

# Package ‘chromDraw’

July 2, 2025

**Type** Package

**Title** chromDraw is a R package for drawing the schemes of karyotypes in the linear and circular fashion.

**Version** 2.38.0

**Date** 2016-06-02

**Author** Jan Janecka, Ing., Mgr. CEITEC Masaryk University

**Maintainer** Jan Janecka <jan.janecka@ceitec.muni.cz>

**biocViews** Software

**Depends** R (>= 3.0.0)

**SystemRequirements** Rtools (>= 3.1)

**Description** ChromDraw is a R package for drawing the schemes of karyotype(s) in the linear and circular fashion. It is possible to visualize cytogenetic marks on the chromosomes. This tool has its own input data format. Input data can be imported from the GenomicRanges data structure. This package can visualize the data in the BED file format. Here is a requirement on the first nine fields of the BED format. 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](http://www.plantcytogenomics.org/chromDraw)

**git\_url** <https://git.bioconductor.org/packages/chromDraw>

**git\_branch** RELEASE\_3\_21

**git\_last\_commit** 09256c9

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-07-02

Contents

|                              |          |
|------------------------------|----------|
| chromDraw-package . . . . .  | 2        |
| chromDraw . . . . .          | 3        |
| chromDrawGR . . . . .        | 4        |
| convertInputColors . . . . . | 5        |
| convertInputData . . . . .   | 5        |
| main_chromDraw . . . . .     | 6        |
| <b>Index</b>                 | <b>8</b> |

---

|                   |                                                         |
|-------------------|---------------------------------------------------------|
| chromDraw-package | <i>chromDraw - simple karyotype visualization tool.</i> |
|-------------------|---------------------------------------------------------|

---

Description

ChromDraw is a R package for drawing the schemes of karyotype(s) in the linear and circular fashion. It is possible to visualized cytogenetic marsk on the chromosomes. This tool has own input data format. Input data can be imported from the GenomicRanges data structure. This package can visualized the data in the BED file format. Here is requirement on to the first nine fields of the BED format. Output files format are \*.eps and \*.svg.

Details

Package: chromDraw  
Type: Package  
Date: 2015-12-12  
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.

Author(s)

Jan Janecka, Ing. Mgr. CEITEC MU Masaryk University Kamenice 5, Building A26 CZ-625 00, Brno Czech Republic tel.: 549 49 8190  
Email: jan.janecka@ceitec.muni.cz

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 calls the main C++ function.</i> |
|-----------|------------------------------------------------------------------------------|

---

**Description**

Main chromDraw function. This R function calls the main C++ function.

**Usage**

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

**Arguments**

|      |                                           |
|------|-------------------------------------------|
| argc | count of the input parameters.            |
| argv | vector with the 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>Function chromDrawGR uses Genomic Ranges as input data format.<br/>This R function call the main C++ function.</i> |
|-------------|-----------------------------------------------------------------------------------------------------------------------|

---

## Description

Function chromDrawGR uses Genomic Ranges as input data format. This R function call the main C++ function. If the output directory is not set, then it is use working directory for the outputs.

## Usage

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

## Arguments

|            |                                                                                      |
|------------|--------------------------------------------------------------------------------------|
| karyotypes | vector of the Genomic Ranges structures per karyotype.                               |
| colors     | data frame definition of coloros, containing color name and RGB of the 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>The R function for converting the data frame with colors to chrom-DRAW color data format.</i> |
|--------------------|--------------------------------------------------------------------------------------------------|

---

### Description

The R function for converting the data frame with colors to chromDraw color data format. Output of this function is file "colors.txt" in the 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>The R function for converting Genomic Ranges data structure to the chromDraw dat format.</i> |
|------------------|-------------------------------------------------------------------------------------------------|

---

### Description

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

**Usage**

```
convertInputData(karyotypes)
```

**Arguments**

karyotypes      vector of the Genomic Ranges structures per karyotype.

**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);

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

---

main\_chromDraw

*The main chromDraw function, that controls all other C++ functions.*


---

**Description**

The main chromDraw function, that controls all other C++ functions.

**Usage**

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

**Arguments**

argc      Count of the input parameters.  
 argv      Vector with the 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));
```

# Index

\* **package, libBoard, getopt, Rcpp,**  
    **chromosome visualization,**  
    **karyotype visualization,**  
    **comparing karyotypes**  
chromDraw-package, [2](#)

chromDraw, [3](#), [3](#)

chromDraw-package, [2](#)

chromDrawGR, [4](#)

convertInputColors, [5](#)

convertInputData, [5](#)

main\_chromDraw, [3](#), [6](#)