

Package ‘chromoMap’

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Type Package

Title Interactive Visualization and Mapping of Human Chromosomes

Version 0.1

Maintainer Lakshay Anand <lakshayanand15@gmail.com>

Description

Provides interactive, configurable and elegant graphics visualization of the human chromosomes 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 location 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 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 (>= 3.4.0)

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Encoding UTF-8

LazyData false

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

Suggests knitr, rmarkdown, shiny

VignetteBuilder knitr

RoxygenNote 6.0.1

NeedsCompilation no

Author Lakshay Anand [aut, cre]

Repository CRAN

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chromoMap	<i>render interactive chromosome plots</i>
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Description

render an interactive graphics of human chromosome. It creates an HTML widget that calls the JavaScript library chromoMap.js that generates the chromosome graphics required for creating widgets

Usage

```
chromoMap(chData, type = c("annotation", "heatmap-single", "heatmap-double"),
  align = "horizontal", bgCol = "white", bgBorder = "white",
  chCol = "#c70039", chBorder = "#c70039", annoColor = "orange",
  textCol = "black", HeatColRange = c("red", "white", "blue"),
  dim = c(640, 480), width = NULL, height = NULL)
```

Arguments

chData	The chromosome data required for annotating chromosome and creating heatmaps. It is a data.frame with atleast three colums viz. name (specify the name for annotation), chrom (specify chromosome name), and start (specify the start position of element). While for heatmaps additional columns data and/or secondData need to added.
type	Specify the type of chromosome plot.Takes only one value from "annotation" , "heatmap-single", or "heatmap-double". For more information about the type of plots see vignette.
align	specify the alignment of plot. Takes the value "horizontal" or "vertical".
bgCol	specify the background color.
bgBorder	specify the border color.

chCol	specify the body color of chromosomes
chBorder	specify the border color of chromosomes
annoColor	specify the color of annotation bars on the chromosomes.
textCol	specify the text color.
HeatColRange	specify the heat-colors for the heatmap. Takes a character vector with three color values each corresponding to minimum, medium, and maximum data.
dim	specify dimension of plot. Takes two values for width and height of the plot.
width	use to define width of widget. Usually ignore and do not change
height	height of widget. ignore

Examples

```
library(chromoMap)
data("pancadata")
#dataset contains two data
#view data set
head(pancadata$data1)
head(pancadata$data2)

#plotting simple annotation
chromoMap(pancadata$data1)

#plotting heatmap-single
chromoMap(pancadata$data1, type="heatmap-single")

#plotting heatmap double
chromoMap(pancadata$data2, type="heatmap-double")

#change orientation of plot
chromoMap(pancadata$data1, align="vertical")

#change chromosome color
chromoMap(pancadata$data1, chCol="green", chBorder="green")

#change chromosome plot background and text color
chromoMap(pancadata$data2, type="heatmap-double", textCol="white", bgCol="black")
```

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.

chromoMapToHTML	<i>convert chromoMap plots into customizable HTML documents</i>
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Description

Helpful in sharing the graphics. Also give options to add text

Usage

```
chromoMapToHTML(chromoMap, file = "chromoMap.html",
  title = "Choose attractive Title for your chromoMap", dir = "",
  description = "", openAfterSave = FALSE)
```

Arguments

chromoMap	an object of the chromoMap plot
file	name of the file to save with, default is chromoMap.html
title	A string for the Title that can be included in the document
dir	specify the directory of the file.default is current directory.
description	A string for adding description of the plot
openAfterSave	A boolean to specify whether to open the document after save

Examples

```
library(chromoMap)
data("pancandata")
chmap = chromoMap(pancandata$data2, type="heatmap-double")

#saving plot to HTML document
#for description
my_desc = "you can write a paragraph to describe your plot"
chromoMapToHTML(chmap, title = "Expression profile Comparison in normal vs tumor",
description = my_desc, openAfterSave = TRUE, dir=tempdir())
```

pancandata	<i>Gene Expression RNAseq data for Pancreatic Adenocarcinoma from TCGA</i>
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Description

Data extracted from The Cancer Genome Atlas database and further processed, consist of Two datasets- data1- 630 selected differentially expressed genes in pancreatic cancer condition as predicted from R limma package, also includes the logFC(log tranformed Fold Change) for each gene data2 - normalized expression values of 25,465 genes for one control sample and one tumor sample (Pancreatic cancer), the data is converted into the format for analysis, consist of five columns as name(gene-names), chrom,start,data(control),secondData(tumor)

Usage

```
data(pancandata)
```

Format

A List of 2 elements

References

The Cancer Genome Atlas

Examples

```
data(pancandata)

chromoMap(pancandata$data1, type="annotation")
chromoMap(pancandata$data1, type="heatmap-single")
chromoMap(pancandata$data2, type="heatmap-double")
```

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