Package ‘TreeAndLeaf’

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Type   Package
Title  Displaying binary trees with focus on dendrogram leaves
Version 1.14.0

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

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
treeAndLeaf

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**  
`data(phylo_species)`

**Format**  
An object of class "data.frame"

**References**  

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**phylo_tree**  
*Species tree from STRING-db v11*

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

**Usage**  
`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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