Package: diffeRenTES (via r-universe)

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Title Computation of TES-Based Cell Differentiation Trees

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Description Computes the ATM (Attractor Transition Matrix) structure and the tree-like structure describing the cell differentiation process (based on the Threshold Ergodic Set concept introduced by Serra and Villani), starting from the Boolean networks with synchronous updating scheme of the 'BoolNet' R package. TESs (Threshold Ergodic Sets) are the mathematical abstractions that represent the different cell types arising during ontogenesis. TESs and the powerful model of biological differentiation based on Boolean networks to which it belongs have been firstly described in ``A Dynamical Model of Genetic Networks for Cell Differentiation'' Villani M, Barbieri A, Serra R (2011) A Dynamical Model of Genetic Networks for Cell Differentiation. PLOS ONE 6(3): e17703.

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Depends R (>= 3.3)

Imports BoolNet, DOT, igraph, tools

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

Encoding UTF-8

RoxygenNote 7.1.2

NeedsCompilation no

Repository CRAN

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Contents

`getATM` *Compute ATM*

Description

`getATM` returns the ATM (Attractor Transition Matrix) structure. The ATM computes the probability of a transition between the attractors of the Boolean network upon the introduction of noise in the form of a logic negation to each node of each state of each attractor, checking in which attractor the dynamics relaxes. The diagonal of the ATM accounts for attractor robustness, as diagonal values represent the probability of returning to the same attractor after a perturbation.

Usage

```
getATM(net, synchronous_attractors, MAX_STEPS_TO_FIND_ATTRACTORS = 1000)
```

Arguments

`net`	The Boolean network previously loaded with loadNetwork() of BoolNet package
`synchronous_attractors`	Synchronous attractors of the Boolean network
`MAX_STEPS_TO_FIND_ATTRACTORS`	Number of steps after that the dynamics after the perturbation gives up

Value

The output will be a named list containing the computed ATM structure, the number of the lost flips (i.e., the number of perturbations that have not reach another attractor within the provided MAX_STEPS_TO_FIND_ATTRACTORS), and lastly the attractors in two formats: the one returned by the BoolNet package (called decimal) and their binary translation (called binary).

Examples

```
net <- BoolNet::generateRandomNKNetwork(10, 2)
attractors <- BoolNet::getAttractors(net)
getATM(net, attractors)
```

`getTESs` *Compute TES*

Description

Creates a structure for constructing the TES as described in "A Dynamical Model of Genetic Networks for Cell Differentiation Villani M, Barbieri A, Serra R (2011) A Dynamical Model of Genetic Networks for Cell Differentiation. PLOS ONE 6(3): e17703. https://doi.org/10.1371/journal.pone.0017703"

Usage

```
getTESs(ATM)
```

Arguments

`ATM`	ATM structure as returned from the `getATM` method.

Value

The output will be a named list that contains the list of computed TESs, the noise thresholds at which they emerged and lastly the ATM structure.

Examples

```
net <- BoolNet::generateRandomNKNetwork(10, 2)
attractors <- BoolNet::getAttractors(net)
ATM <- getATM(net, attractors)
getTESs(ATM)
```

`saveDifferentiationTreeToFile` *Save the graphic representation of the differentiation tree.*

Description

`saveDifferentiationTreeToFile` saves the image of the computed differentiation tree into a file.

Usage

```
saveDifferentiationTreeToFile(TESs, filename)
```

Arguments

`TESs`	TES structure computed with `getTESs`.
`filename`	Defines the filename for exporting the image of the differentiation tree. The only file extension accepted is "svg", filenames omitting the extensions and those with other extensions will be forced to SVG format.

Value

None

Examples

```
net <- BoolNet::generateRandomNKNetwork(10, 2)
attractors <- BoolNet::getAttractors(net)
ATM <- getATM(net, attractors)
TESs <- getTESs(ATM)
saveDifferentiationTreeToFile(TESs, tempfile(tmpdir = tempdir(), fileext = ".svg"))
```

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