

# Package ‘TreeSummarizedExperiment’

March 14, 2025

**Type** Package

**Title** TreeSummarizedExperiment: a S4 Class for Data with Tree Structures

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**Date** 2021-01-01

**Description** TreeSummarizedExperiment has extended SingleCellExperiment to include hierarchical information on the rows or columns of the rectangular data.

**Depends** R(>= 3.6.0), SingleCellExperiment, S4Vectors (>= 0.23.18), Biostrings

**License** GPL (>=2)

**Encoding** UTF-8

**LazyData** true

**biocViews** DataRepresentation, Infrastructure

**Imports** methods, BiocGenerics, utils, ape, rlang, dplyr, SummarizedExperiment, BiocParallel, IRanges, treeio

**VignetteBuilder** knitr

**Suggests** ggtree, ggplot2, BiocStyle, knitr, rmarkdown, testthat

**RoxygenNote** 7.1.1

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TreeSummarizedExperiment-package

*The TreeSummarizedExperiment package*

---

### Description

TreeSummarizedExperiment implement a class of the same name, which extends SingleCellExperiment to include hierarchical information on the rows or columns of the rectangular data.

### Details

It also includes an additional slot for storing reference sequences per feature.

### See Also

[TreeSummarizedExperiment](#) class

---

`.all_equal_in_list`     *test all elements in a list are equal*

---

### Description

test all elements in a list are equal

### Usage

```
.all_equal_in_list(x)
```

### Examples

```
## Not run:
l1 <- list(a = 1, b = 2, c = 3)
l2 <- list(a = 1, b = 1, c = 1)
.all_equal_in_list(l1)
.all_equal_in_list(l2)

## End(Not run)
```

---

```
.all_have_DNAStringSet
```

*test all TSEs have DNAStringSet in the referenceSeq slot*

---

**Description**

test all TSEs have DNAStringSet in the referenceSeq slot

**Usage**

```
.all_have_DNAStringSet(args)
```

---

```
.all_have_DNAStringSetList
```

*test all TSEs have DNAStringSetList in the referenceSeq slot*

---

**Description**

test all TSEs have DNAStringSetList in the referenceSeq slot

**Usage**

```
.all_have_DNAStringSetList(args)
```

---

```
.all_nonnull_in_list    all elements in the list are NULL
```

---

**Description**

all elements in the list are NULL

**Usage**

```
.all_nonnull_in_list(x)
```

---

```
.all_null_in_list      all elements in the list are NULL
```

---

**Description**

all elements in the list are NULL

**Usage**

```
.all_null_in_list(x)
```

---

`.any_null_in_list`      *Any element in the list is NULL*

---

**Description**

Any element in the list is NULL

**Usage**

`.any_null_in_list(x)`

---

`.auto_rename_list`      *rename a list automatically to avoid duplicated names*

---

**Description**

rename a list automatically to avoid duplicated names

**Usage**

`.auto_rename_list(x)`

---

`.bind_link_tree`      *bind links & trees when combine TSE*

---

**Description**

bind links & trees when combine TSE

**Usage**

`.bind_link_tree(x, args, drop.rowLinks, drop.colLinks, bind = "cbind")`

---

`.is_equal_link`      *The links & trees in the specified dim are consistent*

---

**Description**

The links & trees in the specified dim are consistent

**Usage**

`.is_equal_link(args, dim = "row")`

---

*.match\_phylo*                    *match a phylo to a list of phylo*

---

**Description**

match a phylo to a list of phylo

**Usage**

`.match_phylo(phy, phys)`

---

*.match\_phylo\_list*            *match a list of phylo (x.phys) against to a list of phylo (y.phys)*

---

**Description**

match a list of phylo (x.phys) against to a list of phylo (y.phys)

**Usage**

`.match_phylo_list(x.phys, y.phys)`

---

*.match\_x\_dupY*                    *convert char. indicator to num. indicator*

---

**Description**

This differs to match with that the duplicated values in dy are not ignored.

**Usage**

`.match_x_dupY(x, dy)`

**Arguments**

x                    A vector. The values to be matched.  
 dy                    A vector. The values to be matched agaist.

**Author(s)**

Ruizhu Huang

---

.name\_y\_with\_x            *name y with x*

---

**Description**

name y with x

**Usage**

```
.name_y_with_x(x, y)
```

**Examples**

```
## Not run:  
x <- letters[1:5]  
y <- 1:5  
.name_y_with_x(x, y)  
  
## End(Not run)
```

---

.numeric\_ij            *convert char. indicator to num. indicator*

---

**Description**

convert char. indicator to num. indicator

**Usage**

```
.numeric_ij(ij, x, dim = "row")
```

**Arguments**

ij	A character or numeric indicator on rows/columns of x
x	It provides row/col names for ij to be matched against.
dim	"row" or "col" to specify row/col names of x to be matched against.

**Author(s)**

Ruizhu Huang

---

.rbind\_refSeq            *rbind referenceSeq*

---

**Description**

rbind referenceSeq

**Usage**

```
.rbind_refSeq(args)
```

---

`.replace_link_tree_1d` *replace row/col links & trees*

---

**Description**

replace row/col links & trees

**Usage**

```
.replace_link_tree_1d(x, value, ij, dim = "row")
```

**Arguments**

x	A TSE with ij rows/cols to be replaced by value
value	A TSE to replace some rows/cols of x.
ij	A character or numeric vector to specify which rows/cols to be replaced.
dim	"row" or "col" to specify the dimension is in rows or columns

**Author(s)**

Ruizhu Huang

---

`.subset_leaf` *update dimLinks and dimTree (used in subsetByLeaf)*

---

**Description**

update dimLinks and dimTree (used in subsetByLeaf)

**Usage**

```
.subset_leaf(x, leaf, dim = "row", updateTree = TRUE)
```

**Author(s)**

Ruizhu Huang



---

.update\_whichTree      *update the 'whichTree' column in row/column link data*

---

### Description

update the 'whichTree' column in row/column link data

### Usage

```
.update_whichTree(x, y)
```

### Examples

```
## Not run:
(ld <- LinkDataFrame(nodeLab = letters[1:5],
                    nodeLab_alias = LETTERS[1:5],
                    nodeNum = 1:5,
                    isLeaf = TRUE,
                    whichTree = LETTERS[1:5],
                    right = 1:5))
newWhich <- setNames(letters[1:5], LETTERS[1:5])
.update_whichTree(ld, y = newWhich)

## End(Not run)
```

---

addLabel      *add labels to nodes of a tree*

---

### Description

addLabel label nodes of a tree (phylo object)

### Usage

```
addLabel(tree, label = NULL, on = c("all", "leaf", "internal"))
```

### Arguments

tree	A phylo object
label	A character vector to provide node labels. The label is passed to nodes that are sorted by their node number in ascending order. The default is NULL, nodes are labeled by adding a prefix Node_ to their node number.
on	Chosen from "all", "leaf", "internal". If "all", all nodes are labeled; if "leaf", leaves are labeled; if "internal", internal nodes are labeled.

### Value

a phylo object

**Author(s)**

Ruizhu Huang

**Examples**

```

data(tinyTree)
library(ggtree)

# PLOT tree
# The node labels are in orange texts and the node numbers are in blue
ggtree(tinyTree, branch.length = 'none')+
  geom_text2(aes(label = label), color = "darkorange",
             hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
             hjust = -0.5, vjust = 0.7)

# change labels
nodes <- showNode(tree = tinyTree, only.leaf = FALSE)
tt <- addLabel(tree = tinyTree, label = LETTERS[nodes],
              on = "all")

ggtree(tt, branch.length = 'none')+
  geom_text2(aes(label = label), color = "darkorange",
             hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
             hjust = -0.5, vjust = 0.7)

```

---

aggTSE

*Perform data aggregations based on the available tree structures*


---

**Description**

aggTSE aggregates values on the leaf nodes of a tree to a specific arbitrary level of the tree. The level is specified via the nodes of the tree. Users could decide on which dimension (row or column) and how should the aggregation be performed.

**Usage**

```

aggTSE(
  x,
  rowLevel = NULL,
  rowBlock = NULL,
  colLevel = NULL,
  colBlock = NULL,
  rowFun = sum,
  colFun = sum,
  whichRowTree = 1,
  whichColTree = 1,
  whichAssay = NULL,
  message = FALSE,
  rowDataCols,

```

```

    colDataCols,
    rowFirst = TRUE,
    BPPARAM = NULL
  )

```

## Arguments

x	A <code>TreeSummarizedExperiment</code> object.
rowLevel	A numeric (node numbers) or character (node labels) vector. It provides the level on the tree that data is aggregated to. The aggregation is on the row dimension. The default is <code>rowLevel = NULL</code> , and no aggregation is performed.
rowBlock	A column name in the <code>rowData</code> to separate the aggregation.
colLevel	A numeric (node numbers) or character (node labels) vector. It provides the level on the tree that data is aggregated to. The aggregation is on the column dimension. The default is <code>colLevel = NULL</code> , and no aggregation is performed.
colBlock	A column name in the <code>colData</code> to separate the aggregation.
rowFun	A function to be applied on the row aggregation. It's similar to the FUN in <a href="#">apply</a> .
colFun	A function to be applied on the col aggregation. It's similar to the FUN in <a href="#">apply</a> .
whichRowTree	A integer scalar or string indicating which row tree is used in the aggregation. The first row tree is used as default.
whichColTree	A integer scalar or string indicating which row tree is used in the aggregation. The first row tree is used as default.
whichAssay	A integer scalar or string indicating which assay of x to use in the aggregation. If <code>NULL</code> , all assay tables are used in aggregation.
message	A logical value. The default is <code>TRUE</code> . If <code>TRUE</code> , it will print out the running process.
rowDataCols	The <code>rowData</code> columns to include.
colDataCols	The <code>colData</code> columns to include.
rowFirst	<code>TRUE</code> or <code>FALSE</code> . If the aggregation is in both dims., it is performed firstly on the row dim for <code>rowFirst = TRUE</code> or on the column dim for <code>rowFirst = FALSE</code> .
BPPARAM	Default is <code>NULL</code> and the computation isn't run in parallel. To run computation parallelly, an optional <a href="#">BiocParallelParam</a> instance determining the parallel back-end to be used during evaluation, or a list of <a href="#">BiocParallelParam</a> instances, to be applied in sequence for nested calls to <b>BiocParallel</b> functions.

## Value

A [TreeSummarizedExperiment](#) object

## Author(s)

Ruizhu HUANG

## Examples

```

# assays data
set.seed(1)
toyTable <- matrix(rnbinom(20, size = 1, mu = 10), nrow = 5)
colnames(toyTable) <- paste(rep(LETTERS[1:2], each = 2),

```

```

      rep(1:2, 2), sep = "_")
rownames(toyTable) <- paste("entity", seq_len(5), sep = "")

toyTable

# the column data
colInf <- DataFrame(gg = c(1, 2, 3, 3),
                   group = rep(LETTERS[1:2], each = 2),
                   row.names = colnames(toyTable))

colInf

# the toy tree
library(ape)
set.seed(4)
treeC <- rtree(4)
treeC$node.label <- c("All", "GroupA", "GroupB")

library(ggtree)
ggtree(treeC, size = 2) +
  geom_text2(aes(label = node), color = "darkblue",
            hjust = -0.5, vjust = 0.7, size = 6) +
  geom_text2(aes(label = label), color = "darkorange",
            hjust = -0.1, vjust = -0.7, size = 6)

tse <- TreeSummarizedExperiment(assays = list(toyTable),
                               colData = colInf,
                               colTree = treeC,
                               colNodeLab = treeC$tip.label,
                               metadata = list(test = 1:4))

aggCol <- aggTSE(x = tse, colLevel = c("GroupA", "GroupB"),
                colFun = sum)

assays(aggCol)[[1]]

```

---

aggValue

---

*Perform data aggregations based on the available tree structures*


---

## Description

aggValue aggregates values on the leaf nodes of a tree to a specific arbitrary level of the tree. The level is specified via the nodes of the tree. Users could decide on which dimension (row or column) and how should the aggregation be performed.

## Usage

```

aggValue(
  x,
  rowLevel = NULL,
  rowBlock = NULL,
  colLevel = NULL,
  colBlock = NULL,

```

```

FUN = sum,
assay = NULL,
message = FALSE
)

```

### Arguments

x	A TreeSummarizedExperiment object.
rowLevel	A numeric (node numbers) or character (node labels) vector. It provides the level on the tree that data is aggregated to. The aggregation is on the row dimension. The default is rowLevel = NULL, and no aggregation is performed.
rowBlock	A column name in the rowData to separate the aggregation.
colLevel	A numeric (node numbers) or character (node labels) vector. It provides the level on the tree that data is aggregated to. The aggregation is on the column dimension. The default is colLevel = NULL, and no aggregation is performed.
colBlock	A column name in the colData to separate the aggregation.
FUN	A function to be applied on the aggregation. It's similar to the FUN in <a href="#">apply</a> .
assay	A integer scalar or string indicating which assay of x to use in the aggregation. If NULL, all assay tables are used in aggregation.
message	A logical value. The default is TRUE. If TRUE, it will print out the running process.

### Value

A TreeSummarizedExperiment object or a matrix. The output has the same class of the input x.

### Author(s)

Ruizhu HUANG

### See Also

[aggTSE](#)

---

asLeaf	<i>change internal nodes to leaf nodes</i>
--------	--

---

### Description

asLeaf updates a phylo tree by changing the specified internal nodes to leaf nodes. In other words, the descendant nodes of the specified internal nodes are removed.

### Usage

```
asLeaf(tree, node)
```

### Arguments

tree	A phylo object.
node	A numeric or character vector. It specifies internal nodes that are changed to leaves via their node labels or numbers.

**Value**

A phylo object.

**Examples**

```
library(ggtree)
data(tinyTree)
ggtree(tinyTree, ladderize = FALSE) +
  geom_text2(aes(label = label), color = "darkorange",
             hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
             hjust = -0.5, vjust = 0.7) +
  geom_highlight(node = 16) +
  geom_point2()

# remove the blue branch
NT1 <- asLeaf(tree = tinyTree, node = 16)

ggtree(NT1, ladderize = FALSE) +
  geom_text2(aes(label = label), color = "darkorange",
             hjust = -0.1, vjust = -0.7) +
  geom_point2()

# if mergeSingle = TRUE, the node (Node_17) is removed.
NT2 <- asLeaf(tree = tinyTree, node = c(15, 13))

ggtree(NT2, ladderize = FALSE) +
  geom_text2(aes(label = label), color = "darkorange",
             hjust = -0.1, vjust = -0.7) +
  geom_point2()
```

---

asPhylo

---

*Convert a data frame to a phylo object*


---

**Description**

asPhylo converts a data frame to a phylo object. Compared to toTree, asPhylo allows the output tree to have different number of nodes in paths connecting leaves to the root.

**Usage**

```
asPhylo(data, column_order = NULL, asNA = NULL)
```

**Arguments**

data	A data frame or matrix.
column_order	A vector that includes the column names of data to reorder columns of data. Default is NULL, the original order of data is kept.
asNA	This specifies strings that are considered as NA

**Details**

The last column is used as the leaf nodes

**Value**

a phylo object

**Author(s)**

Ruizhu Huang

**Examples**

```
library(ggtree)

# Example 0:
taxTab <- data.frame(R1 = rep("A", 5),
                    R2 = c("B1", rep("B2", 4)),
                    R3 = paste0("C", 1:5))
# Internal nodes: their labels are prefixed with colnames of taxTab
# e.g., R2:B2
taxTree <- asPhylo(data = taxTab)
ggtree(taxTree) +
  geom_text2(aes(label = label), color = "red", vjust = 1) +
  geom_nodepoint()

# (Below gives the same output as toTree)
taxTab$R1 <- paste0("R1:", taxTab$R1)
taxTab$R2 <- paste0("R2:", taxTab$R2)
taxTree <- asPhylo(data = taxTab)
# viz the tree
ggtree(taxTree) +
  geom_text2(aes(label = label), color = "red", vjust = 1) +
  geom_nodepoint()

# Example 1
df1 <- rbind.data.frame(c("root", "A1", "A2", NA),
                      c("root", "B1", NA, NA))
colnames(df1) <- paste0("L", 1:4)
tree1 <- asPhylo(df1)

ggtree(tree1, color = "grey") +
  geom_nodepoint() +
  geom_text2(aes(label = label), angle = 90,
            color = "red", vjust = 2,
            size = 4)

# Example 2
df2 <- data.frame(Group_1 = rep("Root", 11),
                 Group_2 = rep(c(13, 21), c(9, 2)),
                 Group_3 = rep(c(14, 18, "unknown"), c(5, 4, 2)),
                 Group_4 = rep(c(15, "unknown", 19, "unknown"), c(4, 1, 3, 3)),
                 Group_5 = rep(c(16, "unknown", 20, "unknown"), c(3, 2, 2, 4)),
                 Group_6 = rep(c(17, "unknown"), c(2, 9)),
                 LEAF = 1:11)
```

```

tree2 <- asPhylo(df2, asNA = "unknown")

ggtree(tree2, color = "grey") +
  geom_nodepoint() +
  geom_text2(aes(label = label), angle = 90,
             color = "red", vjust = 2,
             size = 4)

# Example 3
df3 <- df2
df3[10:11, 3] <- ""

tree3 <- asPhylo(df3, asNA = c("unknown", ""))

ggtree(tree3, color = "grey") +
  geom_nodepoint() +
  geom_text2(aes(label = label), angle = 90,
             color = "red", vjust = 2,
             size = 4)

```

---

changeTree

*Change the row or column tree*


---

## Description

changeTree changes a row or column tree in a TreeSummarizedExperiment object.

## Usage

```

changeTree(
  x,
  rowTree = NULL,
  rowNodeLab = NULL,
  colTree = NULL,
  colNodeLab = NULL,
  whichRowTree = 1,
  whichColTree = 1
)

```

## Arguments

x	A TreeSummarizedExperiment object
rowTree	A phylo object. A new row tree.
rowNodeLab	A character string. It provides the labels of nodes that the rows of assays tables corresponding to. If NULL (default), the row names of the assays tables are used.
colTree	A phylo object. A new column tree.
colNodeLab	A character string. It provides the labels of nodes that the columns of assays tables corresponding to. If NULL (default), the column names of the assays tables are used.
whichRowTree	Which row tree to be replaced? Default is 1 (the first tree in the rowTree slot).
whichColTree	Which column tree to be replaced? Default is 1 (the first tree in the colTree slot).



**Value**

A TreeSummarizedExperiment object

**Author(s)**

Ruizhu Huang

**Examples**

```
library(ape)
set.seed(1)
treeR <- ape::rtree(10)

# the count table
count <- matrix(rpois(160, 50), nrow = 20)
rownames(count) <- paste0("entity", 1:20)
colnames(count) <- paste("sample", 1:8, sep = "_")
# The sample information
sampC <- data.frame(condition = rep(c("control", "trt"),
                                each = 4),
                    gender = sample(x = 1:2, size = 8,
                                    replace = TRUE))

rownames(sampC) <- colnames(count)
# build a TreeSummarizedExperiment object
tse <- TreeSummarizedExperiment(assays = list(count),
                               colData = sampC,
                               rowTree = treeR,
                               rowNodeLab = rep(treeR$tip.label, each = 2))

treeR2 <- drop.tip(phy = treeR, tip = c("t10", "t9", "t8"))

# if rownames are not used in node labels of the tree, provide rowNodeLab
use <- changeTree(x = tse, rowTree = treeR2,
                 rowNodeLab = rep(treeR$tip.label, each = 2))

use

# if rownames are used in node labels of tree, rowNodeLab is not required.

rownames(tse) <- rep(treeR$tip.label, each = 2)
cse <- changeTree(x = tse, rowTree = treeR2)
cse
```

---

countLeaf

*count the number of leaf nodes*

---

**Description**

countLeaf calculates the number of leaves on a phylo tree.

**Usage**

```
countLeaf(tree)
```

**Arguments**

tree            A phylo object

**Value**

a numeric value

**Author(s)**

Ruizhu Huang

**Examples**

```
library(ggtree)

data(tinyTree)

ggtree(tinyTree, branch.length = 'none') +
  geom_text2(aes(label = label), hjust = -0.3) +
  geom_text2(aes(label = node), vjust = -0.8,
            hjust = -0.3, color = 'blue')

(n <- countLeaf(tinyTree))
```

---

countNode

*count the number of nodes*

---

**Description**

countNode calculates the number of nodes on a phylo tree.

**Usage**

```
countNode(tree)
```

**Arguments**

tree            A phylo object

**Value**

a numeric value

**Author(s)**

Ruizhu Huang



```

      R5 = paste0("E", 1:6))
detectLoop(tax_tab = df)

df <- data.frame(R1 = rep("A", 7),
                 R2 = c("B1", rep("B2", 4), "B3", "B3"),
                 R3 = c("C1", "C2", "C3", "", "", "", ""),
                 R4 = c("D1", "D2", "D3", "", "", "", ""),
                 R5 = paste0("E", 1:7))
detectLoop(tax_tab = df)

df <- data.frame(R1 = rep("A", 7),
                 R2 = c("B1", rep("B2", 4), "B3", "B3"),
                 R3 = c("C1", "C2", "C3", NA, NA, NA, NA),
                 R4 = c("D1", "D2", "D3", NA, NA, NA, NA),
                 R5 = paste0("E", 1:7))
detectLoop(tax_tab = df)

```

---

distNode	<i>Calculate the distance between any two nodes on the tree</i>
----------	---

---

## Description

distNode is to calculate the distance between any two nodes on a phylo tree

## Usage

```
distNode(tree, node)
```

## Arguments

tree	A phylo object.
node	A numeric or character vector of length two.

## Value

A numeric value.

## Examples

```

library(ggtree)
data(tinyTree)
ggtree(tinyTree) +
  geom_text2(aes(label = node), color = "darkorange",
             hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = branch.length), color = "darkblue",
             vjust = 0.7)

distNode(tree = tinyTree, node = c(10, 11))
distNode(tree = tinyTree, node = c(12, 13))
distNode(tree = tinyTree, node = c(13, 15))
distNode(tree = tinyTree, node = c(12, 14))

```

---

findAncestor	<i>Find the ancestors of specified nodes</i>
--------------	--

---

### Description

findAncestor finds the ancestor in the nth generation above specified nodes.

### Usage

```
findAncestor(tree, node, level, use.alias = FALSE)
```

### Arguments

tree	A phylo object
node	A vector of node numbers or node labels
level	A vector of numbers to define nth generation before the specified nodes
use.alias	A logical value, TRUE or FALSE. The default is FALSE, and the node label would be used to name the output; otherwise, the alias of node label would be used to name the output. The alias of node label is created by adding a prefix "alias_" to the node number.

### Value

A vector of nodes. The numeric value is the node number, and the vector name is the corresponding node label. If a node has no label, it would have NA as name when use.alias = FALSE, and have the alias of node label as name when use.alias = TRUE.

### Author(s)

Ruizhu Huang

### Examples

```
library(ggtree)
data(tinyTree)
ggtree(tinyTree, branch.length = 'none') +
  geom_text2(aes(label = label), color = "darkorange",
            hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
            hjust = -0.5, vjust = 0.7)

findAncestor(tree = tinyTree, node = c(18, 13), level = 1)
```

---

`findChild`*Find the children*

---

**Description**

`findChild` finds children of an internal node.

**Usage**

```
findChild(tree, node = 11, use.alias = FALSE)
```

**Arguments**

<code>tree</code>	A phylo object.
<code>node</code>	An internal node. It could be the node number or the node label.
<code>use.alias</code>	A logical value, TRUE or FALSE. The default is FALSE, and the node label would be used to name the output; otherwise, the alias of node label would be used to name the output. The alias of node label is created by adding a prefix "alias_" to the node number.

**Value**

A vector of nodes. The numeric value is the node number, and the vector name is the corresponding node label. If a node has no label, it would have NA as name when `use.alias = FALSE`, and have the alias of node label as name when `use.alias = TRUE`.

**Author(s)**

Ruizhu Huang

**Examples**

```
data(tinyTree)

library(ggtree)
ggtree(tinyTree) +
  geom_text2(aes(label = node), color = "darkblue",
             hjust = -0.5, vjust = 0.7) +
  geom_highlight(node = 17, fill = 'steelblue', alpha = 0.5) +
  geom_text2(aes(label = label), color = "darkorange",
             hjust = -0.1, vjust = -0.7)

(tips <- findChild(tree = tinyTree, node = 17))
```

---

findOS	<i>Find descendants (or offsprings)</i>
--------	---

---

### Description

findDescendant finds descendants of a node.

### Usage

```
findOS(tree, node, only.leaf = TRUE, self.include = FALSE, use.alias = FALSE)
```

```
findDescendant(
  tree,
  node,
  only.leaf = TRUE,
  self.include = FALSE,
  use.alias = FALSE
)
```

### Arguments

tree	A phylo object.
node	An internal node. It could be the node number or the node label.
only.leaf	A logical value, TRUE or FALSE. The default is TRUE. If default, only the leaf nodes in the descendant nodes would be returned.
self.include	A logical value, TRUE or FALSE. The default is FALSE. If TRUE, the node specified in <b>node</b> is included and the leaf node itself is returned as its descendant.
use.alias	A logical value, TRUE or FALSE. The default is FALSE, and the node label would be used to name the output; otherwise, the alias of node label would be used to name the output. The alias of node label is created by adding a prefix "alias_" to the node number.

### Value

A vector of nodes. The numeric value is the node number, and the vector name is the corresponding node label. If a node has no label, it would have NA as name when use.alias = FALSE, and have the alias of node label as name when use.alias = TRUE.

### Author(s)

Ruizhu Huang

### Examples

```
data(tinyTree)

library(ggtree)
ggtree(tinyTree) +
  geom_text2(aes(label = node), color = "darkblue",
             hjust = -0.5, vjust = 0.7) +
  geom_highlight(node = 17, fill = 'steelblue', alpha = 0.5) +
```

```
geom_text2(aes(label = label), color = "darkorange",
           hjust = -0.1, vjust = -0.7)

(tips <- findDescendant(tree = tinyTree, node = c(17), only.leaf = TRUE))
```

---

findSibling	<i>find the sibling node</i>
-------------	------------------------------

---

### Description

findSibling is to find the sibling node of an node node.

### Usage

```
findSibling(tree, node, use.alias = FALSE)
```

### Arguments

tree	A phylo object.
node	A numeric or character vector. Node labels or node numbers.
use.alias	A logical value, TRUE or FALSE. The default is FALSE, and the original node label would be used to name the output; otherwise, the alias of node label would be used to name the output. The alias of node label is created by adding a prefix "alias_" to the node number.

### Value

A vector of nodes. The numeric value is the node number, and the vector name is the corresponding node label. If a node has no label, it would have NA as name when use.alias = FALSE, and have the alias of node label as name when use.alias = TRUE.

### Examples

```
library(ggtree)
data(tinyTree)
ggtree(tinyTree, branch.length = 'none') +
  geom_text2(aes(label = label), color = "darkorange",
            hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
            hjust = -0.5, vjust = 0.7)

findSibling(tree = tinyTree, node = 17)
findSibling(tree = tinyTree, node = c(13, 17))
```



---

isLeaf	<i>To test whether the specified nodes are leaf nodes</i>
--------	---

---

**Description**

isLeaf is to test whether some specified nodes are leaf nodes of a tree.

**Usage**

```
isLeaf(tree, node)
```

**Arguments**

tree	A phylo object.
node	A numeric or character vector. Node labels or node numbers.

**Value**

a logical vector with the same length as the input node.

**Author(s)**

Ruizhu HUANG

**Examples**

```
data(tinyTree)
library(ggtree)

# PLOT tree
# The node labels are in orange texts and the node numbers are in blue
ggtree(tinyTree,branch.length = 'none')+
  geom_text2(aes(label = label), color = "darkorange",
             hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
             hjust = -0.5, vjust = 0.7)

isLeaf(tree = tinyTree, node = c(5, 4, 18))
isLeaf(tree = tinyTree, node = c("t4", "t9", "Node_18" ))
```

---

LinkDataFrame-class	<i>LinkDataFrame: A S4 class extended from DataFrame An S4 class LinkDataFrame</i>
---------------------	--

---

**Description**

The **LinkDataFrame** is extended from the class **DataFrame** to include at least four columns: nodeLab, nodeLab\_alias, nodeNum, and isLeaf.

**Constructor**

See [LinkDataFrame-constructor](#) for constructor functions.

LinkDataFrame-constructor

*Construct a LinkDataFrame Construct a LinkDataFrame object*

---

## Description

Construct a LinkDataFrame Construct a LinkDataFrame object

## Usage

```
LinkDataFrame(nodeLab, nodeLab_alias, nodeNum, isLeaf, whichTree, ...)
```

## Arguments

nodeLab	A character vector
nodeLab_alias	A character vector
nodeNum	A numeric vector
isLeaf	A logical vector
whichTree	A character vector
...	All arguments accepted by <a href="#">DataFrame-class</a> .

## Value

A LinkDataFrame object

## See Also

[LinkDataFrame](#) [DataFrame](#)

## Examples

```
(ld <- LinkDataFrame(nodeLab = letters[1:5],
  nodeLab_alias = LETTERS[1:5],
  nodeNum = 1:5,
  isLeaf = TRUE,
  whichTree = LETTERS[1:5],
  right = 1:5))
```

---

makeTSE	<i>A toy TreeSummarizedExperiment object</i>
---------	--

---

## Description

makeTSE creates a toy TreeSummarizedExperiment object.

## Usage

```
makeTSE(nrow = 10, ncol = 4, include.rowTree = TRUE, include.colTree = TRUE)
```

## Arguments

nrow	a numeric value to specify the number of rows of TreeSummarizedExperiment
ncol	a numeric value to specify the number of columns of TreeSummarizedExperiment
include.rowTree	TRUE or FALSE. Default is TRUE, so the output TreeSummarizedExperiment has a phylo object in rowTree.
include.colTree	TRUE or FALSE. Default is TRUE, so the output TreeSummarizedExperiment has a phylo object in colTree.

## Details

The assays contains a matrix with values from 1:(nrow\*ncol). The rowData has two columns, var1 and var2. var1 is created with rep\_len(letters, nrow). var2 is created with rep\_len(c(TRUE, FALSE), nrow). The colData has two columns, ID and group. ID is created with seq\_len(ncol). group is created with rep\_len(LETTERS[1:2], ncol). The row/col tree is generated with ape::rtree(). So, to generate reproducible trees, set.seed() is required.

## Value

A TreeSummarizedExperiment object

## Author(s)

Ruizhu Huang

## Examples

```
set.seed(1)
makeTSE()
```

---

matTree	<i>Transform a phylo object into a matrix.</i>
---------	--

---

**Description**

matTree transforms a phylo tree into a matrix. The entry of the matrix is node number. Each row represents a path connecting a leaf node and the root. The columns are arranged in the order as the path passing the nodes to reach the root.

**Usage**

```
matTree(tree)
```

**Arguments**

tree	A phylo object
------	----------------

**Value**

A matrix

**Author(s)**

Ruizhu Huang

**Examples**

```
library(ggtree)

data(tinyTree)
ggtree(tinyTree, branch.length = 'none') +
  geom_text2(aes(label = node))

# each row of the matrix representing a path.
# the first column is leaf nodes; the last non-NA value in a row is the root
mat <- matTree(tree = tinyTree)
```

---

phylo	<i>phylo: A S3 class for the phylogenetic tree</i>
-------	--

---

**Description**

The **ape** package does not export its phylo class, probably because it is not really defined formally anywhere. Technically, it is an S3 class extended from the class list. Any exported definitions from the **ape** package would be preferred to use if available.

**Usage**

```
phylo
```

**Format**

An object of class phylo of length 0.

---

printNode	<i>To print out the node labels</i>
-----------	-------------------------------------

---

**Description**

nodeLabel is to print out the node labels of a phylo tree.

**Usage**

```
printNode(tree, type = c("leaf", "internal", "all"))
```

**Arguments**

tree	A phylo object.
type	A character value choose from leaf, all, and internal. If leaf, the output is a data frame including only leaf nodes; if internal, the output is a data frame including only internal nodes; if all, the output is a data frame including all nodes.

**Value**

a data frame

**Author(s)**

Ruizhu HUANG

**Examples**

```
data(tinyTree)
library(ggtree)

# PLOT tree
# The node labels are in orange texts and the node numbers are in blue
ggtree(tinyTree,branch.length = 'none')+
  geom_text2(aes(label = label), color = "darkorange",
            hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
            hjust = -0.5, vjust = 0.7)

(pn1 <- printNode(tinyTree, type = "leaf"))
(pn2 <- printNode(tinyTree, type = "internal"))
(pn3 <- printNode(tinyTree, type = "all"))
```

---

rbind,TreeSummarizedExperiment-method  
*Combine TSEs by rows or columns*

---

### Description

rbind and cbind take one or more TreeSummarizedExperiment objects and combine them by columns or rows, respectively.

### Usage

```
## S4 method for signature 'TreeSummarizedExperiment'  
rbind(..., deparse.level = 1)  
  
## S4 method for signature 'TreeSummarizedExperiment'  
cbind(..., deparse.level = 1)
```

### Arguments

... One or more TreeSummarizedExperiment objects.  
deparse.level See [cbind](#)

### Value

A TreeSummarizedExperiment object

### Author(s)

Ruizhu Huang

### Examples

```
# rbind works :  
# a) TSE without rowTree and without colTree  
# b) TSE with rowTree but without colTree  
# c) TSE without rowTree but with colTree  
# d) TSE with rowTree & colTree  
  
set.seed(1)  
# a)  
(tse_a <- makeTSE(include.colTree = FALSE))  
(tse_b <- makeTSE(include.colTree = FALSE))  
  
# b)  
(tse_c <- makeTSE(include.rowTree = FALSE))  
(tse_d <- makeTSE(include.rowTree = FALSE))  
  
rbind(tse_a, tse_b)  
cbind(tse_c, tse_d)
```

---

resolveLoop	<i>Resolve loops resolveLoop resolve loops by adding suffix to the child node. The suffix is "_i" where 'i' is a number. Please see examples.</i>
-------------	---

---

## Description

Resolve loops resolveLoop resolve loops by adding suffix to the child node. The suffix is "\_i" where 'i' is a number. Please see examples.

## Usage

```
resolveLoop(tax_tab)
```

## Arguments

`tax_tab` a data frame where columns store hierarchical levels. The columns from the left to the right correspond nodes from the root to the leaf.

## Value

a data frame

## Author(s)

Ruizhu Huang

## Examples

```
# example 1
df <- data.frame(A = rep("a", 8),
                 B = rep(c("b1", "b2", "b3", "b4"), each = 2),
                 C = paste0("c", c(1, 2, 2, 3:7)),
                 D = paste0("d", 1:8))

# The result means that a loop is caused by 'b1' and 'b2' in column 'B' and
# 'c2' in column 'C' (a-b1-c2; a-b2-c2)
resolveLoop(tax_tab = df)

# example 2
taxTab <- data.frame(R1 = rep("A", 5),
                    R2 = c("B1", rep("B2", 3), ""),
                    R3 = c("C1", "C2", "C3", "", ""),
                    R4 = c("D1", "D2", "D3", "", ""),
                    R5 = paste0("E", 1:5))

resolveLoop(tax_tab = taxTab)

# example 3
taxTab <- data.frame(R1 = rep("A", 6),
                    R2 = c("B1", rep("B2", 4), ""),
                    R3 = c("C1", "C2", "C3", "", "", ""),
                    R4 = c("D1", "D2", "D3", "", "", ""),
                    R5 = paste0("E", 1:6))

resolveLoop(tax_tab = taxTab)
```

```
# example 3
taxTab <- data.frame(
  R1 = rep("A", 5),
  R2 = c("B1", rep("B2", 3), "B3"),
  R3 = c("C1", "C2", "C3", NA, NA),
  R4 = c("D1", "D2", "D3", NA, NA),
  R5 = paste0("E", 1:5)
)
resolveLoop(tax_tab = taxTab)
```

---

rowLinks

*TreeSummarizedExperiment-accessors*


---

### Description

All accessor functions that work on [SingleCellExperiment](#) should work on **TreeSummarizedExperiment**. Additionally, new accessors `rowLinks`, `colLinks`, `rowTree` and `colTree` accessor function are available for **TreeSummarizedExperiment**.

### Usage

```
rowLinks(x)

## S4 method for signature 'TreeSummarizedExperiment'
rowLinks(x)

colLinks(x)

## S4 method for signature 'TreeSummarizedExperiment'
colLinks(x)

rowTree(x, whichTree = 1, value)

## S4 method for signature 'TreeSummarizedExperiment'
rowTree(x, whichTree = 1, value)

rowTree(x, whichTree = 1) <- value

## S4 replacement method for signature 'TreeSummarizedExperiment'
rowTree(x, whichTree = 1) <- value

colTree(x, whichTree = 1)

## S4 method for signature 'TreeSummarizedExperiment'
colTree(x, whichTree = 1)

colTree(x, whichTree = 1) <- value

## S4 replacement method for signature 'TreeSummarizedExperiment'
colTree(x, whichTree = 1) <- value
```



```
rowTreeNames(x, value)

## S4 method for signature 'TreeSummarizedExperiment'
rowTreeNames(x, value)

rowTreeNames(x) <- value

## S4 replacement method for signature 'TreeSummarizedExperiment'
rowTreeNames(x) <- value

colTreeNames(x, value)

## S4 method for signature 'TreeSummarizedExperiment'
colTreeNames(x, value)

colTreeNames(x) <- value

## S4 replacement method for signature 'TreeSummarizedExperiment'
colTreeNames(x) <- value

referenceSeq(x)

## S4 method for signature 'TreeSummarizedExperiment'
referenceSeq(x)

referenceSeq(x) <- value

## S4 replacement method for signature 'TreeSummarizedExperiment'
referenceSeq(x) <- value

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

## S4 replacement method for signature
## 'TreeSummarizedExperiment,ANY,ANY,TreeSummarizedExperiment'
x[i, j, ...] <- value

## S4 replacement method for signature 'TreeSummarizedExperiment'
rownames(x) <- value

## S4 replacement method for signature 'TreeSummarizedExperiment'
colnames(x) <- value

subsetByLeaf(
  x,
  rowLeaf,
  colLeaf,
  whichRowTree,
  whichColTree,
  updateTree = TRUE
)
```

```
## S4 method for signature 'TreeSummarizedExperiment'
subsetByLeaf(
  x,
  rowLeaf,
  colLeaf,
  whichRowTree,
  whichColTree,
  updateTree = TRUE
)

subsetByNode(x, rowNode, colNode, whichRowTree, whichColTree)

## S4 method for signature 'TreeSummarizedExperiment'
subsetByNode(x, rowNode, colNode, whichRowTree, whichColTree)
```

### Arguments

x	A <code>TreeSummarizedExperiment</code> object
whichTree	A numeric indicator or name character to specify which tree in the <code>rowTree</code> or <code>colTree</code> to be extracted. The default is to extract the first tree. If <code>whichTree = NULL</code> , a list of all trees is extracted.
value	<ul style="list-style-type: none"> <li>the new rownames or colnames as a character value. See <a href="#">BiocGenerics</a>.</li> <li>A <code>DNAStrngSet</code> object or an object coercible to one</li> </ul>
i, j	The row, column index to subset x. The arguments of the subset function <code>[]</code>
...	The argument from the subset function <code>[]</code>
drop	A logical value, <code>TRUE</code> or <code>FALSE</code> . The argument from the subset function <code>[]</code>
rowLeaf	A vector of leaves that are used to subset rows. One could use the leaf number, or the leaf label to specify nodes, but not a mixture of them.
colLeaf	A vector of leaves that are used to subset columns. One could use the leaf number, or the leaf label to specify nodes, but not a mixture of them.
whichRowTree	A numeric indicator or name character to specify which tree in the <code>rowTree</code> .
whichColTree	A numeric indicator or name character to specify which tree in the <code>colTree</code> .
updateTree	<code>TRUE</code> or <code>FALSE</code> . Default is <code>TRUE</code> , which updates tree structures after subsetting.
rowNode	A vector of nodes that are used to subset rows. One could use the node number, the node label or the node alias to specify nodes, but not a mixture of them.
colNode	A vector of nodes that are used to subset columns. One could use the node number, the node label or the node alias to specify nodes, but not a mixture of them.

### Value

Elements from `TreeSummarizedExperiment`.

### Author(s)

Ruizhu HUANG

**See Also**

[TreeSummarizedExperiment](#) [SingleCellExperiment](#)

**Examples**

```
# the assay table
set.seed(1)
y <- matrix(rnbinom(300,size=1,mu=10),nrow=10)
colnames(y) <- paste(rep(LETTERS[1:3], each = 10), rep(1:10,3), sep = "_")
rownames(y) <- tinyTree$tip.label

# the row data
rowInf <- DataFrame(var1 = sample(letters[1:3], 10, replace = TRUE),
                   var2 = sample(c(TRUE, FALSE), 10, replace = TRUE))

# the column data
colInf <- DataFrame(gg = factor(sample(1:3, 30, replace = TRUE)),
                   group = rep(LETTERS[1:3], each = 10))

# the tree structure on the rows of assay tables
data("tinyTree")

# the tree structure on the columns of assay tables
sampTree <- ape::rtree(30)
sampTree$tip.label <- colnames(y)

# create the TreeSummarizedExperiment object
toy_tse <- TreeSummarizedExperiment(assays = list(y),
                                   rowData = rowInf,
                                   colData = colInf,
                                   rowTree = tinyTree,
                                   colTree = sampTree)

## extract the rowData
(rowD <- rowData(x = toy_tse))

## extract the colData
(colD <- colData(x = toy_tse))

## extract the linkData
# on rows
(rowL <- rowLinks(x = toy_tse))
# on columns
(colL <- colLinks(x = toy_tse))

## extract the treeData
# on rows
(rowT <- rowTree(x = toy_tse))
# on columns
(colT <- colTree(x = toy_tse))

# the referenceSeq data
refSeq <- DNASTringSetList(one = DNASTringSet(rep("A",nrow(toy_tse))),
                          two = DNASTringSet(rep("B",nrow(toy_tse))))
referenceSeq(toy_tse) <- refSeq
toy_tse
```

```

# subset treeSE by leaves
library(ape)
set.seed(1)
z <- makeTSE(nrow = 5, ncol = 4, include.rowTree = TRUE, include.colTree = FALSE)
y <- makeTSE(nrow = 4, ncol = 4, include.rowTree = TRUE, include.colTree = FALSE)
tr <- ape::rtree(4)
zy <- rbind(z, y)
x <- changeTree(x = zy, rowTree = tr, whichRowTree = 2, rowNodeLab = tr$tip.label)
rowLinks(zy)
rowLinks(x)
## 1) rowLeaf exist only in one of trees
rf <- c("t1", "t3")
sx <- subsetByLeaf(x = x, rowLeaf = rf)
rowLinks(sx)

sx <- subsetByLeaf(x = x, rowLeaf = rf, updateTree = FALSE)
rowLinks(sx)

## 2) rowLeaf exist in all trees
rf <- 1:3
sxx <- subsetByLeaf(x = x, rowLeaf = rf)
rowLinks(sxx)

## 3) rowLeaf exist in all trees, but subset and update only the specified
trees
rf <- c(3:4)
sxx <- subsetByLeaf(x = x, rowLeaf = rf, whichRowTree = "phylo")
rowLinks(sxx)

```

---

shareNode

*Find the share node*


---

## Description

shareNode is to find the node where the specified nodes first meet.

## Usage

```
shareNode(tree, node, use.alias = FALSE)
```

## Arguments

tree	A phylo object.
node	A vector of node numbers or node labels.
use.alias	A logical value, TRUE or FALSE. The default is FALSE, and the node label would be used to name the output; otherwise, the alias of node label would be used to name the output. The alias of node label is created by adding a prefix "alias_" to the node number.

**Value**

A vector of nodes. The numeric value is the node number, and the vector name is the corresponding node label. If a node has no label, it would have NA as name when `use.alias = FALSE`, and have the alias of node label as name when `use.alias = TRUE`.

**Author(s)**

Ruizhu Huang

**Examples**

```
library(ggtree)
data(tinyTree)

# PLOT tree
ggtree(tinyTree, branch.length = 'none') +
  geom_text2(aes(label = label), color = "darkorange",
    hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
    hjust = -0.5, vjust = 0.7)

## find the node shared by provided node labels
shareNode(node = c('t4','t9'), tree = tinyTree,
  use.alias = FALSE)

shareNode(node = c('t10','Node_17'), tree = tinyTree,
  use.alias = FALSE)

## find the node shared by provided node numbers
shareNode(node = c(2, 3), tree = tinyTree)
```

---

showNode

*Find nodes on the tree*

---

**Description**

showNode is to get nodes from the tree.

**Usage**

```
showNode(tree, only.leaf = FALSE, use.alias = FALSE)
```

**Arguments**

tree	A phylo object.
only.leaf	A logical value, TRUE or FALSE. The default is FALSE, all nodes are output; otherwise, leaves are output
use.alias	A logical value, TRUE or FALSE. The default is FALSE, and the node label would be used to name the output; otherwise, the alias of node label would be used to name the output. The alias of node label is created by adding a prefix "alias_" to the node number.

**Value**

A vector of nodes. The numeric value is the node number, and the vector name is the corresponding node label. If a node has no label, it would have NA as name when `use.alias = FALSE`, and have the alias of node label as name when `use.alias = TRUE`.

**Author(s)**

Ruizhu Huang

**Examples**

```
library(ggtree)
data(tinyTree)

# PLOT tree
ggtree(tinyTree, branch.length = 'none') +
  geom_text2(aes(label = label), color = "darkorange",
             hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
             hjust = -0.5, vjust = 0.7)

## find the node shared by provided node labels
showNode(tree = tinyTree, only.leaf = TRUE,
         use.alias = FALSE)

showNode(tree = tinyTree, only.leaf = FALSE,
         use.alias = FALSE)
```

---

signalNode

*Join nodes*

---

**Description**

`joinNode` is to use as few as possible nodes to represent the provided nodes so that descendant leaves covered by the input nodes and output nodes are exactly the same.

**Usage**

```
signalNode(tree, node, use.alias = FALSE)
```

```
joinNode(tree, node, use.alias = FALSE)
```

**Arguments**

<code>tree</code>	A tree (phylo object)
<code>node</code>	A vector of node numbers or node labels
<code>use.alias</code>	A logical value, TRUE or FALSE. The default is FALSE, and the node label would be used to name the output; otherwise, the alias of node label would be used to name the output. The alias of node label is created by adding a prefix "alias_" to the node number.

**Value**

A vector of nodes. The numeric value is the node number, and the vector name is the corresponding node label. If a node has no label, it would have NA as name when `use.alias = FALSE`, and have the alias of node label as name when `use.alias = TRUE`.

**Author(s)**

Ruizhu Huang

**Examples**

```
data(tinyTree)
library(ggtree)

# PLOT tree
# The node labels are in orange texts and the node numbers are in blue
ggtree(tinyTree,branch.length = 'none')+
  geom_text2(aes(label = label), color = "darkorange",
            hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
            hjust = -0.5, vjust = 0.7)

## find the node shared by provided node labels
joinNode(node = c('t4','t9'), tree = tinyTree)
joinNode(node = c('t4','t9'), tree = tinyTree)
joinNode(node = c('t10','Node_18', 't8'),
         tree = tinyTree,
         use.alias = FALSE)
joinNode(node = c('t10','Node_18', 't8'),
         tree = tinyTree,
         use.alias = TRUE)

## find the node shared by provided node numbers
joinNode(node = c(2, 3), tree = tinyTree)
joinNode(node = c(2, 3, 16), tree = tinyTree)
```

---

tinyTree

*A simulated phylogenetic tree with 10 tips and 9 internal nodes*

---

**Description**

A random phylo object created using the function [rtree](#)

**Usage**

```
tinyTree
```

**Format**

A phylo object with 10 tips and 9 internal nodes:

**Tip labels** t1, t2, ..., t10.

**Node labels** Node\_11, Node\_12, ..., Node\_19

---

`toTree`*Translate a data frame to a phylo object*

---

**Description**

`toTree` translates a data frame to a phylo object

**Usage**

```
toTree(data, column_order = NULL)
```

**Arguments**

<code>data</code>	A data frame or matrix.
<code>column_order</code>	A vector that includes the column names of data to reorder columns of data. Default is <code>NULL</code> , the original order of data is kept.

**Details**

The last column is used as the leaf nodes

**Value**

a phylo object

**Author(s)**

Ruizhu HUANG

**Examples**

```
library(ggtree)
# Example 1:
taxTab <- data.frame(R1 = rep("A", 5),
                    R2 = c("B1", rep("B2", 4)),
                    R3 = paste0("C", 1:5))
# Internal nodes: their labels are prefixed with colnames of taxTab
# e.g., R2:B2
tree <- toTree(data = taxTab)
# viz the tree
ggtree(tree) +
  geom_text2(aes(label = label), color = "red", vjust = 1) +
  geom_nodepoint()

# Example 2: duplicated rows in the 3rd and 4th rows
taxTab <- data.frame(R1 = rep("A", 5),
                    R2 = c("B1", rep("B2", 4)),
                    R3 = c("C1", "C2", "C3", "C3", "C4"))
# duplicated rows are removed with warnings
tree <- toTree(data = taxTab)

# Example 3: NA values in R2 column
# results: the internal node with the label 'R2:'
```



```

taxTab <- data.frame(R1 = rep("A", 5),
                    R2 = c("B1", rep("B2", 2), NA, "B2"),
                    R3 = c("C1", "C2", "C3", NA, "C4"))
tree <- toTree(data = taxTab)
# viz the tree
ggtree(tree) +
  geom_text2(aes(label = label), color = "red", vjust = 1) +
  geom_nodepoint()

# Example 4: duplicated values in the leaf column (R4)
# Not allowed and give errors
# taxTab <- data.frame(R1 = rep("A", 5),
#                     R2 = c("B1", rep("B2", 3), "B3"),
#                     R3 = c("C1", "C2", "C3", "C3", NA),
#                     R4 = c("D1", "D2", "D3", NA, NA))

# Example 5: loops caused by missing values in B2-C4, B3-C4
taxTab <- data.frame(R1 = rep("A", 6),
                    R2 = c("B1", rep("B2", 4), "B3"),
                    R3 = c("C1", "C2", "C3", "C3", "C4", "C4"),
                    R4 = c("D1", "D2", "D3", "D3", "D4", "D4"),
                    R5 = paste0("E", 1:6))
# resolve loops before run to Tree
# Suffix are adding to C4
taxNew <- resolveLoop(taxTab)
tree <- toTree(data = taxNew)

# viz the tree
ggtree(tree) +
  geom_text2(aes(label = label), color = "red", vjust = 1) +
  geom_nodepoint()

```

---

trackNode

*track the nodes of a phylo tree*


---

## Description

trackNode track nodes of a phylo tree by adding the alias labels to them

## Usage

```
trackNode(tree)
```

## Arguments

tree                    A phylo object

## Value

a phylo object

## Author(s)

Ruizhu Huang

**Examples**

```

library(ggtree)

data(tinyTree)

ggtree(tinyTree, branch.length = 'none') +
  geom_text2(aes(label = label), hjust = -0.3) +
  geom_text2(aes(label = node), vjust = -0.8,
            hjust = -0.3, color = 'blue')

#check whether the node number and node label are matched
trackTree <- trackNode(tinyTree)
ggtree(trackTree, branch.length = 'none') +
  geom_text2(aes(label = label), hjust = -0.3) +
  geom_text2(aes(label = node), vjust = -0.8,
            hjust = -0.3, color = 'blue')

```

---

transNode

*Transfer between node number and node label*


---

**Description**

convertNode does the transformation between the number and the label of a node on a tree

**Usage**

```
transNode(tree, node, use.alias = FALSE, message = FALSE)
```

```
convertNode(tree, node, use.alias = FALSE, message = FALSE)
```

**Arguments**

tree	A phylo object
node	A character or numeric vector representing tree node label(s) or tree node number(s)
use.alias	A logical value, TRUE or FALSE. This is an optional argument that only required when the input node is a numeric vector. The default is FALSE, and the node label would be returned; otherwise, the alias of node label would be output. The alias of node label is created by adding a prefix "alias_" to the node number.
message	A logical value, TRUE or FALSE. The default is FALSE. If TRUE, message will show when a tree have duplicated labels for some internal nodes.

**Value**

a vector

**Author(s)**

Ruizhu Huang

**Examples**

```

library(ggtree)

data(tinyTree)

ggtree(tinyTree, branch.length = 'none') +
  geom_text2(aes(label = label), hjust = -0.3) +
  geom_text2(aes(label = node), vjust = -0.8,
            hjust = -0.3, color = 'blue')

#check whether the node number and node label are matched
convertNode(tinyTree, node = c(11, 2, 4, 15))

convertNode(tree = tinyTree, node = c("Node_16", "Node_11"))
convertNode(tree = tinyTree, node = c("alias_16", "alias_11"))

```

---

TreeSummarizedExperiment-class

*An S4 class TreeSummarizedExperiment*


---

**Description**

The class **TreeSummarizedExperiment** is an extension class of standard [SingleCellExperiment](#) class. It has four more slots that are not in [SingleCellExperiment](#) class: `rowTree`, `rowLinks`, `colTree` and `colLinks`. The hierarchical information of rows (columns) is stored in `rowTree` (`colTree`) and the link between the rows (columns) of assays tables and nodes of the tree is given in `rowLinks` (`colLinks`).

**Details**

The class **TreeSummarizedExperiment** is designed to store rectangular data for entities (e.g., microbes or cell types) (assays), information about the hierarchical structure (`rowTree` on rows; `colTree` on columns), and the mapping information between the tree nodes and the rows or the columns of the rectangular data. Users could provide the hierarchical structure of the rows, columns or both) of the assays tables, and the link data will be automatically generated in `rowLinks`, `colData` or both, respectively. It's required that the object in `rowLinks` or `colLinks` has the `LinkDataFrame` class. Please see the page [LinkDataFrame](#) for more details.

**Slots**

`rowTree` A phylo object or NULL. It gives information about the hierarchical structure of rows of assays tables.

`colTree` A phylo object or NULL. It gives information about the hierarchical structure of columns of assays tables.

`rowLinks` A `LinkDataFrame`. It gives information about the link between the nodes of the `rowTree` and the rows of assays tables.

`colLinks` A `LinkDataFrame`. It gives information about the link between the nodes of the `colTree` and the columns of assays tables.

`referenceSeq` A `DNAStrngSet/DNAStrngSetList` object or some object coercible to a `DNAStrngSet/DNAStrngSet` object. See [DNAStrngSet](#) for more details.

... Other slots from [SingleCellExperiment](#)

**Constructor**

See [TreeSummarizedExperiment-constructor](#) for constructor functions.

**Accessor**

See [TreeSummarizedExperiment-accessor](#) for accessor functions.

**See Also**

[TreeSummarizedExperiment](#) [TreeSummarizedExperiment-accessor](#) [SingleCellExperiment](#)

---

TreeSummarizedExperiment-constructor

*Construct a TreeSummarizedExperiment object*

---

**Description**

TreeSummarizedExperiment constructs a TreeSummarizedExperiment object.

**Usage**

```
TreeSummarizedExperiment(
  ...,
  rowTree = NULL,
  colTree = NULL,
  rowNodeLab = NULL,
  colNodeLab = NULL,
  referenceSeq = NULL
)
```

**Arguments**

...	Arguments passed to the <a href="#">SummarizedExperiment</a> constructor to fill the slots of the base class.
rowTree	A phylo object that provides hierarchical information of rows of assay tables.
colTree	A phylo object that provides hierarchical information of columns of assay tables.
rowNodeLab	A character string. It provides the labels of nodes that the rows of assays tables corresponding to. If NULL (default), the row names of the assays tables are used.
colNodeLab	A character string. It provides the labels of nodes that the columns of assays tables corresponding to. If NULL (default), the column names of the assays tables are used.
referenceSeq	A DNASTringSet/DNASTringSetList object or some object coercible to a DNASTringSet/DNASTring object. See <a href="#">DNASTringSet</a> for more details.

## Details

The output `TreeSummarizedExperiment` object has very similar structure as the [SingleCellExperiment](#). The differences are summarized below.

- **rowTree** A slot exists in `TreeSummarizedExperiment` but not in `SingleCellExperiment`. It stores the tree structure(s) that provide(s) hierarchical information of assays rows or columns or both.
- **rowData** If a phylo object is available in the slot `treeData` to provide the hierarchical information about the rows of the assays table, the `rowData` would be a [LinkDataFrame-class](#) instead of `DataFrame`. The data on the right side of the vertical line provides the link information between the assays rows and the tree phylo object, and could be accessed via `linkData`; The data on the left side is the original `rowData` like `SingleCellExperiment` object.
- **colData** Similar to the explanation for **rowData** as above.

More details about the `LinkDataFrame` in the `rowData` or `colData`.

- `nodeLab` The labels of nodes on the tree.
- `nodeLab\_alias` The alias of node labels on the tree.
- `nodeNum` The numbers of nodes on the tree.
- `isLeaf` It indicates whether the node is a leaf node or internal node.

## Value

a `TreeSummarizedExperiment` object

## Author(s)

Ruizhu HUANG

## See Also

[TreeSummarizedExperiment](#) [TreeSummarizedExperiment-accessor](#) [SingleCellExperiment](#)

## Examples

```
data("tinyTree")

# the count table
count <- matrix(rpois(100, 50), nrow = 10)
rownames(count) <- c(tinyTree$tip.label)
colnames(count) <- paste("C_", 1:10, sep = "_")

# The sample information
sampC <- data.frame(condition = rep(c("control", "trt"), each = 5),
                    gender = sample(x = 1:2, size = 10, replace = TRUE))
rownames(sampC) <- colnames(count)

# build a TreeSummarizedExperiment object
tse <- TreeSummarizedExperiment(assays = list(count),
                               colData = sampC,
                               rowTree = tinyTree)
```

---

TreeSummarizedExperiment-internal  
*TreeSummarizedExperiment internals*

---

### Description

Internal functions which should only be used in TreeSummarizedExperiment

### Usage

```
## S4 method for signature 'TreeSummarizedExperiment'
vertical_slot_names(x)
```

---

unionLeaf                    *list leaf nodes that are the descendants of at least one specified node*

---

### Description

unionLeaf list the leaf nodes that are the descendants of (at least one) specified nodes.

### Usage

```
unionLeaf(tree, node)
```

### Arguments

tree	A phylo object.
node	A numeric or character vector. It specifies internal nodes that are changed to leaves via their node labels or numbers.

### Value

A phylo object.

### Examples

```
library(ggtree)
data(tinyTree)
ggtree(tinyTree, ladderize = FALSE) +
  geom_text2(aes(label = label), color = "darkorange",
            hjust = -0.1, vjust = -0.7) +
  geom_text2(aes(label = node), color = "darkblue",
            hjust = -0.5, vjust = 0.7) +
  geom_highlight(node = 18) +
  geom_point2()

u1 <- unionLeaf(tree = tinyTree, node = c(19, 17))
u2 <- unionLeaf(tree = tinyTree, node = c(19, 17, 7))
(u3 <- unionLeaf(tree = tinyTree, node = c(11, 17, 7)))
```

---

updateObject, TreeSummarizedExperiment-method

*Update a TreeSummarizedExperiment object*

---

### Description

Update `TreeSummarizedExperiment` objects to the latest version of the class structure. This is usually called by methods in the `TreeSummarizedExperiment` package rather than by users or downstream packages.

### Usage

```
## S4 method for signature 'TreeSummarizedExperiment'  
updateObject(object, ..., verbose = FALSE)
```

### Arguments

<code>object</code>	A <code>TreeSummarizedExperiment</code> object
<code>...</code>	additional arguments, for use in specific <code>updateObject</code> methods.
<code>verbose</code>	TRUE or FALSE, indicating whether information about the update should be reported.

### Value

An updated `TreeSummarizedExperiment` object

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