

# 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

**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

### Author(s)

Maintainer: Elana J. Fertig <ejfertig@jhmi.edu>, Thomas D. Sherman <tsherma4@jhu.edu>

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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

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getAxisAngle                      *getAxisAngle get the axis angle of each cell*

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**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

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

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

**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

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getNumberOfCells	getNumberOfCells <i>get the number of cells alive</i>
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**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>
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**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))
```

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

**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

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

**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

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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>
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---

**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)
```

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```
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*

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### 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))
```

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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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