Package: heattree (via r-universe)

May 8, 2026

Type Package

Title A Self-Contained Widget for Interactive Phylogenetic Tree Visualization

Version 0.3.1

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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

Roxygen list(markdown = TRUE)

Config/pak/sysreqs cmake make libuv1-dev

Repository https://grunwaldlab.r-universe.dev

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`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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