

Package ‘seqcombo’

January 3, 2025

Title Visualization Tool for Genetic Reassortment

Version 1.28.0

Description Provides useful functions for visualizing virus reassortment events.

Depends R (>= 3.4.0)

Imports ggplot2, grid, igraph, utils, yulab.utils

Suggests emojiFont, knitr, rmarkdown, prettydoc, tibble

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

Encoding UTF-8

BugReports <https://github.com/GuangchuangYu/seqcombo/issues>

biocViews Alignment, Software, Visualization

RoxygenNote 7.3.0

git_url <https://git.bioconductor.org/packages/seqcombo>

git_branch RELEASE_3_20

git_last_commit b18fa7c

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2025-01-02

Author Guangchuang Yu [aut, cre]

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

Contents

seqcombo-package	2
geom_genotype	2
geom_hybrid	3
hybrid_plot	4
set_layout	6
Index	7

 seqcombo-package

seqcombo: Visualization Tool for Genetic Reassortment

Description

Provides useful functions for visualizing virus reassortment events.

Author(s)

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

See Also

Useful links:

- Report bugs at <https://github.com/GuangchuangYu/seqcombo/issues>

 geom_genotype

geom_genotype

Description

geom layer of genotype

Usage

```
geom_genotype(
  virus_info,
  v_color = "darkgreen",
  v_fill = "steelblue",
  v_shape = "ellipse",
  l_color = "black",
  asp = 1,
  g_height = 0.65,
  g_width = 0.65
)
```

Arguments

virus_info	virus information
v_color	the color of outer boundary of virus; can use expression (e.g. v_color=~Host) to color virus by specific variable
v_fill	the color to fill viruses; can use expression (e.g. v_fill=~Host) to fill virus by specific variable
v_shape	one of 'hexagon' or 'ellipse'
l_color	color of the lines that indicate genetic flow
asp	aspect ratio of the plotting device
g_height	height of regions to plot gene segments relative to the virus
g_width	width of gene segment relative to width of the virus (the hexagon)

Value

geom layer

Author(s)

Guangchuang Yu

Examples

```
library(tibble)
library(ggplot2)
n <- 8
virus_info <- tibble(id = 1:7,
  x = c(rep(1990, 4), rep(2000, 2), 2009),
  y = c(1,2,3,5, 1.5, 3, 4),
  segment_color = list(rep('purple', n),
    rep('red', n), rep('darkgreen', n), rep('lightgreen', n),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'red', 'purple', 'red', 'purple'),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'),
    c('darkgreen', 'lightgreen', 'lightgreen', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'))))
ggplot() + geom_genotype(virus_info)
```

geom_hybrid

*geom_hybrid***Description**

geom layer for reassortment events

Usage

```
geom_hybrid(
  virus_info,
  flow_info,
  v_color = "darkgreen",
  v_fill = "steelblue",
  v_shape = "ellipse",
  l_color = "black",
  asp = 1,
  parse = FALSE,
  g_height = 0.65,
  g_width = 0.65,
  t_size = 3.88,
  t_color = "black"
)
```

Arguments

virus_info	virus information
flow_info	flow information
v_color	the color of outer boundary of virus; can use expression (e.g. v_color=~Host) to color virus by specific variable

<code>v_fill</code>	the color to fill viruses; can use expression (e.g. <code>v_fill=~Host</code>) to fill virus by specific variable
<code>v_shape</code>	one of 'hexagon' or 'ellipse'
<code>l_color</code>	color of the lines that indicate genetic flow
<code>asp</code>	aspect ratio of the plotting device
<code>parse</code>	whether parse label, only works if 'label' and 'label_position' exist
<code>g_height</code>	height of regions to plot gene segments relative to the virus
<code>g_width</code>	width of gene segment relative to width of the virus (the hexagon)
<code>t_size</code>	size of text label
<code>t_color</code>	color of text label

Value

geom layer

Author(s)

Guangchuang Yu

Examples

```
library(tibble)
library(ggplot2)
n <- 8
virus_info <- tibble(id = 1:7,
  x = c(rep(1990, 4), rep(2000, 2), 2009),
  y = c(1,2,3,5, 1.5, 3, 4),
  segment_color = list(rep('purple', n),
    rep('red', n), rep('darkgreen', n), rep('lightgreen', n),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'red', 'purple', 'red', 'purple'),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'),
    c('darkgreen', 'lightgreen', 'lightgreen', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'))))

flow_info <- tibble(from = c(1,2,3,3,4,5,6), to = c(5,5,5,6,7,6,7))

ggplot() + geom_hybrid(virus_info, flow_info)
```

hybrid_plot

hyrid_plot

Description

visualize virus reassortment events

Usage

```

hybrid_plot(
  virus_info,
  flow_info,
  v_color = "darkgreen",
  v_fill = "steelblue",
  v_shape = "ellipse",
  l_color = "black",
  asp = 1,
  parse = FALSE,
  g_height = 0.65,
  g_width = 0.65,
  t_size = 3.88,
  t_color = "black"
)

```

Arguments

virus_info	virus information
flow_info	flow information
v_color	the color of outer boundary of virus; can use expression (e.g. v_color=~Host) to color virus by specific variable
v_fill	the color to fill viruses; can use expression (e.g. v_fill=~Host) to fill virus by specific variable
v_shape	one of 'hexagon' or 'ellipse'
l_color	color of the lines that indicate genetic flow
asp	aspect ratio of the plotting device
parse	whether parse label, only works if 'label' and 'label_position' exist
g_height	height of regions to plot gene segments relative to the virus
g_width	width of gene segment relative to width of the virus (the hexagon)
t_size	size of text label
t_color	color of text label

Value

ggplot object

Author(s)

Guangchuang Yu

Examples

```

library(tibble)
n <- 8
virus_info <- tibble(id = 1:7,
  x = c(rep(1990, 4), rep(2000, 2), 2009),
  y = c(1,2,3,5, 1.5, 3, 4),
  segment_color = list(rep('purple', n),
    rep('red', n), rep('darkgreen', n), rep('lightgreen', n),

```

```
c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'red', 'purple', 'red', 'purple'),
c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'),
c('darkgreen', 'lightgreen', 'lightgreen', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'))

flow_info <- tibble(from = c(1,2,3,3,4,5,6), to = c(5,5,5,6,7,6,7))

hybrid_plot(virus_info, flow_info)
```

set_layout

set_layout

Description

set layout for reassortment plot

Usage

```
set_layout(virus_info, flow_info, layout = "layout.auto")
```

Arguments

virus_info	virus information
flow_info	flow information
layout	layout method

Value

updated virus_info

Author(s)

Guangchuang Yu

Index

* **internal**

seqcombo-package, [2](#)

geom_genotype, [2](#)

geom_hybrid, [3](#)

hybrid_plot, [4](#)

seqcombo (seqcombo-package), [2](#)

seqcombo-package, [2](#)

set_layout, [6](#)