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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), pairwise (ARACNE and Chow-Liu), score-based (Hill-Climbing and Tabu Search) and hybrid (MMHC and RSMAX2) 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 and cross-validation. Development snapshots with the latest bugfixes are available from <http://www.bnlearn.com>.

URL http://www.bnlearn.com/

License GPL (>= 2)

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bnlearn-package

Bayesian network structure learning, parameter learning and inference

Description

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

Details

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This package implements some algorithms for learning the structure of Bayesian networks.

Constraint-based algorithms, also known as conditional independence learners, are all optimized derivatives of the Inductive Causation algorithm (Verma and Pearl, 1991). These algorithms use conditional independence tests to detect the Markov blankets of the variables, which in turn are used to compute the structure of the Bayesian network.

Score-based learning algorithms are general purpose heuristic optimization algorithms which 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.
Several functions for parameter estimation, parametric inference, bootstrap, cross-validation and stochastic simulation are available. Furthermore, advanced plotting capabilities are implemented on top of the Rgraphviz and lattice packages.

Available Constraint-Based Learning Algorithms

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

This package includes three implementations of each algorithm:

- an optimized implementation (used when the optimized argument is set to TRUE), which uses backtracking to initialize the learning process of each node.
- an unoptimized implementation (used when the optimized argument is set to FALSE) which is better at uncovering possible erratic behaviour of the statistical tests.
- a cluster-aware implementation, which requires a running cluster set up with the makeCluster function from the parallel package.

The computational complexity of these algorithms is polynomial in the number of tests, usually \(O(N^2)\) (but super-exponential in the worst case scenario), where \(N\) is the number of variables. Execution time scales linearly with the size of the data set.

Available Score-based Learning Algorithms

- **Hill-Climbing (hc)**: a hill climbing greedy search on the space of the directed graphs. 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.

Random restart with a configurable number of perturbing operations is implemented for both algorithms.

Available Hybrid Learning Algorithms

- **Max-Min Hill-Climbing (mmhc)**: a hybrid algorithm which combines the Max-Min Parents and Children algorithm (to restrict the search space) and the Hill-Climbing algorithm (to find the optimal network structure in the restricted space).
- **Restricted Maximization (rsmax2)**: a more general implementation of the Max-Min Hill-Climbing, which can use any combination of constraint-based and score-based algorithms.
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 or the (partial) correlation graph. Therefore all the arcs are undirected, and no attempt is made to detect their orientation. They are often used in hybrid learning algorithms.

- **Max-Min Parents and Children** (mmpc): a forward selection technique for neighbourhood detection based on the maximization of the minimum association measure observed with any subset of the nodes selected in the previous iterations.
- **Hiton Parents and Children** (si.hiton.pc): a fast forward selection technique for neighbourhood detection designed to exclude nodes early based on the marginal association. The implementation follows the Semi-Interleaved variant of the algorithm.
- **Chow-Liu** (chow.liu): an application of the minimum-weight spanning tree and the information inequality. It learns the tree structure closest to the true one in the probability space.
- **ARACNE** (aracne): an improved version of the Chow-Liu algorithm that is able to learn polytrees.

All these algorithms have three implementations (unoptimized, optimized and cluster-aware) like other constraint-based algorithms.

Bayesian Network Classifiers

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 algorithms uses Chow-Liu to approximate the dependence structure of the classifiers.

Available (Conditional) Independence Tests

The conditional independence tests used in constraint-based algorithms in practice are statistical tests on the data set. Available tests (and the respective labels) are:

- **discrete case** (categorical variables)
  - mutual information: an information-theoretic distance measure. It’s proportional to the log-likelihood ratio (they differ by a 2n factor) and is related to the deviance of the tested models. The asymptotic $\chi^2$ test (mi and mi-adf, with adjusted degrees of freedom), the Monte Carlo permutation test (mc-mi), the sequential Monte Carlo permutation test (smc-mi), and the semiparametric test (sp-mi) are implemented.
  - shrinkage estimator for the mutual information (mi-sh): an improved asymptotic $\chi^2$ test based on the James-Stein estimator for the mutual information.
  - Pearson’s $X^2$: the classical Pearson’s $X^2$ test for contingency tables. The asymptotic $\chi^2$ test (x2 and x2-adf, with adjusted degrees of freedom), the Monte Carlo permutation test (mc-x2), the sequential Monte Carlo permutation test (smc-x2) and semiparametric test (sp-x2) are implemented.
• **discrete case** (ordered factors)
  - **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.

• **continuous case** (normal variables)
  - **linear correlation**: Pearson’s linear correlation. The exact Student’s t test (cor), the Monte Carlo permutation test (mc-cor) and the sequential Monte Carlo permutation test (smc-cor) are implemented.
  - **Fisher’s Z**: a transformation of the linear correlation with asymptotic normal distribution. Used by commercial software (such as TETRAD II) for the PC algorithm (an R implementation is present in the pcalg package on CRAN). 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 $\chi^2$ test (mi-g), the Monte Carlo permutation test (mc-mi-g) and the sequential Monte Carlo permutation test (smc-mi-g) are implemented.
  - **shrinkage estimator for the mutual information** (mi-g-sh): an improved asymptotic $\chi^2$ test based on the James-Stein estimator for the mutual information.

• **hybrid case** (mixed discrete and normal variables)
  - **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 $\chi^2$ test (mi-cg) is implemented.

**Available Network Scores**

Available scores (and the respective labels) are:

• **discrete case** (categorical variables)
  - the multinomial log-likelihood (loglik) score, which is equivalent to the entropy measure used in Weka.
  - the Akaike Information Criterion score (aic).
  - the Bayesian Information Criterion score (bic), which is equivalent to the Minimum Description Length (MDL) and is also known as Schwarz Information Criterion.
  - the logarithm of the Bayesian Dirichlet equivalent score (bde), a score equivalent Dirichlet posterior density.
  - the logarithm of the Bayesian Dirichlet sparse score (bds), a sparsity-inducing Dirichlet posterior density (not score equivalent).
  - the logarithm of the Bayesian Dirichlet score with Jeffrey’s prior (not score equivalent).
  - the logarithm of the modified Bayesian Dirichlet equivalent score (mbde) for mixtures of experimental and observational data (not score equivalent).
  - the logarithm of the locally averaged Bayesian Dirichlet score (bdla, not score equivalent).
  - the logarithm of the K2 score (k2), a Dirichlet posterior density (not score equivalent).

• **continuous case** (normal variables)
– the multivariate Gaussian log-likelihood (loglik-g) score.
– the corresponding Akaike Information Criterion score (aic-g).
– the corresponding Bayesian Information Criterion score (bic-g).
– a score equivalent Gaussian posterior density (bge).

• hybrid case (mixed discrete and normal variables)
  – the conditional linear Gaussian log-likelihood (loglik-cg) score.
  – the corresponding Akaike Information Criterion score (aic-cg).
  – the corresponding Bayesian Information Criterion score (bic-cg).

**Whitelist and Blacklist Support**

All learning algorithms support arc whitelisting and blacklisting:

• blacklisted arcs are never present in the 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 graph.
• arcs whitelisted in both directions (i.e. both $A \rightarrow B$ and $B \rightarrow A$ are whitelisted) are present in the 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.

In algorithms that learn undirected graphs, such as ARACNE and Chow-Liu, an arc must be blacklisted in both directions to blacklist the underlying undirected arc.

**Error Detection and Correction: the Strict Mode**

Optimized implementations of constraint-based algorithms rely heavily on backtracking to reduce the number of tests needed by the learning algorithm. This approach may sometimes hide errors either in the Markov blanket or the neighbourhood detection steps, such as when hidden variables are present or there are external (logical) constraints on the interactions between the variables.

On the other hand, in the unoptimized implementations of constraint-based algorithms the learning of the Markov blanket and neighbourhood of each node is completely independent from the rest of the learning process. Thus it may happen that the Markov blanket or the neighbourhoods are not symmetric (i.e. $A$ is in the Markov blanket of $B$ but not vice versa), or that some arc directions conflict with each other.

The strict argument enables some measure of error correction for such inconsistencies, which may help to retrieve a good model when the learning process would otherwise fail:

• if `strict` is set to `TRUE`, every error stops the learning process and results in an error message.
• if `strict` is set to `FALSE`:
  1. v-structures are applied to the network structure in lowest-p-value order; if any arc is already oriented in the opposite direction, the v-structure is discarded.
  2. nodes which cause asymmetries in any Markov blanket are removed from that Markov blanket; they are treated as false positives.
  3. nodes which cause asymmetries in any neighbourhood are removed from that neighbourhood; again they are treated as false positives (see Tsamardinos, Brown and Aliferis, 2006).

Each correction results in a warning.
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References


Examples

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

## Simple learning
# first try the Grow-Shrink algorithm
res = gs(learning.test)
# plot the network structure.
plot(res)
# now try the Incremental Association algorithm.
res2 = iamb(learning.test)
# plot the new network structure.
plot(res2)
# the network structures seem to be identical, don't they?
all.equal(res, res2)
# how many tests each of the two algorithms used?
ntests(res)
ntests(res2)
# and the unoptimized implementation of these algorithms?
## Not run: ntests(gs(learning.test, optimized = FALSE))
## Not run: ntests(iamb(learning.test, optimized = FALSE))

## Greedy search
res = hc(learning.test)
plot(res)

## Another simple example (Gaussian data)
```
data(gaussian.test)
# first try the Grow-Shrink algorithm
res = gs(gaussian.test)
plot(res)

## Blacklist and whitelist use
# the arc B - F should not be there?
blacklist = data.frame(from = c("B", "F"), to = c("F", "B"))
blacklist
res3 = gs(learning.test, blacklist = blacklist)
plot(res3)
# force E - F direction (E -> F).
whitelist = data.frame(from = c("E"), to = c("F"))
whitelist
res4 = gs(learning.test, whitelist = whitelist)
plot(res4)
# use both blacklist and whitelist.
res5 = gs(learning.test, whitelist = whitelist, blacklist = blacklist)
plot(res5)

## Debugging
# use the debugging mode to see the learning algorithms
# in action.
res = gs(learning.test, debug = TRUE)
res = hc(learning.test, debug = TRUE)
# log the learning process for future reference.
## Not run:
sink(file = "learning-log.txt")
res = gs(learning.test, debug = TRUE)
sink()
# if something seems wrong, try the unoptimized version
# in strict mode (inconsistencies trigger errors):
res = gs(learning.test, optimized = FALSE, strict = TRUE, debug = TRUE)
# or disable strict mode to let the algorithm fix errors on the fly:
res = gs(learning.test, optimized = FALSE, strict = FALSE, debug = TRUE)

## End(Not run)

---

**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)
The `alarm` data set contains the following 37 variables:

- CVP (central venous pressure): a three-level factor with levels LOW, NORMAL and HIGH.
- PCWP (pulmonary capillary wedge pressure): a three-level factor with levels LOW, NORMAL and HIGH.
- HIST (history): a two-level factor with levels TRUE and FALSE.
- TPR (total peripheral resistance): a three-level factor with levels LOW, NORMAL and HIGH.
- BP (blood pressure): a three-level factor with levels LOW, NORMAL and HIGH.
- CO (cardiac output): a three-level factor with levels LOW, NORMAL and HIGH.
- HRBP (heart rate/blood pressure): a three-level factor with levels LOW, NORMAL and HIGH.
- HREK (heart rate measured by an EKG monitor): a three-level factor with levels LOW, NORMAL and HIGH.
- HRSA (heart rate/oxygen saturation): a three-level factor with levels LOW, NORMAL and HIGH.
- PAP (pulmonary artery pressure): a three-level factor with levels LOW, NORMAL and HIGH.
- SAO2 (arterial oxygen saturation): a three-level factor with levels LOW, NORMAL and HIGH.
- FI02 (fraction of inspired oxygen): a two-level factor with levels LOW and NORMAL.
- PRSS (breathing pressure): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
- ECO2 (expelled CO2): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
- MINV (minimum volume): a four-level factor with levels ZERO, LOW, NORMAL and HIGH.
- MVS (minimum volume set): a three-level factor with levels LOW, NORMAL and HIGH.
- HYP (hypovolemia): a two-level factor with levels TRUE and FALSE.
- LVF (left ventricular failure): a two-level factor with levels TRUE and FALSE.
- APL (anaphylaxis): a two-level factor with levels TRUE and FALSE.
- ANES (insufficient anesthesia/analgesia): a two-level factor with levels TRUE and FALSE.
- PMB (pulmonary embolus): a two-level factor with levels TRUE and FALSE.
- INT (intubation): a three-level factor with levels NORMAL, ESOPHAGEAL and ONSIDED.
- 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.
- ERL0 (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 http://www.bnlearn.com/bnrepository.

Source


Examples

```r
# 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][HRSAR|ERCA:HR][ANES]",
"[APL][TPR|APL][ECO2|ACO2:VLNG][KINS][MINV:INT:VLNG][FI02][PVS|FI02:VALV]",
"[SAO2|PVS:SHNT][PAP|PMB][PMB][SHNT:INT:PMB][INT][PRSS:INT:KINS:VTUB][DISC]",
"[MVS][VMCH|MVS][VTUB:DISC:VMCH][VLNG:INT:KINS:VTUB][VALV:INT:VLNG]",
"[ACO2|VALV][CCCHL|ACO2:ANES:SAO2:TPR][HR|CCCHL][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)
```
arc operations

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

Value

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

Author(s)

Marco Scutari

References


Examples

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

for (i in 1:3) {
    a = alpha.star(dag, learning.test)
dag = hc(learning.test, score = "bde", iss = a)
}

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.
ddebug 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.
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 = NULL, R = 200, m = nrow(data),
   algorithm, algorithm.args = list(), cpdag = 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, nodes, threshold)
Arguments

x an object of class bnNstrength (for mean()) or of class bn (for all other functions).
networks a list, containing either object of class bn or arc sets (matrices or data frames with two columns, optionally labeled “from” and “to”); or an object of class bn.kcv or bn.kcv.list from bn.cv().
data a data frame containing the data the Bayesian network was learned from (for arcNstrength()) or that will be used to compute the arc strengths (for bootNstrength() and bfNstrength()).
cluster an optional cluster object from package parallel.
strength an object of class bnNstrength, see below.
threshold a numeric value, the minimum strength required for an arc to be included in the averaged network. The default value is the threshold attribute of the strength argument.
nodes a vector of character strings, the labels of the nodes in the network. In averagedNnetwork, it defaults to the set of the unique node labels in the strength argument.
criterion,score a character string. For arcNstrength(), the label of a score function or an independence test; see bnlearn-package for details. For bfNstrength(), 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 meanI()) or network structures (in customNstrength()) to compute strength coefficients. If NULL, weights are assumed to be uniform.
cpdag a boolean value. If TRUE the (PDAG of) the equivalence class is used instead of the network structure itself. It should make it easier to identify score-equivalent arcs.
algorithm a character string, the learning algorithm to be applied to the bootstrap replicates. Possible values are gs, iamb, fastI.iamb, inter.I.iamb, mmrp, hc, tabu, mmhc and rsmax2. See bnlearn-package and the documentation of each algorithm for details.
algorithmNargs a list of extra arguments to be passed to the learning algorithm.
... in arcNstrength(), the additional tuning parameters for the network score (if criterion is the label of a score function, see score for details), the conditional independence test (currently the only one is B, the number of permutations). In mean, additional objects of class bnNstrength to average.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

arcNstrength() 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 possible additional argument is `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 including the arc and the score of the network in which the arc is not 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.

`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).

`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.

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

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

**Value**

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

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

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

**Note**

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

**Author(s)**

Marco Scutari

**References**

for model averaging and bootstrap strength (confidence):


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

See Also

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

Examples

data(learning.test)
res = gs(learning.test)
res = set.arc(res, "A", "B")
arc.strength(res, learning.test)

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

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

## End(Not run)

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

\---

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 http://www.bnlearn.com/bnrepository.

Source

Examples
# load the data.
data(asia)

# create and plot the network structure.
dag = model2network("[A][S][T][A][L][S][B][S][B]:[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 \texttt{bn}, corresponding to the numerator and the denominator models in the Bayes factor.

data a data frame containing the data to be used to compute the Bayes factor.

score a character string, the label of a posterior network score. If none is specified, the default score is the \textit{Bayesian Dirichlet equivalent} score (\texttt{bde}) for discrete networks and the \textit{Bayesian Gaussian score} (\texttt{bge}) for Gaussian networks. Other kinds of Bayesian networks are not currently supported.

\dots extra tuning arguments for the posterior scores. See \texttt{bnlearn-package} for details.

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

Value

A single numeric value, the Bayes factor of the two network structures \texttt{num} and \texttt{den}.

Note

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

Author(s)

Marco Scutari

See Also

\texttt{score}, \texttt{compare}, \texttt{bf.strength}.

Examples

data(learning.test)

dag1 = model2network("[A][B][F][C][B][E][D][A:B:C]"

dag2 = model2network("[A][C][B][A][D][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.
    * phi: a character string, either heckerman or bottcher; used by the bge score.
    * k: a positive numeric value, the penalty coefficient used by the aic, aic-g, bic and bic-g scores.
    * prob: the probability of each arc to be present in a graph generated by the ordered graph generation algorithm.
    * burn.in: the number of iterations for the ic-dag graph generation algorithm to converge to a stationary (and uniform) probability distribution.
    * max.degree: the maximum degree for any node in a graph generated by the ic-dag graph generation algorithm.
    * max.in.degree: the maximum in-degree for any node in a graph generated by the ic-dag graph generation algorithm.
    * max.out.degree: the maximum out-degree for any node in a graph generated by the ic-dag graph generation algorithm.
* training: a character string, the label of the training node in a Bayesian network classifier.
* threshold: the threshold used to determine which arcs are significant when averaging network structures.

- 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).
- maxNsx: the maximum allowed size of the conditioning sets in the conditional independence tests used in constraint-based algorithms.

Author(s)
Marco Scutari

bn.boot  Parametric and 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), sim = "ordinary",
algorithm, algorithm.args = list(), statistic.args = list(),
cluster = NULL, debug = FALSE)

Arguments

data a data frame containing the variables in the model.
statistic a function or a character string (the name of a function) to be applied to each
bootstrap replicate.
R a positive integer, the number of bootstrap replicates.
m a positive integer, the size of each bootstrap replicate.
sim a character string indicating the type of simulation required. Possible values are
"ordinary" (the default, for nonparametric bootstrap) and "parametric".
algorithm a character string, the learning algorithm to be applied to the bootstrap replicates.
Possible values are gs, iamb, fast.iamb, inter.iamb, mmpc, hc, tabu, mmhc
and rsmx2. See bnlearn-package and 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 statistics.args are extracted from the list and
passed to statistic 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 Boot-
strap Approach". Proceedings of the 15th Annual Conference on Uncertainty in Artificial Intelli-
gence, pp. 196–201.

See Also

bn.cv, rbn.
### Cross-validation for Bayesian networks

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

**Usage**

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

**Arguments**

- `data`: a data frame containing the variables in the model.
- `bn`: either a character string (the label of the learning algorithm to be applied to the training data in each iteration) or an object of class `bn` (a fixed network structure).
- `loss`: a character string, the label of a loss function. If none is specified, the default loss function is the *Classification Error* for Bayesian networks classifiers; otherwise, the *Log-Likelihood Loss* for both discrete and continuous data sets. See below for additional details.
- `algorithm.args`: a list of extra arguments to be passed to the learning algorithm.
- `loss.args`: a list of extra arguments to be passed to the loss function specified by `loss`.
- `fit`: a character string, the label of the method used to fit the parameters of the network. See `bn.fit` for details.
- `fit.args`: additional arguments for the parameter estimation procedure, see again `bn.fit` for details.
method: a character string, either k-fold, custom-folds or hold-out. See below for details.

cluster: an optional cluster object from package `parallel`.

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

x: an object of class `bn.kcv` or `bn.kcv.list` returned by `bn.cv()`.

...additional objects of class `bn.kcv` or `bn.kcv.list` to plot alongside the first.

main, xlab, ylab: the title of the plot, an array of labels for the boxplot, the label for the y axis.

connect: a logical value. If TRUE, the medians points in the boxplots will be connected by a segmented line.

Value

`bn.cv()` returns an object of class `bn.kcv.list` if `runs` is at least 2, an object of class `bn.kcv` if `runs` is equal to 1.

`loss()` returns a numeric vector with a length equal to `runs`.

Cross-Validation Strategies

The following cross-validation methods are implemented:

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

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

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

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

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

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

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

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

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

The following loss functions are implemented:

- **Log-Likelihood Loss** ($\log l$): also known as negative entropy or negentropy, it is the negated expected log-likelihood of the test set for the Bayesian network fitted from the training set.
- **Gaussian Log-Likelihood Loss** ($\log l_{Mg}$): the negated expected log-likelihood for Gaussian Bayesian networks.
- **Classification Error** ($\text{pred}$): the prediction error for a single node in a discrete network. Frequentist predictions are used, so the values of the target node are predicted using only the information present in its local distribution (from its parents).
- **Posterior Classification Error** ($\text{predMlw}$ and $\text{predMlwMcg}$): similar to the above, but predictions are computed from an arbitrary set of nodes using likelihood weighting to obtain Bayesian posterior estimates. $\text{predMlw}$ applies to discrete Bayesian networks, $\text{predMlwMcg}$ to (discrete nodes in) hybrid networks.
- **Predictive Correlation** ($\text{cor}$): the correlation between the observed and the predicted values for a single node in a Gaussian Bayesian network.
- **Posterior Predictive Correlation** ($\text{corMlw}$ and $\text{corMlwMcg}$): similar to the above, but predictions are computed from an arbitrary set of nodes using likelihood weighting to obtain Bayesian posterior estimates. $\text{corMlw}$ applies to Gaussian networks and $\text{corMlwMcg}$ to (continuous nodes in) hybrid networks.
- **Mean Squared Error** ($\text{mse}$): the mean squared error between the observed and the predicted values for a single node in a Gaussian Bayesian network.
- **Posterior Mean Squared Error** ($\text{mseMlw}$ and $\text{mseMlwMcg}$): similar to the above, but predictions are computed from an arbitrary set of nodes using likelihood weighting to obtain Bayesian posterior estimates. $\text{mseMlw}$ applies to Gaussian networks and $\text{mseMlwMcg}$ to (continuous nodes in) hybrid networks.

Optional arguments that can be specified in `lossNargs` are:

- **target**: a character string, the label of target node for prediction in all loss functions but $\log l$, $\log l_{Mg}$ and $\log l_{Mlw}$.
- **from**: a vector of character strings, the labels of the nodes used to predict the target node in $\text{pred}$, $\text{predMlw}$, $\text{cor}$, $\text{corMlw}$, $\text{mse}$ and $\text{mseMlw}$. The default is to use all the other nodes in the network. Loss functions $\text{pred}$, $\text{cor}$ and $\text{mse}$ implicitly predict only from the parents of the target node.
- **n**: a positive integer, the number of particles used by likelihood weighting for $\text{pred}$, $\text{predMlw}$, $\text{cor}$, $\text{corMlw}$, $\text{mse}$ and $\text{mseMlw}$. The default value is 500.

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

Plotting Results from Cross-Validation

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

Marco Scutari

References


See Also

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

Examples

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

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

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

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)
**Description**

Fit the parameters of a Bayesian network conditional on its structure.

**Usage**

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

**Arguments**

- `x` an object of class `bn` (for `bn.fit()` and `custom.fit()`) or an object of class `bn.fit` (for `bn.net`).
- `data` a data frame containing the variables in the model.
- `cluster` an optional cluster object from package `parallel`.
- `dist` a named list, with element for each node of `x`. See below.
- `method` a character string, either `mle` for **Maximum Likelihood parameter estimation** or `bayes` for **Bayesian parameter estimation** (currently implemented only for discrete data).
- `...` additional arguments for the parameter estimation procedure, see below.
- `ordinal` a vector of character strings, the labels of the discrete nodes which should be saved as ordinal random variables (`bn.fit.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.

Additional arguments for the `bn.fit()` function:

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

If `FALSE` (the default), the conditional probabilities in the local distributions of discrete nodes have a maximum likelihood estimate of NaN for all parents configurations that are not observed in data. Similarly, regression coefficients are set to NA if the linear regressions corresponding to the local distributions of continuous nodes are singular. Such missing values propagate to the results of functions such as `predict()`.
An in-place replacement method is available to change the parameters of each node in a `bn.fit` object; see the examples for discrete, continuous and hybrid networks below. For a discrete node (class `bn.fit.dnode` or `bn.fit.onode`), the new parameters must be in a table object. For a Gaussian node (class `bn.fit.gnode`), the new parameters can be defined either by an `lm`, `glm` or `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 `pdag2dag` for two ways of manually setting the direction of one or more arcs. The bayes and mle methods handle missing values by estimating the parameters of each distribution using the observations that are complete for the variables involved in that local distribution.

Author(s)

Marco Scutari

See Also

`bn.fit utilities`, `bn.fit plots`.

Examples

data(learning.test)

# learn the network structure.
res = gs(learning.test)
# set the direction of the only undirected arc, A - B.
res = set.arc(res, "A", "B")
# estimate the parameters of the Bayesian network.
fitted = bn.fit(res, learning.test)
# replace the parameters of the node B.
new cpt = matrix(c(0.1, 0.2, 0.3, 0.2, 0.5, 0.6, 0.7, 0.3, 0.1),
bn.fit class

bn.fit class

byrow = TRUE, ncol = 3,
dimnames = list(B = c("a", "b", "c"), A = c("a", "b", "c"))
fitted$B = as.table(new.cpt)
# the network structure is still the same.
all.equal(res, bn.net(fitted))

# learn the network structure.
res = hc(gaussian.test)
# estimate the parameters of the Bayesian network.
fitted = bn.fit(res, 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.
net = model2network("[A][B][C|A:B]")
cpta = matrix(c(0.4, 0.6), ncol = 2, dimnames = list(NULL, c("LOW", "HIGH")))
cptb = matrix(c(0.8, 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(net, dist = list(A = cpta, B = cptb, C = cptc))
# for ordinal nodes it is nearly the same.
cfit = custom.fit(net, dist = list(A = cpta, B = cptb, C = cptc),
                  ordinal = c("A", "B"))

dista = list(coef = c("(Intercept)" = 2), sd = 1)
distb = list(coef = c("(Intercept)" = 1), sd = 1.5)
distc = list(coef = c("(Intercept)" = 0.5, "A" = 0.75, "B" = 1.32), sd = 0.4)
cfit = custom.fit(net, dist = list(A = distA, B = distB, C = distC))

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

bn.fit class

The bn.fit class structure

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.cgnode. Each node contains the following elements:

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

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

Author(s)

Marco Scutari

### bn.fit plots

**Plot fitted Bayesian networks**

**Description**

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

**Usage**

```r
## for Gaussian Bayesian networks.
bn.fit.qqplot(fitted, xlab = "Theoretical Quantiles",
             ylab = "Sample Quantiles", main = "Normal Q-Q Plot", ...)
bn.fit.histogram(fitted, density = TRUE, xlab = "Residuals",
                 ylab = ifelse(density, "Density", ""),
                 main = "Histogram of the residuals", ...)
bn.fit.xyplot(fitted, xlab = "Fitted values",
              ylab = "Residuals", main = "Residuals vs Fitted", ...)
## for discrete (multinomial and ordinal) Bayesian networks.
bn.fit.barchart(fitted, xlab = "Probabilities",
                ylab = "Levels", main = "Conditional Probabilities", ...)
bn.fit.dotplot(fitted, xlab = "Probabilities",
               ylab = "Levels", main = "Conditional Probabilities", ...)
```

**Arguments**

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

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

Value

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

Author(s)

Marco Scutari

See Also

bn.fit, bn.fit class.

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

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

object an object of class `bn.fit`, `bn.fit.dnode`, `bn.fit.gnode`, `bn.fit.cgnode` or `bn.fit.onode`.

nodes a vector of character strings, the label of a node whose log-likelihood components are to be computed.

data a data frame containing the variables in the model.

... additional arguments, currently ignored.

k a numeric value, the penalty coefficient to be used; the default $k = 1$ gives the expression used to compute AIC.

by.sample a boolean value. If TRUE, `logLik()` returns a vector containing the log-likelihood of each observation in the sample. If FALSE, `logLik()` returns a single value, the likelihood of the whole sample.

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.

**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**

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

data(learning.test)
res2 = hc(learning.test)
fitted2 = bn.fit(res2, learning.test)
coefficients(fitted2$E)
```

---

**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 \texttt{bn.kcv.list} is a list whose elements are objects of class \texttt{bn.kcv}.

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

- \texttt{test}: an integer vector, the indexes of the observations used as a test set.
- \texttt{fitted}: an object of class \texttt{bn.fit}, the Bayesian network fitted from the training set.
- \texttt{loss}: the value of the loss function.

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

- \texttt{predicted}: a factor or a numeric vector, the predicted values for the target node in the test set.
- \texttt{observed}: a factor or a numeric vector, the observed values for the target node in the test set.

In addition, an object of class \texttt{bn.kcv} has the following attributes:

- \texttt{loss}: a character string, the label of the loss function.
- \texttt{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”.
- \texttt{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 \texttt{bn} (a fixed network structure).

Author(s)

Marco Scutari

\begin{center}
\begin{tabular}{ll}
\textbf{bn.strength class} & \textit{The bn.strength class structure} \\
\end{tabular}
\end{center}

Description

The structure of an object of S3 class \texttt{bn.strength}.

Details

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

- \texttt{from, to}: the nodes incident on the arc.
- \texttt{strength}: the strength of the arc. See \texttt{arc.strength, boot.strength, custom.strength} and \texttt{strength.plot} for details.

and some additional attributes:
choose.direction

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

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

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

Author(s)

Marco Scutari

choose.direction  

Try to infer the direction of an undirected arc

Description

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

Usage

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

Arguments

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

Details

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

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

choose.direction returns invisibly an updated copy of x.

Author(s)

Marco Scutari

See Also

score, arc.strength.

Examples

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

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

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

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

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

## End(Not run)

---

ci.test

Independence and conditional independence tests

Description

Perform an independence or a conditional independence test.

Usage

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

x  a character string (the name of a variable), a data frame, a numeric vector or a factor object.
y  a character string (the name of another variable), a numeric vector or a factor object.
z  a vector of character strings (the names of the conditioning variables), a numeric vector, a factor object or a data frame. If NULL an independence test will be executed.
data  a data frame containing the variables to be tested.
test  a character string, the label of the conditional independence test to be used in the algorithm. If none is specified, the default test statistic is the mutual information for categorical variables, the Jonckheere-Terpstra test for ordered factors and the linear correlation for continuous variables. See bnlearn-package for details.
b  a positive integer, the number of permutations considered for each permutation test. It will be ignored with a warning if the conditional independence test specified by the test argument is not a permutation test.
debug  a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Value

An object of class htest containing the following components:

- statistic  the value the test statistic.
- parameter  the degrees of freedom of the approximate chi-squared or t distribution of the test statistic; the number of permutations computed by Monte Carlo tests. Semi-parametric tests have both.
- p.value  the p-value for the test.
- method  a character string indicating the type of test performed, and whether Monte Carlo simulation or continuity correction was used.
- data.name  a character string giving the name(s) of the data.
- null.value  the value of the test statistic under the null hypothesis, always 0.
- alternative  a character string describing the alternative hypothesis.

Author(s)

Marco Scutari

References

for parametric and discrete permutation tests:


for shrinkage tests:


**for continuous permutation tests:**


**for semiparametric discrete tests:**


See Also

choose.direction, arc.strength.

Examples

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

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

---

**clgaussian.test**

*Synthetic (mixed) data set to test learning algorithms*

---

**Description**

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

**Usage**

```r
data(clgaussian.test)
```

**Format**

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

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

Examples

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

**compare**

Compare two or more different Bayesian networks

Description

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

Usage

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

shd(learned, true, wlbl = FALSE, debug = FALSE)
hamming(learned, true, debug = FALSE)

graphviz.compare(x, ..., groups, layout = "dot", shape = "circle", main = NULL,
sub = NULL, diff = "from-first", diff.args = list())
```

Arguments

target, learned

an object of class bn.

current, true

another object of class bn.

... extra arguments from the generic method (for all.equal(), currently ignored); or a set of one or more objects of class bn (for graphviz.compare).

wlbl

a boolean value. If TRUE arcs whose directions have been fixed by a whitelist or a by blacklist are preserved when constructing the CPDAGs of learned and true.

debug

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

arcs a boolean value. See below.
compare

x an object of class bn.
groups a list of character vectors, representing groups of node labels of nodes that should be plotted close to each other.
layout a character string, the layout argument that will be passed to Rgraphviz. Possible values are dots, neato, twopi, circo and fdp. See Rgraphviz documentation for details.
shape a character string, the shape of the nodes. Can be circle, ellipse or rectangle.
main a vector of character strings, one for each network. They are plotted at the top of the corresponding figure(s).
sub a vector of character strings, the subtitles that are plotted at the bottom of the corresponding figure(s).
diff a character string, the label of the method used to compare and format the figure(s) created by graphviz.compare(). The default value is from-first, see below for details.
diff.args a list of optional arguments to control the formatting of the figure(s) created by graphviz.compare(). See below for details.

Details

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

• none: differences are not highlighted.
• from-first: the first bn object, x, is taken as the reference network. All the other networks, passed via the ... argument, are compared to that first network and their true positive, false positive, false negative arcs relative to that first network are highlighted. Colours, line types and line widths for each category of arcs can be specified as the elements of a list via the diff.args argument, with names tp.col, tp.lty, tp.lwd, fp.col, fp.lty, fp.lwd, fn.col, fn.lty, tp.lwd.

Regardless of the visualization, the nodes are arranged to be in the same position for all the networks to make it easier to compare them.

Value

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

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

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

graphviz.compare() plots one or more figures and returns NULL invisibly.

Note

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

Marco Scutari

References


Examples

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)
unlist(compare(e1, e2))
compare(target = e1, current = e2, arcs = TRUE)
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

- **data**
  - a data frame containing factor columns.
- **all**
  - 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), Max-Min Parents and Children (MMPC) or Semi-Interleaved HITON-PC constraint-based algorithms.

Usage

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

Arguments

x
a data frame containing the variables in the model.

cluster
an optional cluster object from package parallel.

whitelist
a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs to be included in the graph.

blacklist
a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs not to be included in the graph.

test
a character string, the label of the conditional independence test to be used in the algorithm. If none is specified, the default test statistic is the mutual information for categorical variables, the Jonckheere-Terpstra test for ordered factors and the linear correlation for continuous variables. See bnlearn-package for details.
alpha a numeric value, the target nominal type I error rate.
B a positive integer, the number of permutations considered for each permutation test. It will be ignored with a warning if the conditional independence test specified by the test argument is not a permutation test.
max.sx a positive integer, the maximum allowed size of the conditioning sets used in conditional independence tests. The default is that there is no limit on size.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
optimized a boolean value. See bnlearn-package for details.
strict a boolean value. If TRUE conflicting results in the learning process generate an error; otherwise they result in a warning.
undirected a boolean value. If TRUE no attempt will be made to determine the orientation of the arcs; the returned (undirected) graph will represent the underlying structure of the Bayesian network.

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

Author(s)
Marco Scutari

References
for PC:

for GS:

for IAMB:

for Fast-IAMB and Inter-IAMB:

for MMPC:

for the Semi-Interleaved HITON-PC:


See Also

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

coronary

| coronary | Coronary heart disease data set |

Description

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

Usage

data(coronary)

Format

The coronary data set contains the following 6 variables:

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

Source


Examples

# This is the undirected graphical model from Whittaker (1990).
data(coronary)
ug = empty.graph(names(coronary))
arcs(ug, check.cycles = FALSE) = matrix(
c("Family", "M. Work", "M. Work", "Family",
   "P. Work", "Smoking", "Smoking", "P. Work",
   "Smoking", "Pressure", "Pressure", "Smoking",
   "Pressure", "Proteins", "Proteins", "Pressure"),
ncol = 2, byrow = TRUE,
dimnames = list(c(), c("from", "to")))
## Not run: graphviz.plot(ug, shape = "ellipse")

---

**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

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

Arguments

- **x**
  - an object of class `bn` or `bn.fit` (with the exception of `cextend`, which only accepts objects of class `bn`).
- **arcs**
  - a boolean value. If `TRUE` the arcs that are part of at least one v-structure are returned instead of the v-structures themselves.
- **moral**
  - a boolean value. If `FALSE` we define a v-structure as in Pearl (2000); if `TRUE`, as in Koller and Friedman (2009). See below.
- **wlbl**
  - a boolean value. If `TRUE` arcs whose directions have been fixed by a whitelist or a by blacklist are preserved when constructing the CPDAG.
- **strict**
  - a boolean value. If no consistent extension is possible and `strict` is `TRUE`, an error is generated; otherwise a partially extended graph is returned with a warning.
debug

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

Details

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

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

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

Value

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

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

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

Author(s)

Marco Scutari

References


Examples

data(learning.test)
res = gs(learning.test)
cpdag(res)
vstructs(res)
cpquery  \hspace{1cm} \textit{Perform conditional probability queries}

\textbf{Description}

Perform conditional probability queries (CPQs).

\textbf{Usage}

\begin{verbatim}
cpquery(fitted, event, evidence, cluster = NULL, method = "ls", ..., debug = FALSE)
cpdist(fitted, nodes, evidence, cluster = NULL, method = "ls", ..., debug = FALSE)

mutilated(x, evidence)
\end{verbatim}

\textbf{Arguments}

- \texttt{fitted} \hspace{1cm} an object of class \texttt{bn.fit}.
- \texttt{x} \hspace{1cm} an object of class \texttt{bn} or \texttt{bn.fit}.
- \texttt{event, evidence} \hspace{1cm} see below.
- \texttt{nodes} \hspace{1cm} a vector of character strings, the labels of the nodes whose conditional distribution we are interested in.
- \texttt{cluster} \hspace{1cm} an optional cluster object from package \texttt{parallel}.
- \texttt{method} \hspace{1cm} a character string, the method used to perform the conditional probability query. Currently only \textit{logic sampling} (\texttt{ls}, the default) and \textit{likelihood weighting} (\texttt{lw}) are implemented.
- \ldots \hspace{1cm} additional tuning parameters.
- \texttt{debug} \hspace{1cm} a boolean value. If \texttt{TRUE} a lot of debugging output is printed; otherwise the function is completely silent.

\textbf{Details}

cpquery estimates the conditional probability of \texttt{event} given \texttt{evidence} using the method specified in the \texttt{method} argument.

cpdist generates random samples conditional on the \texttt{evidence} using the method specified in the \texttt{method} argument.

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

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

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

Logic Sampling

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

Three tuning parameters are available:

- **n**: a positive integer number, the number of random samples to generate from fitted. The
default value is 5000 * log10(nparams(fitted)) for discrete and conditional Gaussian net-
  works and 500 * nparams(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 net-
  work, so cpquery and cpdist try to identify which nodes are used in event and evidence and
  reduce the network to their upper closure. query.nodes may be used to manually specify
  these nodes when automatic identification fails; there is no reason to use it otherwise.

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

Likelihood Weighting

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

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

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

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

Author(s)
Marco Scutari

References

Examples

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

cmd = paste("cpquery(fitted, ", str2 , ",", str , ")", sep = "")
eval(parse(text = cmd))
# ... but note that predict works better in this particular case.
attr(predict(fitted, "C", learning.test[obs, -3], prob = TRUE), "prob")
# do the same with likelihood weighting.
cpquery(fitted, event = eval(parse(text = str2)),
    evidence = as.list(learning.test[2, -3]), method = "lw")
attr(predict(fitted, "C", learning.test[obs, -3],
    method = "bayes-lw", prob = TRUE), "prob")
# conditional distribution of A given C == "c".
table(cpdist(fitted, "A", (C == "c")))

## Gaussian Bayesian network.
data(gaussian.test)
fitted = bn.fit(hc(gaussian.test), gaussian.test)
```
ctsdag

# the result should be around 0.04.
cpquery(fitted,
    event = ((A >= 0) & (A <= 1)) & ((B >= 0) & (B <= 3)),
    evidence = (C + D < 10))

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

---

### ctsdag

**Equivalence classes in the presence of interventions**

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

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

**Value**

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

References


See Also
cpdag, score.

dsep

*Test d-separation*

Description
Check whether two nodes are d-separated.

Usage
dsep(bn, x, y, z)

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

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

Author(s)
Marco Scutari
References


Examples

```r
bn = model2network("[A][C][B][C]")
dsep(bn, "A", "B", "C")
bn = model2network("[A][C][B|A;C]")
dsep(bn, "A", "B", "C")
```

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

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

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

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

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

Arguments

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

Value

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

Note

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

Author(s)

Marco Scutari

References


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

Description

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

Usage

data(gaussian.test)

Format

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

Note

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

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

Description

Import and export networks from the gRain package

Usage

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

Arguments

- `x`: an object of class `grain` (for `as.bn.fit`) or `bn.fit` (for `as.grain`).
- `...`: 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 `grain` (for `as.grain`) or `bn.fit` (for `as.bn.fit`).

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 SmS codegrain objects by replacing the missing conditional probability distributions with uniform distributions.

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

Ordinal nodes will be treated as categorical by `as.grain`, disregarding the ordering of the levels.

Author(s)

Marco Scutari
Examples

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

---

**graph enumeration**  
*Count graphs with specific characteristics*

**Description**

Count directed acyclic graphs of various sizes with specific characteristics.

**Usage**

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

**Arguments**

- `type`  
  a character string, the label describing the types of graphs to be counted (see below).
- `nodes`  
  a vector of positive integers, the graph sizes as given by the numbers of nodes.
- `...`  
  additional parameters (see below).
- `debug`  
  a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent. Ignored in some generation methods.

**Details**

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

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

**Value**

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

**Author(s)**

Marco Scutari
References


Examples

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

---

**graph generation utilities**

*Generate empty or random graphs*

---

**Description**

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

**Usage**

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

**Arguments**

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

Available graph generation algorithms are:

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

Additional arguments for the random.graph function are:

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

Value

Both empty.graph( ) and random.graph( ) return an object of class bn (if 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


## Examples

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

## graph integration

**Import and export networks from the graph package**

### Description

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

### Usage

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

### Arguments

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

### Value

An object of the relevant class.

### Note

The corresponding S4 methods are exported as well, and are just wrappers around the S3 ones. So, for example, both `as.graphNEL(x)` and `as(x, "graphNEL")` work and return identical objects.

### 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)
# check whether there is a path between two nodes.
path(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. skeleton(), acyclic(), directed() and path() also accept objects of class bn.fit.
from a character string, the label of a node.
to a character string, the label of a node (different from from).
direct a boolean value. If FALSE ignore any arc between from and to when looking for a path.
underlying.graph a boolean value. If TRUE the underlying undirected graph is used instead of the (directed) one from the x argument.
ordering the labels of all the nodes in the graph; their order is the node ordering used to set the direction of undirected arcs.
nodes the labels of the nodes that induce the subgraph.
directed a boolean value. If TRUE only completely directed cycles are considered; otherwise undirected arcs will also be considered and treated as arcs present in both directions.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
Value
acyclic(), path() and directed() return a boolean value.
skeleton(), pdag2dag() and subgraph() return an object of class bn.

Author(s)
Marco Scutari

References

Examples
```r
data(learning.test)
res = gs(learning.test)

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

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

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

Arguments
- **x**: an object of class bn.fit representing a discrete Bayesian network.
- **type**: a character string, the type of graph used to plot the probability distributions in the nodes. Possible values are barchart, dotplot and barprob (a brachart with probabilities printed over the bars).
graphviz.chart

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

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

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

scale a vector of two positive numbers, used by \texttt{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

\texttt{graphviz.chart()} invisibly returns \texttt{NULL}.

Author(s)

Marco Scutari

Examples

## Not run:

\begin{verbatim}
modelstring = paste("[HIST|LYF][CVLV][PCV|LVV][HYP|LVV][HYP|LYF][LYF]",
                 "[STK|LYF][ERLO][HRBP][ERLO|HR][HERKE][ERKA][HERKA][ERKA][ERKA][ERKA]|ANES",
                 "[APL][TPR|APL][EC20][AO2:VLNG][KINK][MINV|INT:VLNG][FI02][PSV][FI02:VALV]",
                 "[SAO2:PSV:SHNT][PAP][PMB][SHNT:INT:PMB][INT][PRSS:INT:KINK:VTUB][DISC]",
                 "[MV][MVCH][MVCH][VTUB][DISC:VMCH][VLNG][INT:KINK:VTUB][VALV][INT:VLNG][AC02:VALV]",
                 "[CCHL][AC02:ANES:SAO2:TPR][HR][CCHL][C][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.
\end{verbatim}
graphviz.plot

plot = graphviz.plot(fitted, type = "dotplot")

## End(Not run)

---

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

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

and optionally one or more of the following graphical parameters:

- **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.
hailfinder

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

Value

graphviz.plot() returns invisibly the graph object produced by Rgraphviz.

Author(s)
Marco Scutari

See Also
plot.bn.

data(hailfinder)

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 (10.7 mu 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.
• CldShade0th (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.
• CompPFlfcst (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.
- **CapInScn** (*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.
- **AMDewptCalP** (*AM dewpoint calculations, plains*): a three-level factor with levels Instability, Neutral and Stability.
- **AMInsWliScn** (*AM instability within scenario*): a three-level factor with levels LessUnstable, Average and MoreUnstable.
- **InsSclInScn** (*instability scaling within scenario*): a three-level factor with levels LessUnstable, Average and MoreUnstable.
- **ScnRel34** (*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.
- **ScnRePlfCfst** (*scenario relevant to plains forecast*): an eleven-level factor with levels A, B, C, D, E, F, G, H, I, J and K.
- **PlainsFcast** (*plains forecast*): a three-level factor with levels XNIL, SIG and SVR.
- **N34StarFcast** (*regions 2/3/4 forecast*): a three-level factor with levels XNIL, SIG and SVR.
- **R5Fcast** (*region 5 forecast*): a three-level factor with levels XNIL, SIG and SVR.
- **Dewpoints** (*dewpoints*): a seven-level factor with levels Low Everywhere, Low At Station, LowShHighN, LowNHighS, LowMtsHighPl, HighEverywhere, Other.
- **LowLLapse** (*low-level lapse rate*): a four-level factor with levels Close To Dry Ad, Steep, Moderate Or Less and Stable.
- **MeanRH** (*mean relative humidity*): a three-level factor with levels Very Moist, Average and Dry.
- **MidLLapse** (*mid-level lapse rate*): a three-level factor with levels Close To Dry Ad, Steep and Moderate Or Less.
- **MvmtFeatures** (*movement of features*): a four-level factor with levels Strong Front, Marked Upper, Other Rapid and No Major.
- **RHRatio** (*relative humidity ratio*): a three-level factor with levels Moist MDry L, Dry M Moist L and other.
- **SfcWndShfDis** (*surface wind shifts and discontinuities*): a seven-level factor with levels Denv Cyclone, E_W_N, E_W_S, Movig Ftor Ot, Dry Line, None and Other.
- **SynForcng** (*synoptic forcing*): a five-level factor with levels Sig Negative, Neg To Pos, Sig Positive, Pos To Neg and Little Change.
• 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 WidespdDns1.

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

Source

Examples
# load the data.
data(hailfinder)
# create and plot the network structure.
modelstring = paste0("[N07muVerMo][SubjVertMo][QGVertMotion][SatContMoist][RaoContMoist]",
                  "[VISCloudCov][IRCldCover][AMInstabMt][WindHodograph][MorningBound][LoLevMoistAd][Date]",
                  "[MorningCIN][LiFr12ZDENs][AMDewptCalPl][LatestCIN][LLIW]",
                  "[CombVerMo][N07muVerMo][SubjVertMo][QGVertMotion][CombMoisture][SatContMoist][RaoContMoist]",
                  "[CombClouds][VISCloudCov][IRCldCover][Scenario][Date][CurPropConv][LatestCIN][LLIW]",
                  "$[AreaMesoALS][CombVerMo][ScenRelAMCIN][Scenario][ScenRelAMIns][Scenario][ScenRel134][Scenario]",
                  "$[ScnRelPlFcs][Scenario][Dewpoints][Scenario][LowLLapse][Scenario][MeanRH][Scenario]",
                  "$[MidLLapse][Scenario][MvmtFeatures][Scenario][RHRatio][Scenario][SfcWndShfDis][Scenario]",
                  "$[SynForcg][Scenario][TempDis][Scenario][WindAloft][Scenario][WindFieldMt][Scenario]",
                  "$[WindFieldPln][Scenario][AreaMoDryAir][AreaMesoALS][CombMoisture]",
                  "$[AMCINinScn][ScenRelAMCIN][MorningCIN][AMInsWliScn][ScenRelAMIns][LiFr12ZDENs][AMDewptCalPl]",
                  "$[ClShdShade0th][AreaMesoALS][AreaMoDryAir][CombClouds][InsInMt][ClShdShade0th][AInstabMt]",
                  "$[OutFwFrMt][InsInMt][WindHodograph][ClShdShadeConv][InsInMt][WindHodograph][MountainFcs][InsInMt]",
                  "$[Boundaries][WindHodograph][OutFlowFwFrMt][MorningBound][N34StarFcs][ScenRel34][PlainsFcs]",
                  "$[CompPlFcs][AreaMesoALS][ClShdShade0th][Boundaries][ClShdShadeConv][CapChange][CompPlFcs]",
                  "$[InsChange][CompPlFcs][LoLevMoistAd][CapInScn][CapChange][AMCINinScn]",
                  "$[InsClnScn][InsChange][AMInsWliScn][R5Fcs][MountainFcs][N34StarFcs]",
                  "$[PlainsFcs][CapInScn][InsClnScn][CurPropConv][ScnRel1PlFcs]")
dag = model2network(modelstring)
## Not run: graphviz.plot(dag, shape = "ellipse")
Usage

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

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 bnlearn-package and the documentation of each
            algorithm for details.
maximize    a character string, the score-based algorithm to be used in the “maximize” phase.
            Possible values are hc and tabu. See bnlearn-package for details.
restrict.args a list of arguments to be passed to the algorithm specified by restrict,
               such as test or alpha.
maximize.args a list of arguments to be passed to the algorithm specified by maximize,
               such as restart for hill-climbing or tabu for tabu search.
debug       a boolean value. If TRUE a lot of debugging output is printed; otherwise the
            function is completely silent.

Value

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

Note

mmhc() is simply rsmax2() with restrict set to mmpc and maximize set to hc.

Author(s)

Marco Scutari

References


See Also

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

Predict or impute missing data from a Bayesian network

Description

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

Usage

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

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

Arguments

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

Details

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

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

**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.

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

**Examples**

```r
# 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")
```
Description

Insurance is a network for evaluating car insurance risks.

Usage
data(insurance)

Format

The insurance data set contains the following 27 variables:

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

Note

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

Source


Examples

# 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:MakeModel:MakeModel]", "[Airbag][VehicleYear:MakeModel: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")
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 http://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


Examples

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

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

**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

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

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

Value

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

Author(s)

Marco

Examples

```r
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

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

Arguments

- **x**: a data frame containing the variables in the model.
- **whitelist**: a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs to be included in the graph.
- **blacklist**: a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs not to be included in the graph.
- **mi**: a character string, the estimator used for the pairwise (i.e. unconditional) mutual information coefficients in the ARACNE and Chow-Liu algorithms. Possible values are `mi` (discrete mutual information) and `mi-g` (Gaussian mutual information).
marks

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

References

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
misc utilities

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 of bn.f it.

Usage

## nodes
mb(x, node)
nbr(x, node)
parents(x, node)
parents(x, node, debug = FALSE) <- value
children(x, node)
children(x, node, debug = FALSE) <- value
spouses(x, node)
ancestors(x, node)
descendants(x, node)
in.degree(x, node)
out.degree(x, node)
root.nodes(x)
leaf.nodes(x)
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, effective = FALSE, debug = FALSE)
ntests(x)
whitelist(x)
blacklist(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)
# re-label the nodes.
## S4 replacement method for signature 'bn'
nodes(object) <- value
## S4 replacement method for signature 'bn.fit'
nodes(object) <- value

Arguments

x, object an object of class bn or bn.fit. The replacement form of parents, children, arcs and amat requires an object of class bn.

node, Nodes a character string, the label of a node.

value either a vector of character strings (for parents and children), an adjacency matrix (for amat) or a data frame with two columns (optionally labeled "from" and "to", for arcs).

data a data frame containing the data the Bayesian network was learned from. It’s only needed if x is an object of class bn.

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

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

effective a boolean value. If TRUE the number of non-zero free parameters is returned, that is, the effective degrees of freedom of the network; otherwise the theoretical number of parameters is returned.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

Details

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

Value

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

arcs, directed.arcs, undirected.arcs, incoming.arcs, outgoing.arcs, incident.arcs, compelled.arcs, reversible.arcs, whitelist and blacklist 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


Examples

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

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

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

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

## the nodes of the graph.
nodes(res)
## the adjacency matrix for the nodes of the graph.
amat(res)
## the parents of D.
parents(res, "D")
## the children of A.
children(res, "A")
## the root nodes of the graph.
root.nodes(res)
## the leaf nodes of the graph.
leaf.nodes(res)
## number of parameters of the Bayesian network.
res = set.arc(res, "A", "B")
nparams(res, learning.test)

model string utilities

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

**Description**

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

**Usage**

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

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

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

**Arguments**

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

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

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

Value

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

Author(s)

Marco Scutari

Examples

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

Description

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

Usage

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

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

- **training**: a character string, the label of the training variable.
- **explanatory**: a vector of character strings, the labels of the explanatory variables.
- **object**: an object of class `bn.naive`, either fitted or not.
- **x, data**: a data frame containing the variables in the model, which must all be factors.
- **prior**: a numeric vector, the prior distribution for the training variable. It is automatically normalized if not already so. The default prior is the probability distribution of the training variable in `object`.
- **whitelist**: a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs to be included in the graph.
- **blacklist**: a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs not to be included in the graph.
- **mi**: a character string, the estimator used for the mutual information coefficients for the Chow-Liu algorithm in TAN. Possible values are `mi` (discrete mutual information) and `miMg` (Gaussian mutual information).
- **root**: a character string, the label of the explanatory variable to be used as the root of the tree in the TAN classifier.
- **...**: extra arguments from the generic method (currently ignored).
- **prob**: a boolean value. If `TRUE` the posterior probabilities used for prediction are attached to the predicted values as an attribute called `prob`.
- **debug**: a boolean value. If `TRUE` a lot of debugging output is printed; otherwise the function is completely silent.

Details

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

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

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

Value

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

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


**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"])

node ordering utilities

Utilities dealing with partial node orderings

Description

Find the partial node ordering implied by a network or generate the blacklist implied by a complete node ordering.

Usage

nodeNordering(x, debug = FALSE)
orderingRblacklist(nodes)
tiersRblacklist(tiers)

Arguments

x an object of class bn or bn.fit.
nodes a vector of character strings, the node ordering.
tiers a vector of character strings or a list, see below.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.

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.

Value

nodeNordering() returns a vector of character strings, an ordered set of node labels.
ordering2blacklist() and tiers2blacklist() return a sanitized blacklist (a two-column matrix, whose columns are labeled from and to).

Note

nodeNordering() and ordering2blacklist() support only completely directed Bayesian networks.
### Examples

```r
data(learning.test)
res = gs(learning.test, optimized = TRUE)
ntests(res)
res = set.arc(res, "A", "B")
ord = node.ordering(res)
ord

## partial node ordering saves us two tests in the v-structure
## detection step of the algorithm.
ntests(gs(learning.test, blacklist = ordering2blacklist(ord)))
tiers2blacklist(list(LETTERS[1:3], LETTERS[4:6]))
```

---

### Description

Convert pcAlgo objects to bn objects.

### Usage

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

### Arguments

- `x`: an object of class pcAlgo.
- `...`: extra arguments from the generic method (currently ignored).

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

### Value

An object of class bn.

### Author(s)

Marco Scutari
plot.bn  

**Plot a Bayesian network**

**Description**

Plot the graph associated with a small Bayesian network.

**Usage**

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

**Arguments**

- `x`: an object of class `bn`.
- `ylim`: a numeric vector with two components containing the range of the y-axis.
- `xlim`: a numeric vector with two components containing the range of the x-axis.
- `radius`: a numeric value containing the radius of the nodes.
- `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)
res = gs(learning.test)

plot(res)

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

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

Description

Plot arc strengths derived from bootstrap resampling.

Usage

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

Arguments

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

Note

The xlim and ylim arguments are always overridden.

Author(s)

Marco Scutari
Examples

```r
data(learning.test)

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

---

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

Description

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

Usage

```r
# discretize continuous data into factors.
 discretize(data, method, breaks = 3, ordered = FALSE, ..., debug = FALSE)
# screen continuous data for highly correlated pairs of variables.
 dedup(data, threshold, debug = FALSE)
```

Arguments

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

Details

discretize() takes a data frame of continuous variables as its first argument and returns a second data frame of discrete variables, transformed using of three methods: interval, quantile or hartemink.
derdup() screens the data for pairs of highly correlated variables, and discards one in each pair.
Value

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

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

Note

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

Author(s)

Marco Scutari

References


Examples

data(gaussian.test)
d = discretize(gaussian.test, method = 'hartemink', breaks = 4, ibreaks = 20)
plot(hc(d))
d2 = dedup(gaussian.test)

rbn Simulate random data from a given Bayesian network

Description

Simulate random data from a given Bayesian network.

Usage

## S3 method for class 'bn'
rbn(x, n = 1, data, fit = "mle", ..., debug = FALSE)
## S3 method for class 'bn.fit'
rbn(x, n = 1, ..., debug = FALSE)
Arguments

- **x**: an object of class `bn` or `bn.fit`.
- **n**: a positive integer giving the number of observations to generate.
- **data**: a data frame containing the data the Bayesian network was learned from.
- **fit**: a character string, the label of the method used to fit the parameters of the network. See `bn.fit` for details.
- **...**: 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.

Value

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

Author(s)

Marco Scutari

References


See Also

`bn.boot`, `bn.cv`.

Examples

```r
## Not run:
data(learning.test)
res = gs(learning.test)
res = set.arc(res, "A", "B")
par(mfrow = c(1,2))
plot(res)
sim = rbn(res, 500, learning.test)
plot(gs(sim))
## End(Not run)
```
Identify relevant nodes without learning the Bayesian network

Description

Identify all the nodes relevant to compute all the conditional probability distributions for a given set of nodes.

Usage

relevant(target, context, data, test, alpha, B, debug = FALSE)

Arguments

target a vector of character strings, the labels of nodes whose conditional probability distributions are of interest.

context a vector of character strings, the labels of nodes on which to condition the independence tests.

data a data frame containing either numeric or factor columns.

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

alpha a numeric value, the target nominal type I error rate. If none is specified, the default value is 0.05.

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

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

Value

relevant() returns a vector of character strings, the labels of the relevant nodes.

Note

This algorithms selects all the nodes that are relevant at all, not only those that are significantly so. Therefore, to be discarded a node must be completely unrelated to any of the target nodes, not just weakly dependent. On the good side, relevant nodes are correctly identified even for data sets whose probability structure is not faithful to any directed acyclic graph.

Author(s)

Marco Scutari
References


Examples

```r
data(learning.test)
X = as.factor(sample(c("x1", "x2"), nrow(learning.test), replace = TRUE))
relevant("A", data = cbind(learning.test, X))
relevant("A", context = "B", data = learning.test)
```

---

ROCR integration Generating a prediction object for ROCR

Description

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

Usage

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

Arguments

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

Details

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

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

**Author(s)**

Robert Ness

**Examples**

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

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][FI02][PVS][FI02:VALV]",
  "[SAO2][PVS:SHNT][PAP][PMB][PMB][SHNT][INT:PMB][INT][PSS][INT:KINK:VTUB][DISC]",
  "[MVS][VMCH][MVS][VTUB][DISC:VMCH][VLNG][INT:KINK:VTUB][VALV][INT:VLNG][ACO2:VALV]",
  "[CCHL][ACO2][ANES:SAO2:TPR][HR][CCHL][CO][HR:STKV][BP][CO:TPR]"
true.dag = model2network(modelstring)
strength = boot.strength(alarm, R = 200, m = 30, algorithm = "hc")
pred = as.prediction(strength, true.dag)
perf = performance(pred, "tpr", "fpr")
plot(perf, main = "Arc Detection")
performance(pred, "auc")
```

## End(Not run)

<table>
<thead>
<tr>
<th>score</th>
<th>Score of the Bayesian network</th>
</tr>
</thead>
</table>

**Description**

Compute the score of the Bayesian network.

**Usage**

```r
score(x, data, type = NULL, ..., by.node = FALSE, debug = FALSE)

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

Arguments

- **x**, object: an object of class `bn`.
- **data**: a data frame containing the data the Bayesian network that will be used to compute the score.
- **type**: a character string, the label of a network score. If none is specified, the default score is the **Bayesian Information Criterion** for both discrete and continuous data sets. See `bnlearn-package` 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`, `nbde`, `bds`, `bdj`) and the Bayesian Gaussian score (`bge`). It is also known as “equivalent sample size”. The default value is equal to 1 for the Dirichlet scores and 10 for `bge`.
- **exp**: a list of indexes of experimental observations (those that have been artificially manipulated). Each element of the list must be named after one of the nodes, and must contain a numeric vector with indexes of the observations whose value has been manipulated for that node.
- **k**: the penalty coefficient to be used by the AIC and BIC scores. The default value is 1 for AIC and `log(nrow(data))/2` for BIC.
- **phi**: the prior phi matrix formula to use in the Bayesian Gaussian equivalent (`bge`) score. Possible values are `heckerman` (default) and `bottcher` (the one used by default in the `deal` package.)
- **prior**: the prior distribution to be used with the various Bayesian Dirichlet scores (`bde`, `nbde`, `bds`) and the Bayesian Gaussian score (`bge`). Possible values are `uniform` (the default), `vsp` (the Bayesian variable selection prior, which puts a probability of inclusion on parents), `marginal` (an independent marginal uniform for each arc) and `cs` (the Castelo & Siebes prior, which puts an independent prior probability on each arc and direction).
- **beta**: the parameter associated with `prior`.
  - If `prior` is `uniform`, `beta` is ignored.
  - If `prior` is `vsp`, `beta` is the probability of inclusion of an additional parent. The default is `1/ncol(data)`.
-- If prior is marginal, beta is the probability of inclusion of an arc. Each direction has a probability of inclusion of beta / 2 and the probability that the arc is not included is therefore 1 - beta. The default value is 0.5, so that arc inclusion and arc exclusion have the same probability.

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

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 logLik(x) - k * npargs(x), that is, the classic definition rescaled by -2. Therefore higher values are better, and for large sample sizes BIC converges to log(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

References


See Also

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

Examples

```r
# Load data
data(learning.test)
res = set.arc(gs(learning.test), "A", "B")
score(res, learning.test, type = "bde")

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

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

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

# Equivalent to logLik(res, learning.test)
score(res, learning.test, type = "loglik")

# Equivalent to AIC(res, learning.test)
score(res, learning.test, type = "aic")
```

Description

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

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

x a data frame containing the variables in the model.
start an object of class bn, the preseeded directed acyclic graph used to initialize the algorithm. If none is specified, an empty one (i.e. without any arc) is used.
whitelist a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs to be included in the graph.
blacklist a data frame with two columns (optionally labeled "from" and "to"), containing a set of arcs not to be included in the graph.
score a character string, the label of the network score to be used in the algorithm. If none is specified, the default score is the Bayesian Information Criterion for both discrete and continuous data sets. See bnlearn-package for details.
... additional tuning parameters for the network score. See score for details.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
restart an integer, the number of random restarts.
tabu a positive integer number, the length of the tabu list used in the tabu function.
max.tabu a positive integer number, the iterations tabu search can perform without improving the best network score.
perturb an integer, the number of attempts to randomly insert/remove/reverse an arc on every random restart.
max.iter an integer, the maximum number of iterations.
maxp the maximum number of parents for a node. The default value is Inf.
optimized a boolean value. See bnlearn-package for details.

Value

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

Author(s)

Marco Scutari

References

single-node local discovery


See Also

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

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

Arguments

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

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

Author(s)

Marco Scutari

See Also

constraint-based algorithms.

Examples

learn.mbn(learning.test, node = "D", method = "iamb")
learn.mbn(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 = "circle", main = NULL, sub = NULL, render = TRUE,
debug = FALSE)

Arguments

x  
an object of class bn.

strength  
an object of class bn::strength computed from the object of class bn corre-
sponding 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. Possi-
ble values are dots, neato, twopi, circo and fdp. See Rgraphviz documenta-
tion for details.
shape a character string, the shape of the nodes. Can be circle, ellipse or rectangle.
main a character string, the main title of the graph. It's plotted at the top of the graph.
sub a character string, a subtitle which is plotted at the bottom of the graph.
debug a boolean value. If TRUE a lot of debugging output is printed; otherwise the function is completely silent.
render a logical value. If TRUE, strength.plot() actually draws the figure in addition to returning the corresponding graph object. If FALSE, no figure is produced.

Details

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

- if arc strengths have been computed using conditional independence tests, any strength coefficient (which is the p-value of the test) lesser or equal than the threshold is considered significant. In this case the default value of threshold is equal to the value of the alpha argument used in the call to arc.strength(), which in turn defaults to the one used by the learning algorithm (if any) or to 0.05.

- 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. In this case the default value of threshold is 0.

- if arc strengths have been computed using bootstrap, any strength coefficient (which is the relative frequency of the arc in the networks learned from the bootstrap replicates) greater or equal than the threshold is considered significant. In this case the default value of threshold is 0.5.

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

```
1 - unique(c(0, threshold/c(10, 5, 2, 1.5, 1), 1))
```

for bootstrap estimates or by the quantiles

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

of the significant coefficients if network scores are used.

Value

The object of class `graphAM` used to format and render the plot. It can be further modified using the commands present in the `graph` and `Rgraphviz` packages.

Author(s)

Marco Scutari
Examples

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

## End(Not run)
```

### Description

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

### Usage

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

### Arguments

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

Author(s)

Marco Scutari

References


See Also

`score-based algorithms`, `bn.fit`, `impute`.

### 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()
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