

# Package ‘ctbn’

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## Description

The ctn package provides an interface between R and the Continuous Time Bayesian Network Reasoning and Learning Engine (CTBN-RLE) C++ code. The main functionalities of the CTBN-RLE code are designed and implemented in the R environment.

**License** GPL (>= 3)

## R topics documented:

ctbn-package . . . . .	2
CloneCtbn . . . . .	3
DeleteCtbn . . . . .	4
DeleteInfEngine . . . . .	5
GetBnCPTs . . . . .	5
GetBnStruct . . . . .	6
GetCtbnJointDyn . . . . .	7
GetCtbnVars . . . . .	8
GetDynIntMats . . . . .	8
GetDynStruct . . . . .	9
GetInfEngineType . . . . .	10
LearnCtbnParams . . . . .	11
LearnCtbnStruct . . . . .	12
LoadRCtbn . . . . .	13
NewCtbn . . . . .	14
NewInfEngine . . . . .	15
QueryCtbnFilter . . . . .	17
QueryCtbnSmooth . . . . .	18

QueryCtbnStats . . . . .	20
QueryCtbnTime . . . . .	21
ReadProbStruct . . . . .	22
SampleFullTrjs . . . . .	23
SamplePartialTrjs . . . . .	24
SaveRCtbn . . . . .	25
SetBnCPTs . . . . .	26
SetBnStruct . . . . .	27
SetDynIntMats . . . . .	28
SetDynStruct . . . . .	29
WriteProbStruct . . . . .	29

**Index****31**

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ctbn-package*R Package for Continuous Time Bayesian Networks*

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**Description**

The *ctbn* package provides an interface between R and the Continuous Time Bayesian Network Reasoning and Learning Engine (CTBN-RLE) C++ code. The main functionalities of the CTBN-RLE code are designed and implemented in the R environment.

This interface is built using the *Rcpp* package.

**Details**

Package: *ctbn*  
 Type: Package  
 Version: 1.0  
 Date: 2014-04-20  
 License: GPL (>= 3).

**Note**

This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details.

**Author(s)**

This project is written by S. Villa in collaboration with Christian Shelton.  
 The CTBN-RLE project is managed by Christian Shelton and development is done in R-LAIR, Riverside Lab for Artificial Intelligence Research at the University of California, Riverside.

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CloneCtbn

CloneCtbn

## Description

Clone a continuous-time Bayesian network (CTBN) object.

## Usage

```
CloneCtbn (xpCtbn)
```

## Arguments

xpCtbn	external pointer to the CTBN C++ model.
--------	---

## Value

External pointer to the CTBN C++ model. NULL in the case of errors.

**Note**

You own the external pointer, so remember to delete it using the [DeleteCtbn](#) function only.

**See Also**

[DeleteCtbn](#), [NewCtbn](#)

**Examples**

```
# create ctbn
vars    <- data.frame(Name=c("X1","X2"), Value=c(2,3), check.names=FALSE)
xpCtbn <- NewCtbn(vars)

# clone ctbn
xpCtbn2 <- CloneCtbn(xpCtbn)

# delete ctbn
xpCtbn <- DeleteCtbn(xpCtbn)
xpCtbn2 <- DeleteCtbn(xpCtbn2)
garbage <- gc()
```

---

**DeleteCtbn**

*DeleteCtbn*

---

**Description**

Delete a continuous-time Bayesian network (CTBN) object.

**Usage**

`DeleteCtbn (xpCtbn)`

**Arguments**

`xpCtbn`            external pointer to the CTPN C++ model.

**Value**

NULL.

**See Also**

[NewCtbn](#), [CloneCtbn](#)

**Examples**

```
# create ctbn
vars    <- data.frame(Name=c("X1","X2"), Value=c(2,3), check.names=FALSE)
xpCtbn <- NewCtbn(vars)

# delete ctbn
xpCtbn <- DeleteCtbn(xpCtbn)
garbage <- gc()
```

---

`DeleteInfEngine`*DeleteInfEngine*

---

**Description**

Delete an inference engine object.

**Usage**

```
DeleteInfEngine (engine)
```

**Arguments**

engine            external pointer to the inference engine C++ object.

**Value**

NULL.

**See Also**

[NewInfEngine](#), [GetInfEngineType](#)

**Examples**

```
# create engine
engine <- NewInfEngine(inf.type="importance", num.samples=1000)

# delete engine
engine <- DeleteInfEngine(engine)
garbage <- gc()
```

---

---

`GetBnCPTs`*GetBnCPTs*

---

**Description**

Get the definition of the initial Bayesian network (conditional probability tables) of the CTBN object.

**Usage**

```
GetBnCPTs (xpCtbn)
```

**Arguments**

xpCtbn            external pointer to the CTBN C++ model.

**Value**

List. List (I) of lists (II) of dataframes (III), in which the I level contains the nodes  $X_n$ , the second level contains the parents of  $X_n$  ( $X_{n|U}$ ), and the III level contains the values of  $X_n$  given a particular instantiation of its parents ( $X_{n|U}$ ) specified as a dataframe. This dataframe is  $1 \times m$ , where  $m$  is number of values that  $X_n$  can assume (specified in the column header that must be from 0 to value-1), and the row contains the respective probabilities (that must sum up to 1). The names contained in the I level list must be  $X_n$  and the names of the II level list must be in the form  $X_n|U=u$ . NULL in the case of errors.

**See Also**

[SetBnCPTs](#)

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn     <- LoadRCTbn(ctbn.file)

bn.cpts   <- GetBnCPTs(xpCtbn)

# delete ctbn
xpCtbn   <- DeleteCtbn(xpCtbn)
garbage <- gc()
```

**GetBnStruct**

*GetBnStruct*

**Description**

Get the structure of the initial Bayesian network of the CTBN object.

**Usage**

```
GetBnStruct (xpCtbn)
```

**Arguments**

xpCtbn            external pointer to the CTBN C++ model.

**Value**

Dataframe  $k \times 2$ . It is used to define the structure of the initial Bayesian network (specified as a directed acyclic graph). Each row consists of the name of the parent of  $X_n$  (from) and the name of  $X_n$  (to). Both names are contained in the variables definition of the CTBN model (case sensitive). NULL in the case of errors.

**See Also**

[SetBnStruct](#)

## Examples

```
# load ctn
ctn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctn")
xpCtn <- LoadRCtn(ctn.file)

bn.str <- GetBnStruct(xpCtn)

# delete ctn
xpCtn <- DeleteCtn(xpCtn)
garbage <- gc()
```

GetCtnJointDyn

*GetCtnJointDyn*

## Description

Get the joint intensity matrix for the entire CTBN object.

## Usage

```
GetCtnJointDyn (xpCtn)
```

## Arguments

xpCtn external pointer to the CTBN C++ model.

## Value

Matrix. Joint intensity matrix for the entire CTBN model (not recommended if your CTBN is large).

## Examples

```
# load ctn
ctn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctn")
xpCtn <- LoadRCtn(ctn.file)

jointIntsMat <- GetCtnJointDyn(xpCtn)

# delete ctn
xpCtn <- DeleteCtn(xpCtn)
garbage <- gc()
```

GetCtbnVars

*GetCtbnVars***Description**

Get the variables definition of the CTBN object.

**Usage**

```
GetCtbnVars (xpCtbn)
```

**Arguments**

xpCtbn	external pointer to the CTBN C++ model.
--------	---

**Value**

Dataframe n x 2. It is used to define the variables of the CTBN model. Each row consists of the name (string) of n variables Xn and a value (integer) corresponding of the number of values that the variable can assume (defined from 0 to value-1, -1 if unknown). NULL in the case of errors.

**See Also**

[NewCtbn](#)

**Examples**

```
# create ctbn
vars   <- data.frame(Name=c("X1", "X2"), Value=c(2,3), check.names=FALSE)
xpCtbn <- NewCtbn(vars)

vars2  <- GetCtbnVars(xpCtbn)

# delete ctbn
xpCtbn <- DeleteCtbn(xpCtbn)
garbage <- gc()
```

GetDynIntMats

*GetDynIntMats***Description**

Get the definition of the dynamic component (conditional intensity matrices) of the CTBN object.

**Usage**

```
GetDynIntMats (xpCtbn)
```

**Arguments**

xpCtbn	external pointer to the CTBN C++ model.
--------	---

**Value**

List. List (I) of lists (II) of dataframes (III), in which the I level contains the nodes  $X_n$ , the second level contains the parents of  $X_n$  ( $X_{n|U}$ ), and the III level contains the values of  $X_n$  given a particular instantiation of its parents ( $X_{n|U}$ ) specified as a dataframe. This dataframe is  $m \times m$ , where  $m$  is number of values that  $X_n$  can assume (specified in the column header that must be from 0 to value-1) and it contains the conditional intensity probabilities (each row must sum up to 0). The names contained in the I level list must be  $X_n$  and the names of the II level list must be in the form  $X_n|U=u$ . NULL in the case of errors.

**See Also**

[SetDynIntMats](#)

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn    <- LoadRCTbn(ctbn.file)

dyn.cims  <- GetDynIntMats(xpCtbn)

# delete ctbn
xpCtbn    <- DeleteCtbn(xpCtbn)
garbage   <- gc()
```

GetDynStruct

*GetDynStruct*

**Description**

Get the structure of the dynamic component of the CTBN object.

**Usage**

`GetDynStruct (xpCtbn)`

**Arguments**

`xpCtbn`      external pointer to the CTBN C++ model.

**Value**

Dataframe  $k \times 2$ . It is used to define the structure of the dynamic structure (possibly cycle). Each row consists of the name of the parent of  $X_n$  (from) and the name of  $X_n$  (to). Both names are contained in the variables definition of the CTBN model (case sensitive). NULL in the case of errors.

**See Also**

[SetDynStruct](#)

**Examples**

```
# load ctn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtn     <- LoadRCtn(ctbn.file)

dyn.str   <- GetDynStruct(xpCtn)

# delete ctn
xpCtn    <- DeleteCtn(xpCtn)
garbage <- gc()
```

GetInfEngineType

*GetInfEngineType***Description**

Get the type of the inference engine C++ object.

**Usage**

```
GetInfEngineType (engine)
```

**Arguments**

engine	external pointer to the inference engine C++ object.
--------	--

**Value**

Character. Inference engine type.

**See Also**

[NewInfEngine](#), [DeleteInfEngine](#)

**Examples**

```
# create engine
engine <- NewInfEngine(inf.type="importance", num.samples=1000)

print(GetInfEngineType(engine))

# delete engine
engine <- DeleteInfEngine(engine)
garbage <- gc()
```

---

`LearnCtbnParams`*LearnCtbnParams*

---

**Description**

Learn the parameters of the CTBN object (both static and dynamic components) given fully or partially observed trajectories. It is possible to specify an inference engine used to perform learning in the missing data case.

**Usage**

```
LearnCtbnParams (xpCtbn, trjs, inf.type="exact", num.samples=100,
                  burn.iters=100, eps=1e-5, inf.engine=NULL)
```

**Arguments**

<code>xpCtbn</code>	external pointer to the CTBN C++ model.
<code>trjs</code>	list. List of dataframes in which each dataframe represents a trajectory.
<code>inf.type</code>	character. Inference type: exact, importance, gibbs, gibbsaux, meanfield.
<code>num.samples</code>	integer. Number of samples for importance, gibbs, gibbsaux inference engines.
<code>burn.iters</code>	integer. Number of burn-in iterations for gibbs, gibbsaux inference engines.
<code>eps</code>	numeric. Epsilon value for meanfield inference engine.
<code>inf.engine</code>	external pointer to the inference engine C++ model.

**Value**

Character. Status of the learning process. NULL in the case of errors.

**See Also**

[LearnCtbnStruct](#), [SampleFullTrjs](#), [SamplePartialTrjs](#), [GetBnCPTs](#), [GetDynIntMats](#).

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn     <- LoadRCtbn(ctbn.file)

# parameters learning from fully observed data
samples    <- SampleFullTrjs(xpCtbn, num=100)
xpCtbn2    <- CloneCtbn(xpCtbn)
LearnCtbnParams(xpCtbn2, samples)
cptOut2   <- GetBnCPTs(xpCtbn2)
cimsOut2  <- GetDynIntMats(xpCtbn2)
xpCtbn2    <- DeleteCtbn(xpCtbn2)
garbage    <- gc()

# parameters learning from partially observed data
samples    <- SamplePartialTrjs(xpCtbn, num=10, rem.frac=0.01)
```

```

xpCtbn2  <- CloneCtbn(xpCtbn)
inf      <- "importance";
LearnCtbnParams(xpCtbn2, samples, inf.type=inf, num.samples=100)
cptsoOut2 <- GetBnCPTs(xpCtbn2)
cimsOut2 <- GetDynIntMats(xpCtbn2)
xpCtbn2  <- DeleteCtbn(xpCtbn2)
garbage   <- gc()

# delete ctbn
xpCtbn   <- DeleteCtbn(xpCtbn)
garbage   <- gc()

```

**LearnCtbnStruct***LearnCtbnStruct***Description**

Learn the structure (and the relative parameters) of the CTBN object (both static and dynamic components) given fully or partially observed trajectories. It is possible to specify an inference engine used to perform learning in the missing data case.

**Usage**

```
LearnCtbnStruct (xpCtbn, trjs, alpha=1.0, tau=0.1, inf.type="exact",
                  num.samples=100, burn.iters=100, eps=1e-5, inf.engine=NULL)
```

**Arguments**

xpCtbn	external pointer to the CTBN C++ model.
trjs	list. List of dataframes in which each dataframe represents a trajectory.
alpha	numeric. Hyperparameter: pseudo-counts of the number of transitions from one state to another.
tau	numeric. Hyperparameter: imaginary amount of time spent in each state.
inf.type	character. Inference type: exact, importance, gibbs, gibbsaux, meanfield.
num.samples	integer. Number of samples for importance, gibbs, gibbsaux inference engines.
burn.iters	integer. Number of burn-in iterations for gibbs, gibbsaux inference engines.
eps	numeric. Epsilon value for meanfield inference engine.
inf.engine	external pointer to the inference engine C++ model.

**Value**

Character. Status of the learning process. NULL in the case of errors.

**See Also**

[LearnCtbnParams](#), [SampleFullTrjs](#), [SamplePartialTrjs](#), [GetBnStruct](#), [GetDynStruct](#), [GetBnCPTs](#), [GetDynIntMats](#).

**Examples**

```

# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn    <- LoadRCtbn(ctbn.file)

# structural learning from fully observed data
samples   <- SampleFullTrjs(xpCtbn, num=100)
xpCtbn2   <- NewCtbn(GetCtbnVars(xpCtbn))
LearnCtbnStruct(xpCtbn2, samples)
dynStr2   <- GetDynStruct(xpCtbn2)
stcStr2   <- GetBnStruct(xpCtbn2)
cimsOut2  <- GetDynIntMats(xpCtbn2)
cptsoOut2 <- GetBnCPTs(xpCtbn2)
xpCtbn2   <- DeleteCtbn(xpCtbn2)
garbage   <- gc()

# parameters learning from partially observed data
samples   <- SamplePartialTrjs(xpCtbn, num=10, rem.frac=0.01)
xpCtbn2   <- CloneCtbn(xpCtbn)
inf       <- "importance";
LearnCtbnStruct(xpCtbn2, samples, inf.type=inf, num.samples=100)
dynStr2   <- GetDynStruct(xpCtbn2)
stcStr2   <- GetBnStruct(xpCtbn2)
cimsOut2  <- GetDynIntMats(xpCtbn2)
cptsoOut2 <- GetBnCPTs(xpCtbn2)
xpCtbn2   <- DeleteCtbn(xpCtbn2)
garbage   <- gc()

# delete ctbn
xpCtbn    <- DeleteCtbn(xpCtbn)
garbage   <- gc()

```

LoadRCtbn

*LoadRCtbn***Description**

Load a new CTBN object saved in a rctbn format file.

**Usage**

```
LoadRCtbn (pathfile)
```

**Arguments**

pathfile	character. File to be read.
----------	-----------------------------

**Value**

External pointer to the CTBN C++ model. NULL in the case of errors.

**Note**

You own the external pointer, so remember to delete it using the [DeleteCtbn](#) function only.

**See Also**

[DeleteCtbn](#), [SaveRCtbn](#).

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn     <- LoadRCtbn(ctbn.file)

# delete ctbn
xpCtbn     <- DeleteCtbn(xpCtbn)
garbage    <- gc()
```

NewCtbn

*NewCtbn***Description**

Creation of a new continuous-time Bayesian network (CTBN) object calling the respective C++ function.

**Usage**

```
NewCtbn (vars, bn.str=NULL, bn.cpts=NULL, dyn.str=NULL, dyn.cims=NULL)
```

**Arguments**

vars	dataframe n x 2. It is used to define the variables of the CTBN model. Each row consists of the name (string) of n variables Xn and a value (integer) corresponding of the number of values that the variable can assume (defined from 0 to value-1, -1 if unknown).
bn.str	dataframe k x 2. It is used to define the structure of the initial Bayesian network (specified as a directed acyclic graph). Each row consists of the name of the parent of Xn (from) and the name of Xn (to). Both names must be contained in the vars dataframe (case sensitive).
bn.cpts	list. List (I) of lists (II) of dataframes (III), in which the I level contains the nodes Xn, the second level contains the parents of Xn (Xn U), and the III level contains the values of Xn given a particular instantiation of its parents (Xn lu) specified as a dataframe. This dataframe is 1 x m, where m is number of values that Xn can assume (specified in the column header that must be from 0 to value-1), and the row contains the respective probabilities (that must sum up to 1). The names contained in the I level list must be Xn and the names of the II level list must be in the form Xn\$U=u.
dyn.str	dataframe k x 2. It is used to define the structure of the dynamic structure (possibly cycle). Each row consists of the name of the parent of Xn (from) and the name of Xn (to). Both names must be contained in the vars dataframe (case sensitive).

`dyn.cims` list. List (I) of lists (II) of dataframes (III), in which the I level contains the nodes  $X_n$ , the second level contains the parents of  $X_n$  ( $X_{n|U}$ ), and the III level contains the values of  $X_n$  given a particular instantiation of its parents ( $X_{n|u}$ ) specified as a dataframe. This dataframe is  $m \times m$ , where  $m$  is number of values that  $X_n$  can assume (specified in the column header that must be from 0 to value-1) and it contains the conditional intensity probabilities (each row must sum up to 0). The names contained in the I level list must be  $X_n$  and the names of the II level list must be in the form  $X_n|U=u$ .

### Value

External pointer to the CTBN C++ model. NULL in the case of errors.

### Note

You own the external pointer, so remember to delete it using the [DeleteCtbn](#) function only.

### See Also

[DeleteCtbn](#), [CloneCtbn](#)

### Examples

```
# files
vars.file     <- system.file("DrugNetwork", "DrugNetwork_Vars.txt",      package="ctbn")
bn.str.file   <- system.file("DrugNetwork", "DrugNetwork_BN_Struct.txt",  package="ctbn")
bn.cpts.file  <- system.file("DrugNetwork", "DrugNetwork_BN_CPTs.txt",   package="ctbn")
dyn.str.file  <- system.file("DrugNetwork", "DrugNetwork_Dyn_Struct.txt", package="ctbn")
dyn.cims.file <- system.file("DrugNetwork", "DrugNetwork_Dyn_CIMs.txt",   package="ctbn")

# variables
vars         <- read.table(    vars.file ,    sep=",", header=TRUE)
# static part
bn.str       <- read.table(    bn.str.file,  sep=",", header=TRUE)
bn.cpts     <- ReadProbStruct(bn.cpts.file)
# dynamic part
dyn.str     <- read.table(    dyn.str.file, sep=",", header=TRUE)
dyn.cims   <- ReadProbStruct(dyn.cims.file)

# default constructor
xpCtbn     <- NewCtbn(vars, bn.str=bn.str, bn.cpts=bn.cpts, dyn.str=dyn.str, dyn.cims=dyn.cims)

# delete ctbn
xpCtbn     <- DeleteCtbn(xpCtbn)
garbage    <- gc()
```

### Description

Creation of a new inference engine object.

## Usage

```
NewInfEngine (inf.type="exact", hold=FALSE,
              num.samples=100, burn.iters=100, eps=1e-5)
```

## Arguments

inf.type	character. Inference type: exact, importance, gibbs, gibbsaux, meanfield.
hold	logical. If you are using the same model and the same data, you can preserve the past inference computations using hold=TRUE.
num.samples	integer. Number of samples for importance, gibbs, gibbsaux inference engines.
burn.iters	integer. Number of burn-in iterations for gibbs, gibbsaux inference engines.
eps	numeric. Epsilon value for meanfield inference engine.

## Value

External pointer to the inference engine C++ model. NULL in the case of errors.

## Note

You own the external pointer, so remember to delete it using the [DeleteInfEngine](#) function only.

## See Also

[DeleteInfEngine](#), [GetInfEngineType](#)

## Examples

```
# load ctn and trajectory
ctn.file <- system.file("DrugNetwork", "DrugNetwork.rctn", package="ctn")
trj.file <- system.file("DrugNetwork", "Trajectory.csv", package="ctn")
trj <- read.table(trj.file, sep=",", header=TRUE, check.names=FALSE)
xpCtn <- LoadRCtn(ctn.file)

# advanced option: use an inference engine object for queries
var1 <- "Concentration"
var2 <- "Hungry"
sample.part <- trj
sample.part[,var1] <- -1
sample.part[,var2] <- -1

engine <- NewInfEngine(inf.type="importance", num.samples=1000)
print(GetInfEngineType(engine))
QueryCtnStats(xpCtn, sample.part, c("Hungry"), inf.engine=engine)
engine <- DeleteInfEngine(engine)
garbage <- gc()

# if you are using the same model and the same data,
# you can preserve the past inference computations using the hold flag
engine <- NewInfEngine(inf.type="importance", num.samples=1000, hold=TRUE)
print(GetInfEngineType(engine))
QueryCtnStats(xpCtn, sample.part, c("Hungry"), inf.engine=engine)
QueryCtnStats(xpCtn, sample.part, c("Concentration"), inf.engine=engine)
```

```

print(GetInfEngineType(engine))
engine <- DeleteInfEngine(engine)
garbage <- gc()

# this reset the past computations (the model has been changed)
xpCtbn2 <- CloneCtbn(xpCtbn)
QueryCtbnStats(xpCtbn2, sample.part, c("Hungry"), inf.engine=engine)
engine <- DeleteInfEngine(engine)
xpCtbn2 <- DeleteCtbn(xpCtbn2)
garbage <- gc()

# delete ctbn
xpCtbn <- DeleteCtbn(xpCtbn)
garbage <- gc()

```

**QueryCtbnFilter***QueryCtbnFilter***Description**

Perform the filtering query (i.e. the probability of the state  $x$  at time  $t$  given the trajectory up to time  $t$ ).

**Usage**

```
QueryCtbnFilter (xpCtbn, evid, insts, inf.type="exact",
                 num.samples=100, burn.iters=100, eps=1e-5, inf.engine=NULL)
```

**Arguments**

xpCtbn	external pointer to the CTBN C++ model.
evid	dataframe. Evidence specified as a trajectory.
insts	dataframe $k \times n+1$ . Dataframe of $k$ instantiations in which the first column represents the time $t$ .
inf.type	character. Inference type: exact, importance, gibbs, gibbsaux, meanfield.
num.samples	integer. Number of samples for importance, gibbs, gibbsaux inference engines.
burn.iters	integer. Number of burn-in iterations for gibbs, gibbsaux inference engines.
eps	numeric. Epsilon value for meanfield inference engine.
inf.engine	external pointer to the inference engine C++ model.

**Value**

Dataframe  $k \times 2$ . Each row contains the time and the probability according to the `insts` dataframe. NULL in the case of errors.

**See Also**

[QueryCtbnStats](#), [QueryCtbnTime](#), [QueryCtbnSmooth](#).

## Examples

```

# load ctbn and trajectory
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
trj.file  <- system.file("DrugNetwork", "Trajectory.csv",    package="ctbn")
trj       <- read.table(trj.file, sep=",", header=TRUE, check.names=FALSE)
xpCtbn    <- LoadRCtbn(ctbn.file)

# sample.part is a partial trajectory (Concentration and Hungry are not observed at some time)
# insts dataframe of times and instantiations (Concentration=1, Hungry=0)
var1 <- "Concentration"
var2 <- "Hungry"
val1 <- 1
val2 <- 0
sample.part <- trj
sample.part[,var1] <- -1
sample.part[,var2] <- -1
time  <- seq(0,10,0.01)
vals1 <- rep(val1,length(time))
vals2 <- rep(val2,length(time))
insts <- data.frame(time,vals1,vals2)
names(insts) <- c("Time",var1,var2)

# output: dataframe (time, probability)
x <- QueryCtbnFilter(xpCtbn,sample.part,insts)

# plot output
tgt <- paste(paste(var1,val1,sep="="),paste(var2,val2,sep="="),sep=" ", )
plot(x,main=tgt,xlab="Time",ylab="Probability",type="l")

# delete ctbn
xpCtbn <- DeleteCtbn(xpCtbn)
garbage <- gc()

```

## Description

Perform the smoothing query (i.e. the probability of the state x at time t given the whole trajectory).

## Usage

```
QueryCtbnSmooth (xpCtbn, evid, insts, inf.type="exact",
                  num.samples=100, burn.iters=100, eps=1e-5, inf.engine=NULL)
```

## Arguments

xpCtbn	external pointer to the CTBN C++ model.
evid	dataframe. Evidence specified as a trajectory.
insts	dataframe k x n+1. Dataframe of k instantiations in which the first column represents the time t.

inf.type	character. Inference type: exact, importance, gibbs, gibbsaux, meanfield.
num.samples	integer. Number of samples for importance, gibbs, gibbsaux inference engines.
burn.iters	integer. Number of burn-in iterations for gibbs, gibbsaux inference engines.
eps	numeric. Epsilon value for meanfield inference engine.
inf.engine	external pointer to the inference engine C++ model.

**Value**

Dataframe k x 2. Each row contains the time and the probability according to the `insts` dataframe.  
NULL in the case of errors.

**See Also**

[QueryCtbnStats](#), [QueryCtbnTime](#), [QueryCtbnFilter](#).

**Examples**

```
# load ctbn and trajectory
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
trj.file  <- system.file("DrugNetwork", "Trajectory.csv",    package="ctbn")
trj       <- read.table(trj.file, sep=",", header=TRUE, check.names=FALSE)
xpCtbn   <- LoadRCtbn(ctbn.file)

# sample.part is a partial trajectory (Concentration and Hungry are not observed at some time)
# insts dataframe of times and instantiations (Concentration=1, Hungry=0)
var1 <- "Concentration"
var2 <- "Hungry"
val1 <- 1
val2 <- 0
sample.part <- trj
sample.part[,var1] <- -1
sample.part[,var2] <- -1
time  <- seq(0,10,0.01)
vals1 <- rep(val1,length(time))
vals2 <- rep(val2,length(time))
insts <- data.frame(time,vals1,vals2)
names(insts) <- c("Time",var1,var2)

# output: dataframe (time, probability)
x <- QueryCtbnSmooth(xpCtbn,sample.part,insts)

# plot output
tlt <- paste (paste(var1,val1,sep="="),paste(var2,val2,sep="="),sep=" ", ")
plot(x,main=tlt,xlab="Time",ylab="Probability",type="l")

# delete ctbn
xpCtbn <- DeleteCtbn(xpCtbn)
garbage <- gc()
```

QueryCtbnStats

*QueryCtbnStats*

## Description

Perform the query to the CTBN model about the expected time spent in a state and the expected number of transitions from one state to another state of the given variables.

## Usage

```
QueryCtbnStats (xpCtbn, evid, vars, inf.type="exact",
                 num.samples=100, burn.iters=100, eps=1e-5, inf.engine=NULL)
```

## Arguments

xpCtbn	external pointer to the CTBN C++ model.
evid	dataframe. Evidence specified as a trajectory.
vars	vector of characters. This vector contains the n variables names to perform the query.
inf.type	character. Inference type: exact, importance, gibbs, gibbsaux, meanfield.
num.samples	integer. Number of samples for importance, gibbs, gibbsaux inference engines.
burn.iters	integer. Number of burn-in iterations for gibbs, gibbsaux inference engines.
eps	numeric. Epsilon value for meanfield inference engine.
inf.engine	external pointer to the inference engine C++ model.

## Value

List of n dataframes. Each dataframe contains the expected time spent in a state (diagonal elements) and the expected number of transitions from one state to another state (off-diagonal elements). Each state is specified in the row (from) and column (to) headers. NULL in the case of errors.

## See Also

[QueryCtbnTime](#), [QueryCtbnFilter](#), [QueryCtbnSmooth](#).

## Examples

```
# load ctbn and trajectory
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
trj.file  <- system.file("DrugNetwork", "Trajectory.csv",    package="ctbn")
trj       <- read.table(trj.file, sep=",", header=TRUE, check.names=FALSE)
xpCtbn   <- LoadRCTbn(ctbn.file)

# sample.part is a partial trajectory (Eating and Drowsy are not observed at some time)
# v1 vector of variable Eating
# v2 vector of variables Eating and Drowsy
var1 <- "Eating"
var2 <- "Drowsy"
```

```

sample.part <- trj
sample.part[5,var1]=-1
sample.part[6,var2]=-1
v1 <- c(var1)
v2 <- c(var1,var2)

print(QueryCtbnStats(xpCtbn, sample.part, v1))
print(QueryCtbnStats(xpCtbn, sample.part, v2))

# delete ctbn
xpCtbn <- DeleteCtbn(xpCtbn)
garbage <- gc()

```

**QueryCtbnTime***QueryCtbnTime***Description**

Perform the query to the CTBN model about the expected time that the process stays in some states.

**Usage**

```
QueryCtbnTime (xpCtbn, evid, insts, inf.type="exact",
                num.samples=100, burn.iters=100, eps=1e-5, inf.engine=NULL)
```

**Arguments**

xpCtbn	external pointer to the CTBN C++ model.
evid	dataframe. Evidence specified as a trajectory.
insts	dataframe k x n. Dataframe of k instantiations.
inf.type	character. Inference type: exact, importance, gibbs, gibbsaux, meanfield.
num.samples	integer. Number of samples for importance, gibbs, gibbsaux inference engines.
burn.iters	integer. Number of burn-in iterations for gibbs, gibbsaux inference engines.
eps	numeric. Epsilon value for meanfield inference engine.
inf.engine	external pointer to the inference engine C++ model.

**Value**

Dataframe k x 1. Each row contains the expected time that the process stays in the specified state. NULL in the case of errors.

**See Also**

[QueryCtbnStats](#), [QueryCtbnFilter](#), [QueryCtbnSmooth](#).

## Examples

```
# load ctn and trajectory
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
trj.file  <- system.file("DrugNetwork", "Trajectory.csv",    package="ctbn")
trj       <- read.table(trj.file, sep=",", header=TRUE, check.names=FALSE)
xpCtbn    <- LoadRCtbn(ctbn.file)

# sample.part is a partial trajectory (Eating and Drowsy are not observed at some time)
# insts dataframe of instantiations
var1 <- "Eating"
var2 <- "Drowsy"
sample.part <- trj
sample.part[5,var1]=-1
sample.part[6,var2]=-1
insts <- trj[7:8,c(3:4)]
print(insts)

print(QueryCtbnTime(xpCtbn,sample.part,insts))

# delete ctn
xpCtbn <- DeleteCtbn(xpCtbn)
garbage <- gc()
```

**ReadProbStruct**

*ReadProbStruct*

## Description

Read the definition of both static and dynamic parts of the CTBN object from a textual file.

## Usage

```
ReadProbStruct (pathfile, s.tag=NULL, e.tag=NULL)
```

## Arguments

- pathfile      character. File to be read.
- s.tag          character. Initial tag, NULL from the start of the file.
- e.tag          character. End tag, NULL to the end of the file.

## Value

List. List (I) of lists (II) of dataframes (III), in which the I level contains the nodes Xn, the second level contains the parents of Xn (Xn|U), and the III level contains the values of Xn given a particular instantiation of its parents (Xn|u) specified as a dataframe. This dataframe can be 1 x m (bn.cpts) or m x m (dyn.cims), where m is number of values that Xn can assume (specified in the column header that must be from 0 to value-1). The names contained in the I level list must be Xn and the names of the II level list must be in the form Xn\$U=u.

### Note

The file format should be defined as: a row that identifies the variable  $X_n$  given a particular instantiation of its parents ( $X_{nlu}$ ) and the definition of the respective probabilities in terms of a vector (Vec) or a matrix (Mat). See the following two examples.

An excerpt of the definition file of the static component:

```
Eating$Hungry=0
Vec,0,1
"0",0.1,0.9
Concentration$Full stomach=0,Uptake=0
Vec,0,1,2
"0",0.7,0.2,0.1
```

An excerpt of the definition file of the dynamic component:

```
Eating$Hungry=0
Mat,0,1
"0",-0.01,0.01
"1",10.0,-10.0
Concentration$Full stomach=0,Uptake=0
Mat,0,1,2
"0",-0.02,0.01,0.01
"1",0.25,-0.26,0.01
"2",0.01,0.5,-0.51
```

---

### See Also

[WriteProbStruct](#)

### Examples

```
# cpts and cims files
bn.cpts.file <- system.file("DrugNetwork", "DrugNetwork_BN_CPTs.txt", package="ctbn")
dyn.cims.file <- system.file("DrugNetwork", "DrugNetwork_Dyn_CIMs.txt", package="ctbn")

bn.cpts <- ReadProbStruct(bn.cpts.file)
dyn.cims <- ReadProbStruct(dyn.cims.file)
```

---



---

### Description

Sample fully observed trajectories from a given CTBN object.

### Usage

```
SampleFullTrjs (xpCtbn, t.begin=0.0, t.end=10.0, num=10)
```

**Arguments**

xpCtbn	external pointer to the CTBN C++ model.
t.begin	numeric. Begin time of the trajectory.
t.end	numeric. End time of the trajectory.
num	integer. Number of trajectories.

**Value**

List. List of length num of dataframes k x n+1. Each dataframe represents a trajectory in which the columns names are the time and the n variables of the CTBN model and the k rows (that can be different from each trajectory) contain the the temporal evolution of the variables. Recall that in the CTBN model, only one single variable can change at any single instant, so each row of the dataframe contains at most one state transition of a variable. The last row contains all -1 (unknown state) because the variables are observed in the [t1;t2],[t2;t3], ..., [tk-1;tk) time intervals. NULL in the case of errors.

**See Also**

[SamplePartialTrjs](#)

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn    <- LoadRCTbn(ctbn.file)

samplesFull <- SampleFullTrjs(xpCtbn, num=100)

sampleFull  <- samplesFull[[1]]

plot(sampleFull[1:nrow(sampleFull)-1,c(1,4)], type="s", main="Full Trajectory")

# delete ctbn
xpCtbn    <- DeleteCtbn(xpCtbn)
garbage   <- gc()
```

**Description**

Sample partially observed trajectories from a given CTBN object.

**Usage**

```
SamplePartialTrjs (xpCtbn, t.begin=0.0, t.end=10.0, num=10,
                  rem.frac=0.1, rem.ite=1)
```

**Arguments**

xpCtbn	external pointer to the CTBN C++ model.
t.begin	numeric. Begin time of the trajectory.
t.end	numeric. End time of the trajectory.
num	integer. Number of trajectories.
rem.frac	numeric. Fraction of information removed in each iteration.
rem.ite	integer. Number of iterations.

**Value**

List. List of length num of dataframes k x n+1. Each dataframe represents a trajectory in which the columns names are the time and the n variables of the CTBN model and the k rows (that can be different from each trajectory) contain the the temporal evolution of the variables. Recall that in the CTBN model, only one single variable can change at any single instant, so each row of the dataframe contains at most one state transition of a variable. Some information is randomly removed (-1 values) from each trajectory according to the given parameters. The last row contains all -1 (unknown state) because the variables are observed in the [t1;t2],[t2;t3), ..., [tk-1,tk) time intervals. NULL in the case of errors.

**See Also**

[SampleFullTrjs](#)

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn    <- LoadRCtbn(ctbn.file)

samplesPart <- SamplePartialTrjs(xpCtbn, num=100, rem.frac=0.01)

samplePart  <- samplesPart[[1]]

plot(samplePart[1:nrow(samplePart)-1,c(1,4)],type="s",main="Partial Trajectory")

# delete ctbn
xpCtbn    <- DeleteCtbn(xpCtbn)
garbage <- gc()
```

**Description**

Save the CTBN object in a rctbn format file.

**Usage**

SaveRCtbn (xpCtbn, pathfile)

**Arguments**

- `xpCtn` external pointer to the CTBN C++ model.  
`pathfile` character. File to save the CTBN C++ model.

**See Also**

[LoadRCtbn](#)

**Examples**

```
# load ctn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtn     <- LoadRCtbn(ctbn.file)

SaveRCtbn(xpCtn, "myDrugNetwork.rctbn")

# delete ctn
xpCtn     <- DeleteCtbn(xpCtn)
garbage   <- gc()
```

**Description**

Set the definition of the initial Bayesian network (conditional probability tables) of the CTBN object.

**Usage**

`SetBnCPTs (xpCtn, bn.cpts)`

**Arguments**

- `xpCtn` external pointer to the CTBN C++ model.  
`bn.cpts` list. List (I) of lists (II) of dataframes (III), in which the I level contains the nodes Xn, the second level contains the parents of Xn (Xn|U), and the III level contains the values of Xn given a particular instantiation of its parents (Xn|lu) specified as a dataframe. This dataframe is 1 x m, where m is number of values that Xn can assume (specified in the column header that must be from 0 to value-1), and the row contains the respective probabilities (that must sum up to 1). The names contained in the I level list must be Xn and the names of the II level list must be in the form Xn\$U=u.

**Value**

0 if it is set correctly, NULL in the case of errors.

**See Also**

[SetBnCPTs](#), [ReadProbStruct](#)

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn    <- LoadRCTbn(ctbn.file)
bn.cpts   <- GetBnCPTs(xpCtbn)

SetBnCPTs(xpCtbn, bn.cpts)

# delete ctbn
xpCtbn    <- DeleteCtbn(xpCtbn)
garbage   <- gc()
```

SetBnStruct

*SetBnStruct***Description**

Set the structure of the initial Bayesian network of the CTBN object.

**Usage**

```
SetBnStruct (xpCtbn, bn.str)
```

**Arguments**

- |        |   |
|--------|---|
| xpCtbn | external pointer to the CTBN C++ model.   |
| bn.str | dataframe k x 2. It is used to define the structure of the initial Bayesian network (specified as a directed acyclic graph). Each row consists of the name of the parent of Xn (from) and the name of Xn (to). Both names must be contained in the variables definition of the CTBN model (case sensitive). |

**Value**

0 if it is set correctly, NULL in the case of errors.

**See Also**

[GetBnStruct](#)

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn    <- LoadRCTbn(ctbn.file)
bn.str    <- GetBnStruct(xpCtbn)

SetBnStruct(xpCtbn, bn.str)

# delete ctbn
xpCtbn    <- DeleteCtbn(xpCtbn)
garbage   <- gc()
```

**SetDynIntMats***SetDynIntMats***Description**

Set the definition of the dynamic component (conditional intensity matrices) of the CTBN object.

**Usage**

```
SetDynIntMats (xpCtbn, dyn.cims)
```

**Arguments**

- |                       |   |
|-----------------------|---|
| <code>xpCtbn</code>   | external pointer to the CTBN C++ model.   |
| <code>dyn.cims</code> | list. List (I) of lists (II) of dataframes (III), in which the I level contains the nodes $X_n$ , the second level contains the parents of $X_n$ ( $X_{n U}$ ), and the III level contains the values of $X_n$ given a particular instantiation of its parents ( $X_{n U}$ ) specified as a dataframe. This dataframe is $m \times m$ , where $m$ is number of values that $X_n$ can assume (specified in the column header that must be from 0 to value-1) and it contains the conditional intensity probabilities (each row must sum up to 0). The names contained in the I level list must be $X_n$ and the names of the II level list must be in the form $X_n U=u$ . |

**Value**

0 if it is set correctly, NULL in the case of errors.

**See Also**

[GetDynIntMats](#), [ReadProbStruct](#)

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn    <- LoadRCtbn(ctbn.file)
dyn.cims  <- GetDynIntMats(xpCtbn)

SetDynIntMats (xpCtbn, dyn.cims)

# delete ctbn
xpCtbn    <- DeleteCtbn(xpCtbn)
garbage   <- gc()
```

SetDynStruct

*SetDynStruct***Description**

Set the structure of the dynamic component of the CTBN object.

**Usage**

```
SetDynStruct (xpCtbn, dyn.str)
```

**Arguments**

xpCtbn	external pointer to the CTBN C++ model.
dyn.str	dataframe k x 2. It is used to define the structure of the dynamic structure (possibly cycle). Each row consists of the name of the parent of Xn (from) and the name of Xn (to). Both names must be contained in the variables definition of the CTBN model (case sensitive).

**Value**

0 if it is set correctly, NULL in the case of errors.

**See Also**

[GetDynStruct](#)

**Examples**

```
# load ctbn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtbn    <- LoadRCtbn(ctbn.file)
dyn.str   <- GetDynStruct(xpCtbn)

SetDynStruct(xpCtbn, dyn.str)

# delete ctbn
xpCtbn    <- DeleteCtbn(xpCtbn)
garbage   <- gc()
```

WriteProbStruct

*WriteProbStruct***Description**

Write the definition of both static and dynamic parts of the CTBN object to a textual file.

**Usage**

```
WriteProbStruct (prob.struct, pathfile, append=FALSE)
```

**Arguments**

- `prob.struct` list. List (I) of lists (II) of dataframes (III), in which the I level contains the nodes  $X_n$ , the second level contains the parents of  $X_n$  ( $X_n|U$ ), and the III level contains the values of  $X_n$  given a particular instantiation of its parents ( $X_n|U$ ) specified as a dataframe. This dataframe can be  $1 \times m$  (`bn.cpts`) or  $m \times m$  (`dyn.cims`), where  $m$  is number of values that  $X_n$  can assume (specified in the column header that must be from 0 to value-1). The names contained in the I level list must be  $X_n$  and the names of the II level list must be in the form  $X_n|U=u$ .
- `pathfile` character. File to write.
- `append` boolean. Append to pathfile.

**See Also**

[ReadProbStruct](#), [GetBnCPTs](#), [GetDynIntMats](#)

**Examples**

```
# load ctn
ctbn.file <- system.file("DrugNetwork", "DrugNetwork.rctbn", package="ctbn")
xpCtn <- LoadRCTbn(ctbn.file)
bn.cpts <- GetBnCPTs(xpCtn)

WriteProbStruct(bn.cpts, "myDrugNetwork_BN_CPTs.txt")

# delete ctn
xpCtn <- DeleteCtn(xpCtn)
garbage <- gc()
```

# Index

- \*Topic **clone ctbn**  
CloneCtbn, 3
- \*Topic **create ctbn**  
NewCtbn, 14
- \*Topic **create inference engine**  
NewInfEngine, 15
- \*Topic **delete ctbn**  
DeleteCtbn, 4
- \*Topic **delete inference engine**  
DeleteInfEngine, 5
- \*Topic **get ctbn variables**  
GetCtbnVars, 8
- \*Topic **get dynamic definition**  
GetDynIntMats, 8
- \*Topic **get dynamic structure**  
GetDynStruct, 9
- \*Topic **get static definition**  
GetBnCPTs, 5
- \*Topic **get static structure**  
GetBnStruct, 6
- \*Topic **inference engine type**  
GetInfEngineType, 10
- \*Topic **joint intensity matrix**  
GetCtbnJointDyn, 7
- \*Topic **load R ctbn model**  
LoadRCtbn, 13
- \*Topic **parameters learning**  
LearnCtbnParams, 11
- \*Topic **query: expected time and transitions given variables**  
QueryCtbnStats, 20
- \*Topic **query: expected time given states**  
QueryCtbnTime, 21
- \*Topic **query: filtering**  
QueryCtbnFilter, 17
- \*Topic **query: smoothing**  
QueryCtbnSmooth, 18
- \*Topic **read probability structure**  
ReadProbStruct, 22
- \*Topic **sample full trajectories**  
SampleFullTrjs, 23
- \*Topic **sample partial trajectories**  
SamplePartialTrjs, 24
- \*Topic **save R ctbn model**  
SaveRCtbn, 25
- \*Topic **set dynamic definition**  
SetDynIntMats, 28
- \*Topic **set dynamic structure**  
SetDynStruct, 29
- \*Topic **set static definition**  
SetBnCPTs, 26
- \*Topic **set static structure**  
SetBnStruct, 27
- \*Topic **structural learning**  
LearnCtbnStruct, 12
- \*Topic **write probability structure**  
WriteProbStruct, 29

CloneCtbn, 3, 4, 15

ctbn-package, 2

DeleteCtbn, 4, 4, 14, 15

DeleteInfEngine, 5, 10, 16

GetBnCPTs, 5, 11, 12, 30

GetBnStruct, 6, 12, 27

GetCtbnJointDyn, 7

GetCtbnVars, 8

GetDynIntMats, 8, 11, 12, 28, 30

GetDynStruct, 9, 12, 29

GetInfEngineType, 5, 10, 16

LearnCtbnParams, 11, 12

LearnCtbnStruct, 11, 12

LoadRCtbn, 13, 26

NewCtbn, 4, 8, 14

NewInfEngine, 5, 10, 15

QueryCtbnFilter, 17, 19–21

QueryCtbnSmooth, 17, 18, 20, 21

QueryCtbnStats, 17, 19, 20, 21

QueryCtbnTime, 17, 19, 20, 21

ReadProbStruct, 22, 26, 28, 30

SampleFullTrjs, 11, 12, 23, 25

SamplePartialTrjs, [11](#), [12](#), [24](#), [24](#)

SaveRCtbn, [14](#), [25](#)

SetBnCPTs, [6](#), [26](#), [26](#)

SetBnStruct, [6](#), [27](#)

SetDynIntMats, [9](#), [28](#)

SetDynStruct, [9](#), [29](#)

WriteProbStruct, [23](#), [29](#)