# Package 'seqcombo'

October 16, 2025

**Title** Visualization Tool for Genetic Reassortment

**Version** 1.30.0

**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_21

**git_last_commit** 6e872ec

**git_last_commit_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-10-15

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

**Maintainer** Guangchuang Yu <guangchuangyu@gmail.com>

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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 *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

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