

# Package: phylocanvas (via r-universe)

August 16, 2024

**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'

**Repository** <https://phylotastic.r-universe.dev>

**RemoteUrl** <https://github.com/zachcp/phylocanvas>

**RemoteRef** HEAD

**RemoteSha** afc7dc0646f699873c4ff675ae5f69bcb923bd36