

# Package: gRain (via r-universe)

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**Version** 1.4.5

**Title** Bayesian Networks

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**Description** Probability propagation in Bayesian networks, also known as graphical independence networks. Documentation of the package is provided in vignettes included in the package and in the paper by Højsgaard (2012, <[doi:10.18637/jss.v046.i10](https://doi.org/10.18637/jss.v046.i10)>). See 'citation(` `gRain")' for details.

**License** GPL (>= 2)

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**Suggests** bnlearn, gRim, knitr, markdown, microbenchmark, testthat (>= 2.1.0)

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**URL** <https://people.math.aau.dk/~sorenh/software/gR/>

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**VignetteBuilder** knitr

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**Repository** <https://hojsgaard.r-universe.dev>

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compileCPT	<i>Compile conditional probability tables / cliques potentials.</i>
------------	---

---

### Description

Compile conditional probability tables / cliques potentials as a preprocessing step for creating a graphical independence network

### Usage

```
compileCPT(x, ..., forceCheck = TRUE)
```

```
compilePOT(x, ..., forceCheck = TRUE)
```

**Arguments**

x	To compileCPT x is a list of conditional probability tables; to compilePOT, x is a list of clique potentials.
...	Additional arguments; currently not used.
forceCheck	Controls if consistency checks of the probability tables should be made.

**Details**

\* `compileCPT` is relevant for turning a collection of `cptable`'s into an object from which a network can be built. For example, when specification of a `cpt` is made with `cptable` then the levels of the node is given but not the levels of the parents. `compileCPT` checks that the levels of variables in the `cpt`'s are consistent and also that the specifications define a dag.

\* `compilePOT` is not of direct relevance for the user for the moment. However, the elements of the input should be arrays which define a chordal undirected graph and the arrays should, if multiplied, form a valid probability density.

**Value**

A list with a class attribute.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the `gRain` Package for R. *Journal of Statistical Software*, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[extract\\_cpt](#), [extract\\_pot](#), [extract\\_marg](#)

**Examples**

```
example("example_chest_cpt")
x <- compile_cpt(chest_cpt)
class(x)
grain(x)
```

---

components\_extract      *Extract conditional probabilities and clique potentials from data.*

---

### Description

Extract list of conditional probability tables and list of clique potentials from data.

### Usage

```
extract_cpt(data_, graph, smooth = 0)
extract_pot(data_, graph, smooth = 0)
extract_marg(data_, graph, smooth = 0)
marg2pot(marg_rep)
pot2marg(pot_rep)
```

### Arguments

data_	A named array or a dataframe.
graph	An igraph object or a list or formula which can be turned into a igraph object by calling <code>ug</code> or <code>dag</code> . For <code>extract_cpt</code> , <code>graph</code> must be/define a DAG while for <code>extract_pot</code> , <code>graph</code> must be/define undirected triangulated graph.
smooth	See 'details' below.
marg_rep	An object of class <code>marg_rep</code>
pot_rep	An object of class <code>pot_representation</code>

### Details

If `smooth` is non-zero then `smooth` is added to all cell counts before normalization takes place.

### Value

- `extract_cpt`: A list of conditional probability tables.
- `extract_pot`: A list of clique potentials.
- `extract_marg`: A list of clique marginals.

### Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

### References

Søren Højsgaard (2012). Graphical Independence Networks with the `gRain` Package for R. *Journal of Statistical Software*, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[compileCPT](#), [compilePOT](#), [grain](#)

**Examples**

```
## Extract cpts / clique potentials from data and graph
# specification and create network. There are different ways:

data(lizard, package="gRbase")

# DAG: height <- species -> diam
daG <- dag(~species + height:species + diam:species, result="igraph")

# UG : [height:species][diam:species]
uG <- ug(~height:species + diam:species, result="igraph")

pt <- extract_pot(lizard, ~height:species + diam:species)
cp <- extract_cpt(lizard, ~species + height:species + diam:species)

pt
cp

# Both specify the same probability distribution
tabListMult(pt) |> as.data.frame.table()
tabListMult(cp) |> as.data.frame.table()

## Not run:
# Bayesian networks can be created as
bn.uG <- grain(pt)
bn.daG <- grain(cp)

# The steps above are wrapped into a convenience method which
# builds a network from at graph and data.
bn.uG <- grain(uG, data=lizard)
bn.daG <- grain(daG, data=lizard)

## End(Not run)
```

---

components\_gather

*Compile conditional probability tables / cliques potentials.*

---

**Description**

Compile conditional probability tables / cliques potentials as a preprocessing step for creating a graphical independence network

**Usage**

```
compile_cpt(x, ..., forceCheck = TRUE)
```

```
compile_pot(x, ..., forceCheck = TRUE)
```

```
parse_cpt(xi)
```

**Arguments**

x	To compileCPT x is a list of conditional probability tables; to compilePOT, x is a list of clique potentials.
...	Additional arguments; currently not used.
forceCheck	Controls if consistency checks of the probability tables should be made.
xi	cpt in some representation

**Details**

\* `compileCPT` is relevant for turning a collection of `cptable`'s into an object from which a network can be built. For example, when specification of a `cpt` is made with `cptable` then the levels of the node is given but not the levels of the parents. `compileCPT` checks that the levels of variables in the `cpt`'s are consistent and also that the specifications define a dag.

\* `compilePOT` is not of direct relevance for the user for the moment. However, the elements of the input should be arrays which define a chordal undirected graph and the arrays should, if multiplied, form a valid probability density.

**Value**

A list with a class attribute.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the `gRain` Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[extract\\_cpt](#), [extract\\_pot](#), [extract\\_marg](#)

**Examples**

```
example("example_chest_cpt")
x <- compile_cpt(chest_cpt)
class(x)
grain(x)
```

---

 cpt
 

---



---

*Create conditional probability tables (CPTs)*


---

**Description**

Creates conditional probability tables of the form  $p(v|pa(v))$ .

**Usage**

```
cpt(names, levels, values, normalize = "first", smooth = 0)
```

```
cptable(vpar, levels = NULL, values = NULL, normalize = TRUE, smooth = 0)
```

**Arguments**

names	Specifications of the names in $P(v pa1, \dots, pa_k)$ . See section 'details' for information about the form of the argument.
levels	1. a list with specification of the levels of the factors in names or 2) a vector with number of levels of the factors in names. See 'examples' below.
values	Probabilities; recycled if necessary. Regarding the order, please see section 'details' and the examples.
normalize	See 'details' below.
smooth	Should values be smoothed, see 'Details' below.
vpar	node an its parents

**Details**

cptable is simply a wrapper for cpt and the functions can hence be used synonymously.

If smooth is non-zero, then this value is added to all cells **before** normalization takes place.

Regarding the form of the argument names: To specify  $P(a|b, c)$  one may write  $\sim a|b:c$ ,  $\sim a:b:c$ ,  $\sim a|b+c$ ,  $\sim a+b+c$  or  $c("a", "b", "c")$ . Internally, the last form is used. Notice that the + and : operator are used as a separators only. The order of the variables IS important so the operators DO NOT commute.

The first variable in levels varies fastest.

**Value**

An array.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[andtable](#), [ortable](#), [extract\\_cpt](#), [compileCPT](#), [extract\\_cpt](#), [compilePOT](#), [grain](#)

**Examples**

```
## See the wet grass example at
## https://en.wikipedia.org/wiki/Bayesian_network

yn <- c("yes", "no")
ssp <- list(R=yn, S=yn, G=yn) # state space

## Different forms
t1 <- cpt(c("S", "R"), levels=ssp, values=c(.01, .99, .4, .6))
t2 <- cpt(~S:R, levels=ssp, values=c(.01, .99, .4, .6))
t3 <- cpt(~S:R, levels=c(2, 2), values=c(.01, .99, .4, .6))
t4 <- cpt(~S:R, levels=yn, values=c(.01, .99, .4, .6))
t1; t2; t3; t4

varNames(t1)
valueLabels(t1)

## Wet grass example
ssp <- list(R=yn, S=yn, G=yn) # state space
p.R <- cpt(~R, levels=ssp, values=c(.2, .8))
p.S_R <- cpt(~S:R, levels=ssp, values=c(.01, .99, .4, .6))
p.G_SR <- cpt(~G:S:R, levels=ssp, values=c(.99, .01, .8, .2, .9, .1, 0, 1))

wet.cpt <- compileCPT(p.R, p.S_R, p.G_SR)
wet.cpt
wet.cpt$S # etc

# A Bayesian network is created with:
wet.bn <- grain(wet.cpt)
```

---

example\_chest

*Chest clinic example*

---

**Description**

Conditional probability tables for the chest clinic example.



**Examples**

```

yn <- c("yes", "no")
a <- cpt(~asia, values=c(1,99),levels=yn)
t.a <- cpt(~tub|asia, values=c(5,95,1,99),levels=yn)
s <- cpt(~smoke, values=c(5,5), levels=yn)
l.s <- cpt(~lung|smoke, values=c(1,9,1,99), levels=yn)
b.s <- cpt(~bronc|smoke, values=c(6,4,3,7), levels=yn)
e.lt <- cpt(~either|lung:tub,values=c(1,0,1,0,1,0,0,1),levels=yn)
x.e <- cpt(~xray|either, values=c(98,2,5,95), levels=yn)
d.be <- cpt(~dysp|bronc:either, values=c(9,1,7,3,8,2,1,9), levels=yn)

chest_cpt <- list(a, t.a, s, l.s, b.s, e.lt, x.e, d.be)
## bn <- grain(compile_cpt(chest_cpt))

```

example\_grass

*Wet grass example***Description**

Conditional probability tables for the wet grass example.

**Examples**

```

yn <- c("yes", "no")
p.R <- cpt(~R, values=c(.2, .8), levels=yn)
p.S_R <- cpt(~S:R, values=c(.01, .99, .4, .6), levels=yn)
p.G_SR <- cpt(~G:S:R, values=c(.99, .01, .8, .2, .9, .1, 0, 1), levels=yn)

grass_cpt <- list(p.R, p.S_R, p.G_SR)
## bn <- grain(compile_cpt(grass_cpt))

```

finding

*Set, retrieve, and retract finding in Bayesian network.***Description**

Set, retrieve, and retract finding in Bayesian network. NOTICE: The functions described here are kept only for backward compatibility; please use the corresponding evidence-functions in the future.

**Usage**

```
setFinding(object, nodes = NULL, states = NULL, flist = NULL, propagate = TRUE)
```

**Arguments**

object	A "grain" object
nodes	A vector of nodes
states	A vector of states (of the nodes given by 'nodes')
flist	An alternative way of specifying findings, see examples below.
propagate	Should the network be propagated?

**Note**

NOTICE: The functions described here are kept only for backward compatibility; please use the corresponding evidence-functions in the future:

`setEvidence()` is an improvement of `setFinding()` (and as such `setFinding` is obsolete). Users are recommended to use `setEvidence()` in the future.

`setEvidence()` allows to specification of "hard evidence" (specific values for variables) and likelihood evidence (also known as virtual evidence) for variables.

The syntax of `setEvidence()` may change in the future.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[setEvidence](#), [getEvidence](#), [retractEvidence](#), [pEvidence](#), [querygrain](#)

**Examples**

```
## setFindings
yn <- c("yes", "no")
a   <- cpt(~asia, values=c(1, 99), levels=yn)
t.a <- cpt(~tub+asia, values=c(5, 95, 1, 99), levels=yn)
s   <- cpt(~smoke, values=c(5,5), levels=yn)
l.s <- cpt(~lung+smoke, values=c(1, 9, 1, 99), levels=yn)
b.s <- cpt(~bronc+smoke, values=c(6, 4, 3, 7), levels=yn)
e.lt <- cpt(~either+lung+tub, values=c(1, 0, 1, 0, 1, 0, 0, 1), levels=yn)
x.e <- cpt(~xray+either, values=c(98, 2, 5, 95), levels=yn)
d.be <- cpt(~dysp+bronc+either, values=c(9, 1, 7, 3, 8, 2, 1, 9), levels=yn)
chest.cpt <- compileCPT(a, t.a, s, l.s, b.s, e.lt, x.e, d.be)
chest.bn <- grain(chest.cpt)

## These two forms are equivalent
bn1 <- setFinding(chest.bn, nodes=c("chest", "xray"), states=c("yes", "yes"))
bn2 <- setFinding(chest.bn, flist=list(c("chest", "yes"), c("xray", "yes")))
```

```
getFinding(bn1)
getFinding(bn2)

pFinding(bn1)
pFinding(bn2)

bn1 <- retractFinding(bn1, nodes="asia")
bn2 <- retractFinding(bn2, nodes="asia")

getFinding(bn1)
getFinding(bn2)

pFinding(bn1)
pFinding(bn2)
```

---

generics

*gRain generics*

---

## Description

Generic functions etc for the gRain package

## Usage

```
nodeNames(object)

## S3 method for class 'grain'
nodeNames(object)

nodeStates(object, nodes = nodeNames(object))

## S3 method for class 'grain'
nodeStates(object, nodes = nodeNames(object))

universe(object, ...)

## S3 method for class 'grain'
universe(object, ...)

isCompiled(object)

isPropagated(object)

## S3 method for class 'cpt_spec'
vpar(object, ...)
```

```
## S3 method for class 'cpt_grain'
vpar(object, ...)
```

```
## S3 method for class 'grain'
rip(object, ...)
```

### Arguments

object	A relevant object.
nodes	Some nodes of the object.
...	Additional arguments; currently not used.

---

grain-main

*Create Bayesian network*

---

### Description

Create Bayesian network (grain objects (graphical independence network)).

### Usage

```
grain(x, ...)

## S3 method for class 'cpt_spec'
grain(x, control = list(), smooth = 0, compile = TRUE, details = 0, ...)

## S3 method for class 'CPTspec'
grain(x, control = list(), smooth = 0, compile = TRUE, details = 0, ...)

## S3 method for class 'pot_spec'
grain(x, control = list(), smooth = 0, compile = TRUE, details = 0, ...)

## S3 method for class 'igraph'
grain(
  x,
  control = list(),
  smooth = 0,
  compile = TRUE,
  details = 0,
  data = NULL,
  ...
)

## S3 method for class 'dModel'
grain(
```

```

x,
control = list(),
smooth = 0,
compile = TRUE,
details = 0,
data = NULL,
...
)

```

### Arguments

x	An argument to build an independence network from. Typically a list of conditional probability tables, a DAG or an undirected graph. In the two latter cases, data must also be provided.
...	Additional arguments, currently not used.
control	A list defining controls, see 'details' below.
smooth	A (usually small) number to add to the counts of a table if the grain is built from a graph plus a dataset.
compile	Should network be compiled.
details	Debugging information.
data	An optional data set (currently must be an array/table)

### Details

If 'smooth' is non-zero then entries of 'values' which are zero are replaced by the value of 'smooth' - BEFORE any normalization takes place.

### Value

An object of class "grain"

### Note

A change from earlier versions of this package is that grain objects are now compiled upon creation.

### Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

### References

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

### See Also

[cptable](#), [compile.grain](#), [propagate.grain](#), [setFinding](#), [setEvidence](#), [getFinding](#), [pFinding](#), [retractFinding](#), [extract\\_cpt](#), [extract\\_pot](#), [compileCPT](#), [compilePOT](#)

**Examples**

```

## Create network from conditional probability tables CPTs:

yn <- c("yes", "no")
a <- cpt(~asia, values=c(1,99), levels=yn)
t.a <- cpt(~tub + asia, values=c(5,95,1,99), levels=yn)
s <- cpt(~smoke, values=c(5,5), levels=yn)
l.s <- cpt(~lung + smoke, values=c(1,9,1,99), levels=yn)
b.s <- cpt(~bronc + smoke, values=c(6,4,3,7), levels=yn)
e.lt <- cpt(~either + lung + tub, values=c(1,0,1,0,1,0,0,1), levels=yn)
x.e <- cpt(~xray + either, values=c(98,2,5,95), levels=yn)
d.be <- cpt(~dysp + bronc + either, values=c(9,1,7,3,8,2,1,9), levels=yn)
cpt_list <- list(a, t.a, s, l.s, b.s, e.lt, x.e, d.be)
chest_cpt <- compileCPT(cpt_list)
## Alternative: chest_cpt <- compileCPT(a, t.a, s, l.s, b.s, e.lt, x.e, d.be)

chest_bn <- grain(chest_cpt)

## Create network from data and graph specification.

data(lizard, package="gRbase")

## From a DAG: height <- species -> diam
daG <- dag(~species + height:species + diam:species)

## From an undirected graph UG : [height:species][diam:species]
uG <- ug(~height:species + diam:species)

liz_ug <- grain(uG, data=lizard)
liz_dag <- grain(daG, data=lizard)

```

---

grain-simulate

*Simulate from Bayesian network*


---

**Description**

Simulate data from an independence network.

**Usage**

```

## S3 method for class 'grain'
simulate(object, nsim = 1, seed = NULL, ...)

```

**Arguments**

object	An independence network.
nsim	Number of cases to simulate.
seed	An optional integer controlling the random number generation.
...	Not used.

**Value**

A data frame

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**Examples**

```
tf <- system.file("huginex", "chest_clinic.net", package = "gRain")

chest <- loadHuginNet(tf, details=1)
simulate(chest, n=10)

chest2 <- setFinding(chest, c("VisitToAsia", "Dyspnoea"),
                     c("yes", "yes"))
simulate(chest2, n=10)
```

---

grain\_compile

*Compile Bayesian network.*

---

**Description**

Compiles a Bayesian network. This means creating a junction tree and establishing clique potentials.

**Usage**

```
## S3 method for class 'grain'
compile(
  object,
  propagate = FALSE,
  tug = NULL,
  root = NULL,
  control = object$control,
  details = 0,
  ...
)
```

**Arguments**

object	A grain object.
propagate	If TRUE the network is also propagated meaning that the cliques of the junction tree are calibrated to each other.
tug	A triangulated undirected graph.
root	A set of variables which must be in the root of the junction tree
control	Controlling the compilation process.
details	For debugging info. Do not use.
...	Currently not used.

**Value**

A compiled Bayesian network; an object of class grain.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[grain](#), [propagate](#), [propagate.grain](#), [triangulate](#), [rip](#), [junctionTree](#)

---

grain_evidence	<i>Set, update and remove evidence.</i>
----------------	---

---

**Description**

Set, update and remove evidence.

**Usage**

```
evidence_add(object, evidence, propagate = TRUE, details = 0)
```

```
evidence_get(object, short = TRUE)
```

```
evidence_drop(object, nodes = NULL, propagate = TRUE)
```

```
evidence_prob(object, evidence = NULL)
```



**Arguments**

object	A "grain" object
evidence	A list of name=value. See examples below.
propagate	Should the network be propagated?
details	Debugging information
short	If TRUE a dataframe with a summary is returned; otherwise a list with all details.
nodes	A vector of nodes.

**Value**

A list of tables with potentials.

**Note**

setEvidence() is an improvement of setFinding() (and as such setFinding is obsolete). Users are recommended to use setEvidence() in the future.

setEvidence() allows to specification of "hard evidence" (specific values for variables) and likelihood evidence (also known as virtual evidence) for variables.

The syntax of setEvidence() may change in the future.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[setFinding](#), [getFinding](#), [retractFinding](#), [pFinding](#)

**Examples**

```
example("grain")
chest_bn <- grain(compileCPT(chest_cpt))

bn2 <- chest_bn |> evidence_add(list(asia="yes", xray="yes"))
bn3 <- chest_bn |> evidence_add(list(asia=c(0.8, 0.1), xray="yes"))

bn2 |> evidence_get()
bn3 |> evidence_get()

bn2 |> evidence_prob()
bn3 |> evidence_prob()

bn2 |> evidence_drop("xray")
```

```

bn3 |> evidence_drop("xray")

bn2 |> evidence_drop("xray") |> evidence_get()
bn3 |> evidence_drop("xray") |> evidence_get()

## For backward compatibility these functions are available now but
# may be deprecated later.
bb2 <- setEvidence(chest_bn, c("asia", "xray"), c("yes", "yes"))
bb3 <- setEvidence(chest_bn, c("asia", "xray"), list(c(0.8, 0.2), "yes"))
bb4 <- setFinding(chest_bn, c("asia", "xray"), c("yes", "yes"))

bb2 |> getEvidence()
bb3 |> getEvidence()

bb2 |> retractEvidence("xray")
bb3 |> retractEvidence("xray")

bb2 |> pEvidence()
bb3 |> pEvidence()

bb2 |> retractEvidence("xray") |> getEvidence()
bb3 |> retractEvidence("xray") |> getEvidence()

```

---

grain\_predict

*Make predictions from Bayesian network*


---

### Description

Makes predictions (either as the most likely state or as the conditional distributions) of variables conditional on finding (evidence) on other variables in an independence network.

### Usage

```

## S3 method for class 'grain'
predict(
  object,
  response,
  predictors = setdiff(names(newdata), response),
  newdata,
  type = "class",
  ...
)

```

### Arguments

object	A grain object
response	A vector of response variables to make predictions on

predictors	A vector of predictor variables to make predictions from. Defaults to all variables that are not responses.
newdata	A data frame
type	If "class", the most probable class is returned; if "distribution" the conditional distribution is returned.
...	Not used

**Value**

A list with components

pred	A list with the predictions
pFinding	A vector with the probability of the finding (evidence) on which the prediction is based

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[grain](#)

**Examples**

```
example("example_chest_cpt")
data(chestSim500)

chest.bn <- grain(compileCPT(chest_cpt))
nd <- chestSim500[1:4]

predict(chest.bn, response="bronc", newdata=nd)
predict(chest.bn, response="bronc", newdata=nd, type="distribution")
```

---

grain_propagate	<i>Propagate in a Bayesian network</i>
-----------------	--

---

### Description

Propagation refers to calibrating the cliques of the junction tree so that the clique potentials are consistent on their intersections; refer to the reference below for details.

### Usage

```
## S3 method for class 'grain'  
propagate(object, details = object$details, engine = "cpp", ...)  
  
propagateLS(cq_pot_list, rip, initialize = TRUE, details = 0)
```

### Arguments

object	A grain object
details	For debugging info
engine	Either "R" or "cpp"; "cpp" is the default and the fastest.
...	Currently not used
cq_pot_list	List of clique potentials
rip	A rip ordering
initialize	Always true.

### Details

The propagate method invokes propagateLS which is a pure R implementation of the Lauritzen-Spiegelhalter algorithm. The c++ based version is several times faster than the purely R based version.

### Value

A compiled and propagated grain object.

### Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

### References

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

### See Also

[grain](#), [compile](#)

**Examples**

```

example("grain")

## Uncompiled and unpropagated network:
bn0 <- grain(chest_cpt, compile=FALSE)
bn0
## Compiled but unpropagated network:
bn1 <- compile(bn0, propagate=FALSE)
## Compiled and propagated network
bn2 <- propagate(bn1)
bn2
## Default is that networks are compiled but not propagated at creation time:
bn3 <- grain(chest_cpt)
bn3

```

---

load-save-hugin

*Load and save Hugin net files*


---

**Description**

These functions can load a net file saved in the 'Hugin format' into R and save a network in R as a file in the 'Hugin format'.

**Usage**

```
loadHuginNet(file, description = NULL, details = 0)
```

```
saveHuginNet(gin, file, details = 0)
```

**Arguments**

file	Name of Hugin net file. Convenient to give the file the extension '.net'
description	A text describing the network, defaults to file
details	Debugging information.
gin	An independence network

**Value**

An object of class grain.

**Note**

- In Hugin, it is possible to specify the potential of a node as a functional relation between other nodes. In a .net file, such a specification will appear as 'function' rather than as 'node'. Such a specification is not recognized by loadHuginNet.
- It is recommended to avoid the text node as part of the name of a node.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. *Journal of Statistical Software*, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[grain](#)

**Examples**

```
## Load HUGIN net file
tf <- system.file("huginex", "chest_clinic.net", package = "gRain")
chest <- loadHuginNet(tf, details=1)
chest

## Save a copy
td <- tempdir()
saveHuginNet(chest, paste(td, "/chest.net", sep=''))

## Load the copy
chest2 <- loadHuginNet(paste(td, "/chest.net", sep=''))

tf <- system.file("huginex", "golf.net", package = "gRain")
golf <- loadHuginNet(tf, details=1)

saveHuginNet(golf, paste(td, "/golf.net", sep=''))
golf2 <- loadHuginNet(paste(td, "/golf.net", sep=''))
```

---

logical

*Conditional probability tables based on logical dependencies*

---

**Description**

Generate conditional probability tables based on the logical expressions AND and OR.

**Usage**

```
booltab(vpa, levels = c(TRUE, FALSE), op = `&`)
andtab(vpa, levels = c(TRUE, FALSE))
ortab(vpa, levels = c(TRUE, FALSE))
```

```
andtable(vpa, levels = c(TRUE, FALSE))
```

```
ortable(vpa, levels = c(TRUE, FALSE))
```

### Arguments

vpa	Node and two parents; as a formula or a character vector.
levels	The levels (or rather labels) of v, see 'examples' below.
op	A logical operator.

### Details

Regarding the form of the argument vpa: To specify  $P(a|b, c)$  one may write  $\sim a|b+c$  or  $\sim a+b+c$  or  $\sim a|b:c$  or  $\sim a:b:c$  or  $c("a", "b", "c")$ . Internally, the last form is used. Notice that the + and : operator are used as separators only. The order of the variables is important so + and : DO NOT commute.

### Value

An array.

### Note

andtable and ortable are aliases for andtab and ortab and are kept for backward compatibility.

### Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

### References

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

### See Also

[cptable](#)

### Examples

```
## Logical OR:

## A variable v is TRUE if either of its parents pa1 and pa2 are TRUE:
ortab( c("v", "pa1", "pa2") ) |> ftable(row.vars="v")
## TRUE and FALSE can be recoded to e.g. yes and no:
ortab( c("v", "pa1", "pa2"), levels=c("yes", "no") ) |> ftable(row.vars="v")

## Logical AND:

## Same story here:
andtab(c("v", "pa1", "pa2") ) |> ftable(row.vars="v")
```

```

andtab(c("v", "pa1", "pa2"), levels=c("yes", "no") ) |> ftable(row.vars="v")

## Combined approach

booltab(c("v", "pa1", "pa2"), op=~&`) |> ftable(row.vars="v") ## AND
booltab(c("v", "pa1", "pa2"), op=~|`) |> ftable(row.vars="v") ## OR

booltab(~v + pa1 + pa2, op=~&`) |> ftable(row.vars="v") ## AND
booltab(~v + pa1 + pa2, op=~|`) |> ftable(row.vars="v") ## OR

```

---

mendel

*Mendelian segregation*


---

### Description

Generate conditional probability table for Mendelian segregation.

### Usage

```

mendel(allele, names = c("child", "father", "mother"))

```

### Arguments

allele	A character vector.
names	Names of columns in dataframe.

### Note

No error checking at all on the input.

### Examples

```

## Inheritance of the alleles "y" and "g"

men <- mendel(c("y", "g"), names=c("ch", "fa", "mo"))
men

```



---

`old_components_extract`*Extract conditional probabilities and clique potentials from data.*

---

**Description**

Extract list of conditional probability tables and list of clique potentials from data.

**Usage**

```
extractCPT(data_, graph, smooth = 0)
```

```
extractPOT(data_, graph, smooth = 0)
```

```
extractMARG(data_, graph, smooth = 0)
```

**Arguments**

<code>data_</code>	A named array or a dataframe.
<code>graph</code>	An igraph object or a list or formula which can be turned into a igraph object by calling <code>ug</code> or <code>dag</code> . For <code>extract_cpt</code> , <code>graph</code> must be/define a DAG while for <code>extract_pot</code> , <code>graph</code> must be/define undirected triangulated graph.
<code>smooth</code>	See 'details' below.

**Details**

If `smooth` is non-zero then `smooth` is added to all cell counts before normalization takes place.

**Value**

- `extract_cpt`: A list of conditional probability tables.
- `extract_pot`: A list of clique potentials.
- `extract_marg`: A list of clique marginals.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[compileCPT](#), [compilePOT](#), [grain](#)

**Examples**

```

## Extract cpts / clique potentials from data and graph
# specification and create network. There are different ways:

data(lizard, package="gRbase")

# DAG: height <- species -> diam
daG <- dag(~species + height:species + diam:species, result="igraph")

# UG : [height:species][diam:species]
uG <- ug(~height:species + diam:species, result="igraph")

pt <- extract_pot(lizard, ~height:species + diam:species)
cp <- extract_cpt(lizard, ~species + height:species + diam:species)

pt
cp

# Both specify the same probability distribution
tabListMult(pt) |> as.data.frame.table()
tabListMult(cp) |> as.data.frame.table()

## Not run:
# Bayesian networks can be created as
bn.uG <- grain(pt)
bn.daG <- grain(cp)

# The steps above are wrapped into a convenience method which
# builds a network from at graph and data.
bn.uG <- grain(uG, data=lizard)
bn.daG <- grain(daG, data=lizard)

## End(Not run)

```

---

old\_grain\_evidence      *Set, update and remove evidence.*

---

**Description**

Set, update and remove evidence.

**Usage**

```

setEvidence(
  object,
  nodes = NULL,
  states = NULL,
  evidence = NULL,

```

```

    propagate = TRUE,
    details = 0
)

retractEvidence(object, nodes = NULL, propagate = TRUE)

absorbEvidence(object, propagate = TRUE)

getEvidence(object, short = TRUE)

pEvidence(object, evidence = NULL)

```

### Arguments

object	A "grain" object
nodes	A vector of nodes.
states	A vector of states (of the nodes given by 'nodes'). Now deprecated; use argument 'evidence' instead.
evidence	A list of name=value. See examples below.
propagate	Should the network be propagated?
details	Debugging information
short	If TRUE a dataframe with a summary is returned; otherwise a list with all details.

### Value

A list of tables with potentials.

### Note

setEvidence() is an improvement of setFinding() (and as such setFinding is obsolete). Users are recommended to use setEvidence() in the future.

setEvidence() allows to specification of "hard evidence" (specific values for variables) and likelihood evidence (also known as virtual evidence) for variables.

The syntax of setEvidence() may change in the future.

### Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

### References

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

### See Also

[setFinding](#), [getFinding](#), [retractFinding](#), [pFinding](#)

**Examples**

```

example("grain")
chest_bn <- grain(compileCPT(chest_cpt))

bn2 <- chest_bn |> evidence_add(list(asia="yes", xray="yes"))
bn3 <- chest_bn |> evidence_add(list(asia=c(0.8, 0.1), xray="yes"))

bn2 |> evidence_get()
bn3 |> evidence_get()

bn2 |> evidence_prob()
bn3 |> evidence_prob()

bn2 |> evidence_drop("xray")
bn3 |> evidence_drop("xray")

bn2 |> evidence_drop("xray") |> evidence_get()
bn3 |> evidence_drop("xray") |> evidence_get()

## For backward compatibility these functions are available now but
# may be deprecated later.
bb2 <- setEvidence(chest_bn, c("asia", "xray"), c("yes", "yes"))
bb3 <- setEvidence(chest_bn, c("asia", "xray"), list(c(0.8, 0.2), "yes"))
bb4 <- setFinding(chest_bn, c("asia", "xray"), c("yes", "yes"))

bb2 |> getEvidence()
bb3 |> getEvidence()

bb2 |> retractEvidence("xray")
bb3 |> retractEvidence("xray")

bb2 |> pEvidence()
bb3 |> pEvidence()

bb2 |> retractEvidence("xray") |> getEvidence()
bb3 |> retractEvidence("xray") |> getEvidence()

```

---

old\_replace\_cpt

*Replace CPTs in Bayesian network*


---

**Description**

Replace CPTs of Bayesian network.

**Usage**

```
replaceCPT(object, value)
```

**Arguments**

object            A grain object.  
value            A named list, see examples below.

**Details**

When a Bayesian network (BN) is constructed from a list of conditional probability tables (CPTs) (e.g. using the function `grain()`), various actions are taken:

1. It is checked that the list of CPTs define a directed acyclic graph (DAG).
2. The DAG is moralized and triangulated.
3. A list of clique potentials (one for each clique in the triangulated graph) is created from the list of CPTs.
4. The clique potentials are, by default, calibrated to each other so that the potentials contain marginal distributions.

The function described here bypass the first two steps which can provide an important gain in speed compared to constructing a new BN with a new set of CPTs with the same DAG.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. *Journal of Statistical Software*, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[grain](#), [propagate](#), [triangulate](#), [rip](#), [junctionTree](#)

**Examples**

```
## See the wet grass example at
## https://en.wikipedia.org/wiki/Bayesian_network

yn <- c("yes", "no")
p.R <- ctable(~R, values=c(.2, .8), levels=yn)
p.S_R <- ctable(~S:R, values=c(.01, .99, .4, .6), levels=yn)
p.G_SR <- ctable(~G:S:R, values=c(.99, .01, .8, .2, .9, .1, 0, 1), levels=yn)

wet.bn <- compileCPT(p.R, p.S_R, p.G_SR) |> grain()
getgrain(wet.bn, "cpt")[c("R", "S")]

# Update some CPTs
wet.bn <- replace_cpt(wet.bn, list(R=c(.3, .7), S=c(.1, .9, .7, .3)))
getgrain(wet.bn, "cpt")[c("R", "S")]
```

---

 querygrain

*Query a Bayesian network*


---

**Description**

Query an independence network, i.e. obtain the conditional distribution of a set of variables - possibly (and typically) given finding (evidence) on other variables.

**Usage**

```
querygrain(
  object,
  nodes = nodeNames(object),
  type = "marginal",
  evidence = NULL,
  exclude = TRUE,
  normalize = TRUE,
  simplify = FALSE,
  result = "array",
  details = 0
)
```

**Arguments**

object	A grain object.
nodes	A vector of nodes; those nodes for which the (conditional) distribution is requested.
type	Valid choices are "marginal" which gives the marginal distribution for each node in nodes; "joint" which gives the joint distribution for nodes and "conditional" which gives the conditional distribution for the first variable in nodes given the other variables in nodes.
evidence	An alternative way of specifying findings (evidence), see examples below.
exclude	If TRUE then nodes on which evidence is given will be excluded from nodes (see above).
normalize	Should the results be normalized to sum to one.
simplify	Should the result be simplified (to a dataframe) if possible.
result	If "data.frame" the result is returned as a data frame (or possibly as a list of dataframes).
details	Debugging information

**Value**

A list of tables with potentials.

**Note**

setEvidence() is an improvement of setFinding() (and as such setFinding is obsolete). Users are recommended to use setEvidence() in the future.

setEvidence() allows to specification of "hard evidence" (specific values for variables) and likelihood evidence (also known as virtual evidence) for variables.

The syntax of setEvidence() may change in the future.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[setEvidence](#), [getEvidence](#), [retractEvidence](#), [pEvidence](#)

**Examples**

```
testfile <- system.file("huginex", "chest_clinic.net", package = "gRain")
chest <- loadHuginNet(testfile, details=0)
qb <- querygrain(chest)
qb

lapply(qb, as.numeric) # Safe
sapply(qb, as.numeric) # Risky
```

---

repeatPattern

*Create repeated patterns in Bayesian networks*

---

**Description**

Repeated patterns is a useful model specification short cut for Bayesian networks

**Usage**

```
repeatPattern(plist, instances, unlist = TRUE, data = NULL)
```

**Arguments**

<code>plist</code>	A list of conditional probability tables. The variable names must have the form <code>name[i]</code> and the <code>i</code> will be substituted by the values given in instances below. See also the <code>data</code> argument.
<code>instances</code>	A vector of consecutive integers
<code>unlist</code>	If <code>FALSE</code> the result is a list in which each element is a copy of <code>plist</code> in which <code>name[i]</code> are substituted. If <code>TRUE</code> the result is the result of applying <code>unlist()</code> .
<code>data</code>	A two column matrix. The first column is the index / name of a node; the second column is the index / name of the node's parent.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[grain](#), [compile\\_cpt](#)

**Examples**

```

yn <- c("yes", "no")
n <- 3

## Example: Markov chain

x_init <- cpt(~x0, values=c(1, 9), levels=yn)          ## p(x0)
x_trans <- cpt(~x[i]|x[i-1], values=c(1, 99, 2, 98), levels=yn) ## p(x[i]|x[i-1])
pat <- list(x_trans)
rep.pat <- repeat_pattern(pat, instances=1:n)

mc <- compile_cpt(c(list(x_init), rep.pat))
mc
mc <- mc |> grain()

## Example: Hidden markov model:
# The x[i]'s are unobserved, the y[i]'s can be observed.

x_init <- cpt(~x0, values=c(1, 9), levels=yn)          ## p(x0)
x_trans <- cpt(~x[i]|x[i-1], values=c(1, 99, 2, 98), levels=yn) ## p(x[i]|x[i-1])
y_emis <- cpt(~y[i]|x[i], values=c(10, 90, 20, 80), levels=yn) ## p(y[i]|x[i])

pat <- list(x_trans, y_emis) ## Pattern to be repeated
rep.pat <- repeat_pattern(pat, instances=1:n)
hmm <- compile_cpt(c(list(x_init), rep.pat))
hmm

```



```

hmm <- hmm |> grain()

## Data-driven variable names

dep <- data.frame(i=c(1, 2, 3, 4, 5, 6, 7, 8),
                 p=c(0, 1, 2, 2, 3, 3, 4, 4))

x0 <- cpt(~x0, values=c(0.5, 0.5), levels=yn)
xa <- cpt(~x[i] | x[data[i, "p"]], values=c(1, 9, 2, 8), levels=yn)
xb <- repeat_pattern(list(xa), instances=1:nrow(dep), data=dep)
tree <- compile_cpt(c(list(x0), xb))
tree
tree <- tree |> grain()
tree

```

---

repeat_pattern	<i>Create repeated patterns in Bayesian networks</i>
----------------	--

---

### Description

Repeated patterns is a useful model specification short cut for Bayesian networks

### Usage

```
repeat_pattern(plist, instances, unlist = TRUE, data = NULL)
```

### Arguments

plist	A list of conditional probability tables. The variable names must have the form name[i] and the i will be substituted by the values given in instances below. See also the data argument.
instances	A vector of consecutive integers
unlist	If FALSE the result is a list in which each element is a copy of plist in which name[i] are substituted. If TRUE the result is the result of applying unlist().
data	A two column matrix. The first column is the index / name of a node; the second column is the index / name of the node's parent.

### Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

### References

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. Journal of Statistical Software, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[grain](#), [compile\\_cpt](#)

**Examples**

```

yn <- c("yes", "no")
n <- 3

## Example: Markov chain

x_init <- cpt(~x0, values=c(1, 9), levels=yn)          ## p(x0)
x_trans <- cpt(~x[i]|x[i-1], values=c(1, 99, 2, 98), levels=yn) ## p(x[i]|x[i-1])
pat <- list(x_trans)
rep.pat <- repeat_pattern(pat, instances=1:n)

mc <- compile_cpt(c(list(x_init), rep.pat))
mc
mc <- mc |> grain()

## Example: Hidden markov model:
# The x[i]'s are unobserved, the y[i]'s can be observed.

x_init <- cpt(~x0, values=c(1, 9), levels=yn)          ## p(x0)
x_trans <- cpt(~x[i]|x[i-1], values=c(1, 99, 2, 98), levels=yn) ## p(x[i]|x[i-1])
y_emis <- cpt(~y[i]|x[i], values=c(10, 90, 20, 80), levels=yn) ## p(y[i]|x[i])

pat <- list(x_trans, y_emis) ## Pattern to be repeated
rep.pat <- repeat_pattern(pat, instances=1:n)
hmm <- compile_cpt(c(list(x_init), rep.pat))
hmm
hmm <- hmm |> grain()

## Data-driven variable names

dep <- data.frame(i=c(1, 2, 3, 4, 5, 6, 7, 8),
                  p=c(0, 1, 2, 2, 3, 3, 4, 4))

x0 <- cpt(~x0, values=c(0.5, 0.5), levels=yn)
xa <- cpt(~x[i] | x[data[i, "p"]], values=c(1, 9, 2, 8), levels=yn)
xb <- repeat_pattern(list(xa), instances=1:nrow(dep), data=dep)
tree <- compile_cpt(c(list(x0), xb))
tree
tree <- tree |> grain()
tree

```

**Description**

Replace CPTs of Bayesian network.

**Usage**

```
replace_cpt(object, value)
```

```
## S3 method for class 'cpt_grain'  
replace_cpt(object, value)
```

**Arguments**

object	A grain object.
value	A named list, see examples below.

**Details**

When a Bayesian network (BN) is constructed from a list of conditional probability tables (CPTs) (e.g. using the function `grain()`), various actions are taken:

1. It is checked that the list of CPTs define a directed acyclic graph (DAG).
2. The DAG is moralized and triangulated.
3. A list of clique potentials (one for each clique in the triangulated graph) is created from the list of CPTs.
4. The clique potentials are, by default, calibrated to each other so that the potentials contain marginal distributions.

The function described here bypass the first two steps which can provide an important gain in speed compared to constructing a new BN with a new set of CPTs with the same DAG.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**

Søren Højsgaard (2012). Graphical Independence Networks with the gRain Package for R. *Journal of Statistical Software*, 46(10), 1-26. <https://www.jstatsoft.org/v46/i10/>.

**See Also**

[grain](#), [propagate](#), [triangulate](#), [rip](#), [junctionTree](#)

## Examples

```
## See the wet grass example at
## https://en.wikipedia.org/wiki/Bayesian_network

yn <- c("yes", "no")
p.R   <- cptable(~R, values=c(.2, .8), levels=yn)
p.S_R <- cptable(~S:R, values=c(.01, .99, .4, .6), levels=yn)
p.G_SR <- cptable(~G:S:R, values=c(.99, .01, .8, .2, .9, .1, 0, 1), levels=yn)

wet.bn <- compileCPT(p.R, p.S_R, p.G_SR) |> grain()
getgrain(wet.bn, "cpt")[c("R", "S")]

# Update some CPTs
wet.bn <- replace_cpt(wet.bn, list(R=c(.3, .7), S=c(.1, .9, .7, .3)))
getgrain(wet.bn, "cpt")[c("R", "S")]
```

---

simplify\_query

*Simplify output query to a Bayesian network*

---

## Description

Simplify output query to a Bayesian network to a dataframe provided that each node has the same levels.

## Usage

```
simplify_query(b)
```

## Arguments

b                      Result from running querygrain.

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