

# Package: RIdeogram (via r-universe)

September 2, 2024

**Type** Package

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

**Version** 0.2.2

**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 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, tidy, utils

**RoxygenNote** 6.1.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**Repository** <https://tickingclock1992.r-universe.dev>

**RemoteUrl** <https://github.com/tickingclock1992/rideogram>

**RemoteRef** HEAD

**RemoteSha** aaaa2b303c2694e4622a6bcba59e29066528919c

## Contents

convertSVG . . . . .	2
Fst_between_CE_and_CW . . . . .	3
gene_density . . . . .	3
GFFex . . . . .	4

human_karyotype . . . . .	4
ideogram . . . . .	5
karyotype_dual_comparison . . . . .	6
karyotype_ternary_comparison . . . . .	6
liriodendron_karyotype . . . . .	7
LTR_density . . . . .	7
Pi_for_CE . . . . .	8
Pi_for_CE_and_CW . . . . .	8
Random_RNAs_500 . . . . .	9
synteny_dual_comparison . . . . .	9
synteny_ternary_comparison . . . . .	10
synteny_ternary_comparison_graident . . . . .	10

## Index 11

---

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, 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.gencodegenes.org/>)

GFFex

*GFFex*

---

**Description**

extract some specific feature information from a gff file

**Usage**

```
GFFex(input, karyotype, feature = "gene", window = 1000000)
```

**Arguments**

input	gff file
karyotype	karyotype file
feature	feature format
window	window size

**Value**

dataframe

**Author(s)**

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

---

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, syteny = 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
syteny	syteny 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, Dolf Weijers, Guangchuan 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.
```

---

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

*Pi of two Liriodendron groups*

---

**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>
-----------------	---------------------------

---

**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/>)

---

synteny_dual_comparison	<i>Synteny for two genome comparison</i>
-------------------------	--

---

**Description**

Genome Synteny between Grape and Populus

**Usage**

```
data(synteny_dual_comparison)
```

**Format**

data frame

**Source**

MCscan

synten\_ternary\_comparison

*Synten for three genome comparison*

---

**Description**

Genome Synten among Amborella, Grape and Liriodendron

**Usage**

```
data(synten_ternary_comparison)
```

**Format**

data frame

**Source**

MCscan

---

synten\_ternary\_comparison\_graident

*Synten for three genome comparison with gradient fill*

---

**Description**

Genome Synten among Amborella, Grape and Liriodendron with gradient fill

**Usage**

```
data(synten_ternary_comparison_graident)
```

**Format**

data frame

**Source**

MCscan

# Index

## \* datasets

- Fst\_between\_CE\_and\_CW, [3](#)
  - gene\_density, [3](#)
  - human\_karyotype, [4](#)
  - karyotype\_dual\_comparison, [6](#)
  - karyotype\_ternary\_comparison, [6](#)
  - liriodendron\_karyotype, [7](#)
  - LTR\_density, [7](#)
  - Pi\_for\_CE, [8](#)
  - Pi\_for\_CE\_and\_CW, [8](#)
  - Random\_RNAs\_500, [9](#)
  - synteny\_dual\_comparison, [9](#)
  - synteny\_ternary\_comparison, [10](#)
  - synteny\_ternary\_comparison\_graident,  
[10](#)
- convertSVG, [2](#)
- Fst\_between\_CE\_and\_CW, [3](#)
- gene\_density, [3](#)
- GFFex, [4](#)
- human\_karyotype, [4](#)
- ideogram, [5](#)
- karyotype\_dual\_comparison, [6](#)
- karyotype\_ternary\_comparison, [6](#)
- liriodendron\_karyotype, [7](#)
- LTR\_density, [7](#)
- Pi\_for\_CE, [8](#)
- Pi\_for\_CE\_and\_CW, [8](#)
- Random\_RNAs\_500, [9](#)
- svg2jpg (convertSVG), [2](#)
- svg2pdf (convertSVG), [2](#)
- svg2png (convertSVG), [2](#)
- svg2tiff (convertSVG), [2](#)
- synteny\_dual\_comparison, [9](#)
- synteny\_ternary\_comparison, [10](#)
- synteny\_ternary\_comparison\_graident,  
[10](#)