

# Package ‘seqcombo’

April 12, 2022

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

**Version** 1.16.1

**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, utils, yulab.utils

**Suggests** emojiFont, knitr, rmarkdown, 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** 7.1.2

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

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

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

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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)
```

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

*seqdiff*

---

**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                    *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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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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