Package ‘data.tree’

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Maintainer  Christoph Glur <christoph.glur@ipub.com>
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R topics documented:

  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.Node.rpart .......................................... 20
  as.phylo.Node .......................................... 21
  averageBranchingFactor ................................. 21
  CheckNameReservedWord ................................ 22
  Climb ................................................... 22
  Clone ..................................................... 23
  CreateRandomTree ....................................... 24
  CreateRegularTree ..................................... 25
  Cumulate ................................................ 25
  data.tree ............................................... 26
  DefaultPlotHeight ...................................... 28
  Distance ................................................ 29
  Do ......................................................... 29
  FindNode ............................................... 30
  FormatFixedDecimal .................................... 31
  FormatPercent .......................................... 32
  Get ....................................................... 32
  GetAttribute ............................................ 34
  GetPhyloNr ............................................... 35
  isLeaf ................................................... 36
  isNotLeaf ............................................... 36
  isNotRoot ............................................... 37
  isRoot .................................................. 37
  mushroom ................................................. 38
  Navigate ................................................ 38
  Node ..................................................... 39
  NODE_RESERVED_NAMES_CONST .............................. 41
acme

Sample Data: A Simple Company with Departments

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.

Aggregate

Aggregate child values of a Node, recursively.

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, ...)

Index

acme

3
Arguments

node       the Node on which to aggregate
attribute  determines what is collected. The attribute can be
            • a.) the name of a **field** or a **property/active** of each Node in the tree, e.g.
              acme$Get("p") or acme$Get("position")
            • b.) the name of a **method** of each Node in the tree, e.g. acme$Get("levelZeroBased"),
                where e.g. acme$levelZeroBased <- function() acme$level - 1
            • c.) a **function**, whose first argument must be a Node e.g. acme$Get(function(node)
                node$cost * node$p)

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

Test whether all node names are unique.

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
Convert a data.tree structure to a data.frame

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

```r
## 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 `make.names`) is optional.
- `...` the attributes to be added as columns of the data.frame. See `Get` for details. If a specific Node does not contain the attribute, NA is added to the data.frame.
- `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 `Traverse` 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**

```r
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')
)
p`
as.dendrogram.Node  
*Convert a Node to a dendrogram*

**Description**

Convert a `data.tree` structure to a `dendrogram`

**Usage**

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

**Arguments**

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

**Value**

An object of class dendrogram

**See Also**

Other Conversions from Node: `ToNewick`

**Examples**

```r
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(x, vertexAttributes = character(),
                edgeAttributes = character(), directed = FALSE,
                direction = c("climb", "descend"), ...)

Arguments

x          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")?
...         Currently unused.

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

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

Description

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

Usage

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

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

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

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.
- **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.
- **...**: Additional parameters passed to `as.list.Node`

Examples

```r
data(acme)

str(ToListSimple(acme))
str(ToListSimple(acme, keepOnly = "cost"))
```
as.Node

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

as.Node

Convert an object to a data.tree data structure

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.rpart

as.Node.BinaryTree

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

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.
...
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
  • "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)
  • "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)
  • "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
network  A data.frame in network format, i.e. it must adhere to the following requirements:
  • It must contain as many rows as there are nodes (excluding the root, there is no row for the root)
  • Its first and second columns contain the network relationships. This can be either climbing (from parent to children) or descending (from child to parent)
  • Its subsequent columns contain the attributes to be set as fields on the nodes
  • It must contain a single root
  • There are no cycles in the network

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.rpart, 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")
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
  • "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)
  • "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)
  • "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
...

Additional parameters
as.Node.list

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.rpart, 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
cell. "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

- "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)
- "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)
- "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

...  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.rpart, as.Node

Examples

```r
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")
)
```

as.Node.party

```r
list(head = "Helen",
     born = "1840-17-08",
     died = "1845-01-01")
)
FromListSimple(kingJosephs, nodeName = "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 party from the partykit package to a data.tree structure.*

**Description**

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

**Usage**

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

**Arguments**

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

**Examples**

```r
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

```r
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"))))
```

```r
pn
```

### tree ###

#### party: associate recursive partynode structure with data

```r
py <- party(pn, WeatherPlay)
tree <- as.Node(py)
```

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

```r
SetNodeStyle(tree,
  label = function(node) paste0(node$name, ": ", node$splitname),
  tooltip = function(node) paste0(nrow(node$data), " observations"),
  fontname = "helvetica")
```

```r
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))
  })
)
```

```r
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)
  })
)
```

```r
plot(tree)
```
as.Node.phylo

Convert a phylo object from the ape package to a Node

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.rpart, as.Node

Examples

```r
# which bird families 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.Node.rpart

Convert an rpart object to a data.tree structure

Description

Convert an rpart object to a data.tree structure

Usage

## S3 method for class 'rpart'
as.Node(x, digits = getOption("digits") - 3,
      use.n = FALSE, ...)

Arguments

x the rpart object to be converted
digits the number of digits to be used for numeric values in labels
use.n logical. Add cases to labels, see text.rpart for further information
... any other argument to be passed to generic sub implementations

Value

a data.tree object. The tree contains a field rpart.id which references back to the original node id in the row names of the rpart object.

See Also

Other as.Node: as.Node.data.frame, as.Node.dendrogram, as.Node.list, as.Node.phylo, as.Node

Examples

if (require(rpart)) {
  fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
  as.Node(fit)
}
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
  heightAttribute

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
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
• "check": if the name conformance should be checked and warnings should be printed in case of non-conformance (the default)
• "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)
• "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

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 provided argument.

Usage

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

Arguments

node  The root Node of the tree or subtree to climb
...  an attribute name to searched value pairlist. For brevity, you can also provide a character vector.
Clone

Value

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

See Also

Node

Navigate

Examples

```r
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

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

Arguments

- `node` the root node of the tree or sub-tree to clone
- `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.
- `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)
acline <- Clone(acme)
acline$name <- "New Acme"
# acmeClone does not point to the same reference object anymore:
acline$name

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

---

CreateRandomTree  Create a tree for demo and testing

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
  - a.) the name of a **field** or a **property/active** of each Node in the tree, e.g. acme$Get("p") or acme$Get("position")
  - b.) the name of a **method** of each Node in the tree, e.g. acme$Get("levelZeroBased"), where e.g. acme$levelZeroBased <- function() acme$level - 1
  - c.) a **function**, whose first argument must be a Node e.g. acme$Get(function(node) node$cost * node$p)
- **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

```r
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: Hierarchical Data Structures

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, yml, 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**

```r
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
```
DefaultPlotHeight

Calculates the height of a Node given the height of the root.

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

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

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

**Arguments**

- **nodes**
  The nodes on which to perform the Get (typically obtained via Traverse)
- **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

```r
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**

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

**Arguments**

- `x`  
  a numeric scalar or vector
- `digits`  
  the number of digits to print after the decimal point

**Value**

A string corresponding to `x`, suitable for printing

**Examples**

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

**Format a Number as a Percentage**

**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**

- `x`: A number
- `digits`: The number of digits to print
- `format`: The format to use
- `...`: Any other argument passed to `formatC`

**Value**

A string corresponding to `x`, suitable for printing

**See Also**

`formatC`

**Examples**

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

---

Get

**Traverse a Tree and Collect Values**

**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`. 
Get

Usage

# OO-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 Traverse)

attribute determines what is collected. The attribute can be

  • a.) the name of a field or a property/active of each Node in the tree, e.g.
    acme$Get("p") or acme$Get("position")

  • b.) the name of a method of each Node in the tree, e.g. acme$Get("levelZeroBased"),
    where e.g. acme$levelZeroBased <- function() acme$level - 1

  • c.) a function, whose first argument must be a Node e.g. acme$Get(function(node)
    node$cost * node$p)

... 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 SetFormat). 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 sapply, 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

Get an attribute from a Node.

Description
Get an attribute from a Node.

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

Arguments
node
The Node from which the attribute should be fetched.
attribute
determines what is collected. The attribute can be
  • a.) the name of a field or a property/active of each Node in the tree, e.g.
    acmeGet("p") or acmeGet("position")
  • b.) the name of a method of each Node in the tree, e.g. acmeGet("levelZeroBased"),
    where e.g. acme$levelZeroBased <- function() acme$level - 1
  • c.) a function, whose first argument must be a Node e.g. acmeGet(function(node)
      node$cost * node$p)
GetPhyloNr

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 SetFormat). 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
isNotLeaf

Examples

```r
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

**Check if a Node is a leaf**

**Description**

Check if a Node is a leaf

**Usage**

```r
isLeaf(node)
```

**Arguments**

- `node` The Node to test.

**Value**

TRUE if the Node is a leaf, FALSE otherwise

isNotLeaf

**Check if a Node is not a leaf**

**Description**

Check if a Node is not a leaf

**Usage**

```r
isNotLeaf(node)
```

**Arguments**

- `node` The Node to test.

**Value**

FALSE if the Node is a leaf, TRUE otherwise
isNotRoot

*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

*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 Node 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 ‘/’. 
Node

See Also

Climb

Examples

```r
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**

```r
# 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 = NULL, filterFun = NULL, format = NULL, inheritFromAncestors = FALSE, simplify = c(TRUE, FALSE, "array", "regular")) Traverses the tree and collects values along the way.

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

Set(..., traversal = c("pre-order", "post-order", "in-order", "level", "ancestor"), pruneFun = NULL, filterFun = 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

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

Description

Names that are reserved by the Node class.

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. Note that DiagrammeR is only suggested by data.tree, so 'plot' only works if you have installed it on your system.
Usage

```r
## 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 styleName/value pair. See [http://graphviz.org/Documentation.php](http://graphviz.org/Documentation.php) 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 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 Node of the data.tree structure to visualize.

- **node**
  - The Node 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.html

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 p as label, where available:
SetNodeStyle(acme, label = function(node) node$p)
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 Get for details on the meaning of attribute.

- **pruneMethod**
  The method can be used to prune for printing in a simple way. If NULL, the entire tree is displayed. If "simple", then only the first limit nodes are displayed. If "dist", then Nodes are removed everywhere in the tree, according to their level. If pruneFun is provided, then pruneMethod is ignored.
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
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 Node invisibly (for chaining)

See Also

Node
Sort
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

- a.) the name of a field or a property/active of each Node in the tree, e.g. acme$Get("p") or acme$Get("position")
- b.) the name of a method of each Node in the tree, e.g. acme$Get("levelZeroBased"), where e.g. acme$levelZeroBased <- function() acme$level - 1
- c.) a function, whose first argument must be a Node e.g. acme$Get(function(node) node$cost * node$p)

... 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

```r
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)
Traverse

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 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 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, 50

*Topic datasets  
acme, 3  
mushroom, 38  
Node, 39  
NODE_RESERVED_NAMES_CONST, 41

acme, 3  
Aggregate, 3, 26  
AreNamesUnique, 5, 7, 30, 40  
as.data.frame.Node, 5, 13, 26  
as.dendrogram.Node, 8, 26, 28, 50  
as.igraph.Node, 9  
as.list.Node, 10  
as.Node, 11, 13, 15, 16, 19, 20, 26  
as.Node.BinaryTree, 11  
as.Node.data.frame, 11, 12, 15, 16, 19, 20, 26  
as.Node.dendrogram, 11, 13, 14, 16, 19, 20, 26  
as.Node.list, 11, 13, 15, 16, 19, 20  
as.Node.party, 17  
as.Node.phylo, 11, 13, 15, 16, 19, 20, 21, 26, 35  
as.Node.rpart, 11, 13, 15, 16, 19, 20  
as.phylo.Node, 19, 21, 26, 28, 35  
averageBranchingFactor, 21

CheckNameReservedWord, 22  
Climb, 22, 39, 40  
Clone, 23  
CreateRandomTree, 24  
CreateRegularTree, 25  
Cumulate, 25, 26

data.tree, 26, 27, 41  
data.tree-package (data.tree), 26  
DefaultPlotHeight, 28  
dendrogram, 8, 14

Distance, 29  
Do, 26, 29, 34, 40, 47, 51

FindNode, 30, 40  
FormatFixedDecimal, 31  
FormatPercent, 32  
FromDataFrameNetwork, 31  
(as.Node.data.frame), 12  
FromDataFrameTable, 31  
(as.Node.data.frame), 12  
FromListExplicit, 31  
(as.Node.list), 15  
FromListSimple, 31  
(as.Node.list), 15

Get, 4, 6, 26, 30, 32, 40, 47, 48, 51  
GetAttribute, 34  
GetDefaultTooltip, 34  
(plot.Node), 41  
GetPhyloNr, 19, 21, 35

isLeaf, 36  
isNotLeaf, 36  
isNotRoot, 37  
isRoot, 37

mushroom, 38

Navigate, 23, 38, 40  
Node, 4, 22, 23, 26, 27, 30, 32, 34, 38, 39, 42, 43, 46, 47, 49–51  
NODE_RESERVED_NAMES_CONST, 41

plot.Node, 41  
print, 26  
print.Node, 44  
Prune, 26, 40, 45

R6Class, 39  
Revert, 40, 46, 49  
rpart, 20

sapply, 33  
Set, 26, 30, 34, 40, 47, 51
INDEX

SetEdgeStyle(plot.Node), 41
SetFormat, 33, 35, 48
SetGraphStyle(plot.Node), 41
SetNodeStyle(plot.Node), 41
Sort, 26, 40, 46, 49

text.rpart, 20
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), 41
ToListExplicit (as.list.Node), 10
ToListSimple (as.list.Node), 10
ToNewick, 8, 28, 50
Traverse, 6, 26, 30, 33, 34, 47, 50