

# Package ‘CancerEvolutionVisualization’

January 20, 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.

**License** GPL-2

**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

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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

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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

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.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
use.radians	Unit to be used for "angle" column (degrees or radians)
normal.cex	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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