

# Package ‘RIdeogram’

January 20, 2020

**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.

**License** Artistic-2.0

**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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**Repository** CRAN

**Date/Publication** 2020-01-20 11:20:02 UTC

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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

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*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

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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.
```

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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



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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

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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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