

# Package ‘seqcombo’

January 21, 2025

**Title** Visualization Tool for Genetic Reassortment

**Version** 1.28.0

**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** 7.3.0

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

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** b18fa7c

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2025-01-20

**Author** Guangchuang Yu [aut, cre]

**Maintainer** Guangchuang Yu <[guangchuangyu@gmail.com](mailto:guangchuangyu@gmail.com)>

## Contents

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

---

 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

*hyrid\_plot*

---

**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

virus_info	virus information
flow_info	flow information
layout	layout method

### Value

updated virus\_info

### Author(s)

Guangchuang Yu

# Index

## \* **internal**

seqcombo-package, [2](#)

geom\_genotype, [2](#)

geom\_hybrid, [3](#)

hybrid\_plot, [4](#)

seqcombo (seqcombo-package), [2](#)

seqcombo-package, [2](#)

set\_layout, [6](#)