# Package ‘TreeAndLeaf’

May 20, 2026

**Type** Package

**Title** Displaying binary trees with focus on dendrogram leaves

**Version** 1.25.0

**Depends** R(>= 4.4)

**Imports** RedeR(>= 3.6.1), igraph, ape

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

**Description** TreeAndLeaf implements a hybrid layout strategy that enhances leaf-level visualization in dendrograms. By integrating force-directed graph and tree layout algorithms, it enables projection of multiple layers of information onto graph–tree diagrams.

**License** Artistic-2.0

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**VignetteBuilder** knitr

**BugReports** `https://github.com/sysbiolab/TreeAndLeaf/issues`

**URL** `https://doi.org/10.1093/bioinformatics/btab819`

**biocViews** GraphAndNetwork, Network, Visualization, DataRepresentation, Software, SystemsBiology

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

**git_branch** devel

**git_last_commit** 769dd7d

**git_last_commit_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-19

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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)

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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**, 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.

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# `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.<br>Options:<br>1- A clean black and blue theme, for additional customizations.<br>2- Green palette theme.<br>3- Blue palette theme.<br>4- Purple palette theme.<br>5- Red palette theme.<br>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)
```

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`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.

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

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### 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.

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## `spdata` *Genome statistics for eukaryotes with complete genome sequence*

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### 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.*

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### Description

This function tranforms 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)
hc <- hclust(dist(USArrests), "ave")
tal <- treeAndLeaf(hc)

## Not run:
startRedeR()
addGraphToRedeR(tal)

## End(Not run)
```

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