

Package ‘seqcombo’

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

Description

Provides useful functions for visualizing virus reassortment events.

Author(s)

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com>

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 | <i>hyrid_plot</i> |
|-------------|-------------------|

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**

| | |
|-------------------------|-------------------|
| <code>virus_info</code> | virus information |
| <code>flow_info</code> | flow information |
| <code>layout</code> | layout method |

Value

updated virus_info

Author(s)

Guangchuang Yu

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* **internal**

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