Package ‘bnstruct’

May 9, 2020

Description  Bayesian Network Structure Learning from Data with Missing Values.
   The package implements the Silander-Myllymaki complete search,
   the Max-Min Parents-and-Children, the Hill-Climbing, the
   Max-Min Hill-climbing heuristic searches, and the Structural
   Expectation-Maximization algorithm. Available scoring functions are
   BDeu, AIC, BIC. The package also implements methods for generating and using
   bootstrap samples, imputed data, inference.

Type  Package

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   Values

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add.observations<-  

add further evidence to an existing list of observations of an InferenceEngine.

Description

Add a list of observations to an InferenceEngine that already has observations, using a list composed by the two following vectors:

- observed.vars vector of observed variables;
- observed.vals vector of values observed for the variables in observed.vars in the corresponding position.

Usage

add.observations(x) <- value

## S4 replacement method for signature 'InferenceEngine'
add.observations(x) <- value

Arguments

x an InferenceEngine.
value the list of observations of the InferenceEngine.

Details

In case of multiple observations of the same variable, the last observation is the one used, as the most recent.

See Also

observations<-
Description

Wrapper for a loader for the Asia dataset, with only raw data.

Usage

asia()

Details

The dataset has 10000 items, no missing data, so no imputation needs to be performed.

Value

a BNDataset containing the Child dataset.

See Also

asia_10000

Examples

dataset <- asia()
print(dataset)

Description

The Asia dataset contains 10000 complete (no missing data, no latent variables) randomly generated items of the Asia Bayesian Network. No imputation needs to be performed, so only raw data is present.

Format

a BNDataset with raw data slow filled.

Details

The data the BNDataset object is built from is located in files pkg_folder/extdata/asia_10000.header and pkg_folder/extdata/asia_10000.data.
References


See Also

asia

Description

Wrapper for a loader for a 2-layers dataset derived from the Asia dataset, with only raw data.

Usage

asia_2_layers()

Details

The dataset has 100 items, no missing data, so no imputation needs to be performed.

Value

a BNDataset containing the Child dataset.

See Also

asia_10000

Examples

dataset <- asia_2_layers()
print(dataset)
**belief.propagation**

perform belief propagation.

**Description**

Perform belief propagation for the network of an InferenceEngine, given a set of observations. In the current version of bnstruct, belief propagation can be computed only over a junction tree.

**Usage**

belief.propagation(ie, observations = NULL, return.potentials = FALSE)

## S4 method for signature 'InferenceEngine'

belief.propagation(ie, observations = NULL, return.potentials = FALSE)

**Arguments**

- **ie**
  - an `InferenceEngine` object.
- **observations**
  - list of observations, consisting in two vector, `observed.vars` for the observed variables, and `observed.vals` for the values taken by the variables listed in `observed.vars`. If no observations are provided, the `InferenceEngine` will use the ones it already contains.
- **return.potentials**
  - if TRUE only the potentials are returned, instead of the default `BN`.

**Value**

updated `InferenceEngine` object.

**Examples**

```r
## Not run:
dataset <- BNDataset("file.header", "file.data")
bn <- BN(dataset)
ie <- InferenceEngine(bn)
ie <- belief.propagation.ie

observations.ie <- list("observed.vars"="A","G","X"), "observed.vals"=c(1,2,1))
belief.propagation.ie

## End(Not run)
```
**bn**

get the BN object contained in an InferenceEngine.

---

**Description**

Return a network contained in an InferenceEngine.

**Usage**

bn(x)

```r
## S4 method for signature 'InferenceEngine'
bn(x)
```

**Arguments**

- **x** an InferenceEngine.

**Value**

the BN object contained in an InferenceEngine.

---

**BN-class**

BN class definition.

---

**Description**

Instantiate a BN object.

**Usage**

```r
BN(dataset = NULL, ...)
```

**Arguments**

- **.Object** a BN
- **dataset** a BNDataset object containing the dataset the network is built upon, if any. The remaining parameters are considered only if a starting dataset is provided.
- **...** potential further arguments of methods.
**BN-class**

**Details**

The constructor may be invoked without parameters – in this case an empty network will be created, and its slots will be filled manually by the user. This is usually viable only if the user already has knowledge about the network structure.

**Value**

BN object.

**Slots**

- **name**: name of the network
- **num.nodes**: number of nodes in the network
- **variables**: names of the variables in the network
- **discreteness**: TRUE if variable is discrete, FALSE if variable is continue
- **node.sizes**: if variable i is discrete, node.sizes[i] contains the cardinality of i, if i is instead discrete the value is the number of states variable i takes when discretized
- **cpts**: list of conditional probability tables of the network
- **dag**: adjacency matrix of the network
- **wpdag**: weighted partially dag
- **scoring.func**: scoring function used in structure learning (when performed)
- **struct.algo**: algorithm used in structure learning (when performed)
- **num.time.steps**: number of instants in which the network is observed (1, unless it is a Dynamic Bayesian Network)
- **discreteness**: TRUE if variable is discrete, FALSE if variable is continue

**Examples**

```r
## Not run:
net.1 <- BN()

dataset <- BNDataset()
dataset <- read.dataset(dataset, "file.header", "file.data")
net.2 <- BN(dataset)

## End(Not run)
```
Description

Add an original network to an InferenceEngine.

Usage

bn(x) <- value

## S4 replacement method for signature 'InferenceEngine'
bn(x) <- value

Arguments

x an InferenceEngine.
value the BN object contained in an InferenceEngine.

BNdataset-class

BNDataset class.

Description

Contains the all of the data that can be extracted from a given dataset: raw data, imputed data, raw and imputed data with bootstrap.

Usage

BNdataset(data, discreteness, variables = NULL, node.sizes = NULL, ...)

## S4 method for signature 'BNDataset'
initialize(.Object)

Arguments

.data an empty BNDataset.
.data raw data.frame or path/name of the file containing the raw dataset (see 'Details').
discreteness a vector of booleans indicating if the variables are discrete or continuous (TRUE and FALSE, respectively), or path/name of the file containing header information for the dataset (discreteness, variable names, cardinality - see 'Details').
variables vector of variable names.
node.sizes vector of variable cardinalities (for discrete variables) or quantization ranges (for continuous variables).
... further arguments for reading a dataset from files (see documentation for read.dataset).
Details

There are two ways to build a BNDataset: using two files containing respectively header informations and data, and manually providing the data table and the related header informations (variable names, cardinality and discreteness).

The key informations needed are: 1. the data; 2. the state of variables (discrete or continuous); 3. the names of the variables; 4. the cardinalities of the variables (if discrete), or the number of levels they have to be quantized into (if continuous). Names and cardinalities/leves can be guessed by looking at the data, but it is strongly advised to provide _all_ of the informations, in order to avoid problems later on during the execution.

Data can be provided in form of data.frame or matrix. It can contain NAs. By default, NAs are indicated with ‘?’; to specify a different character for NAs, it is possible to provide also the na.string.symbol parameter. The values contained in the data have to be numeric (real for continuous variables, integer for discrete ones). The default range of values for a discrete variable X is \([1, |X|]\), with \(|X|\) being the cardinality of X. The same applies for the levels of quantization for continuous variables. If the value ranges for the data are different from the expected ones, it is possible to specify a different starting value (for the whole dataset) with the starts.from parameter. E.g. by starts.from=0 we assume that the values of the variables in the dataset have range \([0, |X|-1]\). Please keep in mind that the internal representation of bnstruct starts from 1, and the original starting values are then lost.

It is possible to use two files, one for the data and one for the metadata, instead of providing manually all of the info. bnstruct requires the data files to be in a format subsequently described. The actual data has to be in (a text file containing data in) tabular format, one tuple per row, with the values for each variable separated by a space or a tab. Values for each variable have to be numbers, starting from 1 in case of discrete variables. Data files can have a first row containing the names of the corresponding variables.

In addition to the data file, a header file containing additional informations can also be provided. An header file has to be composed by three rows of tab-delimited values: 1. list of names of the variables, in the same order of the data file; 2. a list of integers representing the cardinality of the variables, in case of discrete variables, or the number of levels each variable has to be quantized in, in case of continuous variables; 3. a list that indicates, for each variable, if the variable is continuous (c or C), and thus has to be quantized before learning, or discrete (d or D). In case of need of more advanced options when reading a dataset from files, please refer to the documentation of the read.dataset method. Imputation and bootstrap are also available as separate routines (impute and bootstrap, respectively).

In case of an evolving system to be modeled as a Dynamic Bayesian Network, it is possible to specify only the description of the variables of a single instant; the information will be replicated for all the num.time.steps instants that compose the dataset, where num.time.steps needs to be set as parameter. In this case, it is assumed that the N variables v1, v2, ..., vN of a single instant appear in the dataset as v1_t1, v2_t1, ..., vN_t1, v1_t2, v2_t2, ..., in this exact order. The user can however provide information for all the variables in all the instants; if it is not the case, the name of the variables will be edited to include the instant. In case of an evolving system, the num.variables slots refers anyway to the total number of variables observed in all the instants (the number of columns in the dataset), and not to a single instant.

Value

BNDataset object.
a BNDataset object.

**Slots**

- **name**: name of the dataset
- **header.file**: name and location of the header file
- **data.file**: name and location of the data file
- **variables**: names of the variables in the network
- **node.sizes**: cardinality of each variable of the network
- **num.variables**: number of variables (columns) in the dataset
- **discreteness**: TRUE if variable is discrete, FALSE if variable is continue
- **quantiles**: list of vectors containing the quantiles, one vector per variable. Each vector is NULL if the variable is discrete, and contains the quantiles if it is continuous
- **num.items**: number of observations (rows) in the dataset
- **has.raw.data**: TRUE if the dataset contains data read from a file
- **has.imputed.data**: TRUE if the dataset contains imputed data (computed from raw data)
- **raw.data**: matrix containing raw data
- **imputed.data**: matrix containing imputed data
- **has.boots**: dataset has bootstrap samples
- **boots**: list of bootstrap samples
- **has.imputed.boots**: dataset has imputed bootstrap samples
- **imp.boots**: list of imputed bootstrap samples
- **num.boots**: number of bootstrap samples
- **num.time.steps**: number of instants in which the network is observed (1, unless it is a dynamic system)

**See Also**

read.dataset, impute, bootstrap

**Examples**

```r
## Not run:
# create from files
dataset <- BNDataset("file.data", "file.header")

# other way: create from raw dataset and metadata
data <- matrix(c(1:16), nrow = 4, ncol = 4)
dataset <- BNDataset(data = data,
                      discreteness = rep('d', 4),
                      variables = c("a", "b", "c", "d"),
                      node.sizes = c(4, 8, 12, 16))

## End(Not run)
```
boot

get selected element of bootstrap list.

Description

Given a `BNDataset`, return the sample corresponding to given index.

Usage

```r
boot(dataset, index, use.imputed.data = FALSE)
```

```r
## S4 method for signature 'BNDataset,numeric'
boot(dataset, index, use.imputed.data = FALSE)
```

Arguments

- `dataset`: a `BNDataset` object.
- `index`: the index of the requested sample.
- `use.imputed.data`: `TRUE` if samples from imputed dataset are to be used. Default if `FALSE`.

See Also

- `bootstrap`
- `bootstrap`

Examples

```r
## Not run:
dataset <- BNDataset("file.data", "file.header")
dataset <- bootstrap(dataset, num.boots = 1000)

for (i in 1:num.boots(dataset))
  print(boot(dataset, i))

## End(Not run)
```
boots<- get list of bootstrap samples of a BNDataset.

Description

Return the list of samples computed from raw data of a dataset.

Usage

boots(x)

## S4 method for signature 'BNDataset'
boots(x)

Arguments

x a BNDataset object.

Value

the list of bootstrap samples.

See Also

has.boots, has.imputed.boots, imp.boots

boots<- set list of bootstrap samples of a BNDataset.

Description

Add to a dataset a list of samples from raw data computed using bootstrap.

Usage

boots(x) <- value

## S4 replacement method for signature 'BNDataset'
boots(x) <- value

Arguments

x a BNDataset object.

value the list of bootstrap samples.
bootstrap

Perform bootstrap.

Description

Create a list of num.boots samples of the original dataset.

Usage

bootstrap(object, num.boots = 100, seed = 0, imputation = FALSE, k.impute = 10)

## S4 method for signature 'BNDataset'
bootstrap(object, num.boots = 100, seed = 0, imputation = FALSE, k.impute = 10)

Arguments

- **object**: the BNDataset object.
- **num.boots**: number of sampled datasets for bootstrap.
- **seed**: random seed.
- **imputation**: TRUE if imputation has to be performed. Default is FALSE.
- **k.impute**: number of neighbours to be used; for discrete variables we use mode, for continuous variables the median value is instead taken (useful only if imputation == TRUE).

Examples

```r
## Not run:
dataset <- BNDataset("file.data", "file.header")
dataset <- bootstrap(dataset, num.boots = 1000)
## End(Not run)
```

build.junction.tree

build a JunctionTree.

Description

Starting from the adjacency matrix of the directed acyclic graph of the network contained in an InferenceEngine, build a JunctionTree for the network and store it into an InferenceEngine.

Usage

build.junction.tree(object, ...)

## S4 method for signature 'InferenceEngine'
build.junction.tree(object, ...)

Arguments

object an InferenceEngine object.
... potential further arguments for methods.

See Also

InferenceEngine

Examples

```r
## Not run:
dataset <- BNDataset("file.header", "file.data")
net <- BN(dataset)
eng <- InferenceEngine()
eng <- build.junction.tree(eng)

## End(Not run)
```

child load Child dataset.

Description

Wrapper for a loader for the Child raw dataset; also perform imputation.

Usage

cild()

details

The dataset has 5000 items, with random missing values (no latent variables). BNDataset object contains the raw dataset and imputed dataset, with k=10 (see impute for related explanation).

Value

a BNDataset containing the Child dataset.

See Also

child_NA_5000

Examples

dataset <- child()
print(dataset)
Description

The Child dataset contains 5000 randomly generated items with missing data (no latent variables) of the Child Bayesian Network. Imputation is performed, so both raw and imputed data is present.

Format

a BNDataset with a raw and imputed data slow filled with 5000 items.

Details

The data the BNDataset object is built from is located in files pkg_folder/extdata/extdata/Child_data_na_5000.header and pkg_folder/extdata/extdata/Child_data_na_5000.data.

References


See Also

child

complete Sub-set a BNDataset to get only complete cases.

Description

Given a BNDataset, return a copy of the original object where the raw data consists only in the observations that do not contain missing values.

Usage

complete(x, complete.vars = seq_len(num.variables(x)))

## S4 method for signature 'BNDataset'
complete(x, complete.vars = seq_len(num.variables(x)))

Arguments

x a BNDataset.

complete.vars vector containing the indices of the variables to be considered for the subsetting; variables not included in the vector can still contain NAs.
Details

Non-missingness can be required on a subset of variables (by default, on all variables).

If present, imputed data and bootstrap samples are eliminated from the new `BNdataset`, as using this method *after* using `impute` or `bootstrap`, there may likely be a loss of correspondence between the subsetted `raw.data` and the previously generated `imputed.data` and bootstrap samples.

Value

a copy of the original `BNdataset` containing only complete observations.

cpts

get the list of conditional probability tables of a BN.

Description

Return the list of conditional probability tables of the variables of a BN object. Each probability table is associated to the corresponding variable, and its dimensions are named according to the variable they represent.

Usage

cpts(x)

## S4 method for signature 'BN'
cpts(x)

Arguments

x an object.

Details

Each conditional probability table is represented as a multidimensional array. The ordering of the dimensions of each variable is not guaranteed to follow the actual conditional distribution. E.g. dimensions for conditional probability $P(C|A,B)$ can be either $(C,A,B)$ or $(A,B,C)$, depending on if some operations have been performed, or how the probability table has been computed. Users should not rely on dimension numbers, but should instead select the dimensions using their names.

Value

list of the conditional probability tables of the desired object.
\textit{cpts<-} \textit{set the list of conditional probability tables of a network.}

\textbf{Description}

Set the list of conditional probability tables of a \texttt{BN} object.

\textbf{Usage}

\begin{verbatim}
cpts(x) <- value
\end{verbatim}

\begin{verbatim}
## S4 replacement method for signature 'BN'
cpts(x) <- value
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} an object.
  \item \texttt{value} \hspace{1cm} list of the conditional probability tables of the object.
\end{itemize}

\textbf{Details}

Each conditional probability table is represented as a multidimensional array. To retrieve single dimensions (e.g. to compute marginals), users should provide dimensions names.

\textit{dag} \textit{get adjacency matrix of a network.}

\textbf{Description}

Return the adjacency matrix of the directed acyclic graph representing the structure of a network.

\textbf{Usage}

\begin{verbatim}
dag(x)
\end{verbatim}

\begin{verbatim}
## S4 method for signature 'BN'
dag(x)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} an object.
\end{itemize}

\textbf{Value}

matrix containing the adjacency matrix of the directed acyclic graph representing the structure of the object.
dag.to.cpdag  

`convert a DAG to a CPDAG`

**Description**

Convert the adjacency matrix representing the DAG of a BN into the adjacency matrix representing a CPDAG for the network.

**Usage**

`dag.to.cpdag(dag.adj.matrix, layering = NULL)`

**Arguments**

- `dag.adj.matrix`: the adjacency matrix representing the DAG of a BN.
- `layering`: vector containing the layers each node belongs to.

**Value**

the adjacency matrix representing a CPDAG for the network.

**See Also**

`wpdag.from.dag`

**Examples**

```r
## Not run:
net <- learn.network(dataset, layering=layering)
pdag <- dag.to.cpdag(dag(net), layering)
wpdag(net) <- pdag
## End(Not run)
```

dag<-  

`set adjacency matrix of an object.`

**Description**

Set the adjacency matrix of the directed acyclic graph representing the structure of a network.

**Usage**

`dag(x) <- value`

```r
## S4 replacement method for signature 'BN'
dag(x) <- value
```
data.file

Arguments

x an object.
value matrix containing the adjacency matrix of the directed acyclic graph representing the structure of the object.

data.file get data file of a BNDataset.

Description

Return the data filename of a dataset (with the path to its position, as given by the user). The data filename may contain a header in the first row, containing the list of names of the variables, in the same order as in the header file. After the header, if present, the file contains a data.frame with the observations, one item per row.

Usage

data.file(x)

## S4 method for signature 'BNDataset'
data.file(x)

Arguments

x a BNDataset.

Value

data filename of the dataset.

See Also

data.file

data.file<- set data file of a BNDataset.

Description

Set the data filename of a dataset (with the path to its position, as given by the user). The data filename may contain a header in the first row, containing the list of names of the variables, in the same order as in the header file. After the header, if present, the file contains a data.frame with the observations, one item per row.
Usage

data.file(x) <- value

## S4 replacement method for signature 'BNdataset'
data.file(x) <- value

Arguments

x          a BNDataset.
value      data filename.

See Also

header.file<-

---

discreteness  get status (discrete or continuous) of the variables of an object.

Description

Get a vector representing the status of the variables (with their names) of a BN or BNDataset. Elements of the vector are c if the variable is continue, and d if the variable is discrete.

Usage

discreteness(x)

## S4 method for signature 'BN'
discreteness(x)

## S4 method for signature 'BNDataset'
discreteness(x)

Arguments

x          an object.

Value

vector containing, for each variable of the desired object, c if the variable is continue, and d if the variable is discrete.
discreteness<-

`discreteness<-`  
set status (discrete or continuous) of the variables of an object.

**Description**

Set the list of variable status for the variables in a network or a dataset.

**Usage**

```r
discreteness(x) <- value
```

## S4 replacement method for signature 'BN'
```r
discreteness(x) <- value
```

## S4 replacement method for signature 'BNDataset'
```r
discreteness(x) <- value
```

**Arguments**

- **x**  
an object.

- **value**  
a vector of elements in \{c,d\} for continuous and discrete variables (respectively).

---

edge.dir.wpdag  
counts the edges in a WPDAG with their directionality

**Description**

Given a BN with a WPDAG, it counts the edges, with their directionality.

**Usage**

```r
dir.wpdag(x, use.node.names = TRUE)
```

**Arguments**

- **x**  
the BN

- **use.node.names**  
use node names rather than number (TRUE by default).

**Value**

a matrix containing the node pairs with the count of the edges between them in the WPDAG.
em

*expectation-maximization algorithm.*

**Description**

Learn parameters of a network using the Expectation-Maximization algorithm.

**Usage**

```r
em(x, dataset, threshold = 0.001, max.em.iterations = 10, ess = 1)
```

## S4 method for signature 'InferenceEngine,BNDataset'

```r
e(x, dataset, threshold = 0.001, max.em.iterations = 10, ess = 1)
```

**Arguments**

- `x`: an `InferenceEngine`.
- `dataset`: observed dataset with missing values for the Bayesian Network of `x`.
- `threshold`: threshold for convergence, used as stopping criterion.
- `max.em.iterations`: maximum number of iterations to run in case of no convergence.
- `ess`: Equivalent Sample Size value.

**Value**

a list containing: an `InferenceEngine` with a new updated network ("InferenceEngine"), and the imputed dataset ("BNDataset").

**Examples**

```r
## Not run:
em(x, dataset)
## End(Not run)
```

---

get.most.probable.values

*compute the most probable values to be observed.*

**Description**

Return an array containing the values that each variable of the network is more likely to take, according to the CPTS. In case of ties take the first value.
has.boots

Usage

get.most.probable.values(x, prev.values = NULL)

## S4 method for signature 'BN'
get.most.probable.values(x, prev.values = NULL)

## S4 method for signature 'InferenceEngine'
get.most.probable.values(x, prev.values = NULL)

Arguments

x

a BN or InferenceEngine object.

prev.values

vector of size num.nodes containing an existing observation to complete (NULL if none).

Value

array containing, in each position, the most probable value for the corresponding variable.

Examples

## Not run:
# try with a BN object x
get.most.probable.values(x)

# now build an InferenceEngine object
eng <- InferenceEngine(x)
ge.get.most.probable.values(eng)

## End(Not run)

------------------

has.boots

check whether a BNDataset has bootstrap samples or not.

Description

Return TRUE if the given dataset contains samples for bootstrap, FALSE otherwise.

Usage

has.boots(x)

## S4 method for signature 'BNDataset'
has.boots(x)
Arguments

x  a BNDataset object.

Value

TRUE if dataset has bootstrap samples.

See Also

has.imputed.boots, boots, imp.boots

Description

Return TRUE if the given dataset contains samples for bootstrap from imputed dataset, FALSE otherwise.

Usage

has.imputed.boots(x)

## S4 method for signature 'BNDataset'
has.imputed.boots(x)

Arguments

x  a BNDataset object.

Value

TRUE if dataset has bootstrap samples from imputed data.

See Also

has.boots, boots, imp.boots
has.imputed.data check if a BN.Dataset contains imputed data.

Description

Check whether a BN.Dataset object actually contains imputed data.

Usage

has.imputed.data(x)

## S4 method for signature 'BN.Dataset'
has.imputed.data(x)

Arguments

x a BN.Dataset.

See Also

has.raw.data, raw.data, imputed.data

Examples

## Not run:
x <- BN.Dataset()
has.imputed.data(x) # FALSE

x <- read.dataset(x, "file.header", "file.data")
has.imputed.data(x) # FALSE, since read.dataset() actually reads raw data.

x <- impute(x)
has.imputed.data(x) # TRUE

## End(Not run)

has.raw.data check if a BN.Dataset contains raw data.

Description

Check whether a BN.Dataset object actually contains raw data.
Usage

has.raw.data(x)

## S4 method for signature 'BNDataSet'
has.raw.data(x)

Arguments

x a BNDataSet.

See Also

has.imputed.data, raw.data, imputed.data

Examples

## Not run:
x <- BNDataSet()
has.raw.data(x) # FALSE

x <- read.dataset(x, "file.header", "file.data")
has.raw.data(x) # TRUE, since read.dataset() actually reads raw data.

## End(Not run)

header.file

get header file of a BNDataSet.

Description

Return the header filename of a dataset (with the path to its position, as given by the user), present if the dataset has been read from a file and not manually inserted. The header file contains three rows:

1. list of names of the variables, in the same order as in the data file;
2. list of cardinalities of the variables, if discrete, or levels for quantization if continuous;
3. list of status of the variables: c for continuous variables, d for discrete ones.

Usage

header.file(x)

## S4 method for signature 'BNDataSet'
header.file(x)
header.file<-  

Arguments  
  x  a BNDataset.

Value  

header filename of the dataset.

See Also  
  data.file

Description  

Set the header filename of a dataset (with the path to its position, as given by the user). The header file has to contain three rows:

1. list of names of the variables, in the same order as in the data file;
2. list of cardinalities of the variables, if discrete, or levels for quantization if continuous;
3. list of status of the variables: c for continuous variables, d for discrete ones.

Further rows are ignored.

Usage  

header.file(x) <- value

## S4 replacement method for signature 'BNDataset'
header.file(x) <- value

Arguments  

x  a BNDataset.

value  header filename.

See Also  
  data.file<-
imp.boots<- get list of bootstrap samples from imputed data of a BNDataset.

Description

Return the list of samples computed from raw data of a dataset.

Usage

imp.boots(x)

## S4 method for signature 'BNDataset'
imp.boots(x)

Arguments

x a BNDataset object.

Value

the list of bootstrap samples from imputed data.

See Also

has.boots, has.imputed.boots, boots

imp.boots<- set list of bootstrap samples from imputed data of a BNDataset.

Description

Add to a dataset a list of samples from imputed data computed using bootstrap.

Usage

imp.boots(x) <- value

## S4 replacement method for signature 'BNDataset'
imp.boots(x) <- value

Arguments

x a BNDataset object.

value the list of bootstrap samples from imputed data.
Impute a `BNDataset` raw data with missing values.

### Usage

```r
impute(object, k.impute = 10)
```

#### Arguments

- **object**: the `BNDataset` object.
- **k.impute**: number of neighbours to be used; for discrete variables we use mode, for continuous variables the median value is instead taken.

#### Examples

```r
## Not run:
dataset <- BNDataset("file.data", "file.header")
dataset <- impute(dataset)
## End(Not run)
```

---

Get imputed data contained in a `BNDataset` object, if any.

### Usage

```r
imputed.data(x)
```

#### Arguments

- **x**: a `BNDataset`.
imputed.data<-  

**Description**

Insert imputed data in a `BNDataset` object.

**Usage**

```r
imputed.data(x) <- value
```

**Arguments**

- `x`: a `BNDataset`.
- `value`: a matrix of integers containing a dataset.

**See Also**

- `has.imputed.data`, `imputed.data`, `read.dataset`
Arguments

,Object an empty InferenceEngine object.

..., potential further arguments of methods.

bn a BN object.

observations a list of observations composed by the two following vectors:

• observed.vars: vector of observed variables;
• observed.vals: vector of values observed for the variables in observed.vars in the corresponding position.

interventions a list of interventions composed of the following two vectors:

• intervention.vars: vector of variables for which an intervention has been performed;
• intervention.vals: vector of values chosen for the variables in intervention.vals in the corresponding position.

Value

an InferenceEngine object.

InferenceEngine object.

Slots

junction.tree: junction tree adjacency matrix.
num.nodes: number of nodes in the junction tree.
cliques: list of cliques composing the nodes of the junction tree.
triangulated.graph: adjacency matrix of the original triangulated graph.
jpts: inferred joint probability tables.

bn: original Bayesian Network (as object of class BN) as provided by the user, or learnt from a dataset. NULL if missing.

updated.bn: Bayesian Network (as object of class BN) as modified by a belief propagation computation. In particular, it will have different conditional probability tables with respect to its original version. NULL if missing.

observed.vars: list of observed variables, by name or number.

observed.vals: list of observed values for the corresponding variables in observed.vars.

intervention.vars: list of manipulated variables, by name or number.

intervention.vals: list of specified values for the corresponding variables in intervention.vars.

Examples

## Not run:
dataset <- BNDataset()
dataset <- read.dataset(dataset, "file.header", "file.data")
bn <- BN(dataset)
eng <- InferenceEngine(bn)
obs <- list(c("A","G","X"),c(1,2,1))
eng.2 <- InferenceEngine(bn, obs)
## End(Not run)

---

**interventions**

*get the list of interventions of an InferenceEngine.*

**Description**

Return the list of interventions added to an InferenceEngine.

**Usage**

```r
interventions(x)
```

## S4 method for signature 'InferenceEngine'

`interventions(x)`

**Arguments**

- `x` an `InferenceEngine`.

**Details**

Output is a list in the following format:

- `intervention.vars` vector of manipulated variables;
- `intervention.vals` vector of values for the variables in `observed.vars` in the corresponding position.

**Value**

the list of interventions of the `InferenceEngine`.
interventions<-  set the list of interventions for an InferenceEngine.

Description

Add a list of interventions to an InferenceEngine, using a list composed by the two following vectors:

- intervention.vars: vector of the variables we manipulate;
- intervention.vals: vector of values for the variables in observed.vars in the corresponding position.

Usage

interventions(x) <- value

## S4 replacement method for signature 'InferenceEngine'
interventions(x) <- value

Arguments

- x: an InferenceEngine.
- value: the list of interventions of the InferenceEngine.

Details

An intervention can be applied only when building an InferenceEngine. In case of multiple interventions of the same variable, the last intervention is the one used.

jpts  get the list of joint probability tables compiled by an InferenceEngine.

Description

Return the list of joint probability tables for the cliques of the junction tree obtained after belief propagation has been performed.

Usage

jpts(x)

## S4 method for signature 'InferenceEngine'
jpts(x)
Arguments

x an InferenceEngine.

Details

Each joint probability table is represented as a multidimensional array. To retrieve single dimensions (e.g. to compute marginals), users should not rely on dimension numbers, but should instead select the dimensions using their names.

Value

the list of joint probability tables compiled by the InferenceEngine.

Description

Add a list of joint probability tables for the cliques of the junction tree.

Usage

jpts(x) <- value

## S4 replacement method for signature 'InferenceEngine'
jpts(x) <- value

Arguments

x an InferenceEngine.

value the list of joint probability tables compiled by the InferenceEngine.

Details

Each joint probability table is represented as a multidimensional array. To retrieve single dimensions (e.g. to compute marginals), users should provide dimension names.
**jt.cliques**

get the list of cliques of the junction tree of an `InferenceEngine`.

### Description

Return the list of cliques containing the variables associated to each node of a junction tree.

### Usage

```r
jt.cliques(x)
```

```r
## S4 method for signature 'InferenceEngine'
jt.cliques(x)
```

### Arguments

- **x**: an `InferenceEngine`.

### Value

the list of cliques of the junction tree contained in the `InferenceEngine`.

---

**jt.cliques<-**

set the list of cliques of the junction tree of an `InferenceEngine`.

### Description

Add to the `InferenceEngine` a list containing the cliques of variables composing the nodes of the junction tree.

### Usage

```r
jt.cliques(x) <- value
```

```r
## S4 replacement method for signature 'InferenceEngine'
jt.cliques(x) <- value
```

### Arguments

- **x**: an `InferenceEngine`.
- **value**: the list of cliques of the junction tree contained in the `InferenceEngine`.
junction.tree <- get the junction tree of an InferenceEngine.

Description

Return the adjacency matrix representing the junction tree computed for a network.

Usage

junction.tree(x)

## S4 method for signature 'InferenceEngine'
junction.tree(x)

Arguments

x an InferenceEngine.

Details

Rows and columns are named after the (variables in the) cliques that each node of the junction tree represent.

Value

the junction tree contained in the InferenceEngine.

See Also

build.junction.tree

junction.tree<- set the junction tree of an InferenceEngine.

Description

Set the adjacency matrix of the junction tree computed for a network.

Usage

junction.tree(x) <- value

## S4 replacement method for signature 'InferenceEngine'
junction.tree(x) <- value
knn.impute

Arguments

- `x`: an `InferenceEngine`.
- `value`: the junction tree to be inserted in the `InferenceEngine`.

Description

Perform imputation of missing data in a data frame using the k-Nearest Neighbour algorithm. For discrete variables we use the mode, for continuous variables the median value is instead taken.

Usage

```r
knn.impute(
  data,  # a numerical matrix.
  k = 10,  # number of neighbours to be used; for categorical variables the mode of the neighbours is used, for continuous variables the median value is used instead. Default: 10.
  cat.var = 1:ncol(data),  # vector containing the indices of the variables to be considered as categorical. Default: all variables.
  to.impute = 1:nrow(data),  # vector indicating which rows of the dataset are to be imputed. Default: impute all rows.
  using = 1:nrow(data)  # vector indicating which rows of the dataset are to be used to search for neighbours. Default: use all rows.
)
```

Value

imputed matrix.
**layering**

*return the layering of the nodes.*

---

**Description**

Compute the topological ordering of the nodes of a network, in order to divide the network in layers.

**Usage**

`layering(x)`

```r
## S4 method for signature 'BN'
layering(x)
```

**Arguments**

- `x`: a `BN` object.

**Value**

A vector containing layers the nodes can be divided into.

**Examples**

```r
## Not run:
dataset <- BNDataset("file.header", "file.data")
x <- BN(dataset)
x <- learn.network(x, dataset)
layering(x)
## End(Not run)
```

---

**learn.dynamic.network**

*learn a dynamic network (structure and parameters) of a BN from a BNDataset.*

---

**Description**

Learn a dynamic network (structure and parameters) of a BN from a BNDataset (see the Details section). This method is a wrapper for `learn.network` to simplify the learning of a dynamic network. It provides an automated generation of the layering required to represent the set of time constraints encoded in a dynamic network. In this function, it is assumed that the dataset contains the observations for each variable in all the time steps: \( V_1^{t_1}, V_2^{t_1}, V_n^{t_1}, V_1^{t_2}, \ldots, V_n^{t_k} \). Variables in time step \( j \) can be parents for any variable in time steps \( k \geq j \), but not for variables \( i < j \). If a layering is provided for a time step, it is valid in each time step, and not throughout the whole dynamic network; a global layering can however be provided.
### Usage

```r
learn.dynamic.network(x,...)
```

```r
## S4 method for signature 'BN'
learn.dynamic.network(
  x,
  y = NULL,
  num.time.steps = num.time.steps(y),
  algo = "mmhc",
  scoring.func = "BDeu",
  initial.network = NULL,
  alpha = 0.05,
  ess = 1,
  bootstrap = FALSE,
  layering = c(),
  max.fanin = num.variables(y) - 1,
  max.fanin.layers = NULL,
  max.parents = num.variables(y) - 1,
  max.parents.layers = NULL,
  layer.struct = NULL,
  cont.nodes = c(),
  use.imputed.data = FALSE,
  use.cpc = TRUE,
  mandatory.edges = NULL,
  ...
)
```

```r
## S4 method for signature 'BNDataset'
learn.dynamic.network(
  x,
  num.time.steps = num.time.steps(x),
  algo = "mmhc",
  scoring.func = "BDeu",
  initial.network = NULL,
  alpha = 0.05,
  ess = 1,
  bootstrap = FALSE,
  layering = c(),
  max.fanin = num.variables(x) - 1,
  max.fanin.layers = NULL,
  max.parents = num.variables(x) - 1,
  max.parents.layers = NULL,
  layer.struct = NULL,
  cont.nodes = c(),
  use.imputed.data = FALSE,
  use.cpc = TRUE,
  mandatory.edges = NULL,
  ...
)
```
Arguments

x can be a BN or a BNDataset. If x is a BN, then also the dataset parameter must be given.

... potential further arguments for methods.

y a BNDataset object, to be provided only if x is a BN.

num.time.steps the number of time steps to be represented in the dynamic BN.

algo the algorithm to use. Currently, one among sm (Silander-Myllymaki), mmpc (Max-Min Parent-and-Children), mmhc (Max-Min Hill Climbing, default), hc (Hill Climbing) and sem (Structural Expectation Maximization).

scoring.func the scoring function to use. Currently, one among BDeu, AIC, BIC.

initial.network network structure to be used as starting point for structure search. Can take different values: a BN object, a matrix containing the adjacency matrix of the structure of the network, or the string random.chain to sample a random chain as starting point.

alpha confidence threshold (only for mmhc).

ess Equivalent Sample Size value.

bootstrap TRUE to use bootstrap samples.

layering vector containing the layers each node belongs to.

max.fanin maximum number of parents for each node (only for hc, mmhc).

max.fanin.layers matrix of available parents in each layer (only for sm – DEPRECATED, use max.parents.layers instead).

max.parents maximum number of parents for each node (for sm, hc, mmhc).

max.parents.layers matrix of available parents in each layer (only for sm).

layer.struct 0/1 matrix for indicating which layers can contain parent nodes for nodes in a layer (only for mmhc, mmpc).

cont.nodes vector containing the index of continuous variables.

use.imputed.data TRUE to learn the structure from the imputed dataset (if available, a check is performed). Default is to use raw dataset

use.cpc (when using mmhc) compute Candidate Parent-and-Children sets instead of starting the Hill Climbing from an empty graph.

mandatory.edges binary matrix, where a 1 in cell [i,j] indicates that an edge from node i to node j must be present in the final network.

Details

The other parameters available are the ones of learn.network, refer to the documentation of that function for more details. See also the documentation for learn.structure and learn.params for more informations.
**Value**

new BN object with structure (DAG) and conditional probabilities as learnt from the given dataset.

**See Also**

learn.network learn.structure learn.params

**Examples**

```r
## Not run:
mydataset <- BNDataset("data.file", "header.file")
net <- learn.dynamic.network(mydataset, num.time.steps=2)
## End(Not run)
```

---

**Description**

Learn a network (structure and parameters) of a BN from a BNDataset (see the Details section).

**Usage**

```r
learn.network(x, ...)
```

```
# S4 method for signature 'BN'
learn.network(
  x,
  y = NULL,
  algo = "mmhc",
  scoring.func = "BDeu",
  initial.network = NULL,
  alpha = 0.05,
  ess = 1,
  bootstrap = FALSE,
  layering = c(),
  max.fanin = num.variables(y) - 1,
  max.fanin.layers = NULL,
  max.parents = num.variables(y) - 1,
  max.parents.layers = NULL,
  layer.struct = NULL,
  cont.nodes = c(),
  use.imputed.data = FALSE,
  use.cpc = TRUE,
)```
mandatory.edges = NULL,
...
)

## S4 method for signature 'BNDataset'
learn.network(
  x,
  algo = "mmhc",
  scoring.func = "BDeu",
  initial.network = NULL,
  alpha = 0.05,
  ess = 1,
  bootstrap = FALSE,
  layering = c(),
  max.fanin = num.variables(x) - 1,
  max.fanin.layers = NULL,
  max.parents = num.variables(x) - 1,
  max.parents.layers = NULL,
  layer.struct = NULL,
  cont.nodes = c(),
  use.imputed.data = FALSE,
  use.cpc = TRUE,
  mandatory.edges = NULL,
  ...
)

Arguments

x can be a BN or a BNDataset. If x is a BN, then also the dataset parameter must be given.

... potential further arguments for methods.

y a BNDataset object, to be provided only if x is a BN.

algo the algorithm to use. Currently, one among sm (Silander-Myllymaki), mmhc (Max-Min Parent-and-Children), mmhc (Max-Min Hill Climbing, default), hc (Hill Climbing) and sem (Structural Expectation Maximization).

scoring.func the scoring function to use. Currently, one among BDeu, AIC, BIC.

initial.network network structure to be used as starting point for structure search. Can take different values: a BN object, a matrix containing the adjacency matrix of the structure of the network, or the string random.chain to sample a random chain as starting point.

alpha confidence threshold (only for mmhc).

ess Equivalent Sample Size value.

bootstrap TRUE to use bootstrap samples.

layering vector containing the layers each node belongs to.

max.fanin maximum number of parents for each node (only for hc, mmhc).
Learn the structure (the directed acyclic graph) of a BN object according to a BNDataset. We provide five algorithms for learning the structure of the network, that can be chosen with the algo parameter. The first one is the Silander-Myllymäki (sm) exact search-and-score algorithm, that performs a complete evaluation of the search space in order to discover the best network; this algorithm may take a very long time, and can be inapplicable when discovering networks with more than 25–30 nodes. Even for small networks, users are strongly encouraged to provide meaningful parameters such as the layering of the nodes, or the maximum number of parents – refer to the documentation in package manual for more details on the method parameters.

The second method is the constraint-based Max-Min Parents-and-Children (mmpc), that returns the skeleton of the network. Given the possible presence of loops, due to the non-directionality of the edges discovered, no parameter learning is possible using this algorithm. Also note that in the case of a very dense network and lots of observations, the statistical evaluation of the search space may take a long time. Also for this algorithm there are parameters that may need to be tuned, mainly the confidence threshold of the statistical pruning. Please refer to the rest of this documentation for their explanation.

The third algorithm is another heuristic, the Hill-Climbing (hc). It can start from the complete space of possibilities (default) or from a reduced subset of possible edges, using the cpc argument.

The fourth algorithm (and the default one) is the Max-Min Hill-Climbing heuristic (mmhc), that performs a statistical sieving of the search space followed by a greedy evaluation, by combining the MMPC and the HC algorithms. It is considerably faster than the complete method, at the cost of a (likely) lower quality. As for MMPC, the computational time depends on the density of the network, the number of observations and the tuning of the parameters.

The fifth method is the Structural Expectation-Maximization (sem) algorithm, for learning a network from a dataset with missing values. It iterates a sequence of Expectation-Maximization (in order to “fill in” the holes in the dataset) and structure learning from the guessed dataset, until convergence. The structure learning used inside SEM, due to computational reasons, is MMHC. Conver-
gence of SEM can be controlled with the parameters `struct.threshold` and `param.threshold`, for the structure and the parameter convergence, respectively.

Search-and-score methods also need a scoring function to compute an estimated measure of each configuration of nodes. We provide three of the most popular scoring functions, BDeu (Bayesian-Dirichlet equivalent uniform, default), AIC (Akaike Information Criterion) and BIC (Bayesian Information Criterion). The scoring function can be chosen using the `scoring.func` parameter.

Structure learning sets the dag field of the BN under study, unless bootstrap or the `mmpc` algorithm are employed. In these cases, given the possible presence of loops, the `wpdag` field is set.

In case of missing data, the default behaviour (with no other indication from the user) is to learn the structure using `mmhc` starting from the raw dataset, using only the available cases with no imputation.

In case of learning from a dataset containing observations of a dynamic system, `learn.dynamic.network` will be employed.

Then, the parameters of the network are learnt using MAP (Maximum A Posteriori) estimation (when not using bootstrap or `mmpc`).

See documentation for `learn.structure` and `learn.params` for more informations.

Value

new `BN` object with structure (DAG) and conditional probabilities as learnt from the given dataset.

See Also

`learn.structure` `learn.params` `learn.dynamic.network`

Examples

```r
## Not run:
mydataset <- BNDataset("data.file", "header.file")

# starting from a BN
net <- BN(mydataset)
net <- learn.network(net, mydataset)

# start directly from the dataset
net <- learn.network(mydataset)

## End(Not run)
```

---

**learn.params**

*learn the parameters of a BN.*

**Description**

Learn the parameters of a `BN` object according to a `BNDataset` using MAP (Maximum A Posteriori) estimation.
Usage

learn.params(bn, dataset, ess = 1, use.imputed.data = F)

## S4 method for signature 'BN,BNDataset'
learn.params(bn, dataset, ess = 1, use.imputed.data = FALSE)

Arguments

bn a BN object.
dataset a BNDataset object.
ess Equivalent Sample Size value.
use.imputed.data use imputed data.

Details

Parameter learning is not possible in case of networks learnt using the mmpc algorithm, or from bootstrap samples, as there may be loops.

Value

new BN object with conditional probabilities.

See Also

learn.network

Examples

## Not run:
## first create a BN and learn its structure from a dataset
dataset <- BNDataset("file.header", "file.data")
bn <- BN(dataset)
bn <- learn.structure(bn, dataset)
bn <- learn.params(bn, dataset, ess=1)

## End(Not run)
Usage

learn.structure(
  bn,
  dataset,
  algo = "mmhc",
  scoring.func = "BDeu",
  initial.network = NULL,
  alpha = 0.05,
  ess = 1,
  bootstrap = FALSE,
  layering = c(),
  max.fanin = num.variables(dataset),
  max.fanin.layers = NULL,
  max.parents = num.variables(dataset),
  max.parents.layers = NULL,
  layer.struct = NULL,
  cont.nodes = c(),
  use.imputed.data = FALSE,
  use.cpc = TRUE,
  mandatory.edges = NULL,
  ...
)

## S4 method for signature 'BN,BNDataset'
learn.structure(
  bn,
  dataset,
  algo = "mmhc",
  scoring.func = "BDeu",
  initial.network = NULL,
  alpha = 0.05,
  ess = 1,
  bootstrap = FALSE,
  layering = c(),
  max.fanin = num.variables(dataset) - 1,
  max.fanin.layers = NULL,
  max.parents = num.variables(dataset) - 1,
  max.parents.layers = NULL,
  layer.struct = NULL,
  cont.nodes = c(),
  use.imputed.data = FALSE,
  use.cpc = TRUE,
  mandatory.edges = NULL,
  ...
)
Arguments

bn a BN object.
dataset a BNDataset.
algo the algorithm to use. Currently, one among sm (Silander-Myllymäki), mmpc (Max-Min Parent-and-Children), mmhc (Max-Min Hill Climbing, default), hc (Hill Climbing) and sem (Structural Expectation Maximization).
scoring.func the scoring function to use. Currently, one among BDeu, AIC, BIC.
initial.network network srtructure to be used as starting point for structure search. Can take different values: a BN object, a matrix containing the adjacency matrix of the structure of the network, or the string random.chain to sample a random chain as starting point.
alpha confidence threshold (only for mmhc).
ess Equivalent Sample Size value.
bootstrap TRUE to use bootstrap samples.
layering vector containing the layers each node belongs to (only for sm).
max.fanin maximum number of parents for each node (only for hc, mmhc).
max.fanin.layers matrix of available parents in each layer (only for sm – DEPRECATED, use max.parents.layers instead).
max.parents maximum number of parents for each node (for sm, hc, mmhc).
max.parents.layers matrix of available parents in each layer (only for sm).
layer.struct 0/1 matrix for indicating which layers can contain parent nodes for nodes in a layer (only for mmhc, mmpc).
cont.nodes vector containing the index of continuous variables.
use.imputed.data TRUE to learn the structure from the imputed dataset (if available, a check is performed). Default is to use raw dataset.
use.cpc (when using mmhc) compute Candidate Parent-and-Children sets instead of starting the Hill Climbing from an empty graph.
mandatory.edges binary matrix, where a 1 in cell [i,j] indicates that an edge from node i to node j must be present in the final network.
...
potential further arguments for method.

Details

We provide three algorithms in order to learn the structure of the network, that can be chosen with the algo parameter. The first is the Silander-Myllymäki (sm) exact search-and-score algorithm, that performs a complete evaluation of the search space in order to discover the best network; this algorithm may take a very long time, and can be inapplicable when discovering networks with more than 25–30 nodes. Even for small networks, users are strongly encouraged to provide meaningful
parameters such as the layering of the nodes, or the maximum number of parents – refer to the documentation in package manual for more details on the method parameters.

The second method is the constraint-based Max-Min Parents-and-Children (mmpc), that returns the skeleton of the network. Given the possible presence of loops, due to the non-directionality of the edges discovered, no parameter learning is possible using this algorithm. Also note that in the case of a very dense network and lots of observations, the statistical evaluation of the search space may take a long time. Also for this algorithm there are parameters that may need to be tuned, mainly the confidence threshold of the statistical pruning. Please refer to the rest of this documentation for their explanation.

The third algorithm is another heuristic, the Hill-Climbing (hc). It can start from the complete space of possibilities (default) or from a reduced subset of possible edges, using the cpc argument.

The fourth algorithm (and the default one) is the Max-Min Hill-Climbing heuristic (mhmhc), that performs a statistical sieving of the search space followed by a greedy evaluation, by combining the MMPC and the HC algorithms. It is considerably faster than the complete method, at the cost of a (likely) lower quality. As for MMPC, the computational time depends on the density of the network, the number of observations and the tuning of the parameters.

The fifth method is the Structural Expectation-Maximization (sem) algorithm, for learning a net- work from a dataset with missing values. It iterates a sequence of Expectation-Maximization (in order to “fill in” the holes in the dataset) and structure learning from the guessed dataset, until convergence. The structure learning used inside SEM, due to computational reasons, is MMHC. Conver- gence of SEM can be controlled with the parameters struct.threshold and param.threshold, for the structure and the parameter convergence, respectively, for learning a network from a dataset with missing values. It iterates a sequence of Expectation-Maximization (in order to “fill in” the holes in the dataset) and structure learning from the guessed dataset, until convergence. The structure learning used inside SEM, due to computational reasons, is MMHC. Convergence of SEM can be controlled with the parameters struct.threshold and param.threshold, for the structure and the parameter convergence, respectively.

Search-and-score methods also need a scoring function to compute an estimated measure of each configuration of nodes. We provide three of the most popular scoring functions, BDeu (Bayesian-Dirichlet equivalent uniform, default), AIC (Akaike Information Criterion) and BIC (Bayesian Information Criterion). The scoring function can be chosen using the scoring.func parameter.

Structure learning sets the dag field of the BN under study, unless bootstrap or the mmpc algorithm are employed. In these cases, given the possible presence of loops, the wpdag field is set.

In case of missing data, the default behaviour (with no other indication from the user) is to learn the structure using mmhc starting from the raw dataset.

Value

new BN object with DAG.

See Also

learn.network learn.dynamic.network

Examples

## Not run:
dataset <- BNDataset("file.header", "file.data")
bn <- BN(dataset)
# use MMHC
bn <- learn.structure(bn, dataset, alpha=0.05, ess=1, bootstrap=FALSE)

# now use Silander-Myllymaki
layers <- layering(bn)
mfl <- as.matrix(read.table(header=F, 
text="0 1 1 1 0 1 1 1 0 1 0 0 8 7 7 0 0 0 14 6 0 0 0 0 19"))
bn <- learn.structure(bn, dataset, algo='sm', max.fanin=3, cont.nodes=c(), 
    layering=layers, max.fanin.layers=mfl, use.imputed.data=FALSE)

## End(Not run)

marginals

compute the list of inferred marginals of a BN.

Description

Given an InferenceEngine, it returns a list containing the marginals for the variables in the network, according to the propagated beliefs.

Usage

marginals(x, ...)

## S4 method for signature 'InferenceEngine'
marginals(x, ...)

Arguments

x an InferenceEngine

... potential further arguments of methods.

Value

a list containing the marginals of each variable, as probability tables.

Examples

## Not run:
eng <- InferenceEngine(net)
marginals(eng)

## End(Not run)
name  

get name of an object.

Description

Return the name of an object, of class BN or BNDataset.

Usage

name(x)

## S4 method for signature 'BN'
name(x)

## S4 method for signature 'BNDataset'
name(x)

Arguments

x  an object.

Value

name of the object.

name<-

set name of an object.

Description

Set the name slot of an object of type BN or BNDataset.

Usage

name(x) <- value

## S4 replacement method for signature 'BN'
name(x) <- value

## S4 replacement method for signature 'BNDataset'
name(x) <- value

Arguments

x  an object.

value the new name of the object.
node.sizes

get size of the variables of an object.

Description

Return a list containing the size of the variables of an object. It is the actual cardinality of discrete variables, and the cardinality of the discretized variable for continuous variables.

Usage

node.sizes(x)

## S4 method for signature 'BN'
node.sizes(x)

## S4 method for signature 'BNDataset'
node.sizes(x)

Arguments

x

an object.

Value

vector containing the size of each variable of the desired object.

node.sizes<- set the size of variables of an object.

Description

Set the size of the variables of a BN or BNDataset object. It represents the actual cardinality of discrete variables, and the cardinality of the discretized variable for continuous variables.

Usage

node.sizes(x) <- value

## S4 replacement method for signature 'BN'
node.sizes(x) <- value

## S4 replacement method for signature 'BNDataset'
node.sizes(x) <- value
Arguments

x

an object.

value

vector containing the size of each variable of the object.

---

num.boots

get number of bootstrap samples of a \texttt{BNData}\texttt{set}.

---

Description

Return the number of bootstrap samples computed from a dataset.

Usage

\texttt{num.boots(x)}

\texttt{## S4 method for signature 'BNData'}\texttt{set} \texttt{num.boots(x)}

Arguments

x

a \texttt{BNData} object.

Value

the number of bootstrap samples.

---

num.boots<- 

set number of bootstrap samples of a \texttt{BNData}.

---

Description

Set the length of the list of samples of a dataset computed using bootstrap.

Usage

\texttt{num.boots(x) <- value}

\texttt{## S4 replacement method for signature 'BNData'}\texttt{num.boots(x) <- value}

Arguments

x

a \texttt{BNData} object.

value

the number of bootstrap samples.
num.items

get number of items of a BNDataset.

Description

Return the number of items in a dataset, that is, the number of rows in its data slot.

Usage

num.items(x)

## S4 method for signature 'BNDataset'
num.items(x)

Arguments

x a BNDataset object.

Value

number of items of the desired dataset.

num.items<-

set number of items of a BNDataset.

Description

Set the number of observed items (rows) in a dataset.

Usage

num.items(x) <- value

## S4 replacement method for signature 'BNDataset'
num.items(x) <- value

Arguments

x a BNDataset object.

value number of items of the desired dataset.
num.nodes <-

---

num.nodes <- get number of nodes of an object.

---

**Description**

Return the name of an object, of class **BN** or **InferenceEngine**.

**Usage**

```r
num.nodes(x)
```

```r
## S4 method for signature 'BN'
num.nodes(x)
```

```r
## S4 method for signature 'InferenceEngine'
num.nodes(x)
```

**Arguments**

- `x` an object.

**Value**

number of nodes of the desired object.

---

num.nodes <- set number of nodes of an object.

---

**Description**

Set the number of nodes of an object of type **BN** (number of nodes of the network) or **InferenceEngine** (where parameter contains the number of nodes of the junction tree).

**Usage**

```r
num.nodes(x) <- value
```

```r
## S4 replacement method for signature 'BN'
num.nodes(x) <- value
```

```r
## S4 replacement method for signature 'InferenceEngine'
num.nodes(x) <- value
```

**Arguments**

- `x` an object.
- `value` the number of nodes in the object.
num.time.steps

**Description**

Return the number of time steps observed in a dataset.

**Usage**

```r
num.time.steps(x)
```

```r
## S4 method for signature 'BN'
num.time.steps(x)
```

```r
## S4 method for signature 'BNDataset'
num.time.steps(x)
```

**Arguments**

- **x**
  - a `BN` or a `BNDataset` object.

**Value**

- the number of time steps.

---

num.time.steps<-

**Description**

Set the number of time steps of a dataset.

**Usage**

```r
num.time.steps(x) <- value
```

```r
## S4 replacement method for signature 'BN'
num.time.steps(x) <- value
```

```r
## S4 replacement method for signature 'BNDataset'
num.time.steps(x) <- value
```

**Arguments**

- **x**
  - a `BN` or a `BNDataset` object.
- **value**
  - the number of time steps.
num.variables <- get number of variables of a `BNDataset`.

Description

Return the number of the variables contained in a dataset. This value corresponds to the value of `num.nodes` of a network built upon the same dataset.

Usage

```r
num.variables(x)
```

Arguments

- `x` a `BNDataset` object.

Value

number of variables of the desired dataset.

See Also

`num.nodes`

num.variables <- set number of variables of a `BNDataset`.

Description

Set the number of variables observed in a dataset.

Usage

```r
num.variables(x) <- value
```

Arguments

- `x` a `BNDataset` object.
- `value` number of variables of the dataset.
observations

get the list of observations of an InferenceEngine.

Description

Return the list of observations added to an InferenceEngine.

Usage

observations(x)

## S4 method for signature 'InferenceEngine'
observations(x)

Arguments

x an InferenceEngine.

Details

Output is a list in the following format:

• observed.vars vector of observed variables;
• observed.vals vector of values observed for the variables in observed.vars in the corresponding position.

Value

the list of observations of the InferenceEngine.

observations<- set the list of observations of an InferenceEngine.

Description

Add a list of observations to an InferenceEngine, using a list of observations composed by the two following vectors:

• observed.vars vector of observed variables;
• observed.vals vector of values observed for the variables in observed.vars in the corresponding position.
Usage

observations(x) <- value

## S4 replacement method for signature 'InferenceEngine'
observations(x) <- value

Arguments

x                  an InferenceEngine.
value              the list of observations of the InferenceEngine.

Details

Replace previous list of observations, if present. In order to add evidence, and not just replace it, one must use the add.observations<- method.

In case of multiple observations of the same variable, the last observation is the one used, as the most recent.

See Also

add.observations<-
print

Arguments

x a BN object.
method either default of qgraph. The default method requires the Rgraphviz package, while qgraph requires the qgraph package and allows for a greater customization.
use.node.names TRUE if node names have to be printed. If FALSE, numbers are used instead.
frac minimum fraction [0,1] of presence of an edge to be plotted (used in case of plot.wpdag=TRUE).
max.weight maximum possible weight of an edge (used in case of plot.wpdag=TRUE).
node.size.lab font size for the node labels in the default mode.
node.col list of (R) colors for the nodes.
plot.wpdag if TRUE plot the network according to the WPDAG computed using bootstrap instead of the DAG.
... potential further arguments when using method="qgraph". Please refer to the qgraph documentation for the parameters available for the qgraph() method.

print

Description

print a BN, BNDataset or InferenceEngine to stdout.

Usage

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

## S3 method for class 'BNDataset'
print(x, show.raw.data = FALSE, show.imputed.data = FALSE, ...)

## S3 method for class 'InferenceEngine'
print(x, engine = "jt", ...)

Arguments

x a BN, BNDataset or InferenceEngine.
... potential other arguments.
show.raw.data if x is a BNDataset, print also raw dataset, if available.
show.imputed.data if x is a BNDataset, print also imputed dataset, if available.
engine if x is an InferenceEngine, specify the inference engine to be shown. Currently only engine = 'jt' is supported.
quantiles<-  

get the list of quantiles of an object.

Description

Return the list of quantiles of a BN or a BNDataset. It is set when a discretization needs to be performed.

Usage

quantiles(x)

## S4 method for signature 'BN'
quantiles(x)

## S4 method for signature 'BNDataset'
quantiles(x)

Arguments

x  
a list of vectors.

Details

Output is a list of num.nodes vectors, one per variable. Each vector is NULL if the corresponding variable is discrete in the original dataset, and contains the cut points for the quantiles if the corresponding variable is continuous.

Value

the list of quantiles of the BN of BNDataset.

quantiles<-  

set the list of quantiles of an object.

Description

Set the list of quantiles of a BN or a BNDataset.

Usage

quantiles(x) <- value

## S4 replacement method for signature 'BN'
quantiles(x) <- value

## S4 replacement method for signature 'BNDataset'
quantiles(x) <- value
Arguments

x  a BN or BNDataset.

value  a list of vectors.

Details

It is used when a discretization needs to be performed.

See Also

quantiles

Description

Return raw data contained in a BNDataset object, if any.

Usage

raw.data(x)

## S4 method for signature 'BNDataset'
raw.data(x)

Arguments

x  a BNDataset.

See Also

has.raw.data, has.imputed.data
raw.data <-  

add raw data.

Description
Insert raw data in a `BNdataset` object.

Usage
```r
raw.data(x) <- value
```

## S4 replacement method for signature 'BNdataset'
```r
raw.data(x) <- value
```

Arguments
- `x` a `BNdataset`
- `value` a matrix of integers containing a dataset.

See Also
- `has.raw.data`, `raw.data`, `read.dataset`

read.bif  

Read a network from a `.bif` file.

Description
Read a network described in a `.bif`-formatted file, and build a `BN` object.

Usage
```r
read.bif(x)
```

## S4 method for signature 'character'
```r
read.bif(x)
```

Arguments
- `x` the `.bif` file, with absolute/relative position.

Details
The method relies on a coherent ordering of variable values and parameters in the file.

Value
- a `BN` object.
Description

There are two ways to build a BNDataset: using two files containing respectively header informations and data, and manually providing the data table and the related header informations (variable names, cardinality and discreteness).

Usage

read.dataset(
  object,
  data.file,
  header.file,
  data.with.header = FALSE,
  na.string.symbol = "?",
  sep.symbol = "",
  starts.from = 1,
  num.time.steps = 1
)

Arguments

object the BNDataset object.
data.file the data file.
header.file the header file.
data.with.header TRUE if the first row of dataset file is an header (e.g. it contains the variable names).
na.string.symbol character that denotes NA in the dataset.
sep.symbol separator among values in the dataset.
starts.from starting value for entries in the dataset (observed values, default is 1).
num. time. steps  number of instants composing the observations (1, unless it is a dynamic system).

Details

The key informations needed are: 1. the data; 2. the state of variables (discrete or continuous); 3. the names of the variables; 4. the cardinalities of the variables (if discrete), or the number of levels they have to be quantized into (if continuous). Names and cardinalities/levels can be guessed by looking at the data, but it is strongly advised to provide _all_ of the informations, in order to avoid problems later on during the execution.

Data can be provided in form of data.frame or matrix. It can contain NAs. By default, NAs are indicated with '?'; to specify a different character for NAs, it is possible to provide also the na.string.symbol parameter. The values contained in the data have to be numeric (real for continuous variables, integer for discrete ones). The default range of values for a discrete variable $X$ is $[1, |X|]$, with $|X|$ being the cardinality of $X$. The same applies for the levels of quantization for continuous variables. If the value ranges for the data are different from the expected ones, it is possible to specify a different starting value (for the whole dataset) with the starts.from parameter. E.g. by starts.from=0 we assume that the values of the variables in the dataset have range $[0, |X| - 1]$. Please keep in mind that the internal representation of bnstruct starts from 1, and the original starting values are then lost.

It is possible to use two files, one for the data and one for the metadata, instead of providing manually all of the info. bnstruct requires the data files to be in a format subsequently described. The actual data has to be in (a text file containing data in) tabular format, one tuple per row, with the values for each variable separated by a space or a tab. Values for each variable have to be numbers, starting from 1 in case of discrete variables. Data files can have a first row containing the names of the corresponding variables.

In addition to the data file, a header file containing additional informations can also be provided. An header file has to be composed by three rows of tab-delimited values: 1. list of names of the variables, in the same order of the data file; 2. a list of integers representing the cardinality of the variables, in case of discrete variables, or the number of levels each variable has to be quantized in, in case of continuous variables; 3. a list that indicates, for each variable, if the variable is continuous (c or C), and thus has to be quantized before learning, or discrete (d or D).

See Also

BNDataset

Examples

```r
## Not run:
dataset <- BNDataset()
dataset <- read.dataset(dataset, "file.data", "file.header")
## End(Not run)
```
**read.dsc**  
*Read a network from a .dsc file.*

**Description**  
Read a network described in a .dsc-formatted file, and build a `BN` object.

**Usage**  
```r
read.dsc(x)
```

## S4 method for signature 'character'
```r
read.dsc(x)
```

**Arguments**  
- `x` the .dsc file, with absolute/relative position.

**Details**  
The method relies on a coherent ordering of variable values and parameters in the file.

**Value**  
a `BN` object.

**read.net**  
*Read a network from a .net file.*

**Description**  
Read a network described in a .net-formatted file, and build a `BN` object.

**Usage**  
```r
read.net(x)
```

## S4 method for signature 'character'
```r
read.net(x)
```

**Arguments**  
- `x` the .net file, with absolute/relative position.

**Details**  
The method relies on a coherent ordering of variable values and parameters in the file.
sample.dataset

sample a \texttt{BNDataset} from a network of an inference engine.

Description

sample a \texttt{BNDataset} from a network of an inference engine.

Usage

\begin{verbatim}
sample.dataset(x, n = 100, mar = 0)

## S4 method for signature 'BN'
sample.dataset(x, n = 100, mar = 0)

## S4 method for signature 'InferenceEngine'
sample.dataset(x, n = 100)
\end{verbatim}

Arguments

- \texttt{x}: a \texttt{BN} or \texttt{InferenceEngine} object.
- \texttt{n}: number of items to sample.
- \texttt{mar}: fraction \([0,1]\) of missing values in the sampled dataset (missing at random), default value is 0 (no missing values).

Value

- a \texttt{BNDataset}

sample.row

sample a row vector of values for a network.

Description

sample a row vector of values for a network.

Usage

\begin{verbatim}
sample.row(x, mar = 0)

## S4 method for signature 'BN'
sample.row(x, mar = 0)
\end{verbatim}
Arguments

- `x`: a BN or InferenceEngine object.
- `mar`: fraction [0,1] of missing values in the sampled vector (missing at random), default value is 0 (no missing values).

Value

a vector of values.

Description

Save an image of a Bayesian Network as an .eps file.

Usage

```r
save.to.eps(x, filename, ...)
## S4 method for signature 'BN,character'
save.to.eps(x, filename, ...)
```

Arguments

- `x`: a BN object
- `filename`: name (with path, if needed) of the file to be created
- `...`: parameters for the plot method.

See Also

plot

Examples

```r
## Not run:
save.to.eps(x, "out.eps")

## End(Not run)
```
Read the scoring function used to learn the structure of a network.

Description
Read the scoring function used in the learn.structure method. Outcome is meaningful only if the structure of a network has been learnt.

Usage
scoring.func(x)

## S4 method for signature 'BN'
scoring.func(x)

Arguments
x the BN object.

Value
the scoring function used.

Set the scoring function used to learn the structure of a network.

Description
Set the scoring function used in the learn.structure method.

Usage
scoring.func(x) <- value

## S4 replacement method for signature 'BN'
scoring.func(x) <- value

Arguments
x the BN object.
value the scoring function used.

Value
updated BN.
Compute the Structural Hamming Distance between two adjacency matrices.

**Description**

Compute the Structural Hamming Distance between two adjacency matrices, that is, the distance, in terms of edges, between two network structures. The lower the \texttt{shd}, the more similar are the two network structures.

**Usage**

\texttt{shd(g1, g2)}

**Arguments**

- \texttt{g1} first adjacency matrix.
- \texttt{g2} second adjacency matrix.

**Description**

The \texttt{show} method allows to provide a custom aspect for the output that is generated when the name of an instance is gives as command in an R session.

**Usage**

\texttt{show(object)}

**Arguments**

- \texttt{object} an object.
struct.algo

Read the algorithm used to learn the structure of a network.

Description
Read the algorithm used in the learn.structure method. Outcome is meaningful only if the structure of a network has been learnt.

Usage
struct.algo(x)

## S4 method for signature 'BN'
struct.algo(x)

Arguments
x the BN object.

Value
the structure learning algorithm used.

struct.algo<- Set the algorithm used to learn the structure of a network.

Description
Set the algorithm used in the learn.structure method.

Usage
struct.algo(x) <- value

## S4 replacement method for signature 'BN'
struct.algo(x) <- value

Arguments
x the BN object.
value the scoring function used.

Value
updated BN.
Description

Check if an InferenceEngine actually contains an updated network, in order to provide the chance of a fallback and use the original network if no belief propagation has been performed. An InferenceEngine built specifying a set of interventions will contain an updated BN with altered structure and no conditional probability tables (unless they are computed by a belief propagation operation.)

Usage

test.updated.bn(x)

## S4 method for signature 'InferenceEngine'
test.updated.bn(x)

Arguments

x an InferenceEngine.

Value

TRUE if an updated network is contained in the InferenceEngine, FALSE otherwise.

Examples

## Not run:
dataset <- BNDataset("file.header", "file.data")
bn <- BN(dataset)
ie <- InferenceEngine(bn)
test.updated.bn.ie # FALSE

observations.ie <- list("observed.vars"="A","G","X"), "observed.vals"=c(1,2,1))
ie <- belief.propagation.ie
test.updated.bn.ie # TRUE

interventions <- list("intervention.vars"="A","G","X"), "intervention.vals"=c(1,2,1))
ie2 <- InferenceEngine(bn, interventions = interventions)
test.updated.bn.ie2 # TRUE

## End(Not run)
tune.knn.impute  
*tune the parameter k of the knn algorithm used in imputation.*

**Description**

Tune the parameter k of the knn algorithm used in imputation.

**Usage**

```r
tune.knn.impute(
  data,
  cat.var = 1:ncol(data),
  k.min = 1,
  k.max = 20,
  frac.miss = 0.1,
  n.iter = 20,
  seed = 0
)
```

**Arguments**

- `data`: a numerical matrix.
- `cat.var`: vector containing the categorical variables
- `k.min`: minimum value for k
- `k.max`: maximum value for k
- `frac.miss`: fraction of missing values to add
- `n.iter`: number of iterations for each k
- `seed`: random seed

**Value**

matrix of error distributions

---

**updated.bn**

*get the updated BN object contained in an InferenceEngine.*

**Description**

Return an updated network contained in an InferenceEngine.

**Usage**

```r
updated.bn(x)
```

### S4 method for signature 'InferenceEngine'

```r
updated.bn(x)
```
**updated.bn<-**

**Arguments**

- **x** an *InferenceEngine*.

**Value**

- the updated *BN* object contained in an *InferenceEngine*.

**Description**

Add an updated network to an *InferenceEngine*.

**Usage**

```r
updated.bn(x) <- value
```

```
## S4 replacement method for signature 'InferenceEngine'
updated.bn(x) <- value
```

**Arguments**

- **x** an *InferenceEngine*.
- **value** the updated *BN* object contained in an *InferenceEngine*.

**variables**

*get variables of an object.*

**Description**

Get the list of variables (with their names) of a *BN* or *BNDataset*.

**Usage**

```r
variables(x)
```

```
## S4 method for signature 'BN'
variables(x)
```

```
## S4 method for signature 'BNDataset'
variables(x)
```

**Arguments**

- **x** an object.
Value

vector of the variables names of the desired object.

variables<- set variables of an object.

Description

Set the list of variable names in a BN or BNDataset object.

Usage

variables(x) <- value

## S4 replacement method for signature 'BN'
variables(x) <- value

## S4 replacement method for signature 'BNDataset'
variables(x) <- value

Arguments

x an object.

value vector containing the variable names of the object. Overwrites num.nodes slot if non-matching.

wpdag get the WPDAG of an object.

Description

Return the weighted partially directed acyclic graph of a network, when available (e.g. when bootstrap on dataset is performed).

Usage

wpdag(x)

## S4 method for signature 'BN'
wpdag(x)

Arguments

x an object.

Value

matrix containing the WPDAG of the object.
**wpdag.from.dag**

Initialize a WPDAG from a DAG.

**Description**

Given a BN object with a dag, return a network with its wpdag set as the CPDAG computed starting from the dag.

**Usage**

```r
wpdag.from.dag(x, layering = NULL)
```

## S4 method for signature 'BN'

```r
wpdag.from.dag(x, layering = NULL)
```

**Arguments**

- `x`: a BN object.
- `layering`: vector containing the layers each node belongs to.

**Value**

a BN object with an initialized wpdag.

**See Also**

dag.to.cpdag

**Examples**

```r
## Not run:
net <- learn.network(dataset, layering=layering)
wp.net <- wpdag.from.dag(net, layering)

## End(Not run)
```

---

**wpdag<-**

set WPDAG of the object.

**Description**

Set the weighted partially directed acyclic graph of a network (e.g. in case bootstrap on dataset is performed).
**Usage**

```r
wpdag(x) <- value
```

## S4 replacement method for signature 'BN'

```r
wpdag(x) <- value
```

**Arguments**

- **x**: an object.
- **value**: matrix containing the WPDAG of the object.

---

**write.dsc**

*Write a network saving it in a .dsc file.*

**Description**

Write a network on disk, saving it in a .dsc-formatted file.

**Usage**

```r
write.dsc(x, path = "./"
```

## S4 method for signature 'BN'

```r
write.dsc(x, path = "./"
```

**Arguments**

- **x**: the `BN` object.
- **path**: the relative or absolute path of the directory of the created file.

---

**write_xgmml**

*Write a network saving it in an XGMML file.*

**Description**

Write a network on disk, saving it in an XGMML file, for importing it in Cytoscape.
Usage

write_xgmml(
  x,
  path = "./network",
  write.wpdag = FALSE,
  node.col = rep("white", num.nodes(x)),
  frac = 0.2,
  max.weight = max(wpdag(x))
)

## S4 method for signature 'BN'
write_xgmml(
  x,
  path = "./network",
  write.wpdag = FALSE,
  node.col = rep("white", num.nodes(x)),
  frac = 0.2,
  max.weight = max(wpdag(x))
)

Arguments

x the BN object.
path file name with relative or absolute path to be written.
write.wpdag write the weighted PDAG computed using bootstrap samples or the MMPC structure algorithm, instead of the normaldag (default FALSE).
node.col vector of colors for each node of the network (in R colornames).
frac minimum fraction [0,1] of presence of an edge to be plotted (used in case of write.wpdag=TRUE).
max.weight maximum possible weight of an edge (used in case of write.wpdag=TRUE).
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