

# Package ‘seqcombo’

September 27, 2020

**Title** Visualization Tool for Sequence Recombination and Reassortment

**Version** 1.11.0

**Description** Provides useful functions for visualizing sequence recombination and virus reassortment events.

**Depends** R (>= 3.4.0)

**Imports** Biostrings, cowplot, dplyr, ggplot2, grid, igraph, magrittr, methods, rvcheck, utils

**Suggests** emojiFont, knitr, prettydoc, tibble

**VignetteBuilder** knitr

**ByteCompile** true

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** true

**BugReports** <https://github.com/GuangchuangYu/seqcombo/issues>

**biocViews** Alignment, Software, Visualization

**RoxygenNote** 6.1.1

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|               |                      |
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| geom_genotype | <i>geom_genotype</i> |
|---------------|----------------------|

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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*

---

## 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)

```

---

plot

*plot method for SeqDiff object*


---

**Description**

plot method for SeqDiff object

**Usage**

```

## S4 method for signature 'SeqDiff,ANY'
plot(x, width = 50, title = "auto",
  xlab = "Nucleotide Position", by = "bar", fill = "firebrick",
  colors = c(A = "#E495A5", C = "#ABB065", G = "#39BEB1", T = "#ACA4E2"),
  xlim = NULL)

```

**Arguments**

|        |                                      |
|--------|--------------------------------------|
| x      | SeqDiff object                       |
| width  | bin width                            |
| title  | plot title                           |
| xlab   | xlab                                 |
| by     | one of 'bar' and 'area'              |
| fill   | fill color of upper part of the plot |
| colors | color of lower part of the plot      |
| xlim   | limits of x-axis                     |

**Value**

plot

**Author(s)**

guangchuang yu

**Examples**

```
fas <- list.files(system.file("examples", "GVariation", package="seqcombo"), pattern="fas", full.names=TRUE)
x1 <- seqdiff(fas[1], reference=1)
plot(x1)
```

---

|         |                |
|---------|----------------|
| seqdiff | <i>seqdiff</i> |
|---------|----------------|

---

**Description**

calculate difference of two aligned sequences

**Usage**

```
seqdiff(fasta, reference = 1)
```

**Arguments**

|           |   |
|-----------|---|
| fasta     | fasta file                                |
| reference | which sequence serve as reference, 1 or 2 |

**Value**

SeqDiff object

**Author(s)**

guangchuang yu

**Examples**

```
fas <- list.files(system.file("examples", "GVariation", package="seqcombo"), pattern="fas", full.names=TRUE)
seqdiff(fas[1], reference=1)
```

---

|            |                   |
|------------|-------------------|
| set_layout | <i>set_layout</i> |
|------------|-------------------|

---

**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

---

show

*show method*

---

**Description**

show method

**Usage**

show(object)

**Arguments**

object            SeqDiff object

**Value**

message

**Examples**

```
fas <- list.files(system.file("examples", "GVariation", package="seqcombo"), pattern="fas", full.names=TRUE)
x1 <- seqdiff(fas[1], reference=1)
x1
```

---

simplot

*simplot*

---

**Description**

Sequence similarity plot

**Usage**

```
simplot(file, query, window = 200, step = 20, group = FALSE, id, sep,
sd = FALSE)
```

**Arguments**

|        |   |
|--------|---|
| file   | alignment fast file   |
| query  | query sequence  |
| window | sliding window size (bp)  |
| step   | step size to slide the window (bp)  |
| group  | whether grouping sequence   |
| id     | position to extract id for grouping; only works if group = TRUE                             |
| sep    | separator to split sequence name; only works if group = TRUE                                |
| sd     | whether display standard deviation of similarity among each group; only works if group=TRUE |

**Value**

ggplot object

**Author(s)**

guangchuang yu

**Examples**

```
fas <- system.file("examples/GVariation/sample_alignment.fa", package="seqcombo")
simplot(fas, 'CF_YL21')
```

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