

# Package ‘seqcombo’

May 17, 2024

**Title** Visualization Tool for Genetic Reassortment

**Version** 1.26.0

**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>

**biocViews** Alignment, Software, Visualization

**RoxygenNote** 7.1.2

**git\_url** <https://git.bioconductor.org/packages/seqcombo>

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## Contents

|                         |          |
|-------------------------|----------|
| geom_genotype . . . . . | 2        |
| geom_hybrid . . . . .   | 3        |
| hybrid_plot . . . . .   | 4        |
| set_layout . . . . .    | 6        |
| <b>Index</b>            | <b>7</b> |

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geom\_genotype      *geom\_genotype*

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### 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)

```

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geom\_hybrid

*geom\_hybrid*


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**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)
```

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hybrid\_plot

*hyrid\_plot*

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**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*

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**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

# Index

`geom_genotype`, 2

`geom_hybrid`, 3

`hybrid_plot`, 4

`set_layout`, 6