Package 'seqcombo'

October 16, 2019

Title Visualization Tool for Sequence Recombination and Reassortment

Version 1.6.0

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

git_url https://git.bioconductor.org/packages/seqcombo

git_branch RELEASE_3_9

git_last_commit 5862979

git_last_commit_date 2019-05-02

Date/Publication 2019-10-15

Author Guangchuang Yu [aut, cre]

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

R topics documented:

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)
```

---

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

---

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')
```

Index