Package ‘CancerEvolutionVisualization’

October 12, 2022

Title   Publication Quality Phylogenetic Tree Plots
Version  1.0.1
Date     2022-10-03

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.

License    GPL-2
Depends    R (>= 3.5.0), graphics, grid, gridExtra, gtable,
Imports    plyr, grDevices, utils, stringr
Suggests   testthat, knitr
VignetteBuilder knitr
LazyLoad   yes
LazyData   yes
NeedsCompilation no

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Repository  CRAN
Date/Publication  2022-10-04 10:10:09 UTC

R topics documented:

  colours ................................................................. 2
  SRCGrob .............................................................. 2

Index                                                  6
colours  

**Description**

Default colours used by CP polygons, etc.

**Format**

Character vector

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**SRCGrob**  

**Subclone Tree Plot**

**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**

```r
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.col = "grey29",
  seg1.col = "black",
  seg2.col = "green",
  line.lwd = 3,
)```
```r
node.text.line.dist = 0.1,
colour.scheme = CancerEvolutionVisualization::colours,
draw.nodes = TRUE,
add.normal = FALSE,
normal.cex = 1,
sig.shape = 3,
label.nodes = TRUE,
disable.polygons = FALSE,
length.from.node.edge = TRUE,
size.units = "npc"
);

Arguments

tree Tree structure data.frame
node.text Dataframe for text labels to be displayed next to nodes
main Main plot title
horizontal.padding Increase/reduce the plot’s horizontal padding proportionally. A positive value will expand the padding, and a negative value will reduce it.
scale1 Proportionally scale the values of the first branch length column in the tree input.
scale2 Proportionally scale the values of the second branch length column in the tree input.
yat Specific values to be used for the y-axis ticks. A list is required, with each element corresponding to an axis.
yaxis1.label Text label for the first, leftmost y-axis
yaxis2.label Text label for the second, rightmost y-axis
xlab.cex Font size for the x-axis label
ylab.cex Font size for the y-axis labels
xaxis.cex Font size for the x-axis tick labels
yaxis.cex Font size for the y-axis tick labels
xaxis.label Text label for the x-axis
label.cex Font size for the node labels
node.text.cex Font size for the node text
main.y Move the main plot title position up or down
main.cex Font size for the main plot title
node.radius Node size
node.col Node colour
seg1.col Colour of the first set of tree branch segments
seg2.col Colour of the second set of tree branch segments
line.lwd Branch segment thickness
```
node.text.line.dist
  Distance between node text and tree branches (as a value between 0 and 1)

colour.scheme
  Vector of colour values to be used for CP polygons

draw.nodes
  Enable or disable drawing tree nodes

add.normal
  Adds a normal

normal.cex
  Font size within the normal "box"

sig.shape
  Changes the shape of the CP shading. Lower values are smoother.

label.nodes
  Enable/disable node labels

disable.polygons
  Disables CP polygon drawing (even when CP values are provided)

length.from.node.edge
  Sets the branch length to be calculated from the edge of the node instead of the centre

size.units
  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
);

# 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
);
Index

colours, 2
SRCGrob, 2