Package ‘chromoMap’

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Type Package
Title Interactive Genomic Visualization of Biological Data
Version 0.3
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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 heat-maps, group annotations, adding hyperlinks, and labelling.

Depends R (>= 4.0)
License GPL-3 | file LICENSE
Encoding UTF-8
LazyData false
Imports htmltools (>= 0.3.6), htmlwidgets (>= 1.0)
Suggests knitr, rmarkdown
VignetteBuilder knitr
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R topics documented:

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## 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

```r
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 = 500,  
)```
canvas_height = 520,
data_colors = list(),
anno_col = c("#10B85F"),
chr_text = c(TRUE),
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)),
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, 5, 20, 45, 100),
grid_color = "grey",
plot_filter = list(c("none", 0)),
id = c("chromap")
)

Arguments

ch.files filename(s) containing co-ordinates of the chromosomes to render
data.files filename(s) 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 chromosomes 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 chromosome
chr_length specify the length of each chromosome.
chr_color a vector specifying the color of each chromosome 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 distance 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 chromosome texts for each ploidy set

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 specify 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))

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). default: c(0,5,20,45,100)

grid_color  
specify the color of the grid lines. default: "grey"

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")
Examples

## Not run:

```r
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 chromosome 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)
```

---

**Shiny bindings for chromoMap**

### Description

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

### Usage

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

```r
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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