

Package ‘CancerInSilico’

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Type Package

Title An R interface for computational modeling of tumor progression

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Description The CancerInSilico package provides an R interface for running mathematical models of tumor progression. This package has the underlying models implemented in C++ and the output and analysis features implemented in R.

License GPL (>= 2)

Imports methods, grDevices, graphics, stats

Depends Rcpp

LinkingTo Rcpp, testthat, BH

Suggests testthat, knitr, rmarkdown, BiocStyle

VignetteBuilder knitr

biocViews MathematicalBiology, SystemsBiology, CellBiology,
BiomedicalInformatics

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NeedsCompilation yes

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CancerInSilico	<i>CancerInSilico</i>
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Description

Package: CellModel
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 Version: 0.99.0
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Author(s)

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CellModel-class	<i>CellModel</i>
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Description

An S4 class to represent the output of a cell-based model

Slots

mCells A list object where each row of the list describes the state of all the cells in the model at a given time. Each cell is described over 6 columns: [1] x-coordinate, [2] y-coordinate, [3] radius, [4] axis length, [5] axis angle, [6] growth rate. For instance, the x-coordinates of the first 3 cells will be in columns 1,7,13.

mInitialNumCells the initial number of cells in the model

mRunTime the total run time (hours) of the model

mInitialDensity the density the cells were seeded at

mInheritGrowth whether or not cells inherit growth rates from their parent

mOutputIncrement the frequency of print statements during the run

mRandSeed the random seed

mEpsilon model specific parameter
mNG model specific parameter
mTimeIncrement amount of time elapsed in each model step
mCycleLengthDist initial distribution of cell-cycle lengths

getAxisAngle *getAxisAngle get the axis angle of each cell*

Description

getAxisAngle get the axis angle of each cell

Usage

getAxisAngle(model, time)

Arguments

model A CellModel
time time in model hours

Value

vector containing the axis angle of each cell at time

getAxisLength *getAxisLength get the axis length of each cell*

Description

getAxisLength get the axis length of each cell

Usage

getAxisLength(model, time)

Arguments

model A CellModel
time time in model hours

Value

vector containing the axis length of each cell at time

getCoordinates	getCoordinates <i>get a two dimensional matrix of all the cell coordinates</i>
----------------	--

Description

getCoordinates get a two dimensional matrix of all the cell coordinates

Usage

```
getCoordinates(model, time)
```

Arguments

model	A CellModel
time	time in model hours

Value

an N X 2 matrix of cell coordinates at time

getCycleLengths	getCycleLengths <i>return the cycle lengths of each cells at time</i>
-----------------	---

Description

getCycleLengths return the cycle lengths of each cells at time

Usage

```
getCycleLengths(model, time)
```

Arguments

model	a CellModel object
time	time in model hours

Value

the cycle lengths of each cell at time

Examples

```
getCycleLengths(runCancerSim(1,1), 1)
```

getDensity	getDensity gets the density of cells at a given time
------------	--

Description

getDensity gets the density of cells at a given time

Usage

```
getDensity(model, time)
```

Arguments

model	A Cell Model
time	time in model hours

Value

The density of cells at that time (not quite the same as confluency)

Examples

```
getDensity(runCancerSim(1,1),1)
```

getGrowthRates	getGrowthRates get the model growth rates of each cell
----------------	--

Description

getGrowthRates get the model growth rates of each cell

Usage

```
getGrowthRates(model, time)
```

Arguments

model	A CellModel
time	time in model hours

Value

vector containing the growth rate of each cell at time

getNumberOfCells	getNumberOfCells <i>get the number of cells alive</i>
------------------	---

Description

getNumberOfCells get the number of cells alive

Usage

```
getNumberOfCells(model, time)
```

Arguments

model	A CellModel
time	time in model hours

Value

the number of cells at this time

Examples

```
getNumberOfCells(runCancerSim(1,1), 1)
```

getParameters	getParameters <i>get a named list of parameters in the model</i>
---------------	--

Description

getParameters get a named list of parameters in the model

Usage

```
getParameters(model, fullDist = FALSE)
```

Arguments

model	A CellModel
fullDist	[bool] return full distribution of cycle length

Value

a named list of parameters in the model

Examples

```
getParameters(runCancerSim(1,1))
```

<code>getRadii</code>	<code>getRadii</code> <i>get the radius of each cell</i>
-----------------------	--

Description

`getRadii` get the radius of each cell

Usage

```
getRadii(model, time)
```

Arguments

<code>model</code>	A <code>CellModel</code>
<code>time</code>	time in model hours

Value

vector containing the radius of each cell at time

<code>interactivePlot</code>	<code>interactivePlot</code> <i>plots a CellModel and allows the user to control the plot with various commands</i>
------------------------------	---

Description

`interactivePlot` plots a `CellModel` and allows the user to control the plot with various commands

Usage

```
interactivePlot(model, time = 0)
```

Arguments

<code>model</code>	A <code>CellModel</code>
<code>time</code>	time in model hours

Value

plot a visual representation of cells that takes in command-line-like inputs, type 'h' for help and a list of all available commands

plotCells	plotCell <i>plots a CellModel at a given time</i>
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Description

plotCell plots a CellModel at a given time

Usage

```
plotCells(model, time)
```

Arguments

model	A CellModel
time	time in model hours

Value

plot a visual representation of cells

Examples

```
plotCells(runCancerSim(10,1), 1)
```

runCancerSim	runCancerSim <i>runs a cell-based model of cancer</i>
--------------	---

Description

runCancerSim runs a cell-based model of cancer

Usage

```
runCancerSim(initialNum, runTime, density = 0.01, cycleLengthDist = 12,
  inheritGrowth = FALSE, outputIncrement = 6, randSeed = 0,
  modelType = "DrasdoHohme2003", ...)
```

Arguments

initialNum	how many cells initially (integer)
runTime	how long the simulation runs (model hours)
density	the density the cells are seeded at, must be in (0,0.1]
cycleLengthDist	cycle time distribution
inheritGrowth	whether or not daughter cells have the same cycle-length as parents
outputIncrement	time increment to print status at
randSeed	seed for the model
modelType	the name of the cell-based model to use
...	model specific parameters (depends on modelType)

Details

This function provides a centralized R interface to run c++ code for cell-based models implemented in this package. Standard parameters, as well as model-specific parameters, are passed in to this function along with a model name. This function then runs the model and returns a CellModel object containing all the information from the model. This object can then be accessed with various functions designed to interact with the class. To see a list of available functions, there is a show() command implemented for CellModel objects.

Value

A CellModel containing all info from the model run

Examples

```
runCancerSim(1,4)
```

```
runDrasdoHohme          runDrasdoHohme runs the model based on Drasdo and Hohme (2003)
```

Description

runDrasdoHohme runs the model based on Drasdo and Hohme (2003)

Usage

```
runDrasdoHohme(initialNum, runTime, density, cycleLengthDist, inheritGrowth,
  outputIncrement, randSeed, ...)
```

Arguments

initialNum	how many cells initially
runTime	how long the simulation represents in realtime
density	the density the cells are seeded at
cycleLengthDist	cycle time distribution
inheritGrowth	whether or not daughter cells have the same cycle-length as parents
outputIncrement	time increment to print status at
randSeed	seed for the model
...	nG, epsilon parameters (specific to this model)

Details

This function calls the C++ implementation of the Drasdo and Hohme (2003) model.

Value

A CellModel containing all info from the model run

show, CellModel-method show *display summary of CellModel class*

Description

show display summary of CellModel class

Usage

```
## S4 method for signature 'CellModel'
show(object)
```

Arguments

object A CellModel Object

Value

shows all available functions and parameters of model

Examples

```
show(runCancerSim(1,1))
```

timeToRow	<i>timeToRow return the correct row in the mCells list corresponding to a given time</i>
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Description

timeToRow return the correct row in the mCells list corresponding to a given time

Usage

```
timeToRow(model, time)
```

Arguments

model A CellModel
time time in model hours

Value

corresponding row in mCells list

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