

Package ‘seqcombo’

June 7, 2023

Title Visualization Tool for Genetic Reassortment

Version 1.23.0

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 7.1.2

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

git_branch devel

git_last_commit 7f263f2

git_last_commit_date 2023-04-25

Date/Publication 2023-06-06

Author Guangchuang Yu [aut, cre]

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

R topics documented:

geom_genotype	2
geom_hybrid	3
hybrid_plot	4
set_layout	6
Index	7

geom_genotype	<i>geom_genotype</i>
---------------	----------------------

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	<i>geom_hybrid</i>
-------------	--------------------

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
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

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	<i>set_layout</i>
------------	-------------------

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

`geom_genotype`, [2](#)

`geom_hybrid`, [3](#)

`hybrid_plot`, [4](#)

`set_layout`, [6](#)