

Package ‘RIdeogram’

January 15, 2019

Type Package

Title Drawing SVG Graphics to Visualize and Map Genome-Wide Data in Idiograms

Version 0.1.1

Maintainer Zhaodong Hao <haozd1992@163.com>

Description For whole-genome analysis, idiograms are virtually the most intuitive and effective way to map and visualize the genome-wide information. RIdeogram was developed to visualize and map whole-genome data in idiograms with no restriction of species.

License Artistic-2.0

Encoding UTF-8

LazyData true

Depends R (>= 3.4.0)

Imports ggplot2, grDevices, grImport2, rsvg, scales, tools

RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Zhaodong Hao [aut, cre],
Dekang Lv [aut],
Ying Ge [aut],
Jisen Shi [aut],
Guangchuang Yu [aut],
Jinhui Chen [aut]

Repository CRAN

Date/Publication 2019-01-15 15:50:11 UTC

R topics documented:

convertSVG	2
gene_density	3

human_karyotype	3
ideogram	4
LTR_density	5
Random_RNAs_500	5

Index	6
--------------	----------

convertSVG	<i>convertSVG</i>
------------	-------------------

Description

convert svg to png or other format

Usage

```
convertSVG(svg, file = "chromosome", device = NULL, width = 8.2677,
           height = 11.6929, dpi = 300)
```

```
svg2pdf(svg, file = "chromosome", width = 8.2677, height = 11.6929,
         dpi = 300)
```

```
svg2png(svg, file = "chromosome", width = 8.2677, height = 11.6929,
         dpi = 300)
```

```
svg2tiff(svg, file = "chromosome", width = 8.2677, height = 11.6929,
          dpi = 300)
```

```
svg2jpg(svg, file = "chromosome", width = 8.2677, height = 11.6929,
         dpi = 300)
```

Arguments

svg	svg file
file	output file name
device	target format
width	output width
height	output height
dpi	output dpi

Value

invisible grob object

Author(s)

Zhaodong Hao, Dekang Lv, Ying Ge, Jisen Shi, Guangchuang Yu, Jinhui Chen

gene_density

Gene distribution across the human genome

Description

Gene numbers was counted with a window of 1 Mb

Usage

```
data(gene_density)
```

Format

data frame

Source

Gencode (<https://www.genecodegenes.org/>)

human_karyotype

Karyotype information of the human genome

Description

The version of this geome is gencode.v29.

Usage

```
data(human_karyotype)
```

Format

data frame

Source

Gencode (<https://www.genecodegenes.org/>)

ideogram	<i>ideogram</i>
----------	-----------------

Description

ideogram with overlaid heatmap annotation and optional track label

Usage

```
ideogram(karyotype, overlaid = NULL, label = NULL,  
         colorset1 = c("#4575b4", "#ffffff", "#d73027"),  
         colorset2 = c("#b35806", "#f7f7f7", "#542788"), width = 170,  
         Lx = 160, Ly = 35, output = "chromosome.svg")
```

Arguments

karyotype	karyotype data
overlaid	overlaid data
label	track label data
colorset1	overlaid heatmap-1 color
colorset2	overlaid heatmap-2 color
width	width of plot region
Lx	position of legend (x)
Ly	position of legend (y)
output	output file, only svg is supported

Value

output file

Author(s)

Zhaodong Hao, Dekang Lv, Ying Ge, Jisen Shi, Guangchuang Yu, Jinhui Chen

Examples

```
# Loading the package  
require(RIdeogram)  
  
# Loading the testing data  
data(human_karyotype, package="RIdeogram")  
data(gene_density, package="RIdeogram")  
data(Random_RNAs_500, package="RIdeogram")  
  
# Checking the data format  
head(human_karyotype)
```

```
head(gene_density)
head(Random_RNAs_500)

# Running the function
ideogram(karyotype = human_karyotype)
convertSVG("chromosome.svg", device = "png")

# Then, you will find a SVG file and a PNG file in your Working Directory.
```

LTR_density	<i>LTR distribution across the human genome</i>
-------------	---

Description

LTR numbers was counted with a window of 1 Mb

Usage

```
data(LTR_density)
```

Format

data frame

Source

UCSC (<http://genome.ucsc.edu/index.html>)

Random_RNAs_500	<i>500 RNAs' position</i>
-----------------	---------------------------

Description

500 RNAs randomly selected from all tRNAs, rRNAs and miRNA in the human genome.

Usage

```
data(Random_RNAs_500)
```

Format

data frame

Source

Gencode (<https://www.gencodegenes.org/>)

Index

*Topic **datasets**

- gene_density, [3](#)
- human_karyotype, [3](#)
- LTR_density, [5](#)
- Random_RNAs_500, [5](#)

convertSVG, [2](#)

gene_density, [3](#)

human_karyotype, [3](#)

ideogram, [4](#)

LTR_density, [5](#)

Random_RNAs_500, [5](#)

svg2jpg (convertSVG), [2](#)

svg2pdf (convertSVG), [2](#)

svg2png (convertSVG), [2](#)

svg2tiff (convertSVG), [2](#)