Package ‘TreeAndLeaf’

May 4, 2024

Type Package

Title Displaying binary trees with focus on dendrogram leaves

Version 1.16.0

Description The TreeAndLeaf package combines unrooted and force-directed graph algorithms in order to lay- out binary trees, aiming to represent multiple layers of information onto dendrogram leaves.

Author Leonardo W. Kume, Luis E. A. Rizzardi, Milena A. Cardoso, Mauro A. A. Castro

Maintainer Milena A. Cardoso <milenandreuzo@gmail.com>

Depends R(>= 4.0)

Imports RedeR(>= 1.40.4), igraph, ape

Suggests knitr, rmarkdown, BiocStyle, RUnit, BiocGenerics, stringr, geneplast, ggtree, ggplot2, dplyr, dendextend, RColorBrewer

License Artistic-2.0

Encoding UTF-8

RoxygenNote 7.1.1

VignetteBuilder knitr

biocViews Infrastructure, GraphAndNetwork, Software, Network, Visualization, DataRepresentation

NeedsCompilation no

git_url https://git.bioconductor.org/packages/TreeAndLeaf

git_branch RELEASE_3_19

git_last_commit 8dc2d27

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-03
TreeAndLeaf-package

Contents

TreeAndLeaf-package .................................................. 2
formatTree .............................................................. 3
phylo_species ........................................................... 4
phylo_tree ............................................................... 4
spdata ................................................................. 5
treeAndLeaf ............................................................ 5

Index

TreeAndLeaf-package  TreeAndLeaf: A graph layout for binary trees with focus on dendrogram leaves.

Description

The TreeAndLeaf package combines unrooted and force-directed graph algorithms in order to lay-out binary trees, aiming to represent multiple layers of information onto dendrogram leaves.

Details

Package: TreeAndLeaf
Type: Package
 Depends: R (>= 4.0)
 Imports: RedeR, igraph, ape
 Suggests: knitr, rmarkdown, BiocStyle, RUnit, BiocGenerics, stringr, RColorBrewer
 License: Artistic-2.0
 biocViews: NetworkEnrichment, GraphAndNetwork

Index

formatTree: A theme function for tree-and-leaf igraph objects.
treeAndLeaf: Layout a TreeAndLeaf diagram.

Further information is available from the vignettes vignette("TreeAndLeaf").

Author(s)

Leonardo W. Kume, Luis E. A. Rizzardi, Milena A. Cardoso, Mauro A. A. Castro
References


---

**formatTree**

A theme function for tree-and-leaf igraph objects.

**Description**

This function sets attributes of a tree-and-leaf igraph object for plotting in the RedeR app interface.

**Usage**

```r
formatTree(tal, theme = 1)
```

**Arguments**

- `tal`: An igraph object generated by the `TreeAndLeaf` function.
- `theme`: An integer ranging from 1 to 5 with desired theme. Options:
  1- A clean black and blue theme, for additional customizations.
  2- Green palette theme.
  3- Blue palette theme.
  4- Purple palette theme.
  5- Red palette theme.
  For detailed customization, see attributes in the `addGraph` method.

**Value**

An igraph object with attributes for RedeR application.

**See Also**

- `addGraph`
- `treeAndLeaf`

**Examples**

```r
library(RedeR)
hc <- hclust(dist(USArrests), "ave")
tal <- treeAndLeaf(hc)
tal <- formatTree(tal, theme = 5)
```
Species metadata from STRING-db v11

**Description**

Species metadata used in a phylo object.

**Usage**

```r
data(phylo_species)
```

**Format**

An object of class "data.frame"

**References**


Species tree from STRING-db v11

**Description**

A phylo object for the species tree available from the STRING-db v11.

**Usage**

```r
data(phylo_tree)
```

**Format**

An object of class "phylo"

**References**

**spdata**

*Genome statistics for eukaryotes with complete genome sequence*

**Description**

Data from the NCBI Genome Database for eukaryotes with complete genome sequence. The list of organisms were obtained from the KEGG Organisms Database, and taxonomy IDs were obtained from the NCBI Taxonomy Database.

**Usage**

`data(spdata)`

**Format**

An object of class "data.frame"

**References**


**Examples**

`data(spdata)`

---

**treeAndLeaf**

*Layout a TreeAndLeaf diagram.*

**Description**

This function transforms hclust and phylo objects into tree-and-leaf igraph objects.

**Usage**

`treeAndLeaf(obj)`

**Arguments**

`obj` An object of class 'hclust' or 'phylo'.

**Value**

A tree-and-leaf igraph object.
See Also

formatTree
hclust
as.phylo
addGraph
relax

Examples

library(ResdeR)
rdp <- RedPort()
hc <- hclust(dist(USArrests), "ave")
tal <- treeAndLeaf(hc)

## Not run:
calld(rdp)
addGraph(obj=rdp, tal)

## End(Not run)
Index

* datasets
  phylo_species, 4
  spdata, 5

* package
  TreeAndLeaf-package, 2

* phylotree
  phylo_tree, 4

  addGraph, 3, 6
  as.phylo, 6

  formatTree, 2, 3, 6
  hclust, 6

  phylo_species, 4
  phylo_tree, 4

  relax, 6

  spdata, 5

  TreeAndLeaf, 3
  TreeAndLeaf (TreeAndLeaf-package), 2
  treeAndLeaf, 2, 3, 5
  TreeAndLeaf-package, 2