

# Package ‘phylocanvas’

July 23, 2025

**Title** Interactive Phylogenetic Trees Using the 'Phylocanvas'  
JavaScript Library

**Version** 0.1.3

**Description** Create and customize interactive phylogenetic trees using the 'phylocanvas' JavaScript library and the 'htmlwidgets' package. These trees can be used directly from the R console, from 'RStudio', in Shiny apps, and in R Markdown documents. See <http://phylocanvas.org/> for more information on the 'phylocanvas' library.

**URL** <https://github.com/zachcp/phylocanvas>, <http://phylocanvas.org/>

**BugReports** <https://github.com/zachcp/phylocanvas/issues>

**Depends** R (>= 3.3.1)

**Imports** ape (>= 4.0), phylobase, htmlwidgets, methods (>= 3.3.0)

**Suggests** magrittr, knitr, rmarkdown

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**VignetteBuilder** knitr

**Collate** 'load.tree.R' 'as\_tree.R' 'get.descendants.R'  
'nodes.branches.R' 'phylocanvas.R'

**NeedsCompilation** no

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**Repository** CRAN

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## Contents

|                           |   |
|---------------------------|---|
| as_tree . . . . .         | 2 |
| collapse_branch . . . . . | 2 |

|                             |          |
|-----------------------------|----------|
| get.descendants . . . . .   | 3        |
| highlight_node . . . . .    | 4        |
| load.tree . . . . .         | 4        |
| phylocanvas . . . . .       | 5        |
| phylocanvas-shiny . . . . . | 6        |
| prune_branch . . . . .      | 6        |
| rotate_branch . . . . .     | 7        |
| select_branch . . . . .     | 7        |
| style_node . . . . .        | 8        |
| <b>Index</b>                | <b>9</b> |

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|         |                |
|---------|----------------|
| as_tree | <i>as_tree</i> |
|---------|----------------|

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**Description**

Convert objects to newick strings

**Usage**

```
as_tree(phy)

## S4 method for signature 'phylo'
as_tree(phy)

## S4 method for signature 'phylo4'
as_tree(phy)
```

**Arguments**

|     |                                                                                                                                                                                     |
|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| phy | Required. phy is either a <a href="#">phylo</a> class object, <a href="#">phylo4</a> class object, or a character that can be a newick literal or a path to newick-containing file. |
|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

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|                 |                        |
|-----------------|------------------------|
| collapse_branch | <i>collapse branch</i> |
|-----------------|------------------------|

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**Description**

given a [phylocanvas](#) object and an id node, collapse the node.

**Usage**

```
collapse_branch(phycnv, nodeid, collapse = TRUE)
```

**Arguments**

|          |                                                       |
|----------|-------------------------------------------------------|
| phycnv   | Required.                                             |
| nodeid   | Required.                                             |
| collapse | Optional. Default TRUE. Whether to collapse the node. |

**See Also**

<http://phylocanvas.org/docs/features/#collapse-branches>

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|                 |                        |
|-----------------|------------------------|
| get.descendants | <i>get_descendants</i> |
|-----------------|------------------------|

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**Description**

get the names of the tips of descendants given a tree and the name of an internal node.

**Usage**

```
get.descendants(tree, nodename)
```

**Arguments**

|          |                                                          |
|----------|----------------------------------------------------------|
| tree     | Required. A <a href="#">phylo4</a> object.               |
| nodename | Required. A character corresponding to an internal node. |

**Value**

a character vector of descendant names

**Examples**

```
birdfile <- system.file("treedata/birdfamilies.tree", package="phylocanvas")
tree <- load.tree(birdfile)
node <- phylobase::MRCA(tree, c("Cerylidae", "Upupidae"))
get.descendants(tree, node)
```

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|                |                       |
|----------------|-----------------------|
| highlight_node | <i>highlight node</i> |
|----------------|-----------------------|

---

### Description

given a [phylocanvas](#) object and an nodeid, highlight the node.

### Usage

```
highlight_node(phycnv, nodeid)
```

### Arguments

|        |           |
|--------|-----------|
| phycnv | Required. |
| nodeid | Required. |

### See Also

<http://phylocanvas.org/docs/features/#highlight-leaves>

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|           |                  |
|-----------|------------------|
| load.tree | <i>load tree</i> |
|-----------|------------------|

---

### Description

load a newick tree.

### Usage

```
load.tree(treefile, ...)
```

### Arguments

|          |                                                 |
|----------|-------------------------------------------------|
| treefile | Required. Path of phylogenetic tree to read     |
| ...      | Optional. Pass any other arguments to read.tree |

### Details

this is the recommended way to load a tree for use with phylocanvas. The reason is that all of the javascript selector methods require that the nodes are named and the selection of nodes based on names is straightforward with [phylo4](#) objects. Therefore this function will read your newick tree, add names, and return a [phylo4](#) object that can be easily manipulated and subsetted generating custom displays.

**Value**

a [phylo4](#) tree object.

**Examples**

```
birdfile <- system.file("treedata/birdfamilies.tree", package="phylocanvas")
tree <- load.tree(birdfile)
```

---

phylocanvas

*phylocanvas*


---

**Description**

An html widget wrapper of the [phylocanvas.js](#) JS library.

**Usage**

```
phylocanvas(tree, treetype = "rectangular", nodestyles = NULL,
  nodesize = 30, textsize = 30, linewidth = 3, showlabels = TRUE,
  alignlabels = FALSE, showhistory = FALSE, showcontextmenu = TRUE,
  showscalebar = FALSE, width = NULL, height = NULL, elementId = NULL)
```

**Arguments**

|                 |                                                                                                                                                          |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|
| tree            | Required. Newick string of a phyloseq tree, <a href="#">phylo</a> class object, <a href="#">phylo4</a> class object,, or path to newick-containing file. |
| treetype        | Optional. Default "rectangular". Can be one of "rectangular", "circular", "hierarchical", "diagonal", or "radial".                                       |
| nodestyles      | Optional. Default NULL. Let nodes b stylized.                                                                                                            |
| nodesize        | Optional. Default 30. Global nodesize.                                                                                                                   |
| textsize        | Optional. Default 30. Global textsize.                                                                                                                   |
| linewidth       | Optional. Default 3. Global linewidth.                                                                                                                   |
| showlabels      | Optional. Default TRUE. Whether to show labels.                                                                                                          |
| alignlabels     | Optional. Default FALSE. Whether to align node labels                                                                                                    |
| showhistory     | Optional. Default FALSE. Whether to use/show the history plugin.                                                                                         |
| showcontextmenu | Optional. Default TRUE. Whether to use/show the mouse context menu.                                                                                      |
| showscalebar    | Optional. Default FALSE. Whether to use/show the scalebar.                                                                                               |
| width           | Optional. Default NULL. HTMLWidget width                                                                                                                 |
| height          | Optional. Default NULL. HTMLWidget width                                                                                                                 |
| elementId       | Optional. Default NULL. HTMLWidget ID                                                                                                                    |

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phylocanvas-shiny      *Shiny bindings for phylocanvas*

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### Description

Output and render functions for using phylocanvas within Shiny applications and interactive Rmd documents.

### Usage

```
phylocanvasOutput(outputId, width = "100%", height = "400px")

renderPhylocanvas(expr, env = parent.frame(), quoted = FALSE)
```

### Arguments

|               |                                                                                                                                |
|---------------|--------------------------------------------------------------------------------------------------------------------------------|
| outputId      | output variable to read from                                                                                                   |
| width, height | Must be a valid CSS unit (like '100%', '400px', 'auto') or a number, which will be coerced to a string and have 'px' appended. |
| expr          | An expression that generates a phylocanvas                                                                                     |
| env           | The environment in which to evaluate expr.                                                                                     |
| quoted        | Is expr a quoted expression (with quote())? This is useful if you want to save an expression in a variable.                    |

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prune\_branch      *prune branch*

---

### Description

given a [phylocanvas](#) object and an nodeid for an internal node, prune the branch.

### Usage

```
prune_branch(phycnv, nodeid)
```

### Arguments

|        |           |
|--------|-----------|
| phycnv | Required. |
| nodeid | Required. |

### See Also

<http://phylocanvas.org/docs/features/#prune-branches>

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|               |                        |
|---------------|------------------------|
| rotate_branch | <i>rotate a branch</i> |
|---------------|------------------------|

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**Description**

given a [phyloanvas](http://phyloanvas.org/docs/features/#rotate-branches) object and an nodeid for an internal node, rotate the branch defined by the node

**Usage**

```
rotate_branch(phycnv, nodeid)
```

**Arguments**

|        |           |
|--------|-----------|
| phycnv | Required. |
| nodeid | Required. |

**See Also**

<http://phyloanvas.org/docs/features/#rotate-branches>

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|               |                      |
|---------------|----------------------|
| select_branch | <i>select branch</i> |
|---------------|----------------------|

---

**Description**

given a [phyloanvas](http://phyloanvas.org/docs/features/#select-branches) object and an nodeid for an internal node, select the branch defined by the node

**Usage**

```
select_branch(phycnv, nodeid, cascade = FALSE)
```

**Arguments**

|         |                         |
|---------|-------------------------|
| phycnv  | Required.               |
| nodeid  | Required.               |
| cascade | Optional. Default FALSE |

**See Also**

<http://phyloanvas.org/docs/features/#select-branches>

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style\_node

*style node*


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## Description

add styles to a node

## Usage

```
style_node(phycnv, nodeid, highlighted = FALSE, color = "black",
  shape = "circle", nodesizeratio = 1, strokecolor = "black",
  fillcolor = "black", linewidth = 1, labelcolor = "black",
  labeltextsize = 20, labelfont = "Arial", labelformat = "bold")
```

## Arguments

|               |                                                                                                               |
|---------------|---------------------------------------------------------------------------------------------------------------|
| phycnv        | Required.                                                                                                     |
| nodeid        | Required.                                                                                                     |
| highlighted   | Optional. Default FALSE. Whether to highlight the node.                                                       |
| color         | Optional. Color of the node/branch                                                                            |
| shape         | Optional. Default 'circle'. Can be either 'circle', 'square' or 'triangle'.                                   |
| nodesizeratio | Optional. Default 1. Scale ratio of the nodesize to the base node size.                                       |
| strokecolor   | Optional. Default "black". Colors are strings in the format of names, rgb strings or hex values.              |
| fillcolor     | Optional. Default "black". Scale ratio of the node.                                                           |
| linewidth     | Optional. Default 1.                                                                                          |
| labelcolor    | Optional. Default "black". Label color. Colors are strings in the format of names, rgb strings or hex values. |
| labeltextsize | Optional. Default 20. Label size.                                                                             |
| labelfont     | Optional. Default "Arial". Label font.                                                                        |
| labelformat   | Optional. Default "bold". Label format.                                                                       |

## Details

given a [phylocanvas](#) object and nodeid, apply the given styles to that node.

## See Also

<http://phylocanvas.org/docs/features/#style-branches-individually>

# Index

`as_tree`, [2](#)  
`as_tree, (as_tree)`, [2](#)  
`as_tree, phylo-method (as_tree)`, [2](#)  
`as_tree, phylo4-method (as_tree)`, [2](#)  
  
`collapse_branch`, [2](#)  
  
`get.descendants`, [3](#)  
  
`highlight_node`, [4](#)  
  
`load.tree`, [4](#)  
  
`phylo`, [2](#), [5](#)  
`phylo, (as_tree)`, [2](#)  
`phylo-method (as_tree)`, [2](#)  
`phylo4`, [2–5](#)  
`phylo4, (as_tree)`, [2](#)  
`phylo4-method (as_tree)`, [2](#)  
`phylocanvas`, [2](#), [4](#), [5](#), [6–8](#)  
`phylocanvas-shiny`, [6](#)  
`phylocanvasOutput (phylocanvas-shiny)`, [6](#)  
`prune_branch`, [6](#)  
  
`renderPhylocanvas (phylocanvas-shiny)`, [6](#)  
`rotate_branch`, [7](#)  
  
`select_branch`, [7](#)  
`style_node`, [8](#)