

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

License GPL(>=2)

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| ctgGEMset | <i>The ctgGEMset class</i> |
|-----------|----------------------------|

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

sinccellInfo A list containing named parameters used by `generate_tree(treeType = "sinccell")` 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) <- "ENSG0000000003.10"

# 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

```
dataSet      a ctgGEMset object  
treeType     the type of tree to display. Must be one of names(originalTrees(dataSet))
```

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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