if criterion is the label of a score function, see score for details), the conditional independence test (currently the only one is B, the number of permutations). In mean(), additional objects of class bn.strength to average.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

arc.strength() computes a measure of confidence or strength for each arc, while keeping fixed the rest of the network structure.

If criterion is a conditional independence test, the strength is a p-value (so the lower the value, the stronger the relationship). The conditional independence test would be that to drop the arc from the network. The only two possible additional arguments are alpha, which sets the significance threshold that is used in strength.plot(); and B, the number of permutations to be generated for each permutation test.

If criterion is the label of a score function, the strength is measured by the score gain/loss which would be caused by the arc’s removal. In other words, it is the difference between the score of the network in which the arc is not present and the score of the network in which the arc is present. Negative values correspond to decreases in the network score and positive values correspond to increases in the network score (the stronger the relationship, the more negative the difference). There may be additional arguments depending on the choice of the score, see score for details. The significance threshold is set to 0.
boot.strength() estimates the strength of each arc as its empirical frequency over a set of networks learned from bootstrap samples. It computes the probability of each arc (modulo its direction) and the probabilities of each arc’s directions conditional on the arc being present in the graph (in either direction). The significance threshold is computed automatically from the strength estimates.

bf.strength() estimates the strength of each arc using Bayes factors to overcome the fact that Bayesian posterior scores are not normalised, and uses the latter to estimate the probabilities of all possible states of an arc given the rest of the network. The significance threshold is set to 1.

custom.strength() takes a list of networks and estimates arc strength in the same way as boot.strength().

Model averaging is supported for objects of class bn.strength returned by boot.strength, custom.strength and bf.strength. The returned network contains the arcs whose strength is greater than the threshold attribute of the bn.strength object passed to averaged.network().

Value

arc.strength(), boot.strength(), custom.strength(), bf.strength() and mean() return an object of class bn.strength; boot.strength() and custom.strength() also include information about the relative probabilities of arc directions.

averaged.network() returns an object of class bn.

See bn.strength class and bn-class for details.

Note

averaged.network() typically returns a completely directed graph; an arc can be undirected if and only if the probability of each of its directions is exactly 0.5. This may happen, for example, if the arc is undirected in all the networks being averaged.

Author(s)

Marco Scutari

References

for model averaging and bootstrap strength (confidence):


for the computation of the bootstrap strength (confidence) significance threshold:


See Also

strength.plot, choose.direction, score, ci.test.
Examples

```r
data(learning.test)
res <- gs(learning.test)
res <- set.arc(res, "A", "B")
arc.strength(res, learning.test)

## Not run:
arcs <- boot.strength(learning.test, algorithm = "hc")
arcs[(arcs$strength > 0.85) & (arcs$direction > -0.5), ]
averaged.network(arcs)

start <- random.graph(nodes = names(learning.test), num = 50)
netlist <- lapply(start, function(net) {
  hc(learning.test, score = "bde", iss = 10, start = net)
})
arcs <- custom.strength(netlist, nodes = names(learning.test),
  cpdag = FALSE)
arcs[(arcs$strength > 0.85) & (arcs$direction > -0.5), ]
modelstring(averaged.network(arcs))

## End(Not run)

bf.strength(res, learning.test, score = "bds", prior = "marginal")
```

Description

Small synthetic data set from Lauritzen and Spiegelhalter (1988) about lung diseases (tuberculosis, lung cancer or bronchitis) and visits to Asia.

Usage

```r
data(asia)
```

Format

The `asia` data set contains the following variables:

- `D` (*dyspnoea*), a two-level factor with levels yes and no.
- `T` (*tuberculosis*), a two-level factor with levels yes and no.
- `L` (*lung cancer*), a two-level factor with levels yes and no.
- `B` (*bronchitis*), a two-level factor with levels yes and no.
- `A` (*visit to Asia*), a two-level factor with levels yes and no.
- `S` (*smoking*), a two-level factor with levels yes and no.
- `X` (*chest X-ray*), a two-level factor with levels yes and no.
- `E` (*tuberculosis versus lung cancer/bronchitis*), a two-level factor with levels yes and no.
Note

Lauritzen and Spiegelhalter (1988) motivate this example as follows:

“Shortness-of-breath (dyspnoea) may be due to tuberculosis, lung cancer or bronchitis, or none of them, or more than one of them. A recent visit to Asia increases the chances of tuberculosis, while smoking is known to be a risk factor for both lung cancer and bronchitis. The results of a single chest X-ray do not discriminate between lung cancer and tuberculosis, as neither does the presence or absence of dyspnoea.”

Standard learning algorithms are not able to recover the true structure of the network because of the presence of a node (E) with conditional probabilities equal to both 0 and 1. Monte Carlo tests seems to behave better than their parametric counterparts.

The complete BN can be downloaded from http://www.bnlearn.com/bnrepository.

Source


Examples

# load the data.
data(asia)
# create and plot the network structure.
dag = model2network("[A][S][T|A][L|S][B|S][D|B:E][E|T:L][X|E]"
## Not run: graphviz.plot(dag)

BF

Bayes factor between two network structures

Description

Compute the Bayes factor between the structures of two Bayesian networks.

Usage

BF(num, den, data, score, ..., log = TRUE)

Arguments

num, den two objects of class bn, corresponding to the numerator and the denominator models in the Bayes factor.
data a data frame containing the data to be used to compute the Bayes factor.
score a character string, the label of a posterior network score. If none is specified, the default score is the Bayesian Dirichlet equivalent score (bde) for discrete networks and the Bayesian Gaussian score (bge) for Gaussian networks. Other kinds of Bayesian networks are not currently supported.
... extra tuning arguments for the posterior scores. See `score` for details.

log

a boolean value. If `TRUE` the Bayes factor is given as \( \log(\text{BF}) \).

**Value**

A single numeric value, the Bayes factor of the two network structures `num` and `den`.

**Note**

The Bayes factor for two network structures, by definition, is the ratio of the respective marginal likelihoods which is equivalent to the ratio of the corresponding posterior probabilities if we assume the uniform prior over all possible DAGs. However, note that it is possible to specify different priors using the "..." arguments of `BF()`; in that case the value returned by the function will not be the classic Bayes factor.

**Author(s)**

Marco Scutari

**See Also**

`score`, `compare`, `bf.strength`.

**Examples**

data(learning.test)

dag1 = model2network("[A][B][F][C][E][B][D][A:B:C]")
dag2 = model2network("[A][C][B][A][D][E][F][A:C:E]")
BF(dag1, dag2, learning.test, score = "bds", iss = 1)

---

**bn class**

_The bn class structure_

**Description**

The structure of an object of S3 class `bn`.

**Details**

An object of class `bn` is a list containing at least the following components:

- `learning`: a list containing some information about the results of the learning algorithm. It’s never changed afterward.
  - `whitelist`: a copy of the `whitelist` argument (a two-column matrix, whose columns are labeled from `from` and `to`) as transformed by sanitization functions.
  - `blacklist`: a copy of the `blacklist` argument (a two-column matrix, whose columns are labeled from `from` and `to`) as transformed by sanitization functions.
- `test`: the label of the conditional independence test used by the learning algorithm (a character string); the label of the network score is used for score-based algorithms; the label of the network score used in the “Maximize” phase of hybrid algorithms; "none" for randomly generated graphs. For hybrid algorithms, `test` always has the same value as `maxscore` (see below).
- `ntests`: the number of conditional independence tests or score comparisons used in the learning (an integer value).
- `algo`: the label of the learning algorithm or the random generation algorithm used to generate the network (a character string).
- `args`: a list. The values of the parameters of either the conditional tests or the scores used in the learning process. Only the relevant ones are stored, so this may be an empty list.
  * `alpha`: the target nominal type I error rate (a numeric value) of the conditional independence tests.
  * `iss`: a positive numeric value, the imaginary sample size used by the bge and bde scores.
  * `k`: a positive numeric value, the penalty coefficient used by the aic, aic-g, bic and bic-g scores.
  * `prob`: the probability of each arc to be present in a graph generated by the ordered graph generation algorithm.
  * `burn.in`: the number of iterations for the ic-dag graph generation algorithm to converge to a stationary (and uniform) probability distribution.
  * `max.degree`: the maximum degree for any node in a graph generated by the ic-dag graph generation algorithm.
  * `max.in.degree`: the maximum in-degree for any node in a graph generated by the ic-dag graph generation algorithm.
  * `max.out.degree`: the maximum out-degree for any node in a graph generated by the ic-dag graph generation algorithm.
  * `training`: a character string, the label of the training node in a Bayesian network classifier.
  * `threshold`: the threshold used to determine which arcs are significant when averaging network structures.
  * `prior`: the graphical prior used in combination with a Bayesian score such as bde or bge.
  * `beta`: the parameters of the graphical prior.

- `nodes`: a list. Each element is named after a node and contains the following elements:
  - `mb`: the Markov blanket of the node (a vector of character strings).
  - `nbr`: the neighbourhood of the node (a vector of character strings).
  - `parents`: the parents of the node (a vector of character strings).
  - `children`: the children of the node (a vector of character strings).
- `arcs`: the arcs of the Bayesian network (a two-column matrix, whose columns are labeled from and to). Undirected arcs are stored as two directed arcs with opposite directions between the corresponding incident nodes.

Additional (optional) components under `learning`:
• **optimized**: whether additional optimizations have been used in the learning algorithm (a boolean value).
• **illegal**: arcs that are illegal according to the parametric assumptions used to learn the network structure (a two-column matrix, whose columns are labeled from and to).
• **restrict**: the label of the constraint-based algorithm used in the “Restrict” phase of a hybrid learning algorithm (a character string).
• **rtest**: the label of the conditional independence test used in the “Restrict” phase of a hybrid learning algorithm (a character string).
• **maximize**: the label of the score-based algorithm used in the “Maximize” phase of a hybrid learning algorithm (a character string).
• **maxscore**: the label of the network score used in the “Maximize” phase of a hybrid learning algorithm (a character string).
• **max.sx**: the maximum allowed size of the conditioning sets in the conditional independence tests used in constraint-based algorithms.

**Author(s)**
Marco Scutari

---

**bn.boot**

*Nonparametric bootstrap of Bayesian networks*

**Description**

Apply a user-specified function to the Bayesian network structures learned from bootstrap samples of the original data.

**Usage**

```r
bn.boot(data, statistic, R = 200, m = nrow(data), algorithm, 
algorithm.args = list(), statistic.args = list(), cluster = NULL, 
debug = FALSE)
```

**Arguments**

- **data**: a data frame containing the variables in the model.
- **statistic**: a function or a character string (the name of a function) to be applied to each bootstrap replicate.
- **R**: a positive integer, the number of bootstrap replicates.
- **m**: a positive integer, the size of each bootstrap replicate.
- **algorithm**: a character string, the learning algorithm to be applied to the bootstrap replicates. See structure learning and the documentation of each algorithm for details.
- **algorithm.args**: a list of extra arguments to be passed to the learning algorithm.
- **statistic.args**: a list of extra arguments to be passed to the function specified by statistic.
cluster  an optional cluster object from package **parallel**.

degub     a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

**Details**

The first argument of statistic is the bn object encoding the network structure learned from the bootstrap sample; the arguments specified in statistics.args are extracted from the list and passed to statistics as the 2nd, 3rd, etc. arguments.

**Value**

A list containing the results of the calls to statistic.

**Author(s)**

Marco Scutari

**References**


**See Also**

bn.cv, rbn.

**Examples**

```r
## Not run:
data(learning.test)
bn.boot(data = learning.test, R = 2, m = 500, algorithm = "gs",
       statistic = arcs)
## End(Not run)
```

---

**bn.cv**  

*Cross-validation for Bayesian networks*

**Description**

Perform a k-fold or hold-out cross-validation for a learning algorithm or a fixed network structure.
**bn.cv**

**Usage**

```r
bn.cv(data, bn, loss = NULL, ..., algorithm.args = list(),
loss.args = list(), fit = "mle", fit.args = list(), method = "k-fold",
cluster = NULL, debug = FALSE)
```

```r
## S3 method for class 'bn.kcv'
plot(x, ..., main, xlab, ylab, connect = FALSE)
```

```r
## S3 method for class 'bn.kcv.list'
plot(x, ..., main, xlab, ylab, connect = FALSE)
```

```r
loss(x)
```

**Arguments**

- `data`: a data frame containing the variables in the model.
- `bn`: either a character string (the label of the learning algorithm to be applied to the training data in each iteration) or an object of class `bn` (a fixed network structure).
- `loss`: a character string, the label of a loss function. If none is specified, the default loss function is the *Classification Error* for Bayesian networks classifiers; otherwise, the *Log-Likelihood Loss* for both discrete and continuous data sets. See below for additional details.
- `algorithm.args`: a list of extra arguments to be passed to the learning algorithm.
- `loss.args`: a list of extra arguments to be passed to the loss function specified by `loss`.
- `t`: a character string, the label of the method used to fit the parameters of the network. See `bn.t` for details.
- `t.args`: additional arguments for the parameter estimation procedure, see again `bn.t` for details.
- `method`: a character string, either *k-fold*, *custom-folds* or *hold-out*. See below for details.
- `cluster`: an optional cluster object from package `parallel`.
- `debug`: a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
- `x`: an object of class `bn.kcv` or `bn.kcv.list` returned by `bn.cv()`.
- `...`: additional objects of class `bn.kcv` or `bn.kcv.list` to plot alongside the first.
- `main, xlab, ylab`: the title of the plot, an array of labels for the boxplot, the label for the y axis.
- `connect`: a logical value. If TRUE, the medians points in the boxplots will be connected by a segmented line.

**Value**

- `bn.cv()` returns an object of class `bn.kcv.list` if `runs` is at least 2, an object of class `bn.kcv` if `runs` is equal to 1.
- `loss()` returns a numeric vector with a length equal to `runs`. 
Cross-Validation Strategies

The following cross-validation methods are implemented:

- **k-fold**: the data are split in k subsets of equal size. For each subset in turn, bn is fitted (and possibly learned as well) on the other k-1 subsets and the loss function is then computed using that subset. Loss estimates for each of the k subsets are then combined to give an overall loss for data.

- **custom-folds**: the data are manually partitioned by the user into subsets, which are then used as in k-fold cross-validation. Subsets are not constrained to have the same size, and every observation must be assigned to one subset.

- **hold-out**: k subsamples of size m are sampled independently without replacement from the data. For each subsample, bn is fitted (and possibly learned) on the remaining m -row(data) samples and the loss function is computed on the m observations in the subsample. The overall loss estimate is the average of the k loss estimates from the subsamples.

If either cross-validation is used with multiple runs, the overall loss is the average of the loss estimates from the different runs.

To clarify, cross-validation methods accept the following optional arguments:

- **k**: a positive integer number, the number of groups into which the data will be split (in k-fold cross-validation) or the number of times the data will be split in training and test samples (in hold-out cross-validation).

- **m**: a positive integer number, the size of the test set in hold-out cross-validation.

- **runs**: a positive integer number, the number of times k-fold or hold-out cross-validation will be run.

- **folds**: a list in which element corresponds to one fold and contains the indices for the observations that are included to that fold; or a list with an element for each run, in which each element is itself a list of the folds to be used for that run.

Loss Functions

The following loss functions are implemented:

- **Log-Likelihood Loss (logl)**: also known as negative entropy or negentropy, it is the negated expected log-likelihood of the test set for the Bayesian network fitted from the training set.

- **Gaussian Log-Likelihood Loss (logl-g)**: the negated expected log-likelihood for Gaussian Bayesian networks.

- **Classification Error (pred)**: the prediction error for a single node in a discrete network. Frequentist predictions are used, so the values of the target node are predicted using only the information present in its local distribution (from its parents).

- **Posterior Classification Error (pred-lw and pred-lw-cg)**: similar to the above, but predictions are computed from an arbitrary set of nodes using likelihood weighting to obtain Bayesian posterior estimates. pred-lw applies to discrete Bayesian networks, pred-lw-cg to (discrete nodes in) hybrid networks.

- **Exact Classification Error (pred-exact)**: closed-form exact posterior predictions are available for Bayesian network classifiers.
- **Predictive Correlation** (cor): the correlation between the observed and the predicted values for a single node in a Gaussian Bayesian network.

- **Posterior Predictive Correlation** (cor-lw and cor-lw-cg): similar to the above, but predictions are computed from an arbitrary set of nodes using likelihood weighting to obtain Bayesian posterior estimates. cor-lw applies to Gaussian networks and cor-lw-cg to (continuous nodes in) hybrid networks.

- **Mean Squared Error** (mse): the mean squared error between the observed and the predicted values for a single node in a Gaussian Bayesian network.

- **Posterior Mean Squared Error** (mse-lw and mse-lw-cg): similar to the above, but predictions are computed from an arbitrary set of nodes using likelihood weighting to obtain Bayesian posterior estimates. mse-lw applies to Gaussian networks and mse-lw-cg to (continuous nodes in) hybrid networks.

Optional arguments that can be specified in `loss.args` are:

- **target**: a character string, the label of target node for prediction in all loss functions but `logl`, `logl-g` and `logl-cg`.

- **from**: a vector of character strings, the labels of the nodes used to predict the target node in `pred-lw`, `pred-lw-cg`, `cor-lw`, `cor-lw-cg`, `mse-lw` and `mse-lw-cg`. The default is to use all the other nodes in the network. Loss functions `pred`, `cor` and `mse` implicitly predict only from the parents of the target node.

- **n**: a positive integer, the number of particles used by likelihood weighting for `pred-lw`, `pred-lw-cg`, `cor-lw`, `cor-lw-cg`, `mse-lw` and `mse-lw-cg`. The default value is 500.

Note that if `bn` is a Bayesian network classifier, `pred` and `pred-lw` both give exact posterior predictions computed using the closed-form formulas for naive Bayes and TAN.

**Plotting Results from Cross-Validation**

Both plot methods accept any combination of objects of class `bn.kcv` or `bn.kcv.list` (the first as the `x` argument, the remaining as the `...` argument) and plot the respected expected loss values side by side. For a `bn.kcv` object, this mean a single point; for a `bn.kcv.list` object this means a boxplot.

**Author(s)**

Marco Scutari

**References**


**See Also**

`bn.boot`, `rbn`, `bn.kcv-class`. 

bn.cv
Examples

```
bn.cv(learning.test, 'hc', loss = "pred", loss.args = list(target = "F"))

folds = list(1:2000, 2001:3000, 3001:5000)
bn.cv(learning.test, 'hc', loss = "logl", method = "custom-folds",
    folds = folds)

xval = bn.cv(gaussian.test, 'mmhc', method = "hold-out",
    k = 5, m = 50, runs = 2)

bn.cv(gaussian.test, 'mmhc', metho d = "hold-out",
    k = 5, m = 50, runs = 2)

## Not run:
# comparing algorithms with multiple runs of cross-validation.

xval = bn.cv(learning.test, 'hc', loss = "logl", method = "custom-folds",
    folds = folds)

# multiple runs, with custom folds.
bn.cv(gaussian.test, 'mmhc', metho d = "hold-out",
    k = 5, m = 50, runs = 2)

```

---

**bn.fit**

*Fit the parameters of a Bayesian network*

---

**Description**

Fit, assign or replace the parameters of a Bayesian network conditional on its structure.

**Usage**

```
bn.fit(x, data, cluster = NULL, method = "mle", ..., keep.fitted = TRUE, debug = FALSE)
custom.fit(x, dist, ordinal, debug = FALSE)
bn.net(x, debug = FALSE)
```
Arguments

- **x**: an object of class bn (for bn.fit() and custom.fit()) or an object of class bn.fit (for bn.net).
- **data**: a data frame containing the variables in the model.
- **cluster**: an optional cluster object from package parallel.
- **dist**: a named list, with element for each node of **x**. See below.
- **method**: a character string, either mle for Maximum Likelihood parameter estimation or bayes for Bayesian parameter estimation (currently implemented only for discrete data).
- **...**: additional arguments for the parameter estimation procedure, see below.
- **ordinal**: a vector of character strings, the labels of the discrete nodes which should be saved as ordinal random variables (bn.fit.dnode) instead of unordered factors (bn.fit.dnode).
- **keep.fitted**: a boolean value. If TRUE, the object returned by bn.fit will contain fitted values and residuals for all Gaussian and conditional Gaussian nodes, and the configurations of the discrete parents for conditional Gaussian nodes.
- **debug**: a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

bn.fit() fits the parameters of a Bayesian network given its structure and a data set; bn.net returns the structure underlying a fitted Bayesian network.

Additional arguments for the bn.fit() function:

- **iss**: a numeric value, the imaginary sample size used by the bayes method to estimate the conditional probability tables associated with discrete nodes (see score for details).
- **replace.unidentifiable**: a boolean value. If TRUE and method is mle, unidentifiable parameters are replaced by zeroes (in the case of regression coefficients and standard errors in Gaussian and conditional Gaussian nodes) or by uniform conditional probabilities (in discrete nodes).

  If FALSE (the default), the conditional probabilities in the local distributions of discrete nodes have a maximum likelihood estimate of NaN for all parents configurations that are not observed in data. Similarly, regression coefficients are set to NA if the linear regresions corresponding to the local distributions of continuous nodes are singular. Such missing values propagate to the results of functions such as predict().

An in-place replacement method is available to change the parameters of each node in a bn.fit object; see the examples for discrete, continuous and hybrid networks below. For a discrete node (class bn.fit.dnode or bn.fit.onode), the new parameters must be in a table object. For a Gaussian node (class bn.fit.gnode), the new parameters can be defined either by an lm, glm or penalized object (the latter is from the penalized package) or in a list with elements named coef, sd and optionally fitted and resid. For a conditional Gaussian node (class bn.fit.cgnode), the new parameters can be defined by a list with elements named coef, sd and optionally fitted, resid and configs. In both cases coef should contain the new regression coefficients, sd the standard deviation of the residuals,
fitted the fitted values and resid the residuals. config should contain the configurations if the discrete parents of the conditional Gaussian node, stored as a factor.

custom.fit() takes a set of user-specified distributions and their parameters and uses them to build a bn.fit object. Its purpose is to specify a Bayesian network (complete with the parameters, not only the structure) using knowledge from experts in the field instead of learning it from a data set. The distributions must be passed to the function in a list, with elements named after the nodes of the network structure x. Each element of the list must be in one of the formats described above for in-place replacement.

Value

bn.fit() and custom.fit() returns an object of class bn.fit, bn.net() an object of class bn. See bn class and bn.fit class for details.

Note

Due to the way Bayesian networks are defined it is possible to estimate their parameters only if the network structure is completely directed (i.e. there are no undirected arcs). See set.arc and pdag2dag for two ways of manually setting the direction of one or more arcs.

The bayes and mle methods in bn.fit() handle missing values in data by estimating the parameters of each local distribution using the observations that are complete for the variables involved (the node and its parents).

When method is set to mle, bn.fit() produces NA parameter estimates for discrete and conditional Gaussian nodes when there are (discrete) parents configurations that are not observed in data. To avoid this either set replace:unidentifiable to TRUE or, in the case of discrete networks, use method = "bayes".

Author(s)

Marco Scutari

See Also

bn.fit utilities, bn.fit plots.

Examples

data(learning.test)

# learn the network structure.
res = gs(learning.test)
# set the direction of the only undirected arc, A - B.
res = set.arc(res, "A", "B")
# estimate the parameters of the Bayesian network.
fitted = bn.fit(res, learning.test)
# replace the parameters of the node B.
new.cpt = matrix(c(0.1, 0.2, 0.3, 0.2, 0.5, 0.6, 0.7, 0.3, 0.1), byrow = TRUE, ncol = 3, dimnames = list(B = c("a", "b", "c"), A = c("a", "b", "c")))
fitted$B = as.table(new.cpt)
# the network structure is still the same.
all.equal(res, bn.net(fitted))

# learn the network structure.
res = hc(gaussian.test)

# estimate the parameters of the Bayesian network.
res = bn.fit(res, gaussian.test)

# replace the parameters of the node F.
res = fitted$F = list(coef = c(1, 2, 3, 4, 5), sd = 3)

# set again the original parameters
res = fitted$F = lm(F ~ A + D + E + G, data = gaussian.test)

# discrete Bayesian network from expert knowledge.
net = model2network("[A][B][C|A:B]"

cptA = matrix(c(0.4, 0.6), ncol = 2, dimnames = list(NULL, c("LOW", "HIGH")))
cptB = matrix(c(0.3, 0.7), ncol = 2, dimnames = list(NULL, c("GOOD", "BAD")))
cptC = c(0.5, 0.3, 0.4, 0.6, 0.7, 0.2, 0.8)
dim(cptC) = c(2, 2, 2)
dimnames(cptC) = list("C" = c("TRUE", "FALSE"), "A" = c("LOW", "HIGH"),
                      "B" = c("GOOD", "BAD"))
cfit = custom.fit(net, dist = list(A = cptA, B = cptB, C = cptC))

# for ordinal nodes it is nearly the same.
cfit = custom.fit(net, dist = list(A = cptA, B = cptB, C = cptC),
                   ordinal = c("A", "B"))

# Gaussian Bayesian network from expert knowledge.
distA = list(coef = c("(Intercept)" = 2), sd = 1)
distB = list(coef = c("(Intercept)" = 1), sd = 1.5)
distC = list(coef = c("(Intercept)" = 0.5, "A" = 0.75, "B" = 1.32), sd = 0.4)
cfit = custom.fit(net, dist = list(A = distA, B = distB, C = distC))

# conditional Gaussian Bayesian network from expert knowledge.
cptA = matrix(c(0.4, 0.6), ncol = 2, dimnames = list(NULL, c("LOW", "HIGH")))
distB = list(coef = c("(Intercept)" = 1), sd = 1.5)
distC = list(coef = matrix(c(1.2, 2.3, 3.4, 4.5), ncol = 2,
                          dimnames = list(c("(Intercept)", "B")), NULL),
                      sd = c(0.3, 0.6))
cgfit = custom.fit(net, dist = list(A = cptA, B = distB, C = distC))
bn.fit class

- node: a character string, the label of the node.
- parents: a vector of character strings, the labels of the parents of the node.
- children: a vector of character strings, the labels of the children of the node.
- prob: a (multi)dimensional numeric table, the conditional probability table of the node given its parents.

Nodes encoding ordinal variables (i.e. ordered factors) have class `bn.fit.onode` and contain the same elements as `bn.fit.dnode` nodes. Networks containing only ordinal nodes also have class `bn.fit.onet`, while those containing both ordinal and multinomial nodes also have class `bn.fit.donet`.

If on the other hand the network is continuous (i.e. the nodes are Gaussian random variables), the object also has class `bn.fit.gnet`; each node has class `bn.fit.gnode` and contains the following elements:

- node: a character string, the label of the node.
- parents: a vector of character strings, the labels of the parents of the node.
- children: a vector of character strings, the labels of the children of the node.
- coefficients: a numeric vector, the linear regression coefficients of the parents against the node.
- residuals: a numeric vector, the residuals of the linear regression.
- fitted.values: a numeric vector, the fitted mean values of the linear regression.
- sd: a numeric value, the standard deviation of the residuals (i.e. the standard error).

Hybrid (i.e. conditional linear Gaussian) networks also have class `bn.fit.gnet`. Gaussian nodes have class `bn.fit.gnode`, discrete nodes have class `bn.fit.dnode` and conditional Gaussian nodes have class `bn.fit.cgnode`. Each node contains the following elements:

- node: a character string, the label of the node.
- parents: a vector of character strings, the labels of the parents of the node.
- children: a vector of character strings, the labels of the children of the node.
- dparents: an integer vector, the indexes of the discrete parents in `parents`.
- gparents: an integer vector, the indexes of the continuous parents in `parents`.
- dlevels: a list containing the levels of the discrete parents in `parents`.
- coefficients: a numeric matrix, the linear regression coefficients of the continuous parents. Each column corresponds to a configuration of the discrete parents.
- residuals: a numeric vector, the residuals of the linear regression.
- fitted.values: a numeric vector, the fitted mean values of the linear regression.
- configs: an integer vector, the indexes of the configurations of the discrete parents.
- sd: a numeric vector, the standard deviation of the residuals (i.e. the standard error) for each configuration of the discrete parents.

Furthermore, Bayesian network classifiers store the label of the training node in an additional attribute named `training`.

Author(s)

Marco Scutari
bn.fit plots

Plot fitted Bayesian networks

Description

Plot functions for the bn.fit, bn.fit.dnode and bn.fit.gnode classes, based on the lattice package.

Usage

### for Gaussian Bayesian networks.
bn.fit.qqplot(fitted, xlab = "Theoretical Quantiles",
              ylab = "Sample Quantiles", main, ...)
bn.fit.histogram(fitted, density = TRUE, xlab = "Residuals",
                 ylab = ifelse(density, "Density", ""), main, ...)
bn.fit.xyplot(fitted, xlab = "Fitted values", ylab = "Residuals", main, ...)

### for discrete (multinomial and ordinal) Bayesian networks.
bn.fit.barchart(fitted, xlab = "Probabilities", ylab = "Levels", main, ...)
bn.fit.dotplot(fitted, xlab = "Probabilities", ylab = "Levels", main, ...)

Arguments

- fitted: an object of class bn.fit, bn.fit.dnode or bn.fit.gnode.
- xlab, ylab, main: the label of the x axis, of the y axis, and the plot title.
- density: a boolean value. If TRUE the histogram is plotted using relative frequencies, and the matching normal density is added to the plot.
- ... additional arguments to be passed to lattice functions.

Details

bn.fit.qqplot() draws a quantile-quantile plot of the residuals.
bn.fit.histogram() draws a histogram of the residuals, using either absolute or relative frequencies.
bn.fit.xyplot() plots the residuals versus the fitted values.
bn.fit.barchart() and bn.fit.dotplot plot the probabilities in the conditional probability table associated with each node.

Value

The lattice plot objects. Note that if auto-printing is turned off (for example when the code is loaded with the source function), the return value must be printed explicitly for the plot to be displayed.

Author(s)

Marco Scutari

See Also

bn.fit, bn.fit class.
Utilities to manipulate fitted Bayesian networks

Description

Assign, extract or compute various quantities of interest from an object of class \texttt{bn.fit}, \texttt{bn.fit.dnode}, \texttt{bn.fit.gnode}, \texttt{bn.fit.cgnode} or \texttt{bn.fit.onode}.

Usage

```r
## methods available for "bn.fit"
## S3 method for class 'bn.fit'
fitted(object, ...)
## S3 method for class 'bn.fit'
coef(object, ...)
## S3 method for class 'bn.fit'
residuals(object, ...)
## S3 method for class 'bn.fit'
sigma(object, ...)
## S3 method for class 'bn.fit'
logLik(object, data, nodes, by.sample = FALSE, ...)
## S3 method for class 'bn.fit'
AIC(object, data, ..., k = 1)
## S3 method for class 'bn.fit'
BIC(object, data, ...)

## methods available for "bn.fit.dnode"
## S3 method for class 'bn.fit.dnode'
coef(object, for.parents, ...)

## methods available for "bn.fit.onode"
## S3 method for class 'bn.fit.onode'
coef(object, for.parents, ...)

## methods available for "bn.fit.gnode"
## S3 method for class 'bn.fit.gnode'
fitted(object, ...)
## S3 method for class 'bn.fit.gnode'
coef(object, ...)
## S3 method for class 'bn.fit.gnode'
residuals(object, ...)
## S3 method for class 'bn.fit.gnode'
sigma(object, ...)

## methods available for "bn.fit.cgnode"
## S3 method for class 'bn.fit.cgnode'
fitted(object, ...)
```
bn.fit utilities

## S3 method for class 'bn.fit.cnodo'
coef(object, for.parents, ...)

## S3 method for class 'bn.fit.cnodo'
residuals(object, ...)

## S3 method for class 'bn.fit.cnodo'
sigma(object, for.parents, ...)

Arguments

object an object of class bn.fit, bn.fit.cnodo, bn.fit.cnodo, bn.fit.cnodo or bn.fit.onode.
nodes a vector of character strings, the label of a node whose log-likelihood components are to be computed.
data a data frame containing the variables in the model.
... additional arguments, currently ignored.
k a numeric value, the penalty coefficient to be used; the default k = 1 gives the expression used to compute AIC.
by.sample a boolean value. If TRUE, logLik() returns a vector containing the the log-likelihood of each observation in the sample. If FALSE, logLik() returns a single value, the likelihood of the whole sample.
for.parents a named list in which each element contains

Details

ccoef() (and its alias coefficients()) extracts model coefficients (which are conditional probabilities for discrete nodes and linear regression coefficients for Gaussian and conditional Gaussian nodes).

residuals() (and its alias resid()) extracts model residuals and fitted() (and its alias fitted.values()) extracts fitted values from Gaussian and conditional Gaussian nodes. If the bn.fit object does not include the residuals or the fitted values for the node of interest both functions return NULL.

sigma() extracts the standard deviations of the residuals from Gaussian and conditional Gaussian networks and nodes.

logLik() returns the log-likelihood for the observations in data.

The for.parents argument in the methods for coef() and sigma() can be used to have both functions return the parameters associated with a specific configuration of the discrete parents of a node. If for.parents is not specified, all relevant parameters are returned.

Value

logLik() returns a numeric vector or a single numeric value, depending on the value of by.sample. AIC and BIC always return a single numeric value.

All the other functions return a list with an element for each node in the network (if object has class bn.fit) or a numeric vector or matrix (if object has class bn.fit.cnodo, bn.fit.cnodo, bn.fit.cnodo or bn.fit.onode).

Author(s)

Marco Scutari
See Also

bn.fit, bn.fit-class.

Examples

data(gaussian.test)
res <- hc(gaussian.test)
fitted <- bn.fit(res, gaussian.test)
coefficients(fitted)
coefficients(fitted$C)
str(residuals(fitted))

data(learning.test)
res2 <- hc(learning.test)
fitted2 <- bn.fit(res2, learning.test)
coefficients(fitted2$E)
coefficients(fitted2$E, for.parents = list(F = "a", B = "b"))

bn.kcv class

The bn.kcv class structure

Description

The structure of an object of S3 class bn.kcv or bn.kcv.list.

Details

An object of class bn.kcv.list is a list whose elements are objects of class bn.kcv.

An object of class bn.kcv is a list whose elements correspond to the iterations of a k-fold cross-validation. Each element contains the following objects:

- `test`: an integer vector, the indexes of the observations used as a test set.
- `fitted`: an object of class bn.fit, the Bayesian network fitted from the training set.
- `learning`: the learning element of the bn object that was used for parameter learning from the training set (either learned from the training set as well or specified by the user).
- `loss`: the value of the loss function.

If the loss function requires to predict values from the test sets, each element also contains:

- `predicted`: a factor or a numeric vector, the predicted values for the target node in the test set.
- `observed`: a factor or a numeric vector, the observed values for the target node in the test set.

In addition, an object of class bn.kcv has the following attributes:

- `loss`: a character string, the label of the loss function.
- `mean`: the mean of the values of the loss function computed in the k iterations of the cross-validation, which is printed as the "expected loss" or averaged to compute the "average loss over the runs".
- `bn`: either a character string (the label of the learning algorithm to be applied to the training data in each iteration) or an object of class bn (a fixed network structure).
bn.strength class

Author(s)
Marco Scutari

---

**bn.strength class**  
*The bn.strength class structure*

---

**Description**

The structure of an object of S3 class bn.strength.

**Details**

An object of class bn.strength is a data frame with the following columns (one row for each arc):

- **from,to**: the nodes incident on the arc.
- **strength**: the strength of the arc. See `arc.strength`, `boot.strength`, `custom.strength` and `strength.plot` for details.

and some additional attributes:

- **method**: a character string, the method used to compute the strength coefficients. It can be equal to `test`, `score` or `bootstrap`.
- **threshold**: a numeric value, the threshold used to determine if a strength coefficient is significant.

An optional column called `direction` may also be present, giving the probability of the direction of an arc given its presence in the graph.

Only the `plot()` method is defined for this class; therefore, it can be manipulated as a standard data frame.

**Author(s)**

Marco Scutari
choose.direction

Try to infer the direction of an undirected arc

Description

Check both possible directed arcs for existence, and choose the one with the lowest p-value, the highest score or the highest bootstrap probability.

Usage

choose.direction(x, arc, data, criterion = NULL, ..., debug = FALSE)

Arguments

  x                  an object of class bn.
  arc                a character string vector of length 2, the labels of two nodes of the graph.
  data               a data frame containing the data the Bayesian network was learned from.
  criterion          a character string, the label of a score function, the label of an independence test or bootstrap. See network scores and independence tests for details on the first two possibilities.
  ...                additional tuning parameters for the network score. See score for details.
  debug              a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

If criterion is bootstrap, choose.directions accepts the same arguments as boot.strength(): R (the number of bootstrap replicates), m (the bootstrap sample size), algorithm (the structure learning algorithm), algorithm.args (the arguments to pass to the structure learning algorithm) and cpdag (whether to transform the network structure to the CPDAG representation of the equivalence class it belongs to).

If criterion is a test or a score function, any node connected to one of the nodes in arc by an undirected arc is treated as a parent of that node (with a warning).

Value

choose.direction returns invisibly an updated copy of x.

Author(s)

Marco Scutari

See Also

score, arc.strength.
Examples

```r
data(learning.test)
res <- gs(learning.test)
## the arc A - B has no direction.
choose.direction(res, learning.test, arc = c("A", "B"), debug = TRUE)

## let's see score equivalence in action.
choose.direction(res, learning.test, criterion = "aic",
    arc = c("A", "B"), debug = TRUE)

## arcs which introduce cycles are handled correctly.
res <- set.arc(res, "A", "B")
# now A -> B -> E -> A is a cycle.
choose.direction(res, learning.test, arc = c("E", "A"), debug = TRUE)

## Not run:
choose.direction(res, learning.test, arc = c("D", "E"), criterion = "bootstrap",
    R = 100, algorithm = "iamb", algorithm.args = list(test = "x2"), cpdag = TRUE,
    debug = TRUE)

## End(Not run)
```

---

**ci.test**  
Independence and conditional independence tests

### Description

Perform an independence or a conditional independence test.

### Usage

```r
ci.test(x, y, z, data, test, B, debug = FALSE)
```

### Arguments

- **x**
  - a character string (the name of a variable), a data frame, a numeric vector or a factor object.

- **y**
  - a character string (the name of another variable), a numeric vector or a factor object.

- **z**
  - a vector of character strings (the names of the conditioning variables), a numeric vector, a factor object or a data frame. If NULL an independence test will be executed.

- **data**
  - a data frame containing the variables to be tested.

- **test**
  - a character string, the label of the conditional independence test to be used in the algorithm. If none is specified, the default test statistic is the **mutual information** for categorical variables, the Jonckheere-Terpstra test for ordered factors and the **linear correlation** for continuous variables. See independence tests for details.
ci.test

B a positive integer, the number of permutations considered for each permutation test. It will be ignored with a warning if the conditional independence test specified by the test argument is not a permutation test.

debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Value

An object of class htest containing the following components:

statistic the value the test statistic.

parameter the degrees of freedom of the approximate chi-squared or t distribution of the test statistic; the number of permutations computed by Monte Carlo tests. Semi-parametric tests have both.

p.value the p-value for the test.

method a character string indicating the type of test performed, and whether Monte Carlo simulation or continuity correction was used.

data.name a character string giving the name(s) of the data.

null.value the value of the test statistic under the null hypothesis, always 0.

alternative a character string describing the alternative hypothesis.

Author(s)

Marco Scutari

See Also

choose.direction, arc.strength.

Examples

data(gaussian.test)
data(learning.test)

# using a data frame and column labels.
ci.test(x = "F", y = "B", z = c("C", "D"), data = gaussian.test)
# using a data frame.
ci.test(gaussian.test)
# using factor objects.
attach(learning.test)
ci.test(x = F, y = B, z = data.frame(C, D))
clgaussian.test

Synthetic (mixed) data set to test learning algorithms

Description

This a synthetic data set used as a test case in the bnlearn package.

Usage

data(clgaussian.test)

Format

The clgaussian.test data set contains one normal (Gaussian) variable, 4 discrete variables and 3 conditional Gaussian variables.

Note

The R script to generate data from this network is available from http://www.bnlearn.com/documentation/networks.

Examples

# load the data.
data(clgaussian.test)
# create and plot the network structure.
dag = model2network("[A][B][C][H][D][A:H][F][B:C][E][B:D][G][A:D:E:F]")
## Not run: graphviz.plot(dag)

compare

Compare two or more different Bayesian networks

Description

Compare two different Bayesian networks; compute their Structural Hamming Distance (SHD) or the Hamming distance between their skeletons. Or graphically compare them by plotting them side by side.

Usage

compare(target, current, arcs = FALSE)
## S3 method for class 'bn'
all.equal(target, current, ...)

shd(learned, true, wlbl = FALSE, debug = FALSE)
hamming(learned, true, debug = FALSE)
graphviz.compare(x, ..., groups, layout = "dot", shape = "circle", main = NULL,
sub = NULL, diff = "from-first", diff.args = list())

Arguments

target, learned  an object of class bn.
current, true   another object of class bn.
...            extra arguments from the generic method (for all.equal(), currently ignored); or
               a set of one or more objects of class bn (for graphviz.compare).
wlbl            a boolean value. If TRUE arcs whose directions have been fixed by a whitelist
               or a by blacklist are preserved when constructing the CPDAGs of learned and
               true.
debug          a boolean value. If TRUE a lot of debugging output is printed; otherwise the
               function is completely silent.
archs           a boolean value. See below.
x              an object of class bn.
groups         a list of character vectors, representing groups of node labels of nodes that
               should be plotted close to each other.
layout         a character string, the layout argument that will be passed to Rgraphviz. Possible
               values are dots, neato, twopi, circo and fdp. See Rgraphviz documentation
               for details.
shape          a character string, the shape of the nodes. Can be circle, ellipse or rectangle.
main           a vector of character strings, one for each network. They are plotted at the top
               of the corresponding figure(s).
sub            a vector of character strings, the subtitles that are plotted at the bottom of the
               corresponding figure(s).
diff           a character string, the label of the method used to compare and format the figure(s)
               created by graphviz.compare(). The default value is from-first, see below
               for details.
diff.args      a list of optional arguments to control the formatting of the figure(s) created by
               graphviz.compare(). See below for details.

Details

graphviz.compare() can visualize differences between graphs in various way depending on the
value of the diff and diff.args arguments:

- none: differences are not highlighted.
- from-first: the first bn object, x, is taken as the reference network. All the other networks,
passed via the ... argument, are compared to that first network and their true positive, false
positive, false negative arcs relative to that first network are highlighted. Colours, line types
and line widths for each category of arcs can be specified as the elements of a list via the
diff.args argument, with names tp.col, tp.pty, tp.lwd, fp.col, fp.pty, fp.lwd, fn.col, fn.pty,
tp.lwd. In addition, it is possible not to plot the reference network at all by setting show.first
to FALSE.
Regardless of the visualization, the nodes are arranged to be in the same position for all the networks to make it easier to compare them.

Value

`compare()` returns a list containing the number of true positives (`tp`, the number of arcs in `current` also present in `target`), of false positives (`fp`, the number of arcs in `current` not present in `target`) and of false negatives (`fn`, the number of arcs not in `current` but present in `target`) if `arcs` is `FALSE`; or the corresponding arc sets if `arcs` is `TRUE`.

`all.equal()` returns either `TRUE` or a character string describing the differences between `target` and `current`.

`shd()` and `hamming()` return a non-negative integer number.

`graphviz.compare()` plots one or more figures and returns invisibly a list containing the graph objects produced by `Rgraphviz`.

Note

Note that SHD, as defined in the reference, is defined on CPDAGs; therefore `cpdag()` is called on both `learned` and `true` before computing the distance.

Author(s)

Marco Scutari

References


Examples

```r
data(learning.test)

e1 <- model2network("[A][B][C|A:B][D][E|C][F|A:E]"
)
e2 <- model2network("[A][B][C|A:B][D][E|C:F][F|A]"
)
shd(e2, e1, debug = TRUE)
unlist(compare(e1, e2))
## Not run: graphviz.compare(e1, e2, diff = "none")
```

---

**configs**  
**Construct configurations of discrete variables**

**Description**

Create configurations of discrete variables, which can be used in modelling conditional probability tables.
Usage

```r
congs(data, all = TRUE)
```

Arguments

data: a data frame containing factor columns.
all: a boolean value. If TRUE all configurations are included as levels in the return value; otherwise only configurations which are actually observed are considered.

Value

A factor with one element for each row of `data`, and levels as specified by `all`.

Author(s)

Marco Scutari

Examples

```r
data(learning.test)
congs(learning.test, all = TRUE)
congs(learning.test, all = FALSE)
```

---

**constraint-based algorithms**

*Constraint-based structure learning algorithms*

Description

Learn the equivalence class of a directed acyclic graph (DAG) from data using the PC, Grow-Shrink (GS), Incremental Association (IAMB), Fast Incremental Association (Fast-IAMB), Interleaved Incremental Association (Inter-IAMB), Incremental Association with FDR (IAMB-FDR), Max-Min Parents and Children (MMPC), Semi-Interleaved HITON-PC or Hybrid Parents and Children (HPC) constraint-based algorithms.

Usage

```r
pc.stable(x, cluster = NULL, whitelist = NULL, blacklist = NULL, test = NULL,
          alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE, undirected = FALSE)
gs(x, cluster = NULL, whitelist = NULL, blacklist = NULL, test = NULL,
   alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE, undirected = FALSE)
iamb(x, cluster = NULL, whitelist = NULL, blacklist = NULL, test = NULL,
    alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE, undirected = FALSE)
fast.iamb(x, cluster = NULL, whitelist = NULL, blacklist = NULL, test = NULL,
          alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE, undirected = FALSE)
inter.iamb(x, cluster = NULL, whitelist = NULL, blacklist = NULL, test = NULL,
           alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE, undirected = FALSE)
```
constraint-based algorithms

iam.bdr(x, cluster = NULL, whitelist = NULL, blacklist = NULL, test = NULL, alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE, undirected = FALSE)
mmpc(x, cluster = NULL, whitelist = NULL, blacklist = NULL, test = NULL, alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE, undirected = TRUE)
si.hiton.pc(x, cluster = NULL, whitelist = NULL, blacklist = NULL, test = NULL, alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE, undirected = TRUE)
hpc(x, cluster = NULL, whitelist = NULL, blacklist = NULL, test = NULL, alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE, undirected = TRUE)

Arguments

x a data frame containing the variables in the model.
cluster an optional cluster object from package parallel.
whitelist a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs to be included in the graph.
blacklist a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs not to be included in the graph.
test a character string, the label of the conditional independence test to be used in the algorithm. If none is specified, the default test statistic is the mutual information for categorical variables, the Jonckheere-Terpstra test for ordered factors and the linear correlation for continuous variables. See independence tests for details.
alpha a numeric value, the target nominal type I error rate.
B a positive integer, the number of permutations considered for each permutation test. It will be ignored with a warning if the conditional independence test specified by the test argument is not a permutation test.
max.sx a positive integer, the maximum allowed size of the conditioning sets used in conditional independence tests. The default is that there is no limit on size.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
undirected a boolean value. If TRUE no attempt will be made to determine the orientation of the arcs; the returned (undirected) graph will represent the underlying structure of the Bayesian network.

Value

An object of class bn. See bn-class for details.

Note

Note that even when undirected is set to FALSE there is no guarantee that all arcs in the returned network will be directed; some arc directions are impossible to learn just from data due to score equivalence.

See structure learning for a complete list of structure learning algorithms with the respective references.
**Author(s)**

Marco Scutari

**See Also**

local discovery algorithms, score-based algorithms, hybrid algorithms.

---

**coronary**

*Coronary heart disease data set*

**Description**

Probable risk factors for coronary thrombosis, comprising data from 1841 men.

**Usage**

data(coronary)

**Format**

The coronary data set contains the following 6 variables:

- Smoking (*smoking*): a two-level factor with levels no and yes.
- M. Work (*strenuous mental work*): a two-level factor with levels no and yes.
- P. Work (*strenuous physical work*): a two-level factor with levels no and yes.
- Pressure (*systolic blood pressure*): a two-level factor with levels <140 and >140.
- Proteins (*ratio of beta and alpha lipoproteins*): a two-level factor with levels <3 and >3.
- Family (*family anamnesis of coronary heart disease*): a two-level factor with levels neg and pos.

**Source**


**Examples**

```r
# This is the undirected graphical model from Whittaker (1990).

data(coronary)
ug <- empty.graph(names(coronary))
arcs(ug, check.cycles = FALSE) <- matrix(
  c("Family", "M. Work", "M. Work", "Family",
  "P. Work", "Smoking", "Smoking", "P. Work",
  "Smoking", "Pressure", "Pressure", "Smoking",
  "Pressure", "Proteins", "Proteins", "Pressure"),
  ncol = 2, byrow = TRUE,
  dimnames = list(c(), c("from", "to")))
## Not run: graphviz.plot(ug, shape = "ellipse")
```

---

**Description**

Find the equivalence class and the v-structures of a Bayesian network, construct its moral graph, or create a consistent extension of an equivalent class.

**Usage**

```r
cpdag(x, moral = FALSE, wlbl = FALSE, debug = FALSE)
cextend(x, strict = TRUE, debug = FALSE)
moral(x, debug = FALSE)

colliders(x, arcs = FALSE, debug = FALSE)
shielded.colliders(x, arcs = FALSE, debug = FALSE)
unshielded.colliders(x, arcs = FALSE, debug = FALSE)
vstructs(x, arcs = FALSE, moral = FALSE, debug = FALSE)
```

**Arguments**

- **x**: an object of class `bn` or `bn.fit` (with the exception of `cextend`, which only accepts objects of class `bn`).
- **arcs**: a boolean value. If TRUE the arcs that are part of at least one v-structure are returned instead of the v-structures themselves.
- **moral**: a boolean value. If FALSE we define a v-structure as in Pearl (2000); if TRUE, as in Koller and Friedman (2009). See below.
- **wlbl**: a boolean value. If TRUE arcs whose directions have been fixed by a whitelist or a by blacklist are preserved when constructing the CPDAG.
strict

A boolean value. If no consistent extension is possible and strict is TRUE, an error is generated; otherwise a partially extended graph is returned with a warning.

debug

A boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

What kind of arc configuration is called a v-structure is not uniquely defined in literature. The original definition from Pearl (2000), which is still followed by most texts and papers, states that the two parents in the v-structure must not be connected by an arc. However, Koller and Friedman (2009) call that a immoral v-structure and call a moral v-structure a v-structure in which the parents are linked by an arc. This mirrors the unshielded versus shielded collider naming convention, but it is confusing.

Setting moral to TRUE in cpdag() and vstructs() makes those functions follow the definition from Koller and Friedman (2009); the default value of FALSE, on the other hand, makes those functions follow the definition from Pearl (2000). The former call v-structures both shielded and unshielded colliders (respectively moral v-structures and immoral v-structures); the latter requires v-structures to be unshielded colliders. Hence, the moral argument controls whether moral v-structures (shielded colliders) are returned along with immoral v-structures (unshielded colliders).

Note that arcs whose directions are dictated by the parametric assumptions of conditional linear Gaussian networks are preserved as directed arcs in cpdag().

Value

cpdag() returns an object of class bn, representing the equivalence class. moral on the other hand returns the moral graph. See bn-class for details.

extend() returns an object of class bn, representing a DAG that is the consistent extension of x.

vstructs() returns a matrix with either 2 or 3 columns, according to the value of the arcs argument.

Author(s)

Marco Scutari

References


Examples

data(learning.test)
res <- gs(learning.test)
cpdag(res)
Perform conditional probability queries (CPQs).

Usage

cpquery(fitted, event, evidence, cluster = NULL, method = "ls", ...,
        debug = FALSE)
cpdist(fitted, nodes, evidence, cluster = NULL, method = "ls", ...,
       debug = FALSE)

mutilated(x, evidence)

Arguments

- fitted: an object of class bn.fit.
- x: an object of class bn or bn.fit.
- event, evidence: see below.
- nodes: a vector of character strings, the labels of the nodes whose conditional distribution we are interested in.
- cluster: an optional cluster object from package parallel.
- method: a character string, the method used to perform the conditional probability query. Currently only logic sampling (ls, the default) and likelihood weighting (lw) are implemented.
- ...: additional tuning parameters.
- debug: a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

cpquery estimates the conditional probability of event given evidence using the method specified in the method argument.
cpdist generates random samples conditional on the evidence using the method specified in the method argument.

mutilated constructs the mutilated network arising from an ideal intervention setting the nodes involved to the values specified by evidence. In this case evidence must be provided as a list in the same format as for likelihood weighting (see below).

Note that both cpquery and cpdist are based on Monte Carlo particle filters, and therefore they may return slightly different values on different runs.


Value

cpquery() returns a numeric value, the conditional probability of event() conditional on evidence. cpdist() returns a data frame containing the samples generated from the conditional distribution of the nodes conditional on evidence(). The data frame has class c("bn.cpdist","data.frame"), and a method attribute storing the value of the method argument. In the case of likelihood weighting, the weights are also attached as an attribute called weights.

mutilated returns a bn or bn.fit object, depending on the class of x.

Logic Sampling

The event and evidence arguments must be two expressions describing the event of interest and the conditioning evidence in a format such that, if we denote with data the data set the network was learned from, data[evidence,] and data[event,] return the correct observations. If either event or evidence is set to TRUE an unconditional probability query is performed with respect to that argument.

Three tuning parameters are available:

- n: a positive integer number, the number of random samples to generate from fitted. The default value is $5000 \times \log_{10}(\text{npars}(\text{fitted}))$ for discrete and conditional Gaussian networks and $500 \times \text{npars}(\text{fitted})$ for Gaussian networks.
- batch: a positive integer number, the number of random samples that are generated at one time. Defaults to $10^4$. If the n is very large (e.g. $10^{12}$), R would run out of memory if it tried to generate them all at once. Instead random samples are generated in batches of size batch, discarding each batch before generating the next.
- query.nodes: a vector of character strings, the labels of the nodes involved in event and evidence. Simple queries do not require to generate samples from all the nodes in the network, so cpquery and cpdist try to identify which nodes are used in event and evidence and reduce the network to their upper closure. query.nodes may be used to manually specify these nodes when automatic identification fails; there is no reason to use it otherwise.

Note that the number of samples returned by cpdist() is always smaller than n, because logic sampling is a form of rejection sampling. Therefore, only the observations matching evidence (out of the n that are generated) are returned, and their number depends on the probability of evidence.

Likelihood Weighting

The event argument must be an expression describing the event of interest, as in logic sampling. The evidence argument must be a named list:

- Each element corresponds to one node in the network and must contain the value that node will be set to when sampling.
- In the case of a continuous node, two values can also be provided. In that case, the value for that node will be sampled from a uniform distribution on the interval delimited by the specified values.
- In the case of a discrete or ordinal node, two or more values can also be provided. In that case, the value for that node will be sampled with uniform probability from the set of specified values.
If either event or evidence is set to TRUE an unconditional probability query is performed with respect to that argument.

Tuning parameters are the same as for logic sampling: n, batch and query nodes.

Note that the samples returned by cpdist() are generated from the mutilated network, and need to be weighted appropriately when computing summary statistics (for more details, see the references below). cpquery does that automatically when computing the final conditional probability. Also note that the batch argument is ignored in cpdist for speed and memory efficiency.

### Author(s)

Marco Scutari

### References


### Examples

```r
## discrete Bayesian network (it is the same with ordinal nodes).
data(learning.test)
fitted = bn.fit(hc(learning.test), learning.test)
# the result should be around 0.025.
cpquery(fitted, (B == "b"), (A == "a"))
# programmatically build a conditional probability query...
var = names(learning.test)
obs = 2
str = paste("(", names(learning.test)[-3], " == ",
          sapply(learning.test[obs, -3], as.character), ",")",
          sep = "", collapse = " & ")
str
str2 = paste("(", names(learning.test)[3], " == ",
          as.character(learning.test[obs, 3]), ",")",
          sep = "")
str2

cmd = paste("cpquery(fitted, ", str2, ", ", str, ",")", sep = "")
eval(parse(text = cmd))
# ... but note that predict works better in this particular case.
attr(predict(fitted, "C", learning.test[obs, -3], prob = TRUE), "prob")
# do the same with likelihood weighting.

cpquery(fitted, event = eval(parse(text = str2)),
         evidence = as.list(learning.test[2, -3]), method = "lw")
attr(predict(fitted, "C", learning.test[obs, -3],
       method = "bayes-lw", prob = TRUE), "prob")
# conditional distribution of A given C == "c".
table(cpdist(fitted, "A", (C == "c")))

## Gaussian Bayesian network.
data(gaussian.test)
fitted = bn.fit(hc(gaussian.test), gaussian.test)
```
# the result should be around 0.04.
cpquery(fitted,
  event = ((A >= 0) & (A <= 1)) & ((B >= 0) & (B <= 3)),
  evidence = (C + D < 10))

## ideal interventions and mutilated networks.
mutilated(fitted, evidence = list(F = 42))

---

### ctsdag

**Equivalence classes in the presence of interventions**

#### Description
Generate the partially directed acyclic graph representing the equivalence class of a Bayesian network learned using interventions.

#### Usage
```r
ctsdag(x, exp, learning = FALSE, debug = FALSE)
```

#### Arguments
- `x`: an object of class `bn`, the network from which to compute the PDAG.
- `exp`: a vector of character strings, the labels of the node that are the targets of the interventions. If no targets are provided, `ctsdag()` just reverts to `cpdag()`.
- `learning`: a boolean value. If `TRUE`, interventions, whitelists and blacklists used in learning the structure of `x` will be taken into account in constructing the PDAG. These interventions will be applied in addition to those provided via the `exp` argument.
- `debug`: a boolean value. If `TRUE` a lot of debugging output is printed; otherwise the function is completely silent.

#### Details
`ctsdag()` extends `cpdag()` by incorporating interventions in constructing the partially directed acyclic graph that represents the equivalence class of `x`; it preserves the directions of arcs that are compelled because they are incident on the target nodes specified by the `exp` argument. This assumes do-calculus model of targeted interventions with no unknown side-effects.

It also takes into account prior arc probabilities used in structure learning, ensuring that DAGs are equivalent in posterior probability only if they are equivalent in prior probability. This is not the case for graph priors other than the uniform (`uniform`) and marginal uniform priors (`marginal`, see `bn-class` for details).

#### Value
`ctsdag` returns an object of class `bn`, representing the equivalence class. See `bn-class` for details.
Author(s)

Robert Osazuwa Ness

References


See Also

cpdag, score.

dsep

**Description**

Check whether two nodes are d-separated.

**Usage**

dsep(bn, x, y, z)

**Arguments**

- **bn**: an object of class *bn*.
- **x, y**: a character string, the label of a node.
- **z**: an optional vector of character strings, the label of the (candidate) d-separating nodes. It defaults to the empty set.

**Value**

dsep() returns TRUE if x and y are d-separated by z, and FALSE otherwise.

Author(s)

Marco Scutari
References


Examples

bn = model2network("[A][C|A][B|C]")
dsep(bn, "A", "B", "C")
bn = model2network("[A][C][B:A:C]")
dsep(bn, "A", "B", "C")

---

foreign files utilities

Read and write BIF, NET, DSC and DOT files

Description

Read networks saved from other programs into bn.fit objects, and dump bn and bn.fit objects into files for other programs to read.

Usage

# Old (non-XML) Bayesian Interchange format.
read.bif(file, debug = FALSE)
write.bif(file, fitted)

# Microsoft Interchange format.
read.dsc(file, debug = FALSE)
write.dsc(file, fitted)

# HUGIN flat network format.
read.net(file, debug = FALSE)
write.net(file, fitted)

# Graphviz DOT format.
write.dot(file, graph)

Arguments

file a connection object or a character string.
fitted an object of class bn.fit.
graph an object of class bn or bn.fit.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
gaussian.test

Value

read.bif(), read.dsc() and read.net() return an object of class bn.fit.
write.bif(), write.dsc(), write.net() and write.dot() return NULL invisibly.

Note

All the networks present in the Bayesian Network Repository have associated BIF, DSC and NET files that can be imported with read.bif(), read.dsc() and read.net().
HUGIN can import and export NET files; Netica can read (but not write) DSC files; and GeNIe can read and write both DSC and NET files.
DOT files can be read by Graphviz, Gephi and a variety of other programs.
Please note that these functions work on a “best effort” basis, as the parsing of these formats have been implemented by reverse engineering the file format from publicly available examples.

Author(s)

Marco Scutari

References


| gaussian.test                        | Synthetic (continuous) data set to test learning algorithms |

Description

This a synthetic data set used as a test case in the bnlearn package.

Usage

data(gaussian.test)

Format

The gaussian.test data set contains seven normal (Gaussian) variables.

Note

The R script to generate data from this network is available from http://www.bnlearn.com/documentation/networks.
Examples

```r
# load the data.
data(gaussian.test)
# create and plot the network structure.
dag = model2network("A|B|E|G|C|A:B|D|B|F|A:D:E:G")
## Not run: graphviz.plot(dag)
```

---

### gRain integration

import and export networks from the gRain package

---

Description

Convert `bn.fit` objects to `grain` objects and vice versa.

Usage

```r
## S3 method for class 'grain'
as.bn.fit(x, including.evidence = FALSE, ...)
## S3 method for class 'bn.fit'
as.grain(x)
## S3 method for class 'grain'
as.bn(x, ...)
```

Arguments

- **x**: an object of class `grain(code)` (for `as.bn.fit`) or `bn.fit()` (for `as.grain`).
- **including.evidence**: a boolean value. If `FALSE`, the `grain` object is converted without considering any evidence that has been set into it. If `TRUE`, any hard evidence is carried over into the `bn.fit` object as a zero-one probability distribution.
- **...**: extra arguments from the generic method (currently ignored).

Value

An object of class `grain` (for `as.grain`), `bn.fit` (for `as.bn.fit`) or `bn` (for `as.bn`).

Note

Conditional probability tables in `grain` objects must be completely specified; on the other hand, `bn.fit` allows `NaN` values for unobserved parents’ configurations. Such `bn.fit` objects will be converted to `$m$ codegrain objects by replacing the missing conditional probability distributions with uniform distributions.

Another solution to this problem is to fit another `bn.fit` with `method = "bayes"` and a low `iss` value, using the same data and network structure.

Ordinal nodes will be treated as categorical by `as.grain`, disregarding the ordering of the levels.
Author(s)
Marco Scutari

Examples
```r
## Not run:
library(gRain)
a <- bn.fit(hc(learning.test), learning.test)
b <- as.grain(a)
c <- as.bn.fit(b)
## End(Not run)
```

description

Count directed acyclic graphs of various sizes with specific characteristics.

Usage

```r
count.graphs(type = "all.dags", nodes, ..., debug = FALSE)
```

Arguments

type a character string, the label describing the types of graphs to be counted (see below).

nodes a vector of positive integers, the graph sizes as given by the numbers of nodes.

... additional parameters (see below).

debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent. Ignored in some generation methods.

Details

The types of graphs, and the associated additional parameters, are:

- all-dags: all directed acyclic graphs.
- dags-given-ordering: all directed acyclic graphs with a specific topological ordering.
- dags-with-k-roots: all directed acyclic graphs with k root nodes.
- dags-with-r-arcs: all directed acyclic graphs with r arcs.

Value

`count.graphs()` returns an objects of class `bigz` from the `gmp` package, a vector with the graph counts.
graph generation utilities

Author(s)
Marco Scutari

References

Examples
```r
## Not run:
count.graphs("dags.with.r.arcs", nodes = 3:6, r = 2)
## End(Not run)
```

---

graph generation utilities

*Generate empty or random graphs*

Description
Generate empty or random directed acyclic graphs from a given set of nodes.

Usage
```r
empty.graph(nodes, num = 1)
random.graph(nodes, num = 1, method = "ordered", ..., debug = FALSE)
```

Arguments
- **nodes**
  - a vector of character strings, the labels of the nodes.
- **num**
  - an integer, the number of graphs to be generated.
- **method**
  - a character string, the label of a score. Possible values are ordered (full ordering based generation), ic-dag (Ide’s and Cozman’s Generating Multi-connected DAGs algorithm), melancon (Melancon’s and Philippe’s Uniform Random Acyclic Digraphs algorithm) and empty (generates empty graphs).
- **...**
  - additional tuning parameters (see below).
- **debug**
  - a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent. Ignored in some generation methods.
Details

Available graph generation algorithms are:

- **full ordering** based generation (ordered): generates graphs whose node ordering is given by the order of the labels in the nodes argument. The same algorithm is used in the randomDAG function in package pcalg.
- Ide’s and Cozman’s *Generating Multi-connected DAGs* algorithm (ic-dag): generates graphs with a uniform probability distribution over the set of multiconnected graphs.
- Melancon’s and Philippe’s *Uniform Random Acyclic Digraphs* algorithm (melancon): generates graphs with a uniform probability distribution over the set of all possible graphs.
- **empty graphs** (empty): generates graphs without any arc.

Additional arguments for the random.graph function are:

- prob: the probability of each arc to be present in a graph generated by the ordered algorithm. The default value is \(2 / (\text{length}(\text{nodes}) - 1)\), which results in a sparse graph (the number of arcs should be of the same order as the number of nodes).
- burn.in: the number of iterations for the ic-dag and melancon algorithms to converge to a stationary (and uniform) probability distribution. The default value is \(6 * \text{length}(\text{nodes})^2\).
- every: return only one graph every number of steps instead of all the graphs generated with ic-dag and melancon. Since both algorithms are based on Markov Chain Monte Carlo approaches, high values of every result in a more diverse set of networks. The default value is 1, i.e. to return all the networks that are generated.
- max.degree: the maximum degree for any node in a graph generated by the ic-dag and melancon algorithms. The default value is Inf.
- max.in.degree: the maximum in-degree for any node in a graph generated by the ic-dag and melancon algorithms. The default value is Inf.
- max.out.degree: the maximum out-degree for any node in a graph generated by the ic-dag and melancon algorithms. The default value is Inf.

Value

Both empty.graph() and random.graph() return an object of class bn (if n is equal to 1) or a list of objects of class bn (otherwise). If every is greater than 1, random.graph always returns a list, regardless of the number of graphs it contains.

Author(s)

Marco Scutari

References


Examples

```r
empty.graph(LETTERS[1:8])
random.graph(LETTERS[1:8])
plot(random.graph(LETTERS[1:8], method = "ic-dag", max.in.degree = 2))
plot(random.graph(LETTERS[1:8]))
plot(random.graph(LETTERS[1:8], prob = 0.2))
```

---

**graph integration**

Import and export networks from the graph package

---

**Description**

Convert bn and bn.fit objects to graphNEL and graphAM objects and vice versa.

**Usage**

```r
## S3 method for class 'graphNEL'
as.bn(x, ..., check.cycles = TRUE)
## S3 method for class 'graphAM'
as.bn(x, ..., check.cycles = TRUE)
## S3 method for class 'bn'
as.graphNEL(x)
## S3 method for class 'bn.fit'
as.graphNEL(x)
## S3 method for class 'bn'
as.graphAM(x)
## S3 method for class 'bn.fit'
as.graphAM(x)
```

**Arguments**

- `x` an object of class bn, bn.fit, graphNEL, graphAM.
- `...` extra arguments from the generic method (currently ignored).
- `check.cycles` a boolean value. If FALSE the returned network will not be checked for cycles.

**Value**

An object of the relevant class.

**Author(s)**

Marco Scutari
graph utilities

Examples

```r
## Not run:
library(graph)
a <- bn.fit(hc(learning.test), learning.test)
b <- as.graphNEL(a)
c <- as.bn(b)
## End(Not run)
```

Description

Utilities to manipulate graphs

Usage

```r
# check whether the graph is acyclic/completely directed.
acyclic(x, directed = FALSE, debug = FALSE)
directed(x)

# check whether there is a path between two nodes.
path.exists(x, from, to, direct = TRUE, underlying.graph = FALSE, debug = FALSE)

# deprecated alias of path.exists().
## S4 method for signature 'bn'
path(object, from, to, direct = TRUE, underlying.graph = FALSE, debug = FALSE)

## S4 method for signature 'bn.fit'
path(object, from, to, direct = TRUE, underlying.graph = FALSE, debug = FALSE)

# build the skeleton or a complete orientation of the graph.
skeleton(x)
pdag2dag(x, ordering)

# build a subgraph spanning a subset of nodes.
subgraph(x, nodes)
```

Arguments

- `x, object` an object of class `bn`. `skeleton()`, `acyclic()`, `directed()`, `path.exists()` and `path()` also accept objects of class `bn.fit`.
- `from` a character string, the label of a node.
- `to` a character string, the label of a node (different from `from`).
- `direct` a boolean value. If `FALSE` ignore any arc between `from` and `to` when looking for a path.
- `underlying.graph` a boolean value. If `TRUE` the underlying undirected graph is used instead of the (directed) one from the `x` argument.
ordering

the labels of all the nodes in the graph; their order is the node ordering used to set the direction of undirected arcs.

nodes

the labels of the nodes that induce the subgraph.

directed

a boolean value. If TRUE only completely directed cycles are considered; otherwise undirected arcs will also be considered and treated as arcs present in both directions.

debug

a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Value

acyclic(), path() and directed() return a boolean value.
skeleton(), pdag2dag() and subgraph() return an object of class bn.

Author(s)

Marco Scutari

References


Examples

data(learning.test)
res <- gs(learning.test)

acyclic(res)
directed(res)
res <- pdag2dag(res, ordering = LETTERS[1:6])
res
directed(res)
skeleton(res)

Description

Plot a Bayesian network as a graph whose nodes are barplots representing the marginal probability distributions of the corresponding variables. Requires the *Rgraphviz* and *gRain* packages.

Usage

graphviz.chart(x, type = "barchart", layout = "dot", draw.levels = TRUE,
grid = FALSE, scale = c(0.75, 1.1), col = "black", bg = "transparent",
text.col = "black", bar.col = "black", strip.bg = bg, main = NULL,
sub = NULL)
Arguments

x an object of class bn.fit representing a discrete Bayesian network.

type a character string, the type of graph used to plot the probability distributions in the nodes. Possible values are barchart, dotplot and barprob (a barchart with probabilities printed over the bars).

layout a character string, the layout argument that will be passed to Rgraphviz. Possible values are dots, neato, twopi, circo and fdp. See Rgraphviz documentation for details.

draw.levels a boolean value, whether to print the labels of the levels of each variable.

grid a boolean value, whether to draw to a reference grid for the probability distributions. If grid is TRUE, a vertical grid is drawn at probabilities c(0,0.25, 0.50,0.75). If grid is a numeric vector, a vertical grid is drawn at the specified probabilities.

scale a vector of two positive numbers, used by Rgraphviz to determine the size and the aspect ratio of the nodes.

col, bg, text.col, bar.col, strip.bg the colours of the node border, of the barchart background, of the text, of the bars and of the strip background.

main a character string, the main title of the graph. It’s plotted at the top of the graph.

sub a character string, a subtitle which is plotted at the bottom of the graph.

Value

graphviz.chart() invisibly returns NULL.

Author(s)

Marco Scutari

Examples

```r
## Not run:
modelstring = paste("[HIST|LVE][CVP|LVV][PCWP|LVV][HYP|LVV][HYP|LVF][LVF]",
"[STK|HYP:LVF][ERLO][HRBP][ERLO:HR][HREK][ERCA:HR][ERCA][HRSA][ERCA:HR][ALES]",
"[APL][TPR][APL][ECO2][ACO2:VLAN][KINK][MINV][INT:VLNG][FIO2][FIO2:VALV]",
"[SAO2][PVS:SHNT][PAP][PMB][PMB][SHNT][INT:PMB][INT][FRSS][INT-KINK:VTUB][DISC]",
"[MVS][VCMCH][MVS][VTUB][DISC:VMCH][VLNG][INT:KINK:VTUB][VALV][INT:VLNG][ACO2][VALV]",
"[CCHL][ACO2][ANES:SAO2:TPR][HR][CCHL][CO][HR:STKV][BP][CO:TPR]", sep = " "
)
dag = model2network(modelstring)
fitted = bn.fit(dag, alarm)
```

```r
# Netica style.
graphviz.chart(fitted, grid = TRUE, bg = "beige", bar.col = "black")
```

```r
# Hugin style.
graphviz.chart(fitted, type = "barprob", grid = TRUE, bar.col = "green",
strip.bg = "LightYellow")
```

```r
# GeNi style.
graphviz.chart(fitted, col = "darkblue", bg = "azure", bar.col = "darkblue")
```
personal favourites.

```r
graphviz.plot

# dot-plot version.

## End(Not run)
```

---

**graphviz.plot**

**Advanced Bayesian network plots**

---

**Description**

Plot the graph associated with a Bayesian network using the **Rgraphviz** package.

**Usage**

```r
graphviz.plot(x, highlight = NULL, groups, layout = "dot", shape = "circle", main = NULL, sub = NULL, render = TRUE)
```

**Arguments**

- `x` an object of class `bn` or `bn.fit`.
- `highlight` a list, see below.
- `groups` a list of character vectors, representing groups of node labels of nodes that should be plotted close to each other.
- `layout` a character string, the layout argument that will be passed to **Rgraphviz**. Possible values are dots, neato, twopi, circo and fdp. See **Rgraphviz** documentation for details.
- `shape` a character string, the shape of the nodes. Can be circle, ellipse or rectangle.
- `main` a character string, the main title of the graph. It’s plotted at the top of the graph.
- `sub` a character string, a subtitle which is plotted at the bottom of the graph.
- `render` a logical value. If TRUE, `graphviz.plot()` actually draws the figure in addition to returning the corresponding graph object. If FALSE, no figure is produced.

**Details**

The `highlight` argument is a list with at least one of the following elements:

- `nodes`: a character vector, the labels of the nodes to be highlighted.
- `arcs`: the arcs to be highlighted (a two-column matrix, whose columns are labeled from and to).

and optionally one or more of the following graphical parameters:
hailfinder

• col: an integer or character string (the highlight colour for the arcs and the node frames). The default value is red.
• textCol: an integer or character string (the highlight colour for the labels of the nodes). The default value is black.
• fill: an integer or character string (the colour used as a background colour for the nodes). The default value is white.
• lwd: a positive number (the line width of highlighted arcs). It overrides the line width settings in strength.plot(). The default value is to use the global settings of Rgraphviz.
• lty: the line type of highlighted arcs. Possible values are 0, 1, 2, 3, 4, 5, 6, "blank", "solid", "dashed", "dotted", "dotdash", "longdash" and "twodash". The default value is to use the global settings of Rgraphviz.

Value

graphviz.plot() returns invisibly the graph object produced by Rgraphviz. It can be further modified using the commands present in the graph and Rgraphviz packages.

Author(s)
Marco Scutari

See Also
plot.bn.

hailfinder The HailFinder weather forecast system (synthetic) data set

Description
Hailfinder is a Bayesian network designed to forecast severe summer hail in northeastern Colorado.

Usage
data(hailfinder)

Format
The hailfinder data set contains the following 56 variables:

• N07nuVerMo (10.7nu vertical motion): a four-level factor with levels StrongUp, WeakUp, Neutral and Down.
• SubjVertMo (subjective judgment of vertical motion): a four-level factor with levels StrongUp, WeakUp, Neutral and Down.
• QGVertMotion (quasigeostrophic vertical motion): a four-level factor with levels StrongUp, WeakUp, Neutral and Down.
• **CombVerMo** (*combined vertical motion*): a four-level factor with levels StrongUp, WeakUp, Neutral and Down.
• **AreaMesoALS** (*area of meso-alpha*): a four-level factor with levels StrongUp, WeakUp, Neutral and Down.
• **SatContMoist** (*satellite contribution to moisture*): a four-level factor with levels VeryWet, Wet, Neutral and Dry.
• **RaoContMoist** (*reading at the forecast center for moisture*): a four-level factor with levels VeryWet, Wet, Neutral and Dry.
• **CombMoisture** (*combined moisture*): a four-level factor with levels VeryWet, Wet, Neutral and Dry.
• **AreaMoDryAir** (*area of moisture and dry air*): a four-level factor with levels VeryWet, Wet, Neutral and Dry.
• **VISCloudCo v** (*visible cloud cover*): a three-level factor with levels Cloudy, PC and Clear.
• **IRCloudCover** (*infrared cloud cover*): a three-level factor with levels Cloudy, PC and Clear.
• **CombClouds** (*combined cloud cover*): a three-level factor with levels Cloudy, PC and Clear.
• **CldShadeOth** (*cloud shading, other*): a three-level factor with levels Cloudy, PC and Clear.
• **AMInstabMt** (*AM instability in the mountains*): a three-level factor with levels None, Weak and Strong.
• **InsInMt** (*instability in the mountains*): a three-level factor with levels None, Weak and Strong.
• **WndHodograph** (*wind hodograph*): a four-level factor with levels DCVZFavor, StrongWest, Westerly and Other.
• **OutflowFrMt** (*outflow from mountains*): a three-level factor with levels None, Weak and Strong.
• **MorningBound** (*morning boundaries*): a three-level factor with levels None, Weak and Strong.
• **Boundaries** (*boundaries*): a three-level factor with levels None, Weak and Strong.
• **CldShadeConv** (*cloud shading, convection*): a three-level factor with levels None, Some and Marked.
• **CompPlF cst** (*composite plains forecast*): a three-level factor with levels IncCapDecIns, LittleChange and DecCapIncIns.
• **CapChange** (*capping change*): a three-level factor with levels Decreasing, LittleChange and Increasing.
• **LoLevMoistAd** (*low-level moisture advection*): a four-level factor with levels StrongPos, WeakPos, Neutral and Negative.
• **InsChange** (*instability change*): three-level factor with levels Decreasing, LittleChange and Increasing.
• **MountainF cst** (*mountains (region 1) forecast*): a three-level factor with levels XNIL, SIG and SVR.
• **Date** (*date*): a six-level factor with levels May15_Jun14, Jun15_Jul1, Jul2_Jul15, Jul16_Aug10, Aug11_Aug20 and Aug20_Sep15.
• **Scenario (scenario):** an eleven-level factor with levels A, B, C, D, E, F, G, H, I, J and K.
• **Scenario relevant to AM convective inhibition (Scenario relevant to AM convective inhibition):** a two-level factor with levels AB and CThruK.
• **Morning convective inhibition (morning convective inhibition):** a four-level factor with levels None, PartInhibit, Stiffing and TotalInhibit.
• **AM convective inhibition in scenario (AM convective inhibition in scenario):** a three-level factor with levels LessThanAve, Average and MoreThanAve.
• **Capping within scenario (capping within scenario):** a three-level factor with levels LessThanAve, Average and MoreThanAve.
• **Scenario relevant to AM instability (scenario relevant to AM instability):** a six-level factor with levels ABI, CDEJ, F, G, H and K.
• **LI from 12Z DEN sounding (LI from 12Z DEN sounding):** a four-level factor with levels LIGt0, N1GtLIGt_4, N5GtLIGt_8 and LILT_8.
• **AM dewpoint calculations, plains (AM dewpoint calculations, plains):** a three-level factor with levels Instability, Neutral and Stability.
• **AM instability within scenario (AM instability within scenario):** a three-level factor with levels LessUnstable, Average and MoreUnstable.
• **Instability scaling within scenario (instability scaling within scenario):** a three-level factor with levels LessUnstable, Average and MoreUnstable.
• **Scenario relevant to regions 2/3/4 (scenario relevant to regions 2/3/4):** a five-level factor with levels A CEFK, B, D, GJ and HI.
• **Latest convective inhibition (latest convective inhibition):** a four-level factor with levels None, PartInhibit, Stiffing and TotalInhibit.
• **LLIW (LLIW severe weather index):** a four-level factor with levels Unfavorable, Weak, Moderate and Strong.
• **Current propensity to convection (current propensity to convection):** a four-level factor with levels None, Slight, Moderate and Strong.
• **Scenario relevant to plains forecast (scenario relevant to plains forecast):** an eleven-level factor with levels A, B, C, D, E, F, G, H, I, J and K.
• **Plains forecast (plains forecast):** a three-level factor with levels XNIL, SIG and SVR.
• **Regions 2/3/4 forecast (regions 2/3/4 forecast):** a three-level factor with levels XNIL, SIG and SVR.
• **Region 5 forecast (region 5 forecast):** a three-level factor with levels XNIL, SIG and SVR.
• **Dewpoints (dewpoints):** a seven-level factor with levels LowEverywhere, LowAtStation, LowSHighN, LowNHighS, LowMtsHighPl, HighEverywhere, Other.
• **Low level lapse rate (low-level lapse rate):** a four-level factor with levels CloseToDryAd, Steep, ModerateOrLe and Stable.
• **Mean relative humidity (mean relative humidity):** a three-level factor with levels VeryMoist, Average and Dry.
• **Mid-level lapse rate (mid-level lapse rate):** a three-level factor with levels CloseToDryAd, Steep and ModerateOrLe.
• **Movement of features (movement of features):** a four-level factor with levels StrongFront, MarkedUpper, OtherRapid and NoMajor.
• **RHRatio** (relative humidity ratio): a three-level factor with levels MoistMDryL, DryMMoistL and other.

• **SfcWndShfDis** (surface wind shifts and discontinuities): a seven-level factor with levels DenvCyclone, E_W_N, E_W_S, MovigFtorOt, DryLine, None and Other.

• **SynForcng** (synoptic forcing): a five-level factor with levels SigNegative, NegToPos, SigPositive, PosToNeg and LittleChange.

• **TempDis** (temperature discontinuities): a four-level factor with levels QStationary, Moving, None, Other.

• **WindAloft** (wind aloft): a four-level factor with levels LV, SWQuad, NWQuad, AllElse.

• **WindFieldMt** (wind fields, mountains): a two-level factor with levels Westerly and LVorOther.

• **WindFieldPln** (wind fields, plains): a six-level factor with levels LV, DenvCyclone, LongAnticyc, E_NE, SEquad and WidespdDnsl.

**Note**

The complete BN can be downloaded from [http://www.bnlearn.com/bnrepository](http://www.bnlearn.com/bnrepository).

**Source**


**Examples**

```r
# load the data.
data(hailfinder)
# create and plot the network structure.
modelstring <- paste0("[N07mnVerMo]|[SubjVertMo]|[QGVertMotion]|[SatContMoist]|[RaoContMoist]", 
                     "[MorningCIN]|[Lfr12ZDEN3d]|[AMDewptCalPI]|[LatestCIN]|[LLIW]", 
                     "[CombVerMo]|[N07mnVerMo]|[SubjVertMo]|[QGVertMotion]|[CombMoisture]|[SatContMoist]|[RaoContMoist]", 
                     "[AreaMesoALS]|[CombVerMo]|[ScenRelA|MCIN]|[Scenario]|[ScenRelAMins]|[Scenario]|[ScenRelB34|Scenario]", 
                     "[ScenRelPIFcst|Scenario]|[Dewpoints|Scenario]|[LawLLapse|Scenario]|[MeanRH|Scenario]", 
                     "[MidLLapse|Scenario]|[MovtFeatures|Scenario]|[RHRatio|Scenario]|[SfcWndShfDis|Scenario]", 
                     "[SynForcng|Scenario]|[TempDis|Scenario]|[WindAloft|Scenario]|[WindFieldMt|Scenario]", 
                     "[WindFieldPln|Scenario]|[AreaMoDryAir|AreaMesoALS]|[CombMoisture]", 
                     "[AMCINInScen|ScenRelAMCIN|MorningCIN]|[AMInsWliScen|ScenRelAMIns|Lfr12ZDEN3d]|[AMDewptCalPI]", 
                     "[CldShadeOth|AreaMesoALS]|[AreaMoDryAir|CombClouds]|[InsInMt|CldShadeOth|AMInstabMt]", 
                     "[OutflowFrMt|InsInMt|WindHodograph]|[CldShadeConv|InsInMt|WindHodograph]|[MountainFest|InsInMt]", 
                     "[Boundaries|WindHodograph]|[OutflowFrMt|MorningBound]|[N34StarFcst|ScenRelB34|PlainsFcst]", 
                     "[CompPlFcst|AreaMesoALS]|[CldShadeOth|Boundaries|CldShadeConv]|CapChange|CompPlFcst]", 
                     "[InsChange|CompPlFcst]|LoLevMoistAd]|CapInScen|CapChange|AMCINInScen]", 
                     "[InsScInScen|InsChange|AmMsWhScen]|[R5Fcst|MountainFest|N34StarFcst]", 
                     "[PlainsFcst|CapInScen|InsScInScen|CurPropConv|ScnRelPlFcst]"
)
dag <- modelnetwork(modelstring)
## Not run: graphviz.plot(dag, shape = "ellipse")
hybrid algorithms

Hybrid structure learning algorithms

Description

Learn the structure of a Bayesian network with Max-Min Hill Climbing (MMHC), Hybrid HPC (H2PC), and the more general 2-phase Restricted Maximization (RSMAX2) hybrid algorithms.

Usage

```r
rsmax2(x, whitelist = NULL, blacklist = NULL, restrict = "si.hiton.pc", maximize = "hc", restrict.args = list(), maximize.args = list(), debug = FALSE)
mmhc(x, whitelist = NULL, blacklist = NULL, restrict.args = list(), maximize.args = list(), debug = FALSE)
h2pc(x, whitelist = NULL, blacklist = NULL, restrict.args = list(), maximize.args = list(), debug = FALSE)
```

Arguments

- `x`: a data frame containing the variables in the model.
- `whitelist`: a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs to be included in the graph.
- `blacklist`: a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs not to be included in the graph.
- `restrict`: a character string, the constraint-based or local search algorithm to be used in the "restrict" phase. See structure learning and the documentation of each algorithm for details.
- `maximize`: a character string, the score-based algorithm to be used in the "maximize" phase. Possible values are `hc` and `tabu`. See structure learning for details.
- `restrict.args`: a list of arguments to be passed to the algorithm specified by `restrict`, such as `test` or `alpha`.
- `maximize.args`: a list of arguments to be passed to the algorithm specified by `maximize`, such as `restart` for hill-climbing or `tabu` for tabu search.
- `debug`: a boolean value. If `TRUE` a lot of debugging output is printed; otherwise the function is completely silent.

Value

An object of class `bn`. See `bn-class` for details.

Note

- `mmhc()` is simply `rsmax2()` with `restrict` set to `mmpc` and `maximize` set to `hc`. Similarly, `h2pc` is simply `rsmax2()` with `restrict` set to `hp` and `maximize` set to `hc`.
- See structure learning for a complete list of structure learning algorithms with the respective references.
igraph integration

Import and export networks from the igraph package

Author(s)

Marco Scutari

See Also

local discovery algorithms, score-based algorithms, constraint-based algorithms.

Description

Convert bn and bn.fit objects to igraph and vice versa.

Usage

## S3 method for class 'igraph'
as.bn(x, ..., check.cycles = TRUE)
## S3 method for class 'bn'
as.igraph(x, ...)
## S3 method for class 'bn.fit'
as.igraph(x, ...)

Arguments

x an object of class bn, bn.fit, or igraph.

... extra arguments from the generic method (currently ignored).

check.cycles a boolean value. If FALSE the returned network will not be checked for cycles.

Value

An object of the relevant class.

Author(s)

Marco Scutari

Examples

## Not run:
a <- bn.fit(hc(learning.test), learning.test)
b <- as.igraph(a)
plot(b, edge.arrow.mode = 2L * igraph::which.mutual(b))
c <- as.bn(b)
## End(Not run):
**impute**  
*Predict or impute missing data from a Bayesian network*

**Description**
Impute missing values in a data set or predict a variable from a Bayesian network.

**Usage**
```r
## S3 method for class 'bn.fit'
predict(object, node, data, method = "parents", ..., prob = FALSE, debug = FALSE)
```
```r
impute(object, data, method, ..., debug = FALSE)
```

**Arguments**
- `object`: an object of class `bn.fit` for `impute`; or an object of class `bn` or `bn.fit` for `predict`.
- `data`: a data frame containing the data to be imputed. Complete observations will be ignored.
- `node`: a character string, the label of a node.
- `method`: a character string, the method used to impute the missing values or predict new ones. The default value is `parents`.
- `...`: additional arguments for the imputation method. See below.
- `prob`: a boolean value. If TRUE and `object` is a discrete network, the probabilities used for prediction are attached to the predicted values as an attribute called `prob`.
- `debug`: a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

**Details**
`predict()` returns the predicted values for `node` given the data specified by `data` and the fitted network. Depending on the value of `method`, the predicted values are computed as follows.

- **parents**: the predicted values are computed by plugging in the new values for the parents of `node` in the local probability distribution of `node` extracted from fitted.
- **bayes-lw**: the predicted values are computed by averaging likelihood weighting simulations performed using all the available nodes as evidence (obviously, with the exception of the node whose values we are predicting). The number of random samples which are averaged for each new observation is controlled by the `n` optional argument; the default is 500. If the variable being predicted is discrete, the predicted level is that with the highest conditional probability. If the variable is continuous, the predicted value is the expected value of the conditional distribution. The variables that are used to compute the predicted values can be...
specified with the from optional argument; the default is to use all the relevant variables from the data. Note that the predicted values will differ in each call to predict() since this method is based on a stochastic simulation.

impute() is based on predict(), and can impute missing values with the same methods (parents and bayes-lw). The latter can take an additional argument n with the number of random samples which are averaged for each observation. As in predict(), imputed values will differ in each call to impute() when method is set to bayes-lw.

If object contains NA parameter estimates (because of unobserved discrete parents configurations in the data the parameters were learned from), predict will predict NAs when those parents configurations appear in data. See bn.fit for details on how to make sure bn.fit objects contain no NA parameter estimates.

Value

predict() returns a numeric vector (for Gaussian and conditional Gaussian nodes), a factor (for categorical nodes) or an ordered factor (for ordinal nodes). If prob = TRUE and the network is discrete, the probabilities used for prediction are attached to the predicted values as an attribute called prob.

impute() returns a data frame with the same structure as data.

Note

Ties in prediction are broken using Bayesian tie breaking, i.e. sampling at random from the tied values. Therefore, setting the random seed is required to get reproducible results.

Classifiers have a separate predict() method, see naive.bayes.

Author(s)

Marco Scutari

Examples

# missing data imputation.
with.missing.data <- gaussian.test
with.missing.data[sample(nrow(with.missing.data), 500), "F"] <- NA
fitted <- bn.fit(model2network("[A][B][E][G][C|A:B][D|B][F|A:D:E:G]"),
                 gaussian.test)
imputed <- impute(fitted, with.missing.data)

# predicting a variable in the test set.
training <- bn.fit(model2network("[A][B][E][G][C|A:B][D|B][F|A:D:E:G]"),
                   gaussian.test[1:2000, ])
test <- gaussian.test[nrow(gaussian.test), ]
predicted <- predict(training, node = "F", data = test)

# obtain the conditional probabilities for the values of a single variable
# given a subset of the rest, they are computed to determine the predicted
# values.
fitted <- bn.fit(model2network("[A][C][F][B][A][D|A:C][E:B:F]"), learning.test)
independence-tests

evidence <- data.frame(A = factor("a", levels = levels(learning.test$A)),
                       F = factor("b", levels = levels(learning.test$F)))
predicted <- predict(fitted, "C", evidence,
                      method = "bayes-fw", prob = TRUE)
attr(predicted, "prob")

independence-tests

Conditional independence tests

Description
Overview of the conditional independence tests implemented in bnlearn, with the respective reference publications.

Details
Unless otherwise noted, the reference publication for conditional independence tests is:

Additionally for continuous permutation tests:

and for semiparametric discrete tests:

Available conditional independence tests (and the respective labels) for discrete Bayesian networks (categorical variables) are:

- **mutual information**: an information-theoretic distance measure. It’s proportional to the log-likelihood ratio (they differ by a $2n$ factor) and is related to the deviance of the tested models. The asymptotic $\chi^2$ test (mi and mi-adf, with adjusted degrees of freedom), the Monte Carlo permutation test (mc-mi), the sequential Monte Carlo permutation test (smc-mi), and the semiparametric test (sp-mi) are implemented.

- **shrinkage estimator** for the **mutual information** (mi-sh): an improved asymptotic $\chi^2$ test based on the James-Stein estimator for the mutual information.


- **Pearson’s $X^2$**: the classical Pearson’s $X^2$ test for contingency tables. The asymptotic $\chi^2$ test (x2 and x2-adf, with adjusted degrees of freedom), the Monte Carlo permutation test (mc-x2), the sequential Monte Carlo permutation test (smc-x2) and semiparametric test (sp-x2) are implemented.

Available conditional independence tests (and the respective labels) for discrete Bayesian networks (ordered factors) are:
• Jonckheere-Terpstra: a trend test for ordinal variables. The asymptotic normal test (jt), the Monte Carlo permutation test (mc-jt) and the sequential Monte Carlo permutation test (smc-jt) are implemented.

Available conditional independence tests (and the respective labels) for Gaussian Bayesian networks (normal variables) are:

- **linear correlation**: Pearson’s linear correlation. The exact Student’s t test (cor), the Monte Carlo permutation test (mc-cor) and the sequential Monte Carlo permutation test (smc-cor) are implemented.

- **Fisher’s Z**: a transformation of the linear correlation with asymptotic normal distribution. The asymptotic normal test (zf), the Monte Carlo permutation test (mc-zf) and the sequential Monte Carlo permutation test (smc-zf) are implemented.

- **mutual information**: an information-theoretic distance measure. Again it is proportional to the log-likelihood ratio (they differ by a \(2/n\) factor). The asymptotic \(\chi^2\) test (mi-g), the Monte Carlo permutation test (mc-mi-g) and the sequential Monte Carlo permutation test (smc-mi-g) are implemented.

- **shrinkage estimator** for the mutual information (mi-g-sh): an improved asymptotic \(\chi^2\) test based on the James-Stein estimator for the mutual information.


Available conditional independence tests (and the respective labels) for hybrid Bayesian networks (mixed discrete and normal variables) are:

- **mutual information**: an information-theoretic distance measure. Again it is proportional to the log-likelihood ratio (they differ by a \(2/n\) factor). Only the asymptotic \(\chi^2\) test (mi-cg) is implemented.

### insurance

**Insurance evaluation network (synthetic) data set**

**Description**

Insurance is a network for evaluating car insurance risks.

**Usage**

data(insurance)

**Format**

The `insurance` data set contains the following 27 variables:

- **GoodStudent** *(good student)*: a two-level factor with levels False and True.
- **Age** *(age)*: a three-level factor with levels Adolescent, Adult and Senior.
• SocioEcon (socio-economic status): a four-level factor with levels Prole, Middle, UpperMiddle and Wealthy.
• RiskAversion (risk aversion): a four-level factor with levels Psychopath, Adventurous, Normal and Cautious.
• VehicleYear (vehicle age): a two-level factor with levels Current and older.
• ThisCarDam (damage to this car): a four-level factor with levels None, Mild, Moderate and Severe.
• RuggedAuto (ruggedness of the car): a three-level factor with levels EggShell, Football and Tank.
• Accident (severity of the accident): a four-level factor with levels None, Mild, Moderate and Severe.
• MakeModel (car’s model): a five-level factor with levels SportsCar, Economy, FamilySedan, Luxury and SuperLuxury.
• DrivQuality (driving quality): a three-level factor with levels Poor, Normal and Excellent.
• Mileage (mileage): a four-level factor with levels FiveThou, TwentyThou, FiftyThou and Domino.
• AntiLock (ABS): a two-level factor with levels False and True.
• DrivingSkill (driving skill): a three-level factor with levels SubStandard, Normal and Expert.
• SeniorTrain (senior training): a two-level factor with levels False and True.
• ThisCarCost (costs for the insured car): a four-level factor with levels Thousand, TenThou, HundredThou and Million.
• Theft (theft): a two-level factor with levels False and True.
• CarValue (value of the car): a five-level factor with levels FiveThou, TenThou, TwentyThou, FiftyThou and Million.
• HomeBase (neighbourhood type): a four-level factor with levels Secure, City, Suburb and Rural.
• AntiTheft (anti-theft system): a two-level factor with levels False and True.
• PropCost (ratio of the cost for the two cars): a four-level factor with levels Thousand, TenThou, HundredThou and Million.
• OtherCarCost (costs for the other car): a four-level factor with levels Thousand, TenThou, HundredThou and Million.
• OtherCar (other cars involved in the accident): a two-level factor with levels False and True.
• MedCost (cost of the medical treatment): a four-level factor with levels Thousand, TenThou, HundredThou and Million.
• Cushioning (cushioning): a four-level factor with levels Poor, Fair, Good and Excellent.
• Airbag (airbag): a two-level factor with levels False and True.
• ILiCost (inspection cost): a four-level factor with levels Thousand, TenThou, HundredThou and Million.
• DrivHist (driving history): a three-level factor with levels Zero, One and Many.
Note

The complete BN can be downloaded from http://www.bnlearn.com/bnrepository.

Source


Examples

```r
# load the data.
data(insurance)
# create and plot the network structure.
modelstring <- paste0("[Age][Mileage][SocioEcon][Age][Good Student][Age:SocioEcon]",
"[Risk Aversion][Age][SocioEcon][Other Car][SocioEcon][Vehicle Year][SocioEcon][Risk Aversion]",
"[Make Model][SocioEcon][Risk Aversion][Senior Train][Age][Risk Aversion]",
"[Home Base][SocioEcon][Risk Aversion][Anti Theft][SocioEcon][Risk Aversion]",
"[Rugged Auto][Vehicle Year: Make Model][Anti Theft][Vehicle Year: Make Model]",
"[Driving Skill][Age][Senior Train][Car Value][Vehicle Year: Make Model: Mileage]",
"[Airbag][Vehicle Year: Make Model][Driving Quality][Risk Aversion][Driving Skill]",
"[Theft][Car Value][Home Base: Anti Theft][Cushioning][Rugged Auto: Airbag]",
"[Driving Skill][Risk Aversion][Driving Skill][Accident][Driving Quality][Mileage: Anti Theft]",
"[This Car Dam][Rugged Auto: Accident][Other Car Cost][Rugged Auto: Accident]",
"[Med Cost][Age][Accident: Cushioning][ILL Cost][Accident]",
"[This Car Cost][This Car Dam: Theft][Car Value][Prop Cost][This Car Cost: Other Car Cost]")
dag <- make.augmented.dag(modelstring)
## Not run: graphviz.plot(dag, shape = "ellipse")
```

*learning.test*  
*Synthetic (discrete) data set to test learning algorithms*

Description

This a synthetic data set used as a test case in the bnlearn package.

Usage

```r
data(learning.test)
```

Format

The learning.test data set contains the following variables:

- A, a three-level factor with levels a, b and c.
- B, a three-level factor with levels a, b and c.
- C, a three-level factor with levels a, b and c.
- D, a three-level factor with levels a, b and c.
- E, a three-level factor with levels a, b and c.
- F, a two-level factor with levels a and b.
lizards

Note

The R script to generate data from this network is available from http://www.bnlearn.com/documentation/networks.

Examples

```r
# load the data.
data(learning.test)
# create and plot the network structure.
dag <- model2network("[A][C][F][B][D][A:C][E][B:F]")
## Not run: graphviz.plot(dag)
```

lizards                      Lizards’ perching behaviour data set

Description

Real-world data set about the perching behaviour of two species of lizards in the South Bimini island, from Shoener (1968).

Usage

data(lizards)

Format

The lizards data set contains the following variables:

- Species (the species of the lizard): a two-level factor with levels Sagrei and Distichus.
- Height (perch height): a two-level factor with levels high (greater than 4.75 feet) and low (lesser or equal to 4.75 feet).
- Diameter (perch diameter): a two-level factor with levels narrow (greater than 4 inches) and wide (lesser or equal to 4 inches).

Source


Examples

```r
# load the data.
data(lizards)
# create and plot the network structure.
dag <- model2network("[Species][Diameter|Species][Height|Species]")
## Not run: graphviz.plot(dag, shape = "ellipse")

# This data set is useful as it offers nominal values for
# the conditional mutual information and X^2 tests.
ci.test("Height", "Diameter", "Species", test = "mi", data = lizards)
ci.test("Height", "Diameter", "Species", test = "x2", data = lizards)
```

Description

Take a bn object or bn.fit object encoding a Gaussian network and refit all the local distributions using lm(). This makes it possible to use all the functions provided by R for lm objects (summary, anova, etc.) to investigate the network.

Usage

```r
## S3 method for class 'bn'
as.lm(x, data, ...)
## S3 method for class 'bn.fit'
as.lm(x, data, ...)
## S3 method for class 'bn.fit.gnode'
as.lm(x, data, ...)
```

Arguments

- `x` an object of class bn, bn.fit or bn.fit.gnode.
- `data` a data frame containing the variables in the model.
- `...` additional arguments, currently ignored.

Value

If `x` is an object of class bn or bn.fit, as.lm() returns a list of lm objects, one for each node in `x`. If `x` is an object of class bn or bn.fit.gnode, as.lm() returns a single lm object.

Author(s)

Marco
local discovery algorithms

Examples

dag <- hc(gaussian.test)
fitted <- bn.fit(dag, gaussian.test)
as.lm(dag, gaussian.test)
as.lm(fitted, gaussian.test)
as.lm(fitted$F, gaussian.test)

Description

ARACNE and Chow-Liu learn simple graphs structures from data using pairwise mutual information coefficients.

Usage

aracne(x, whitelist = NULL, blacklist = NULL, mi = NULL, debug = FALSE)
chow.liu(x, whitelist = NULL, blacklist = NULL, mi = NULL, debug = FALSE)

Arguments

x             a data frame containing the variables in the model.
whitelist     a data frame with two columns (optionally labeled "from" and "to"), containing
              a set of arcs to be included in the graph.
blacklist     a data frame with two columns (optionally labeled "from" and "to"), containing
              a set of arcs not to be included in the graph.
mi             a character string, the estimator used for the pairwise (i.e. unconditional)
              mutual information coefficients in the ARACNE and Chow-Liu algorithms. Possible
              values are mi (discrete mutual information) and mi-g (Gaussian mutual
              information).
debug         a boolean value. If TRUE a lot of debugging output is printed; otherwise the
              function is completely silent.

Value

An object of class bn. See bn-class for details.

Author(s)

Marco Scutari

See Also

costRAINT-based algorithms, score-based algorithms, hybrid algorithms.
marks

Description

Examination marks of 88 students on five different topics, from Mardia (1979).

Usage

data(marks)

Format

The marks data set contains the following variables, one for each topic in the examination:

- MECH (mechanics)
- VECT (vectors)
- ALG (algebra)
- ANL (analysis)
- STAT (statistics)

All are measured on the same scale (0-100).

Source


Examples

```r
# This is the undirected graphical model from Edwards (2000).
data(marks)
ug <- empty.graph(names(marks))
arc('ug', check.cycles = FALSE) = matrix(
c("MECH", "VECT", "MECH", "ALG", "VECT", "MECH", "VECT", "ALG", 
"ALG", "MECH", "ALG", "VECT", "ALG", "ANL", "ALG", "STAT", 
"ANL", "ALG", "ANL", "STAT", "STAT", "ALG", "STAT", "ANL"), 
ncol = 2, byrow = TRUE, 
dimnames = list(c(), c("from", "to"))
)
## Not run: graphviz.plot(ug)
```

Description

Assign or extract various quantities of interest from an object of class bn of bn.fit.

Usage

```r
## nodes
mb(x, node)
nbr(x, node)
parents(x, node)
parents(x, node, debug = FALSE) <- value
children(x, node)
children(x, node, debug = FALSE) <- value
spouses(x, node)
ancestors(x, node)
descendants(x, node)
in.degree(x, node)
out.degree(x, node)
root.nodes(x)
leaf.nodes(x)
nodes(x)

## arcs
arcs(x)
arcs(x, check.cycles = TRUE, check.illegal = TRUE, debug = FALSE) <- value
directed.arcs(x)
undirected.arcs(x)
incoming.arcs(x, node)
outgoing.arcs(x, node)
incident.arcs(x, node)
compelled.arcs(x)
reversible.arcs(x)
narcs(x)

## adjacency matrix
amat(x)
amat(x, check.cycles = TRUE, check.illegal = TRUE, debug = FALSE) <- value

## graphs
nparams(x, data, effective = FALSE, debug = FALSE)
ngates(x)

## shared with the graph package.
# these used to be a simple nodes(x) function.
```
## S4 method for signature 'bn'

nodes(object)

## S4 method for signature 'bn.fit'

nodes(object)

# these used to be a simple degree(x, node) function.

## S4 method for signature 'bn'

degree(object, Nodes)

## S4 method for signature 'bn.fit'

degree(object, Nodes)

### Arguments

- `x, object` an object of class `bn` or `bn.fit`. The replacement form of `parents`, `children`, `arcs` and `amat` requires an object of class `bn`.
- `node, Nodes` a character string, the label of a node.
- `value` either a vector of character strings (for `parents` and `children`), an adjacency matrix (for `amat`) or a data frame with two columns (optionally labeled "from" and "to", for `arcs`).
- `data` a data frame containing the data the Bayesian network was learned from. It’s only needed if `x` is an object of class `bn`.
- `check.cycles` a boolean value. If `FALSE` the returned network will not be checked for cycles.
- `check.illegal` a boolean value. If `TRUE` arcs that break the parametric assumptions of `x`, such as those from continuous to discrete nodes in conditional Gaussian networks, cause an error.
- `effective` a boolean value. If `TRUE` the number of non-zero free parameters is returned, that is, the effective degrees of freedom of the network; otherwise the theoretical number of parameters is returned.
- `debug` a boolean value. If `TRUE` a lot of debugging output is printed; otherwise the function is completely silent.

### Details

The number of parameters of a discrete Bayesian network is defined as the sum of the number of logically independent parameters of each node given its parents (Chickering, 1995). For Gaussian Bayesian networks the distribution of each node can be viewed as a linear regression, so it has a number of parameters equal to the number of the parents of the node plus one (the intercept) as per Neapolitan (2003). For conditional linear Gaussian networks, the number of parameters of discrete and Gaussian nodes is as above. The number of parameters of conditional Gaussian nodes is equal to 1 plus the number of continuous parents (who get one regression coefficient each, plus the intercept) times the number of configurations of the discrete parents (each configuration has an associated regression model).

### Value

`mb`, `nbr`, `nodes`, `parents`, `children`, `spouses`, `ancestors`, `descendants`, `root.nodes` and `leaf.nodes` return a vector of character strings.
misc utilities

arcs, directed.arcs, undirected.arcs, incoming.arcs, outgoing.arcs, incident.arcs, compelled.arcs, reversible.arcs, return a matrix of two columns of character strings.
narcs and n_nodes return the number of arcs and nodes in the graph, respectively.
amat returns a matrix of 0/1 integer values.
degree, in_degree, out_degree, n_params and n_tests return an integer.

Author(s)

Marco Scutari

References


Examples

data(learning.test)
res <- gs(learning.test)

## the Markov blanket of A.
mb(res, "A")

## the neighbourhood of F.
nbr(res, "F")

## the arcs in the graph.
arcs(res)

## the nodes of the graph.
nodes(res)

## the adjacency matrix for the nodes of the graph.
amat(res)

## the parents of D.
parents(res, "D")

## the children of A.
children(res, "A")

## the root nodes of the graph.
root.nodes(res)

## the leaf nodes of the graph.
leaf.nodes(res)

## number of parameters of the Bayesian network.
res <- set.arc(res, "A", "B")
nparams(res, learning.test)
model string utilities

Build a model string from a Bayesian network and vice versa

Description

Build a model string from a Bayesian network and vice versa.

Usage

```r
modelstring(x)
modelstring(x, debug = FALSE) <- value
model2network(string, ordering = NULL, debug = FALSE)
```

```r
## S3 method for class 'bn'
as.character(x, ...)
## S3 method for class 'character'
as.bn(x, ...)
```

Arguments

- `x`: an object of class `bn`. `modelstring()` (but not its replacement form) accepts also objects of class `bn.fit`.
- `string`: a character string describing the Bayesian network.
- `ordering`: the labels of all the nodes in the graph; their order is the node ordering used in the construction of the `bn` object. If `NULL` the nodes are sorted alphabetically.
- `value`: a character string, the same as the `string`.
- `debug`: a boolean value. If `TRUE` a lot of debugging output is printed; otherwise the function is completely silent.
- `...`: extra arguments from the generic method (currently ignored).

Details

The strings returned by `modelstring()` have the same format as the ones returned by the `modelstring()` function in package `deal`; network structures may be easily exported to and imported from that package (via the `model2network` function).

The format of the model strings is as follows. The local structure of each node is enclosed in square brackets (`"[]"`); the first string is the label of that node. The parents of the node (if any) are listed after a (`"|"`) and separated by colons (`"::"`). All nodes (including isolated and root nodes) must be listed.

Value

- `model2network()` and `as.bn()` return an object of class `bn`;
- `modelstring()` and `as.character.bn()` return a character string.
naive.bayes

Author(s)
Marco Scutari

Examples

data(learning.test)
res = set.arc(gs(learning.test), "A", "B")
res
modelstring(res)
res2 = model2network(modelstring(res))
res2
all.equal(res, res2)

naive.bayes Naive Bayes classifiers

Description
Create, fit and perform predictions with naive Bayes and Tree-Augmented naive Bayes (TAN) classifiers.

Usage

naive.bayes(x, training, explanatory)
## S3 method for class 'bn.naive'
predict(object, data, prior, ..., prob = FALSE, debug = FALSE)

tree.bayes(x, training, explanatory, whitelist = NULL, blacklist = NULL,
mi = NULL, root = NULL, debug = FALSE)
## S3 method for class 'bn.tan'
predict(object, data, prior, ..., prob = FALSE, debug = FALSE)

Arguments

training a character string, the label of the training variable.
explanatory a vector of character strings, the labels of the explanatory variables.
object an object of class bn.naive, either fitted or not.
x, data a data frame containing the variables in the model, which must all be factors.
prior a numeric vector, the prior distribution for the training variable. It is automatically normalized if not already so. The default prior is the probability distribution of the training variable in object.
whitelist a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs to be included in the graph.
blacklist a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs not to be included in the graph.
mi  a character string, the estimator used for the mutual information coefficients for the Chow-Liu algorithm in TAN. Possible values are mi (discrete mutual information) and mi-g (Gaussian mutual information).

root  a character string, the label of the explanatory variable to be used as the root of the tree in the TAN classifier.

...  extra arguments from the generic method (currently ignored).

prob  a boolean value. If TRUE the posterior probabilities used for prediction are attached to the predicted values as an attribute called prob.

debug  a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details
The naive.bayes() function creates the star-shaped Bayesian network form of a naive Bayes classifier; the training variable (the one holding the group each observation belongs to) is at the center of the star, and it has an outgoing arc for each explanatory variable.

If data is specified, explanatory will be ignored and the labels of the explanatory variables will be extracted from the data.

predict() performs a supervised classification of the observations by assigning them to the group with the maximum posterior probability.

Value
naive.bayes() returns an object of class c("bn.naive","bn"), which behaves like a normal bn object unless passed to predict(). tree.bayes() returns an object of class c("bn.tan","bn"), which again behaves like a normal bn object unless passed to predict().

predict() returns a factor with the same levels as the training variable from data. If prob = TRUE, the posterior probabilities used for prediction are attached to the predicted values as an attribute called prob.

See network classifiers for a complete list of network classifiers with the respective references.

Note
Since bnlearn does not support networks containing both continuous and discrete variables, all variables in data must be discrete.

Ties in prediction are broken using Bayesian tie breaking, i.e. sampling at random from the tied values. Therefore, setting the random seed is required to get reproducible results.

tan.tree() supports whitelisting and blacklisting arcs but not their directions. Moreover it is not possible to whitelist or blacklist arcs incident on training.

predict() accepts either a bn or a bn.fit object as its first argument. For the former, the parameters of the network are fitted on data, that is, the observations whose class labels the function is trying to predict.

Author(s)
Marco Scutari
network-classifiers

References


Examples

data(learning.test)
# this is an in-sample prediction with naive Bayes (parameter learning
# is performed implicitly during the prediction).
bn <- naive.bayes(learning.test, "A")
pred <- predict(bn, learning.test)
table(pred, learning.test[, "A"])

# this is an in-sample prediction with TAN (parameter learning is
# performed explicitly with bn.fit).
tan <- tree.bayes(learning.test, "A")
fitted <- bn.fit(tan, learning.test, method = "bayes")
pred <- predict(fitted, learning.test)
table(pred, learning.test[, "A"])

# this is an out-of-sample prediction, from a training test to a separate
# test set.
training.set <- learning.test[1:4000, ]
test.set <- learning.test[4001:5000, ]
bn <- naive.bayes(training.set, "A")
fitted <- bn.fit(bn, training.set)
pred <- predict(fitted, test.set)
table(pred, test.set[, "A"])

---

network-classifiers Bayesian network Classifiers

Description

Structure learning algorithms for Bayesian network classifiers.

Details

The algorithms are aimed at classification, and favour predictive power over the ability to recover the correct network structure. The implementation in *bnlearn* assumes that all variables, including the classifiers, are discrete.

- *Naive Bayes* (*naive.bayes*): a very simple algorithm assuming that all classifiers are independent and using the posterior probability of the target variable for classification.
• Tree-Augmented Naive Bayes (tree.bayes): an improvement over naive Bayes, this algorithm uses Chow–Liu to approximate the dependence structure of the classifiers.


---

**Description**

Overview of the network scores implemented in *bnlearn*, with the respective reference publications.

**Details**

Available scores (and the respective labels) for discrete Bayesian networks (categorical variables) are:

- the multinomial log-likelihood (loglik) score, which is equivalent to the entropy measure used in Weka.
- the Akaike Information Criterion score (aic).
- the Bayesian Information Criterion score (bic), which is equivalent to the Minimum Description Length (MDL) and is also known as Schwarz Information Criterion.
- the predictive log-likelihood (pred-loglik) computed on a separate test set.
- the logarithm of the Bayesian Dirichlet equivalent (uniform) score (bdeu) (also denoted BDeu), a score equivalent Dirichlet posterior density.
- the logarithm of the Bayesian Dirichlet sparse score (bds) (BDs), a sparsity-inducing Dirichlet posterior density (not score equivalent).
- the logarithm of the Bayesian Dirichlet score with Jeffrey’s prior (not score equivalent).
• the logarithm of the modified Bayesian Dirichlet equivalent score (mbde) for mixtures of experimental and observational data (not score equivalent).


• the logarithm of the locally averaged Bayesian Dirichlet score (lada, not score equivalent).


• the logarithm of the $K2$ score (k2), a Dirichlet posterior density (not score equivalent).


Available scores (and the respective labels) for Gaussian Bayesian networks (normal variables) are:

• the multivariate Gaussian log-likelihood (loglik-g) score.

• the corresponding Akaike Information Criterion score (aic-g).

• the corresponding Bayesian Information Criterion score (bic-g).


• the predictive log-likelihood (pred-loglik-g) computed on a separate test set. The reference paper is the same as that for pred-loglik. It is currently implemented to be score-equivalent like pred-loglik, but that may be subject to change.

• a score equivalent Gaussian posterior density (bge).


Available scores (and the respective labels) for hybrid Bayesian networks (mixed categorical and normal variables) are:

• the conditional linear Gaussian log-likelihood (loglik-cg) score.

• the corresponding Akaike Information Criterion score (aic-cg).

• the corresponding Bayesian Information Criterion score (bic-cg).

• the predictive log-likelihood (pred-loglik-cg) computed on a separate test set. The reference paper is the same as that for pred-loglik.

Other scores (and the respective labels):

• a custom decomposable (custom) score interface that takes an R function as an argument. It can be used to trial experimental score functions without having to code them in C and hook them up to the internals of bnlearn.
node operations

Manipulate nodes in a graph

Description

Add, remove and rename nodes in a graph.

Usage

```r
# add and remove nodes.
add.node(x, node)
remove.node(x, node)

# re-label nodes.
rename.nodes(x, names)
```

### S4 replacement method for signature 'bn'
```r
evaluate(object) <- value
```

### S4 replacement method for signature 'bn.fit'
```r
evaluate(object) <- value
```

Arguments

- `x` : an object of class `bn` for `add.node()` and `remove.node()`; an object of class `bn` or `bn.fit` for `rename.nodes()`.
- `object` : an object of class `bn` or `bn.fit`.
- `node` : a character string, the label of a node.
- `value, names` : a vector of character strings, the new set of labels that will be used as to rename the nodes.

Details

- `add.node()` adds a new (isolated) node to an existing `bn` object.
- `remove.node()` removes a node from a `bn` object.
- `rename.nodes()` replaces the node labels with new ones, relabelling the whole node set. The assignment method for `nodes()` is an alias of `rename.nodes()`.

Value

- `add.node()`, `remove.node()` and `rename.nodes()` return an updated `bn` object.

Author(s)

Marco Scutari
Examples

dag = random.graph(LETTERS[1:5])
add.node(dag, "Z")
remove.node(dag, "A")

nodes(dag)
nodes(dag) = LETTERS[6:10]
nodes(dag)

---

node ordering utilities

Partial node orderings

Description

Find the partial node ordering implied by a network.

Usage
	node.ordering(x, debug = FALSE)

Arguments

x an object of class bn or bn.fit.

default a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Value

node.ordering() returns a vector of character strings, an ordered set of node labels.

Note

node.ordering() supports only completely directed Bayesian networks.

Author(s)

Marco Scutari

Examples

dag = random.graph(LETTERS[1:10])
ord = node.ordering(dag)
ord
pcalg integration

Import and export networks from the pcalg package

Description

Convert pcalgo objects to bn objects.

Usage

```r
## S3 method for class 'pcAlgo'
as.bn(x, ..., check.cycles = TRUE)
```

Arguments

- `x` an object of class pcAlgo.
- `...` extra arguments from the generic method (currently ignored).
- `check.cycles` a boolean value. If FALSE the returned network will not be checked for cycles.

Value

An object of class bn.

Author(s)

Marco Scutari

plot.bn

Plot a Bayesian network

Description

Plot the graph associated with a small Bayesian network.

Usage

```r
## S3 method for class 'bn'
plot(x, ylim = c(0,600), xlim = ylim, radius = 250,
     arrow = 35, highlight = NULL, color = "red", ...)
```
Arguments

x an object of class bn.
ylim a numeric vector with two components containing the range of the y-axis.
xlim a numeric vector with two components containing the range of the x-axis.
radius a numeric value containing the radius of the nodes.
arow a numeric value containing the length of the arrow heads.
highlight a vector of character strings, representing the labels of the nodes (and corresponding arcs) to be highlighted.
color an integer or character string (the highlight colour).
... other graphical parameters to be passed through to plotting functions.

Note

The following arguments are always overridden:

- axes is set to FALSE.
- xlab is set to an empty string.
- ylab is set to an empty string.

Author(s)

Marco Scutari

See Also

graphviz.plot.

Examples

data(learning.test)
res = gs(learning.test)
plot(res)

## highlight node B and related arcs.
plot(res, highlight = "B")

## highlight B and its Markov blanket.
plot(res, highlight = c("B", mb(res, "B")))

## a more compact plot.
par oma = rep(0, 4), mar = rep(0, 4), mai = rep(0, 4),
plt = c(0.06, 0.94, 0.12, 0.88)
plot(res)
Description

Plot arc strengths derived from bootstrap resampling.

Usage

```r
## S3 method for class 'bn.strength'
plot(x, draw.threshold = TRUE, main = NULL,
     xlab = "arc strengths", ylab = "CDF(arc strengths)", ...)
```

Arguments

- `x`: an object of class `bn.strength`.
- `draw.threshold`: a boolean value. If `TRUE`, a dashed vertical line is drawn at the threshold.
- `main`, `xlab`, `ylab`: character strings, the main title and the axes labels.
- `...`: other graphical parameters to be passed through to plotting functions.

Note

The `xlim` and `ylim` arguments are always overridden.

Author(s)

Marco Scutari

Examples

```r
data(learning.test)
start <- random.graph(nodes = names(learning.test), num = 50)
netlist <- lapply(start, function(net) {
  hc(learning.test, score = "bde", iss = 10, start = net) })
arcs <- custom.strength(netlist, nodes = names(learning.test), cpdag = FALSE)
plot(arcs)
```
**Preprocess**

**Pre-process data to better learn Bayesian networks**

**Description**

Screen and transform the data to make them more suitable for structure and parameter learning.

**Usage**

```r
# discretize continuous data into factors.
discretize(data, method, breaks = 3, ordered = FALSE, ..., debug = FALSE)

# screen continuous data for highly correlated pairs of variables.
dedup(data, threshold, debug = FALSE)
```

**Arguments**

- `data`: a data frame containing numeric columns (for `dedup()`) or a combination of numeric or factor columns (for `discretize()`).
- `threshold`: a numeric value between zero and one, the absolute correlation used a threshold in screening highly correlated pairs.
- `method`: a character string, either `interval` for *interval discretization*, `quantile` for *quantile discretization* (the default) or `hartemink` for *Hartemink’s pairwise mutual information* method.
- `breaks`: if `method` is set to `hartemink`, an integer number, the number of levels the variables are to be discretized into. Otherwise, a vector of integer numbers, one for each column of the data set, specifying the number of levels for each variable.
- `ordered`: a boolean value. If `TRUE` the discretized variables are returned as ordered factors instead of unordered ones.
- `...`: additional tuning parameters, see below.
- `debug`: a boolean value. If `TRUE` a lot of debugging output is printed; otherwise the function is completely silent.

**Details**

`discretize()` takes a data frame of continuous variables as its first argument and returns a second data frame of discrete variables, transformed using of three methods: `interval`, `quantile` or `hartemink`.

`dedup()` screens the data for pairs of highly correlated variables, and discards one in each pair.

**Value**

- `discretize()` returns a data frame with the same structure (number of columns, column names, etc.) as `data`, containing the discretized variables.
- `dedup()` returns a data frame with a subset of the columns of `data`. 
Note

Hartemink’s algorithm has been designed to deal with sets of homogeneous, continuous variables; this is the reason why they are initially transformed into discrete variables, all with the same number of levels (given by the ibreaks argument). Which of the other algorithms is used is specified by the idisc argument (quantile is the default). The implementation in \texttt{bnlearn} also handles sets of discrete variables with the same number of levels, which are treated as adjacent interval identifiers. This allows the user to perform the initial discretization with the algorithm of his choice, as long as all variables have the same number of levels in the end.

Author(s)

Marco Scutari

References


Examples

\begin{verbatim}
data(gaussian.test) d = discretize(gaussian.test, method = 'hartemink', breaks = 4, ibreaks = 20) plot(hc(d)) d2 = dedup(gaussian.test)
\end{verbatim}

---

\textbf{rbn} \hspace{2cm} \textit{Simulate random samples from a given Bayesian network}

Description

Simulate random samples from a given Bayesian network.

Usage

\begin{verbatim}
## S3 method for class 'bn'
rbn(x, n = 1, data, t = "mle", ..., debug = FALSE)
## S3 method for class 'bn.fit'
rbn(x, n = 1, ..., debug = FALSE)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{x} \hspace{2cm} an object of class \texttt{bn} or \texttt{bn.fit}.
  \item \texttt{n} \hspace{2cm} a positive integer giving the number of observations to generate.
  \item \texttt{data} \hspace{2cm} a data frame containing the data the Bayesian network was learned from.
  \item \texttt{fit} \hspace{2cm} a character string, the label of the method used to fit the parameters of the network. See \texttt{bn.fit} for details.
\end{itemize}
additional arguments for the parameter estimation procedure, see again \texttt{bn.fit}
for details.

- \texttt{debug}:
a boolean value. If \texttt{TRUE} a lot of debugging output is printed; otherwise the
function is completely silent.

\section*{Details}

\texttt{rbn()} implements forward/logic sampling: values for the root nodes are sampled from their (un-
conditional) distribution, then those of their children conditional on the respective parent sets. This
is done iteratively until values have been sampled for all nodes.

If \texttt{x} contains \texttt{NA} parameter estimates (because of unobserved discrete parents configurations in the
data the parameters were learned from), \texttt{rbn} will produce samples that contain \texttt{NA}s when those
parents configurations appear in the simulated samples. See \texttt{bn.fit} for details on how to make sure
\texttt{bn.fit} objects contain no \texttt{NA} parameter estimates.

\section*{Value}

A data frame with the same structure (column names and data types) of the data argument (if \texttt{x} is an object of class \texttt{bn}) or with the same structure as the data originally used to fit the parameters
of the Bayesian network (if \texttt{x} is an object of class \texttt{bn.fit}).

\section*{Author(s)}

Marco Scutari

\section*{References}


\section*{See Also}

\texttt{bn.boot}, \texttt{bn.cv}.

\section*{Examples}

```r
## Not run:
data(learning.test)
res <- gs(learning.test)
res <- set.arc(res, "A", "B")
par(mfrow = c(1,2))
plot(res)
sim <- rbn(res, 500, learning.test)
plot(gs(sim))
## End(Not run)
```
**ROCR integration**

*Generating a prediction object for ROCR*

---

**Description**

Evaluate structure learning accuracy with **ROCR**. This function views the arcs in a `bn.strength` object as a set of predictions and the arcs in a `true` reference graph as a set of labels, and produces a prediction object from the **ROCR** package. This facilitates evaluation of structure learning with traditional machine learning metrics such as ROC curves and AUC.

**Usage**

```r
## S3 method for class 'bn.strength'
as.prediction(x, true, ..., consider.direction = TRUE)
```

**Arguments**

- `x` an object of class `bn.strength` returned by `boot.strength()`, representing learning results targeting the object of class `bn` specified by the `true` argument.
- `true` an object of class `bn`, the target of structure learning.
- `...` additional arguments, currently ignored.
- `consider.direction` a boolean value. If `TRUE` an arc’s prediction value is set to the product of its `strength` and `direction` values in `x` (interpreted as the probability an arc is both present and has the specified direction). If `FALSE` the arc’s prediction value is set to its `strength` value.

**Details**

One way of evaluating the overall performance of a network structure learning algorithm is to evaluate how well it detects individual arcs. `as.prediction()` takes each pair of nodes in a ground truth network and labels them with a `1` if an arc exists between them and `0` if not. It uses the arc presence probabilities in a `bn.strength` object returned by `boot.strength()` as the predictions.

**Value**

An object of class `prediction` from the **ROCR** package.

**Author(s)**

Robert Ness
Examples

```r
## Not run:
library(ROCR)

modellingstring <- paste0("[HIST|LVF][CVP|LVV][PCWP|LVV][HYP][LVV|HYP:LVF][LVF]",
  "[STKV|HYP:LVF][ERLO][HRRP][ERLO:HR][HREK][ERCA:HRR][HREK][ERCA:HRR][ANES]",
  "[APL][TPR][APL][ECO2][ACO2:VLNG][KINK][MINV][INT:VLNG][FIO2][FIO2:VALV]",
  "[SAO2][PVS:SHNT][SAP][PMB][PMB][SHNT][INT:PMB][INT][PRSS][INT:KINK:VTUB][DISC]",
  "[MVS][VMCH][MVS][VTUB][DISC:VMCH][VLNG][INT:KINK:VTUB][VALV][INT:VLNG][ACO2][VALV]",
  "[CCHL][ACO2:ANES:SAO2:TPR][HR][CCHL][CO:HR][STKV][BP][CO:TPR]")
true.dag <- model2network(modelstring)
strength <- boot.strength(alarm, R = 200, m = 30, algorithm = "hc")
pred <- as.prediction(strength, true.dag)
perf <- performance(pred, "tpr", "fpr")
plot(perf, main = "Arc Detection")
performance(pred, "auc")

## End(Not run)
```

---

**score**

*Score of the Bayesian network*

**Description**

Compute the score of the Bayesian network.

**Usage**

```r
## S4 method for signature 'bn'
score(x, data, type = NULL, ..., by.node = FALSE, debug = FALSE)
## S4 method for signature 'bn.naive'
score(x, data, type = NULL, ..., by.node = FALSE, debug = FALSE)
## S4 method for signature 'bn.tan'
score(x, data, type = NULL, ..., by.node = FALSE, debug = FALSE)

## S3 method for class 'bn'
logLik(object, data, ...)
## S3 method for class 'bn'
AIC(object, data, ..., k = 1)
## S3 method for class 'bn'
BIC(object, data, ...)
```

**Arguments**

- `x, object` an object of class bn.
- `data` a data frame containing the data the Bayesian network that will be used to compute the score.
type

a character string, the label of a network score. If none is specified, the default score is the *Bayesian Information Criterion* for both discrete and continuous data sets. See network scores for details.

by.node

a boolean value. If `TRUE` and the score is decomposable, the function returns the score terms corresponding to each node; otherwise it returns their sum (the overall score of `x`).

debug

a boolean value. If `TRUE` a lot of debugging output is printed; otherwise the function is completely silent.

... extra arguments from the generic method (for the AIC and logLik functions, currently ignored) or additional tuning parameters (for the score function).

k

a numeric value, the penalty coefficient to be used; the default `k = 1` gives the expression used to compute the AIC in the context of scoring Bayesian networks.

Details

Additional arguments of the `score()` function:

- `iss`: the imaginary sample size used by the Bayesian Dirichlet scores (`bde`, `mbde`, `bds`, `bdj`). It is also known as “equivalent sample size”. The default value is equal to 1.
- `iss.mu`: the imaginary sample size for the normal component of the normal-Wishart prior in the Bayesian Gaussian score (`bge`). The default value is 1.
- `iss.w`: the imaginary sample size for the Wishart component of the normal-Wishart prior in the Bayesian Gaussian score (`bge`). The default value is `ncol(data) + 2`.
- `mu`: the mean vector of the normal component of the normal-Wishart prior in the Bayesian Gaussian score (`bge`). The default value is equal to `colMeans(data)`.
- `l`: the number of scores to average in the locally averaged Bayesian Dirichlet score (`bdl`). The default value is 5.
- `exp`: a list of indexes of experimental observations (those that have been artificially manipulated). Each element of the list must be named after one of the nodes, and must contain a numeric vector with indexes of the observations whose value has been manipulated for that node.
- `k`: the penalty coefficient to be used by the AIC and BIC scores. The default value is 1 for AIC and `log(nrow(data))/2` for BIC.
- `prior`: the prior distribution to be used with the various Bayesian Dirichlet scores (`bde`, `mbde`, `bds`, `bdj`, `bdl`) and the Bayesian Gaussian score (`bge`). Possible values are uniform (the default), vsp (the Bayesian variable selection prior, which puts a probability of inclusion on parents), marginal (an independent marginal uniform for each arc) and cs (the Castelo & Siebes prior, which puts an independent prior probability on each arc and direction).
- `beta`: the parameter associated with `prior`.
  - If `prior` is uniform, `beta` is ignored.
  - If `prior` is vsp, `beta` is the probability of inclusion of an additional parent. The default is `1/ncol(data)`.
- If prior is marginal, beta is the probability of inclusion of an arc. Each direction has a probability of inclusion of $\beta / 2$ and the probability that the arc is not included is therefore $1 - \beta$. The default value is 0.5, so that arc inclusion and arc exclusion have the same probability.

- If prior is cs, beta is a data frame with columns from, to and prob specifying the prior probability for a set of arcs. A uniform probability distribution is assumed for the remaining arcs.

- newdata: the test set whose predictive likelihood will be computed by pred-loglik, pred-loglik-g or pred-loglik-cg. It should be a data frame with the same variables as data.

**Value**

For score() with by.node = TRUE, a vector of numeric values, the individual node contributions to the score of the Bayesian network. Otherwise, a single numeric value, the score of the Bayesian network.

**Note**

AIC and BIC are computed as $\text{logLik}(x) - k \times \text{nparams}(x)$, that is, the classic definition rescaled by -2. Therefore higher values are better, and for large sample sizes BIC converges to $\log(\text{BDe})$.

When using the Castelo & Siebes prior in structure learning, the prior probabilities associated with an arc are bound away from zero and one by shrinking them towards the uniform distribution as per Hausser and Strimmer (2009) with a lambda equal to $3 \times \sqrt{\text{Machine}\$\text{double\.eps}}$. This dramatically improves structure learning, which is less likely to get stuck when starting from an empty graph. As an alternative to prior probabilities, a blacklist can be used to prevent arcs from being included in the network, and a whitelist can be used to force the inclusion of particular arcs. beta is not modified when the prior is used from functions other than those implementing score-based and hybrid structure learning.

**Author(s)**

Marco Scutari

**See Also**

choose.direction, arc.strength, alpha.star.

**Examples**

data(learning.test)
res <- set.arc(gs(learning.test), "A", "B")
score(res, learning.test, type = "bde")

### let’s see score equivalence in action!
res2 <- set.arc(gs(learning.test), "B", "A")
score(res2, learning.test, type = "bde")

### K2 score on the other hand is not score equivalent.
score(res, learning.test, type = "k2")
score(res2, learning.test, type = "k2")
score-based algorithms

### BDe with a prior.
```r
data.frame(from = c("A", "D"), to = c("B", "F"),
prob = c(0.2, 0.5), stringsAsFactors = FALSE)
score(res, learning.test, type = "bde", prior = "cs", beta = beta)
```

### equivalent to logLik(res, learning.test)
```r
code(res, learning.test, type = "loglik")
```

### equivalent to AIC(res, learning.test)
```r
code(res, learning.test, type = "aic")
```

---

score-based algorithms  Score-based structure learning algorithms

### Description

Learn the structure of a Bayesian network using a hill-climbing (HC) or a Tabu search (TABU) greedy search.

### Usage

```r
hc(x, start = NULL, whitelist = NULL, blacklist = NULL, score = NULL, ..., 
  debug = FALSE, restart = 0, perturb = 1, max.iter = Inf, maxp = Inf, optimized = TRUE)
tabu(x, start = NULL, whitelist = NULL, blacklist = NULL, score = NULL, ..., 
  debug = FALSE, tabu = 10, max.tabu = tabu, max.iter = Inf, maxp = Inf, optimized = TRUE)
```

### Arguments

- **x**: a data frame containing the variables in the model.
- **start**: an object of class `bn`, the preseeded directed acyclic graph used to initialize the algorithm. If none is specified, an empty one (i.e. without any arc) is used.
- **whitelist**: a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs to be included in the graph.
- **blacklist**: a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs not to be included in the graph.
- **score**: a character string, the label of the network score to be used in the algorithm. If none is specified, the default score is the [Bayesian Information Criterion](#) for both discrete and continuous data sets. See network scores for details.
- **...**: additional tuning parameters for the network score. See `score` for details.
- **debug**: a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
- **restart**: an integer, the number of random restarts.
- **tabu**: a positive integer number, the length of the tabu list used in the `tabu` function.
- **max.tabu**: a positive integer number, the iterations tabu search can perform without improving the best network score.
Discover the structure around a single node

Learn the Markov blanket or the neighbourhood centered on a node.

Usage

```r
learn.mbl(x, node, method, whitelist = NULL, blacklist = NULL, start = NULL, test = NULL, alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE)
learnnbr(x, node, method, whitelist = NULL, blacklist = NULL, test = NULL, alpha = 0.05, B = NULL, max.sx = NULL, debug = FALSE)
```
Arguments

- **x**: a data frame containing the variables in the model.
- **node**: a character string, the label of the node whose local structure is being learned.
- **method**: a character string, the label of a structure learning algorithm. Possible choices are listed in structure learning.
- **whitelist**: a vector of character strings, the labels of the whitelisted nodes.
- **blacklist**: a vector of character strings, the labels of the blacklisted nodes.
- **start**: a vector of character strings, the labels of the nodes to be included in the Markov blanket before the learning process (in `learn.mb`). Note that the nodes in `start` can be removed from the Markov blanket by the learning algorithm, unlike the nodes included due to whitelisting.
- **test**: a character string, the label of the conditional independence test to be used in the algorithm. If none is specified, the default test statistic is the mutual information for categorical variables, the Jonckheere-Terpstra test for ordered factors and the linear correlation for continuous variables. See independence tests for details.
- **alpha**: a numeric value, the target nominal type I error rate.
- **B**: a positive integer, the number of permutations considered for each permutation test. It will be ignored with a warning if the conditional independence test specified by the `test` argument is not a permutation test.
- **max.sz**: a positive integer, the maximum allowed size of the conditioning sets used in conditional independence tests. The default is that there is no limit on size.
- **debug**: a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Value

A vector of character strings, the labels of the nodes in the Markov blanket (for `learn.mb`) or in the neighbourhood (for `learn.nbr`).

Author(s)

Marco Scutari

See Also

constraint-based algorithms.

Examples

```r
learn.mb(learning.test, node = "D", method = "iamb")
learn.mb(learning.test, node = "D", method = "iamb", blacklist = c("A", "F"))
learn.nbr(gaussian.test, node = "F", method = "si.hiton.pc", whitelist = "D")
```
**strength.plot**  

**Arc strength plot**

**Description**

Plot a Bayesian network and format its arcs according to the strength of the dependencies they represent. Requires the *Rgraphviz* package.

**Usage**

```r
strength.plot(x, strength, threshold, cutpoints, highlight = NULL, groups,  
layout = "dot", shape = "circle", main = NULL, sub = NULL, render = TRUE,  
debug = FALSE)
```

**Arguments**

- **x**: an object of class `bn`.
- **strength**: an object of class `bn.strength` computed from the object of class `bn` corresponding to the `x` argument.
- **threshold**: a numeric value. See below.
- **cutpoints**: an array of numeric values. See below.
- **highlight**: a list, see *graphviz.plot* for details.
- **groups**: a list of character vectors, representing groups of node labels of nodes that should be plotted close to each other.
- **layout**: a character string, the layout argument that will be passed to *Rgraphviz*. Possible values are `dots`, `neato`, `twopi`, `circo` and `fdp`. See *Rgraphviz* documentation for details.
- **shape**: a character string, the shape of the nodes. Can be `circle`, `ellipse` or `rectangle`.
- **main**: a character string, the main title of the graph. It's plotted at the top of the graph.
- **sub**: a character string, a subtitle which is plotted at the bottom of the graph.
- **debug**: a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
- **render**: a logical value. If TRUE, `strength.plot()` actually draws the figure in addition to returning the corresponding graph object. If FALSE, no figure is produced.

**Details**

The `threshold` argument is used to determine which arcs are supported strongly enough by the data to be deemed significant:

- if arc strengths have been computed using conditional independence tests, any strength coefficient (which is the p-value of the test) lesser than or equal to the threshold is considered significant.
if arc strengths have been computed using network scores, any strength coefficient (which is the increase/decrease of the network score caused by the removal of the arc) lesser than the threshold is considered significant.

if arc strengths have been computed using bootstrap or using Bayes factors, any strength coefficient (which can be interpreted as a probability for inclusion) greater or equal than the threshold is considered significant.

The default value is the value of the strength attribute of the bn.strength object passed via the strength argument.

Non-significant arcs are plotted as dashed lines.

The cutpoints argument is an array of numeric values used to divide the range of the strength coefficients into intervals. The interval each strength coefficient falls into determines the line width of the corresponding arc in the plot. The default intervals are delimited by

```
unique(c(0,threshold/c(10,5,2,1,5,1),1))
```

if the coefficients are computed from conditional independence tests, by

```
unique(c(0,(1-threshold)/c(10,5,2,1,5,1),1))
```

for bootstrap estimates or by the quantiles

```
quantile(s[s < threshold],1-c(0.50,0.75,0.90,0.95,1))
```

of the significant differences if network scores are used.

Value

`graphviz.plot()` returns invisibly the graph object produced by `Rgraphviz`. It can be further modified using the commands present in the `graph` and `Rgraphviz` packages, and it contains the arc strengths in the edge weight attribute.

Author(s)

Marco Scutari

Examples

```r
## Not run:
# plot the network learned by gs().
res <- set.arc(gs(learning.test), "A", "B")
strength <- arc.strength(res, learning.test, criterion = "x2")
\dontrun{strength.plot(res, strength)}
# add another (non-significant) arc and plot the network again.
res <- set.arc(res, "A", "C")
strength <- arc.strength(res, learning.test, criterion = "x2")
\dontrun{strength.plot(res, strength)}

## End(Not run)
```
structural.em

Structure learning from missing data

Description

Learn the structure of a Bayesian network from a data set containing missing values using Structural EM.

Usage

structural.em(x, maximize = "hc", maximize.args = list(), fit = "mle",
fit.args = list(), impute, impute.args = list(), return.all = FALSE,
start = NULL, max.iter = 5, debug = FALSE)

Arguments

x a data frame containing the variables in the model.
maximize a character string, the score-based algorithm to be used in the “maximization” step. See structure learning for details.
maximize.args a list of arguments to be passed to the algorithm specified by maximize, such as restart for hill-climbing or tabu for tabu search.
fitt a character string, the parameter learning method to be used in the “maximization” step. See bn.t for details.
fitt.args a list of arguments to be passed to the parameter learning method specified by fit.
impute a character string, the imputation method to be used in the “expectation” step. See impute for details.
impute.args a list of arguments to be passed to the imputation method specified by impute.
return.all a boolean value. See below for details.
start a bn or bn.fit object, the network used to perform the first imputation and as a starting point for for the score-based algorithm specified by maximize.
max.iter an integer, the maximum number of iterations.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Value

If return.all is FALSE, structural.em() returns an object of class bn. (See bn-class for details.)
If return.all is TRUE, structural.em() returns a list with three elements named dag (an object of class bn), imputed (a data frame containing the imputed data from the last iteration) and fitted (an object of class bn.fit, again from the last iteration; see bn.fit-class for details).
Note

If at least one of the variables in the data x does not contain any observed value, the start network must be specified and it must be a bn.fit object. Otherwise, structural.em() is unable to complete the first maximization step because it cannot fit the corresponding local distribution(s).

Note that if impute is set to bayes-lw, each call to structural.em may produce a different model since the imputation is based on a stochastic simulation.

Author(s)

Marco Scutari

References


See Also

score-based algorithms, bn.fit, impute.

---

structure-learning

Structure learning algorithms

Description

Overview of the structure learning algorithms implemented in bnlearn, with the respective reference publications.

Available Constraint-Based Learning Algorithms

- **PC** (pc.stable), a modern implementation of the first practical constraint-based structure learning algorithm.
- **Grow-Shrink** (gs): based on the Grow-Shrink Markov Blanket, the first (and simplest) Markov blanket detection algorithm used in a structure learning algorithm.
- **Incremental Association** (iamb): based on the Markov blanket detection algorithm of the same name, which is based on a two-phase selection scheme (a forward selection followed by an attempt to remove false positives).
- **Fast Incremental Association** (fast.iamb): a variant of IAMB which uses speculative stepwise forward selection to reduce the number of conditional independence tests.
- **Interleaved Incremental Association** (*inter iamb*): another variant of IAMB which uses forward stepwise selection to avoid false positives in the Markov blanket detection phase.

- **Incremental Association with FDR** (*iamb.fdr*): a variant of IAMB which adjusts the tests significance threshold with FDR.

**bnlearn** includes two implementations of each algorithm: a vanilla implementation, and a parallel one that requires a running cluster set up with the `makeCluster` function from the **parallel** package.

### Available Score-based Learning Algorithms

- **Hill-Climbing** (*hc*): a hill climbing greedy search that explores the space of the directed acyclic graphs by single-arc addition, removal and reversals; with random restarts to avoid local optima. The optimized implementation uses score caching, score decomposability and score equivalence to reduce the number of duplicated tests.

- **Tabu Search** (*tabu*): a modified hill-climbing able to escape local optima by selecting a network that minimally decreases the score function.

### Available Hybrid Learning Algorithms

- **Max-Min Hill-Climbing** (*mmhc*): a hybrid algorithm which combines the Max-Min Parents and Children algorithm (to restrict the search space) and the Hill-Climbing algorithm (to find the optimal network structure in the restricted space).

- **Restricted Maximization** (*rsmax2*): a general implementation of the Sparse Candidate algorithms, which can use any combination of constraint-based and score-based algorithms.

- **Hybrid HPC** (*h2pc*): a hybrid algorithm combining HPC and hill-climbing.
Other (Constraint-Based) Local Discovery Algorithms

These algorithms learn the structure of the undirected graph underlying the Bayesian network, which is known as the skeleton of the network. Therefore by default all arcs are undirected, and no attempt is made to detect their orientation. They are often used in hybrid learning algorithms.

- **Max-Min Parents and Children (mmpc)**: a forward selection technique for neighbourhood detection based on the maximization of the minimum association measure observed with any subset of the nodes selected in the previous iterations.
- **Hiton Parents and Children (si.hiton.pc)**: a fast forward selection technique for neighbourhood detection designed to exclude nodes early based on the marginal association. The implementation follows the Semi-Interleaved variant of the algorithm.
- **Hybrid Parents and Children (hpc)**: an algorithm building on mmhc and si.hiton.pc. The reference publication is the same as that for Hybrid HPC.

Pairwise Mutual Information Algorithms

These algorithms learn approximate network structures using only pairwise mutual information.

- **Chow-Liu (chow.liu)**: an application of the minimum-weight spanning tree and the information inequality. It learns the tree structure closest to the true one in the probability space.
- **ARACNE (aracne)**: an improved version of the Chow-Liu algorithm that is able to learn polytrees.

All these algorithms have two implementations (vanilla and parallel) like other constraint-based algorithms.

<table>
<thead>
<tr>
<th><strong>Description</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>Check, increment or reset the test/score counter used in structure learning algorithms.</td>
</tr>
</tbody>
</table>
utilities for whitelists and blacklists

Usage

```r
test.counter()
increment.test.counter(i = 1)
reset.test.counter()
```

Arguments

- `i` a numeric value, which is added to the test counter.

Value

A numeric value, the current value of the test counter.

Author(s)

Marco Scutari

Examples

```r
data(learning.test)
hc(learning.test)
test.counter()
reset.test.counter()
test.counter()
```

Description

Get or create whitelists and blacklists

Utilities for whitelists and blacklists

```r
whitelist(x)
blacklist(x)
ordering2blacklist(nodes)
tiers2blacklist(tiers)
set2blacklist(set)
```

Arguments

- `x` an object of class `bn`.
- `nodes, set` a vector of character strings, the labels of the nodes.
- `tiers` a vector of character strings or a list, see below.
Details

`ordering2blacklist()` takes a vector of character strings (the labels of the nodes), which specifies a complete node ordering. An object of class `bn` or `bn.fit`; in that case, the node ordering is derived by the graph. In both cases, the blacklist returned by `ordering2blacklist()` contains all the possible arcs that violate the specified node ordering.

`tiers2blacklist()` takes (again) a vector of character strings (the labels of the nodes), which specifies a complete node ordering, or a list of character vectors, which specifies a partial node ordering. In the latter case, all arcs going from a node in a particular element of the list (sometimes known as tier) to a node in one of the previous elements are blacklisted. Arcs between nodes in the same element are not blacklisted.

`set2blacklist()` creates a blacklist containing all the arcs between any two of the nodes whose labels are passed as the argument `set`.

Value

`whitelist()` and `blacklist()` return a matrix of character string with two columns, named `from` and `to`, if whitelist or a blacklist have been used to learn the `bn` object passed as their argument.

`ordering2blacklist()`, `tiers2blacklist()` and `set2blacklist()` return a sanitized blacklist (a two-column matrix, whose columns are labeled `from` and `to`).

Author(s)

Marco Scutari

Examples

```r
  tiers2blacklist(list(LETTERS[1:3], LETTERS[4:6]))
  set2blacklist(LETTERS[1:3])
  ordering2blacklist(LETTERS[1:6])
```

---

**whitelists-blacklists**

Whitelists and blacklists in structure learning

Description

How whitelists and blacklists are used in structure learning.

Constraint-based Algorithms

Constraint-based algorithms support arc whitelisting and blacklisting as follows:

- blacklisted arcs are never present in the learned graph.
- arcs whitelisted in one direction only (i.e. $A \rightarrow B$ is whitelisted but $B \rightarrow A$ is not) have the respective reverse arcs blacklisted, and are always present in the learned graph.
- arcs whitelisted in both directions (i.e. both $A \rightarrow B$ and $B \rightarrow A$ are whitelisted) are present in the learned graph, but their direction is set by the learning algorithm.
Any arc whitelisted and blacklisted at the same time is assumed to be whitelisted, and is thus removed from the blacklist.

**Score-based Algorithms**

Score-based algorithms support arc whitelisting and blacklisting as follows:

- blacklisted arcs are never present in the learned graph.
- arcs can only be whitelisted in a single direction, and are always present in the learned graph; it is not possible to whitelist arcs in both directions.

**Hybrid Algorithms**

Hybrid algorithms use constraint-based (or pairwise mutual information) algorithms in the *restrict phase* and score-based algorithms in the *maximize phase*. Hence whitelists and blacklists are supported as follows:

- whitelists and blacklists should be specified for the algorithm used in the restrict phase.
- if the whitelist contains any undirected arc, its consistent extension is used instead in the maximize phase.

**Pairwise Mutual Information Algorithms**

In algorithms that learn undirected graphs, such as ARACNE and Chow-Liu, arcs are treated as being whitelisted or blacklisted in both directions even if only one direction is listed in the whitelist or blacklist. Again blacklisted arcs are never present in the learned graph and whitelisted arcs are guaranteed to be present in the learned graph.
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