Package 'CancerEvolutionVisualization'

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Title Publication Quality Phylogenetic Tree Plots

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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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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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R topics documented:

| colours | *Colour scheme vector* |

Description

Default colours used by CP polygons, etc.

Format

Character vector

| 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 alonside 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.col = "grey29",
    seg1.col = "black",
    seg2.col = "green",
    line.lwd = 3,
```

```
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
    );
```

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