Package 'chromDraw'

April 22, 2016

Type Package

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

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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 demonstrat-
ing chromosomes structures in karyotype and the circular type of visualization is used for com-
paring of karyotypes between each other. This tool has own input data format or genomi-
cRanges structure can be used as input. Each chromosome containing defini-
tion 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

R topics documented:

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 ARGC 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.

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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 *Main chromDraw function. Thsic R function call main C++ function.*

Description

Main chromDraw function. Thsic 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 sate.

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

Description

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

Usage

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

Arguments

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

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, 400000,0,3300000,6000000,0,2500000,0,3800000,6400000),
        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);
```

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convertInputColors | *R function for converting data frame with colors to chromDraw color data format.*

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);
```

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convertInputData	*R function for converting Genomic Ranges data structure to chromDraw dat format.*

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, 400000,0,3300000,6000000,0,2500000,0,3800000,6400000),
        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(2400000,0,3500000,12200000,0,0,6700000,9200000),
        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	*Main chromDraw function. The main function that controls all other C++ functions.*

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 sate.

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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