

# Package ‘bnstruct’

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**Description** More about what it does (maybe more than one line)

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## R topics documented:

add.observations<-	3
asia	4
asia_10000	5
belief.propagation	5
bn	6
BN-class	7
bn<-	8
BNDataset-class	8
boots	10
boots<-	11
bootstrap	11
build.junction.tree	12
child	13
child_NA_5000	13
cpts	14

cpts<-	15
dag	15
dag<-	16
data.file	16
data.file<-	17
discreteness	17
discreteness<-	18
em	18
get.boot	19
get.data	20
get.imputed.data	21
get.most.probable.values	21
get.raw.data	22
has.boots	23
has.data	23
has.imp.boots	24
has.imputed.data	25
has.raw.data	25
header.file	26
header.file<-	27
imp.boots	28
imp.boots<-	28
impute	29
imputed.data<-	29
InferenceEngine-class	30
jpts	31
jpts<-	32
jt.cliques	32
jt.cliques<-	33
junction.tree	33
junction.tree<-	34
knn.impute	34
layering	35
learn.params	36
learn.structure	37
marginals	38
name	39
name<-	40
node.sizes	40
node.sizes<-	41
num.boots	41
num.boots<-	42
num.items	42
num.items<-	43
num.nodes	43
num.nodes<-	44
num.variables	44
num.variables<-	45

observations . . . . .	45
observations<- . . . . .	46
plot . . . . .	47
print . . . . .	47
query . . . . .	48
raw.data<- . . . . .	49
read.bif . . . . .	49
read.dataset . . . . .	50
read.dsc . . . . .	51
read.net . . . . .	52
sample.dataset . . . . .	52
sample.row . . . . .	53
save.to.eps . . . . .	53
scoring.func . . . . .	54
scoring.func<- . . . . .	54
sem . . . . .	55
show . . . . .	56
struct.algo . . . . .	57
struct.algo<- . . . . .	57
test.updated.bn . . . . .	58
updated.bn . . . . .	58
updated.bn<- . . . . .	59
variables . . . . .	59
variables<- . . . . .	60
wpdag . . . . .	61
wpdag<- . . . . .	61
write.dsc . . . . .	62

**Index****63**


---

add.observations<-	<i>add further evidence to an existing list of observations of an <a href="#">InferenceEngine</a>.</i>
--------------------	--

---

**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<-](#)

---

<code>asia</code>	<i>load Asia dataset.</i>
-------------------	---------------------------

---

**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)
```

---

asia_10000	Asia <i>dataset</i> .
------------	-----------------------

---

### 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

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

### See Also

[asia](#)

---

<code>belief.propagation</code>	<i>perform belief propagation.</i>
---------------------------------	------------------------------------

---

### Description

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

### Usage

```
belief.propagation(ie, net = NULL, observed.vars = NULL,
  observed.vals = NULL, return.potentials = FALSE, ...)

## S4 method for signature 'InferenceEngine'
belief.propagation(ie, net = NULL,
  observed.vars = NULL, observed.vals = NULL, return.potentials = FALSE,
  ...)
```

**Arguments**

ie                    an [InferenceEngine](#) object.  
 net                   a [BN](#) object.  
 observed.vars       list of observed variables.  
 observed.vals       values taken by variables listed in observed.vars.  
 return.potentials   if TRUE only the potentials are returned, instead of the default [BN](#).  
 ...                   potential further arguments of methods.

**Value**

updated [InferenceEngine](#) object.

**Examples**

```
## Not run:
dataset <- BNdataset()
dataset <- read.dataset(dataset, "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	<i>get the <a href="#">BN</a> object contained in an <a href="#">InferenceEngine</a>.</i>
----	---

---

**Description**

Return a network contained in an [InferenceEngine](#).

**Usage**

```
bn(x)

## 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**

BN class definition.

Instantiate a [BN](#) object.

**Usage**

```
## S4 method for signature 'BN'
initialize(.Object, dataset = NULL, ...)

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

**Arguments**

<code>.Object</code>	a BN
<code>dataset</code>	a <a href="#">BNDataset</a> object containing the dataset the network is built upon, if any. The remaining parameters are considered only if a starting dataset is provided.
<code>...</code>	potential further arguments of methods.

**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)

**Examples**

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

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

## End(Not run)
```

---

bn<-	set the original BN object contained in an InferenceEngine.
------	---

---

**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.

initialize a BNDataset object.

constructor for BNDataset object

**Usage**

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

```
BNDataset(name = "", data = NULL, variables = c(), node.sizes = c(),
  discreteness = c(), ...)
```



**Arguments**

<code>.Object</code>	an empty BNDataset.
<code>...</code>	potential further arguments of methods.
<code>name</code>	name of the dataset.
<code>data</code>	raw data.frame.
<code>variables</code>	vector of variable names.
<code>node.sizes</code>	vector of variable cardinalities (for discrete variables) or quantization ranges (for continuous variables).
<code>discreteness</code>	a vector of elements in {c,d} for continuous and discrete variables (respectively)

**Details**

Dataset should be provided in the following format... (describe)

**Value**

a BNDataset object.  
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  
`num.items`: number of observations (rows) in the dataset  
`has.rawdata`: TRUE if the dataset contains data read from a file  
`has.impdata`: TRUE if the dataset contains imputed data (computed from raw data)  
`raw.data`: matrix containing raw data  
`imputation`: TRUE if it dataset contains imputed data  
`imputed.data`: matrix containing imputed data  
`has.boots`: dataset has bootstrap samples  
`boots`: list of bootstrap samples  
`has.imp.boots`: dataset has imputed bootstrap samples  
`imp.boots`: list of imputed bootstrap samples  
`num.boots`: number of bootstrap samples

## Examples

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

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

## End(Not run)
```

---

boots	<i>get list of bootstrap samples of a <a href="#">BNDataset</a>.</i>
-------	--

---

## 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.imp.boots](#), [imp.boots](#)

---

boots<-	<i>set list of bootstrap samples of a <a href="#">BNDataset</a>.</i>
---------	--

---

**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 <a href="#">BNDataset</a> object.
value	the list of bootstrap samples.

---

bootstrap	<i>Perform bootstrap.</i>
-----------	---------------------------

---

**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, na.string.symbol = "?", ...)
```

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

**Arguments**

object	the <a href="#">BNDataset</a> object.
num.boots	number of sampled datasets for bootstrap.
seed	random seed.
imputation	TRUE if imputation has to be performed.
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).

```
na.string.symbol      character that denotes NA in the dataset (useful only if imputation == TRUE).
...                  potential further arguments of methods.
```

### Examples

```
## Not run:
dataset <- BNdataset()
dataset <- read.dataset(dataset, "file.header", "file.data")
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.
```

### Examples

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

## End(Not run)
```

---

child	<i>load Child dataset.</i>
-------	----------------------------

---

**Description**

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

**Usage**

```
child()
```

**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)
```

---

child_NA_5000	<i>Child dataset.</i>
---------------	-----------------------

---

**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.head` and `pkg_folder/extdata/extdata/Child_data_na_5000.data`.

## References

D. J. Spiegelhalter, R. G. Cowell (1992). Learning in probabilistic expert systems. In Bayesian Statistics 4 (J. M. Bernardo, J. O. Berger, A. P. Dawid and A. F. M. Smith, eds.) 447-466. Clarendon Press, Oxford.

## See Also

[child](#)

---

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.

---

cpts<-	<i>set the list of conditional probability tables of a network.</i>
--------	---

---

**Description**

Set the list of conditional probability tables of a [BN](#) object.

**Usage**

```
cpts(x) <- value

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

**Arguments**

x	an object.
value	list of the conditional probability tables of the object.

**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.

---

dag	<i>get adjacency matrix of a network.</i>
-----	---

---

**Description**

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

**Usage**

```
dag(x)

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

**Arguments**

x	an object.
---	------------

**Value**

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

---

dag<-	<i>set adjacency matrix of an object.</i>
-------	---

---

**Description**

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

**Usage**

```
dag(x) <- value

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

**Arguments**

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

---

data.file	<i>get data file of a <a href="#">BNDataset</a>.</i>
-----------	--

---

**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 <a href="#">BNDataset</a> .
---	-------------------------------

**Value**

data filename of the dataset.

**See Also**

[data.file](#)



---

data.file<-	<i>set data file of a <a href="#">BNDataset</a>.</i>
-------------	--

---

**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 <a href="#">BNDataset</a> .
value	data filename.

**See Also**

[header.file<-](#)

---

discreteness	<i>get status (discrete or continuous) of the variables of an object.</i>
--------------	---

---

**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 'BNDataset'
discreteness(x)

## S4 method for signature 'BN'
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<-` *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**

```
discreteness(x) <- value

## S4 replacement method for signature 'BNdataset'
discreteness(x) <- value

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

**Arguments**

`x` an object.

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

---

`em` *expectation-maximization algorithm.*

---

**Description**

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

**Usage**

```
em(x, dataset, threshold = 0.001, k.impute = 10, ...)

## S4 method for signature 'InferenceEngine,BNdataset'
em(x, dataset, threshold = 0.001,
   k.impute = 10, ...)
```

**Arguments**

x	an <a href="#">InferenceEngine</a> .
dataset	observed dataset with missing values for the Bayesian Network of x.
threshold	threshold for convergence, used as stopping criterion.
k.impute	number of neighbours to be used; for discrete variables we use mode, for continuous variables the median value is instead taken.
...	further potential arguments for method.

**Value**

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

**Examples**

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

## End(Not run)
```

---

get.boot	<i>get selected element of bootstrap list.</i>
----------	--

---

**Description**

Given a [BNDataset](#), return the sample corresponding to given index.

**Usage**

```
get.boot(dataset, index, imputed = TRUE, ...)

## S4 method for signature 'BNDataset,numeric'
get.boot(dataset, index, imputed = TRUE, ...)
```

**Arguments**

dataset	a <a href="#">BNDataset</a> object.
index	the index of the requested sample.
imputed	TRUE if samples from imputed dataset are to be used.
...	potential further arguments of methods (ignored).

**See Also**

[bootstrap](#)

**Examples**

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

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

## End(Not run)
```

---

get.data	<i>get data of a BNDataset.</i>
----------	---------------------------------

---

**Description**

Return data contained in a [BNDataset](#) object, if any. Preference is given to imputed data, if available, because the imputed dataset is (supposed to be), in general, more useful. To obtain specifically raw or imputed data, one must revert to [get.raw.data\(\)](#) and [get.imputed.data\(\)](#), respectively.

**Usage**

```
get.data(x)

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

**Arguments**

x                    a [BNDataset](#).

**See Also**

[has.data](#), [has.raw.data](#), [has.imputed.data](#), [get.raw.data](#), [get.imputed.data](#)

**Examples**

```
## Not run:
x <- BNDataset()
x <- read.dataset(x, "file.header", "file.data")
get.data(x) # returns raw dataset, the only one present in dataset

x <- impute(x)
get.data(x) # returns imputed dataset, since it is present now

## End(Not run)
```

---

get.imputed.data	<i>get imputed data of a BNDataset.</i>
------------------	---

---

### Description

Return imputed data contained in a [BNDataset](#) object, if any.

### Usage

```
get.imputed.data(x)

## S4 method for signature 'BNDataset'
get.imputed.data(x)
```

### Arguments

x                    a [BNDataset](#).

### See Also

[has.data](#), [has.raw.data](#), [has.imputed.data](#), [get.data](#), [get.raw.data](#)

---

get.most.probable.values	<i>compute the most probable values to be observed.</i>
--------------------------	---

---

### 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.

### Usage

```
get.most.probable.values(x, ...)
```

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

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

### Arguments

x                    a [BN](#) or [InferenceEngine](#) object.

...                  potential further arguments of methods.

**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)  
get.most.probable.values(eng)  
  
## End(Not run)
```

---

get.raw.data

*get raw data of a BNdataset.*

---

**Description**

Return raw data contained in a [BNdataset](#) object, if any.

**Usage**

```
get.raw.data(x)  
  
## S4 method for signature 'BNdataset'  
get.raw.data(x)
```

**Arguments**

x                    a [BNdataset](#).

**See Also**

[has.data](#), [has.raw.data](#), [has.imputed.data](#), [get.data](#), [get.imputed.data](#)

---

has.boots	<i>check whether a <a href="#">BNDataset</a> has bootstrap samples or not.</i>
-----------	--

---

**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.imp.boots](#), [boots](#), [imp.boots](#)

---

has.data	<i>check if a <a href="#">BNDataset</a> contains any data.</i>
----------	--

---

**Description**

Check whether a [BNDataset](#) object actually contains raw or imputed data.

**Usage**

```
has.data(x)

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

**Arguments**

x                    a [BNDataset](#).

**See Also**

[has.raw.data](#), [has.imputed.data](#), [get.data](#), [get.raw.data](#), [get.imputed.data](#)

### Examples

```
## Not run:
x <- BNDataset()
has.data(x) # FALSE

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

## End(Not run)
```

---

has.imp.boots	<i>check whether a <a href="#">BNDataset</a> has bootstrap samples from imputed data or not.</i>
---------------	--

---

### Description

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

### Usage

```
has.imp.boots(x)

## S4 method for signature 'BNDataset'
has.imp.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	<i>check if a BNDataset contains imputed data.</i>
------------------	--

---

### Description

Check whether a [BNDataset](#) object actually contains imputed data.

### Usage

```
has.imputed.data(x)

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

### Arguments

x                    a [BNDataset](#).

### See Also

[has.data](#), [has.raw.data](#), [get.data](#), [get.raw.data](#), [get.imputed.data](#)

### Examples

```
## Not run:
x <- BNDataset()
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	<i>check if a BNDataset contains raw data.</i>
--------------	--

---

### Description

Check whether a [BNDataset](#) 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.data](#), [has.imputed.data](#), [get.data](#), [get.raw.data](#), [get.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	<i>get header file of a <a href="#">BNDataset</a>.</i>
-------------	--

---

**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)
```

**Arguments**

x                      a [BNDataset](#).

**Value**

header filename of the dataset.

**See Also**

[data.file](#)

---

header.file<-	<i>set header file of a <a href="#">BNDataset</a>.</i>
---------------	--

---

**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 <a href="#">BNDataset</a> .
value	header filename.

**See Also**

[data.file<-](#)

---

imp.boots	<i>get list of bootstrap samples from imputed data of a <a href="#">BNDataset</a>.</i>
-----------	--

---

**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.imp.boots](#), [boots](#)

---

imp.boots<-	<i>set list of bootstrap samples from imputed data of a <a href="#">BNDataset</a>.</i>
-------------	--

---

**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	Impute a <a href="#">BNDataset</a> raw data with missing values.
--------	--

---

### Description

Impute a [BNDataset](#) raw data with missing values.

### Usage

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

## S4 method for signature 'BNDataset'
impute(object, k.impute = 10)
```

### Arguments

object	the <a href="#">BNDataset</a> object.
k.impute	number of neighbours to be used; for discrete variables we use mode, for continuous variables the median value is instead taken.
...	potential further arguments of methods.

### Examples

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

## End(Not run)
```

---

imputed.data<-	add imputed data.
----------------	-------------------

---

### Description

Insert imputed data in a [BNDataset](#) object.

### Usage

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

## S4 replacement method for signature 'BNDataset'
imputed.data(x) <- value
```

**Arguments**

x	a <a href="#">BNDataset</a> .
value	a matrix of integers containing a dataset.

**Details**

Users are encouraged to not use this method whenever possible, in favour of [read.dataset](#) with flag `imputation = TRUE`.

**See Also**

[has.data](#), [has.imputed.data](#), [get.data](#), [read.dataset](#)

---

InferenceEngine-class *InferenceEngine class.*

---

**Description**

InferenceEngine class.

Constructor method of [InferenceEngine](#) class.

constructor for [InferenceEngine](#) object

**Usage**

```
## S4 method for signature 'InferenceEngine'
initialize(.Object, ...)
```

```
InferenceEngine(bn = NULL, observations = NULL, ...)
```

**Arguments**

.Object	an empty InferenceEngine object.
...	potential further arguments of methods.
bn	a <a href="#">BN</a> object.
observations	a list of observations composed by the two following vectors: <ul style="list-style-type: none"> <li>• <code>observed.vars</code>:vector of observed variables;</li> <li>• <code>observed.vals</code>:vector of values observed for the variables in <code>observed.vars</code> in the corresponding position.</li> </ul>

**Value**

an InferenceEngine object.

InferenceEngine object.



**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](#).

---

jpts<-	<i>set the list of joint probability tables compiled by an <a href="#">InferenceEngine</a>.</i>
--------	---

---

**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 <a href="#">InferenceEngine</a> .
value	the list of joint probability tables compiled by the <a href="#">InferenceEngine</a> .

**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	<i>get the list of cliques of the junction tree of an <a href="#">InferenceEngine</a>.</i>
------------	--

---

**Description**

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

**Usage**

```
jt.cliques(x)

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



`jt.cliques<-`

33

### Arguments

`x` an [InferenceEngine](#).

### Value

the list of cliques of the junction tree contained in the [InferenceEngine](#).

---

<code>jt.cliques&lt;-</code>	<i>set the list of cliques of the junction tree of an <a href="#">InferenceEngine</a>.</i>
------------------------------	--

---

### Description

Add to the [InferenceEngine](#) a list containing the cliques of variables composing the nodes of the junction tree.

### Usage

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

## 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](#).

---

<code>junction.tree</code>	<i>get the junction tree of an <a href="#">InferenceEngine</a>.</i>
----------------------------	---

---

### 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 <a href="#">InferenceEngine</a> .
-----------------	---

---

**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
```

**Arguments**

x	an <a href="#">InferenceEngine</a> .
value	the junction tree to be inserted in the <a href="#">InferenceEngine</a> .

---

knn.impute	Perform imputation of a data frame using k-NN.
------------	--

---

**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**

```
knn.impute(data, k = 10, cat.var = 1:ncol(data), to.impute = 1:nrow(data),
  using = 1:nrow(data))
```

**Arguments**

<code>data</code>	a data frame
<code>k</code>	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.
<code>cat.var</code>	vector containing the indices of the variables to be considered as categorical. Default: all variables.
<code>to.impute</code>	vector indicating which rows of the dataset are to be imputed. Default: impute all rows.
<code>using</code>	vector indicating which rows of the dataset are to be used to search for neighbours. Default: use all rows.

**Value**

imputed data frame.

---

<code>layering</code>	<i>return the layering of the nodes.</i>
-----------------------	--

---

**Description**

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

**Usage**

```
layering(x, updated.bn = TRUE, ...)

## S4 method for signature 'BN'
layering(x, updated.bn = TRUE, ...)

## S4 method for signature 'InferenceEngine'
layering(x, updated.bn = TRUE, ...)
```

**Arguments**

<code>x</code>	a <a href="#">BN</a> or <a href="#">InferenceEngine</a> object.
<code>updated.bn</code>	TRUE if <code>x</code> is an <code>InferenceEngine</code> and the updated network is chosen (kept only for compatibility with other methods).
<code>...</code>	potential further arguments for methods.

**Value**

a vector containing layers the nodes can be divided into.

**Examples**

```
## Not run:
dataset <- BNdataset(name="MyDataset")
dataset <- read.dataset(dataset, "file.header", "file.data")
x <- BN(dataset)
layering(x)
eng <- InferenceEngine(x)
layering(x, updated.bn=TRUE)

## 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, ...)

## S4 method for signature 'BN,BNdataset'
learn.params(bn, dataset, ess = 1)
```

**Arguments**

bn	a <a href="#">BN</a> object.
dataset	a <a href="#">BNdataset</a> object.
ess	Equivalent Sample Size value.
...	potential further arguments of methods.

**Value**

new [BN](#) object with conditional probabilities.

**Examples**

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

## End(Not run)
```

---

learn.structure	<i>learn the structure of a network.</i>
-----------------	--

---

## Description

Learn the structure (the directed acyclic graph) of a [BN](#) object according to a [BNDataset](#). Currently, two algorithms are supported (can be specified using the `algo` option): `'sm'`, the Silander-Myllymaki exact algorithm, and `'mmhc'`, the Max-Min Hill-Climbing heuristic algorithm (default). Three scoring functions are also provided: `'BDeu'`, the Bayesian-Dirichlet equivalent uniform score, `'AIC'`, the Akaike Information criterion, and `'BIC'`, the Bayesian Information criterion.

## Usage

```
learn.structure(bn, dataset, algo = "mmhc", scoring.func = "BDeu",
  alpha = 0.05, ess = 1, bootstrap = FALSE, layering = c(),
  max.fanin.layers = NULL, max.fanin = num.variables(dataset),
  cont.nodes = c(), raw.data = FALSE, num.boots = 100,
  imputation = TRUE, k.impute = 10, na.string.symbol = "?", seed = 0,
  ...)

## S4 method for signature 'BN,BNDataset'
learn.structure(bn, dataset, algo = "mmhc",
  scoring.func = "BDeu", alpha = 0.05, ess = 1, bootstrap = FALSE,
  layering = c(), max.fanin.layers = NULL,
  max.fanin = num.variables(dataset), cont.nodes = c(), raw.data = FALSE,
  num.boots = 100, imputation = TRUE, k.impute = 10,
  na.string.symbol = "?", seed = 0)
```

## Arguments

<code>bn</code>	a <a href="#">BN</a> object.
<code>dataset</code>	a <a href="#">BNDataset</a> .
<code>algo</code>	the algorithm to use. Currently, one among <code>sm</code> (Silander-Myllymaki) and <code>mmhc</code> (Max-Min Hill Climbing, default).
<code>scoring.func</code>	the scoring function to use. Currently, one among <code>BDeu</code> , <code>AIC</code> , <code>BIC</code> .
<code>alpha</code>	confidence threshold (only for <code>mmhc</code> ).
<code>ess</code>	Equivalent Sample Size value.
<code>bootstrap</code>	<code>TRUE</code> to use bootstrap samples.
<code>layering</code>	vector containing the layers each node belongs to (only for <code>sm</code> ).
<code>max.fanin.layers</code>	matrix of available parents in each layer (only for <code>sm</code> ).
<code>max.fanin</code>	maximum number of parents for each node (only for <code>sm</code> ).
<code>cont.nodes</code>	vector containing the index of continuous variables.

<code>raw.data</code>	TRUE to learn the structure from the raw dataset. Default is to use imputed dataset (if available, otherwise the raw dataset will be used anyway).
<code>num.boots</code>	number of bootstrap samples to generate, if needed.
<code>imputation</code>	TRUE if imputation is needed; if <code>bootstrap=TRUE</code> , imputed samples will be also used.
<code>k.impute</code>	number of neighbours to be used; for discrete variables we use mode, for continuous variables the median value is instead taken.
<code>na.string.symbol</code>	symbol for NA values (missing data).
<code>seed</code>	random seed.
<code>...</code>	potential further arguments for method.

### Details

The Silander-Myllymaki algorithm can take a very long time, and it is not feasible for networks of more than 20-30 nodes. It is strongly recommended that valid layering, `max.fanin.layers` and `max.fanin` parameters are passed to the method if `algo = 'sm'` is given as parameter to the method.

### Value

new [BN](#) object with DAG.

### Examples

```
## Not run:
dataset <- BNdataset(name = "MyDataset")
dataset <- read.dataset(dataset, "file.header", "file.data")
bn <- BN()
# 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 1 0 1 1 1 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, raw.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	<i>get name of an object.</i>
------	-------------------------------

---

**Description**

Return the name of an object, of class [BN](#) or [BNDataset](#).

**Usage**

```
name(x)

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

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

**Arguments**

x                    an object.

**Value**

name of the object.

---

name<-	<i>set name of an object.</i>
--------	-------------------------------

---

### Description

Set the name slot of an object of type [BN](#) or [BNDataset](#).

### Usage

```
name(x) <- value

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

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

### Arguments

x	an object.
value	the new name of the object.

---

node.sizes	<i>get size of the variables of an object.</i>
------------	--

---

### 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 'BNDataset'
node.sizes(x)

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

### Arguments

x	an object.
---	------------

### Value

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



---

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

---

### 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 'BNDataset'
node.sizes(x) <- value

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

### Arguments

x	an object.
value	vector containing the size of each variable of the object.

---

num.boots	<i>get number of bootstrap samples of a <a href="#">BNDataset</a>.</i>
-----------	--

---

### Description

Return the number of bootstrap samples computed from a dataset.

### Usage

```
num.boots(x)

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

### Arguments

x	a <a href="#">BNDataset</a> object.
---	-------------------------------------

### Value

the number of bootstrap samples.

---

num.boots<-	<i>set number of bootstrap samples of a <a href="#">BNDataset</a>.</i>
-------------	--

---

**Description**

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

**Usage**

```
num.boots(x) <- value

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

**Arguments**

x	a <a href="#">BNDataset</a> object.
value	the number of bootstrap samples.

---

num.items	<i>get number of items of a <a href="#">BNDataset</a>.</i>
-----------	--

---

**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 <a href="#">BNDataset</a> object.
---	-------------------------------------

**Value**

number of items of the desired dataset.

---

num.items<-	<i>set number of items of a <a href="#">BNDataset</a>.</i>
-------------	--

---

**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 <a href="#">BNDataset</a> object.
value	number of items of the desired dataset.

---

num.nodes	<i>get number of nodes of an object.</i>
-----------	--

---

**Description**

Return the name of an object, of class [BN](#) or [InferenceEngine](#).

**Usage**

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

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

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

**Arguments**

x	an object.
---	------------

**Value**

number of nodes of the desired object.

---

num.nodes<-	<i>set number of nodes of an object.</i>
-------------	--

---

### 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

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

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

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

### Arguments

x	an object.
value	the number of nodes in the object.

---

num.variables	<i>get number of variables of a <a href="#">BNDataset</a>.</i>
---------------	--

---

### 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

```
num.variables(x)

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

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

### Arguments

x	a <a href="#">BNDataset</a> object.
---	-------------------------------------

`num.variables<-`

45

### Value

number of variables of the desired dataset.

### See Also

[num.nodes](#)

---

<code>num.variables&lt;-</code>	<i>set number of variables of a <a href="#">BNDataset</a>.</i>
---------------------------------	--

---

### Description

Set the number of variables observed in a dataset.

### Usage

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

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

### Arguments

<code>x</code>	a <a href="#">BNDataset</a> object.
<code>value</code>	number of variables of the dataset.

---

<code>observations</code>	<i>get the list of observations of an <a href="#">InferenceEngine</a>.</i>
---------------------------	--

---

### Description

Return the list of observations added to an [InferenceEngine](#).

### Usage

```
observations(x)

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

### Arguments

<code>x</code>	an <a href="#">InferenceEngine</a> .
----------------	--------------------------------------

## 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](#).

---

<code>observations&lt;-</code>	<i>set the list of observations of an <a href="#">InferenceEngine</a>.</i>
--------------------------------	--

---

## 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

<code>x</code>	an <a href="#">InferenceEngine</a> .
<code>value</code>	the list of observations of the <a href="#">InferenceEngine</a> .

## 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<-](#)

---

plot	<i>plot a BN as a picture.</i>
------	--------------------------------

---

### Description

plot a BN as a picture.

### Usage

```
## S3 method for class 'BN'
plot(x, ..., use.node.names = TRUE, frac = 0.2,
      max.weight = max(dag(x)), node.col = rep("white", ncol(dag(x))),
      plot.wpdag = FALSE)
```

### Arguments

x	a BN object.
...	potential further arguments for methods.
use.node.names	TRUE if node names have to be printed. If FALSE, numbers are used instead.
frac	fraction
max.weight	max.weight
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.

---

print	<i>print an object to stdout.</i>
-------	-----------------------------------

---

### Description

print an object to stdout.

### Usage

```
print(x, ...)

## S4 method for signature 'BNdataset'
print(x, show.raw.data = FALSE,
      show.imputed.data = FALSE, ...)

## S4 method for signature 'BN'
print(x, ...)

## S4 method for signature 'InferenceEngine'
print(x, engine = "jt", ...)
```

**Arguments**

**x** an object.  
**...** potential other arguments.  
**show.raw.data** when x is a [BNDataset](#), print also raw dataset, if available.  
**show.imputed.data** when x is a [BNDataset](#), print also imputed dataset, if available.  
**engine** when x is an [InferenceEngine](#), specify the inference engine to be shown. Currently only engine = 'jt' is supported.

---

query	<i>query BN given observations</i>
-------	------------------------------------

---

**Description**

query BN given observations

**Usage**

```
query(x, observed.vars = c(), observed.vals = c(), ...)
```

```
## S4 method for signature 'BN'
query(x, observed.vars, observed.vals)
```

**Arguments**

**x** a BN.  
**observed.vars** vector of observed variables.  
**observed.vals** vector of observed values for corresponding variables in observed.vars.  
**...** potential further arguments for method.

**Value**

most probable values given observations



---

raw.data<-	<i>add raw data.</i>
------------	----------------------

---

**Description**

Insert raw data in a [BNDataset](#) object.

**Usage**

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

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

**Arguments**

x	a <a href="#">BNDataset</a> .
value	a matrix of integers containing a dataset.

**Details**

Users are encouraged to not use this method whenever possible, in favour of [read.dataset](#).

**See Also**

[has.data](#), [has.raw.data](#), [get.data](#), [read.dataset](#)

---

read.bif	<i>Read a network from a .bif file.</i>
----------	---

---

**Description**

Read a network described in a .bif-formatted file, and build a [BN](#) object.

**Usage**

```
read.bif(x)
```

```
## S4 method for signature 'character'
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.

---

read.dataset	<i>Read a dataset from file.</i>
--------------	----------------------------------

---

## Description

File has to be in format (describe...)

## Usage

```
read.dataset(object, header.file, data.file, imputation = FALSE,
  header.flag = FALSE, na.string.symbol = "?", sep.symbol = "",
  k.impute = 10, bootstrap = FALSE, num.boots = 100, seed = 0,
  starts.from = 0, ...)
```

```
## S4 method for signature 'BNDataset,character,character'
read.dataset(object, header.file,
  data.file, imputation = FALSE, header.flag = FALSE,
  na.string.symbol = "?", sep.symbol = "", k.impute = 10,
  bootstrap = FALSE, num.boots = 100, seed = 0, starts.from = 0, ...)
```

## Arguments

object	the <a href="#">BNDataset</a> object.
header.file	the header file.
data.file	the data file.
imputation	TRUE if imputation has to be performed.
header.flag	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.
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).
bootstrap	TRUE if bootstrap has to be performed; prepares a list of datasets sampled from the original one.
num.boots	number of sampled datasets for bootstrap (useful only if bootstrap == TRUE).

seed                    random seed (useful only if bootstrap == TRUE).  
 starts.from            starting value for entries in the dataset (observed values, default is 0).  
 ...                    potential further arguments of methods.

### Examples

```
## Not run:
dataset <- BNdataset()
dataset <- read.dataset(dataset, header="file.header", dataset="file.data")

## End(Not run)
```

---

read.dsc	<i>Read a network from a .dsc file.</i>
----------	---

---

### Description

Read a network described in a .dsc-formatted file, and build a [BN](#) object.

### Usage

```
read.dsc(x)

## S4 method for signature 'character'
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	<i>Read a network from a .net file.</i>
----------	---

---

### Description

Read a network described in a .net-formatted file, and build a [BN](#) object.

### Usage

```
read.net(x)

## S4 method for signature 'character'
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.

### Value

a [BN](#) object.

---

sample.dataset	<i>sample a <a href="#">BNDataset</a> from a network of an inference engine.</i>
----------------	--

---

### Description

sample a [BNDataset](#) from a network of an inference engine.

### Usage

```
sample.dataset(x, n = 100)

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

## S4 method for signature 'InferenceEngine'
sample.dataset(x, n = 100)
```

### Arguments

x                      a [BN](#) or [InferenceEngine](#) object.  
n                      number of items to sample.

**Value**

a [BNDataset](#)

---

sample.row	<i>sample a row vector of values for a network.</i>
------------	---

---

**Description**

sample a row vector of values for a network.

**Usage**

```
sample.row(x)

## S4 method for signature 'BN'
sample.row(x)

## S4 method for signature 'InferenceEngine'
sample.row(x)
```

**Arguments**

x                      a [BN](#) or [InferenceEngine](#) object.

**Value**

a vector of values.

---

save.to.eps	<i>save a <a href="#">BN</a> picture as .eps file.</i>
-------------	--

---

**Description**

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

**Usage**

```
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

**See Also**[plot](#)**Examples**

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

## End(Not run)
```

scoring.func

*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.

scoring.func&lt;-

*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 <a href="#">BN</a> object.
value	the scoring function used.

**Value**

updated BN.

---

sem	<i>Structural Expectation-Maximization algorithm.</i>
-----	---

---

**Description**

Learn struvture and parameters of a network with the Structural EM algorithm.

**Usage**

```
sem(x, dataset, struct.threshold = 10, param.threshold = 0.001,
    k.impute = 10, algo = "mmhc", scoring.func = "BDeu", alpha = 0.05,
    ess = 1, bootstrap = FALSE, layering = c(), max.fanin.layers = NULL,
    max.fanin = num.variables(dataset), cont.nodes = c(), raw.data = FALSE,
    num.boots = 100, imputation = TRUE, na.string.symbol = "?", seed = 0,
    ...)

## S4 method for signature 'InferenceEngine,BNDataset'
sem(x, dataset, struct.threshold = 10,
    param.threshold = 0.001, k.impute = 10, algo = "mmhc",
    scoring.func = "BDeu", alpha = 0.05, ess = 1, bootstrap = FALSE,
    layering = c(), max.fanin.layers = NULL,
    max.fanin = num.variables(dataset), cont.nodes = c(), raw.data = FALSE,
    num.boots = 100, imputation = TRUE, na.string.symbol = "?", seed = 0,
    ...)
```

**Arguments**

x	an <a href="#">InferenceEngine</a>
dataset	observed dataset with missing values for the Bayesian Network of x.
struct.threshold	threshold for convergence of the structure learning step, used as stopping criterion.
param.threshold	threshold for convergence of the parameter learning step, used as stopping criterion.
k.impute	number of neighbours to be used; for discrete variables we use mode, for continuous variables the median value is instead taken.

<code>algo</code>	the algorithm to use. Currently, one among <code>sm</code> (Silander-Myllymaki) and <code>mmhc</code> (Max-Min Hill Climbing, default).
<code>scoring.func</code>	the scoring function to use. Currently, one among <code>BDeu</code> , <code>AIC</code> , <code>BIC</code> .
<code>alpha</code>	confidence threshold (only for <code>mmhc</code> ).
<code>ess</code>	Equivalent Sample Size value.
<code>bootstrap</code>	TRUE to use bootstrap samples.
<code>layering</code>	vector containing the layers each node belongs to (only for <code>sm</code> ).
<code>max.fanin.layers</code>	matrix of available parents in each layer (only for <code>sm</code> ).
<code>max.fanin</code>	maximum number of parents for each node (only for <code>sm</code> ).
<code>cont.nodes</code>	vector containing the index of continuous variables.
<code>raw.data</code>	TRUE to learn the structure from the raw dataset. Default is to use imputed dataset (if available, otherwise the raw dataset will be used anyway).
<code>num.boots</code>	number of bootstrap samples to generate, if needed.
<code>imputation</code>	TRUE if imputation is needed; if <code>bootstrap=TRUE</code> , imputed samples will be also used.
<code>na.string.symbol</code>	symbol for NA values (missing data).
<code>seed</code>	random seed.
<code>...</code>	further potential arguments for method.

### Value

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

### Examples

```
## Not run:
sem(x, dataset)

## End(Not run)
```

---

<code>show</code>	<i>Show method for objects.</i>
-------------------	---------------------------------

---

### Description

The `show` method allows to provide a custom aspect for the output that is generated when the name of an instance is given as command in an R session.

### Usage

```
show(object)
```



**Arguments**

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.

---

test.updated.bn	<i>check if an updated BN is present in an InferenceEngine.</i>
-----------------	---

---

### 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.

### 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()
dataset <- read.dataset(dataset, "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

## End(Not run)
```

---

updated.bn	<i>get the updated BN object contained in an InferenceEngine.</i>
------------	---

---

### Description

Return an updated network contained in an InferenceEngine.

`updated.bn<-`

59

### Usage

```
updated.bn(x)

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

### Arguments

`x` an [InferenceEngine](#).

### Value

the updated [BN](#) object contained in an [InferenceEngine](#).

---

<code>updated.bn&lt;-</code>	<i>set the updated <a href="#">BN</a> object contained in an <a href="#">InferenceEngine</a>.</i>
------------------------------	---

---

### Description

Add an updated network to an [InferenceEngine](#).

### Usage

```
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](#).

---

<code>variables</code>	<i>get variables of an object.</i>
------------------------	------------------------------------

---

### Description

Get the list of variables (with their names) of a [BN](#) or [BNDataset](#).

**Usage**

```
variables(x)

## S4 method for signature 'BNdataset'
variables(x)

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

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

**Arguments**

x                      an object.

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

---

wpdag	<i>get the WPDAG of an object.</i>
-------	------------------------------------

---

**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<-	<i>set WPDAG of the object.</i>
---------	---------------------------------

---

**Description**

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

**Usage**

```
wpdag(x) <- value

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

**Arguments**

x                      an object.  
value                  matrix containing the WPDAG of the object.

---

write.dsc	<i>Write a network saving it in a .dsc file.</i>
-----------	--

---

**Description**

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

**Usage**

```
write.dsc(x, path = "./")  
  
## S4 method for signature 'BN'  
write.dsc(x, path = "./")
```

**Arguments**

x	the <a href="#">BN</a> object.
path	the relative or absolute path of the directory of the created file.

# Index

add.observations<-, 3  
add.observations<-, InferenceEngine-method  
    (add.observations<-), 3  
asia, 4, 5  
asia\_10000, 4, 5  
  
belief.propagation, 5  
belief.propagation, InferenceEngine  
    (belief.propagation), 5  
belief.propagation, InferenceEngine-method  
    (belief.propagation), 5  
BN, 6–8, 14, 15, 17, 21, 30, 31, 35–40, 43, 44,  
    47, 49–55, 57–60, 62  
BN (BN-class), 7  
bn, 6  
BN, BN-class (BN-class), 7  
bn, InferenceEngine (bn), 6  
bn, InferenceEngine-method (bn), 6  
BN-class, 7  
bn<-, 8  
bn<-, InferenceEngine-method (bn<-), 8  
BNdataset, 5, 7, 8, 10, 11, 13, 16, 17, 19–30,  
    36, 37, 39–45, 48–50, 52, 53, 59, 60  
BNdataset (BNdataset-class), 8  
BNdataset, BNdataset-class  
    (BNdataset-class), 8  
BNdataset-class, 8  
boots, 10, 23, 24, 28  
boots, BNdataset (boots), 10  
boots, BNdataset-method (boots), 10  
boots<-, 11  
boots<-, BNdataset-method (boots<-), 11  
bootstrap, 11, 19  
bootstrap, BNdataset (bootstrap), 11  
bootstrap, BNdataset-method (bootstrap),  
    11  
build.junction.tree, 12, 34  
build.junction.tree, InferenceEngine  
    (build.junction.tree), 12  
  
build.junction.tree, InferenceEngine-method  
    (build.junction.tree), 12  
  
child, 13, 14  
child\_NA\_5000, 13, 13  
cpts, 14  
cpts, BN (cpts), 14  
cpts, BN-method (cpts), 14  
cpts<-, 15  
cpts<-, BN-method (cpts<-), 15  
  
dag, 15  
dag, BN (dag), 15  
dag, BN-method (dag), 15  
dag<-, 16  
dag<-, BN-method (dag<-), 16  
data.file, 16, 16, 27  
data.file, BNdataset (data.file), 16  
data.file, BNdataset-method (data.file),  
    16  
data.file<-, 17  
data.file<-, BNdataset-method  
    (data.file<-), 17  
discreteness, 17  
discreteness, BN (discreteness), 17  
discreteness, BN-method (discreteness),  
    17  
discreteness, BNdataset (discreteness),  
    17  
discreteness, BNdataset-method  
    (discreteness), 17  
discreteness<-, 18  
discreteness<-, BN-method  
    (discreteness<-), 18  
discreteness<-, BNdataset-method  
    (discreteness<-), 18  
  
em, 18  
em, InferenceEngine, BNdataset (em), 18

- em, InferenceEngine, BNDataset-method (em), 18
- get.boot, 19
- get.boot, BNDataset (get.boot), 19
- get.boot, BNDataset, numeric-method (get.boot), 19
- get.data, 20, 21–23, 25, 26, 30, 49
- get.data, BNDataset (get.data), 20
- get.data, BNDataset-method (get.data), 20
- get.imputed.data, 20, 21, 22, 23, 25, 26
- get.imputed.data, BNDataset (get.imputed.data), 21
- get.imputed.data, BNDataset-method (get.imputed.data), 21
- get.most.probable.values, 21
- get.most.probable.values, BN (get.most.probable.values), 21
- get.most.probable.values, BN-method (get.most.probable.values), 21
- get.most.probable.values, InferenceEngine (get.most.probable.values), 21
- get.most.probable.values, InferenceEngine-method (get.most.probable.values), 21
- get.raw.data, 20, 21, 22, 23, 25, 26
- get.raw.data, BNDataset (get.raw.data), 22
- get.raw.data, BNDataset-method (get.raw.data), 22
- has.boots, 10, 23, 24, 28
- has.boots, BNDataset (has.boots), 23
- has.boots, BNDataset-method (has.boots), 23
- has.data, 20–22, 23, 25, 26, 30, 49
- has.data, BNDataset (has.data), 23
- has.data, BNDataset-method (has.data), 23
- has.imp.boots, 10, 23, 24, 28
- has.imp.boots, BNDataset (has.imp.boots), 24
- has.imp.boots, BNDataset-method (has.imp.boots), 24
- has.imputed.data, 20–23, 25, 26, 30
- has.imputed.data, BNDataset (has.imputed.data), 25
- has.imputed.data, BNDataset-method (has.imputed.data), 25
- has.raw.data, 20–23, 25, 25, 49
- has.raw.data, BNDataset (has.raw.data), 25
- has.raw.data, BNDataset-method (has.raw.data), 25
- header.file, 26
- header.file, BNDataset (header.file), 26
- header.file, BNDataset-method (header.file), 26
- header.file<-, 27
- header.file<-, BNDataset-method (header.file<-), 27
- imp.boots, 10, 23, 24, 28
- imp.boots, BNDataset (imp.boots), 28
- imp.boots, BNDataset-method (imp.boots), 28
- imp.boots<-, 28
- imp.boots<-, BNDataset-method (imp.boots<-), 28
- impute, 13, 29
- impute, BNDataset (impute), 29
- impute, BNDataset-method (impute), 29
- imputed.data<-, 29
- imputed.data<-, BNDataset-method (imputed.data<-), 29
- InferenceEngine, 3, 4, 6, 8, 12, 19, 21, 30–35, 38, 39, 43–46, 48, 52, 53, 55, 56, 58, 59
- InferenceEngine (InferenceEngine-class), 30
- InferenceEngine, InferenceEngine-class (InferenceEngine-class), 30
- InferenceEngine-class, 30
- initialize, BN-method (BN-class), 7
- initialize, BNDataset-method (BNDataset-class), 8
- initialize, InferenceEngine-method (InferenceEngine-class), 30
- jpts, 31
- jpts, InferenceEngine (jpts), 31
- jpts, InferenceEngine-method (jpts), 31
- jpts<-, 32
- jpts<-, InferenceEngine-method (jpts<-), 32
- jt.cliques, 32
- jt.cliques, InferenceEngine (jt.cliques), 32



`jt.cliques`, `InferenceEngine`-method  
     (`jt.cliques`), 32  
`jt.cliques<-`, 33  
`jt.cliques<-`, `InferenceEngine`-method  
     (`jt.cliques<-`), 33  
`junction.tree`, 33  
`junction.tree`, `InferenceEngine`  
     (`junction.tree`), 33  
`junction.tree`, `InferenceEngine`-method  
     (`junction.tree`), 33  
`junction.tree<-`, 34  
`junction.tree<-`, `InferenceEngine`-method  
     (`junction.tree<-`), 34  
  
`knn.impute`, 34  
  
`layering`, 35  
`layering`, `BN` (`layering`), 35  
`layering`, `BN`-method (`layering`), 35  
`layering`, `InferenceEngine` (`layering`), 35  
`layering`, `InferenceEngine`-method  
     (`layering`), 35  
`learn.params`, 36  
`learn.params`, `BN`, `BNDataset`  
     (`learn.params`), 36  
`learn.params`, `BN`, `BNDataset`-method  
     (`learn.params`), 36  
`learn.structure`, 37, 54, 57  
`learn.structure`, `BN`, `BNDataset`  
     (`learn.structure`), 37  
`learn.structure`, `BN`, `BNDataset`-method  
     (`learn.structure`), 37  
  
`marginals`, 38  
`marginals`, `InferenceEngine` (`marginals`),  
     38  
`marginals`, `InferenceEngine`-method  
     (`marginals`), 38  
  
`name`, 39  
`name`, `BN` (`name`), 39  
`name`, `BN`-method (`name`), 39  
`name`, `BNDataset` (`name`), 39  
`name`, `BNDataset`-method (`name`), 39  
`name<-`, 40  
`name<-`, `BN`-method (`name<-`), 40  
`name<-`, `BNDataset`-method (`name<-`), 40  
`node.sizes`, 40  
`node.sizes`, `BN` (`node.sizes`), 40  
`node.sizes`, `BN`-method (`node.sizes`), 40  
`node.sizes`, `BNDataset` (`node.sizes`), 40  
`node.sizes`, `BNDataset`-method  
     (`node.sizes`), 40  
`node.sizes<-`, 41  
`node.sizes<-`, `BN`-method (`node.sizes<-`),  
     41  
`node.sizes<-`, `BNDataset`-method  
     (`node.sizes<-`), 41  
`num.boots`, 41  
`num.boots`, `BNDataset` (`num.boots`), 41  
`num.boots`, `BNDataset`-method (`num.boots`),  
     41  
`num.boots<-`, 42  
`num.boots<-`, `BNDataset`-method  
     (`num.boots<-`), 42  
`num.items`, 42  
`num.items`, `BNDataset` (`num.items`), 42  
`num.items`, `BNDataset`-method (`num.items`),  
     42  
`num.items<-`, 43  
`num.items<-`, `BNDataset`-method  
     (`num.items<-`), 43  
`num.nodes`, 43, 44, 45  
`num.nodes`, `BN` (`num.nodes`), 43  
`num.nodes`, `BN`-method (`num.nodes`), 43  
`num.nodes`, `InferenceEngine` (`num.nodes`),  
     43  
`num.nodes`, `InferenceEngine`-method  
     (`num.nodes`), 43  
`num.nodes<-`, 44  
`num.nodes<-`, `BN`-method (`num.nodes<-`), 44  
`num.nodes<-`, `InferenceEngine`-method  
     (`num.nodes<-`), 44  
`num.variables`, 44  
`num.variables`, `BNDataset`  
     (`num.variables`), 44  
`num.variables`, `BNDataset`-method  
     (`num.variables`), 44  
`num.variables<-`, 45  
`num.variables<-`, `BNDataset`-method  
     (`num.variables<-`), 45  
  
`observations`, 45  
`observations`, `InferenceEngine`  
     (`observations`), 45  
`observations`, `InferenceEngine`-method  
     (`observations`), 45  
`observations<-`, 46

- observations<-, InferenceEngine-method  
(observations<-), 46
- plot, 47, 54
- plot, BN (plot), 47
- plot.BN (plot), 47
- plot.BN, BN (plot), 47
- print, 47
- print, BN (print), 47
- print, BN-method (print), 47
- print, BNdataset (print), 47
- print, BNdataset-method (print), 47
- print, InferenceEngine (print), 47
- print, InferenceEngine-method (print), 47
- query, 48
- query, BN (query), 48
- query, BN-method (query), 48
- raw.data<-, 49
- raw.data<-, BNdataset-method  
(raw.data<-), 49
- read.bif, 49
- read.bif, character (read.bif), 49
- read.bif, character-method (read.bif), 49
- read.dataset, 30, 49, 50
- read.dataset, BNdataset, character, character  
(read.dataset), 50
- read.dataset, BNdataset, character, character-method  
(read.dataset), 50
- read.dsc, 51
- read.dsc, character (read.dsc), 51
- read.dsc, character-method (read.dsc), 51
- read.net, 52
- read.net, character (read.net), 52
- read.net, character-method (read.net), 52
- sample.dataset, 52
- sample.dataset, BN (sample.dataset), 52
- sample.dataset, BN-method  
(sample.dataset), 52
- sample.dataset, InferenceEngine  
(sample.dataset), 52
- sample.dataset, InferenceEngine-method  
(sample.dataset), 52
- sample.row, 53
- sample.row, BN (sample.row), 53
- sample.row, BN-method (sample.row), 53
- sample.row, InferenceEngine  
(sample.row), 53
- sample.row, InferenceEngine-method  
(sample.row), 53
- save.to.eps, 53
- save.to.eps, BN, character (save.to.eps),  
53
- save.to.eps, BN, character-method  
(save.to.eps), 53
- scoring.func, 54
- scoring.func, BN (scoring.func), 54
- scoring.func, BN-method (scoring.func),  
54
- scoring.func<-, 54
- scoring.func<-, BN-method  
(scoring.func<-), 54
- sem, 55
- sem, InferenceEngine, BNdataset (sem), 55
- sem, InferenceEngine, BNdataset-method  
(sem), 55
- show, 56
- show, AllTheClasses-method (show), 56
- show, BN-method (show), 56
- show, BNdataset-method (show), 56
- show, InferenceEngine-method (show), 56
- struct.algo, 57
- struct.algo, BN (struct.algo), 57
- struct.algo, BN-method (struct.algo), 57
- struct.algo<-, 57
- struct.algo<-, BN-method  
(struct.algo<-), 57
- test.updated.bn, 58
- test.updated.bn, InferenceEngine  
(test.updated.bn), 58
- test.updated.bn, InferenceEngine-method  
(test.updated.bn), 58
- updated.bn, 58
- updated.bn, InferenceEngine  
(updated.bn), 58
- updated.bn, InferenceEngine-method  
(updated.bn), 58
- updated.bn<-, 59
- updated.bn<-, InferenceEngine-method  
(updated.bn<-), 59
- variables, 59
- variables, BN (variables), 59
- variables, BN-method (variables), 59
- variables, BNdataset (variables), 59

`variables`, `BNdataset-method` (`variables`),  
59  
`variables<-`, 60  
`variables<-`, `BN-method` (`variables<-`), 60  
`variables<-`, `BNdataset-method`  
(`variables<-`), 60  
  
`wpdag`, 61  
`wpdag`, `BN` (`wpdag`), 61  
`wpdag`, `BN-method` (`wpdag`), 61  
`wpdag<-`, 61  
`wpdag<-`, `BN-method` (`wpdag<-`), 61  
`write.dsc`, 62  
`write.dsc`, `BN` (`write.dsc`), 62  
`write.dsc`, `BN-method` (`write.dsc`), 62