

Package ‘RIdeogram’

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Type Package

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

Version 0.2.2

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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 on idiograms with no restriction of species.

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Encoding UTF-8

LazyData true

Depends R (>= 3.5.0)

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

RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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convertSVG

convertSVG

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, Dolf Weijers, Guangchuang Yu, Jinhui Chen

Fst_between_CE_and_CW *Fst between two Liriodendron groups*

Description

Fst values between China east and west groups of *Liriodendron chinense* and being calculated in a 2-Mb sliding window with a 1-Mb step

Usage

```
data(Fst_between_CE_and_CW)
```

Format

data frame

Source

Nature Plants, doi: 10.1038/s41477-018-0323-6

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/>)

GFFex

GFFex

Description

extract some specific feature information from a gff file

Usage

```
GFFex(input, karyotype, feature = "gene", window = 1e+06)
```

Arguments

input	gff file
karyotype	karyotype file
feature	feature name
window	window size

Value

dataframe

Author(s)

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

human_karyotype	<i>Karyotype information of the human genome</i>
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Description

The version of this genome is gencode.v29.

Usage

```
data(human_karyotype)
```

Format

data frame

Source

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

ideogram	<i>ideogram</i>
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Description

ideogram with overlaid heatmap annotation and optional track label

Usage

```
ideogram(karyotype, overlaid = NULL, label = NULL, label_type = NULL,
  synteny = NULL, colorset1 = c("#4575b4", "#ffffbf", "#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
label_type	track label type, only support four types: marker, heatmap, line and polygon
synteny	synteny data
colorset1	overlaid heatmap color
colorset2	label heatmap 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, Dolf Weijers, 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 (Remove "#" before you run the following codes)
# ideogram(karyotype = human_karyotype)
# convertSVG("chromosome.svg", device = "png")

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

karyotype_dual_comparison

Karyotype for two genome comparison

Description

Grape and Populus genomes

Usage

```
data(karyotype_dual_comparison)
```

Format

data frame

Source

MCscan

karyotype_ternary_comparison

Karyotype for three genome comparison

Description

Amborella, Grape and Liriodendron genomes

Usage

data(karyotype_ternary_comparison)

Format

data frame

Source

MCscan

liriodendron_karyotype

Karyotype information of the Liriodendron genome

Description

Liriodendron chinense genome

Usage

data(liriodendron_karyotype)

Format

data frame

Source

Nature Plants, doi: 10.1038/s41477-018-0323-6

LTR_density

LTR distribution across the human genome

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>)

Pi_for_CE

Pi of one Liriodendron group

Description

Pi values of the China east group of *Liriodendron chinense* and being calculated in a 2-Mb sliding window with a 1-Mb step

Usage

```
data(Pi_for_CE)
```

Format

data frame

Source

Nature Plants, doi: 10.1038/s41477-018-0323-6

Pi_for_CE_and_CW	<i>Pi of two Liriodendron groups</i>
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Description

Pi values of the China east and west groups of *Liriodendron chinense* and being calculated in a 2-Mb sliding window with a 1-Mb step

Usage

```
data(Pi_for_CE_and_CW)
```

Format

data frame

Source

Nature Plants, doi: 10.1038/s41477-018-0323-6

Random_RNAs_500	<i>500 RNAs' position</i>
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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.genencodegenes.org/>)

synteny_dual_comparison

Synteny for two genome comparison

Description

Genome Synteny between Grape and Populus

Usage

```
data(synteny_dual_comparison)
```

Format

data frame

Source

MCscan

synteny_ternary_comparison

Synteny for three genome comparison

Description

Genome Synteny among Amborella, Grape and Liriodendron

Usage

```
data(synteny_ternary_comparison)
```

Format

data frame

Source

MCscan

`synteny_ternary_comparison_graident`

Synteny for three genome comparison with gradient fill

Description

Genome Synteny among Amborella, Grape and Liriodendron with gradient fill

Usage

`data(synteny_ternary_comparison_graident)`

Format

data frame

Source

MCscan

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