Package ‘seqcombo’
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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

```r
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)
```

Description

`geom_hybrid` is a geom layer for reassortment events.

Usage

```r
geom_hybrid(
  virus_info,  # virus information
  flow_info,   # flow information
  v_color = "darkgreen",  # the color of outer boundary of virus; can use expression (e.g. v_color=~Host) to color virus by specific variable
  v_fill = "steelblue",   # the color to fill viruses; can use expression (e.g. v_fill=~Host) to fill virus by specific variable
  v_shape = "ellipse",   # shape of virus
  l_color = "black",  # the color of line
  asp = 1,           # aspect ratio
  parse = FALSE,     # parse expressions
  g_height = 0.65,   # height of graph
  g_width = 0.65,    # width of graph
  t_size = 3.88,     # size of text
  t_color = "black"  # color of text
)
```

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
Description

visualize virus reassortment events

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(1,2,3,4,5,6), to = c(5,5,5,6,7,7))
ggplot() + geom_hybrid(virus_info, flow_info)
hybrid_plot

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)

Guangchuan Yu
Examples

```r
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)
```

Description

set layout for reassortment plot

Usage

```r
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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