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

git_branch RELEASE_3_14

git_last_commit d1e889d

git_last_commit_date 2022-03-17

Date/Publication 2022-04-12

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