Package 'CNORdt'

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Type Package

Title Add-on to CellNOptR: Discretized time treatments

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Description This add-on to the package CellNOptR handles time-course data, as opposed to steady state data in CellNOptR. It scales the simulation step to allow comparison and model fitting for time-course data. Future versions will optimize delays and strengths for each edge.

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Depends R (>= 1.8.0), CellNOptR (>= 0.99), abind

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CNOlistPB *Toy data*

Description

This data object contains the data associated with the toy model example from the package vignette, already loaded and formatted as a CNOlist object.

Usage

```
CNOlistPB
```

Format

CNOlistPB is a list with the fields "namesCues" (character vector), "namesStimuli" (character vector), "namesInhibitors" (character vector), "namesSignals" (character vector), "timeSignals" (numerical vector), "valueCues" (numerical matrix), "valueInhibitors" (numerical matrix), "valueStimuli"(numerical matrix), "valueSignals"(numerical matrix).

Source

This data was generated with the CellNOptR add-on package CNORode. Full details of the data can be found in the reference below.

References

A. MacNamara, C. Terfve, D. Henriques, B. Penalver Bernabe and J. Saez-Rodriguez, 2012. State-time spectrum of signal transduction logic models. Physical biology, 9(4), p.045003.

computeScoreDT *Compute the score of a model/data (time-course) set using a bitString to cut the model.*

Description

The bitString made of 0s and 1s encodes a submodel from the model provided. Then, the simulator function is called to compute the objective function. The sizeFac and NAFac are penalties added to the final score as described in `gaBinaryDT`. The indexList and simList arguments can be provided to speed up the code, otherwise they are recomputed from the CNOlist and model.

Usage

```
computeScoreDT(CNOlist, model, bString, simList=NULL, indexList=NULL,
sizeFac=0.0001, NAFac=1, boolUpdates, lowerB=lowerB, upperB=upperB)
```

Arguments

CNOlist	A CNOlist structure, as created by makeCNOlist.
model	A model structure, as created by codereadSIF, normally pre-processed but that is not a requirement of this function.
bString	A bit string of the same size as the number of reactions in the model above.
simList	If provided, simList should be created by prep4sim, and has also already been cut to contain only the reactions to be evaluated.
indexList	If provided, indexList should contain a list of indexes of the species stimulated/inhibited/measured in the model, as created by indexFinder.
sizeFac	The scaling factor for the size term in the objective function, default to 0.0001.
NAFac	The scaling factor for the NA term in the objective function, default to 1.
boolUpdates	The number of synchronous updates performed by the boolean simulator.
lowerB	The lower bound for the optimized value of the scaling factor.
upperB	The upper bound for the optimized value of the scaling factor.

Value

score	See gaBinaryT1 for details.

Author(s)

A. MacNamara

Examples

```
library(CellNOptR)
library(CNORdt)
data(CNOlistPB, package="CNORdt")
data(modelPB, package="CNORdt")

# pre-process model
model = preprocessing(CNOlistPB, modelPB)

# compute score
score = computeScoreDT(CNOlistPB, model, bString=rep(1,16),
boolUpdates=10, lowerB=0.8, upperB=10)
```

---

convert2array *Converts the output of simulatorDT to a 3D array for other functions*

Description

As above.

Usage

```
convert2array(x, nRow, nCol, nBool)
```

Arguments

x	simResults as returned by simulatorDT
nRow	Number of rows of output.
nCol	Number of columns of output.
nBool	The third dimension, which corresponds to the number of simulation updates.

Value

This function returns a 3D array of the simulation results.

Author(s)

A. MacNamara

Examples

```
library(CellNOptR)
library(CNORdt)
data(CNOlistPB, package="CNORdt")
data(modelPB, package="CNORdt")

indexOrig <- indexFinder(CNOlistPB, modelPB, verbose=TRUE)
fields4Sim <- prep4sim(modelPB)
boolUpdates=10

simResults <- simulatorDT(
  CNOlist=CNOlistPB,
  model=modelPB,
  simList=fields4Sim,
  indices=indexOrig,
  boolUpdates=boolUpdates
)
simResults = convert2array(simResults, dim(CNOlistPB$valueSignals[[1]])[1],
length(modelPB$namesSpecies), boolUpdates)
```

---

cutAndPlotResultsDT *Plot the results of a time-course optimization*

Description

This function takes the optimized bit string, cuts the model according to the string and then finds the optimized scaling factor to pass on to plotOptimResultsPan for visualization.

Usage

```
cutAndPlotResultsDT(model, bString, simList=NULL, CNOlist, indexList=NULL,
plotPDF=FALSE, tag=NULL, plotParams=list(maxrow=10), boolUpdates=boolUpdates,
lowerB=lowerB, upperB=upperB, sizeFac = 1e-04, NAFac = 1)
```

Arguments

model	The expanded model used as input for gaBinaryDT.
bString	A bit string as output by gabinaryDT (i.e. a vector of 1s and 0s).
simList	A simlist corresponding to the model, as output by prep4sim.
CNOlist	The CNOlist used in optimization.
indexList	An indexList, produced by indexFinder run on the model and the CNOlist above.
plotPDF	TRUE or FALSE; for pdf output.
tag	NULL or string; prefixes filenames with a tag (replaces the default behavior).
plotParams	A list of options related to the PDF and plotting outputs. (1) maxrow is the maximum number of rows used to plot the results. See plotOptimResultsPan for other fields.
boolUpdates	The number of synchronous updates performed by the boolean simulator.
lowerB	The lower bound for the optimized value of the scaling factor.
upperB	The upper bound for the optimized value of the scaling factor.
sizeFac	The scaling factor for the size term in the objective function, default to 0.0001.
NAFac	The scaling factor for the NA term in the objective function, default to 1.

Value

This function doesn't return anything, it only plots the graph in your graphic window.

Author(s)

A. MacNamara

See Also

plotOptimResultsPan

Examples

```
data(CNOlistPB, package="CNORdt")
data(modelPB, package="CNORdt")

# pre-process model
model <- preprocessing(CNOlistPB, modelPB)
indices = indexFinder(CNOlistPB, model)
fields4Sim <- prep4sim(model=model)
initBstring <- rep(1, length(model$reacID))

# optimize
opt1 <- gaBinaryDT(CNOlist=CNOlistPB, model=model, initBstring=initBstring,
verbose=TRUE, boolUpdates=10, maxTime=30, lowerB=0.8, upperB=10)

cutAndPlotResultsDT(
  model=model,
  CNOlist=CNOlistPB,
  bString=opt1$bString,
  plotPDF=FALSE,
  boolUpdates=10,
  lowerB=0.8,
```

```
  upperB=10
)
```

`gaBinaryDT` *Genetic algorithm for optimizing models using multiple time-points*

Description

The genetic algorithm used to optimize a model by fitting to data consisting of multiple time points. The data can be fitted by applying a single scaling factor to the boolean simulation.

Usage

```
gaBinaryDT(CNOlist, model, initBstring = NULL, sizeFac = 1e-04, NAFac = 1, popSize = 50,
pMutation = 0.5, maxTime = 60, maxGens = 500, stallGenMax = 100, selPress = 1.2,
elitism = 5, relTol = 0.1, verbose = TRUE, priorBitString = NULL, maxSizeHashTable = 5000,
boolUpdates, lowerB = lowerB, upperB = upperB)
```

Arguments

`CNOlist`	A CNOlist on which the score is based.
`model`	A model structure, as created by `readSIF`, normally pre-processed but that is not a requirement of this function.
`initBstring`	An initial bitstring to be tested, should be of the same size as the number of reactions in the model above (model$reacID). The default is all ones.
`sizeFac`	The scaling factor for the size term in the objective function, it defaults to 0.0001.
`NAFac`	The scaling factor for the NA term in the objective function, it defaults to 1.
`popSize`	The population size for the genetic algorithm, it is set to 50.
`pMutation`	the mutation probability for the genetic algorithm, default set to 0.5.
`maxTime`	the maximum optimisation time in seconds, default set to 60.
`maxGens`	The maximum number of generations in the genetic algorithm, default set to 500.
`stallGenMax`	The maximum number of stall generations in the genetic algorithm, default to 100.
`selPress`	The selective pressure in the genetic algorithm, default set to 1.2.
`elitism`	The number of best individuals that are propagated to the next generation in the genetic algorithm, default set to 5.
`relTol`	The relative tolerance for the best bitstring reported by the genetic algorithm, i.e., how different from the best solution, default set to 0.1.
`verbose`	Logical (default to TRUE): do you want the statistics of each generation to be printed on the screen?
`priorBitString`	At each generation, the GA algorithm creates a population of bitstrings that will be used to perform the optimisation. If the user knows the values of some bits, they can be used to overwrite bit values proposed by the GA algorithm. If provided, the priorBitString must have the same length as the initial bitstring and be made of 0, 1 or NA (by default, this bitstring is set to NULL, which is equivalent to setting all bits to NA). Bits that are set to 0 or 1 are used to replace the bits created by the GA itself (see example).

`maxSizeHashTable`
: A hash table is used to store bitstrings and related scores. This allows the GA to be very efficient is the case of small models. The size of the hash table is 5000 by default, which may be too large for large models.

`boolUpdates`
: The number of synchronous updates performed by the boolean simulator.

`lowerB`
: The lower bound for the optimized value of the scaling factor.

`upperB`
: The upper bound for the optimized value of the scaling factor.

Details

This is the modified version of gaBinaryT1 from the CellNOptR package, which is able to use all data from CNOlist$valueSignals.

Value

This function returns a list with elements:

`bString`
: The best bitstring.

`Results`
: A matrix with columns: "Generation", "Best_score", "Best_bitString", "Stall_Generation", "Avg_Score_Gen", "Best_score_Gen", "Best_bit_Gen", "Iter_time".

`StringsTol`
: The bitstrings whose scores are within the tolerance.

`StringsTolScores`
: The scores of the above-mentioned strings.

Author(s)

A. MacNamara

References

A. MacNamara, C. Terfve, D. Henriques, B. Penalver Bernabe and J. Saez-Rodriguez, 2012. State-time spectrum of signal transduction logic models. Physical biology, 9(4), p.045003.

See Also

getFitDT, simulatorDT

Examples

```
library(CellNOptR)
library(CNORdt)
data(CNOlistPB, package="CNORdt")
data(modelPB, package="CNORdt")

# pre-process model
model = preprocessing(CNOlistPB, modelPB)

# optimise
initBstring <- rep(1, length(model$reacID))
opt1 <- gaBinaryDT(CNOlist=CNOlistPB, model=model, initBstring=initBstring,
verbose=TRUE, boolUpdates=10, maxTime=30, lowerB=0.8, upperB=10)
```

getFitDT *The optimization function that finds the scaling factor for the boolean simulation*

Description

This function is called from gaBinaryDT. Using the model passed as input, it finds a scaling factor that minimizes the mean squared error between the data from the boolean simulation and the experimental data. A spline is fitted to the experimental data to allow this.

Usage

```
getFitDT(simResults, CNOlist, model, indexList, sizeFac = 1e-04, NAFac = 1, nInTot, boolUpdates, low
```

Arguments

simResults	The simulation results as output from simulatorDT
CNOlist	A CNOlist on which the score is based (based on all valueSignals).
model	A model list.
indexList	A list of indexes of species stimulated/inhibited/signals, as produced by indexfinder applied on the model and CNOlist above.
sizeFac	The scaling factor for the size term in the objective function, default to 0.0001.
NAFac	The scaling factor for the NA term in the objective function, default to 1.
nInTot	The number of inputs in the model prior to cutting, used to normalise the size penalty.
boolUpdates	The number of synchronous updates performed by the boolean simulator.
lowerB	The lower bound for the optimized value of the scaling factor.
upperB	The upper bound for the optimized value of the scaling factor.

Details

The function optim() is used to find the optimal scaling factor.

Value

This function returns a list with elements:

score	The mean squared error between simulation and experiment with NA and model size penalties.
estimate	The scaling factor used to compare boolean and real data.
xCoords	The x-axis coordinates after multiplication with the scaling factor.
yInter	The interpolated values of the experimental data.
yBool	The boolean simulation results at each time point.

Author(s)

A. MacNamara

See Also

gaBinaryDT, simulatorDT

Examples

```
# this function is usually contained within gaBinaryDT
# but the output can be viewed as follows:

library(CellNOptR)
library(CNORdt)
data(CNOlistPB, package="CNORdt")
data(modelPB, package="CNORdt")

# pre-processing
indexOrig <- indexFinder(CNOlist=CNOlistPB, model=modelPB, verbose=TRUE)
fields4Sim <- prep4sim(model=modelPB)

boolUpdates = 10
simResults <- simulatorDT(
  CNOlist=CNOlistPB,
  model=modelPB,
  simList=fields4Sim,
  indices=indexOrig,
  boolUpdates=boolUpdates
)
simResults = convert2array(simResults, dim(CNOlistPB$valueSignals[[1]])[1],
length(modelPB$namesSpecies), boolUpdates)

optimRes <- getFitDT(
  simResults=simResults,
  CNOlist=CNOlistPB,
  model=modelPB,
  indexList=indexOrig,
  boolUpdates=boolUpdates,
  lowerB=0.8,
  upperB=10,
  nInTot=length(which(modelPB$interMat == -1))
)
```

`modelPB` *modelPB*

Description

This data object contains the toy model from the package vignette, already loaded and formatted as a Model object.

Usage

```
Model
```

Format

modelPB is a list with fields "reacID" (character vector), "namesSpecies" (character vector), "interMat" (numerical matrix), and "notMat"(numerical matrix).

Source

This data and model is from the Physical Biology tutorial, "State-time spectrum of signal transduction logic models". It is used to demonstrate the assumptions and limitations of different logic model formalisms.

References

A. MacNamara, C. Terfve, D. Henriques, B. Penalver Bernabe and J. Saez-Rodriguez, 2012. State-time spectrum of signal transduction logic models. Physical biology, 9(4), p.045003.

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simulatorDT *Discrete time simulation of a boolean model*

Description

Simulates multiple time points within C (for speed).

Usage

```
simulatorDT(CNOlist, model, simList, indices, boolUpdates,
prevSim=NULL)
```

Arguments

CNOlist	A CNOlist.
model	A model that only contains the reactions to be evaluated.
simList	A simList as created by prep4sim, that has also already been cut to contain only the reactions to be evaluated.
indices	An indexList as created by indexFinder.
boolUpdates	The number of update rounds the simulator should run for.
prevSim	The results from `simulatorT0` can be used here as initial conditions.

Value

A 3-dimensional array that gives the value of all species under each condition at each update (conditions, species, update).

Author(s)

A. MacNamara

See Also

gaBinaryDT, getFitDT

Examples

```
# this computes the output of the full model,
# which is normally not done on a stand alone basis,
# but if you have a model and would like to visualise
# its output compared to your data, then this is what you should do.

library(CellNOptR)
library(CNORdt)
data(CNOlistPB, package="CNORdt")
data(modelPB, package="CNORdt")

indexOrig <- indexFinder(CNOlistPB, modelPB, verbose=TRUE)
fields4Sim <- prep4sim(modelPB)
boolUpdates=10

simResults <- simulatorDT(
  CNOlist=CNOlistPB,
  model=modelPB,
  simList=fields4Sim,
  indices=indexOrig,
  boolUpdates=boolUpdates
)
simResults = convert2array(simResults, dim(CNOlistPB$valueSignals[[1]])[1],
length(modelPB$namesSpecies), boolUpdates)
```

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