

# Package ‘data.tree’

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## Enhances

**Description** Create tree structures from hierarchical data, and traverse the tree in various orders. Aggregate, cumulate, print, plot, convert to and from data.frame and more. Useful for decision trees, machine learning, finance, conversion from and to JSON, and many other applications.

**License** GPL (>= 2)

**URL** <http://github.com/gluc/data.tree>

**BugReports** <http://github.com/gluc/data.tree/issues>

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acme . . . . .	3
Aggregate . . . . .	3
AreNamesUnique . . . . .	5
as.data.frame.Node . . . . .	5
as.dendrogram.Node . . . . .	8
as.igraph.Node . . . . .	9
as.list.Node . . . . .	10
as.Node . . . . .	11
as.Node.BinaryTree . . . . .	11
as.Node.data.frame . . . . .	12
as.Node.dendrogram . . . . .	14
as.Node.list . . . . .	15
as.Node.party . . . . .	17
as.Node.phylo . . . . .	19
as.phylo.Node . . . . .	20
averageBranchingFactor . . . . .	20
CheckNameReservedWord . . . . .	21
Climb . . . . .	21
Clone . . . . .	22
CreateRandomTree . . . . .	23
CreateRegularTree . . . . .	24
Cumulate . . . . .	24
data.tree . . . . .	25
DefaultPlotHeight . . . . .	27
Distance . . . . .	28
Do . . . . .	28
FindNode . . . . .	29
FormatFixedDecimal . . . . .	30
FormatPercent . . . . .	31
Get . . . . .	31
GetAttribute . . . . .	33
GetPhyloNr . . . . .	34
isLeaf . . . . .	35
isNotLeaf . . . . .	35
isNotRoot . . . . .	36
isRoot . . . . .	36
mushroom . . . . .	37
Navigate . . . . .	37
Node . . . . .	38
NODE_RESERVED_NAMES_CONST . . . . .	40
plot.Node . . . . .	40
print.Node . . . . .	43
Prune . . . . .	44
Revert . . . . .	45
Set . . . . .	45
SetFormat . . . . .	46

<i>acme</i>	3
Sort . . . . .	47
ToNewick . . . . .	48
Traverse . . . . .	49
<b>Index</b>	<b>51</b>

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<i>acme</i>	<i>Sample Data: A Simple Company with Departments</i>
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### Description

*acme*'s tree representation is accessed through its root, *acme*.

### Usage

`data(acme)`

### Format

A `data.tree` root Node

### Details

- `cost`, only available for leaf nodes. Cost of the project.
- `p` probability that a project will be undertaken.

---

<i>Aggregate</i>	<i>Aggregate child values of a Node, recursively.</i>
------------------	---

---

### Description

The `Aggregate` method lets you fetch an attribute from a Node's children, and then aggregate them using `aggFun`. For example, you can aggregate `cost` by summing costs of child Nodes. This is especially useful in the context of tree traversal, when using post-order traversal mode.

### Usage

`Aggregate(node, attribute, aggFun, ...)`

**Arguments**

node	the Node on which to aggregate
attribute	determines what is collected. The attribute can be <ul style="list-style-type: none"> <li>• a.) the name of a <b>field</b> or a <b>property/active</b> of each Node in the tree, e.g. <code>acme\$Get("p")</code> or <code>acme\$Get("position")</code></li> <li>• b.) the name of a <b>method</b> of each Node in the tree, e.g. <code>acme\$Get("levelZeroBased")</code>, where e.g. <code>acme\$levelZeroBased &lt;- function() acme\$level - 1</code></li> <li>• c.) a <b>function</b>, whose first argument must be a Node e.g. <code>acme\$Get(function(node) node\$cost * ...</code></li> </ul>
aggFun	the aggregation function to be applied to the children's attributes
...	any arguments to be passed on to attribute (in case it's a function)

**Details**

As with [Get](#), the attribute can be a field, a method or a function. If the attribute on a child is NULL, `Aggregate` is called recursively on its children.

**See Also**

[Node](#)

**Examples**

```
data(acme)

#Aggregate on a field
Aggregate(acme, "cost", sum)

#This is the same as:
HomeRolledAggregate <- function(node) {
  sum(sapply(node$children, function(child) {
    if (!is.null(child$cost)) child$cost
    else HomeRolledAggregate(child)
  }))
}
HomeRolledAggregate(acme)

#Aggregate using Get
print(acme, "cost", minCost = acme$Get(Aggregate, "cost", min))

#use Aggregate with a function:
Aggregate(acme, function(x) x$cost * x$p, sum)

#cache values along the way
acme$Do(function(x) x$cost <- Aggregate(x, "cost", sum), traversal = "post-order")
acme$IT$cost
```

---

AreNamesUnique	<i>Test whether all node names are unique.</i>
----------------	--

---

**Description**

This can be useful for some conversions.

**Usage**

```
AreNamesUnique(node)
```

**Arguments**

node	The root Node of the data.tree structure to test
------	--

**Value**

TRUE if all Node\$name == TRUE for all nodes in the tree

**See Also**

as.igraph.Node

**Examples**

```
data(acme)
AreNamesUnique(acme)
acme$name <- "IT"
AreNamesUnique(acme)
```

---

as.data.frame.Node	<i>Convert a data.tree structure to a data.frame</i>
--------------------	--

---

**Description**

If a node field contains data of length > 1, then that is converted into a string in the data.frame.

**Usage**

```
## S3 method for class 'Node'
as.data.frame(x, row.names = NULL, optional = FALSE, ...,
  traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
  pruneFun = NULL, filterFun = NULL, format = FALSE,
  inheritFromAncestors = FALSE)
```

```
ToDataFrameTree(x, ..., pruneFun = NULL)
```

```
ToDataFrameTable(x, ..., pruneFun = NULL)
```

```
ToDataFrameNetwork(x, ..., direction = c("climb", "descend"),
  pruneFun = NULL, format = FALSE, inheritFromAncestors = FALSE)
```

```
ToDataFrameTypeCol(x, ..., type = "level", prefix = type, pruneFun = NULL)
```

**Arguments**

x	The root Node of the tree or sub-tree to be convert to a data.frame
row.names	NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
optional	logical. If TRUE, setting row names and converting column names (to syntactic names: see <code>make.names</code> ) is optional.
...	the attributes to be added as columns of the data.frame. See <a href="#">Get</a> for details. If a specific Node does not contain the attribute, NA is added to the data.frame.
traversal	any of 'pre-order' (the default), 'post-order', 'in-order', 'level', or 'ancestor'. See <a href="#">Traverse</a> for details.
pruneFun	allows providing a a prune criteria, i.e. a function taking a Node as an input, and returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its entire sub-tree will not be considered.
filterFun	a function taking a Node as an argument. See <a href="#">Traverse</a> for details.
format	if FALSE (the default), then no formatting will be applied. If TRUE, then the first formatter (if any) along the ancestor path is used for formatting.
inheritFromAncestors	if FALSE, and if the attribute is a field or a method, then only a Node itself is searched for the field/method. If TRUE, and if the Node does not contain the attribute, then ancestors are also searched.
direction	when converting to a network, should the edges point from root to children ("climb") or from child to parent ("descend")?
type	when converting type columns, the type is the discriminator, i.e. an attribute (e.g. field name) of each node
prefix	when converting type columns, the prefix used for the column names. Can be NULL to omit prefixes.

**Value**

ToDataFrameTree: a data.frame, where each row represents a Node in the tree or sub-tree spanned by x, possibly pruned according to pruneFun.

ToDataFrameTable: a data.frame, where each row represents a leaf Node in the tree or sub-tree spanned by x, possibly pruned according to pruneFun.

ToDataFrameNetwork: a data.frame, where each row represents a Node in the tree or sub-tree spanned by x, possibly pruned according to pruneFun. The first column is called 'from', while the second is called 'to', describing the parent to child edge (for direction "climb") or the child to parent edge (for direction "descend"). If [AreNamesUnique](#) is TRUE, then the Network is based on the Node\$name, otherwise on the Node\$pathString

ToDataFrameTypeCol: a data.frame in table format (i.e. where each row represents a leaf in the tree or sub-tree spanned by x), possibly pruned according to pruneFun. In addition to ..., each distinct type is output to a column.

**Examples**

```

data(acme)
acme$fieldsAll
as.data.frame(acme, row.names = NULL, optional = FALSE, "cost", "p")

ToDataFrameTree(acme, "cost", "p")
ToDataFrameNetwork(acme, "cost", "p", direction = "climb")
ToDataFrameTable(acme, "cost", "p")
ToDataFrameTypeCol(acme)

#use the pruneFun:
acme$Do(function(x) x$totalCost <- Aggregate(x, "cost", sum), traversal = "post-order")
ToDataFrameTree(acme, "totalCost", pruneFun = function(x) x$totalCost > 300000)

#inherit
acme$Set(floor = c(1, 2, 3), filterFun = function(x) x$level == 2)
as.data.frame(acme, row.names = NULL, optional = FALSE, "floor", inheritFromAncestors = FALSE)
as.data.frame(acme, row.names = NULL, optional = FALSE, "floor", inheritFromAncestors = TRUE)

#using a function as an attribute:
acme$Accounting$Head <- "Mrs. Numright"
acme$Research$Head <- "Mr. Stein"
acme$IT$Head <- "Mr. Squarehead"
ToDataFrameTable(acme, department = function(x) x$parent$name, "name", "Head", "cost")

#complex TypeCol
acme$IT$Outsource$AddChild("India")
acme$IT$Outsource$AddChild("Poland")
acme$Set(type = c('company', 'department', 'project', 'project', 'department',
                 'project', 'project', 'department', 'program', 'project',
                 'project', 'project', 'project'
                 )
        )
print(acme, 'type')
ToDataFrameTypeCol(acme, type = 'type')

```

---

as.dendrogram.Node      *Convert a Node to a dendrogram*

---

### Description

Convert a `data.tree` structure to a [dendrogram](#)

### Usage

```
## S3 method for class 'Node'  
as.dendrogram(object, heightAttribute = DefaultPlotHeight,  
  edgetext = FALSE, ...)
```

### Arguments

<code>object</code>	The Node to convert
<code>heightAttribute</code>	The attribute (field name or function) storing the height
<code>edgetext</code>	If TRUE, then the for non-leaf nodes the node name is stored as the dendrogram's edge text.
<code>...</code>	Additional parameters

### Value

An object of class `dendrogram`

### See Also

Other Conversions from Node: [ToNewick](#)

### Examples

```
data(acme)  
acmed <- as.dendrogram(acme)  
plot(acmed, center = TRUE)  
  
#you can take an attribute for the height:  
acme$Do( function(x) x$myPlotHeight <- (10 - x$level))  
acmed <- as.dendrogram(acme, heightAttribute = "myPlotHeight")  
plot(acmed, center = TRUE)  
  
#or directly a function  
acmed <- as.dendrogram(acme, heightAttribute = function(x) 10 - x$level)  
plot(acmed)
```

---

as.igraph.Node                      *Convert a data.tree structure to an igraph network*

---

### Description

This requires the igraph package to be installed. Also, this requires the names of the Nodes to be unique within the data.tree structure.

### Usage

```
as.igraph.Node(node, vertexAttributes = character(),  
               edgeAttributes = character(), directed = FALSE, direction = c("climb",  
                                   "descend"))
```

### Arguments

node	The root Node to convert
vertexAttributes	A vector of strings, representing the attributes in the data.tree structure to add as attributes to the vertices of the igraph
edgeAttributes	A vector of strings, representing the attributes in the data.tree structure to add as edge attributes of the igraph
directed	Logical scalar, whether or not to create a directed graph.
direction	when converting to a network, should the edges point from root to children ("climb") or from child to parent ("descend")?

### Value

an igraph object

### See Also

AreNamesUnique

### Examples

```
data(acme)  
library(igraph)  
ig <- as.igraph(acme, "p", c("level", "isLeaf"))  
plot(ig)
```

---

as.list.Node	<i>Convert a data.tree structure to a list-of-list structure</i>
--------------	--

---

### Description

Convert a data.tree structure to a list-of-list structure

### Usage

```
## S3 method for class 'Node'
as.list(x, mode = c("simple", "explicit"), unname = FALSE,
        nameName = ifelse(unname, "name", ""), childrenName = "children",
        rootName = "", keepOnly = NULL, ...)

ToListSimple(x, nameName = "name", ...)

ToListExplicit(x, unname = FALSE, nameName = ifelse(unname, "name", ""),
              childrenName = "children", ...)
```

### Arguments

x	The Node to convert
mode	How the list is structured. "simple" (the default) will add children directly as nested lists. "explicit" puts children in a separate nested list called childrenName
unname	If TRUE, and if mode is "explicit", then the nested children list will not have named arguments. This can be useful e.g. in the context of conversion to JSON, if you prefer the children to be an array rather than named objects.
nameName	The name that should be given to the name element
childrenName	The name that should be given to the children nested list
rootName	The name of the node. If provided, this overrides Node\$name
keepOnly	A character vector of fields to include in the result. If NULL (the default), all fields are kept.
...	Additional parameters passed to as.list.Node

### Examples

```
data(acme)

str(ToListSimple(acme))
str(ToListSimple(acme, keepOnly = "cost"))

str(ToListExplicit(acme))
str(ToListExplicit(acme, unname = TRUE))
str(ToListExplicit(acme, unname = TRUE, nameName = "id", childrenName = "descendants"))
```

---

as.Node	<i>Convert an object to a data.tree data structure</i>
---------	--

---

**Description**

Convert an object to a data.tree data structure

**Usage**

```
as.Node(x, ...)
```

**Arguments**

x	The object to be converted
...	Additional arguments

**See Also**

Other as.Node: [as.Node.data.frame](#), [as.Node.dendrogram](#), [as.Node.list](#), [as.Node.phylo](#)

---

as.Node.BinaryTree	<i>Convert a a SplitNode from the party package to a data.tree structure.</i>
--------------------	---

---

**Description**

Convert a a SplitNode from the party package to a data.tree structure.

**Usage**

```
## S3 method for class 'BinaryTree'  
as.Node(x, ...)
```

**Arguments**

x	The BinaryTree
...	additional arguments (unused)

**Examples**

```

library(party)
airq <- subset(airquality, !is.na(Ozone))
airct <- ctree(Ozone ~ ., data = airq,
              controls = ctree_control(maxsurrogate = 3))

tree <- as.Node(airct)
tree

print(tree,
      "label",
      criterion = function(x) round(x$criterion$maxcriterion, 3),
      statistic = function(x) round(max(x$criterion$statistic), 3)
      )

FindNode(tree, 6)$path

```

---

as.Node.data.frame      *Convert a data.frame to a data.tree structure*

---

**Description**

Convert a data.frame to a data.tree structure

**Usage**

```

## S3 method for class 'data.frame'
as.Node(x, ..., mode = c("table", "network"),
       pathName = "pathString", pathDelimiter = "/", colLevels = NULL,
       na.rm = TRUE)

FromDataFrameTable(table, pathName = "pathString", pathDelimiter = "/",
                  colLevels = NULL, na.rm = TRUE, check = c("check", "no-warn",
                  "no-check"))

FromDataFrameNetwork(network, check = c("check", "no-warn", "no-check"))

```

**Arguments**

x	The data.frame in the required format.
...	Any other argument implementations of this might need
mode	Either "table" (if x is a data.frame in tree or table format) or "network"
pathName	The name of the column in x containing the path of the row
pathDelimiter	The delimiter used to separate nodes in pathName

colLevels	Nested list of column names, determining on what node levels the attributes are written to.
na.rm	If TRUE, then NA's are treated as NULL and values will not be set on nodes
table	a data.frame in table or tree format, i.e. having a row for each leaf (and optionally for additional nodes). There should be a column called pathName, separated by pathDelimiter, describing the path of each row.
check	Either <ul style="list-style-type: none"> <li>• "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)</li> <li>• "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)</li> <li>• "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors</li> </ul>
network	A data.frame in network format, i.e. it must adhere to the following requirements: <ul style="list-style-type: none"> <li>• It must contain as many rows as there are nodes (excluding the root, there is no row for the root)</li> <li>• Its first and second columns contain the network relationships. This can be either climbing (from parent to children) or descending (from child to parent)</li> <li>• Its subsequent columns contain the attributes to be set as fields on the nodes</li> <li>• It must contain a single root</li> <li>• There are no cycles in the network</li> </ul>

**Value**

The root Node of the data.tree structure

**See Also**

[as.data.frame.Node](#)

Other as.Node: [as.Node.dendrogram](#), [as.Node.list](#), [as.Node.phylo](#), [as.Node](#)

**Examples**

```
data(acme)

#Tree
x <- ToDataFrameTree(acme, "pathString", "p", "cost")
x
xN <- as.Node(x)
print(xN, "p", "cost")

#Table
x <- ToDataFrameTable(acme, "pathString", "p", "cost")
```

```

x
xN <- FromDataFrameTable(x)
print(xN, "p", "cost")

#More complex Table structure, using colLevels
acme$Set(floor = c(1, 2, 3), filterFun = function(x) x$level == 2)
x <- ToDataFrameTable(acme, "pathString", "floor", "p", "cost")
x
xN <- FromDataFrameTable(x, colLevels = list(NULL, "floor", c("p", "cost")), na.rm = TRUE)
print(xN, "floor", "p", "cost")

#Network
x <- ToDataFrameNetwork(acme, "p", "cost", direction = "climb")
x
xN <- FromDataFrameNetwork(x)
print(xN, "p", "cost")

```

---

as.Node.dendrogram      *Convert a [dendrogram](#) to a data.tree Node*

---

## Description

Convert a [dendrogram](#) to a data.tree Node

## Usage

```

## S3 method for class 'dendrogram'
as.Node(x, name = "Root", heightName = "plotHeight",
        check = c("check", "no-warn", "no-check"), ...)

```

## Arguments

x	The dendrogram
name	The name of the root Node
heightName	The name under which the dendrogram's height is stored
check	Either <ul style="list-style-type: none"> <li>• "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)</li> <li>• "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)</li> <li>• "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors</li> </ul>
...	Additional parameters

**Value**

The root Node of a data.tree

**See Also**

Other as.Node: [as.Node.data.frame](#), [as.Node.list](#), [as.Node.phylo](#), [as.Node](#)

**Examples**

```
hc <- hclust(dist(USArrests), "ave")
dend1 <- as.dendrogram(hc)
tree1 <- as.Node(dend1)
tree1$fieldsAll
tree1$totalCount
tree1$leafCount
tree1$height
```

---

as.Node.list

---

*Convert a nested list structure to a data.tree structure*


---

**Description**

Convert a nested list structure to a data.tree structure

**Usage**

```
## S3 method for class 'list'
as.Node(x, mode = c("simple", "explicit"), nameName = "name",
        childrenName = "children", nodeName = NULL, check = c("check",
        "no-warn", "no-check"), ...)
```

```
FromListExplicit(explicitList, nameName = "name", childrenName = "children",
                 nodeName = NULL, check = c("check", "no-warn", "no-check"))
```

```
FromListSimple(simpleList, nameName = "name", nodeName = NULL,
               check = c("check", "no-warn", "no-check"))
```

**Arguments**

x	The list to be converted.
mode	How the list is structured. "simple" (the default) will interpret any list to be a child. "explicit" assumes that children are in a nested list called childrenName
nameName	The name of the element in the list that should be used as the name, can be NULL if mode = explicit and the children lists are named, or if an automatic name (running number) should be assigned

childrenName	The name of the element that contains the child list (applies to mode 'explicit' only).
nodeName	A name suggestion for x, if the name cannot be deferred otherwise. This is for example the case for the root with mode explicit and named lists.
check	Either <ul style="list-style-type: none"> <li>• "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)</li> <li>• "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)</li> <li>• "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors</li> </ul>
...	Any other argument to be passed to generic sub implementations
explicitList	A list in which children are in a separate nested list called childrenName.
simpleList	A list in which children are stored as nested list alongside other fields. Any list is interpreted as a child Node

### See Also

Other as.Node: [as.Node.data.frame](#), [as.Node.dendrogram](#), [as.Node.phylo](#), [as.Node](#)

### Examples

```
kingJosephs <- list(name = "Joseph I",
  spouse = "Mary",
  born = "1818-02-23",
  died = "1839-08-29",
  children = list(
    list(name = "Joseph II",
      spouse = "Kathryn",
      born = "1839-03-28",
      died = "1865-12-19"),
    list(name = "Helen",
      born = "1840-17-08",
      died = "1845-01-01")
  )
)
FromListExplicit(kingJosephs)
```

```
kingJosephs <- list(head = "Joseph I",
  spouse = "Mary",
  born = "1818-02-23",
  died = "1839-08-29",
  list(head = "Joseph II",
    spouse = "Kathryn",
    born = "1839-03-28",
    died = "1865-12-19"),
  list(head = "Helen",
```

```

        born = "1840-17-08",
        died = "1845-01-01")
    )
  FromListSimple(kingJosephs, nameName = "head")

  kingJosephs <- list(spouse = "Mary",
    born = "1818-02-23",
    died = "1839-08-29",
    `Joseph II` = list(spouse = "Kathryn",
      born = "1839-03-28",
      died = "1865-12-19"),
    Helen = list(born = "1840-17-08",
      died = "1845-01-01")

  )
  FromListSimple(kingJosephs, nodeName = "Joseph I")

```

---

as.Node.party

*Convert a a party from the partykit package to a data.tree structure.*


---

## Description

Convert a a party from the partykit package to a data.tree structure.

## Usage

```
## S3 method for class 'party'
as.Node(x, ...)
```

## Arguments

x	The party object
...	other arguments (unused)

## Examples

```

library(partykit)
data("WeatherPlay", package = "partykit")
### splits ###
# split in overcast, humidity, and windy
sp_o <- partysplit(1L, index = 1:3)
sp_h <- partysplit(3L, breaks = 75)
sp_w <- partysplit(4L, index = 1:2)

## query labels
character_split(sp_o)

### nodes ###

```

```

## set up partynode structure
pn <- partynode(1L, split = sp_o, kids = list(
  partynode(2L, split = sp_h, kids = list(
    partynode(3L, info = "yes"),
    partynode(4L, info = "no")),
  partynode(5L, info = "yes"),
  partynode(6L, split = sp_w, kids = list(
    partynode(7L, info = "yes"),
    partynode(8L, info = "no")))))
pn
### tree ###
## party: associate recursive partynode structure with data
py <- party(pn, WeatherPlay)
tree <- as.Node(py)

print(tree,
      "splitname",
      count = function(node) nrow(node$data),
      "splitLevel")

SetNodeStyle(tree,
  label = function(node) paste0(node$name, ": ", node$splitname),
  tooltip = function(node) paste0(nrow(node$data), " observations"),
  fontname = "helvetica")
SetEdgeStyle(tree,
  arrowhead = "none",
  label = function(node) node$splitLevel,
  fontname = "helvetica",
  penwidth = function(node) 12 * nrow(node$data)/nrow(node$root$data),
  color = function(node) {
    paste0("grey",
          100 - as.integer( 100 * nrow(node$data)/nrow(node$root$data))
          )
  }
)
Do(tree$leaves,
  function(node) {
    SetNodeStyle(node,
      shape = "box",
      color = ifelse(node$splitname == "yes", "darkolivegreen4", "lightsalmon4"),
      fillcolor = ifelse(node$splitname == "yes", "darkolivegreen1", "lightsalmon"),
      style = "filled,rounded",
      penwidth = 2
    )
  }
)

plot(tree)

```

---

as.Node.phylo	<i>Convert a phylo object from the ape package to a Node</i>
---------------	--

---

### Description

Convert a phylo object from the ape package to a Node

### Usage

```
## S3 method for class 'phylo'  
as.Node(x, heightName = "plotHeight",  
        replaceUnderscores = TRUE, namesNotUnique = FALSE, ...)
```

### Arguments

x	The phylo object to be converted
heightName	If the phylo contains edge lengths, then they will be converted to a height and stored in a field named according to this parameter (the default is "height")
replaceUnderscores	if TRUE (the default), then underscores in names are replaced with spaces
namesNotUnique	if TRUE, then the name of the Nodes will be prefixed with a unique id. This is useful if the children of a parent have non-unique names.
...	any other parameter to be passed to sub-implementations

### See Also

Other ape phylo conversions: [GetPhyloNr](#), [as.phylo.Node](#)

Other as.Node: [as.Node.data.frame](#), [as.Node.dendrogram](#), [as.Node.list](#), [as.Node](#)

### Examples

```
#which bird familes have the max height?  
library(ape)  
data(bird.families)  
bf <- as.Node(bird.families)  
height <- bf$height  
t <- Traverse(bf, filterFun = function(x) x$level == 25)  
Get(t, "name")
```

---

as.phylo.Node                      *Convert a Node to a phylo object from the ape package.*

---

### Description

This method requires the ape package to be installed and loaded.

### Usage

```
as.phylo.Node(x, heightAttribute = DefaultPlotHeight, ...)
```

### Arguments

x	The root Node of the tree or sub-tree to be converted
heightAttribute	The attribute (field name or function) storing the height
...	any other argument

### See Also

Other ape phylo conversions: [GetPhyloNr](#), [as.Node.phylo](#)

### Examples

```
library(ape)
data(acme)
acmephylo <- as.phylo(acme)
#plot(acmephylo)
```

---

averageBranchingFactor

*Calculate the average number of branches each non-leaf has*

---

### Description

Calculate the average number of branches each non-leaf has

### Usage

```
averageBranchingFactor(node)
```

### Arguments

node	The node
------	----------

---

CheckNameReservedWord *Checks whether name is a reserved word, as defined in NODE\_RESERVED\_NAMES\_CONST.*

---

### Description

Checks whether name is a reserved word, as defined in NODE\_RESERVED\_NAMES\_CONST.

### Usage

```
CheckNameReservedWord(name, check = c("check", "no-warn", "no-check"))
```

### Arguments

name	the name to check
check	Either <ul style="list-style-type: none"> <li>• "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)</li> <li>• "no-warn": if the name conformance should be checked, but no warnings should be printed in case of non-conformance (if you expect non-conformance)</li> <li>• "no-check" or FALSE: if the name conformance should not be checked; use this if performance is critical. However, in case of non-conformance, expect cryptic follow-up errors</li> </ul>

---

Climb *Climb a tree from parent to children, by provided criteria.*

---

### Description

This method lets you climb the tree, from crutch to crutch. On each Node, the Climb finds the first child having attribute value equal to the the provided argument.

### Usage

```
#node$Climb(...)
Climb(node, ...)
```

### Arguments

node	The root <a href="#">Node</a> of the tree or subtree to climb
...	an attribute name to searched value pairlist. For brevity, you can also provide a character vector.

**Value**

the Node having path . . . , or NULL if such a path does not exist

**See Also**

[Node](#)

[Navigate](#)

**Examples**

```
data(acme)

#the following are all equivalent
Climb(acme, 'IT', 'Outsource')
Climb(acme, name = 'IT', name = 'Outsource')
Climb(acme, 'IT')$Climb('Outsource')
Navigate(acme, path = "IT/Outsource")

Climb(acme, name = 'IT')

Climb(acme, position = c(2, 1))
#or, equivalent:
Climb(acme, position = 2, position = 1)
Climb(acme, name = "IT", cost = 250000)

tree <- CreateRegularTree(5, 2)
tree$Climb(c("1", "1"), position = c(2, 2))$path
```

---

Clone

*Clone a tree (creates a deep copy)*

---

**Description**

The method also clones object attributes (such as the formatters), if desired. If the method is called on a non-root, then the parent relationship is not cloned, and the resulting [Node](#) will be a root.

**Usage**

```
Clone(node, pruneFun = NULL, attributes = FALSE)
```

**Arguments**

node	the root node of the tree or sub-tree to clone
pruneFun	allows providing a prune criteria, i.e. a function taking a Node as an input, and returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its entire sub-tree will not be considered.
attributes	if FALSE, then R class attributes (e.g. formatters and grViz styles) are not cloned. This makes the method faster.

**Value**

the clone of the tree or sub-tree

**See Also**

SetFormat

**Examples**

```
data(acme)
acmeClone <- Clone(acme)
acmeClone$name <- "New Acme"
# acmeClone does not point to the same reference object anymore:
acme$name

#cloning a subtree
data(acme)
itClone <- Clone(acme$IT)
itClone$isRoot
```

---

CreateRandomTree	<i>Create a tree for demo and testing</i>
------------------	---

---

**Description**

Create a tree for demo and testing

**Usage**

```
CreateRandomTree(nodes = 100, root = Node$new("1"), id = 1)
```

**Arguments**

nodes	The number of nodes to create
root	the previous node (for recursion, typically use default value)
id	The id (for recursion)

---

CreateRegularTree      *Create a tree for demo and testing*

---

### Description

Create a tree for demo and testing

### Usage

```
CreateRegularTree(height = 5, branchingFactor = 3, parent = Node$new("1"))
```

### Arguments

height	the number of levels
branchingFactor	the number of children per node
parent	the parent node (for recursion)

---

Cumulate      *Cumulate values among siblings*

---

### Description

For example, you can sum up values of siblings before this Node.

### Usage

```
Cumulate(node, attribute, aggFun, ...)
```

### Arguments

node	The node on which we want to cumulate
attribute	determines what is collected. The attribute can be <ul style="list-style-type: none"> <li>a.) the name of a <b>field</b> or a <b>property/active</b> of each Node in the tree, e.g. <code>acme\$Get("p")</code> or <code>acme\$Get("position")</code></li> <li>b.) the name of a <b>method</b> of each Node in the tree, e.g. <code>acme\$Get("levelZeroBased")</code>, where e.g. <code>acme\$levelZeroBased &lt;- function() acme\$level - 1</code></li> <li>c.) a <b>function</b>, whose first argument must be a Node e.g. <code>acme\$Get(function(node) node\$cost * ...)</code></li> </ul>
aggFun	the aggregation function to be applied to the children's attributes
...	any arguments to be passed on to attribute (in case it's a function)

## Examples

```
data(acme)
acme$Do(function(x) x$cost <- Aggregate(x, "cost", sum), traversal = "post-order")
acme$Do(function(x) x$cumCost <- Cumulate(x, "cost", sum))
print(acme, "cost", "cumCost")
```

---

data.tree

*data.tree: Hierarchical Data Structures*

---

## Description

`data.tree` is to hierarchical data what `data.frame` is to tabular data: An extensible, general purpose structure to store, manipulate, and display hierarchical data.

## Introduction

Hierarchical data is ubiquitous in statistics and programming (XML, search trees, family trees, classification, file system, etc.). However, no general-use **tree data structure** is available in R. Where tabular data has `data.frame`, hierarchical data is often modeled in lists of lists or similar makeshifts. These structures are often difficult to manage. This is where the `data.tree` package steps in. It lets you build trees of hierarchical data for various uses: to print, to rapid prototype search algorithms, to test out new classification algorithms, and much more.

## Tree Traversal

`data.tree` allows to [Traverse](#) trees in various orders (pre-order, post-order, level, etc.), and it lets you run operations on [Nodes](#) via [Do](#). Similarly, you can collect and store data while traversing a tree using the [Get](#) and the [Set](#) methods.

## Methods

The package also contains utility functions to [Sort](#), to [Prune](#), to [Aggregate](#) and [Cumulate](#) and to [print](#) in custom formats.

## Construction and Conversion

The package also contains many conversions from and to `data.tree` structures. Check out the see also section of [as.Node](#).

You can construct a tree from a `data.frame` using [as.Node.data.frame](#), and convert it back using [as.data.frame.Node](#). Similar options exist for list of lists. For more specialized conversions, see [as.dendrogram.Node](#), [as.Node.dendrogram](#), [as.phylo.Node](#) and [as.Node.phylo](#)

Finally, easy conversion options from and to JSON, YAML, `igraph`, and more exist.

## Node and Reference Semantics

The entry point to the package is [Node](#). Each tree is composed of a number of Nodes, referencing each other.

One of most important things to note about `data.tree` is that it exhibits **reference semantics**. In a nutshell, this means that you can modify your tree along the way, without having to reassign it to a variable after each modification. By and large, this is a rather exceptional behavior in R, where value-semantics is king most of the time.

## Applications

`data.tree` is not optimised for computational speed, but for implementation speed. Namely, its memory footprint is relatively large compared to traditional R data structures. However, it can easily handle trees with several thousand nodes, and once a tree is constructed, operations on it are relatively fast. `data.tree` is always useful when

- you want to develop and test a new algorithm
- you want to import and convert tree structures (it imports and exports to list-of-list, `data.frame`, `yaml`, `json`, `igraph`, `dendrogram`, `phylo` and more)
- you want to play around with data, display it and get an understanding
- you want to test another package, to compare it with your own results
- you need to do homework

For a quick overview of the features, read the [data.tree](#) vignette by running `vignette("data.tree")`. For stylized applications, see `vignette("applications", package='data.tree')`

## See Also

[Node](#)

For more details, see the `data.tree` vignette by running: `vignette("data.tree")`

## Examples

```
data(acme)
print(acme)
acme$fieldsAll
acme$count
acme$totalCount
acme$isRoot
acme$height
print(acme, "p", "cost")

outsource <- acme$IT$Outsource
class(outsource)
print(outsource)
outsource$fields
outsource$isLeaf
outsource$level
outsource$path
outsource$p
```

```
outsource$parent$name
outsource$root$name
outsource$expCost <- outsource$p * outsource$cost
print(acme, "expCost")

acme$Get("p")
acme$Do(function(x) x$expCost <- x$p * x$cost)
acme$Get("expCost", filterFun = isLeaf)

ToDataFrameTable(acme, "name", "p", "cost", "level", "pathString")
ToDataFrameTree(acme, "name", "p", "cost", "level")
ToDataFrameNetwork(acme, "p", "cost")
```

---

DefaultPlotHeight	<i>Calculates the height of a Node given the height of the root.</i>
-------------------	--

---

## Description

This function puts leafs at the bottom (not hanging), and makes edges equally long. Useful for easy plotting with third-party packages, e.g. if you have no specific height attribute, e.g. with [as.dendrogram.Node](#), [ToNewick](#), and [as.phylo.Node](#)

## Usage

```
DefaultPlotHeight(node, rootHeight = 100)
```

## Arguments

node	The node
rootHeight	The height of the root

## Examples

```
data(acme)
dacme <- as.dendrogram(acme, heightAttribute = function(x) DefaultPlotHeight(x, 200))
plot(dacme, center = TRUE)
```

---

 Distance

*Find the distance between two nodes of the same tree*


---

### Description

The distance is measured as the number of edges that need to be traversed to reach node2 when starting from node1.

### Usage

```
Distance(node1, node2)
```

### Arguments

node1	the first node in the tree
node2	the second node in the same tree

### Examples

```
data(acme)
Distance(FindNode(acme, "Outsource"), FindNode(acme, "Research"))
```

---

 Do

*Executes a function on a set of nodes*


---

### Description

Executes a function on a set of nodes

### Usage

```
# 00-style:
# node$Do(fun,
#       ...,
#       traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
#       pruneFun = NULL,
#       filterFun = NULL)

# traditional:
Do(nodes, fun, ...)
```

**Arguments**

nodes	The nodes on which to perform the Get (typically obtained via <a href="#">Traverse</a> )
fun	the function to execute. The function is expected to be either a Method, or to take a Node as its first argument
...	any additional parameters to be passed on to fun

**See Also**

[Node](#)  
[Get](#)  
[Set](#)  
[Traverse](#)

**Examples**

```
data(acme)
acme$Do(function(node) node$expectedCost <- node$p * node$cost)
print(acme, "expectedCost")
```

---

FindNode

*Find a node by name in the (sub-)tree*

---

**Description**

Scans the entire sub-tree spanned by node and returns the first [Node](#) having the name specified. This is mainly useful for trees whose name is unique. If [AreNamesUnique](#) is FALSE, i.e. if there is more than one Node called name in the tree, then it is undefined which one will be returned. Also note that this method is not particularly fast. See examples for a faster way to index large trees, if you need to do multiple searches. See [Traverse](#) if you need to find multiple Nodes.

**Usage**

```
FindNode(node, name)
```

**Arguments**

node	The root Node of the tree or sub-tree to search
name	The name of the Node to be returned

**Value**

The first Node whose name matches, or NULL if no such Node is found.

**See Also**

AreNamesUnique, Traverse

**Examples**

```
data(acme)
FindNode(acme, "Outsource")

#re-usable hashed index for multiple searches:
if(!AreNamesUnique(acme)) stop("Hashed index works for unique names only!")
trav <- Traverse(acme, "level")
names(trav) <- Get(trav, "name")
nameIndex <- as.environment(trav)
#you could also use hash from package hash instead!
#nameIndex <- hash(trav)
nameIndex$Outsource
nameIndex$IT
```

---

FormatFixedDecimal      *Format a Number as a Decimal*

---

**Description**

Simple function that can be used as a format function when converting trees to a `data.frame`

**Usage**

```
FormatFixedDecimal(x, digits = 3)
```

**Arguments**

<code>x</code>	a numeric scalar or vector
<code>digits</code>	the number of digits to print after the decimal point

**Value**

A string corresponding to `x`, suitable for printing

**Examples**

```
data(acme)
print(acme, prob = acme$Get("p", format = function(x) FormatFixedDecimal(x, 4)))
```

---

FormatPercent	<i>Format a Number as a Percentage</i>
---------------	--

---

**Description**

This utility method can be used as a format function when converting trees to a `data.frame`

**Usage**

```
FormatPercent(x, digits = 2, format = "f", ...)
```

**Arguments**

<code>x</code>	A number
<code>digits</code>	The number of digits to print
<code>format</code>	The format to use
<code>...</code>	Any other argument passed to <code>formatC</code>

**Value**

A string corresponding to `x`, suitable for printing

**See Also**

`formatC`

**Examples**

```
data(acme)
print(acme, prob = acme$Get("p", format = FormatPercent))
```

---

Get	<i>Traverse a Tree and Collect Values</i>
-----	---

---

**Description**

The `Get` method is one of the most important ones of the `data.tree` package. It lets you traverse a tree and collect values along the way. Alternatively, you can call a method or a function on each [Node](#).

## Usage

```
# 00-style:
#node$Get(attribute,
#         ...,
#         traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
#         pruneFun = NULL,
#         filterFun = NULL,
#         format = FALSE,
#         inheritFromAncestors = FALSE)

# traditional:
Get(nodes,
     attribute,
     ...,
     format = FALSE,
     inheritFromAncestors = FALSE,
     simplify = c(TRUE, FALSE, "array", "regular"))
```

## Arguments

nodes	The nodes on which to perform the Get (typically obtained via <a href="#">Traverse</a> )
attribute	determines what is collected. The attribute can be <ul style="list-style-type: none"> <li>a.) the name of a <b>field</b> or a <b>property/active</b> of each Node in the tree, e.g. <code>acme\$Get("p")</code> or <code>acme\$Get("position")</code></li> <li>b.) the name of a <b>method</b> of each Node in the tree, e.g. <code>acme\$Get("levelZeroBased")</code>, where e.g. <code>acme\$levelZeroBased &lt;- function() acme\$level - 1</code></li> <li>c.) a <b>function</b>, whose first argument must be a Node e.g. <code>acme\$Get(function(node) node\$cost * ...</code></li> </ul>
...	in case the attribute is a function or a method, the ellipsis is passed to it as additional arguments.
format	if FALSE (the default), no formatting is being used. If TRUE, then the first formatter (if any) found along the ancestor path is being used for formatting (see <a href="#">SetFormat</a> ). If format is a function, then the collected value is passed to that function, and the result is returned.
inheritFromAncestors	if TRUE, then the path above a Node is searched to get the attribute in case it is NULL.
simplify	same as <a href="#">sapply</a> , i.e. TRUE, FALSE or "array". Additionally, you can specify "regular" if each returned value is of length > 1, and equally named. See below for an example.

## Value

a vector containing the attributes collected during traversal, in traversal order. NULL is converted to NA, such that `length(Node$Get) == Node$totalCount`

**See Also**

[Node](#)  
[Set](#)  
[Do](#)  
[Traverse](#)

**Examples**

```

data(acme)
acme$Get("level")
acme$Get("totalCount")

acme$Get(function(node) node$cost * node$p,
          filterFun = isLeaf)

#This is equivalent:
nodes <- Traverse(acme, filterFun = isLeaf)
Get(nodes, function(node) node$cost * node$p)

#simplify = "regular" will preserve names
acme$Get(function(x) c(position = x$position, level = x$level), simplify = "regular")

```

---

GetAttribute	<i>Get an attribute from a Node.</i>
--------------	--------------------------------------

---

**Description**

Get an attribute from a Node.

**Usage**

```

GetAttribute(node, attribute, ..., format = FALSE,
            inheritFromAncestors = FALSE, nullAsNa = TRUE)

```

**Arguments**

node	The <a href="#">Node</a> from which the attribute should be fetched.
attribute	determines what is collected. The attribute can be <ul style="list-style-type: none"> <li>• a.) the name of a <b>field</b> or a <b>property/active</b> of each Node in the tree, e.g. <code>acme\$Get("p")</code> or <code>acme\$Get("position")</code></li> <li>• b.) the name of a <b>method</b> of each Node in the tree, e.g. <code>acme\$Get("levelZeroBased")</code>, where e.g. <code>acme\$levelZeroBased &lt;- function() acme\$level - 1</code></li> <li>• c.) a <b>function</b>, whose first argument must be a Node e.g. <code>acme\$Get(function(node) node\$cost * ...)</code></li> </ul>

...	in case the attribute is a function or a method, the ellipsis is passed to it as additional arguments.
format	if FALSE (the default), no formatting is being used. If TRUE, then the first formatter (if any) found along the ancestor path is being used for formatting (see <a href="#">SetFormat</a> ). If format is a function, then the collected value is passed to that function, and the result is returned.
inheritFromAncestors	if TRUE, then the path above a Node is searched to get the attribute in case it is NULL.
nullAsNa	If TRUE (the default), then NULL is returned as NA. Otherwise it is returned as NULL.

### Examples

```
data(acme)
GetAttribute(acme$IT$Outsource, "cost")
```

---

GetPhyloNr

*Determine the number a Node has after conversion to a phylo object*

---

### Description

Use this function when plotting a Node as a phylo, e.g. to set custom labels to plot.

### Usage

```
GetPhyloNr(x, type = c("node", "edge"))
```

### Arguments

x	The Node
type	Either "node" (the default) or "edge" (to get the number of the edge from x to its parent)

### Value

an integer representing the node

### See Also

Other ape phylo conversions: [as.Node.phylo](#), [as.phylo.Node](#)

**Examples**

```
library(ape)
library(data.tree)
data(acme)
ap <- as.phylo(acme)
#plot(ap)
#nodeLabels("IT Dep.", GetPhyloNr(Climb(acme, "IT")))
#edgeLabels("Good!", GetPhyloNr(Climb(acme, "IT", "Switch to R"), "edge"))
```

---

isLeaf	<i>Check if a Node is a leaf</i>
--------	----------------------------------

---

**Description**

Check if a Node is a leaf

**Usage**

```
isLeaf(node)
```

**Arguments**

node            The Node to test.

**Value**

TRUE if the Node is a leaf, FALSE otherwise

---

isNotLeaf	<i>Check if a Node is not a leaf</i>
-----------	--------------------------------------

---

**Description**

Check if a Node is not a leaf

**Usage**

```
isNotLeaf(node)
```

**Arguments**

node            The Node to test.

**Value**

FALSE if the Node is a leaf, TRUE otherwise

---

isNotRoot	<i>Check if a Node is not a root</i>
-----------	--------------------------------------

---

**Description**

Check if a Node is not a root

**Usage**

```
isNotRoot(node)
```

**Arguments**

node	The Node to test.
------	-------------------

**Value**

FALSE if the Node is the root, TRUE otherwise

---

isRoot	<i>Check if a Node is the root</i>
--------	------------------------------------

---

**Description**

Check if a Node is the root

**Usage**

```
isRoot(node)
```

**Arguments**

node	The Node to test.
------	-------------------

**Value**

TRUE if the Node is the root, FALSE otherwise

---

mushroom

*Sample Data: Data Used by the ID3 Vignette*

---

### Description

mushroom contains attributes of mushrooms. We can use this data to predict a mushroom's toxicity based on its attributes. The attributes available in the data set are:

### Usage

```
data(mushroom)
```

### Format

```
data.frame
```

### Details

- color the color of a mushroom
- size whether a mushroom is small or large
- points whether a mushroom has points
- edibility whether a mushroom is edible or toxic

---

Navigate

*Navigate to another node by relative path.*

---

### Description

Navigate to another node by relative path.

### Usage

```
Navigate(node, path)
```

### Arguments

node	The starting <a href="#">Node</a> to navigate
path	A string or a character vector describing the path to navigate

### Details

The path is always relative to the node. Navigation to the parent is defined by `..`, whereas navigation to a child is defined via the child's name. If path is provided as a string, then the navigation steps are separated by `'/'`.

**See Also**[Climb](#)**Examples**

```
data(acme)
Navigate(acme$Research, "../IT/Outsource")
Navigate(acme$Research, c("../", "IT", "Outsource"))
```

---

**Node***Create a data.tree Structure With Nodes*

---

**Description**

Node is at the very heart of the `data.tree` package. All trees are constructed by tying together Node objects.

**Usage**

```
# n1 <- Node$new("Node 1")
```

**Format**

An [R6Class](#) generator object

**Details**

Assemble Node objects into a `data.tree` structure and use the traversal methods to set, get, and perform operations on it. Typically, you construct larger tree structures by converting from `data.frame`, `list`, or other formats.

**Fields**

`children` A list of child Nodes

`parent` The node's parent Node

**Methods**

`Node$new(name)` Creates a new Node called `name`. Often used to construct the root when creating trees programmatically.

`AddChild(name)` Creates a new Node called `name` and adds it to this Node as a child.

`AddChildNode(node)` Adds a Node as a child.

`AddSibling(name)` Creates a new Node called `name` and adds it after this Node as a sibling.

`AddSiblingNode(sibling)` Adds a new Node after this Node, as a sibling.

`RemoveChild(name)` Remove the child Node called `name` from a Node and returns it.

`RemoveAttribute(name, stopIfNotAvailable)` Removes attribute called name from this Node. Gives an error if stopIfNotAvailable and the attribute does not exist.

`Climb(...)` Find a node with path ..., where the ... arguments are the names of the Nodes, or other field values.

`Navigate(path)` Find a node by relative path

`FindNode(name)` Find a node with name name. Especially useful if `AreNamesUnique` is TRUE

`Get(attribute, ..., traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"), pruneFun = ...)` Traverses the tree and collects values along the way.

`Do(fun, ..., traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"), pruneFun = ...)` Traverses the tree and call fun on each node.

`Set(..., traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"), pruneFun = NULL)` Traverses the tree and assigns the args along the way, recycling the args.

`Sort(attribute, ..., decreasing = FALSE, recursive = TRUE)` Sort children of a node with respect to an attribute (field, method, active, function)

`Revert(recursive = TRUE)` Revert the sort order of a node

`Prune(pruneFun)` Prune a tree. The pruneFun takes a node as its first argument, and returns TRUE if the node should be kept, FALSE otherwise

### Actives (aka Properties)

`name` Gets or sets the name of a Node. For example `Node$name <- "Acme"`

`parent` Gets or sets the parent Node of a Node. Only set this if you know what you are doing, as you might mess up the tree structure!

`children` Gets or sets the children list of a Node. Only set this if you know what you are doing, as you might mess up the tree structure!

`siblings` Returns a list of the siblings of this Node

`fields` Gets the names of the set properties of a Node

`fieldsAll` Gets the names of the set properties of a Node or any of its sub-Nodes

`isLeaf` Returns TRUE if the Node is a leaf, FALSE otherwise

`isRoot` Returns TRUE if the Node is the root, FALSE otherwise

`count` Returns the number of children of a Node

`totalCount` Returns the total number of Nodes in the tree

`path` Returns a vector of mode character containing the names of the Nodes in the path from the root to this Node

`pathString` Returns a string representing the path to this Node, separated by backslash

`levelName` Returns the name of the Node, preceded by level times '\*'. Useful for printing.

`leafCount` Returns the number of leaves are below a Node

`leaves` Returns a list containing all the leaf Nodes

`level` Returns an integer representing the level of a Node. For example, the root has level 1.

`height` Returns max(level) of any of the Nodes of the tree

`averageBranchingFactor` Returns the average number of crotches below this Node

`root` Returns the root Node of a Node's tree

**See Also**

For more details see the [data.tree](#) documentations, or the `data.tree` vignette: `vignette("data.tree")`

**Examples**

```
library(data.tree)
acme <- Node$new("Acme Inc.")
accounting <- acme$AddChild("Accounting")$
  AddSibling("Research")$
  AddChild("New Labs")$
  parent$
  AddSibling("IT")$
  AddChild("Outsource")
print(acme)
```

---

NODE\_RESERVED\_NAMES\_CONST

*Names that are reserved by the Node class.*

---

**Description**

These are reserved by the Node class, you cannot use these as attribute names. Note also that all fields starting with a `.` are reserved.

**Usage**

NODE\_RESERVED\_NAMES\_CONST

**Format**

An object of class character of length 40.

---

plot.Node

*Plot a graph, or get a graphviz dot representation of the tree*

---

**Description**

Use these methods to style your graph, and to plot it. The functionality is built around the DiagrammeR package, so for anything that goes beyond simple plotting, it is recommended to read its documentation at <http://rich-iannone.github.io/DiagrammeR/docs.html>

**Usage**

```
## S3 method for class 'Node'
plot(x, ..., direction = c("climb", "descend"),
     pruneFun = NULL, output = "graph")

ToDiagrammerGraph(root, direction = c("climb", "descend"), pruneFun = NULL)

SetNodeStyle(node, inherit = TRUE, keepExisting = FALSE, ...)

SetEdgeStyle(node, inherit = TRUE, keepExisting = FALSE, ...)

SetGraphStyle(root, keepExisting = FALSE, ...)

GetDefaultTooltip(node)
```

**Arguments**

x	The root node of the data.tree structure to plot
...	For the SetStyle methods, this can be any stlyeName / value pair. See <a href="http://graphviz.org/Documentation.p">http://graphviz.org/Documentation.p</a> for details. For the plot.Node generic method, this is not used.
direction	when converting to a network, should the edges point from root to children ("climb") or from child to parent ("descend")?
pruneFun	allows providing a a prune criteria, i.e. a function taking a Node as an input, and returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its entire sub-tree will not be considered.
output	a string specifying the output type; graph (the default) renders the graph using the grViz function and visNetwork renders the graph using the visnetwork function.
root	The root <a href="#">Node</a> of the data.tree structure to visualize.
node	The <a href="#">Node</a> of the data.tree structure on which you would like to set style attributes.
inherit	If TRUE, then children will inherit this node's style. Otherwise they inherit from this node's parent. Note that the inherit always applies to the node, i.e. all style attributes of a node and not to a single style attribute.
keepExisting	If TRUE, then style attributes are added to possibly existing style attributes on the node.

**Details**

Use SetNodeStyle and SetEdgeStyle to define the style of your plot. Use plot to display a graphical representation of your tree.

The most common styles that can be set on the nodes are:

- color
- fillcolor

- fixedsize true or false
- fontcolor
- fontname
- fontsize
- height
- penwidth
- shape box, ellipse, polygon, circle, box, etc.
- style
- tooltip
- width

The most common styles that can be set on the edges are:

- arrowhead e.g. normal, dot, vee
- arrowsize
- arrowtail
- color
- dir forward, back, both, none
- fontcolor
- fontname
- fontsize
- headport
- label
- minlen
- penwidth
- tailport
- tooltip

A good source to understand the attributes is <http://graphviz.org/Documentation.php>. Another good source is the DiagrammeR package documentation, or more specifically: <http://rich-iannone.github.io/DiagrammeR/docs.htm>

In addition to the standard GraphViz functionality, the `data.tree` plotting infrastructure takes advantage of the fact that `data.tree` structure are always hierarchic. Thus, style attributes are inherited from parents to children on an individual basis. For example, you can set the `fontcolor` to red on a parent, and then all children will also have red font, except if you specifically disallow inheritance. Labels and tooltips are never inherited.

Another feature concerns functions: Instead of setting a fixed value (e.g. `SetNodeStyle(acme, label = "Acme. Inc")`), you can set a function (e.g. `SetNodeStyle(acme, label = function(x) x$name)`). The function must take a `Node` as its single argument. Together with inheritance, this becomes a very powerful tool.

The `GetDefaultTooltip` method is a utility method that can be used to print all fields of a `Node`.

There are some more examples in the 'applications' vignette, see `vignette('applications', package = "data.tree")`

**Examples**

```

data(acme)
SetGraphStyle(acme, rankdir = "TB")
SetEdgeStyle(acme, arrowhead = "vee", color = "blue", penwidth = 2)
#per default, Node style attributes will be inherited:
SetNodeStyle(acme, style = "filled,rounded", shape = "box", fillcolor = "GreenYellow",
             fontname = "helvetica", tooltip = GetDefaultTooltip)
SetNodeStyle(acme$IT, fillcolor = "LightBlue", penwidth = "5px")
#inheritance can be avoided:
SetNodeStyle(acme$Accounting, inherit = FALSE, fillcolor = "Thistle",
             fontcolor = "Firebrick", tooltip = "This is the accounting department")
SetEdgeStyle(acme$Research$`New Labs`,
             color = "red",
             label = "Focus!",
             penwidth = 3,
             fontcolor = "red")
#use Do to set style on specific nodes:
Do(acme$leaves, function(node) SetNodeStyle(node, shape = "egg"))
plot(acme)

```

---

print.Node

---

*Print a Node in a human-readable fashion.*


---

**Description**

Print a Node in a human-readable fashion.

**Usage**

```

## S3 method for class 'Node'
print(x, ..., pruneMethod = c("simple", "dist", NULL),
      limit = 100, pruneFun = NULL)

```

**Arguments**

x	The Node
...	Node attributes to be printed. Can be either a character (i.e. the name of a Node field), a Node method, or a function taking a Node as a single argument. See <code>Get</code> for details on the meaning of attribute.
pruneMethod	The method can be used to prune for printing in a simple way. If <code>NULL</code> , the entire tree is displayed. If "simple", then only the first <code>limit</code> nodes are displayed. If "dist", then Nodes are removed everywhere in the tree, according to their level. If <code>pruneFun</code> is provided, then <code>pruneMethod</code> is ignored.
limit	The maximum number of nodes to print. Can be <code>NULL</code> if the entire tree should be printed.
pruneFun	allows providing a a prune criteria, i.e. a function taking a Node as an input, and returning <code>TRUE</code> or <code>FALSE</code> . If the <code>pruneFun</code> returns <code>FALSE</code> for a Node, then the Node and its entire sub-tree will not be considered.

**Examples**

```

data(acme)
print(acme, "cost", "p")
print(acme, "cost", probability = "p")
print(acme, expectedCost = function(x) x$cost * x$p)
do.call(print, c(acme, acme$fieldsAll))

tree <- CreateRegularTree(4, 5)
# print entire tree:
print(tree, pruneMethod = NULL)
# print first 20 nodes:
print(tree, pruneMethod = "simple", limit = 20)
# print 20 nodes, removing leafs first:
print(tree, pruneMethod = "dist", limit = 20)
# provide your own pruning function:
print(tree, pruneFun = function(node) node$position != 2)

```

---

Prune

*Prunes a tree.*


---

**Description**

Pruning refers to removing entire subtrees. This function has side-effects, it modifies your data.tree structure!

**Usage**

```
Prune(node, pruneFun)
```

**Arguments**

node	The root of the sub-tree to be pruned
pruneFun	allows providing a a prune criteria, i.e. a function taking a Node as an input, and returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its entire sub-tree will not be considered.

**Value**

the number of nodes removed

**See Also**

[Node](#)

## Examples

```
data(acme)
acme$Do(function(x) x$cost <- Aggregate(x, "cost", sum))
Prune(acme, function(x) x$cost > 700000)
print(acme, "cost")
```

---

Revert

*Reverts the sort order of a Node's children.*

---

## Description

Reverts the sort order of a Node's children.

## Usage

```
Revert(node, recursive = TRUE)
```

## Arguments

node	the Node whose children's sort order is to be reverted
recursive	If TRUE, then revert is called recursively on all children.

## Value

returns the Nodel invisibly (for chaining)

## See Also

[Node](#)  
[Sort](#)

---

Set

*Traverse a Tree and Assign Values*

---

## Description

The method takes one or more vectors as an argument. It traverses the tree, whereby the values are picked from the vector. Also available as OO-style method on [Node](#).

**Usage**

```
#OO-style:
# node$Set(...,
#     traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"),
#     pruneFun = NULL,
#     filterFun = NULL)
#traditional:
Set(nodes, ...)
```

**Arguments**

nodes            The nodes on which to perform the Get (typically obtained via [Traverse](#))  
 ...              each argument can be a vector of values to be assigned. Recycled.

**Value**

invisibly returns the nodes (useful for chaining)

**See Also**

[Node](#)  
[Get](#)  
[Do](#)  
[Traverse](#)

**Examples**

```
data(acme)
acme$Set(departmentId = 1:acme$totalCount, openingHours = NULL, traversal = "post-order")
acme$Set(head = c("Jack Brown",
                 "Mona Moneyhead",
                 "Dr. Frank N. Stein",
                 "Eric Nerdahl"
                ),
        filterFun = function(x) !x$isLeaf
      )
print(acme, "departmentId", "head")
```

---

 SetFormat

*Set a formatter function on a specific node*


---

**Description**

Formatter functions set on a Node act as a default formatter when printing and using the [Get](#) method. The formatter is inherited, meaning that whenever Get fetches an attribute from a Node, it checks on the Node or on any of its ancestors whether a formatter is set.

**Usage**

```
SetFormat(node, name, formatFun)
```

**Arguments**

node	The node on which to set the formatter
name	The attribute name for which to set the formatter
formatFun	The formatter, i.e. a function taking a value as an input, and formatting returning the formatted value

**See Also**

Get  
print.Node

**Examples**

```
data(acme)
acme$Set(id = 1:(acme$totalCount))
SetFormat(acme, "id", function(x) FormatPercent(x, digits = 0))
SetFormat(Climb(acme, "IT"), "id", FormatFixedDecimal)
print(acme, "id")
# Calling Get with an explicit formatter will overwrite the default set on the Node:
print(acme, id = acme$Get("id", format = function(x) paste0("id:", x)))

# Or, to avoid formatters, even though you set them on a Node:
print(acme, id = acme$Get("id", format = identity))
```

---

Sort

---

*Sort children of a Node or an entire data.tree structure*


---

**Description**

You can sort with respect to any argument of the tree. But note that sorting has side-effects, meaning that you modify the underlying, original data.tree object structure.

**Usage**

```
Sort(node, attribute, ..., decreasing = FALSE, recursive = TRUE)
```

**Arguments**

node	The node whose children are to be sorted
attribute	determines what is collected. The attribute can be <ul style="list-style-type: none"> <li>• a.) the name of a <b>field</b> or a <b>property/active</b> of each Node in the tree, e.g. <code>acme\$Get("p")</code> or <code>acme\$Get("position")</code></li> <li>• b.) the name of a <b>method</b> of each Node in the tree, e.g. <code>acme\$Get("levelZeroBased")</code>, where e.g. <code>acme\$levelZeroBased &lt;- function() acme\$level - 1</code></li> <li>• c.) a <b>function</b>, whose first argument must be a Node e.g. <code>acme\$Get(function(node) node\$cost * ...)</code></li> </ul>
...	any parameters to be passed on the the attribute (in case it's a method or a function)
decreasing	sort order
recursive	if TRUE, Sort will be called recursively on the Node's children. This allows sorting an entire tree.

**Value**

Returns the node on which Sort is called, invisibly. This can be useful to chain Node methods.

**See Also**

[Node](#)

[Revert](#)

**Examples**

```
data(acme)
acme$Do(function(x) x$totalCost <- Aggregate(x, "cost", sum), traversal = "post-order")
Sort(acme, "totalCost", decreasing = FALSE)
print(acme, "totalCost")
```

---

ToNewick

*Write a data.tree structure to Newick notation*

---

**Description**

To read from Newick, you can use the `ape` package, and convert the resulting phylo object to a `data.tree` structure.

**Usage**

```
ToNewick(node, heightAttribute = DefaultPlotHeight, ...)
```

**Arguments**

node	The root Node of a tree or sub-tree to be converted
heightAttribute	The attribute (field name, method, or function) storing or calculating the height for each Node
...	parameters that will be passed on the the heightAttributeName, in case it is a function

**See Also**

Other Conversions from Node: [as.dendrogram.Node](#)

**Examples**

```
data(acme)
ToNewick(acme)
ToNewick(acme, heightAttribute = NULL)
ToNewick(acme, heightAttribute = function(x) DefaultPlotHeight(x, 200))
ToNewick(acme, rootHeight = 200)
```

Traverse

*Traverse a tree or a sub-tree*

**Description**

Traverse takes the root of a tree or a sub-tree, and "walks" the tree in a specific order. It returns a list of [Node](#) objects, filtered and pruned by filterFun and pruneFun.

**Usage**

```
Traverse(node, traversal = c("pre-order", "post-order", "in-order", "level",
    "ancestor"), pruneFun = NULL, filterFun = NULL)
```

**Arguments**

node	the root of a tree or a sub-tree that should be traversed
traversal	any of 'pre-order' (the default), 'post-order', 'in-order', 'level', 'ancestor', or a custom function (see details)
pruneFun	allows providing a a prune criteria, i.e. a function taking a Node as an input, and returning TRUE or FALSE. If the pruneFun returns FALSE for a Node, then the Node and its entire sub-tree will not be considered.
filterFun	allows providing a a filter, i.e. a function taking a Node as an input, and returning TRUE or FALSE. Note that if filter returns FALSE, then the node will be excluded from the result (but not the entire subtree).

**Details**

The traversal order is as follows. (Note that these descriptions are not precise and complete. They are meant for quick reference only. See the `data.tree` vignette for a more detailed description).

**pre-order** Go to first child, then to its first child, etc.

**post-order** Go to the first branch's leaf, then to its siblings, and work your way back to the root

**in-order** Go to the first branch's leaf, then to its parent, and only then to the leaf's sibling

**level** Collect root, then level 2, then level 3, etc.

**ancestor** Take a node, then the node's parent, then that node's parent in turn, etc. This ignores the `pruneFun`

**function** You can also provide a function, whose sole parameter is a [Node](#) object. The function is expected to return the node's next node, a list of the node's next nodes, or `NULL`.

**Value**

a list of Nodes

**See Also**

[Node](#)

[Get](#)

[Set](#)

[Do](#)

# Index

## \*Topic **Newick**

ToNewick, [48](#)

## \*Topic **datasets**

acme, [3](#)

mushroom, [37](#)

Node, [38](#)

NODE\_RESERVED\_NAMES\_CONST, [40](#)

acme, [3](#)

Aggregate, [3](#), [25](#)

AreNamesUnique, [5](#), [7](#), [29](#), [39](#)

as.data.frame.Node, [5](#), [13](#), [25](#)

as.dendrogram.Node, [8](#), [25](#), [27](#), [49](#)

as.igraph.Node, [9](#)

as.list.Node, [10](#)

as.Node, [11](#), [13](#), [15](#), [16](#), [19](#), [25](#)

as.Node.BinaryTree, [11](#)

as.Node.data.frame, [11](#), [12](#), [15](#), [16](#), [19](#), [25](#)

as.Node.dendrogram, [11](#), [13](#), [14](#), [16](#), [19](#), [25](#)

as.Node.list, [11](#), [13](#), [15](#), [15](#), [19](#)

as.Node.party, [17](#)

as.Node.phylo, [11](#), [13](#), [15](#), [16](#), [19](#), [20](#), [25](#), [34](#)

as.phylo.Node, [19](#), [20](#), [25](#), [27](#), [34](#)

averageBranchingFactor, [20](#)

CheckNameReservedWord, [21](#)

Climb, [21](#), [38](#), [39](#)

Clone, [22](#)

CreateRandomTree, [23](#)

CreateRegularTree, [24](#)

Cumulate, [24](#), [25](#)

data.tree, [25](#), [26](#), [40](#)

data.tree-package (data.tree), [25](#)

DefaultPlotHeight, [27](#)

dendrogram, [8](#), [14](#)

Distance, [28](#)

Do, [25](#), [28](#), [33](#), [39](#), [46](#), [50](#)

FindNode, [29](#), [39](#)

FormatFixedDecimal, [30](#)

FormatPercent, [31](#)

FromDataFrameNetwork

(as.Node.data.frame), [12](#)

FromDataFrameTable

(as.Node.data.frame), [12](#)

FromListExplicit (as.Node.list), [15](#)

FromListSimple (as.Node.list), [15](#)

Get, [4](#), [6](#), [25](#), [29](#), [31](#), [39](#), [46](#), [50](#)

GetAttribute, [33](#)

GetDefaultTooltip (plot.Node), [40](#)

GetPhyloNr, [19](#), [20](#), [34](#)

isLeaf, [35](#)

isNotLeaf, [35](#)

isNotRoot, [36](#)

isRoot, [36](#)

mushroom, [37](#)

Navigate, [22](#), [37](#), [39](#)

Node, [4](#), [21](#), [22](#), [25](#), [26](#), [29](#), [31](#), [33](#), [37](#), [38](#), [41](#),  
[42](#), [44–46](#), [48–50](#)

NODE\_RESERVED\_NAMES\_CONST, [40](#)

plot.Node, [40](#)

print, [25](#)

print.Node, [43](#)

Prune, [25](#), [39](#), [44](#)

R6Class, [38](#)

Revert, [39](#), [45](#), [48](#)

sapply, [32](#)

Set, [25](#), [29](#), [33](#), [39](#), [45](#), [50](#)

SetEdgeStyle (plot.Node), [40](#)

SetFormat, [32](#), [34](#), [46](#)

SetGraphStyle (plot.Node), [40](#)

SetNodeStyle (plot.Node), [40](#)

Sort, [25](#), [39](#), [45](#), [47](#)

ToDataFrameNetwork  
    (as.data.frame.Node), 5  
ToDataFrameTable (as.data.frame.Node), 5  
ToDataFrameTree (as.data.frame.Node), 5  
ToDataFrameTypeCol  
    (as.data.frame.Node), 5  
ToDiagrammeRGraph (plot.Node), 40  
ToListExplicit (as.list.Node), 10  
ToListSimple (as.list.Node), 10  
ToNewick, 8, 27, 48  
Traverse, 6, 25, 29, 32, 33, 46, 49