

Package ‘CancerEvolutionVisualization’

July 21, 2025

Title Publication Quality Phylogenetic Tree Plots

Version 2.0.1

Date 2023-11-17

Description Generates tree plots with precise branch lengths, gene annotations, and cellular prevalence. The package handles complex tree structures (angles, lengths, etc.) and can be further refined as needed by the user.

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URL <https://github.com/uclahs-cds/package-CancerEvolutionVisualization>

BugReports

<https://github.com/uclahs-cds/package-CancerEvolutionVisualization/issues>

Depends R (>= 3.5.0), graphics, grid, gridExtra, gtable,

Imports plyr, grDevices, utils, stringr, BoutrosLab.plotting.general

Suggests testthat, knitr

VignetteBuilder knitr

LazyLoad yes

LazyData yes

NeedsCompilation no

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Repository CRAN

Date/Publication 2023-11-21 19:40:02 UTC

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colours	<i>Colour scheme vector</i>
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Description

Default colours used by CP polygons, etc.

Format

Character vector

SRCGrob	<i>Subclone Tree Plot</i>
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Description

Creates a phylogenetic tree using subclonal reconstruction data. An optional node text data.frame can be used to annotate notable genes alongside branches.

Usage

```
SRCGrob(  
  tree,  
  node.text = NULL,  
  main = NULL,  
  horizontal.padding = 0.1,  
  scale1 = 1,  
  scale2 = 1,  
  yat = NULL,  
  yaxis1.label = NULL,  
  yaxis2.label = NULL,  
  xlab.cex = 1.55,  
  ylab.cex = 1.55,  
  xaxis.cex = 1.45,  
  yaxis.cex = 1.45,  
  xaxis.label = "CP",  
  label.cex = NA,  
  node.text.cex = 0.85,  
  main.y = NULL,  
  main.cex = 1.7,  
  node.radius = 0.1,  
  node.text.line.dist = 0.1,  
  colour.scheme = CancerEvolutionVisualization::colours,  
  draw.nodes = TRUE,  
  add.normal = FALSE,
```

```

    use.radians = FALSE,
    normal.cex = 1,
    sig.shape = 3,
    label.nodes = TRUE,
    disable.polygons = FALSE,
    length.from.node.edge = TRUE,
    size.units = "npc"
  );

```

Arguments

<code>tree</code>	Tree structure data.frame
<code>node.text</code>	Dataframe for text labels to be displayed next to nodes
<code>main</code>	Main plot title
<code>horizontal.padding</code>	Increase/reduce the plot's horizontal padding proportionally. A positive value will expand the padding, and a negative value will reduce it.
<code>scale1</code>	Proportionally scale the values of the first branch length column in the tree input.
<code>scale2</code>	Proportionally scale the values of the second branch length column in the tree input.
<code>yat</code>	Specific values to be used for the y-axis ticks. A list is required, with each element corresponding to an axis.
<code>yaxis1.label</code>	Text label for the first, leftmost y-axis
<code>yaxis2.label</code>	Text label for the second, rightmost y-axis
<code>xlab.cex</code>	Font size for the x-axis label
<code>ylab.cex</code>	Font size for the y-axis labels
<code>xaxis.cex</code>	Font size for the x-axis tick labels
<code>yaxis.cex</code>	Font size for the y-axis tick labels
<code>xaxis.label</code>	Text label for the x-axis
<code>label.cex</code>	Font size for the node labels
<code>node.text.cex</code>	Font size for the node text
<code>main.y</code>	Move the main plot title position up or down
<code>main.cex</code>	Font size for the main plot title
<code>node.radius</code>	Node size
<code>node.text.line.dist</code>	Distance between node text and tree branches (as a value between 0 and 1)
<code>colour.scheme</code>	Vector of colour values to be used for CP polygons
<code>draw.nodes</code>	Enable or disable drawing tree nodes
<code>add.normal</code>	Adds a normal
<code>use.radians</code>	Unit to be used for "angle" column (degrees or radians)
<code>normal.cex</code>	Font size within the normal "box"

<code>sig.shape</code>	Changes the shape of the CP shading. Lower values are smoother.
<code>label.nodes</code>	Enable/disable node labels
<code>disable.polygons</code>	Disables CP polygon drawing (even when CP values are provided)
<code>length.from.node.edge</code>	Sets the branch length to be calculated from the edge of the node instead of the centre
<code>size.units</code>	Grid units to be used for all specific size/length parameters

Value

A 'grob' of class "SRCGrob"

Author(s)

Dan Knight

Examples

```
# Simple Tree Plot
simple.tree <- data.frame(
  parent = c(NA, 1, 1)
);

SRCGrob(simple.tree);

# Specify Branch Lengths
branch.lengths.tree <- data.frame(
  simple.tree,
  length1 = c(10, 20, 15)
);

SRCGrob(branch.lengths.tree);

# Cellular Prevalence
CP.tree <- data.frame(
  branch.lengths.tree,
  CP = c(1, 0.3, 0.5)
);

SRCGrob(CP.tree);

# Scaled Branch Lengths
SRCGrob(
  branch.lengths.tree,
  scale1 = 0.8
);
```

```
# Override Branch Angles in Degrees
degrees.tree <- data.frame(
  parent = c(NA, 1, 2),
  angle = c(NA, NA, 90)
);

SRCGrob(degrees.tree);
```

```
# Override Branch Angles in Radians
radians.tree <- data.frame(
  parent = c(NA, 1, 2),
  angle = c(NA, NA, pi / 2)
);

SRCGrob(
  radians.tree,
  use.radians = TRUE
);
```

```
# Plot Title
SRCGrob(
  simple.tree,
  main = 'Example Plot'
);
```

```
# Y-Axis Label
SRCGrob(
  branch.lengths.tree,
  yaxis1.label = 'SNVs'
);
```

```
# Y-Axis Ticks
yaxis1.ticks <- seq(0, 10, 2);
```

```
SRCGrob(
  branch.lengths.tree,
  yat = list(yaxis1.ticks)
);
```

```
# Normal
SRCGrob(
  simple.tree,
  add.normal = TRUE
);
```

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