Package 'heattree'

May 4, 2026

Type Package

Title A Self-Contained Widget for Interactive Phylogenetic Tree Visualization

Version 0.3.1

Maintainer Zachary Foster <zacharyfoster1989@gmail.com>

Description Creates self-contained widgets for interactive phylogenetic tree visualization. This package wraps the 'JavaScript' 'heat-tree' package using the 'htmlwidgets' R package.

URL https://grunwaldlab.github.io/heattree/

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

Depends R (>= 3.5)

Imports ape, htmlwidgets

Suggests testthat (>= 3.0.0), knitr

Config/Needs/website rmarkdown

NeedsCompilation no

Author Zachary Foster [aut, cre] (ORCID: <https://orcid.org/0000-0002-5075-0948>), Niklaus Grunwald [aut] (ORCID: <https://orcid.org/0000-0003-1656-7602>), USDA Agricultural Research Service [fnd]

Repository CRAN

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Contents

`bansal_2021_metadata` *Isolate metadata from Bansal et al. 2021*

Description

Isolate metadata from Bansal et al. 2021 (doi:10.1016/j.ygeno.2021.09.021) included for use as an example data set. This is the parsed version of the included "bansal_2021_metadata.tsv" file.

Format

`data.frame`

Source

Bansal, K., Kumar, S., Kaur, A., Singh, A. and Patil, P.B., 2021. Deep phylo-taxono genomics reveals Xylella as a variant lineage of plant associated Xanthomonas and supports their taxonomic reunification along with Stenotrophomonas and Pseudoxanthomonas. Genomics, 113(6), pp.3989-4003.

`bansal_2021_tree` *A phylogeny from Bansal et al. 2021*

Description

A core gene phylogeny from Bansal et al. 2021 (doi:10.1016/j.ygeno.2021.09.021) included for use as an example data set. This is the parsed version of the included "bansal_2021_tree.nwk" file.

Format

`ape::phylo`

Source

Bansal, K., Kumar, S., Kaur, A., Singh, A. and Patil, P.B., 2021. Deep phylo-taxono genomics reveals Xylella as a variant lineage of plant associated Xanthomonas and supports their taxonomic reunification along with Stenotrophomonas and Pseudoxanthomonas. Genomics, 113(6), pp.3989-4003.

`heat_tree` *Create an interactive phylogenetic tree*

Description

Create an interactive phylogenetic tree using the javascript heat-tree package

Usage

```
heat_tree(
  tree = NULL,
  metadata = NULL,
  aesthetics = NULL,
  width = NULL,
  height = NULL,
  elementId = NULL,
  ...
)
```

Arguments

`tree`	One or more trees to plot. Can be a raw newick-formatted string, a `phylo` object, or a list of such inputs. If a list is provided, its names will be used to name trees.
`metadata`	Metadata associated with `tree`. Can be a `data.frame` or `tibble` with a column containing IDs matching the tree labels. The ID column is detected automatically. If there are multiple trees (a list), then a list of tables of equal length is required. If a list is provided, its names will be used to name metadata tables.
`aesthetics`	A named character vector defining which metadata columns are initially used to color/size tree parts. If there are multiple trees (a list), then a list of equal length is required.
`width`	Width of the widget (CSS units or number).
`height`	Height of the widget (CSS units or number).
`elementId`	Optional element ID for the widget.
`...`	Options passed to options parameter of the underlying `HeatTree.heatTree()` javascript function to modify the initial state of the widget.

Value

An htmlwidget object of class `heat_tree` that renders an interactive phylogenetic tree visualization. The object contains:

- `x`: A list with tree data and options passed to JavaScript
- `width`, `height`: Dimensions of the widget
- `elementId`: Optional DOM element ID

The widget can be displayed in R Markdown, Quarto, or using and IDE like RStudio.

Examples

```
# Create an empty tree viewer for loading data interactively
heat_tree()

# Create a tree viewer with example data included with the package
data(weisberg_2020_metadata)
data(weisberg_2020_mlsa)
heat_tree(
  tree = weisberg_2020_mlsa,
  metadata = weisberg_2020_metadata,
  aesthetics = c(tipLabelColor = 'host_type')
)
```

`heat_tree-shiny` *Shiny bindings for heat_tree*

Description

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

Usage

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

renderheat_tree(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 heat_tree
`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.

Value

`heat_treeOutput()` returns an output function that creates a Shiny UI element for displaying a heat_tree widget. Used in the UI definition of a Shiny app.

`renderheat_tree()` returns a render function that can be assigned to an output element in the server function of a Shiny app. It returns a Shiny render binding.

`weisberg_2020_beast` *A BEAST phylogeny from Weisberg et al. 2020*

Description

A BEAST phylogeny from Weisberg et al. 2020 (doi:10.1126/science.aba5256) included for use as an example data set. This is the parsed version of the included "weisberg_2020_beast.tre" file.

Format

`ape::phylo`

Source

Alexandra J. Weisberg et al., Unexpected conservation and global transmission of agrobacterial virulence plasmids.Science368,eaba5256(2020)

`weisberg_2020_metadata` *Isolate metadata from Weisberg et al. 2020*

Description

Isolate metadata from Weisberg et al. 2020 (doi:10.1126/science.aba5256) included for use as an example data set. This is the parsed version of the included "weisberg_2020_metadata.tsv" file.

Format

`data.frame`

Source

Alexandra J. Weisberg et al., Unexpected conservation and global transmission of agrobacterial virulence plasmids.Science368,eaba5256(2020)

`weisberg_2020_mlsa` *A MLSA phylogeny from Weisberg et al. 2020*

Description

A MLSA phylogeny from Weisberg et al. 2020 (doi:10.1126/science.aba5256) included for use as an example data set. This is the parsed version of the included "weisberg_2020_mlsa.tre" file.

Format

`ape::phylo`

Source

Alexandra J. Weisberg et al., Unexpected conservation and global transmission of agrobacterial virulence plasmids.Science368,eaba5256(2020)

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