Package ‘seqcombo’

May 4, 2026

Title Visualization Tool for Genetic Reassortment

Version 1.35.0

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`

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`seqcombo-package` *seqcombo: Visualization Tool for Genetic Reassortment*

Description

Provides useful functions for visualizing virus reassortment events.

Author(s)

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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

`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` *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

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