Package ‘chromoMap’

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Type  Package
Title  Interactive Genomic Visualization of Biological Data
Version  0.3.1
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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)
License  GPL-3 | file LICENSE
Encoding  UTF-8
LazyData  false
Imports  htmltools (>= 0.3.6), htmlwidgets (>= 1.0)
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 = 500,
```r
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)),
scatter.colors = NULL,
scatter.lg_x = 0,
scatter.lg_y = 0,
ref_line = c(FALSE),
refl_pos = c(0),
ref1_color = c("grey"),
ref1_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
)
```

**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 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))
scatter.colors  specify the group colors for visualizing categories on scatter plot
scatter.lg_x  specify the x or horizontal distance of scatter plot legend from the origin(bottom right corner)
scatter.lg_y  specify the y or vertical distance of scatter 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

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 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)

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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.
Is `expr` a quoted expression (with `quote()`)? This is useful if you want to save an expression in a variable.
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