

# Package ‘phylocanvas’

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**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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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

<code>phycnv</code>	Required.
<code>nodeid</code>	Required.
<code>collapse</code>	Optional. Default TRUE. Whether to collapse the node.

### See Also

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

---

`get.descendants`      *get.descendants*

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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

<code>tree</code>	Required. A <a href="#">phylo4</a> object.
<code>nodename</code>	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>
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**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>
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**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 be 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*

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### 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 [phylocanvas](#) 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://phylocanvas.org/docs/features/#rotate-branches>

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select_branch	<i>select branch</i>
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**Description**

given a [phylocanvas](#) 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://phylocanvas.org/docs/features/#select-branches>

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style_node	<i>style node</i>
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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>

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