Package ‘TreeAndLeaf’

May 30, 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.

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Depends R(>= 4.0)
Imports RedeR(>= 1.40.4), igraph, ape
Suggests knitr, markdown, BiocStyle, RUnit, BiocGenerics, stringr, geneplast, ggtree, ggplot2, dplyr, dendextend, RColorBrewer
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Description

The TreeAndLeaf package combines unrooted and force-directed graph algorithms in order to layout 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

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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

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

Examples

library(RedeR)
hc <- hclust(dist(USArrests), "ave")
tal <- treeAndLeaf(hc)
tal <- formatTree(tal, theme = 5)
### phylo_species

**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**


### phylo_tree

**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)
```

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**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(RedeR)
rdp <- RedPort()
hc <- hclust(dist(USArrests), "ave")
tal <- treeAndLeaf(hc)

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

## End(Not run)
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