

# Package ‘scTreeViz’

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**Type** Package

**Title** R/Bioconductor package to interactively explore and visualize single cell RNA-seq datasets with hierarchical annotations

**Version** 1.10.0

**Description** scTreeViz provides classes to support interactive data aggregation and visualization of single cell RNA-seq datasets with hierarchies for e.g. cell clusters at different resolutions. The `TreeIndex` class provides methods to manage hierarchy and split the tree at a given resolution or across resolutions. The `TreeViz` class extends `SummarizedExperiment` and can perform quick aggregations on the count matrix defined by clusters.

**License** Artistic-2.0

**Depends** R (>= 4.0), methods, epivizr, SummarizedExperiment

**Imports** data.table, S4Vectors, digest, Matrix, Rtsne, httr, igraph, clustree, scran, sys, epivizrData, epivizrServer, ggraph, scater, Seurat, SingleCellExperiment, ggplot2, stats, utils

**Suggests** knitr, BiocStyle, testthat, SC3, scRNAseq, rmarkdown, msd16s, metagenomeSeq, epivizrStandalone, GenomeInfoDb

**VignetteBuilder** knitr

**biocViews** Visualization, Infrastructure, GUI, SingleCell

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**RoxygenNote** 7.1.1

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.generate\_hierarchy\_tree

*generate hierarchy tree*

---

### Description

generate hierarchy tree

### Usage

```
.generate_hierarchy_tree(hierarchy, feature_order)
```

**Arguments**

hierarchy      hierarchy as a data.table  
feature\_order   order of the tree if different from colnames

**Value**

a data frame object

---

`.generate_leaf_of_table`  
*generate leaf of table*

---

**Description**

generate leaf of table

**Usage**

```
.generate_leaf_of_table(  
  hierarchy_tree,  
  node_ids_table,  
  nodes_table,  
  feature_order  
)
```

**Arguments**

hierarchy\_tree   hierarchy as a data.table  
node\_ids\_table   node ids  
nodes\_table      nodes table  
feature\_order    order of the tree if different from colnames

**Value**

a data frame object

---

`.generate_nodes_table` *generate nodes table tree*

---

**Description**

generate nodes table tree

**Usage**

```
.generate_nodes_table(hierarchy_tree, node_ids_table, feature_order)
```

**Arguments**

`hierarchy_tree` hierarchy as a `data.table`

`node_ids_table` node ids

`feature_order` order of the tree if different from `colnames`

**Value**

a data frame object

---

`.generate_node_ids` *generate node ids in the tree*

---

**Description**

generate node ids in the tree

**Usage**

```
.generate_node_ids(hierarchy_tree, feature_order)
```

**Arguments**

`hierarchy_tree` hierarchy as a `data.table`

`feature_order` order of the tree if different from `colnames`

**Value**

a data frame object

---

.replaceNAFeatures      *replace if there are NA's in the hierarchy*

---

**Description**

replace if there are NA's in the hierarchy

**Usage**

```
.replaceNAFeatures(replacing_na_obj_fData, feature_order)
```

**Arguments**

replacing\_na\_obj\_fData      hierarchy data table  
feature\_order      order of the tree if different from colnames

**Value**

a data frame object

---

ClusterHierarchy      *Creates a new ClusterHierarchy object.*

---

**Description**

Works as a validation check for multiple issues user passed dataframe might have. For example, multiple root nodes, incompatible naming, multiple parents of a single node, etc This function performs all this checks and tries to resolve the issues by making changes in cluster assignment User can give either col\_regex or columns option to filter the columns or specify the column order

**Usage**

```
ClusterHierarchy(hierarchy, col_regex = NULL, columns = NULL)
```

**Arguments**

hierarchy      hierarchy as a dataframe  
col\_regex      Regular Expression for choosing columns  
columns      Vector containing list of columns to choose from with ordering

**Value**

‘ClusterHierarchy‘ return an object of class ClusterHierarchy containing cluster information that ensures a valid dataframe for treviz input

**Examples**

```
n=64
# create a hierarchy
df<- data.frame(cluster0=rep(1,n))
for(i in seq(1,5)){
  df[[paste0("cluster",i)]]<- rep(seq(1:(2**i)),each=ceiling(n/(2**i)),len=n)
}
clus_hier<-ClusterHierarchy(df, col_regex = "clus")
```

---

**ClusterHierarchy-class***ClusterHierarchy class to manage treeviz cluster data*

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**Description**

ClusterHierarchy class to manage treeviz cluster data

---

**createFromSCE***Creates a ‘TreeViz‘ object from ‘SingleCellExperiment‘. Generates clusters based on Walktrap algorithm if no default is provided*

---

**Description**

Creates a ‘TreeViz‘ object from ‘SingleCellExperiment‘. Generates clusters based on Walktrap algorithm if no default is provided

**Usage**

```
createFromSCE(
  object,
  check_coldata = FALSE,
  col_regex = NULL,
  columns = NULL,
  reduced_dim = c("TSNE")
)
```

**Arguments**

object	‘SingleCellExperiment‘ object to be visualized
check_coldata	whether to colData of ‘SingleCellExperiment‘ object for cluster information or not
col_regex	common regular expression shared across all columns with cluster information
columns	vector containing columns with cluster information
reduced_dim	Vector of Dimensionality reduction information provided in ‘SingleCellExperiment‘ object to be added in ‘TreeViz‘ (if exists)

**Value**

‘TreeViz’ Object

**Examples**

```
library(SingleCellExperiment)
library(scater)
sce <- mockSCE()
sce <- logNormCounts(sce)
sce <- runTSNE(sce)
sce <- runUMAP(sce)
set.seed(1000)
for (i in seq_len(5)) {
  clust.kmeans <- kmeans(reducedDim(sce, "TSNE"), centers = i)
  sce[[paste0("clust", i)]] <- factor(clust.kmeans$cluster)
}
treeviz <- createFromSCE(sce, check_coldata = TRUE, col_regex = "clust", reduced_dim = c("TSNE", "UMAP"))
```

---

createFromSeurat	<i>Creates a ‘TreeViz’ object from ‘Seurat’</i>
------------------	---

---

**Description**

Creates a ‘TreeViz’ object from ‘Seurat’

**Usage**

```
createFromSeurat(
  object,
  check_metadata = FALSE,
  col_regex = "*snn*",
  columns = NULL,
  reduced_dim = c("TSNE")
)
```

**Arguments**

object	‘Seurat’ class containing cluster information at different resolutions
check_metadata	whether to metaData of ‘Seurat’ object for cluster information or not
col_regex	common regular expression shared across all columns with cluster information
columns	vector containing columns with cluster information
reduced_dim	Vector of Dimensionality reduction information provided in ‘Seurat’ object to be added in ‘TreeViz’ (if exists)

**Value**

‘TreeViz’ Object

**Examples**

```
library(Seurat)
data(pbmc_small)
pbmc <- pbmc_small
treeviz<- createFromSeurat(pbmc, check_metadata = TRUE, reduced_dim = c("pca","tsne"))
```

---

<code>createTreeViz</code>	<i>Creates 'TreeViz' object from hierarchy and count matrix</i>
----------------------------	---

---

**Description**

Provided with a count matrix and a dataframe or 'ClusterHierarchy' object, this module runs the necessary checks on the dataframe and tries to convert it to a tree by making necessary changes. Returns the 'TreeViz' object if a tree is successfully generated from dataframe, throws error otherwise

**Usage**

```
createTreeViz(clusters, counts)
```

**Arguments**

<code>clusters</code>	'ClusterHierarchy' object or a dataframe containing cluster information at different resolutions
<code>counts</code>	matrix Dense or sparse matrix containing the count matrix

**Value**

'TreeViz' Object

**Examples**

```
n=64
# create a hierarchy
df<- data.frame(cluster0=rep(1,n))
for(i in seq_len(5)){
  df[[paste0("cluster",i)]]<- rep(seq(1:(2**i)),each=ceiling(n/(2**i)),len=n)
}
# generate a count matrix
counts <- matrix(rpois(6400, lambda = 10), ncol=n, nrow=100)
colnames(counts)<- seq_len(64)
# create a `TreeViz` object
treeViz <- createTreeViz(df, counts)
```



---

EpivizTreeData-class *Data container for MRExperiment objects*

---

## Description

Used to serve hierarchical data (used in e.g., icycle plots and heatmaps).

## Methods

`df_to_tree(root, df)` Helper function to recursively build nested response for `getHierarchy`

**root** Root of subtree

**df** data.frame containing children to process

`get_default_chart_type()` Get name of default chart type for this data type

`get_measurements()` Get description of measurements served by this object

`getCombined( measurements = NULL, seqName, start = 1, end = 1000, order = NULL, nodeSelection = NULL, select`  
Return the counts aggregated to selected nodes for the given samples

**measurements** Samples to get counts for

**seqName** name of datasource

**start** Start of feature range to query

**end** End of feature range to query

**order** Ordering of nodes

**nodeSelection** Node-id and selectionType pairs

**selectedLevels** Current aggregation level

`getHierarchy(nodeId = NULL)` Retrieve feature hierarchy information for subtree with specified  
root

**nodeId** Feature identifier with level info

`getReducedDim(method = NULL, gene = NULL)` Compute PCA over all features for given samples

**method** which dimension to access

**gene** send expression of a gene back with the dimensions

`getRows( measurements = NULL, start = 1, end = 1000, selectedLevels = 3, selections = NULL )`

Return the sample annotation and features within the specified range and level for a given sam-  
ple and features

**measurements** Samples to retrieve for

**start** Start of feature range to query

**end** End of feature range to query

**selections** Node-id and selectionType pairs

**selectedLevels** Current aggregation level

`propagateHierarchyChanges( selection = NULL, order = NULL, selectedLevels = NULL, request_with_labels = F`  
Update internal state for hierarchy

**selection** Node-id and selectionType pairs

**order** Ordering of features

**selectedLevels** Current aggregation level  
**request\_with\_labels** For handling requests using fData entries from MRExperiment  
row\_to\_dict(row) Helper function to format each node entry for getHierarchy response  
**row** Information for current node.  
searchTaxonomy(query = NULL, max\_results = 15) Return list of features matching a text-based query  
**query** String of feature for which to search  
**max\_results** Maximum results to return

---

set\_gene\_list                    *Sets gene list for visualization*

---

### Description

Sets gene list for visualization

### Usage

```
set_gene_list(treeviz, genes)
```

### Arguments

treeviz	TreeViz object
genes	list of genes to use

### Value

TreeViz object set with gene list

---

show, TreeViz-method    *show object*

---

### Description

show object  
Method to aggregate a TreeViz object  
Method to aggregate a TreeViz object  
Generic method to register data to the epiviz data server  
plot tree from TreeViz

**Usage**

```
## S4 method for signature 'TreeViz'
show(object)

aggregateTree(x, ...)

## S4 method for signature 'TreeViz'
aggregateTree(
  x,
  selectedLevel = 3,
  selectedNodes = NULL,
  aggFun = colSums,
  start = 1,
  end = NULL,
  by = "row",
  format = "TreeViz"
)

## S4 method for signature 'TreeViz'
register(object, tree = "row", columns = NULL, ...)

## S4 method for signature 'TreeViz,ANY'
plot(x, y)
```

**Arguments**

object	The object to register to data server
x	treeviz object
...	Additional arguments passed to object constructors
selectedLevel	level to select nodes from
selectedNodes	used to set states on individual nodes to define a cut on the tree
aggFun	aggregate function to use, by default colSums if by="row", rowSums if by="col"
start, end	indices to filter nodes
by	"row" to aggregate the TreeIndex on rowData, "col" to aggregate TreeIndex on colData
format	return format can be one of "counts" or "TreeViz"
tree	Is tree over rows or columns of the object (default: "row")
columns	Name of columns containing data to register
y	none

**Value**

describe a TreeIndex object  
a generic

a Treeviz object or type specified by format

An [EpiVizTreeData-class](#) object

Dataframe containing cluster information at different resolutions

### Functions

- show, TreeViz-method:
- aggregateTree:
- aggregateTree, TreeViz-method:
- register, TreeViz-method:
- plot, TreeViz, ANY-method:

### Examples

```
library(metagenomeSeq)
data(mouseData)
counts <- MRcounts(mouseData)
hierarchy <- fData(mouseData)
tree <- TreeIndex(hierarchy)
mbiome <- TreeViz(SimpleList(counts=counts), rowData=tree)
aggregateTree(mbiome)
```

```
library(metagenomeSeq)
data(mouseData)
counts <- MRcounts(mouseData)
hierarchy <- fData(mouseData)
tree <- TreeIndex(hierarchy)
mbiome <- TreeViz(SimpleList(counts=counts), rowData=tree)
aggregateTree(mbiome)
```

```
library(metagenomeSeq)
data(mouseData)
counts <- MRcounts(mouseData)
hierarchy <- fData(mouseData)
tree <- TreeIndex(hierarchy)
mbiome <- TreeViz(SimpleList(counts=counts), rowData=tree)
plot(mbiome)
```

---

startTreeviz

*Start treeviz app and create [TreeVizApp](#) object to manage connection.*

---

### Description

Start treeviz app and create [TreeVizApp](#) object to manage connection.

**Usage**

```
startTreeviz(
  data = NULL,
  genes = NULL,
  top_genes = 100,
  host = "http://epiviz.cbcb.umd.edu/treeviz",
  register_function = .register_all_treeviz_things,
  delay = 2L,
  ...
)
```

**Arguments**

<code>data</code>	TreeViz object to explore
<code>genes</code>	(character vector) genes (rownames) to include in heatmap
<code>top_genes</code>	(integer) number of top variable genes to include in the heatmap
<code>host</code>	(character) host address to launch.
<code>register_function</code>	(function) function used to register actions and charts on the treeviz app.
<code>delay</code>	(integer) number of seconds to wait for application to load in browser
<code>...</code>	additional parameters passed to <a href="#">startEpiviz</a> .

**Value**

An object of class [TreeVizApp](#)

**See Also**

[TreeVizApp](#)

**Examples**

```
# see package vignette for example usage
app <- startTreeviz(non_interactive=TRUE, open_browser=FALSE)
app$stop_app()
```

---

TreeIndex	<i>create a new TreeIndex object</i>
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---

**Description**

create a new TreeIndex object

**Usage**

```
TreeIndex(hierarchy = NULL, feature_order = NULL)
```

**Arguments**

hierarchy      hierarchy as a data.table  
 feature\_order   order of the tree if different from colnames

**Value**

a 'TreeIndex' object

**Examples**

```
library(metagenomeSeq)
data(mouseData)
counts <- MRcounts(mouseData)
hierarchy <- fData(mouseData)
tree <- TreeIndex(hierarchy)
```

---

TreeIndex-class	<i>TreeIndex class to manage and query hierarchical data</i>
-----------------	--

---

**Description**

TreeIndex class to manage and query hierarchical data

---

TreeViz	<i>The TreeViz class.</i>
---------	---------------------------

---

**Description**

SummarizedExperiment-like class for datasets that have hierarchies on either rowData or colData. For microbiome data, rowData is a tree hierarchy For single cell data, colData is a tree hierarchy

**Usage**

```
TreeViz(assays = SimpleList(), rowData = NULL, colData = NULL, ...)
```

**Arguments**

assays            simple list of counts  
 rowData          rowData  
 colData          colData  
 ...              other parameters for SummarizedExperiment

**Value**

a 'TreeViz' object

**Examples**

```
library(metagenomeSeq)
data(mouseData)
counts <- MRcounts(mouseData)
hierarchy <- fData(mouseData)
tree <- TreeIndex(hierarchy)
mbiome <- TreeViz(SimpleList(counts=counts), rowData=tree)
```

TreeViz-class

*TreeViz class wrapper for SummarizedExperiment objects***Description**

TreeViz class wrapper for SummarizedExperiment objects

TreeVizApp-class

*Class managing connection to metaviz application.***Description**

Class managing connection to metaviz application.

**Methods**

plotGene(gene = NULL, datasource\_name = "SCRNA\_1") Plot a bar plot for a gene across cell types

**gene** gene to extract expression values

**datasource\_name** object to extract from (automatically selected)

[,TreeIndex,ANY,ANY,ANY-method

*Subset TreeIndex***Description**

Subset TreeIndex

Generic method to get nodes at a tree level

Method to get nodes at a tree level

Generic method for possible node states

Method to get possible node states a node state is 0 if removed, 1 if expanded to show children & 2 if counts are aggregated to the node

Generic method to split the tree

splitAt divides the TreeIndex into groups defined by the level, node selections and filters(start, end)

Show the TreeIndex object

**Usage**

```

## S4 method for signature 'TreeIndex,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

getNode(x, ...)

## S4 method for signature 'TreeIndex'
getNode(x, selectedLevel = NULL)

getNodeStates(x)

## S4 method for signature 'TreeIndex'
getNodeStates(x)

splitAt(x, ...)

## S4 method for signature 'TreeIndex'
splitAt(
  x,
  selectedLevel = 3,
  selectedNodes = NULL,
  start = 1,
  end = NULL,
  format = "list"
)

## S4 method for signature 'TreeIndex'
show(object)

```

**Arguments**

x	TreeIndex object
i, j	indices to subset or keep
...	other parameters
drop	drop the dimensions of the object. defaults to FALSE
selectedLevel	tree level to select nodes from
selectedNodes	used to set states on individual nodes to define a cut on the tree
start, end	indices to filter nodes by
format	return format can be one of "list" or "TreeIndex"
object	TreeIndex object

**Value**

a 'TreeIndex' subset object  
a generic



levels at node cut  
node state  
node states  
a generic  
a 'TreeIndex' object or type set in format  
object description of the 'TreeIndex' object

### Examples

```
library(metagenomeSeq)
data(mouseData)
counts <- MRcounts(mouseData)
hierarchy <- fData(mouseData)
tree <- TreeIndex(hierarchy)
getNodeS(tree)
library(metagenomeSeq)
data(mouseData)
counts <- MRcounts(mouseData)
hierarchy <- fData(mouseData)
tree <- TreeIndex(hierarchy)
getNodeS(tree)
```

```
library(metagenomeSeq)
data(mouseData)
counts <- MRcounts(mouseData)
hierarchy <- fData(mouseData)
tree <- TreeIndex(hierarchy)
splitAt(tree)
```

```
library(metagenomeSeq)
data(mouseData)
counts <- MRcounts(mouseData)
hierarchy <- fData(mouseData)
tree <- TreeIndex(hierarchy)
splitAt(tree)
```

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