Package ‘seqcombo’

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Title Visualization Tool for Genetic Reassortment
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Description Provides useful functions for visualizing virus reassortment events.
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Description

geom layer of genotype

Usage

```r
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)
```

### Description
geom layer for reassortment events

### Usage
```
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
  v_fill = "steelblue",  # color virus by specific variable
  v_shape = "ellipse",  # the color to fill viruses; can use expression (e.g. v_fill=~Host) to fill virus by
  l_color = "black",    # specific variable
  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

gem 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', '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)

Description

visualize virus reassortment events
**Usage**

```r
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:n,
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

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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