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
geom_hybrid

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', '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,
  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
hybrid_plot

**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

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**Author(s)**
Guangchuang Yu

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**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'))
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)
```

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**Description**

visualize virus reassortment events
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)

Guangchuang 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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