Package 'chromoMap'

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Type Package

Title Interactive Genomic Visualization of Biological Data

Version 4.1.1

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Description Provides interactive, configurable and elegant graphics visualization of the chromosomes or chromosome regions
of any living organism allowing users to map chromosome elements (like genes, SNPs etc.) on the chromosome plot. It introduces
a special plot viz. the ``chromosome heatmap" that, in addition to mapping elements, can visualize the data
associated with chromosome elements (like gene expression) in the form of heat colors which can be highly
advantageous in the scientific interpretations and research work. Because of the large size of the chromosomes,
it is impractical to visualize each element on the same plot. However, the plot provides a magnified view for each
of chromosome locus to render additional information and visualization specific for that location. You can map
thousands of genes and can view all mappings easily. Users can investigate the detailed information about the mappings
(like gene names or total genes mapped on a location) or can view the magnified single or double stranded view of the
chromosome at a location showing each mapped element in sequential order. The package provide multiple features
like visualizing multiple sets, chromosome heatmaps, group annotations, adding hyperlinks, and labelling.
The plots can be saved as HTML documents that can be customized and shared easily. In addition, you can include them in R Markdown or in R 'Shiny' applications.

Depends R (>= 4.0)

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Encoding UTF-8

Imports htmltools (>= 0.3.6), htmlwidgets (>= 1.0)

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.1.2

NeedsCompilation no

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`chromoMap` *render interactive chromosome plots of any living organism and annotate elements*

Description

render an interactive graphics visualization of entire chromosomes or chromosomal regions of any living organism. Chromosomal elements such as genes can be annotated easily using this tool.

required for creating widgets

Usage

```
chromoMap(
  ch.files,
  data.files,
  title = c(),
  ch_gap = 5,
  ploidy = 1,
  top_margin = 25,
  left_margin = 50,
  chr_width = 15,
  chr_length = 4,
  chr_color = c("black"),
  data_based_color_map = FALSE,
  segment_annotation = FALSE,
  lg_x = 0,
  lg_y = 0,
  data_type = c("numeric", "categorical"),
  labels = FALSE,
  canvas_width = NULL,
  canvas_height = NULL,
```

```
    data_colors = list(),
    anno_col = c("#10B85F"),
    chr_text = c(TRUE),
    discrete.domain = NULL,
    legend = c(FALSE),
    hlinks = FALSE,
    aggregate_func = c("avg"),
    plots = c("none"),
    tag_filter = list(c("none", 0)),
    plot_height = c(30),
    plot_ticks = c(4),
    plot_color = c("blue"),
    plot_y_domain = list(c(0, 0)),
    ch2D.colors = NULL,
    ch2D.cat.order = NULL,
    ch2D.lg_x = 0,
    ch2D.lg_y = 0,
    ref_line = c(FALSE),
    refl_pos = c(0),
    refl_color = c("grey"),
    refl_stroke_w = c(2),
    tagColor = c("red"),
    heat_map = c(TRUE),
    text_font_size = c(10),
    chr_curve = 5,
    title_font_size = 12,
    label_font = 9,
    label_angle = -90,
    vertical_grid = FALSE,
    grid_array = c(0, 5000, 10000),
    grid_color = "grey",
    grid_text = NULL,
    grid_text_size = 12,
    grid_text_y = 20,
    plot_filter = list(c("none", 0)),
    id = c("chromap"),
    region = NULL,
    show.links = FALSE,
    loci_links = "none",
    directed.edges = F,
    y_chr_scale = 0,
    links.colors = NULL,
    links.lg_x = 0,
    links.lg_y = 0,
    n_win.factor = 1,
    chr.scale.ticks = 5,
    export.options = F,
    fixed.window = F,
```

```
  window.size = NULL,
  win.summary.display = F,
  remove.last.window = T,
  guides = F,
  guides_color = "lightgrey",
  ann.h = 1,
  chr.2D.plot = F,
  display.chr = T,
  plot.shift = c(1),
  plot.legend.labels = c(""),
  cat.legend.label = "",
  plot.y.labels = c(""),
  plot.y.lab.x = 10,
  plot.y.lab.y = 0,
  plot.y.lab.size = 15,
  scale.suffix = "bp",
  numeric.domain = NULL,
  interactivity = T
)
```

Arguments

ch.files	filename(s) as character vector OR list of data.frames containing co-ordinates of the chromosomes to render
data.files	filename(s) as character vector OR list of data.frames containing data to annotate on the chromosomes.
title	a character string to be used as a title in plot
ch_gap	provide spacing between chromosomes.
ploidy	specify the number of sets of chromsomes being passed.
top_margin	specify the margin from top of the plot
left_margin	specify the margin from the left of the plot
chr_width	specify the width of each chromsome
chr_length	specify the length of each chromsome.
chr_color	a vector specifying the color of each chromsome in a set. A color can be assigned to each set by passing a different color values as vector
data_based_color_map	a boolean to tell the plot to use the data provided in file for visualizing annotation
segment_annotation	a boolean to use segment-annotation algorithm
lg_x	specify the x or horizontal distance of the legend from origin(bottom right corner)
lg_y	specify the y or vertical distnce of the legend from the origin
data_type	specifying the data type of the data used. takes value either 'categorical' or 'numeric'

labels	a boolean to include labels in plot
canvas_width	width of the plot
canvas_height	height of the plot
data_colors	specify annotation colors for the data
anno_col	a vector to specify annotation color for each set.
chr_text	a boolean vector to enable or disable chromsome texts for each ploidy.set
discrete.domain	manually specify the order of categories.
legend	a boolean vector to enable or disable legend for each set/ploidy
hlinks	a boolean to use hyperlinks supplied in data
aggregate_func	takes either 'sum' or 'avg' to specift aggregate function for each loci
plots	specify the type of plot to visualize. takes either 'scatter' , 'bar' or 'tags'.(default: 'none')
tag_filter	a list to specify the filter operation and operands for each ploidy.
plot_height	specify plot height for each ploidy. default: c(30)
plot_ticks	specify number of ticks for plot axis. default: c(4)
plot_color	specify the plot color for each ploidy. default: c("blue")
plot_y_domain	specify plot y-axis domain. default: list(c(0,0))
ch2D.colors	specify the group colors for visualizing categories on 2D chromosome plots
ch2D.cat.order	manually setting the order of categories for 2D-Chromsome plot
ch2D.lg_x	specify the x or horizontal distance of 2D plot legend from the origin(bottom right corner)
ch2D.lg_y	specify the y or vertical distance of 2D plot legend
ref_line	a boolean to use horizontal reference line in plot. default: c(FALSE)
refl_pos	specify the position of reference line. default: c(0)
refl_color	specify the color of the reference line. default: c("grey")
refl_stroke_w	specify the stroke width of the reference line. default: c(2)
tagColor	specify the color of tags. default: c("red")
heat_map	a boolean to use if chromosome heatmaps are shown. default: c(TRUE),
text_font_size	specify chromosome text font-size. default: c(10)
chr_curve	specify the chromosome curves at the telomeres or centromere loci. default:5
title_font_size	specify the font-size of the title. default:12
label_font	specify the font-size of the labels. default:9
label_angle	specify the angle of rotation of labels. default: -90
vertical_grid	a boolean to use vertical grid lines. default: FALSE
grid_array	specify the position(s) of grid line(s) in bp to highlight locations across genome. default: c(0,5000,10000)

grid_color	specify the color of the grid lines. default: "grey"
grid_text	specify the text to be attached at the top end of gridlines
grid_text_size	specify the font-size of the text
grid_text_y	specify the y-distance (from top) for the text
plot_filter	a list specify the plot filter operation, operands, and filter-color for each ploidy.
id	specify a unique id doe chromoMap plot. default: c("chromap")
region	specify the region of interest for chromosome(s) for zoom-in. Format: "chrName:Ploidy:Start:Stop"
show.links	a boolean to specify whether links are visualized. default: FALSE
loci_links	a character vector specifying file name or a data.frame for links input data
directed.edges	a boolean to visualize directed edges
y_chr_scale	adjust the chromosome scale along y-axis
links.colors	specify the links colors
links.lg_x	specify x or horizontal distance of links legend from the origin
links.lg_y	specify y or vertical distance of links
n_win.factor	specify the factor by which the chr will be scaled;increases number of windows (default:1)
chr.scale.ticks	specify the number of ticks for chr scale (default:5)
export.options	boolean to include export buttons in the plot
fixed.window	Boolean to specify wether to use fixed window visualization
window.size	specify the window size, if fixed.window is TRUE
win.summary.display	boolean to display window summary to console
remove.last.window	For fixed window analysis, boolean to specify whether to include last window of chromosomes
guides	boolean to display guides
guides_color	set guides color.
ann.h	set annotation bar height in 2D-Chromosome plot
chr.2D.plot	boolean to specify visualize 2d Chromosome plot
display.chr	boolean to show.hide chromosome
plot.shift	shifting the plots in y direction in case hiding chromosomes
plot.legend.labels	specify plot legend labels
cat.legend.label	specify categorical-data legends label
plot.y.labels	specify plots y-axis labels
plot.y.lab.x	adjust plot y labels in x-direction
plot.y.lab.y	adjust plot y labels in y-direction

plot.y.lab.size	set size of plot y labels
scale.suffix	set the suffix for chromosome scale(default:'bp')
numeric.domain	manually set data domain(min,max) for heat colors for numeric data
interactivity	boolean to enable/disable interactivity on chromosomes

Examples

```
## Not run:

library(chromoMap)

#simple annotations
chromoMap("chromosome_file.txt","annotation_file.txt")

#polyploidy example
chromoMap(c("chromosome_set1.txt","chromosome_set2.txt"),
          c("annotation_set1.txt","annotation_set2.txt"), ploidy=2)

#plotting group annotation
chromoMap("chromosome_file.txt","annotation_file.txt",
           data_base_color_map=T, data_type="categorical")

#plotting chromsome heatmaps
chromoMap("chromosome_file.txt","annotation_file.txt",
           data_based_color_map=T, data_type="numeric")

#enabling hyperlinks
chromoMap("chromosome_file.txt","annotation_file.txt", hlinks=T)

#enabling labels
chromoMap("chromosome_file.txt","annotation_file.txt", labels=T)

#change chromosome color
chromoMap("chromosome_file.txt","annotation_file.txt", chr_color="red")


## End(Not run)
```

---

chromoMap-shiny *Shiny bindings for chromoMap*

Description

Output and render functions for using chromoMap within Shiny applications and interactive Rmd documents.

Usage

```
chromoMapOutput(outputId, width = "100%", height = "400px")

renderChromoMap(expr, env = parent.frame(), quoted = FALSE)
```

Arguments

outputId	output variable to read from
width, height	Must be a valid CSS unit (like '100%', '400px', 'auto') or a number, which will be coerced to a string and have 'px' appended.
expr	An expression that generates a chromoMap
env	The environment in which to evaluate expr.
quoted	Is expr a quoted expression (with quote())? This is useful if you want to save an expression in a variable.

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