

Package ‘TreeAndLeaf’

January 16, 2022

Type Package

Title Displaying binary trees with focus on dendrogram leaves

Version 1.6.1

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_14

git_last_commit 171d519

git_last_commit_date 2021-10-27

Date/Publication 2022-01-16

R topics documented:

TreeAndLeaf-package	2
formatTree	3

phylo_species	4
phylo_tree	4
spdata	5
treeAndLeaf	5

Index	7
--------------	----------

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

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

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

CASTRO, M. A. et al. RedeR: R/Bioconductor package for representing modular structures, nested networks and multiple levels of hierarchical associations. **Genome Biology**, 13(4):R29, 2012.
 CASTRO, M. A. A. et al. Regulators of genetic risk of breast cancer identified by integrative network analysis. **Nature Genetics**, 48(1):12–21, 2016.

RUSU, A.; SANTIAGO, C. Grid Drawings of Binary Trees: An Experimental Study. **Journal of Graph Algorithms and Applications**, 12(2):131–195, 2008.

formatTree	<i>A theme function for tree-and-leaf igraph objects.</i>
------------	---

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

Szklarczyk D. et al. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 47:D607-613, 2019.

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

Szklarczyk D. et al. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 47:D607-613, 2019.

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

NCBI Genome Database <https://www.ncbi.nlm.nih.gov/genome> Accessed: August 15, 2019.

NCBI Taxonomy Database <https://www.ncbi.nlm.nih.gov/taxonomy> Accessed: August 15, 2019.

KEGG Organisms Database https://www.genome.jp/kegg/catalog/org_list.html Accessed: August 15, 2019.

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(RedeR)
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