

# Package ‘ctgGEM’

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**Type** Package

**Title** Generating Tree Hierarchy Visualizations from Gene Expression Data

**Version** 1.2.0

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## 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)

**Encoding** UTF-8

**LazyData** true

**biocViews** GeneExpression, Visualization, Sequencing, SingleCell, Clustering, RNASeq, ImmunoOncology, DifferentialExpression, MultipleComparison, QualityControl, DataImport

**RoxygenNote** 7.1.0

**Roxygen** list(markdown = TRUE)

**Depends** monocle, SummarizedExperiment,

**Imports** Biobase, BiocGenerics, graphics, grDevices, igraph, methods, utils, sincell, TSCAN, destiny, HSMMSingleCell

**Suggests** BiocStyle, biomaRt, irlba, knitr, VGAM

**Collate** 'ctgGEMset-class.R' 'ctgGEMset-methods.R' 'generate\_tree.R' 'makeDestiny.R' 'makeMonocle.R' 'makeSincell.R' 'makeTSCAN.R' 'plotOriginalTree.R' 'tree2igraph.R'

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## R topics documented:

ctgGEMset . . . . .	2
generate_tree . . . . .	3
plotOriginalTree . . . . .	4

<b>Index</b>	<b>6</b>
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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 <b>cellTreeGenerator</b> 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 <b>cellTreeGenerator</b> workflow
sincellInfo	A list containing named parameters used by generate_tree(treeType = "sincell") in the <b>cellTreeGenerator</b> workflow
treeList	A list containing the simplified igraph representation of the trees generated by the <b>ctgGEM</b> workflow
originalTrees	A list containing the trees generated by the <b>ctgGEM</b> 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)
```

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generate\_tree

*Function to Generate Cell Trees*

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## 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)
```

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plotOriginalTree      *Display Original ctgGEM Plots*

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## 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 <code>names(originalTrees(dataSet))</code>

## Value

For `treeType = "destinyDM"` and `treeType = "destinyDPT"`, returns NULL. For all other tree types, a `ggplot2::ggplot` object.

## Note

In order to reproduce original oncoNEM trees or destiny 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")
```

# Index

- \* **cell**
  - generate\_tree, 3
- \* **tree**
  - generate\_tree, 3
  - .ctgGEMset (ctgGEMset), 2
- ctgGEMset, 2
- ctgGEMset-class (ctgGEMset), 2
- generate\_tree, 3
- originalTrees, 4
- plotOriginalTree, 4
- SummarizedExperiment::SummarizedExperiment,  
2