Package ‘CancerInSilico’

March 22, 2017

Type Package

Title An R interface for computational modeling of tumor progression

Version 1.0.0

Date 2016-06-01

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Description The CancerInSilico package provides an R interface for running mathematical models of tumor progresson. 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

RoxygenNote 5.0.1

NeedsCompilation yes

R topics documented:

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Description

Package: CellModel
Type: Package
Version: 0.99.0
Date: 2016-06-24
License: LGPL

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CellModel-class CellModel

Description

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

Slots

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
getAxisAngle

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

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

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
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

Description
getCycleLengths return the cycle lengths of each cells at time

Usage
getchCycleLengths(model, time)

Arguments
model a CellModel object
time time in model hours

Value
the cycle lengths of each cell at time

Examples
getchCycleLengths(runCancerSim(1,1), 1)
getDensity

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

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

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

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))
getRadii

getRadii get the radius of each cell

Description
getRadii get the radius of each cell

Usage
getRadii(model, time)

Arguments
  model  A CellModel
  time   time in model hours

Value
vector containing the radius of each cell at time

interactivePlot

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

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

Usage
interactivePlot(model, time = 0)

Arguments
  model  A CellModel
  time   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

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

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)
runDrasdoHohme

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)

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
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

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

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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