

Package ‘ctgGEM’

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Type Package

Title Generating Tree Hierarchy Visualizations from Gene Expression Data

Version 1.6.0

Description

Cell Tree Generator for Gene Expression Matrices (ctgGEM) streamlines the building of cell-state hierarchies from single-cell gene expression data across multiple existing tools for improved comparability and reproducibility. It supports pseudotemporal ordering algorithms and visualization tools from monocle, cellTree, TSCAN, sincell, and destiny, and provides a unified output format for integration with downstream data analysis workflows and Cytoscape.

VignetteBuilder knitr

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ctgGEMset	<i>The ctgGEMset class</i>
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Description

The main class used by the **cellTreeGenerator** package to hold single cell gene expression data and generated tree results. ctgGEMset extends the [SummarizedExperiment::SummarizedExperiment](#) class.

Usage

```
ctgGEMset(exprsData, phenoData = NULL, featureData = NULL)
```

Arguments

- exprsData expression data matrix for an experiment
- phenoData a data frame containing attributes of individual samples
- featureData a data frame containing attributes of features (genes)

Details

This class is initialized from a matrix of gene expression values and associated metadata. Methods that operate on ctgGEMset objects comprise the ctgGEM workflow.

Value

a new ctgGEMset object

Fields

monocleInfo A character vector of parameters used by `generate_tree(treeType = "monocle")` in the **cellTreeGenerator** workflow

TSCANInfo A character vector of the row name of a single gene in `exprsData()` to use for a single gene vs. pseudotime plot for `generate_tree(treeType = "TSCAN")` in the **cellTreeGenerator** workflow

sincellInfo A list containing named parameters used by `generate_tree(treeType = "sincell")` in the **cellTreeGenerator** workflow

treeList A list containing the simplified igraph representation of the trees generated by the **ctgGEM** workflow

originalTrees A list containing the trees generated by the **ctgGEM** workflow in their original formats for re-plotting

Examples

```
# load HSMMSingleCell package
library(HSMMSingleCell)

# load the data
data(HSMM_expr_matrix)
data(HSMM_sample_sheet)
data(HSMM_gene_annotation)

# construct a ctgGEMset
dataSet <- ctgGEMset(exprsData = HSMM_expr_matrix,
                    phenoData = HSMM_sample_sheet,
                    featureData = HSMM_gene_annotation)

# load HSMMSingleCell package
library(HSMMSingleCell)

# load the data
data(HSMM_expr_matrix)
data(HSMM_sample_sheet)
data(HSMM_gene_annotation)

# construct a ctgGEMset
dataSet <- ctgGEMset(exprsData = HSMM_expr_matrix,
                    phenoData = HSMM_sample_sheet,
                    featureData = HSMM_gene_annotation)
```

generate_tree

*Function to Generate Cell Trees***Description**

This function builds a cell hierarchy tree of a chosen supported type with a given data set, contained in a **ctgGEMset** object. Different tree types require data from corresponding slots of the **ctgGEMset** object. See vignette for examples, usage details, and instructions on building a **ctgGEMset** object.

Usage

```
generate_tree(dataSet, treeType, outputDir = NULL)
```

Arguments

dataSet	the ctgGEMset object for creating the cell tree
treeType	the type of tree generated
outputDir	the directory where output should be saved, defaults to the temporary location returned by tempdir()

Value

An updated ctgGEMset object. The generated tree is placed in @treeList[treeType] slot, and can be accessed via treeList(dataSet)\$treeType. The function also creates a directory named "treeType-Output" and writes the plot(s) of the generated tree(s) and its SIF file to that directory.

Examples

```
# load HSMMSingleCell package
library(HSMMSingleCell)

# load the data
data(HSMM_expr_matrix)
data(HSMM_sample_sheet)
data(HSMM_gene_annotation)

# construct a ctgGEMset
dataSet <- ctgGEMset(exprsData = HSMM_expr_matrix,
                     phenoData = HSMM_sample_sheet,
                     featureData = HSMM_gene_annotation)

TSCANinfo(dataSet) <- "ENSG00000000003.10"

# choose output directory
od <- getwd()
# run generate_tree()
dataSet <- generate_tree(dataSet = dataSet, treeType = "TSCAN",
                        outputDir = od)
```

plotOriginalTree

Display Original ctgGEM Plots

Description

Displays the original plots created by the ctgGEM package and stored in the [originalTrees](#) slot of a ctgGEMset object.

Usage

```
plotOriginalTree(dataSet, treeType)
```

Arguments

<code>dataSet</code>	a ctgGEMset object
<code>treeType</code>	the type of tree to display. Must be one of <code>names(originalTrees(dataSet))</code>

Value

a `ggplot2::ggplot` object.

Note

In order to reproduce original plots, the respective package(s) must be installed.

Examples

```
# load HSMMSingleCell package
library(HSMMSingleCell)

# load the data for TSCAN and monocle:
data(HSMM_expr_matrix)
data(HSMM_sample_sheet)
data(HSMM_gene_annotation)

# construct a ctgGEMset
dataSet <- ctgGEMset(exprsData = HSMM_expr_matrix,
                    phenoData = HSMM_sample_sheet,
                    featureData = HSMM_gene_annotation)

TSCANinfo(dataSet) <- "ENSG00000000003.10"

# run generate_tree()
dataSet <- generate_tree(dataSet = dataSet, treeType = "TSCAN")

# view names of original trees
names(originalTrees(dataSet))

# plot original trees
plotOriginalTree(dataSet, "TSCANclustering")
plotOriginalTree(dataSet, "TSCANsingleGene")
```

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