Package 'TreeAndLeaf'

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Type Package

Title An alternative to dendrogram visualization and insertion of multiple layers of information

Version 1.0.0

Description TreeAndLeaf package comes as an alternative to solve problems regarding dendrogram plotting, such as the lack of space when the dendrogram is too large and the need for adding more layers of information. It treats a whole dendrogram as a tree, in which the observations are represented by the leaves.

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Depends R (>= 4.0)

Imports RedeR, igraph, ape, methods

Suggests knitr, rmarkdown, BiocStyle, RUnit, BiocGenerics, stringr, RColorBrewer, geneplast

License Artistic-2.0

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`TreeAndLeaf-package` *TreeAndLeaf: An alternative to dendrogram visualization and insertion of multiple layers of information.*

Description

TreeAndLeaf package comes as an alternative to solve problems regarding dendrogram plotting, such as the lack of space when the dendrogram is too large and the need for adding more layers of information. It treats a whole dendrogram as a tree, in which the observations are represented by the 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 function for formatting an igraph to be shown in RedeR.
hclust2igraph:	a function for converting a hclust object to an igraph.
phylo2igraph:	a function for converting a phylo object to an igraph.
treeAndLeaf:	a function for layout creation and plotting of the TreeAndLeaf in RedeR.

Further information is available in the vignettes by typing `vignette("TreeAndLeaf")`. Documented topics are also available in HTML by typing `help.start()` and selecting the TreeAndLeaf package from the menu.

Author(s)

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References

CASTRO, M. A. et al. RedeR: R/Bioconductor package for representing modular structures, nested networks and multiple levels of hierarchical associations. **Genome Biology**, v. 13, n. 4, p. R29, 2012.

CASTRO, M. A. A. et al. Regulators of genetic risk of breast cancer identified by integrative network analysis. **Nature Genetics**, v. 48, n. 1, p. 12–21, jan. 2016.

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

`formatTree` *A theme function for formatting of an igraph to be shown in RedeR*

Description

Applies formatting patterns to an igraph object according to predefined themes. This formatting is used for plotting on the RedeR app interface.

Usage

```
formatTree(gg, theme = 1, cleanalias = FALSE)
```

Arguments

`gg`	An igraph object generated by either `hclust2igraph` or `phylo2igraph`<igraph>.
`theme`	An integer ranging from 1 to 5 with desired theme. Options are: 1- A clean black and blue theme, great for higher levels of user customization. 2- A theme with a palette of greens. 3- A theme with a palette of blues. 4- A theme with a palette of purples. 5- A theme with a palette of reds. For custom formatting, see `addGraph` for accepted parameters <integer>.
`cleanalias`	A logical that removes the node aliases when set to TRUE (default = FALSE) <logical>.

Value

An igraph object with standard formatting for RedeR application.

See Also

`addGraph`

`treeAndLeaf`

Examples

```
hc <- hclust(dist(USArrests), "ave")
gg <- hclust2igraph(hc)
gg <- formatTree(gg = gg,
                 theme = 5)
```

hclust2igraph *Convert an hclust to an igraph*

Description

Function for converting a hclust object to an igraph.

Usage

```
hclust2igraph(hc)
```

Arguments

hc	a hclust object.

Value

An igraph object.

See Also

hclust

Examples

```
hc <- hclust(dist(USArrests), "ave")
gg <- hclust2igraph(hc)
```

phylo2igraph *Convert a phylo object to an igraph*

Description

Function for converting a phylo object to an igraph.

Usage

```
phylo2igraph(phy)
```

Arguments

phy	A phylo object with labeled tips <phylo>.

Value

An igraph object.

Examples

```
phy <- ape::rtree(10, tip.label = c(1:10))
gg <- phylo2igraph(phy)
```

phylo_species *Species metadata for the strings tree from STRING-db v11.0*

Description

Species metadata for phylo_tree object from STRING-db website. Available visiting download page under Accessory Data. Version: 11.0

Usage

```
data(phylo_species)
```

Format

An object of class `"data.frame"`

References

STRING: functional protein association networks. Retrieved August 15, 2019, from https://string-db.org/

phylo_tree *Species tree from STRING-db v11.0*

Description

Species tree from STRING-db website. Available visiting download page under Accessory Data. Version: 11.0

Usage

```
data(phylo_tree)
```

Format

An object of class `"phylo"`

References

STRING: functional protein association networks. Retrieved August 15, 2019, from https://string-db.org/

spdata *Genome statistical data from eukaryotes with complete genome*

Description

Data from NCBI Genome database showing statistical results for eukaryotes with complete genome sequenced. The list of organisms with complete genome is available on KEGG Organisms website and NCBI data was scraped using RCrawler package. Taxonomy ids were obtained using NCBI Tax Identifier.

Usage

```
data(spdata)
```

Format

An object of class `"data.frame"`

References

Genome - NCBI. Retrieved August 15, 2019 from https://www.ncbi.nlm.nih.gov/genome

Taxonomy - NCBI. Tax Identifier. Retrieved August 15, 2019 from https://www.ncbi.nlm.nih.gov/taxonomy

KEGG Organisms: Complete Genomes. Retrieved August 15, 2019 from https://www.genome.jp/kegg/catalog/org_list.h

Examples

```
data(spdata)
View(spdata)
```

treeAndLeaf *Layout creation and plotting of the TreeAndLeaf in RedeR.*

Description

Creates tree-and-leaf layouts and plots. It also returns the given igraph with nodes coordinates added after setting of positions and relaxation by the force based algorithm implemented in the RedeR package.

Usage

```
treeAndLeaf(obj, gg)
```

Arguments

obj	An object of RedPort class, from RedeR package <RedPort>.
gg	An igraph object generated by either hclust2igraph or phylo2igraph<igraph>.

Value

Plotting of igraph in RedeR app and the given igraph with nodes coordinates added.

See Also

formatTree

addGraph

relax

Examples

```
library(RedeR)
rdp <- RedPort()
hc <- hclust(dist(USArrests), "ave")
gg <- hclust2igraph(hc)

## Not run:
calld(rdp)
treeAndLeaf(rdp, gg)

## End(Not run)
```

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