

Package ‘chromDraw’

October 8, 2015

Type Package

Title chromDraw an R package for visualization of linear and circular karyotypes.

Version 1.0.0

Date 2014-08-01

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biocViews Software

Depends R (>= 3.0.0)

SystemRequirements Rtools (>= 3.1)

Description Package chromDraw is a simple package for linear and circular type of karyotype visualization. The linear type of visualization is usually used for demonstrating chromosomes structures in karyotype and the circular type of visualization is used for comparing of karyotypes between each other. This tool has own input data format or genomicRanges structure can be used as input. Each chromosome containing definition of blocks and centromere position. Output file formats are *.eps and *.svg.

License GPL-3

Imports Rcpp (>= 0.11.1), GenomicRanges (>= 1.17.46)

LinkingTo Rcpp

URL www.plantcytogenomics.org/chromDraw

NeedsCompilation yes

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chromDraw-package *chromDraw - simple karyotype visualization tool.*

Description

chromDraw is a simple package for drawing simple caryotype or comparing karyotypes schemes. This tool has own input data format. Each chromosome containing definition of blocks and centromere position. Output file formats are *.eps and *.svg.

Details

Package: chromDraw
Type: Package
Date: 2014-08-01
License: GPL-3
License: LGPL | library Board

This package has only one function with two parameters, such as main function in C. First parameter ARGV is a count of input parameters and second parameter ARGV is vector contain calling parameters. Example: `chromDraw(argc=5, argv=c("chromDraw", "-c", "/home/user/Documents/colors.txt", "-d", "/home/user/Documents/input_data.txt"))`

First string in vector with arguments must be package name. The others strings in vector are parameter string and string with parameter value. As shown in the example.

Author(s)

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References

LibBoard: A vector graphics C++ library (Version 0.9.0). GREYC laboratory. [Software]. <http://libboard.sourceforge.net/>. [accessed Sept. 2014].

See Also

[chromDraw main_chromDraw](#)

Examples

```
OUTPUTPATH = file.path(getwd());  
INPUTPATH = system.file('extdata', 'Ack_and_Stenopetalum_nutans.txt', package = 'chromDraw')  
COLORPATH = system.file('extdata', 'default_colors.txt', package = 'chromDraw')  
chromDraw(argc=7, argv=c("chromDraw", "-c", COLORPATH, "-d", INPUTPATH, "-o", OUTPUTPATH));
```

chromDraw	<i>Main chromDraw function. This R function call main C++ function.</i>
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Description

Main chromDraw function. This R function call main C++ function.

Usage

```
chromDraw(argc, argv)
```

Arguments

argc	count of input parameters.
argv	vector with input parameters strings.

Value

return exit state.

Examples

```
OUTPUTPATH = file.path(getwd());
INPUTPATH = system.file('extdata', 'Ack_and_Stenopetalum_nutans.txt', package = 'chromDraw')
COLORPATH = system.file('extdata', 'default_colors.txt', package = 'chromDraw')
chromDraw(argc=7, argv=c("chromDraw", "-c", COLORPATH, "-d", INPUTPATH, "-o",
OUTPUTPATH));
```

chromDrawGR	<i>Main chromDraw function using Genomic Ranges as input data format. This R function call main C++ function.</i>
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Description

Main chromDraw function using Genomic Ranges as input data format. This R function call main C++ function.

Usage

```
chromDrawGR(karyotypes, colors)
```

Arguments

karyotypes	vector of Genomic Ranges structures per karyotype.
colors	data frame definition of colors, containing color name and RGB of color values.

Value

return exit state.

Examples

```
#load package
library(GenomicRanges)

#data generating
karyotype1 <- GRanges(seqnames =Rle(c("Ack1", "Ack2"), c(5, 5)),ranges =
IRanges(start = c(0, 400000,0,3300000,6000000,0,2500000,0,3800000,6400000),
end = c(400000,3300000,0,6000000,10400000,2500000,3800000,0,6400000,14800000),
names = c("A","B","CENTROMERE","C","D","E","F","CENTROMERE","G","H")),
color = c("orange","yellow","", "orange","red","green","green","", "red","orange"));

karyotype2 <- GRanges(seqnames =Rle(c("Ack3", "Ack4"), c(4, 4)),ranges =
IRanges(start = c(0,0, 2400000,3500000,0,0,2400000,6700000),
end = c(2400000,0,3500000,12200000,2400000,0,6700000,9200000),
names = c("I","CENTROMERE","J","K","L","CENTROMERE","M","N")),
color = c("light_blue","", "orange","red","pink","", "red","light_blue"));

inputData <- list(karyotype1,karyotype2);

#colors generating
name <- c("yellow", "red", "blue", "violet", "orange", "green", "light_blue", "pink");
r <- c(255, 255, 0, 255, 247, 0, 0, 230);
g <- c(255, 0, 0, 0, 148, 255, 255, 170);
b <- c(0, 0, 255, 255, 29, 0, 255, 160);
inputColors <- data.frame(name,r,g,b);

#run the function with generated data and colors
chromDrawGR(inputData,inputColors);
```

convertInputColors	<i>R function for converting data frame with colors to chromDraw color data format.</i>
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Description

R function for converting data frame with colors to chromDraw color data format. Output of this function is file "colors.txt" in working directory.

Usage

```
convertInputColors(colors);
```

Arguments

colors data frame definition of coloros, containing color name and RGB of color values.

Value

return file with colors in working directory.

Examples

```
#colors generating
name <- c("yellow", "red", "blue", "violet", "orange", "green", "light_blue", "pink");
r <- c(255, 255, 0, 255, 247, 0, 0, 230);
g <- c(255, 0, 0, 0, 148, 255, 255, 170);
b <- c(0, 0, 255, 255, 29, 0, 255, 160);
inputColors <- data.frame(name,r,g,b);

#run the function for generate chromDraw color file.
convertInputColors(inputColors);
```

convertInputData	<i>R function for converting Genomic Ranges data structure to chromDraw dat format.</i>
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Description

R function for converting Genomic Ranges data structure to chromDraw dat format. Output of this function is file "data.txt" in working directory.

Usage

```
convertInputData(karyotypes)
```

Arguments

karyotypes vector of Genomic Ranges structures per karyotype.

Value

return exit sate.

Examples

```
#load package
library(GenomicRanges)

#data generating
karyotype1 <- GRanges(seqnames =Rle(c("Ack1", "Ack2"), c(5, 5)),ranges =
IRanges(start = c(0, 400000,3300000,0,6000000,10400000,0,2500000,0,3800000,6400000),
          end = c(400000,3300000,0,6000000,10400000,2500000,3800000,0,6400000,14800000),
          names = c("A","B","CENTROMERE","C","D","E","F","CENTROMERE","G","H")),
          color = c("orange","yellow","", "orange","red", "green", "green", "", "red", "orange"));

karyotype2 <- GRanges(seqnames =Rle(c("Ack3", "Ack4"), c(4, 4)),ranges =
```

```

IRanges(start = c(0,0, 2400000,3500000,0,0,2400000,6700000),
        end = c(2400000,0,3500000,12200000,2400000,0,6700000,9200000),
        names = c("I","CENTROMERE","J","K","L","CENTROMERE","M","N")),
        color = c("light_blue","", "orange","red","pink","", "red","light_blue"));

inputData <- list(karyotype1,karyotype2);

#run the function for generate chromDraw data file.
convertInputData(inputData);

```

main_chromDraw	<i>Main chromDraw function. The main function that controls all other C++ functions.</i>
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Description

Main chromDrawS function. The main function that controls all other C++ functions.

Usage

```
main_chromDraw(argc, argv)
```

Arguments

argc	Count of input parameters.
argv	Vector with input parameters strings.

Value

Return exit state.

Examples

```

OUTPUTPATH = file.path(getwd());
INPUTPATH = system.file('extdata','Ack_and_Stenopetalum_nutans.txt', package = 'chromDraw')
COLORPATH = system.file('extdata','default_colors.txt', package = 'chromDraw')
chromDraw(argc=7, argv=c("chromDraw", "-c", COLORPATH, "-d", INPUTPATH, "-o",
OUTPUTPATH));

```

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