

Package ‘bnlearn’

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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 <<https://www.bnlearn.com/>>.

URL <https://www.bnlearn.com/>

SystemRequirements USE_C17

License GPL (>= 2)

LazyData yes

NeedsCompilation yes

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bnlearn-package	<i>Bayesian network structure learning, parameter learning and inference</i>
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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

bnlearn implements key algorithms covering all stages of Bayesian network modelling: data pre-processing, 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 GeNIe; an associated Bayesian network repository of golden-standard networks at <https://www.bnlearn.com/bnrepository/>.

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

Author(s)

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References

reference books:

Koller D, Friedman N (2009). *Probabilistic Graphical Models: Principles and Techniques*. MIT Press.

Korb K, Nicholson AE (2010). *Bayesian Artificial Intelligence*. Chapman & Hall/CRC, 2nd edition.

Pearl J (1988). *Probabilistic Reasoning in Intelligent Systems: Networks of Plausible Inference*. Morgan Kaufmann.

from the author:

Nagarajan R, Scutari M, Lebre S (2013). "Bayesian Networks in R with Applications in Systems Biology." Springer.

Scutari M (2010). "Learning Bayesian Networks with the bnlearn R Package." *Journal of Statistical Software*, **35**(3):1–22.

Scutari M (20107). "Bayesian Network Constraint-Based Structure Learning Algorithms: Parallel and Optimized Implementations in the bnlearn R Package." *Journal of Statistical Software*, **77**(2):1–20.

Examples

```
## 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...
net = 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 barchart...
## 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.
- FIO2 (*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.
- ACO2 (*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.
- VLNG (*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.

Note

The complete BN can be downloaded from <https://www.bnlearn.com/bnrepository/>.

Source

Beinlich I, Suermondt HJ, Chavez RM, Cooper GF (1989). "The ALARM Monitoring System: A Case Study with Two Probabilistic Inference Techniques for Belief Networks." *Proceedings of the 2nd European Conference on Artificial Intelligence in Medicine*, 247–256.

Examples

```
# load the data.
data(alarm)
# create and plot the network structure.
modelstring = paste0("[HIST|LVF][CVP|LVV][PCWP|LVV][HYP][LVV|HYP:LVF][LVF]",
  "[STKV|HYP:LVF][ERLO][HRBP|ERLO:HR][HREK|ERCA:HR][ERCA][HRSA|ERCA:HR][ANES]",
  "[APL][TPR|APL][ECO2|ACO2:VLNG][KINK][MINV|INT:VLNG][FIO2][PVS|FIO2:VALV]",
  "[SAO2|PVS:SHNT][PAP|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]")
dag = model2network(modelstring)
## Not run: graphviz.plot(dag)
```

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 <code>bn</code> (for <code>bn.fit</code> and <code>custom.fit</code>) or an object of class <code>bn.fit</code> (for <code>bn.net</code>).
data	a data frame containing the variables in the model.
debug	a boolean value. If <code>TRUE</code> 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

Steck H (2008). "Learning the Bayesian Network Structure: Dirichlet Prior versus Data." *Proceedings of the 24th Conference on Uncertainty in Artificial Intelligence*, 511–518.

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)

}#FOR
```

arc operations	<i>Drop, add or set the direction of an arc or an edge</i>
----------------	--

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	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.
debug	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

```
dag = cpdag(model2network("[A][C][F][B|A][D|A:C][E|B:F]"))
dag

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

arc.strength	<i>Measure arc strength</i>
--------------	-----------------------------

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

```
# strength of the arcs present in x.
arc.strength(x, data, criterion = NULL, ..., debug = FALSE)
# strength of all possible arcs, as learned from bootstrapped data.
boot.strength(data, cluster, R = 200, m = nrow(data),
  algorithm, algorithm.args = list(), cpdag = TRUE, shuffle = TRUE,
  debug = FALSE)
# strength of all possible arcs, from a list of custom networks.
custom.strength(networks, nodes, weights = NULL, cpdag = TRUE, debug = FALSE)
# strength of all possible arcs, computed using Bayes factors.
bf.strength(x, data, score, ..., debug = FALSE)

# average arc strengths.
## S3 method for class 'bn.strength'
mean(x, ..., weights = NULL)

# averaged network structure.
averaged.network(strength, threshold)
# strength threshold for inclusion in the averaged network structure.
inclusion.threshold(strength)
```

Arguments

x	an object of class <code>bn.strength</code> (for <code>mean()</code>) or of class <code>bn</code> (for all other functions).
---	---

networks	a list, containing either object of class <code>bn</code> or arc sets (matrices or data frames with two columns, optionally labeled "from" and "to"); or an object of class <code>bn.kcv</code> or <code>bn.kcv.list</code> from <code>bn.cv()</code> .
data	a data frame containing the data the Bayesian network was learned from (for <code>arc.strength()</code>) or that will be used to compute the arc strengths (for <code>boot.strength()</code> and <code>bf.strength()</code>).
cluster	an optional cluster object from package parallel .
strength	an object of class <code>bn.strength</code> , 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 <code>threshold</code> attribute of the <code>strength</code> argument.
nodes	a vector of character strings, the labels of the nodes in the network.
criterion, score	a character string. For <code>arc.strength()</code> , 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 <code>mean()</code>) or network structures (in <code>custom.strength()</code>) to compute strength coefficients. If <code>NULL</code> , weights are assumed to be uniform.
cpdag	a boolean value. If <code>TRUE</code> the (CPDAG of) the equivalence class is used instead of the network structure itself. It should make it easier to identify score-equivalent arcs.
shuffle	a boolean value. If <code>TRUE</code> the columns in the data are permuted in each bootstrap sample to enforce the fact that the ordering of the variables in the data should be an invariant.
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 <code>arc.strength()</code> , the additional tuning parameters for the network score (if <code>criterion</code> is the label of a score function, see score for details), the conditional independence test (currently the only one is <code>B</code> , the number of permutations). In <code>mean()</code> , additional objects of class <code>bn.strength</code> to average.
debug	a boolean value. If <code>TRUE</code> 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):

Friedman N, Goldszmidt M, Wyner A (1999). "Data Analysis with Bayesian Networks: A Bootstrap Approach." *Proceedings of the 15th Annual Conference on Uncertainty in Artificial Intelligence*, 196–201.

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

Scutari M, Nagarajan R (2013). "On Identifying Significant Edges in Graphical Models of Molecular Networks." *Artificial Intelligence in Medicine*, **57**(3):207–217.

See Also

[strength.plot](#), [score](#), [ci.test](#).

Examples

```
data(learning.test)
dag = hc(learning.test)
arc.strength(dag, 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))

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

## End(Not run)
```

asia

Asia (synthetic) data set by Lauritzen and Spiegelhalter

Description

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

Usage

```
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 <https://www.bnlearn.com/bnrepository/>.

Source

Lauritzen S, Spiegelhalter D (1988). "Local Computation with Probabilities on Graphical Structures and their Application to Expert Systems (with discussion)." *Journal of the Royal Statistical Society: Series B*, **50**(2):157–224.

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 or custom for the custom score. If none is specified, the default score is the <i>Bayesian Dirichlet equivalent</i> score (bde) for discrete networks and the <i>Bayesian Gaussian score</i> (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(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 ration 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|B][E|B][D|A:B:C]")
dag2 = model2network("[A][C][B|A][D|A][E|D][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 and to) as transformed by sanitization functions.
 - blacklist: a copy of the blacklist argument (a two-column matrix, whose columns are labeled 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, aic-cg, bic, bic-g, bic-cg, pnal, pnal-g and pnal-cg 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

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

Friedman N, Goldszmidt M, Wyner A (1999). "Data Analysis with Bayesian Networks: A Bootstrap Approach." *Proceedings of the 15th Annual Conference on Uncertainty in Artificial Intelligence*, 196–201.

See Also

[bn.cv](#), [rbn](#).

Examples

```
## 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.

Usage

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

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

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 <i>Classification Error</i> for Bayesian networks classifiers; otherwise, the <i>Log-Likelihood Loss</i> for both discrete and continuous data sets. See below for additional details.

<code>algorithm.args</code>	a list of extra arguments to be passed to the learning algorithm.
<code>loss.args</code>	a list of extra arguments to be passed to the loss function specified by <code>loss</code> .
<code>fit</code>	a character string, the label of the method used to fit the parameters of the network. See bn.fit for details.
<code>fit.args</code>	additional arguments for the parameter estimation procedure, see again bn.fit for details.
<code>method</code>	a character string, either <code>k-fold</code> , <code>custom-folds</code> or <code>hold-out</code> . See below for details.
<code>cluster</code>	an optional cluster object from package parallel .
<code>debug</code>	a boolean value. If <code>TRUE</code> a lot of debugging output is printed; otherwise the function is completely silent.
<code>x</code>	an object of class <code>bn.kcv</code> or <code>bn.kcv.list</code> returned by <code>bn.cv()</code> .
<code>...</code>	additional objects of class <code>bn.kcv</code> or <code>bn.kcv.list</code> to plot alongside the first.
<code>main, xlab, ylab</code>	the title of the plot, an array of labels for the boxplot, the label for the y axis.
<code>connect</code>	a logical value. If <code>TRUE</code> , 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 $m - \text{nrow}(\text{data})$ 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 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. Lower values are better.
- *Classification Error* (`pred`): the *prediction error* for a single discrete node. Lower values are better.
- *Exact Classification Error* (`pred-exact`): closed-form exact posterior predictions are available for Bayesian network classifiers. Lower values are better.
- *Predictive Correlation* (`cor`): the *correlation* between the observed and the predicted values for a single continuous node. Higher values are better.
- *Mean Squared Error* (`mse`): the *mean squared error* between the observed and the predicted values for a single continuous node. Lower values are better.
- *F1 score* (`f1`): the *F1 score* between observed and predicted values for both binary and multi-class target variables.
- *AUROC* (`auroc`): the *area under the ROC curve* for both binary and multiclass target variables. The multiclass AUROC score is computed as one-vs-rest by averaging the AUROC for each level of the target variable.

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

- `predict`: a character string, the label of the method used to predict the observations in the test set. The default is "parents". Other possible values are the same as in `predict()`.
- `predict.args`: a list containing the optional arguments for the prediction method. See the documentation for `predict()` for more details.
- `target`: a character string, the label of target node for prediction in all loss functions but `logl`, `logl-g` and `logl-cg`.

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

Koller D, Friedman N (2009). *Probabilistic Graphical Models: Principles and Techniques*. MIT Press.

See Also

[bn.boot](#), [rbn](#), [bn.kcv-class](#).

Examples

```
bn.cv(learning.test, 'hc', loss = "pred",
      loss.args = list(predict = "bayes-lw", 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)
xval
loss(xval)

## Not run:
# comparing algorithms with multiple runs of cross-validation.
gaussian.subset = gaussian.test[1:50, ]
cv.gs = bn.cv(gaussian.subset, 'gs', runs = 10)
cv.iamb = bn.cv(gaussian.subset, 'iamb', runs = 10)
cv.inter = bn.cv(gaussian.subset, 'inter.iamb', runs = 10)
plot(cv.gs, cv.iamb, cv.inter,
     xlab = c("Grow-Shrink", "IAMB", "Inter-IAMB"), connect = TRUE)

# use custom folds.
folds = split(sample(nrow(gaussian.subset)), seq(5))
bn.cv(gaussian.subset, "hc", method = "custom-folds", folds = folds)

# multiple runs, with custom folds.
folds = replicate(5, split(sample(nrow(gaussian.subset)), seq(5)),
                  simplify = FALSE)
bn.cv(gaussian.subset, "hc", method = "custom-folds", folds = folds)

## End(Not run)
```

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, method, ..., keep.fitted = TRUE,
      debug = FALSE)
custom.fit(x, dist, ordinal, debug = FALSE)
bn.net(x)
```

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, see below for details.
...	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.onode) 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.

bn.fit() accepts data with missing values encoded as NA. If the parameter estimation method was not specifically designed to deal with incomplete data, bn.fit() uses locally complete observations to fit the parameters of each local distribution.

Available methods for *discrete Bayesian networks* are:

- mle: the maximum likelihood estimator for conditional probabilities.
- bayes: the classic Bayesian posterior estimator with a uniform prior matching that in the Bayesian Dirichlet equivalent (bde) score.
- hdir: the hierarchical Dirichlet posterior estimator for related data sets from Azzimonti, Corani and Zaffalon (2019).
- hard-em: the Expectation-Maximization implementation of the estimators above.

Available methods for *Gaussian Bayesian networks* are:

- mle-g: the maximum likelihood estimator for least squares regression models.
- hard-em-g: the Expectation-Maximization implementation of the estimators above.

Available methods for *conditional Gaussian Bayesian networks* are:

- mle-cg: a combination of the maximum likelihood estimators mle and mle-g.
- hard-em-cg: the Expectation-Maximization implementation of the estimators above.

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 one of mle, mle-g or mle-cg, 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 regressions corresponding to the local distributions of continuous nodes are singular. Such missing values propagate to the results of functions such as `predict()`.
- alpha0: a positive number, the amount of information pooling between the related data sets in the hdir estimator.
- group: a character string, the label of the node with the grouping of the observations into the related data sets in the hdir estimator.
- impute and impute.args: a character string, the label of the imputation method (and its arguments) used by hard-em, hard-em-g and hard-em-cg to complete the data in the *expectation* step. The default method is the same as for `impute()`.
- fit and fit.args: a character string, the label of the parameter estimation method used by hard-em, hard-em-g and hard-em-cg to estimate the parameters in the *maximization* step. The default method is the same as for `bn.fit()`.
- loglik.threshold: a non-negative numeric value, the minimum improvement threshold to continue iterating in hard-em, hard-em-g and hard-em-cg. The threshold is defined as the relative likelihood improvement divided by the sample size of data, and defaults to 1e-3. Setting it to zero means that iterations only stop in case of negative improvement, which can happen due to stochastic noise if the imputation of the missing data uses approximate inference.
- params.threshold: a non-negative numeric value, the minimum maximum relative change in the parameter values to continue iterating in hard-em, hard-em-g and hard-em-cg. The threshold is defined as the maximum of the differences between parameter values divided scaled by the parameter value in the lastest iteration. The default value is 1e-3.
- max.iter: a positive integer value, the maximum number of iterations in hard-em, hard-em-g and hard-em-cg. The default value is 5.
- start: a `bn.fit` object, the fitted network used to initialize the hard-em, hard-em-g and hard-em-cg estimators. The default is to use the `bn.fit` object obtained from `x` with the default parameter estimator for the data, which will use locally complete data to fit the local distributions.
- newdata: a data frame, a separate set of data used to assess the convergence of the hard-em, hard-em-g and hard-em-cg estimators. The data in `data` are used by default for this purpose.

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 conditional Gaussian 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 `pensim` 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. `configs` 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 [cextend](#) for two ways of manually setting the direction of one or more arcs.

In the case of maximum likelihood estimators, `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

References

Azzimonti L, Corani G, Zaffalon M (2019). "Hierarchical Estimation of Parameters in Bayesian Networks." *Computational Statistics & Data Analysis*, **137**:67–91.

See Also

[bn.fit utilities](#), [bn.fit plots](#).

Examples

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

```

# learn the network structure.
cpdag = pc.stable(learning.test)
# set the direction of the only undirected arc, A - B.
dag = set.arc(cpdag, "A", "B")
# estimate the parameters of the Bayesian network.
fitted = bn.fit(dag, 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(dag, bn.net(fitted))

# learn the network structure.
dag = hc(gaussian.test)
# estimate the parameters of the Bayesian network.
fitted = bn.fit(dag, gaussian.test)
# replace the parameters of the node F.
fitted$F = list(coef = c(1, 2, 3, 4, 5), sd = 3)
# set again the original parameters
fitted$F = lm(F ~ A + D + E + G, data = gaussian.test)

# discrete Bayesian network from expert knowledge.
dag = model2network("[A][B][C|A:B]")
cptA = matrix(c(0.4, 0.6), ncol = 2, dimnames = list(NULL, c("LOW", "HIGH")))
cptB = matrix(c(0.8, 0.2), ncol = 2, dimnames = list(NULL, c("GOOD", "BAD")))
cptC = c(0.5, 0.5, 0.4, 0.6, 0.3, 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(dag, dist = list(A = cptA, B = cptB, C = cptC))
# for ordinal nodes it is nearly the same.
cfit = custom.fit(dag, 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(dag, 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(dag, dist = list(A = cptA, B = distB, C = distC))

```

Description

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

Details

An object of class `bn.fit` is a list whose elements correspond to the nodes of the Bayesian network. If the latter is discrete (i.e. the nodes are multinomial random variables), the object also has class `bn.fit.dnet`; each node has class `bn.fit.dnode` 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.
- `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.cnode`. 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`.
- `gpairs`: 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

<code>fitted</code>	an object of class <code>bn.fit</code> , <code>bn.fit.dnode</code> or <code>bn.fit.gnode</code> .
<code>xlab</code> , <code>ylab</code> , <code>main</code>	the label of the x axis, of the y axis, and the plot title.
<code>density</code>	a boolean value. If <code>TRUE</code> the histogram is plotted using relative frequencies, and the matching normal density is added to the plot.
<code>...</code>	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](#).

bn.fit utilities

Utilities to manipulate fitted Bayesian networks

Description

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

Usage

```
## 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, na.rm = FALSE, debug = FALSE, ...)
## S3 method for class 'bn.fit'
AIC(object, data, ..., k = 1)
## S3 method for class 'bn.fit'
BIC(object, data, ...)
```

```

## non-method functions for "bn.fit"
identifiable(x, by.node = FALSE)
singular(x, by.node = FALSE)

## 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, ...)
## S3 method for class 'bn.fit.cgnode'
coef(object, for.parents, ...)
## S3 method for class 'bn.fit.cgnode'
residuals(object, ...)
## S3 method for class 'bn.fit.cgnode'
sigma(object, for.parents, ...)

```

Arguments

object	an object of class <code>bn.fit</code> , <code>bn.fit.dnode</code> , <code>bn.fit.gnode</code> , <code>bn.fit.cgnode</code> or <code>bn.fit.onode</code> .
x	an object of class <code>bn.fit</code> .
nodes	a vector of character strings, the label of a nodes 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 <code>k = 1</code> gives the expression used to compute AIC.
by.sample	a boolean value. If <code>TRUE</code> , <code>logLik()</code> returns a vector containing the log-likelihood of each observations in the sample. If <code>FALSE</code> , <code>logLik()</code> returns a single value, the log-likelihood of the whole sample.

<code>by.node</code>	a boolean value. if TRUE, <code>identifiable()</code> and <code>singular()</code> return a vector containing one value for each local distributions. If FALSE, <code>identifiable()</code> and <code>singular()</code> return a single value for the whole model.
<code>na.rm</code>	a boolean value, whether missing values should be used in computing the log-likelihood. See below for details. The default value is FALSE, and it only has an effect if <code>by.sample = FALSE</code> .
<code>debug</code>	a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
<code>for.parents</code>	a named list in which each element contains a set of values for the discrete parents of the nodes. <code>coef()</code> and <code>sigma()</code> will only return the parameters associated with those parent configurations. (Only relevant for conditional Gaussian nodes.)

Details

`coef()` (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. If `na.rm` is set to TRUE, the log-likelihood will be NA if the data contain missing values. If `na.rm` is set to FALSE, missing values will be dropped and the log-likelihood will be computed using only locally-complete observations (effectively returning the node-average log-likelihood times the sample size). Note that the log-likelihood may be NA even if `na.rm = TRUE` if the network contains NA parameters or is singular.

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.dnode`, `bn.fit.gnode`, `bn.fit.cgnode` or `bn.fit.onode`).

Author(s)

Marco Scutari

See Also

[bn.fit](#), [bn.fit-class](#).

Examples

```
data(gaussian.test)
dag = hc(gaussian.test)
fitted = bn.fit(dag, gaussian.test)
coefficients(fitted)
coefficients(fitted$C)
str(residuals(fitted))

data(learning.test)
dag2 = hc(learning.test)
fitted2 = bn.fit(dag2, 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 (for `method = "hold-out"` or `loss = "logl"`), or NA (otherwise).

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).

Author(s)

Marco Scutari

bn.strength class	<i>The bn.strength class structure</i>
-------------------	--

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:

- `nodes`: a vector of character strings, the labels of the nodes of the network(s) the strength were computed from.
- `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

causal inference	<i>Perform causal inference</i>
------------------	---------------------------------

Description

Perform interventions and counterfactuals, using Bayesian networks as causal models.

Usage

```
# network transformations used in causal inference.
mutilated(x, evidence)
twin(x)

# causal inference types.
intervention(x, evidence)
counterfactual(x, evidence, merging = TRUE)
```

Arguments

<code>x</code>	an object of class <code>bn</code> or <code>bn.fit</code> .
<code>evidence</code>	a list, in the same format as the evidence for likelihood weighting (see cpquery).
<code>merging</code>	a boolean value. If <code>TRUE</code> , the twin network is reduced by node merging after introducing the counterfactual.

Details

`mutilated()` constructs the mutilated network arising from an ideal intervention setting the nodes involved to the values specified by evidence.

`twin()` constructs the twin network required to compute counterfactuals, separating noise (exogenous) from functional (factual) nodes and adding counterfactual nodes.

`intervention()` is an alias of `mutilated()`.

`counterfactual()` constructs the twin network and introduces a counterfactual (that is, an intervention on the counterfactual nodes) before applying node merging (optional). The intervention in evidence is specified using the labels of the nodes in `x`, and is then applied to the corresponding counterfactual nodes.

Both `twin()` and `counterfactual()` label nodes as follows:

- a counterfactual node has the label of the corresponding factual node with a period appended (as in `paste0(label, ".")`).
- a noise node has the label of the corresponding factual node with a "u" prepended (as in `paste0("u", label)`).

Value

A `bn` or `bn.fit` object, depending on the class of `x`.

Author(s)

Marco Scutari

References

- Balke A, Pearl J (2022). "Probabilistic Evaluation of Counterfactual Queries." *Probabilistic and Causal Inference: The Works of Judea Pearl*, 237–254. The original is in the Proceedings of AAAI, 1994.
- Graham D, Lee CM, Perov Y (2019). "Copy, Paste, Infer: A Robust Analysis of Twin Networks for Counterfactual Inference." *NeurIPS19 CausalML workshop*.
- Koller D, Friedman N (2009). *Probabilistic Graphical Models: Principles and Techniques*. MIT Press.
- Shpitser I, Pearl J (2007). "What counterfactuals can be tested." *Proceedings of the 23rd Conference on Uncertainty in Artificial Intelligence (UAI)*, 352–359.

Examples

```
# example from Graham, Lee and Perov.
dag = model2network("[C][A|C][B|C][D|A:B]")
intervention(dag, evidence = list(A = 0))
twin(dag)
counterfactual(dag, evidence = list(A = 0), merging = FALSE)
counterfactual(dag, evidence = list(A = 0), merging = TRUE)
```

ci.test

Independence and conditional independence tests

Description

Perform an independence or a conditional independence test.

Usage

```
ci.test(x, y, z, data, test, ..., 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 <i>mutual information</i> for categorical variables, the Jonckheere-Terpstra test for ordered factors and the <i>linear correlation</i> for continuous variables. See independence tests for details.
...	optional arguments to be passed to the test specified by test. See below for details.
debug	a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

Additional arguments of the `ci.test()` function:

- B: a positive integer, the number of permutations used to compute the p-value of permutation tests. The default value is 5000 for nonparametric permutation tests and 100 for semiparametric permutation tests.
- fun: the function that computes the conditional independence test in the custom-test test. fun must have arguments x, y, z, data and args, in this order; in other words, it must have signature `function(x, y, z, data, args)`. x and y will be the labels of the nodes to test for independence (one character string each); z will be the labels of the nodes in the conditioning set (a vector of character strings, possibly NULL for empty sets); data will contain the complete data set, with all the variables (a data frame); and args will be a list containing any additional arguments to the test.
- args: a list containing the optional arguments to fun, for tuning custom-test test functions.

Value

An object of class `hctest` 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

[independence tests](#), [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	<i>Synthetic (mixed) data set to test learning algorithms</i>
-----------------	---

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 <https://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, ...)

sid(learned, true, debug = FALSE)
shd(learned, true, wlbl = FALSE, cpdag = TRUE, debug = FALSE)
hamming(learned, true, debug = FALSE)

graphviz.compare(x, ..., groups, layout = "dot", shape = "rectangle",
  fontsize = 12, 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 <code>all.equal()</code> , currently ignored); or a set of one or more objects of class bn (for <code>graphviz.compare</code>).
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.
cpdag	a boolean value. If TRUE the (CPDAG of) the equivalence class is used instead of the network structures themselves, which is more appropriate if either was learned from data.
debug	a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
arcs	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.

<code>shape</code>	a character string, the shape of the nodes. Can be <code>circle</code> , <code>ellipse</code> or <code>rectangle</code> .
<code>fontsize</code>	a positive number, the font size for the node labels.
<code>main</code>	a vector of character strings, one for each network. They are plotted at the top of the corresponding figure(s).
<code>sub</code>	a vector of character strings, the subtitles that are plotted at the bottom of the corresponding figure(s).
<code>diff</code>	a character string, the label of the method used to compare and format the figure(s) created by <code>graphviz.compare()</code> . The default value is <code>from-first</code> , see below for details.
<code>diff.args</code>	a list of optional arguments to control the formatting of the figure(s) created by <code>graphviz.compare()</code> . 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.lty`, `tp.lwd`, `fp.col`, `fp.lty`, `fp.lwd`, `fn.col`, `fn.lty`, `fn.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.

`shd()` computes the Structural Hamming Distance (SHD). 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.

`sid()` computes the Structural Interventional Distance (SID) between two DAGs, between a CPDAG and a DAG, between a DAG and a CPDAG, or between two CPDAGs.

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.

`sid()` returns a vector of non-negative integer numbers, with additional attributes describing the distribution over all the evaluated graphs.

`graphviz.compare()` plots one or more figures and returns invisibly a list containing the graph objects generated from the networks that were passed as arguments (in the same order). They can be further modified using the **graph** and **Rgraphviz** packages. Unlike the other functions, `graphviz.compare()` accepts networks with different node sets as long as they overlap.

Author(s)

Marco Scutari

References

Tsamardinos I, Brown LE, Aliferis CF (2006). "The Max-Min Hill-Climbing Bayesian Network Structure Learning Algorithm." *Machine Learning*, **65**(1):31–78.

Peters J, Buhlmann P (2015). "Structural Intervention Distance for Evaluating Causal Graphs." *Neural Computation*, **27**(3):771–779.

Examples

```
data(learning.test)

e1 = model2network("[A][B][C|A:B][D|B][E|C][F|A:E]")
e2 = model2network("[A][B][C|A:B][D|B][E|C:F][F|A]")
shd(e2, e1, debug = TRUE)
sid(e2, e1, debug = TRUE)
unlist(compare(e1,e2))
compare(target = e1, current = e2, arcs = TRUE)
## 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

```
configs(data, all = TRUE)
```

Arguments

<code>data</code>	a data frame containing factor columns.
<code>all</code>	a boolean value. If TRUE all configuration 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

```
data(learning.test)
configs(learning.test, all = TRUE)
configs(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 (MMP), Semi-Interleaved HITON-PC or Hybrid Parents and Children (HPC) constraint-based algorithms.

Usage

```
pc.stable(x, cluster, whitelist = NULL, blacklist = NULL, test = NULL,
  alpha = 0.05, ..., max.sx = NULL, debug = FALSE, undirected = FALSE)
gs(x, cluster, whitelist = NULL, blacklist = NULL, test = NULL,
  alpha = 0.05, ..., max.sx = NULL, debug = FALSE, undirected = FALSE)
iamb(x, cluster, whitelist = NULL, blacklist = NULL, test = NULL,
  alpha = 0.05, ..., max.sx = NULL, debug = FALSE, undirected = FALSE)
fast.iamb(x, cluster, whitelist = NULL, blacklist = NULL, test = NULL,
  alpha = 0.05, ..., max.sx = NULL, debug = FALSE, undirected = FALSE)
inter.iamb(x, cluster, whitelist = NULL, blacklist = NULL, test = NULL,
  alpha = 0.05, ..., max.sx = NULL, debug = FALSE, undirected = FALSE)
iamb.fdr(x, cluster, whitelist = NULL, blacklist = NULL, test = NULL,
  alpha = 0.05, ..., max.sx = NULL, debug = FALSE, undirected = FALSE)
mmpc(x, cluster, whitelist = NULL, blacklist = NULL, test = NULL,
  alpha = 0.05, ..., max.sx = NULL, debug = FALSE, undirected = TRUE)
si.hiton.pc(x, cluster, whitelist = NULL, blacklist = NULL, test = NULL,
  alpha = 0.05, ..., max.sx = NULL, debug = FALSE, undirected = TRUE)
hpc(x, cluster, whitelist = NULL, blacklist = NULL, test = NULL,
  alpha = 0.05, ..., 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 .

<code>whitelist</code>	a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs to be included in the graph.
<code>blacklist</code>	a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs not to be included in the graph.
<code>test</code>	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 <i>mutual information</i> for categorical variables, the Jonckheere-Terpstra test for ordered factors and the <i>linear correlation</i> for continuous variables. See independence tests for details.
<code>alpha</code>	a numeric value, the target nominal type I error rate.
<code>...</code>	optional arguments to be passed to the test specified by <code>test</code> . See ci.test for details.
<code>max.sx</code>	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.
<code>debug</code>	a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
<code>undirected</code>	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. `cextend()` provides a consistent extension of partially directed networks into directed acyclic graphs, which can then be used (for instance) for parameter learning.

See [structure learning](#) for a complete list of structure learning algorithms with the respective references. All algorithms accept incomplete data, which they handle by computing individual conditional independence tests on locally complete observations.

Author(s)

Marco Scutari

See Also

[independence tests](#), [local discovery algorithms](#), [score-based algorithms](#), [hybrid algorithms](#), [cextend](#).

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

Edwards DI (2000). *Introduction to Graphical Modelling*. Springer, 2nd edition.

Reinis Z, Pokorny J, Basika V, Tiserova J, Gorican K, Horakova D, Stuchlikova E, Havranek T, Hrabovsky F (1981). "Prognostic Significance of the Risk Profile in the Prevention of Coronary Heart Disease." *Bratisl Lek Listy*, **76**:137–150. Published on Bratislava Medical Journal, in Czech.

Whittaker J (1990). *Graphical Models in Applied Multivariate Statistics*. Wiley.

Examples

```
# 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",
    "M. Work", "P. Work", "P. Work", "M. Work",
    "M. Work", "Proteins", "Proteins", "M. Work",
    "M. Work", "Smoking", "Smoking", "M. Work",
    "P. Work", "Smoking", "Smoking", "P. Work",
    "P. Work", "Proteins", "Proteins", "P. Work",
    "Smoking", "Proteins", "Proteins", "Smoking",
    "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")
```

cpdag

Equivalence classes, moral graphs and consistent extensions

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

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

cextend.all(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, debug = FALSE)
```

Arguments

x	an object of class <code>bn</code> or <code>bn.fit</code> (with the exception of <code>cextend()</code> , which only accepts objects of class <code>bn</code>).
arcs	a boolean value. If <code>TRUE</code> the arcs that are part of at least one v-structure are returned instead of the v-structures themselves.
wlbl	a boolean value. If <code>TRUE</code> 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 <code>strict</code> is <code>TRUE</code> , an error is generated; otherwise a partially extended graph is returned with a warning.
debug	a boolean value. If <code>TRUE</code> a lot of debugging output is printed; otherwise the function is completely silent.

Details

Note that arcs whose directions are dictated by the parametric assumptions of the network are preserved as directed arcs in `cpdag()`. This means that, in a conditional Gaussian network, arcs from discrete nodes to continuous nodes will be treated as whitelisted in their only valid direction.

`cextend.all()` returns all possible consistent extensions of a CPDAG, whereas `cextend()` returns only one.

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.

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

cextend.all() returns an object of class bn or a list of objects of class bn.

vstructs(), colliders(), shielded.colliders() and unshielded.colliders() return a matrix with either 2 or 3 columns, according to the value of the arcs argument.

Author(s)

Marco Scutari

References

Dor D (1992). *A Simple Algorithm to Construct a Consistent Extension of a Partially Oriented Graph*. UCLA, Cognitive Systems Laboratory.

Koller D, Friedman N (2009). *Probabilistic Graphical Models: Principles and Techniques*. MIT Press.

Pearl J (2009). *Causality: Models, Reasoning and Inference*. Cambridge University Press, 2nd edition.

Andersson SA, Madigan D, Perlman MD (1997). "A Characterization of Markov Equivalence Classes for Acyclic Digraphs." *The Annals of Statistics*, **25**(2):505–541.

Wienobst M, Luttermann M, Bannach M, Liskiewicz M (2023). "Efficient Enumeration of Markov Equivalent DAGs." *Proceedings of the Thirty-Seventh AAAI Conference on Artificial Intelligence*, 12313–12320.

Examples

```
data(learning.test)
dag = hc(learning.test)
cpdag(dag)
vstructs(dag)
```

cpquery

Perform conditional probability queries

Description

Perform conditional probability queries (CPQs).

Usage

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

Arguments

<code>fitted</code>	an object of class <code>bn.fit</code> .
<code>event, evidence</code>	see below.
<code>nodes</code>	a vector of character strings, the labels of the nodes whose conditional distribution we are interested in.
<code>cluster</code>	an optional cluster object from package parallel .
<code>method</code>	a character string, the method used to perform the conditional probability query. Currently only <i>logic sampling</i> (<code>ls</code> , the default) and <i>likelihood weighting</i> (<code>lw</code>) are implemented.
<code>...</code>	additional tuning parameters.
<code>debug</code>	a boolean value. If <code>TRUE</code> 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.

Both `cpquery()` and `cpdist()` are based on Monte Carlo particle filters, and therefore they may return slightly different values on different runs due to simulation noise.

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 `meth`, `-80d` attribute storing the value of the `method` argument. In the case of likelihood weighting, the weights are also attached as an attribute called `weights`.

Logic Sampling

Logic sampling is an *approximate inference* algorithm.

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 $5000 * \log_{10}(\text{nparams}(\text{fitted}))$ for discrete and conditional Gaussian networks and $500 * \text{nparams}(\text{fitted})$ 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. Furthermore, the probabilities returned by `cpquery()` are approximate estimates and they will not sum up to 1 even when the corresponding underlying values do if they are computed in separate calls to `cpquery()`.

Likelihood Weighting

Likelihood weighting is an *approximate inference* algorithm based on Monte Carlo sampling.

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. Furthermore, the probabilities returned by `cpquery()` are approximate estimates and they will not sum up to 1 even when the corresponding underlying values do if they are computed in separate calls to `cpquery()`.

Author(s)

Marco Scutari

References

- Koller D, Friedman N (2009). *Probabilistic Graphical Models: Principles and Techniques*. MIT Press.
- Korb K, Nicholson AE (2010). *Bayesian Artificial Intelligence*. Chapman & Hall/CRC, 2nd edition.

Examples

```
## 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))
```

data preprocessing

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

```
# 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, method, threshold, debug = FALSE)
```

Arguments

data	a data frame containing numeric columns (for <code>dedup()</code>) or a combination of numeric or factor columns (for <code>discretize()</code>).
threshold	a numeric value between zero and one, the absolute correlation used a threshold in screening highly correlated pairs.
method	a character string, either <code>interval</code> for <i>interval discretization</i> , <code>quantile</code> for <i>quantile discretization</i> (the default) or <code>hartemink</code> for <i>Hartemink's pairwise mutual information</i> method.
breaks	an integer number, the number of levels the variables will be discretized into; or 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 as its first argument and returns a second data frame of discrete variables, transformed using of three methods: `interval`, `quantile` or `hartemink`. Discrete variables are left unchanged.

The `hartemink` method has two additional tuning parameters:

- `idisc`: the method used for the initial marginal discretization of the variables, either `interval` or `quantile`.
- `ibreaks`: the number of levels the variables are initially discretized into, in the same format as in the `breaks` argument.

It is sometimes the case that the `quantile` method cannot discretize one or more variables in the data without generating zero-length intervals because the quantiles are not unique. If `method = "quantile"`, `discretize()` will produce an error. If `method = "quantile"` and `idisc = "quantile"`, `discretize()` will try to lower the number of breaks set by the `ibreaks` argument until quantiles are distinct. If this is not possible without making `ibreaks` smaller than `breaks`, `discretize()` will produce an error.

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

Both `discretize()` and `dedup()` accept data with missing values.

Value

`discretize()` returns a data frame with the same structure (number of columns, column names, etc.) as `data`, containing the discretized variables. The data frame has an attribute "cutpoints" containing the cutpoints used internally by `discretize()`, which are made available to discretize another data set into the same set of factors.

`dedup()` returns a data frame with a subset of the columns of `data`.

Author(s)

Marco Scutari

References

Hartemink A (2001). *Principled Computational Methods for the Validation and Discovery of Genetic Regulatory Networks*. Ph.D. thesis, School of Electrical Engineering and Computer Science, Massachusetts Institute of Technology.

Examples

```
data(gaussian.test)
d = discretize(gaussian.test, method = 'hartemink', breaks = 4, ibreaks = 10)
plot(hc(d))
d2 = dedup(gaussian.test)
```

dsep	<i>Test d-separation</i>
------	--------------------------

Description

Check whether two nodes are d-separated.

Usage

```
dsep(bn, x, y, z)
```

Arguments

<code>bn</code>	an object of class <code>bn</code> .
<code>x, y</code>	a character string, the label of a node.
<code>z</code>	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

Koller D, Friedman N (2009). *Probabilistic Graphical Models: Principles and Techniques*. MIT Press.

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

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

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

Bayesian Network Repository, <https://www.bnlearn.com/bnrepository/>.

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 <https://www.bnlearn.com/documentation/networks/>.

Examples

```
# 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

```
## 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 `$m$` grain 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

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

graph enumeration

Count graphs with specific characteristics

Description

Count directed acyclic graphs of various sizes and/or with specific characteristics.

Usage

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

Arguments

type	a character string, the label describing the types of graphs to be counted (see below).
...	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 with nodes nodes.
- "dags-given-ordering": all directed acyclic graphs with a specific topological ordering and nodes nodes.
- "dags-with-k-roots": all directed acyclic graphs with k root nodes and nodes nodes.
- "dags-with-r-arcs": all directed acyclic graphs with r arcs and nodes nodes.
- "dags-in-equivalence-class": all directed acyclic arcs in the equivalence class described by eqclass.

Value

count.graphs() returns an object of class bigz from the **gmp** package, a vector with the graph counts.

Author(s)

Marco Scutari

References

- Harary F, Palmer EM (1973). "Graphical Enumeration." Academic Press.
- Rodionov VI (1992). "On the Number of Labeled Acyclic Digraphs." *Discrete Mathematics*, **105**:319–321.
- Liskovets VA (1976). "On the Number of Maximal Vertices of a Random Acyclic Digraph." *Theory of Probability and its Applications*, **20**(2):401–409.
- Wienobst M, Luttermann M, Bannach M, Liskiewicz (2023). "Efficient Enumeration of Markov Equivalent DAGs." *Proceedings of the 37th AAAI Conference on Artificial Intelligence*, 12313–12320.

Examples

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

## End(Not run)
```

graph generation utilities

Generate empty, complete or random graphs

Description

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

Usage

```
empty.graph(nodes, num = 1)
complete.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 (<i>full ordering</i> based generation), ic-dag (Ide's and Cozman's <i>Generating Multi-connected DAGs</i> algorithm) and melancon (Melancon's and Philippe's <i>Uniform Random Acyclic Digraphs</i> algorithm).
...	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

Graph generation algorithms available in `random.graph()` 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.

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`.

`empty.graph()` generates `num` identical empty graphs, while `complete.graph()` generates `num` identical complete directed acyclic graphs.

Value

`empty.graph()`, `complete.graph()` and `random[.graph()` return an object of class `bn` (if `num` 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

- Ide JS, Cozman FG (2002). "Random Generation of Bayesian Networks." *Proceedings of the 16th Brazilian Symposium on Artificial Intelligence*, 366–375.
- Melancon G, Dutour I, Bousquet-Melou M (2001). "Random Generation of Directed Acyclic Graphs." *Electronic Notes in Discrete Mathematics*, **10**:202–207.
- Melancon G, Philippe F (2004). "Generating Connected Acyclic Digraphs Uniformly at Random." *Information Processing Letters*, **90**(4):209–213.

Examples

```
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	<i>Import and export networks from the graph package</i>
-------------------	--

Description

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

Usage

```
## 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

Examples

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

graph utilities

*Utilities to manipulate graphs***Description**

Check and manipulate graph-related properties of an object of class bn.

Usage

```
# check whether the graph is acyclic/completely directed.
acyclic(x, directed = FALSE, debug = FALSE)
directed(x)
valid.dag(x, debug = FALSE)
valid.cpdag(x, debug = FALSE)
valid.ug(x, debug = FALSE)
# check whether there is a path between two nodes.
path.exists(x, 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	an object of class bn. <code>skeleton()</code> , <code>acyclic()</code> , <code>directed()</code> and <code>path.exists()</code> also accept objects of class <code>bn.fit</code> .
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.
 valid.dag(), valid.cpdag() and valid.ug() return a logical value.

Author(s)

Marco Scutari

References

Bang-Jensen J, Gutin G (2009). *Digraphs: Theory, Algorithms and Applications*. Springer, 2nd edition.

Examples

```
data(learning.test)
cpdag = pc.stable(learning.test)

acyclic(cpdag)
directed(cpdag)
dag = pdag2dag(cpdag, ordering = LETTERS[1:6])
dag
directed(dag)
skeleton(dag)
```

graphviz.chart

Plotting networks with probability bars

Description

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

Usage

```
graphviz.chart(x, type = "barchart", layout = "dot", draw.labels = 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 <code>bn.fit</code> .
type	a character string, the type of graph used to plot the probability distributions in the nodes. Possible values are <code>barchart</code> , <code>dotplot</code> and <code>barprob</code> (a <code>barchart</code> with parameter values printed over the bars).
layout	a character string, the layout argument that will be passed to Rgraphviz . Possible values are <code>dots</code> , <code>neato</code> , <code>twopi</code> , <code>circo</code> and <code>fdp</code> . See Rgraphviz documentation for details.
draw.labels	a boolean value, whether to print the labels of the parameters of each variable.
grid	a boolean value, whether to draw to a reference grid for the probability distributions. If <code>grid</code> is <code>TRUE</code> , a vertical grid is drawn at probabilities <code>c(0, 0.25, 0.50, 0.75)</code> for discrete nodes, and at the quartiles of the regression coefficients range for continuous nodes. If <code>grid</code> is a numeric vector, a vertical grid is drawn at the specified values. If <code>grid</code> is a named list, each element is a set of grid points can be specified for the corresponding node.
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

```
## Not run:
modelstring = paste("[HIST|LVF][CVP|LVV][PCWP|LVV][HYP][LVV|HYP:LVF][LVF]",
  "[STKV|HYP:LVF][ERLO][HRBP|ERLO:HR][HREK|ERCA:HR][ERCA][HRSA|ERCA:HR][ANES]",
  "[APL][TPR|APL][ECO2|ACO2:VLNG][KINK][MINV|INT:VLNG][FIO2][PVS|FIO2:VALV]",
  "[SAO2|PVS:SHNT][PAP|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]", sep = "")
```

```

dag = model2network(modelstring)
fitted = bn.fit(dag, alarm)

# Netica style.
graphviz.chart(fitted, grid = TRUE, bg = "beige", bar.col = "black")
# Hugin style.
graphviz.chart(fitted, type = "barprob", grid = TRUE, bar.col = "green",
  strip.bg = "lightyellow")
# GeNIe style.
graphviz.chart(fitted, col = "darkblue", bg = "azure", bar.col = "darkblue")
# personal favourites.
graphviz.chart(fitted, type = "barprob", grid = TRUE, bar.col = "darkgreen",
  strip.bg = "lightskyblue")
graphviz.chart(fitted, type = "barprob", grid = TRUE, bar.col = "gold",
  strip.bg = "lightskyblue")
# dot-plot version.
graphviz.chart(fitted, type = "dotplot")

## End(Not run)

```

graphviz.plot

Advanced Bayesian network plots

Description

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

Usage

```

graphviz.plot(x, highlight = NULL, groups, layout = "dot",
  shape = "rectangle", fontsize = 12, 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.
fontsize	a positive number, the font size for the node labels.
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:

- `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 `transparent`.
- `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**.

Note that all these parameters take a single value that is then applied to all nodes and arcs that will be highlighted.

Value

`graphviz.plot()` returns invisibly the graph object produced from the network passed as the `x` argument. It can be further modified using 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:

- N07muVerMo (*10.7mu 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 adry air*): a four-level factor with levels VeryWet, Wet, Neutral and Dry.
- VISCloudCov (*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.
- CompPlFcst (*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.
- MountainFcst (*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.
- ScenRelAMCIN (*scenario relevant to AM convective inhibition*): a two-level factor with levels AB and CThruK.
- MorningCIN (*morning convective inhibition*): a four-level factor with levels None, PartInhibit, Stifling and TotalInhibit.
- AMCINInScen (*AM convective inhibition in scenario*): a three-level factor with levels LessThanAve, Average and MoreThanAve.
- CapInScen (*capping withing scenario*): a three-level factor with levels LessThanAve, Average and MoreThanAve.
- ScenRelAMIns (*scenario relevant to AM instability*): a six-level factor with levels ABI, CDEJ, F, G, H and K.
- LIfr12ZDENSd (*LI from 12Z DEN sounding*): a four-level factor with levels LIGt0, N1GtLIGt_4, N5GtLIGt_8 and LILt_8.
- AMDewptCalPl (*AM dewpoint calculations, plains*): a three-level factor with levels Instability, Neutral and Stability.
- AMInsWliScen (*AM instability within scenario*): a three-level factor with levels LessUnstable, Average and MoreUnstable.
- InsScIInScen (*instability scaling within scenario*): a three-level factor with levels LessUnstable, Average and MoreUnstable.
- ScenRel134 (*scenario relevant to regions 2/3/4*): a five-level factor with levels ACEFK, B, D, GJ and HI.
- LatestCIN (*latest convective inhibition*): a four-level factor with levels None, PartInhibit, Stifling and TotalInhibit.
- LLIW (*LLIW severe weather index*): a four-level factor with levels Unfavorable, Weak, Moderate and Strong.

- CurPropConv (*current propensity to convection*): a four-level factor with levels None, Slight, Moderate and Strong.
- ScnRelPlFcst (*scenario relevant to plains forecast*): an eleven-level factor with levels A, B, C, D, E, F, G, H, I, J and K.
- PlainsFcst (*plains forecast*): a three-level factor with levels XNIL, SIG and SVR.
- N34StarFcst (*regions 2/3/4 forecast*): a three-level factor with levels XNIL, SIG and SVR.
- R5Fcst (*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, HighEverywher, Other.
- LowLLapse (*low-level lapse rate*): a four-level factor with levels CloseToDryAd, Steep, ModerateOrLe and Stable.
- MeanRH (*mean relative humidity*): a three-level factor with levels VeryMoist, Average and Dry.
- MidLLapse (*mid-level lapse rate*): a three-level factor with levels CloseToDryAd, Steep and ModerateOrLe.
- MvmtFeatures (*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 <https://www.bnlearn.com/bnrepository/>.

Source

Abramson B, Brown J, Edwards W, Murphy A, Winkler RL (1996). "Hailfinder: A Bayesian System for Forecasting Severe Weather." *International Journal of Forecasting*, **12**(1):57–71.

Examples

```
# load the data.
data(hailfinder)
# create and plot the network structure.
```

```

modelstring = paste0("[N07muVerMo|SubjVertMo|QGVertMotion|SatContMoist|RaoContMoist]",
  "[VISCloudCov|IRCloudCover|AMInstabMt|WndHodograph|MorningBound|LoLevMoistAd|Date]",
  "[MorningCIN|LIfr12ZDENSd|AMDewptCalPl|LatestCIN|LLIW]",
  "[CombVerMo|N07muVerMo:SubjVertMo:QGVertMotion|CombMoisture|SatContMoist:RaoContMoist]",
  "[CombClouds|VISCloudCov:IRCloudCover|Scenario|Date|CurPropConv|LatestCIN:LLIW]",
  "[AreaMesoALS|CombVerMo|ScenRelAMCIN|Scenario|ScenRelAMIns|Scenario|ScenRel34|Scenario]",
  "[ScnRelPlFcst|Scenario|Dewpoints|Scenario|LowLLapse|Scenario|MeanRH|Scenario]",
  "[MidLLapse|Scenario|MvmtFeatures|Scenario|RHRatio|Scenario|SfcWndShfDis|Scenario]",
  "[SynForcng|Scenario|TempDis|Scenario|WindAloft|Scenario|WindFieldMt|Scenario]",
  "[WindFieldPln|Scenario|AreaMoDryAir|AreaMesoALS:CombMoisture]",
  "[AMCINInScen|ScenRelAMCIN:MorningCIN|AMInsWliScen|ScenRelAMIns:LIfr12ZDENSd:AMDewptCalPl]",
  "[CldShadeOth|AreaMesoALS:AreaMoDryAir:CombClouds|InsInMt|CldShadeOth:AMInstabMt]",
  "[OutflowFrMt|InsInMt:WndHodograph|CldShadeConv|InsInMt:WndHodograph|MountainFcst|InsInMt]",
  "[Boundaries|WndHodograph:OutflowFrMt:MorningBound|N34StarFcst|ScenRel34:PlainsFcst]",
  "[CompPlFcst|AreaMesoALS:CldShadeOth:Boundaries:CldShadeConv|CapChange|CompPlFcst]",
  "[InsChange|CompPlFcst:LoLevMoistAd|CapInScen|CapChange:AMCINInScen]",
  "[InsScIInScen|InsChange:AMInsWliScen|R5Fcst|MountainFcst:N34StarFcst]",
  "[PlainsFcst|CapInScen:InsScIInScen:CurPropConv:ScnRelPlFcst]")
dag = model2network(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

```

rsmx2(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.

<code>maximize</code>	a character string, the score-based algorithm to be used in the “maximize” phase. Possible values are <code>hc</code> and <code>tabu</code> . See structure learning for details.
<code>restrict.args</code>	a list of arguments to be passed to the algorithm specified by <code>restrict</code> , such as <code>test</code> or <code>alpha</code> .
<code>maximize.args</code>	a list of arguments to be passed to the algorithm specified by <code>maximize</code> , such as <code>restart</code> for hill-climbing or <code>tabu</code> for tabu search.
<code>debug</code>	a boolean value. If <code>TRUE</code> 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 `mmhc` and `maximize` set to `hc`. Similarly, `h2pc` is simply `rsmax2()` with `restrict` set to `h2pc` and `maximize` set to `hc`.

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](#), [constraint-based algorithms](#).

igraph integration *Import and export networks from the igraph package*

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)
```

independence-tests	<i>Conditional independence tests</i>
--------------------	---------------------------------------

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:

Edwards DI (2000). *Introduction to Graphical Modelling*. Springer, 2nd edition.

Additionally for continuous permutation tests:

Legendre P (2000). "Comparison of Permutation Methods for the Partial Correlation and Partial Mantel Tests." *Journal of Statistical Computation and Simulation*, **67**:37–73.

and for semiparametric discrete tests:

Tsamardinos I, Borboudakis G (2010). "Permutation Testing Improves Bayesian Network Learning." *Machine Learning and Knowledge Discovery in Databases*, 322–337.

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 χ^2 test (mi and mi-adf), the Monte Carlo permutation test (mc-mi), the sequential Monte Carlo permutation test (smc-mi), and the semiparametric test (sp-mi) are implemented. Compared to mi, mi-adf adjusts the degrees of freedom for structural zeroes and automatically favours independence if there are fewer than 5 observations per parameter.
- *shrinkage estimator* for the *mutual information* (mi-sh): an improved asymptotic χ^2 test based on the James-Stein estimator for the mutual information.
Hausser J, Strimmer K (2009). "Entropy Inference and the James-Stein Estimator, with Application to Nonlinear Gene Association Networks." *Statistical Applications in Genetics and Molecular Biology*, **10**:1469–1484.
- *Pearson's X^2* : the classical Pearson's X^2 test for contingency tables. The asymptotic χ^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.
Hotelling H (1953). "New Light on the Correlation Coefficient and its Transforms." *Journal of the Royal Statistical Society: Series B*, **15**(2):193–225.
- *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 $2n$ factor). The asymptotic χ^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 χ^2 test based on the James-Stein estimator for the mutual information.
Ledoit O, Wolf M (2003). "Improved Estimation of the Covariance Matrix of Stock Returns with an Application to Portfolio Selection." *Journal of Empirical Finance*, **10**:603–621.

Available conditional independence tests (and the respective labels) for *conditional Gaussian 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 $2n$ factor). Only the asymptotic χ^2 test (mi-cg) is implemented.

information theoretic quantities

Compute the distance between two fitted Bayesian networks

Description

Compute Shannon's entropy of a fitted Bayesian network and the Kullback-Leibler divergence between two fitted Bayesian networks.

Usage

```
H(P)
KL(P, Q)
```

Arguments

P, Q objects of class `bn.fit`.

Value

H() and KL() return a single numeric value.

Note

Note that in the case of Gaussian and conditional Gaussian networks the divergence can be negative. Regardless of the type of network, if at least one of the two networks is singular the divergence can be infinite.

If any of the parameters of the two networks are NAs, the divergence will also be NA.

Author(s)

Marco Scutari

Examples

```
## Not run:
# discrete networks
dag = model2network("[A][C][F][B|A][D|A:C][E|B:F]")
fitted1 = bn.fit(dag, learning.test, method = "mle")
fitted2 = bn.fit(dag, learning.test, method = "bayes", iss = 20)

H(fitted1)
H(fitted2)

KL(fitted1, fitted1)
KL(fitted2, fitted2)
KL(fitted1, fitted2)
```

```
## End(Not run)

# continuous, singular networks.
dag = model2network("[A][B][E][G][C|A:B][D|B][F|A:D:E:G]")
singular = fitted1 = bn.fit(dag, gaussian.test)
singular$A = list(coef = coef(fitted1[["A"]]) + runif(1), sd = 0)

H(singular)
H(fitted1)

KL(singular, fitted1)
KL(fitted1, singular)
```

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 <https://www.bnlearn.com/bnrepository/>.

Source

Binder J, Koller D, Russell S, Kanazawa K (1997). "Adaptive Probabilistic Networks with Hidden Variables." *Machine Learning*, **29**(2–3):213–244.

Examples

```
# load the data.
data(insurance)
# create and plot the network structure.
modelstring = paste0("[Age][Mileage][SocioEcon|Age][GoodStudent|Age:SocioEcon]",
  "[RiskAversion|Age:SocioEcon][OtherCar|SocioEcon][VehicleYear|SocioEcon:RiskAversion]",
  "[MakeModel|SocioEcon:RiskAversion][SeniorTrain|Age:RiskAversion]",
  "[HomeBase|SocioEcon:RiskAversion][AntiTheft|SocioEcon:RiskAversion]",
  "[RuggedAuto|VehicleYear:MakeModel][Antilock|VehicleYear:MakeModel]",
  "[DrivingSkill|Age:SeniorTrain][CarValue|VehicleYear:MakeModel:Mileage]",
```

```

"[Airbag|VehicleYear:MakeModel][DrivQuality|RiskAversion:DrivingSkill]",
"[Theft|CarValue:HomeBase:AntiTheft][Cushioning|RuggedAuto:Airbag]",
"[DrivHist|RiskAversion:DrivingSkill][Accident|DrivQuality:Mileage:Antilock]",
"[ThisCarDam|RuggedAuto:Accident][OtherCarCost|RuggedAuto:Accident]",
"[MedCost|Age:Accident:Cushioning][ILiCost|Accident]",
"[ThisCarCost|ThisCarDam:Theft:CarValue][PropCost|ThisCarCost:OtherCarCost]")
dag = model2network(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

```
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.

Note

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

Examples

```

# load the data.
data(learning.test)
# create and plot the network structure.
dag = model2network("[A][C][F][B|A][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

Edwards DI (2000). *Introduction to Graphical Modelling*. Springer, 2nd edition.

Fienberg SE (1980). *The Analysis of Cross-Classified Categorical Data*. Springer, 2nd edition.

Schoener TW (1968). "The Anolis Lizards of Bimini: Resource Partitioning in a Complex Fauna." *Ecology*, **49**(4):704–726.

Examples

```
# 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)
```

*lm integration**Produce lm objects from Bayesian networks*

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

```
## 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

<code>x</code>	an object of class <code>bn</code> , <code>bn.fit</code> or <code>bn.fit.gnode</code> .
<code>data</code>	a data frame containing the variables in the model.
<code>...</code>	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

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)
```

local discovery algorithms

Local discovery structure learning algorithms

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 <code>mi</code> (discrete mutual information) and <code>mi-g</code> (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

[constraint-based algorithms](#), [score-based algorithms](#), [hybrid algorithms](#).

marks

Examination marks data set

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

Edwards DI (2000). *Introduction to Graphical Modelling*. Springer, 2nd edition.

Mardia KV, Kent JT, Bibby JM (1979). *Multivariate Analysis*. Academic Press.

Whittaker J (1990). *Graphical Models in Applied Multivariate Statistics*. Wiley.

Examples

```
# This is the undirected graphical model from Edwards (2000).
data(marks)
ug = empty.graph(names(marks))
arcs(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)
```

misc utilities

Miscellaneous utilities

Description

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

Usage

```
## nodes
mb(x, node)
nbr(x, node, max.dist = 1)
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)
isolated.nodes(x)
nnodes(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, debug = FALSE)
ntests(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

<code>x, object</code>	an object of class <code>bn</code> or <code>bn.fit</code> . The replacement form of parents, children, arcs and amat requires an object of class <code>bn</code> .
<code>node, Nodes</code>	a character string, the label of a node.
<code>max.dist</code>	a positive integer, the maximum number of arcs (distance) from the node at the center of the neighbourhood.
<code>value</code>	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).
<code>data</code>	a data frame containing the data the Bayesian network was learned from. It's only needed if <code>x</code> is an object of class <code>bn</code> .
<code>check.cycles</code>	a boolean value. If <code>FALSE</code> the returned network will not be checked for cycles.
<code>check.illegal</code>	a boolean value. If <code>TRUE</code> arcs that break the parametric assumptions of <code>x</code> , such as those from continuous to discrete nodes in conditional Gaussian networks, cause an error.
<code>debug</code>	a boolean value. If <code>TRUE</code> 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`, `leaf.nodes` and `isolated.nodes` return a vector of character strings.

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 nnodes 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, nparams and ntests return an integer.

Author(s)

Marco Scutari

References

Chickering DM (1995). "A Transformational Characterization of Equivalent Bayesian Network Structures." *Proceedings of the Eleventh Annual Conference on Uncertainty in Artificial Intelligence*, 87–98.

Neapolitan RE (2003). *Learning Bayesian Networks*. Prentice Hall.

Examples

```
data(learning.test)
cpdag = pc.stable(learning.test)

## the Markov blanket of A.
mb(cpdag, "A")
## the neighbourhood of F.
nbr(cpdag, "F")
## the arcs in the graph.
arcs(cpdag)
## the nodes of the graph.
nodes(cpdag)
## the adjacency matrix for the nodes of the graph.
amat(cpdag)
## the parents of D.
parents(cpdag, "D")
## the children of A.
children(cpdag, "A")
## the root nodes of the graph.
root.nodes(cpdag)
## the leaf nodes of the graph.
leaf.nodes(cpdag)
## number of parameters of the Bayesian network.
dag = set.arc(cpdag, "A", "B")
nparams(dag, 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

```
modelstring(x)
modelstring(x, debug = FALSE) <- value

model2network(string, ordering = NULL, debug = FALSE)

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

Arguments

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

Details

The strings returned by `modelstringi()` 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.

Author(s)

Marco Scutari

Examples

```
data(learning.test)
dag = hc(learning.test)
dag
modelstring(dag)
dag2 = model2network(modelstring(dag))
dag2
all.equal(dag, dag2)
```

multivariate normal distribution

Gaussian Bayesian networks and multivariate normals

Description

Convert a Gaussian Bayesian network into the multivariate normal distribution that is its global distribution, and vice versa.

Usage

```
gbn2mvnorm(fitted)
mvnorm2gbn(dag, mu, sigma)
```

Arguments

fitted	an object of class <code>bn.fit</code> .
dag	an object of class <code>bn</code> , the structure of the network that will be returned.
mu	a numeric vector, the expectation of the multivariate normal.
sigma	a square numeric matrix, the covariance matrix of the multivariate normal.

Value

`gbn2mvnorm()` returns a list with elements "mu" (the vector of expectations) and "sigma" (the covariance matrix).

`mvnorm2gbn()` returns an object of class `bn.fit`.

Author(s)

Marco Scutari

References

Pourahmadi M (2011). "Covariance Estimation: The GLM and Regularization Perspectives." *Statistical Science*, 26(3), 369–387.

See Also[bn.fit](#).**Examples**

```
data(gaussian.test)
dag = model2network("[A][B][E][G][C|A:B][D|B][F|A:D:E:G]")
bn = bn.fit(dag, gaussian.test)
mvn = gbn2mvnorm(bn)
bn2 = mvnorm2gbn(dag, mu = mvn$mu, sigma = mvn$sigma)
all.equal(bn, bn2)
```

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 <code>bn.naive</code> , 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.

<code>mi</code>	a character string, the estimator used for the mutual information coefficients for the Chow-Liu algorithm in TAN. Possible values are <code>mi</code> (discrete mutual information) and <code>mi-g</code> (Gaussian mutual information).
<code>root</code>	a character string, the label of the explanatory variable to be used as the root of the tree in the TAN classifier.
<code>...</code>	extra arguments from the generic method (currently ignored).
<code>prob</code>	a boolean value. If <code>TRUE</code> the posterior probabilities used for prediction are attached to the predicted values as an attribute called <code>prob</code> .
<code>debug</code>	a boolean value. If <code>TRUE</code> 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

References

- Borgelt C, Kruse R, Steinbrecher M (2009). *Graphical Models: Representations for Learning, Reasoning and Data Mining*. Wiley, 2nd edition.
- Friedman N, Geiger D, Goldszmidt M (1997). "Bayesian Network Classifiers." *Machine Learning*, **29**(2–3):131–163.

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	<i>Bayesian network Classifiers</i>
---------------------	-------------------------------------

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.
Friedman N, Geiger D, Goldszmit M (1997). "Bayesian Network Classifiers." *Machine Learning*, **29**:131–163.

network-scores

Network scores

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* (AIC) score (aic).
- the *Bayesian Information Criterion* (BIC) score (bic), which is equivalent to the *Minimum Description Length* (MDL) and is also known as *Schwarz Information Criterion*.
Chickering DM (1995). "A Transformational Characterization of Equivalent Bayesian Network Structures." *Proceedings of the Eleventh Annual Conference on Uncertainty in Artificial Intelligence*, 87–98.
- the *extended Bayesian Information Criterion* (ebic), which adds a second penalty to BIC to penalize dense networks.
Foygel R, Drton M (2010). "Extended Bayesian Information Criteria for Gaussian Graphical Models." *NIPS* 23, 604–612.
- the *predictive log-likelihood* (pred-loglik) computed on a separate test set.
Chickering DM, Heckerman D (2000). "A Comparison of Scientific and Engineering Criteria for Bayesian Model Selection." *Statistics and Computing*, **10**:55–62.
Scutari M, Vitolo C, Tucker A (2019). "Learning Bayesian Networks from Big Data with Greedy Search: Computational Complexity and Efficient Implementation." *Statistics and Computing*, **25**(9):1095–1108.
- the logarithm of the *Bayesian Dirichlet equivalent (uniform)* score (bde) (also denoted BDeu), a score equivalent Dirichlet posterior density.
Heckerman D, Geiger D, Chickering DM (1995). "Learning Bayesian Networks: The Combination of Knowledge and Statistical Data." *Machine Learning*, **20**(3):197–243.
Castelo R, Siebes A (2000). "Priors on Network Structures. Biasing the Search for Bayesian Networks." *International Journal of Approximate Reasoning*, **24**(1):39–57.
- the logarithm of the *Bayesian Dirichlet sparse* score (bds) (BDs), a sparsity-inducing Dirichlet posterior density (not score equivalent).
Scutari M (2016). "An Empirical-Bayes Score for Discrete Bayesian Networks." *Journal of Machine Learning Research*, **52**:438–448.

- the logarithm of the *Bayesian Dirichlet* score with *Jeffrey's prior* (not score equivalent).
Suzuki J (2016). "A Theoretical Analysis of the BDeu Scores in Bayesian Network Structure Learning." *Behaviormetrika*, **44**(1):97–116.
- the logarithm of the modified *Bayesian Dirichlet equivalent* score (mbde) for mixtures of experimental and observational data (not score equivalent).
Cooper GF, Yoo C (1999). "Causal Discovery from a Mixture of Experimental and Observational Data." *Proceedings of the Fifteenth Annual Conference on Uncertainty in Artificial Intelligence*, 116–125.
- the logarithm of the *locally averaged Bayesian Dirichlet* score (bdla, not score equivalent).
Cano A, Gomez-Olmedo M, Masegosa AR, Moral S (2013). "Locally Averaged Bayesian Dirichlet Metrics for Learning the Structure and the Parameters of Bayesian Networks." *International Journal of Approximate Reasoning*, **54**:526–540.
- the logarithm of the *K2* score (k2), a Dirichlet posterior density (not score equivalent).
Korb K, Nicholson AE (2010). *Bayesian Artificial Intelligence*. Chapman & Hall/CRC, 2nd edition.
- the logarithm of the *factorized normalized maximum likelihood* score (fnml, not score equivalent).
Silander T, Roos T, Kontkanen P, Myllymaki P (2008). "Factorized Normalized Maximum Likelihood Criterion for Learning Bayesian Network Structures." *Proceedings of the 4th European Workshop on Probabilistic Graphical Models*, 257–272.
- the logarithm of the *quotient normalized maximum likelihood* (qnml).
Silander T, Leppa-Abo J, Jaasaari, Roos T (2018). "Quotient Normalized Maximum Likelihood Criterion for Learning Bayesian Network Structures." *Proceedings of Machine Learning Research*, **84**:948–957.
- the node-average (log-)likelihood (nal) and the penalized node-average (log-)likelihood (pna1).
Bodewes T, Scutari M (2021). "Learning Bayesian Networks from Incomplete Data with the Node-Averaged Likelihood." *International Journal of Approximate Reasoning*, **138**:145–160.

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* (AIC) score (aic-g).
- the corresponding *Bayesian Information Criterion* (BIC) score (bic-g).
Geiger D, Heckerman D (1994). "Learning Gaussian Networks." *Proceedings of the Tenth Annual Conference on Uncertainty in Artificial Intelligence*, 235–243.
- the *extended Bayesian Information Criterion* (ebic-g), which adds a second penalty to BIC to penalize dense networks.
Foygel R, Drton M (2010). "Extended Bayesian Information Criteria for Gaussian Graphical Models." *NIPS* 23, 604–612.
- 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).
Kuipers J, Moffa G, Heckerman D (2014). "Addendum on the Scoring of Gaussian Directed Acyclic Graphical Models." *The Annals of Statistics*, **42**(4):1689–1691.

- the node-average (log-)likelihood (nal-g) and the penalized node-average (log-)likelihood (pnal-g).

Bodewes T, Scutari M (2021). "Learning Bayesian Networks from Incomplete Data with the Node-Averaged Likelihood." *International Journal of Approximate Reasoning*, **138**:145–160.

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

- the conditional linear Gaussian *log-likelihood* (loglik-cg) score.
- the corresponding *Akaike Information Criterion* (AIC) score (aic-cg).
- the corresponding *Bayesian Information Criterion* (BIC) score (bic-cg).
- the *extended Bayesian Information Criterion* (ebic-cg), which adds a second penalty to BIC to penalize dense networks.
- the *predictive log-likelihood* (pred-loglik-cg) computed on a separate test set. The reference paper is the same as that for pred-loglik.
- the node-average (log-)likelihood (nal-cg) and the penalized node-average (log-)likelihood (pnal-cg).

Bodewes T, Scutari M (2021). "Learning Bayesian Networks from Incomplete Data with the Node-Averaged Likelihood." *International Journal of Approximate Reasoning*, **138**:145–160.

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	<i>Manipulate nodes in a graph</i>
-----------------	------------------------------------

Description

Add, remove and rename nodes in a graph.

Usage

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

Arguments

x	an object of class bn for <code>add.node()</code> and <code>remove.node()</code> ; an object of class bn or <code>bn.fit</code> for <code>rename.nodes()</code> .
object	an object of class bn or <code>bn.fit</code> .
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`.
`debug` 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

```
## 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

```
## 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.
arrow	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)
cpdag = pc.stable(learning.test)

plot(cpdag)

## highlight node B and related arcs.
plot(cpdag, highlight = "B")
## highlight B and its Markov blanket.
plot(cpdag, highlight = c("B", mb(cpdag, "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(cpdag)

```

plot.bn.strength	<i>Plot arc strengths derived from bootstrap</i>
------------------	--

Description

Plot arc strengths derived from bootstrap resampling.

Usage

```

## 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

```
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)
```

predict and impute	<i>Predict or impute missing data from a Bayesian network</i>
--------------------	---

Description

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

Usage

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

impute(object, data, cluster, method, ..., strict = TRUE, debug = FALSE)
```

Arguments

object	a object of class <code>bn.fit</code> for <code>impute</code> ; or an object of class <code>bn</code> or <code>bn.fit</code> for <code>predict</code> .
data	a data frame containing the data to be imputed. Complete observations will be ignored.
node	a character string, the label of a node.
cluster	an optional cluster object from package parallel .
method	a character string, the method used to impute the missing values or predict new ones. The default value is <code>parents</code> .
...	additional arguments for the imputation method. See below.
prob	a boolean value. If <code>TRUE</code> and object is a discrete network, the probabilities used for prediction are attached to the predicted values as an attribute called <code>prob</code> .
strict	a boolean value. If <code>TRUE</code> , <code>impute()</code> will produce an error if the data were not imputed successfully, that is, if they still contain missing values. If <code>FALSE</code> , it will return the partially imputed data with a warning.
debug	a boolean value. If <code>TRUE</code> 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.
- `exact`: the predicted values are computed using exact inference. They are maximum a posteriori estimates obtained using junction trees and belief propagation in the case of discrete networks, or posterior expectations computed using closed-form results for the multivariate normal distribution for Gaussian networks. Conditional Gaussian networks are not supported. The variables that are used to compute the predicted values can be specified with the `from` optional argument; the default is to use those in the Markov blanket of node.

`impute()` is based on `predict()`, and can impute missing values with the same methods (`parents`, `bayes-lw` and `exact`). The method `bayes-lw` 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[2001: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)
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-lw", prob = TRUE)
attr(predicted, "prob")
```

rbn

Simulate random samples from a given Bayesian network

Description

Simulate random samples from a given Bayesian network.

Usage

```
rbn(x, n = 1, ..., debug = FALSE)
```

Arguments

x	an object of class <code>bn.fit</code> .
n	a positive integer giving the number of observations to generate.
...	additional arguments for the parameter estimation procedure, see again bn.fit for details.
debug	a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

`rbn()` implements forward/logic sampling: values for the root nodes are sampled from their (unconditional) 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 `x` contains NA parameter estimates (because of unobserved discrete parents configurations in the data the parameters were learned from), `rbn` will produce samples that contain NAs when those parents configurations appear in the simulated samples. See [bn.fit](#) for details on how to make sure `bn.fit` objects contain no NA parameter estimates.

Value

A data frame with the same structure as the data originally used to fit the parameters of the Bayesian network.

Author(s)

Marco Scutari

References

Korb K, Nicholson AE (2010). *Bayesian Artificial Intelligence*. Chapman & Hall/CRC, 2nd edition.

See Also

[cpdist](#).

Examples

```
data(learning.test)
dag = hc(learning.test)
fitted = bn.fit(dag, learning.test)
rbn(fitted, 5)
```

score

Score of the Bayesian network

Description

Compute the score of the Bayesian network.

Usage

```
## 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 <i>Bayesian Information Criterion</i> 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`.
- nu: 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 (bdla). 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, BIC and penalized node-average log-likelihood scores. The default value is 1 for AIC, $\log(\text{nrow}(\text{data})) / 2$ for BIC and $1 / \text{nnodes}(\text{x}) * \text{nrow}(\text{data})^{-0.25}$ for the node-average log-likelihood scores.
- **gamma**: the additional penalty in the extended BIC scores. The default value is 0.5.
- **prior**: the prior distribution to be used with the various Bayesian Dirichlet scores (bde, mbde, bds, bdj, bdla) 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.
 - **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 $1/\text{ncol}(\text{data})$.
 - If prior is marginal, beta is the probability of inclusion of an arc. Each direction has a probability of inclusion of $\text{beta} / 2$ and the probability that the arc is not included is therefore $1 - \text{beta}$. 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`.
- **fun**: the function that computes the score component for a single node in the custom score. `fun` must have arguments `node`, `parents`, `data` and `args`, in this order; in other words, it must have signature `function(node, parents, data, args)`. `node` will contain the label of the node to be scored (a character string); `parents` will contain the labels of its parents (a character vector); `data` will contain the complete data set, with all the variables (a data frame); and `args` will be a list containing any additional arguments to the score.
- **args**: a list containing the optional arguments to `fun`, for tuning custom score functions.

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 $\text{logLik}(\text{x}) - k * \text{nparams}(\text{x})$, 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 $3 * \sqrt{.Machine\$double.eps}$. 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

[network scores](#), [arc.strength](#), [alpha.star](#).

Examples

```
data(learning.test)
dag = hc(learning.test)
score(dag, learning.test, type = "bde")

## let's see score equivalence in action!
dag2 = set.arc(dag, "B", "A")
score(dag2, learning.test, type = "bde")

## K2 score on the other hand is not score equivalent.
score(dag, learning.test, type = "k2")
score(dag2, learning.test, type = "k2")

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

## equivalent to logLik(dag, learning.test)
score(dag, learning.test, type = "loglik")

## equivalent to AIC(dag, learning.test)
score(dag, learning.test, type = "aic")

## custom score, computing BIC manually.
my.bic = function(node, parents, data, args) {

  n = nrow(data)

  if (length(parents) == 0) {

    counts = table(data[, node])
    nparams = dim(counts) - 1
    sum(counts * log(counts / n)) - nparams * log(n) / 2

  }#THEN
```

```

else {

  counts = table(data[, node], configs(data[, parents, drop = FALSE]))
  nparams = ncol(counts) * (nrow(counts) - 1)
  sum(counts * log(prop.table(counts, 2))) - nparams * log(n) / 2

}#ELSE

}#MY.BIC
score(dag, learning.test, type = "custom-score", fun = my.bic, by.node = TRUE)
score(dag, learning.test, type = "bic", by.node = TRUE)

```

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

```

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

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

<code>max.tabu</code>	a positive integer number, the iterations tabu search can perform without improving the best network score.
<code>perturb</code>	an integer, the number of attempts to randomly insert/remove/reverse an arc on every random restart.
<code>max.iter</code>	an integer, the maximum number of iterations.
<code>maxp</code>	the maximum number of parents allowed for a node in any network that is considered in the search, including that that is returned. The default value is <code>Inf</code> .
<code>optimized</code>	a boolean value. If <code>TRUE</code> (the default), score caching is used to speed up structure learning.

Value

An object of class `bn`. See [bn-class](#) for details.

Note

See [structure learning](#) for a complete list of structure learning algorithms with the respective references.

Author(s)

Marco Scutari

See Also

[network scores](#), [constraint-based algorithms](#), [hybrid algorithms](#), [local discovery algorithms](#), [alpha.star](#).

single-node local discovery

Discover the structure around a single node

Description

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

Usage

```
learn.mb(x, node, method, whitelist = NULL, blacklist = NULL, start = NULL,
  test = NULL, alpha = 0.05, ..., max.sx = NULL, debug = FALSE)
learn.nbr(x, node, method, whitelist = NULL, blacklist = NULL,
  test = NULL, alpha = 0.05, ..., max.sx = NULL, debug = FALSE)
```

Arguments

<code>x</code>	a data frame containing the variables in the model.
<code>node</code>	a character string, the label of the node whose local structure is being learned.
<code>method</code>	a character string, the label of a structure learning algorithm. Possible choices are listed in structure learning .
<code>whitelist</code>	a vector of character strings, the labels of the whitelisted nodes.
<code>blacklist</code>	a vector of character strings, the labels of the blacklisted nodes.
<code>start</code>	a vector of character strings, the labels of the nodes to be included in the Markov blanket before the learning process (in <code>learn.mb()</code>). Note that the nodes in <code>start</code> can be removed from the Markov blanket by the learning algorithm, unlike the nodes included due to whitelisting.
<code>test</code>	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 <i>mutual information</i> for categorical variables, the Jonckheere-Terpstra test for ordered factors and the <i>linear correlation</i> for continuous variables. See independence tests for details.
<code>alpha</code>	a numeric value, the target nominal type I error rate.
<code>...</code>	optional arguments to be passed to the test specified by <code>test</code> . See ci.test for details.
<code>max.sx</code>	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.
<code>debug</code>	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()`).

Note

All algorithms used by `learn.mb()` and `learn.nbr()` accept incomplete data, which they handle by computing individual conditional independence tests on locally complete observations.

Author(s)

Marco Scutari

See Also

[constraint-based algorithms](#).

Examples

```
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

```
strength.plot(x, strength, threshold, cutpoints, highlight = NULL, groups,
  layout = "dot", shape = "rectangle", fontsize = 12, 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.
fontsize	a positive number, the font size for the node labels.
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

```
## Not run:
# plot the network learned by hc().
dag = hc(learning.test)
strength = arc.strength(dag, learning.test, criterion = "x2")
strength.plot(dag, strength)
# add another (non-significant) arc and plot the network again.
dag = set.arc(dag, "A", "C")
strength = arc.strength(dag, learning.test, criterion = "x2")
```

```
strength.plot(dag, strength)

## End(Not run)
```

structural.em	<i>Structure learning from missing data</i>
---------------	---

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,
  fit.args = list(), impute, impute.args = list(), return.all = FALSE,
  start = NULL, max.iter = 5, debug = FALSE)
```

Arguments

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

Friedman N (1997). "Learning Belief Networks in the Presence of Missing Values and Hidden Variables." *Proceedings of the 14th International Conference on Machine Learning*, 125–133.

See Also

[score-based algorithms](#), [bn.fit](#), [impute](#).

Examples

```
data(learning.test)

# learn with incomplete data.
incomplete.data = learning.test
incomplete.data[1:100, 1] = NA
incomplete.data[101:200, 2] = NA
incomplete.data[1:200, 5] = NA
structural.em(incomplete.data)

## Not run:
# learn with a latent variable.
incomplete.data = learning.test
incomplete.data[seq(nrow(incomplete.data)), 1] = NA
start = bn.fit(empty.graph(names(learning.test)), learning.test)
wl = data.frame(from = c("A", "A"), to = c("B", "D"))
structural.em(incomplete.data, start = start,
  maximize.args = list(whitelist = wl))

## End(Not run)
```

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.
Colombo D, Maathuis MH (2014). "Order-Independent Constraint-Based Causal Structure Learning." *Journal of Machine Learning Research*, **15**:3921–3962.
- *Grow-Shrink* ([gs](#)): based on the *Grow-Shrink Markov Blanket*, the first (and simplest) Markov blanket detection algorithm used in a structure learning algorithm.
Margaritis D (2003). *Learning Bayesian Network Model Structure from Data*. Ph.D. thesis, School of Computer Science, Carnegie-Mellon University, Pittsburgh, PA.
- *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).
Tsamardinos I, Aliferis CF, Statnikov A (2003). "Algorithms for Large Scale Markov Blanket Discovery." *Proceedings of the Sixteenth International Florida Artificial Intelligence Research Society Conference*, 376–381.
- *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.
Yamakala S, Margaritis D (2005). "Speculative Markov Blanket Discovery for Optimal Feature Selection." *Proceedings of the Fifth IEEE International Conference on Data Mining*, 809–812.
- *Incremental Association with FDR* ([iamb.fdr](#)): a variant of IAMB which adjusts the tests significance threshold with FDR.
Pena JM (2008). "Learning Gaussian Graphical Models of Gene Networks with False Discovery Rate Control." *Proceedings of the Sixth European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics*, 165–176.
Gasse M, Aussem A, Elghazel H (2014). "A Hybrid Algorithm for Bayesian Network Structure Learning with Application to Multi-Label Learning." *Expert Systems with Applications*, **41**(15):6755–6772.

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.
Russell SJ, Norvig P (2009). *Artificial Intelligence: A Modern Approach*. Prentice Hall, 3rd edition.

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).
Tsamardinos I, Brown LE, Aliferis CF (2006). "The Max-Min Hill-Climbing Bayesian Network Structure Learning Algorithm." *Machine Learning*, **65**(1):31–78.
- *Restricted Maximization* ([rsmx2](#)): a general implementation of the Sparse Candidate algorithms, which can use any combination of constraint-based and score-based algorithms.
Friedman N, Nachman I, Pe'er D (1999). "Learning Bayesian Network Structure from Massive Datasets: the Sparse Candidate Algorithm." *Proceedings of the Fifteenth Conference on Uncertainty in Artificial Intelligence (UAI)*, 206–215.
- *Hybrid HPC* ([h2pc](#)): a hybrid algorithm combining HPC and hill-climbing.
Gasse M, Aussem A, Elghazel H (2014). "A Hybrid Algorithm for Bayesian Network Structure Learning with Application to Multi-Label Learning." *Expert Systems with Applications*, **41**(15):6755–6772.

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.
Tsamardinos I, Aliferis CF, Statnikov A (2003). "Time and Sample Efficient Discovery of Markov Blankets and Direct Causal Relations." *Proceedings of the Ninth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, 673–678.
- *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.
Aliferis FC, Statnikov A, Tsamardinos I, Subramani M, Koutsoukos XD (2010). "Local Causal and Markov Blanket Induction for Causal Discovery and Feature Selection for Classification Part I: Algorithms and Empirical Evaluation." *Journal of Machine Learning Research*, **11**:171–234.
- *Hybrid Parents and Children* ([hpc](#)): an algorithm building on [iamb.fdr](#) to learn the parents and children of each node like [mmpc](#) 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.
Chow CK, Liu CN (1968). "Approximating Discrete Probability Distributions with Dependence Trees." *IEEE Transactions on Information Theory*, IT-14 **3**:462–467.

- *ARACNE* ([aracne](#)): an improved version of the Chow-Liu algorithm that is able to learn polytrees.

Margolin AA, Nemenman I, Basso K, Wiggins C, Stolovitzky G, Dalla Favera R, Califano A (2006). "ARACNE: An Algorithm for the Reconstruction of Gene Regulatory Networks in a Mammalian Cellular Context." *BMC Bioinformatics*, **7**(Suppl 1):S7.

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

test counter

Manipulating the test counter

Description

Check, increment or reset the test/score counter used in structure learning algorithms.

Usage

```
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

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

 utilities for whitelists and blacklists

Get or create whitelists and blacklists

Description

Extract whitelists and blacklists from an object of class `bn`, or create them for use in structure learning.

Usage

```
whitelist(x)
blacklist(x)

ordering2blacklist(nodes)
tiers2blacklist(tiers)
set2blacklist(set)
```

Arguments

<code>x</code>	an object of class <code>bn</code> .
<code>nodes, set</code>	a vector of character strings, the labels of the nodes.
<code>tiers</code>	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

```
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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