# shinyCircos

an R/Shiny application for interactive creation of

Circos plot

Yiming Yu[1], Yidan Ouyang[1,*], Wen Yao[1,2*]

[1]National Key Laboratory of Crop Genetic Improvement, National Center of Plant Gene Research (Wuhan), Huazhong Agricultural University, Wuhan 430070, China, [2]College of Life Science and Technology, Henan Agricultural University, Zhengzhou 450002, China.

Contact: yaowen@henau.edu.cn, diana1983941@mail.hzau.edu.cn

The source code of shinyCircos is deposited in Github (https://github.com/venyao/shinyCircos).

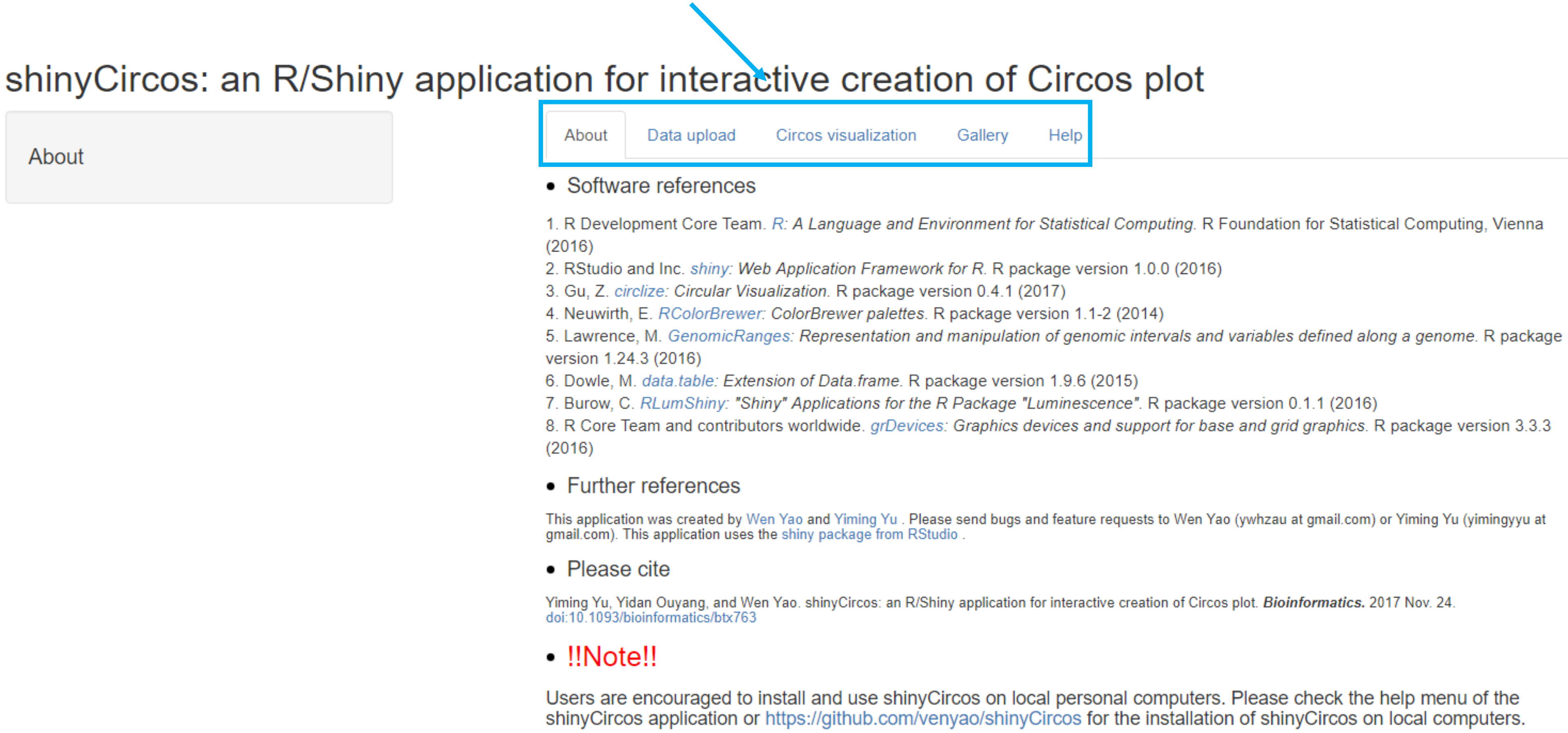
shinyCircos is deployed at https://yimingyu.shinyapps.io/shinycircos/ and http://shinycircos.ncpgr.cn/. Users can use shinyCircos online by accessing either of the two URLs.

Users are encouraged to install and use shinyCircos on local personal computers. Please check the help menu of the shinyCircos application or https://github.com/venyao/shinyCircos for the installation of shinyCircos on local computers.

# 1. Interface of shinyCircos

# Menu in shinyCircos: About

- The shinyCircos application contains five menus, "About", "Data upload", "Circos visualization", "Gallery" and "Help".



shinyCircos: an R/Shiny application for interactive creation of Circos plot

- Software references

1. R Development Core Team. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna (2016)
2. RStudio and Inc. *shiny: Web Application Framework for R*. R package version 1.0.0 (2016)
3. Gu, Z. *circlize: Circular Visualization*. R package version 0.4.1 (2017)
4. Neuwirth, E. *RColorBrewer: ColorBrewer palettes*. R package version 1.1-2 (2014)
5. Lawrence, M. *GenomicRanges: Representation and manipulation of genomic intervals and variables defined along a genome*. R package version 1.24.3 (2016)
6. Dowle, M. *data.table: Extension of Data.frame*. R package version 1.9.6 (2015)
7. Burow, C. *RLumShiny: "Shiny" Applications for the R Package "Luminescence"*. R package version 0.1.1 (2016)
8. R Core Team and contributors worldwide. *grDevices: Graphics devices and support for base and grid graphics*. R package version 3.3.3 (2016)

- Further references

This application was created by Wen Yao and Yiming Yu . Please send bugs and feature requests to Wen Yao (ywhzau at gmail.com) or Yiming Yu (yimingyyu at gmail.com). This application uses the shiny package from RStudio .

- Please cite

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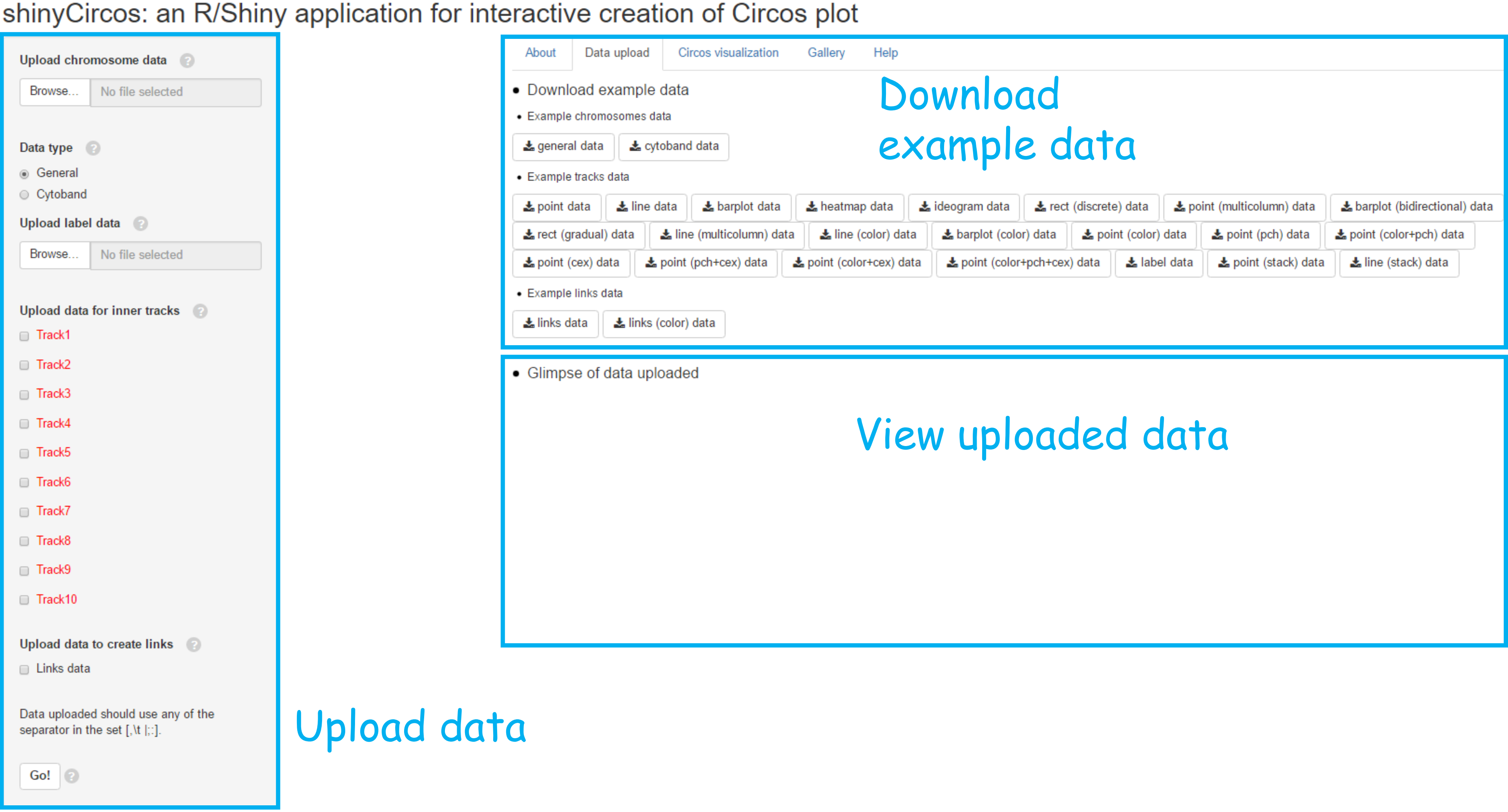
- !!Note!!

Users are encouraged to install and use shinyCircos on local personal computers. Please check the help menu of the shinyCircos application or https://github.com/venyao/shinyCircos for the installation of shinyCircos on local computers.

- The "About" menu lists the R packages used in shinyCircos.

# Menu in shinyCircos: Data upload

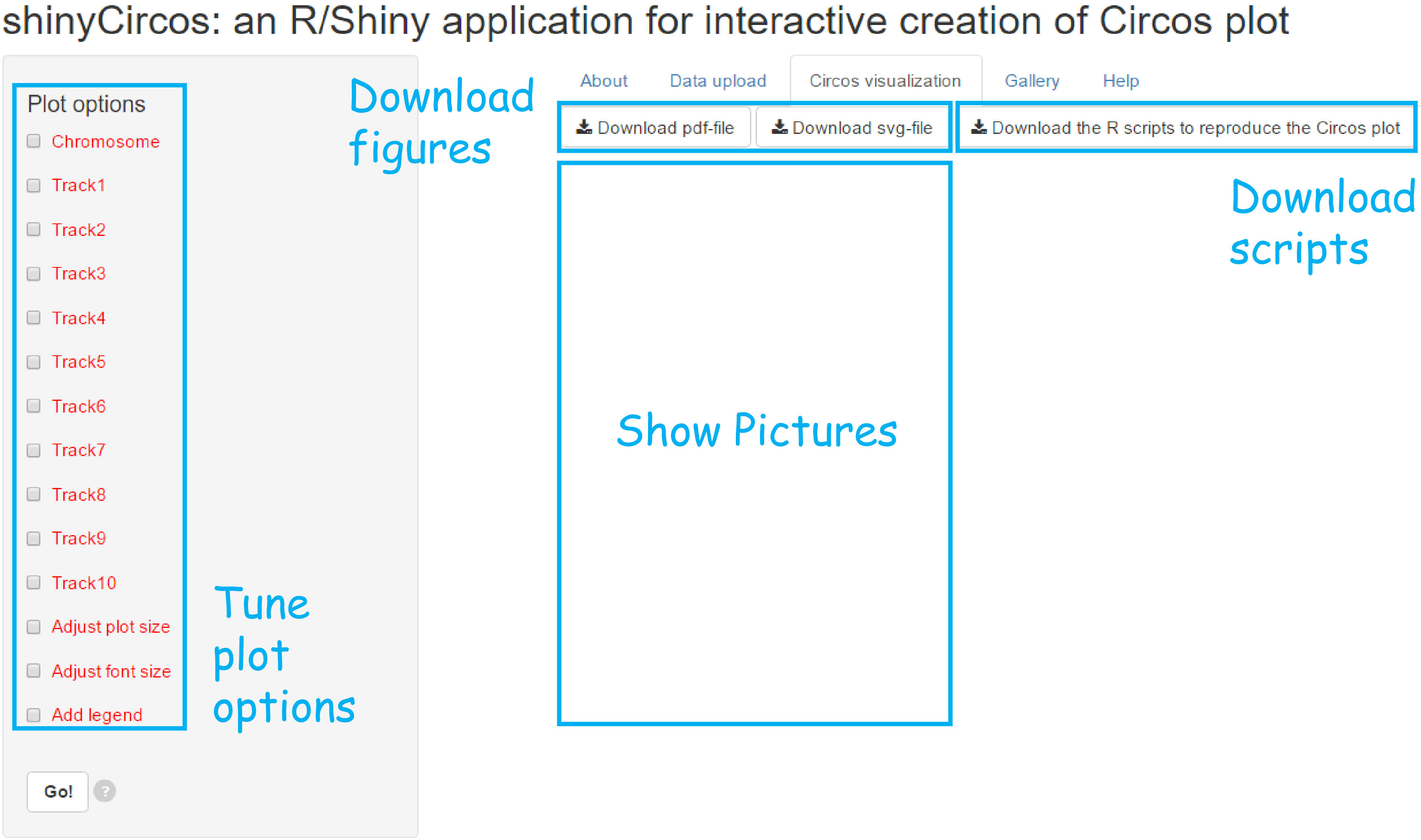


shinyCircos: an R/Shiny application for interactive creation of Circos plot

Data uploaded should use any of the separator in the set [,\t |;:].

- The "Data upload" menu allows uploading of input data for Circos plots.
- A glimpse of the uploaded data will be printed on this page.
- Example datasets could be downloaded from this menu.

# Menu in shinyCircos: Circos visualization



Download figures

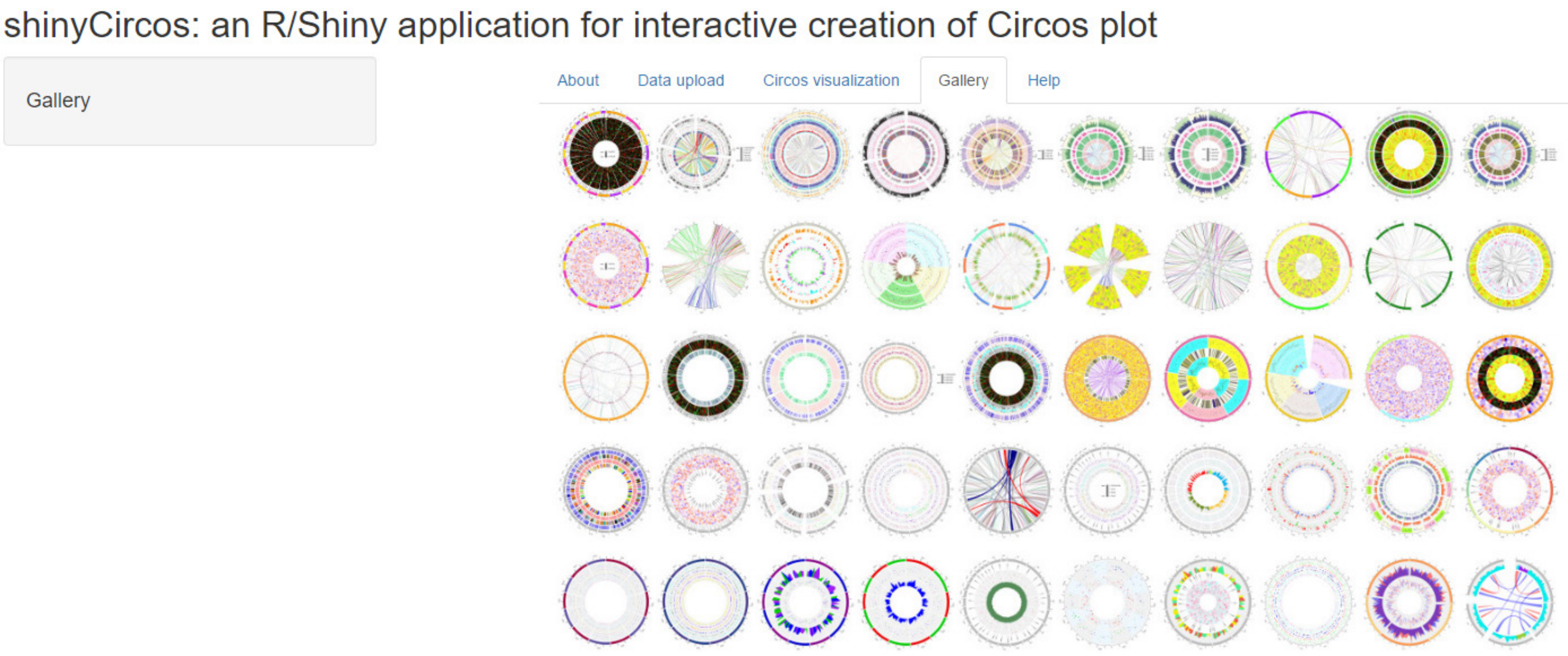
Download scripts

Tune plot options

Show Pictures

- After data uploading, the "Circos visualization" menu allows generation of Circos plot.
- Various options are provided to tune the appearance of the Circos plot.

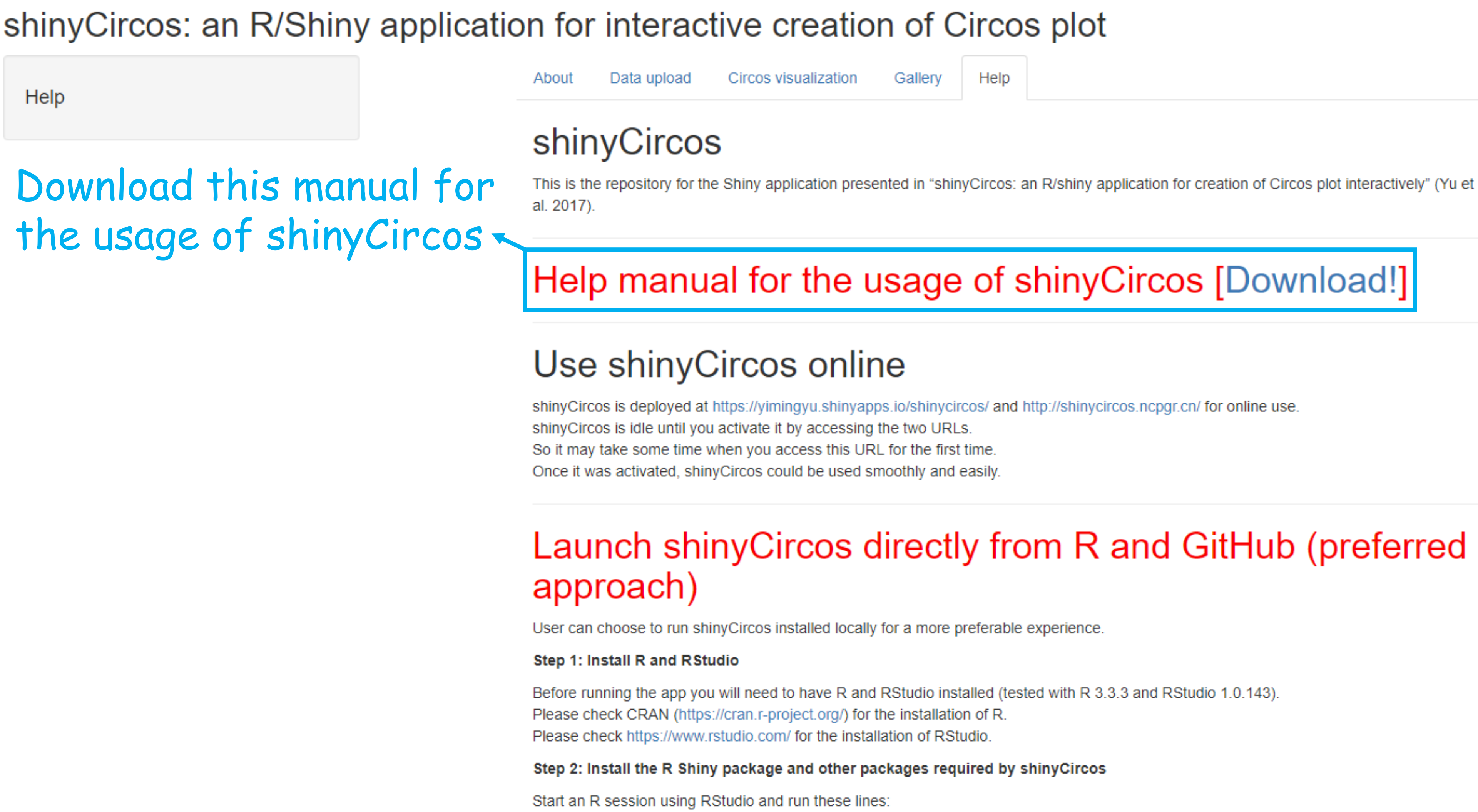
# Menu in shinyCircos: Gallery



shinyCircos: an R/Shiny application for interactive creation of Circos plot

- Fifty example figures generated by shinyCircos are listed in the "Gallery" menu.

# Menu in shinyCircos: Help



shinyCircos: an R/Shiny application for interactive creation of Circos plot

## shinyCircos

This is the repository for the Shiny application presented in “shinyCircos: an R/shiny application for creation of Circos plot interactively” (Yu et al. 2017).

## Help manual for the usage of shinyCircos [Download!]

Download this manual for the usage of shinyCircos

## Use shinyCircos online

shinyCircos is deployed at https://yimingyu.shinyapps.io/shinycircos/ and http://shinycircos.ncpgr.cn/ for online use.
shinyCircos is idle until you activate it by accessing the two URLs.
So it may take some time when you access this URL for the first time.
Once it was activated, shinyCircos could be used smoothly and easily.

## Launch shinyCircos directly from R and GitHub (preferred approach)

User can choose to run shinyCircos installed locally for a more preferable experience.

**Step 1: Install R and RStudio**

Before running the app you will need to have R and RStudio installed (tested with R 3.3.3 and RStudio 1.0.143).
Please check CRAN (https://cran.r-project.org/) for the installation of R.
Please check https://www.rstudio.com/ for the installation of RStudio.

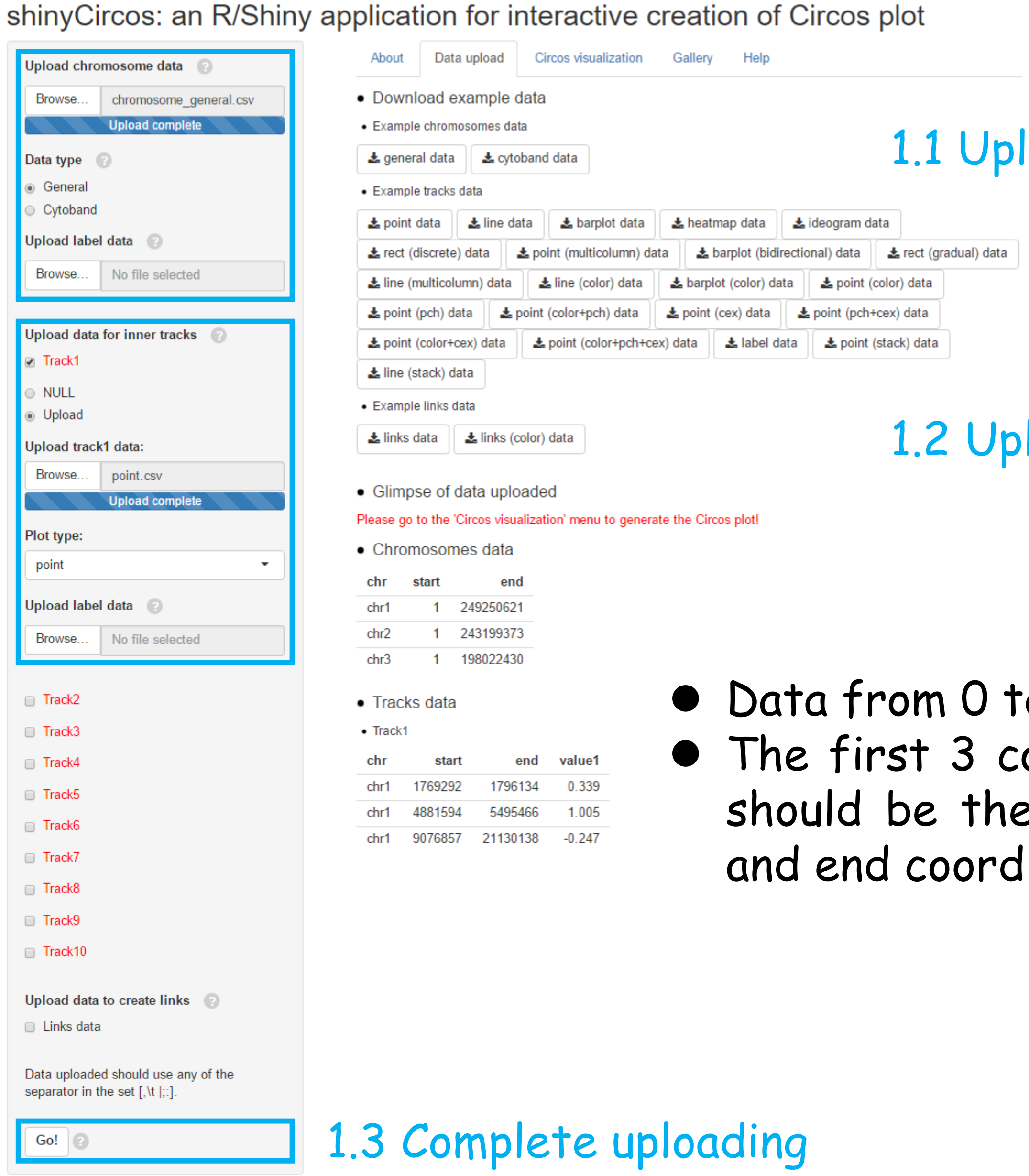
**Step 2: Install the R Shiny package and other packages required by shinyCircos**

Start an R session using RStudio and run these lines:

- Instructions for installation of shinyCircos on local computers or web servers are shown in the “Help” menu.

# 2. Usage of shinyCircos

# Step 1: Data uploading



shinyCircos: an R/Shiny application for interactive creation of Circos plot

**Upload chromosome data**

chromosome_general.csv

Upload complete

**Data type**

● General
○ Cytoband

**Upload label data**

No file selected

**Upload data for inner tracks**

☑ Track1

○ NULL
● Upload

**Upload track1 data:**

point.csv

Upload complete

**Plot type:**

point

**Upload label data**

No file selected

☐ Track2
☐ Track3
☐ Track4
☐ Track5
☐ Track6
☐ Track7
☐ Track8
☐ Track9
☐ Track10

**Upload data to create links**

☐ Links data

Data uploaded should use any of the separator in the set [,\t |;:].

- Download example data
  - Example chromosomes data
  - Example tracks data
  - Example links data

- Glimpse of data uploaded

Please go to the 'Circos visualization' menu to generate the Circos plot!

- Chromosomes data

| chr | start | end |
|---|---|---|
| chr1 | 1 | 249250621 |
| chr2 | 1 | 243199373 |
| chr3 | 1 | 198022430 |

- Tracks data
  - Track1

| chr | start | end | value1 |
|---|---|---|---|
| chr1 | 1769292 | 1796134 | 0.339 |
| chr1 | 4881594 | 5495466 | 1.005 |
| chr1 | 9076857 | 21130138 | -0.247 |

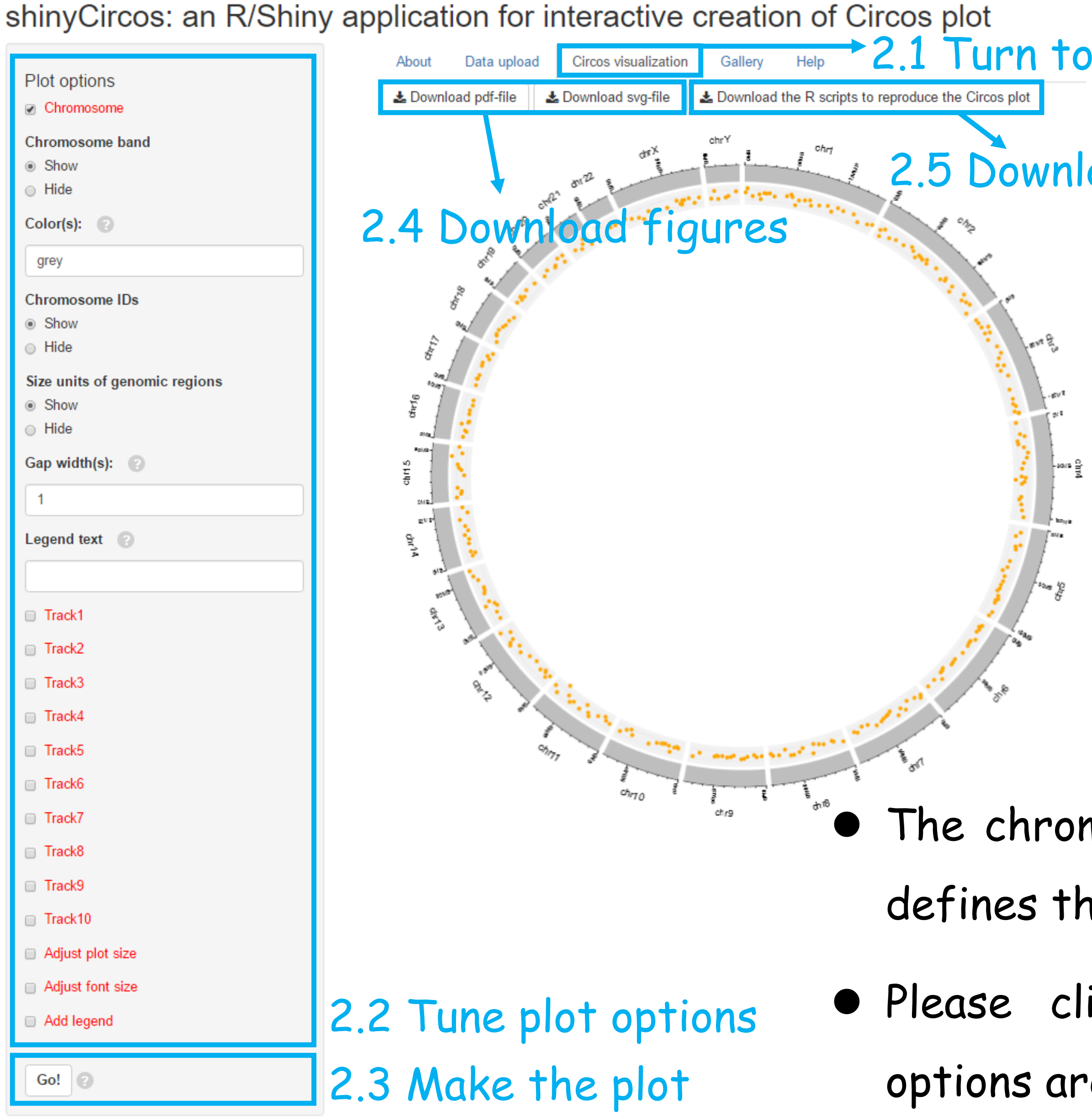
1.1 Upload chromosome data

1.2 Upload track data

- Data from 0 to 10 tracks can be uploaded.
- The first 3 columns of the uploaded data should be the chromosome ID, the start and end coordinates of genomic regions.

1.3 Complete uploading

# Step 2: Circos visualization



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☑ Chromosome

**Chromosome band**

● Show

○ Hide

**Color(s):**

grey

**Chromosome IDs**

● Show

○ Hide

**Size units of genomic regions**

● Show

○ Hide

**Gap width(s):**

1

**Legend text**

☐ Track1

☐ Track2

☐ Track3

☐ Track4

☐ Track5

☐ Track6

☐ Track7

☐ Track8

☐ Track9

☐ Track10

☐ Adjust plot size

☐ Adjust font size

☐ Add legend

2.1 Turn to "Circos visualization" menu

2.2 Tune plot options

2.3 Make the plot

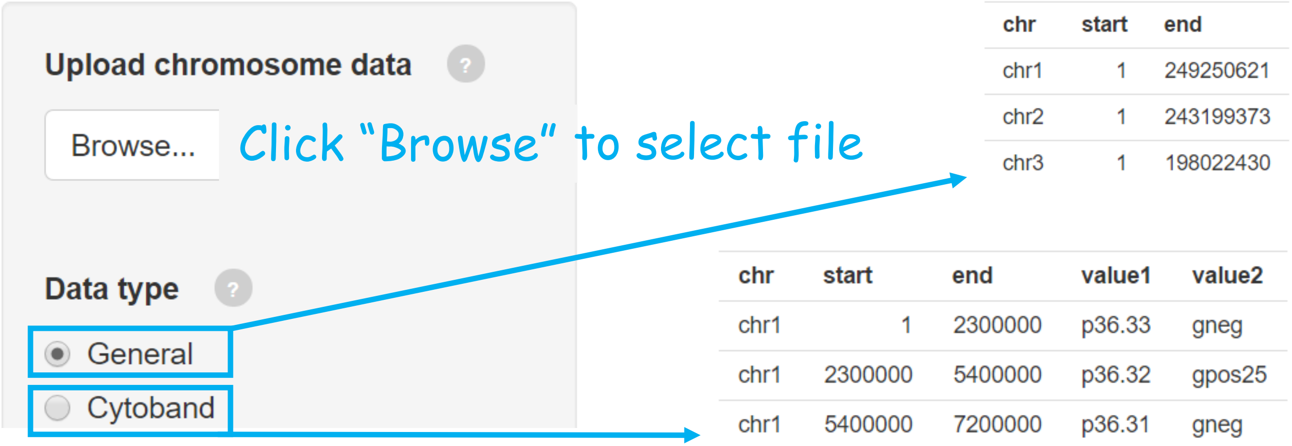
2.4 Download figures

2.5 Download scripts

- The chromosome data is compulsory and defines the frame of a Circos plot.
- Please click the "Go!" button if any options are modified.

## 2.1 Plot chromosomes

# Upload chromosome data



Click “Browse” to select file

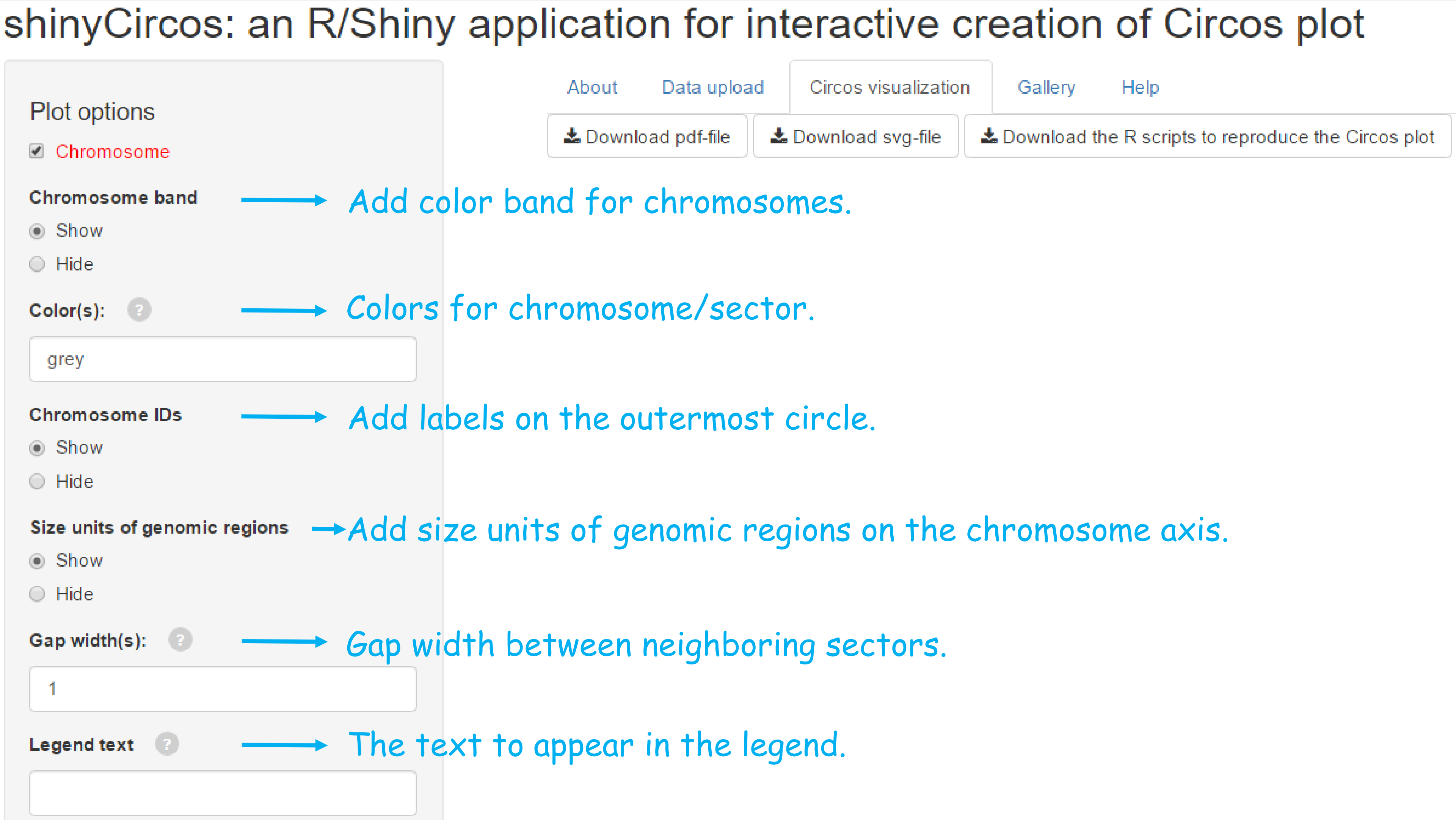
● General
○ Cytoband

| chr | start | end |
|---|---|---|
| chr1 | 1 | 249250621 |
| chr2 | 1 | 243199373 |
| chr3 | 1 | 198022430 |

| chr | start | end | value1 | value2 |
|---|---|---|---|---|
| chr1 | 1 | 2300000 | p36.33 | gneg |
| chr1 | 2300000 | 5400000 | p36.32 | gpos25 |
| chr1 | 5400000 | 7200000 | p36.31 | gneg |

- Use the “Data upload” menu for data input.
- Chromosome data can be either chromosome ideograms (“Cytoband” type, see example data “chromosome_cytoband.csv” for detail) or simple definition of chromosome lengths (“General” type, see example data “chromosome_general.csv” for detail).

# Options



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☑ Chromosome

**Chromosome band** → Add color band for chromosomes.

● Show
○ Hide

**Color(s):** → Colors for chromosome/sector.

grey

**Chromosome IDs** → Add labels on the outermost circle.

● Show
○ Hide

**Size units of genomic regions** → Add size units of genomic regions on the chromosome axis.

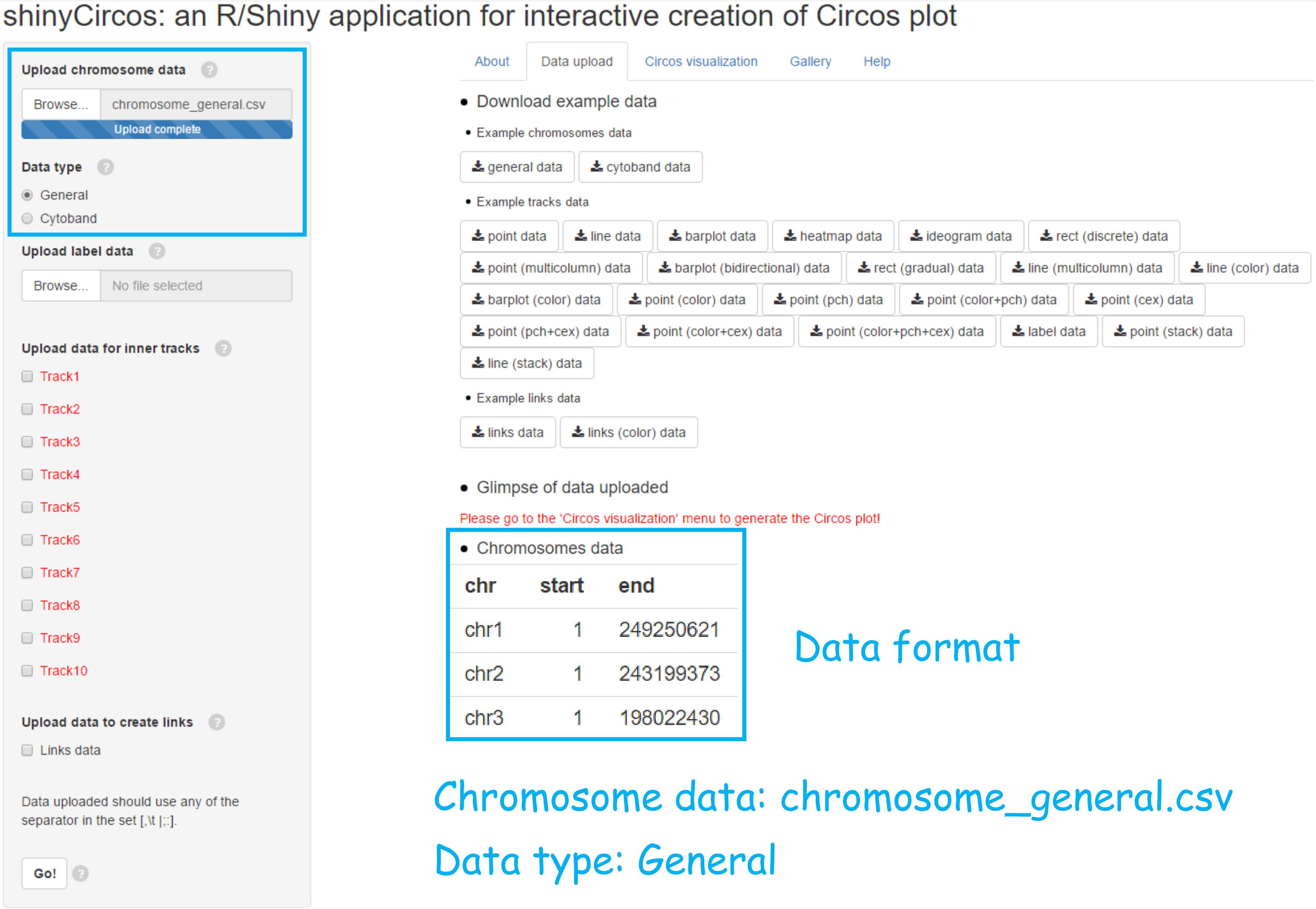
● Show
○ Hide

**Gap width(s):** → Gap width between neighboring sectors.

1

**Legend text** → The text to appear in the legend.

# Example 1



shinyCircos: an R/Shiny application for interactive creation of Circos plot

**Upload chromosome data** ?

Browse... chromosome_general.csv

Upload complete

**Data type** ?

● General

○ Cytoband

**Upload label data** ?

Browse... No file selected

**Upload data for inner tracks** ?

☐ Track1

☐ Track2

☐ Track3

☐ Track4

☐ Track5

☐ Track6

☐ Track7

☐ Track8

☐ Track9

☐ Track10

**Upload data to create links** ?

☐ Links data

Data uploaded should use any of the separator in the set [,\t |;:].

Go! ?

About | Data upload | Circos visualization | Gallery | Help

- Download example data
  - Example chromosomes data

general data | cytoband data

  - Example tracks data

point data | line data | barplot data | heatmap data | ideogram data | rect (discrete) data | point (multicolumn) data | barplot (bidirectional) data | rect (gradual) data | line (multicolumn) data | line (color) data | barplot (color) data | point (color) data | point (pch) data | point (color+pch) data | point (cex) data | point (pch+cex) data | point (color+cex) data | point (color+pch+cex) data | label data | point (stack) data | line (stack) data

  - Example links data

links data | links (color) data

- Glimpse of data uploaded

Please go to the 'Circos visualization' menu to generate the Circos plot!

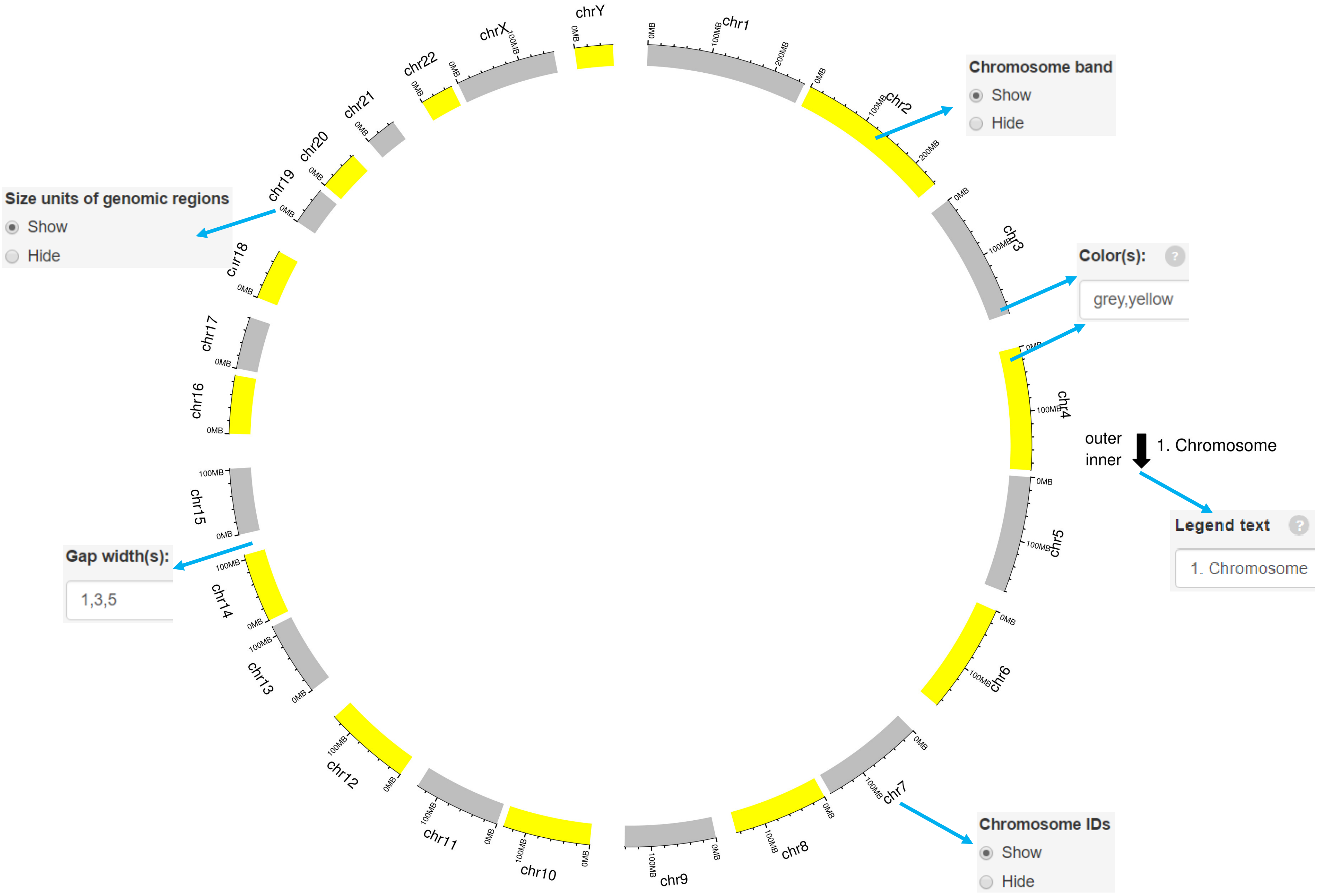
- Chromosomes data

| chr | start | end |
|---|---|---|
| chr1 | 1 | 249250621 |
| chr2 | 1 | 243199373 |
| chr3 | 1 | 198022430 |

Data format

Chromosome data: chromosome_general.csv

Data type: General



**Chromosome band**
● Show
○ Hide

**Color(s):**
grey,yellow

outer
inner
1. Chromosome

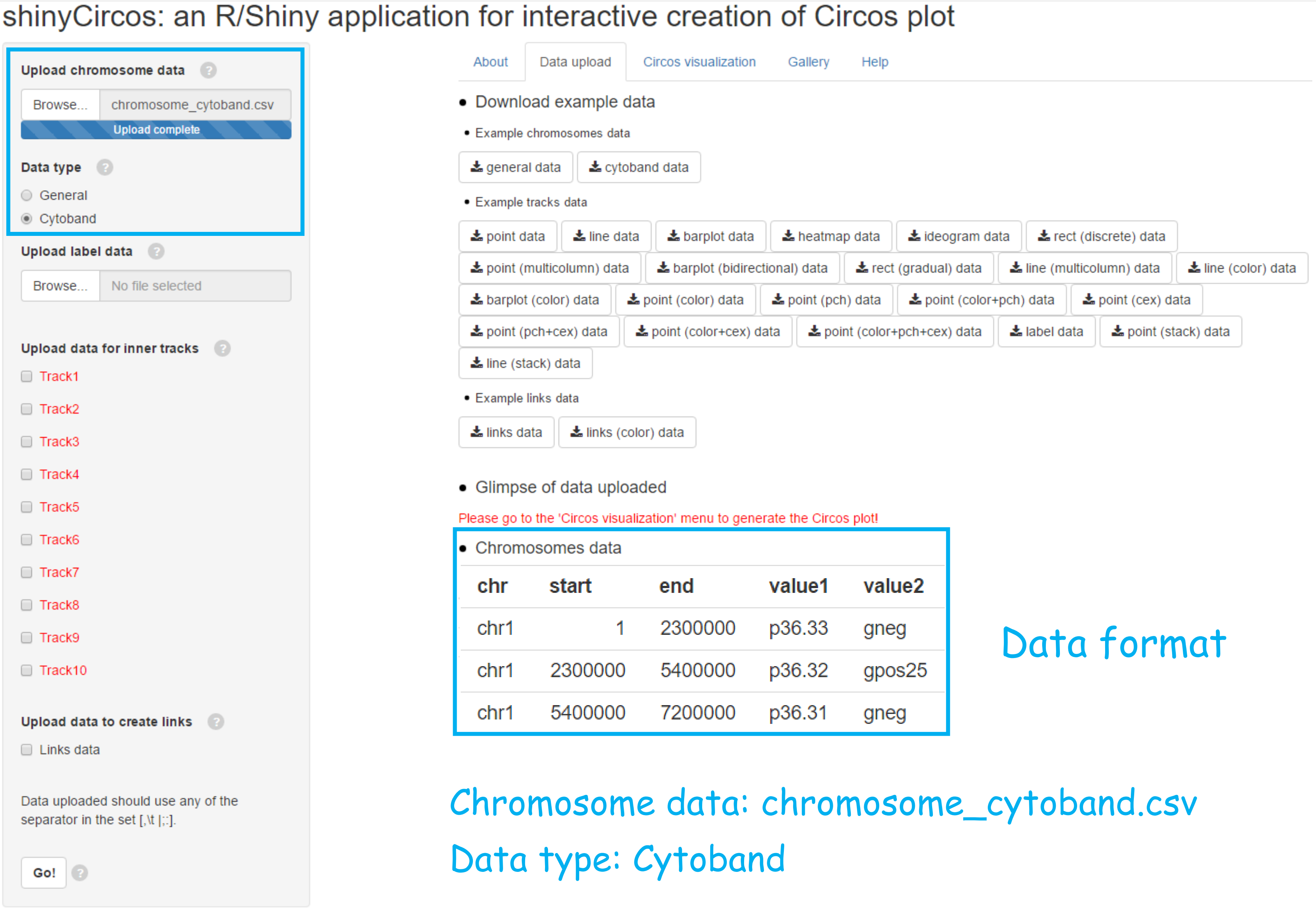
**Legend text**
1. Chromosome

**Chromosome IDs**
● Show
○ Hide

**Size units of genomic regions**
● Show
○ Hide

**Gap width(s):**
1,3,5

# Example 2



shinyCircos: an R/Shiny application for interactive creation of Circos plot

**Upload chromosome data** ?

Browse... chromosome_cytoband.csv

Upload complete

**Data type** ?

○ General

● Cytoband

**Upload label data** ?

Browse... No file selected

**Upload data for inner tracks** ?

☐ Track1

☐ Track2

☐ Track3

☐ Track4

☐ Track5

☐ Track6

☐ Track7

☐ Track8

☐ Track9

☐ Track10

**Upload data to create links** ?

☐ Links data

Data uploaded should use any of the separator in the set [,\t |;:].

Go! ?

- Download example data
  - Example chromosomes data

  - Example tracks data

  - Example links data

- Glimpse of data uploaded

Please go to the 'Circos visualization' menu to generate the Circos plot!

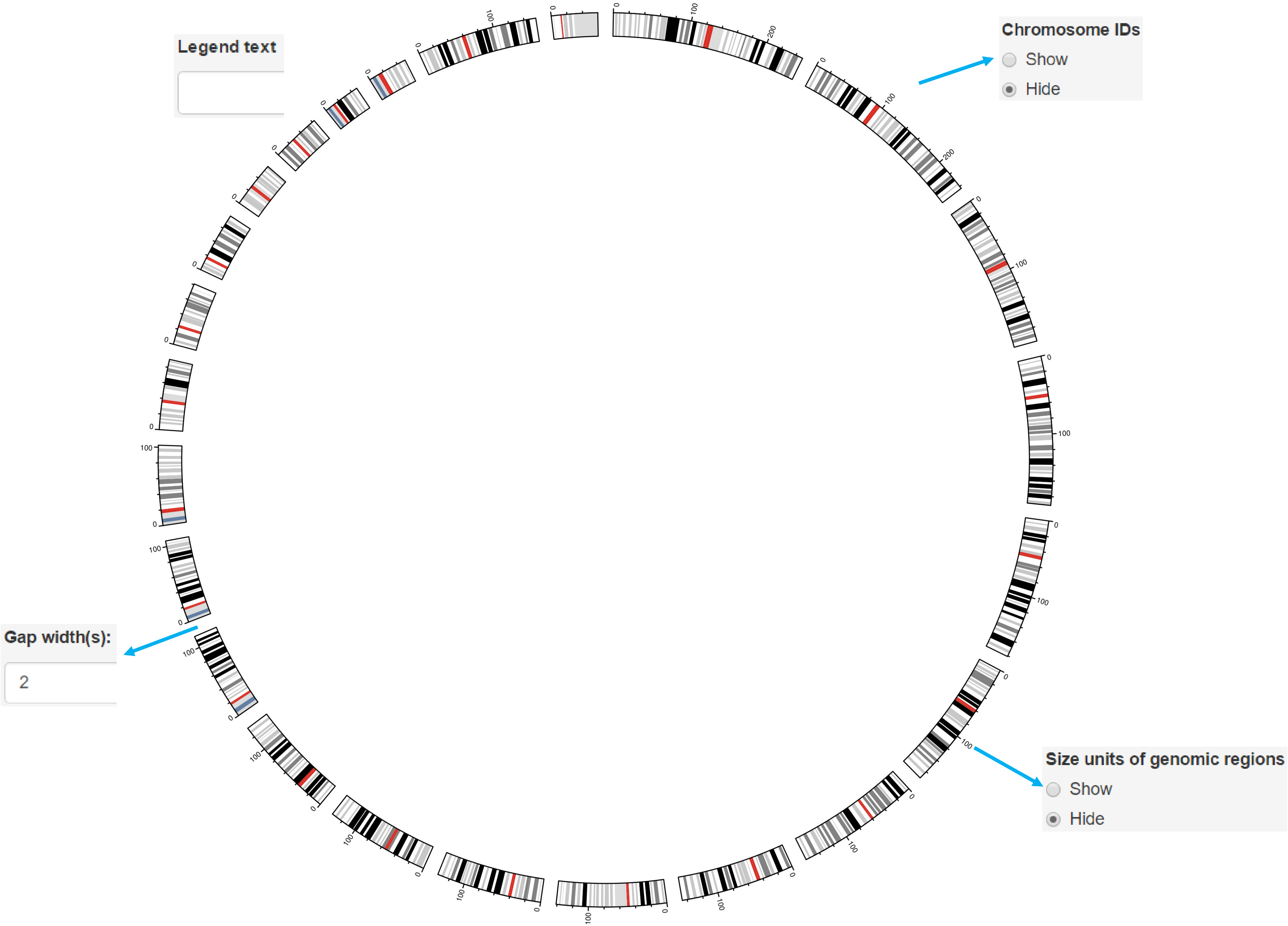
- Chromosomes data

| chr | start | end | value1 | value2 |
|---|---|---|---|---|
| chr1 | 1 | 2300000 | p36.33 | gneg |
| chr1 | 2300000 | 5400000 | p36.32 | gpos25 |
| chr1 | 5400000 | 7200000 | p36.31 | gneg |

Data format

Chromosome data: chromosome_cytoband.csv

Data type: Cytoband



**Legend text**

**Chromosome IDs**

○ Show

● Hide

**Gap width(s):**

2

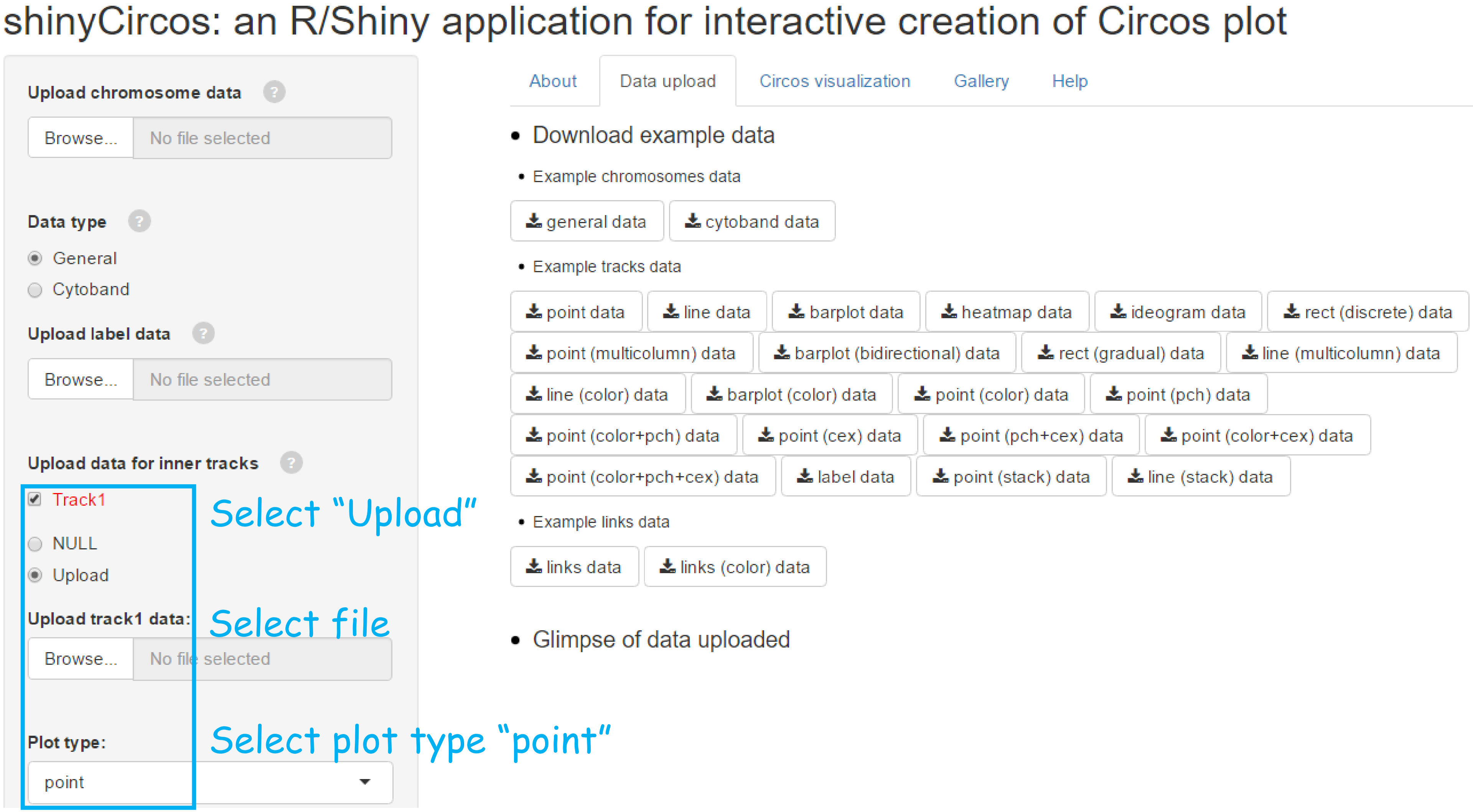
**Size units of genomic regions**

○ Show

● Hide

# 2.2 Plot points

# Upload point data



shinyCircos: an R/Shiny application for interactive creation of Circos plot

**Upload chromosome data** ?

**Data type** ?

● General
○ Cytoband

**Upload label data** ?

**Upload data for inner tracks** ?

☑ Track1

○ NULL
● Upload

**Upload track1 data:**

**Plot type:** point

- Download example data
  - Example chromosomes data

  - Example tracks data

  - Example links data

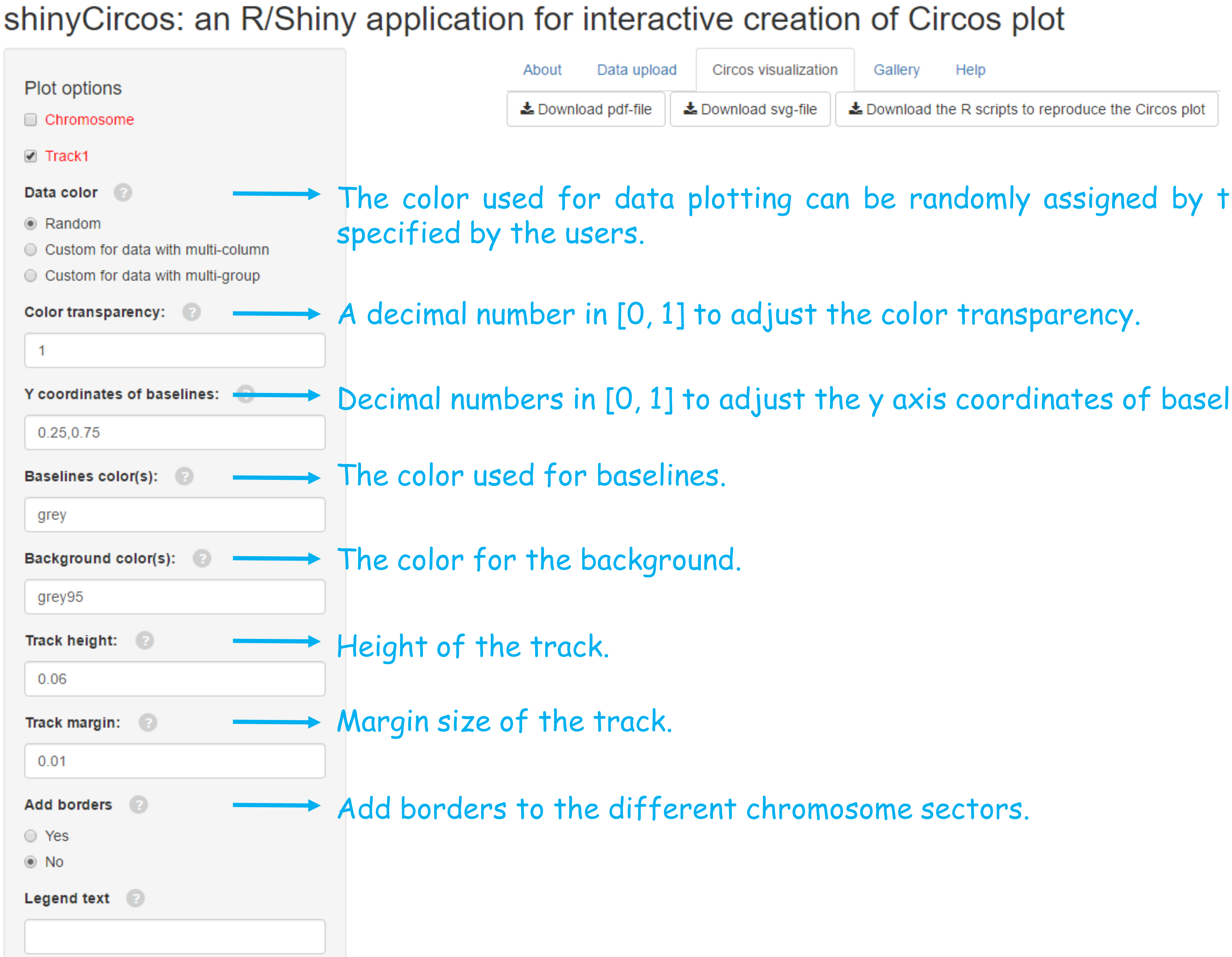
- Glimpse of data uploaded

Select "Upload"

Select file

Select plot type "point"

# Options



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☐ Chromosome

☑ Track1

**Data color**

● Random
○ Custom for data with multi-column
○ Custom for data with multi-group

**Color transparency:** 1

**Y coordinates of baselines:** 0.25,0.75

**Baselines color(s):** grey

**Background color(s):** grey95

**Track height:** 0.06

**Track margin:** 0.01

**Add borders**

○ Yes
● No

**Legend text**

The color used for data plotting can be randomly assigned by the application or specified by the users.

A decimal number in [0, 1] to adjust the color transparency.

Decimal numbers in [0, 1] to adjust the y axis coordinates of baselines.

The color used for baselines.

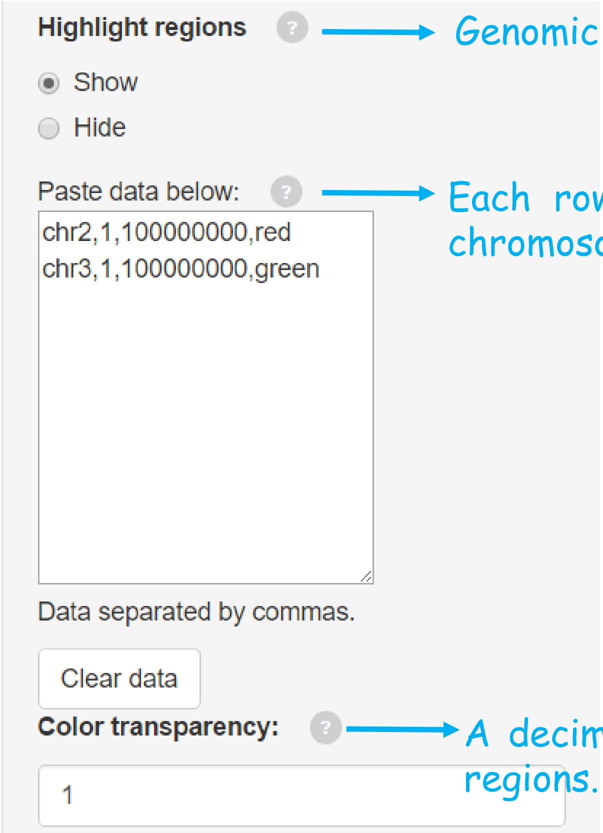
The color for the background.

Height of the track.

Margin size of the track.

Add borders to the different chromosome sectors.

# Options



**Highlight regions**

● Show

○ Hide

Paste data below:

```
chr2,1,100000000,red
chr3,1,100000000,green
```

Data separated by commas.

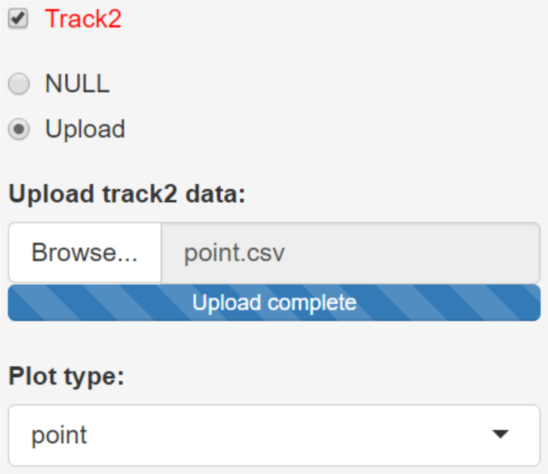
**Color transparency:** 1

Highlight regions: Genomic regions can be highlighted with specified colors.

Paste data below: Each row should contain four components separated by commas including the chromosome ID, start coordinate, end coordinate and the specified color.

Color transparency: A decimal number in [0, 1] to adjust the color transparency for the highlighted regions.

# Example 1



☑ **Track2**

○ NULL
● Upload

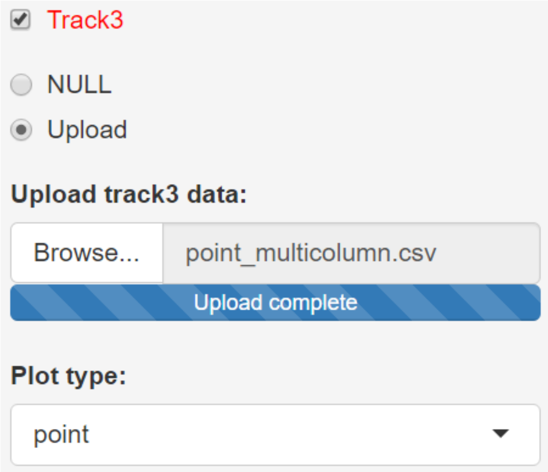
**Upload track2 data:**

Browse... point.csv

Upload complete

**Plot type:**

point



☑ **Track3**

○ NULL
● Upload

**Upload track3 data:**

Browse... point_multicolumn.csv

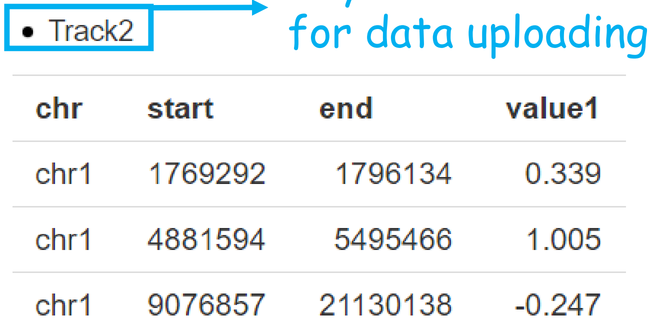
Upload complete

**Plot type:**

point

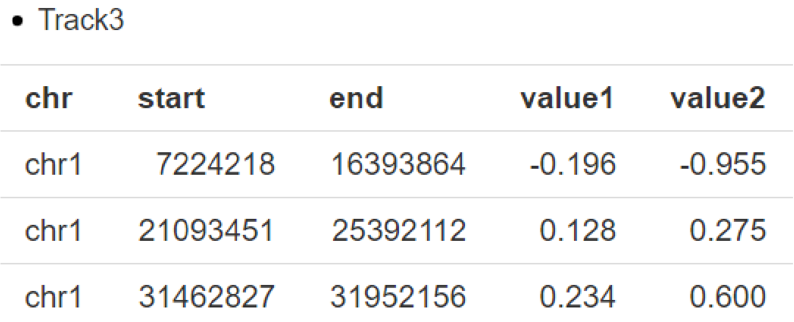
## Data format

Any track can be used for data uploading.



- Track2

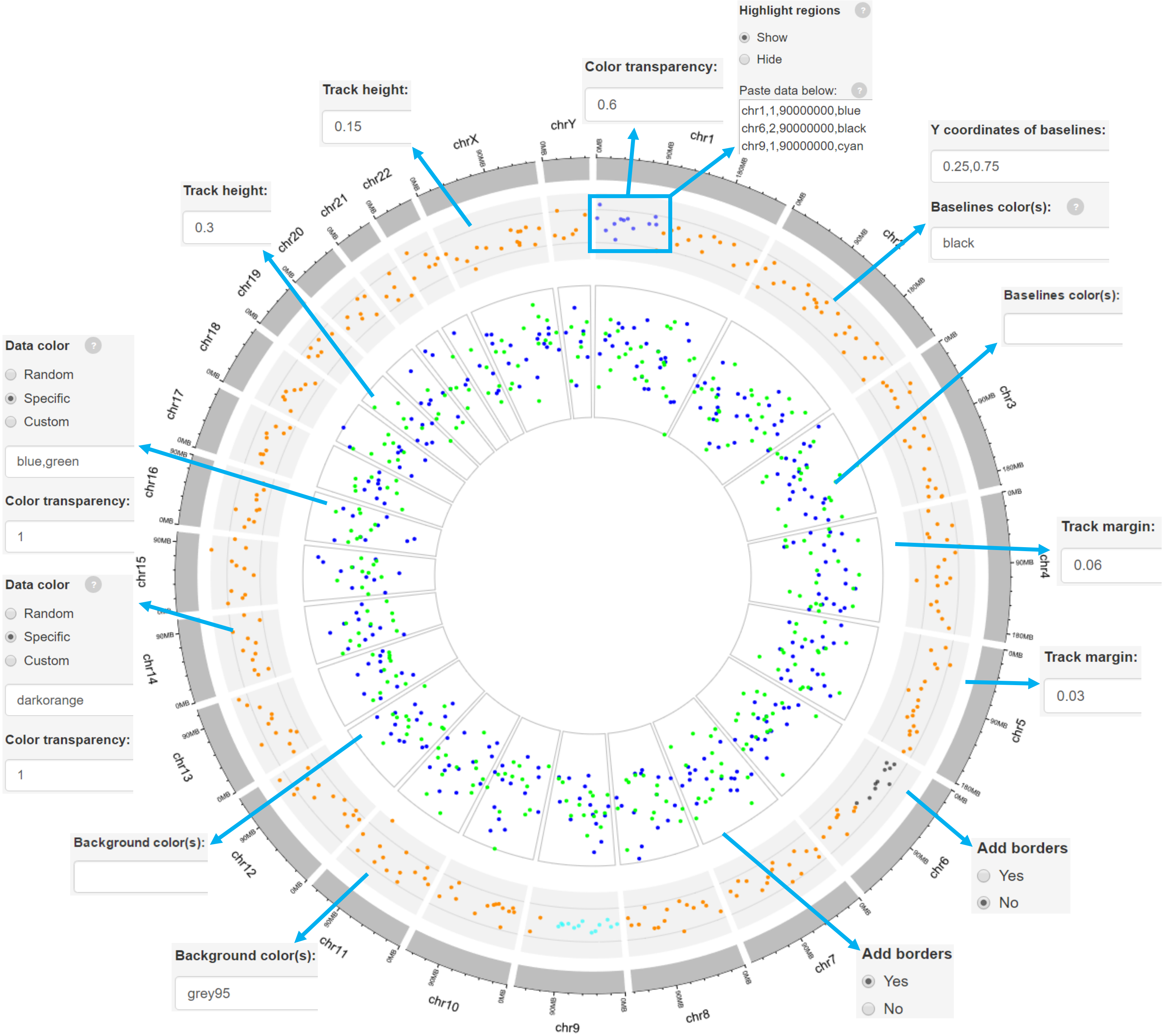
| chr | start | end | value1 |
|---|---|---|---|
| chr1 | 1769292 | 1796134 | 0.339 |
| chr1 | 4881594 | 5495466 | 1.005 |
| chr1 | 9076857 | 21130138 | -0.247 |



- Track3

| chr | start | end | value1 | value2 |
|---|---|---|---|---|
| chr1 | 7224218 | 16393864 | -0.196 | -0.955 |
| chr1 | 21093451 | 25392112 | 0.128 | 0.275 |
| chr1 | 31462827 | 31952156 | 0.234 | 0.600 |

- Simplest data to plot point should contain at least 4 columns including the chromosome ID, start coordinate, end coordinate and multiple columns of values.



**Highlight regions**

● Show

○ Hide

Paste data below:

chr1,1,90000000,blue
chr6,2,90000000,black
chr9,1,90000000,cyan

**Color transparency:** 0.6

**Track height:** 0.15

**Track height:** 0.3

**Y coordinates of baselines:** 0.25,0.75

**Baselines color(s):** black

**Baselines color(s):**

**Data color**

○ Random

● Specific

○ Custom

blue,green

**Color transparency:** 1

**Data color**

○ Random

● Specific

○ Custom

darkorange

**Color transparency:** 1

**Track margin:** 0.06

**Track margin:** 0.03

**Background color(s):**

**Background color(s):** grey95

**Add borders**

○ Yes

● No

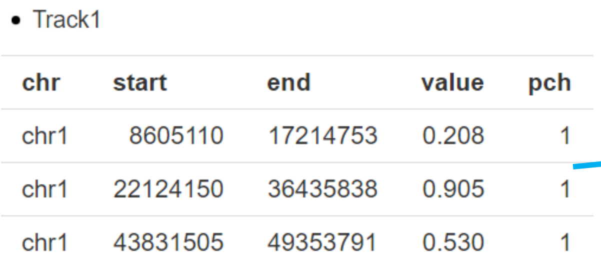
**Add borders**

● Yes

○ No

# Example 2

## Data format

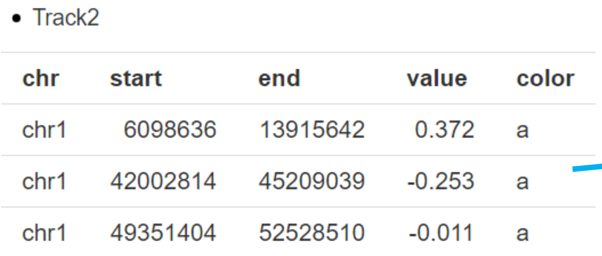


- Track1

| chr | start | end | value | pch |
|---|---|---|---|---|
| chr1 | 8605110 | 17214753 | 0.208 | 1 |
| chr1 | 22124150 | 36435838 | 0.905 | 1 |
| chr1 | 43831505 | 49353791 | 0.530 | 1 |

point_pch.csv

- The last column “pch” indicates different point types for differing data groups.

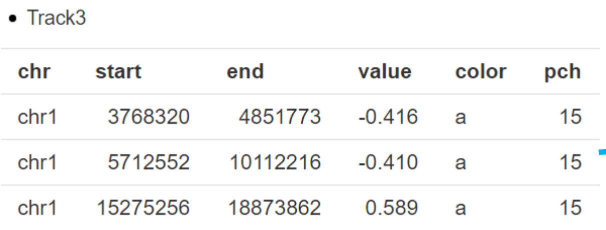


- Track2

| chr | start | end | value | color |
|---|---|---|---|---|
| chr1 | 6098636 | 13915642 | 0.372 | a |
| chr1 | 42002814 | 45209039 | -0.253 | a |
| chr1 | 49351404 | 52528510 | -0.011 | a |

point_color.csv

- The last column “color” indicates different colors for differing data groups.



- Track3

| chr | start | end | value | color | pch |
|---|---|---|---|---|---|
| chr1 | 3768320 | 4851773 | -0.416 | a | 15 |
| chr1 | 5712552 | 10112216 | -0.410 | a | 15 |
| chr1 | 15275256 | 18873862 | 0.589 | a | 15 |

point_color_pch.csv

- The last columns “color” and “pch” represent different colors and point types for different data groups.

**Data color**

○ Random

○ Custom for data with multi-column

● Custom for data with multi-group

a:chartreuse3;b:brown;c:slategray;d:tan2

**Highlight regions**

● Show

○ Hide

Paste data below:

chr1,1,60000000,red

**Highlight regions**

● Show

○ Hide

Paste data below:

chr1,30000000,100000000,darkorange3

**Y coordinates of baselines:**

0.25,0.75

**Baselines color(s):**

red,blue

**Legend text**

1.Chromosome

**Data color**

○ Random

○ Custom for data with multi-column

● Custom for data with multi-group

a:violetred;b:lightseagreen;c:gold3;d:cyan

**Data color**

○ Random

● Custom for data with multi-column

○ Custom for data with multi-group

purple

**Track height:**

0.15

**Track margin:**

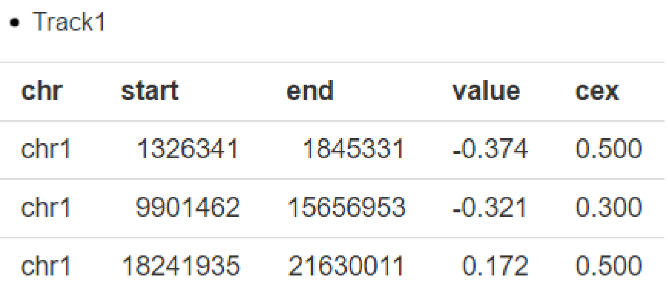
0.01

**Track margin:**

0.03

# Example 3

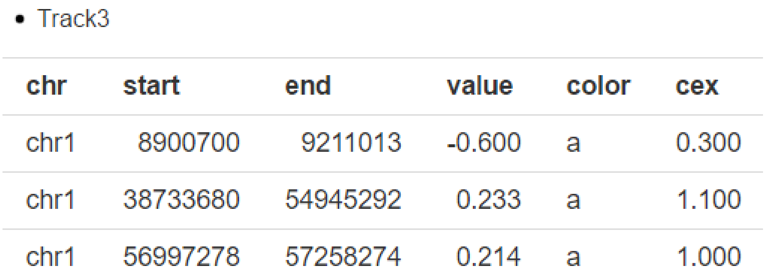
## Data format



- Track1

| chr | start | end | value | cex |
|---|---|---|---|---|
| chr1 | 1326341 | 1845331 | -0.374 | 0.500 |
| chr1 | 9901462 | 15656953 | -0.321 | 0.300 |
| chr1 | 18241935 | 21630011 | 0.172 | 0.500 |

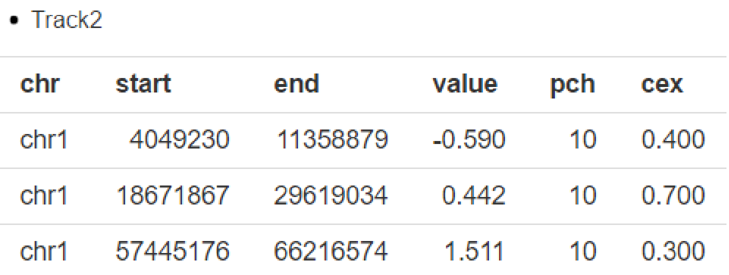
point_cex.csv



- Track3

| chr | start | end | value | color | cex |
|---|---|---|---|---|---|
| chr1 | 8900700 | 9211013 | -0.600 | a | 0.300 |
| chr1 | 38733680 | 54945292 | 0.233 | a | 1.100 |
| chr1 | 56997278 | 57258274 | 0.214 | a | 1.000 |

point_color_cex.csv



- Track2

| chr | start | end | value | pch | cex |
|---|---|---|---|---|---|
| chr1 | 4049230 | 11358879 | -0.590 | 10 | 0.400 |
| chr1 | 18671867 | 29619034 | 0.442 | 10 | 0.700 |
| chr1 | 57445176 | 66216574 | 1.511 | 10 | 0.300 |

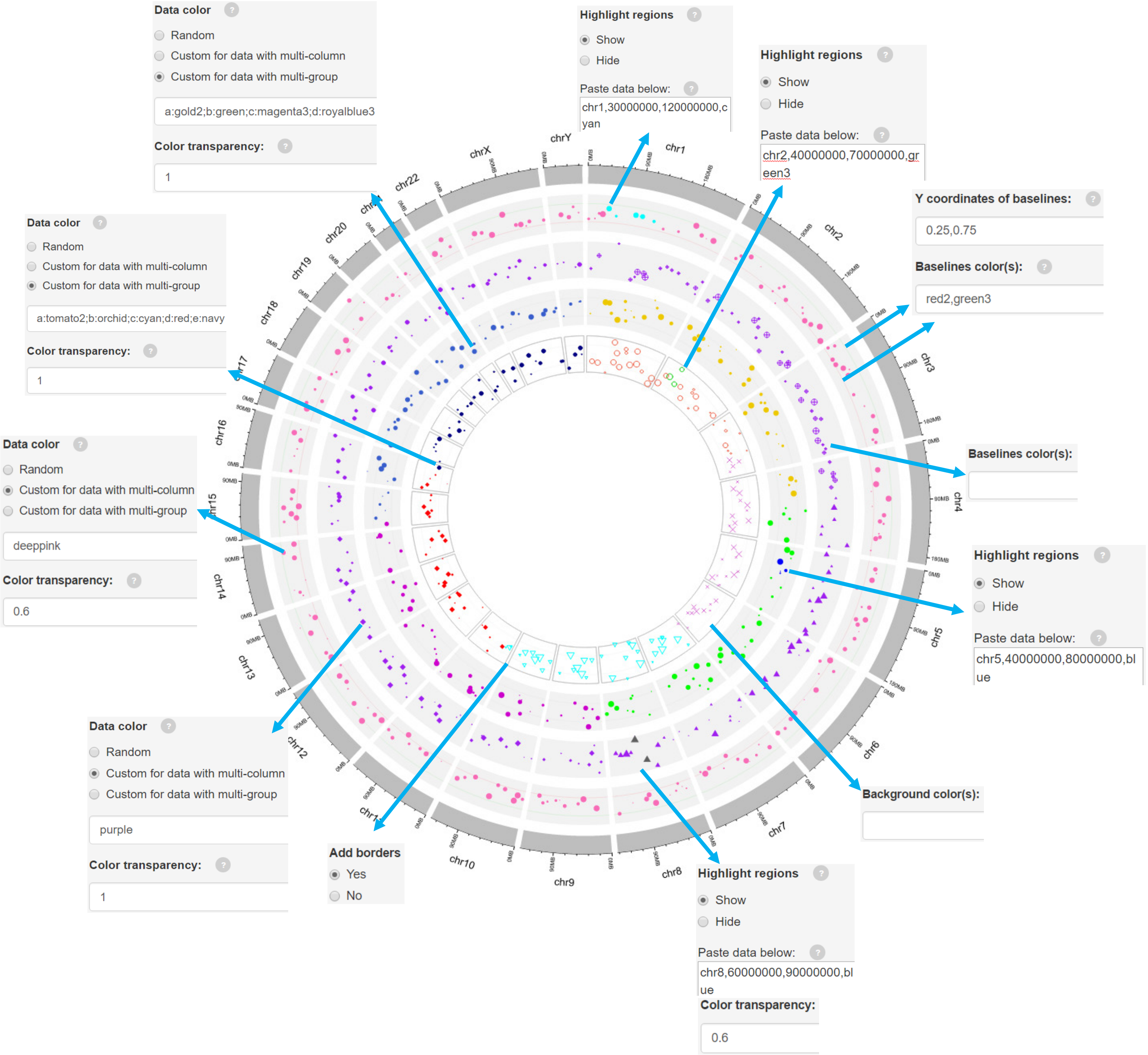
point_pch_cex.csv

- Track4

| chr | start | end | value | color | pch | cex |
|---|---|---|---|---|---|---|
| chr1 | 14053524 | 24878326 | -0.498 | a | 1 | 0.900 |
| chr1 | 29640089 | 49313488 | -0.565 | a | 1 | 1.000 |
| chr1 | 53970010 | 87166913 | -1.159 | a | 1 | 0.300 |

point_color_pch_cex.csv

- The “cex” column is a numeric vector represents different point size.



**Data color**

○ Random
○ Custom for data with multi-column
● Custom for data with multi-group

a:gold2;b:green;c:magenta3;d:royalblue3

**Color transparency:**

1

**Highlight regions**

● Show
○ Hide

Paste data below:

chr1,30000000,120000000,cyan

**Highlight regions**

● Show
○ Hide

Paste data below:

chr2,40000000,70000000,green3

**Y coordinates of baselines:**

0.25,0.75

**Baselines color(s):**

red2,green3

**Data color**

○ Random
○ Custom for data with multi-column
● Custom for data with multi-group

a:tomato2;b:orchid;c:cyan;d:red;e:navy

**Color transparency:**

1

**Baselines color(s):**

**Data color**

○ Random
● Custom for data with multi-column
○ Custom for data with multi-group

deeppink

**Color transparency:**

0.6

**Highlight regions**

● Show
○ Hide

Paste data below:

chr5,40000000,80000000,blue

**Data color**

○ Random
● Custom for data with multi-column
○ Custom for data with multi-group

purple

**Color transparency:**

1

**Add borders**

● Yes
○ No

**Background color(s):**

**Highlight regions**

● Show
○ Hide

Paste data below:

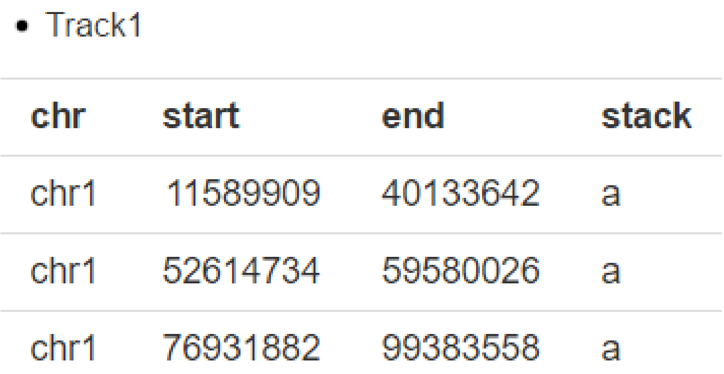
chr8,60000000,90000000,blue

**Color transparency:**

0.6

# Example 4

## Data format

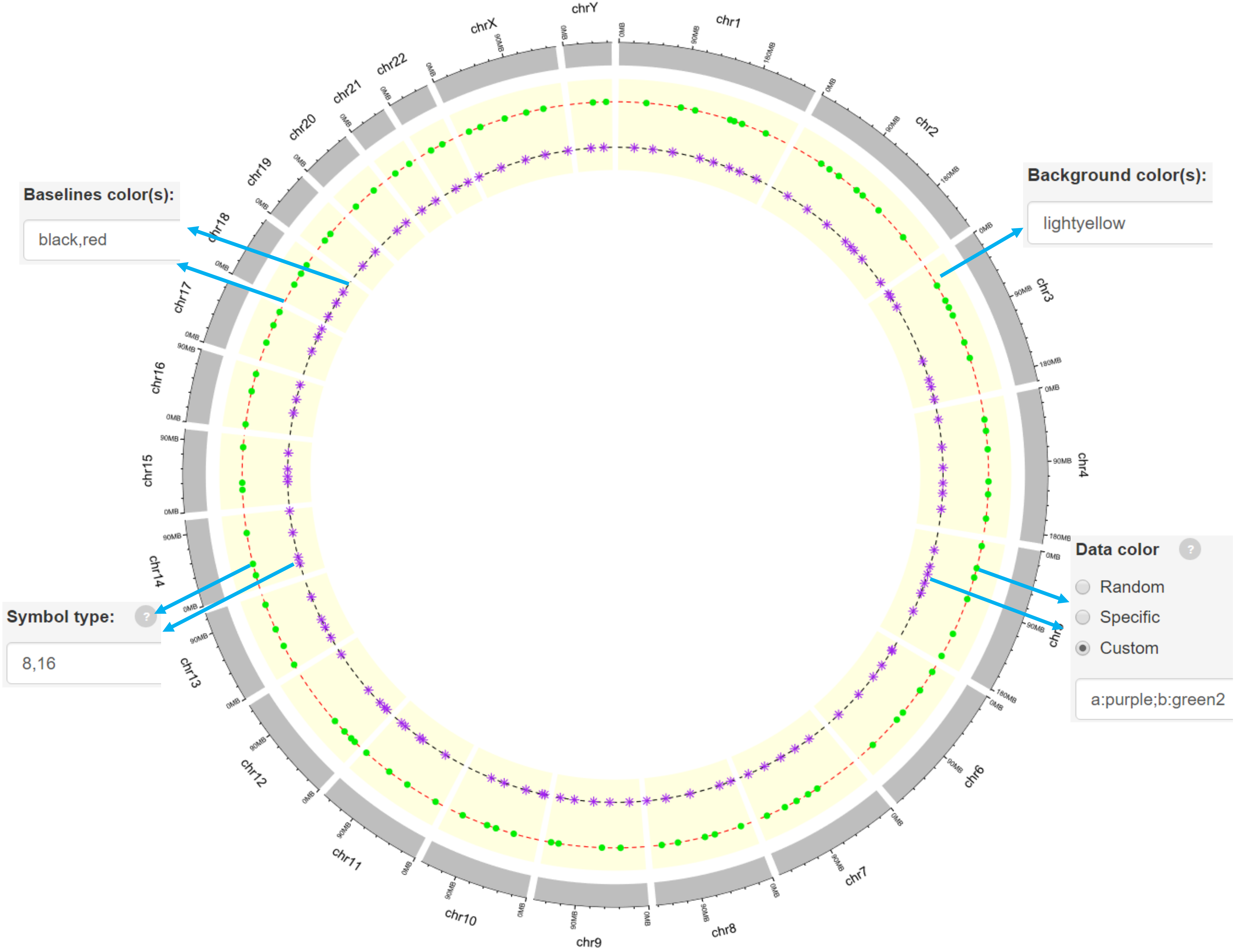


- Track1

| chr | start | end | stack |
|---|---|---|---|
| chr1 | 11589909 | 40133642 | a |
| chr1 | 52614734 | 59580026 | a |
| chr1 | 76931882 | 99383558 | a |

stack_point.csv

- The last column "stack" is a numeric vector or a character vector.
- In stack mode, the y-axis is split into several bins with equal height and all data points are put onto different "horizontal" bins based on the "stack" column.



**Baselines color(s):**
black,red

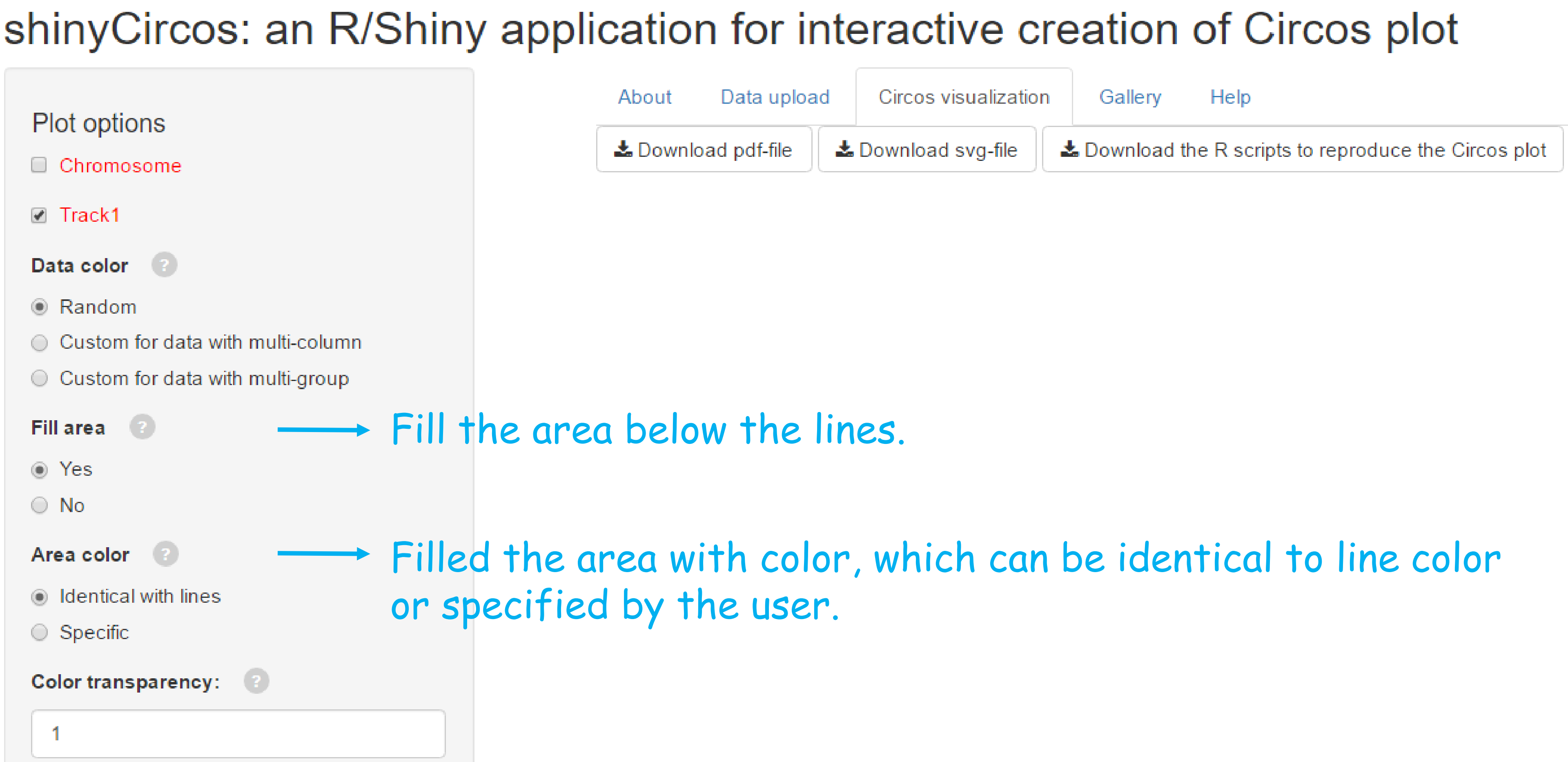
**Background color(s):**
lightyellow

**Symbol type:**
8,16

**Data color**
○ Random
○ Specific
● Custom
a:purple;b:green2

# 2.3 Plot lines

# Options



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☐ Chromosome

☑ Track1

**Data color**

● Random
○ Custom for data with multi-column
○ Custom for data with multi-group

**Fill area** → Fill the area below the lines.

● Yes
○ No

**Area color** → Filled the area with color, which can be identical to line color or specified by the user.

● Identical with lines
○ Specific

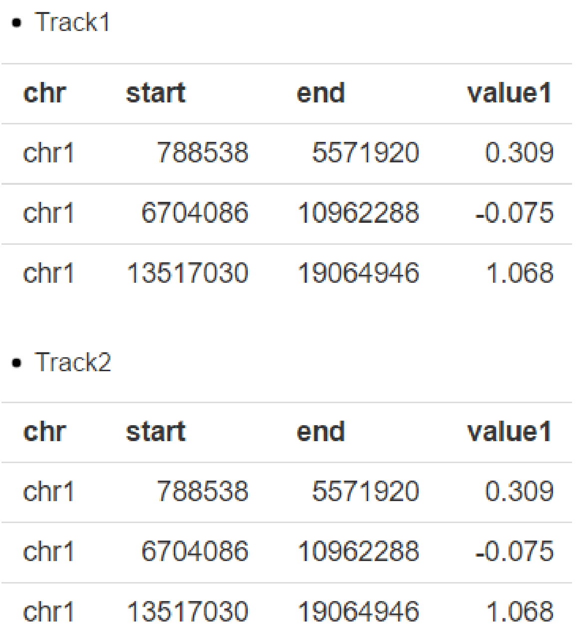
**Color transparency:**

1

- See section 2.2 for more plot options.

# Example 1

## Data format



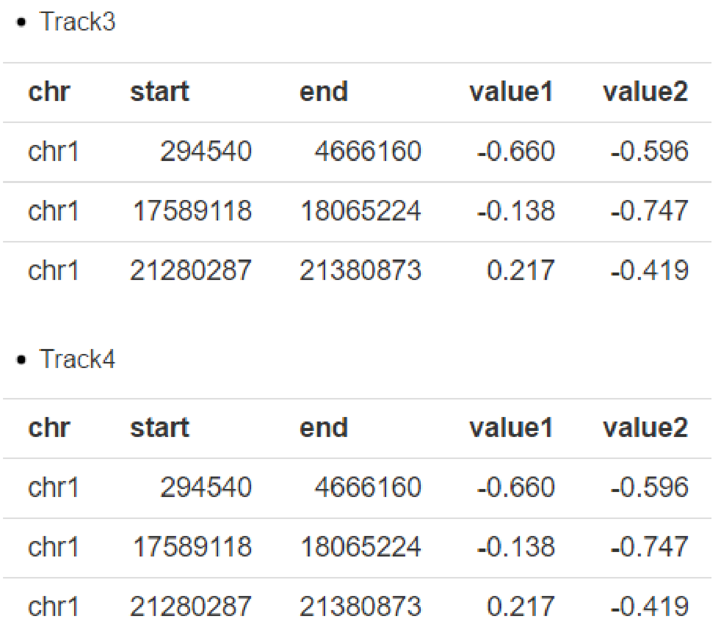
- Track1

| chr | start | end | value1 |
|---|---|---|---|
| chr1 | 788538 | 5571920 | 0.309 |
| chr1 | 6704086 | 10962288 | -0.075 |
| chr1 | 13517030 | 19064946 | 1.068 |

- Track2

| chr | start | end | value1 |
|---|---|---|---|
| chr1 | 788538 | 5571920 | 0.309 |
| chr1 | 6704086 | 10962288 | -0.075 |
| chr1 | 13517030 | 19064946 | 1.068 |

line.csv



- Track3

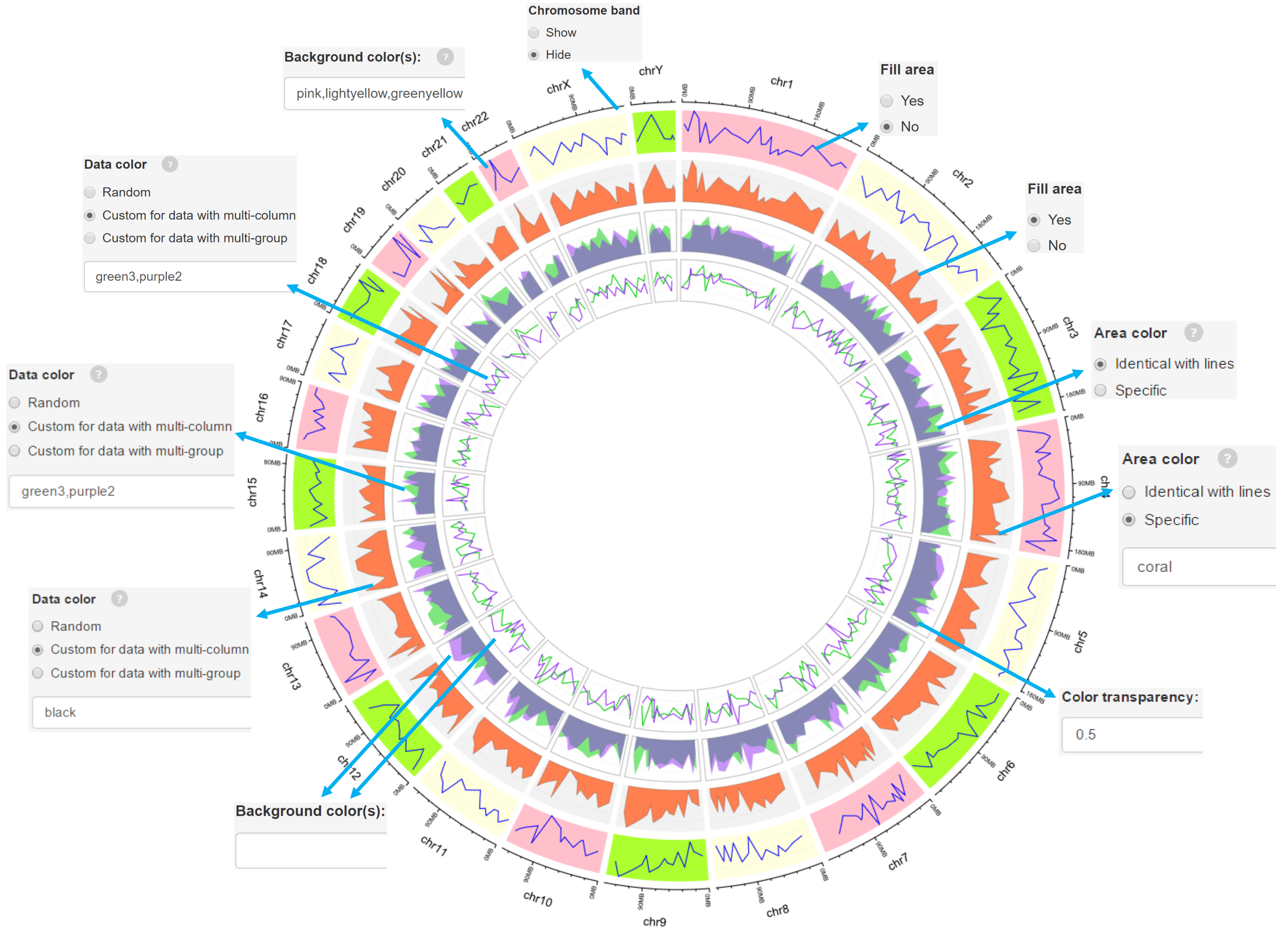
| chr | start | end | value1 | value2 |
|---|---|---|---|---|
| chr1 | 294540 | 4666160 | -0.660 | -0.596 |
| chr1 | 17589118 | 18065224 | -0.138 | -0.747 |
| chr1 | 21280287 | 21380873 | 0.217 | -0.419 |

- Track4

| chr | start | end | value1 | value2 |
|---|---|---|---|---|
| chr1 | 294540 | 4666160 | -0.660 | -0.596 |
| chr1 | 17589118 | 18065224 | -0.138 | -0.747 |
| chr1 | 21280287 | 21380873 | 0.217 | -0.419 |

line_multicolumn.csv

- Simplest data to plot line should contain at least 4 columns including the chromosome ID, start coordinate, end coordinate and multiple columns of values.



**Chromosome band**

○ Show

● Hide

**Background color(s):**

pink,lightyellow,greenyellow

**Fill area**

○ Yes

● No

**Data color**

○ Random

● Custom for data with multi-column

○ Custom for data with multi-group

green3,purple2

**Fill area**

● Yes

○ No

**Area color**

● Identical with lines

○ Specific

**Data color**

○ Random

● Custom for data with multi-column

○ Custom for data with multi-group

green3,purple2

**Area color**

○ Identical with lines

● Specific

coral

**Data color**

○ Random

● Custom for data with multi-column

○ Custom for data with multi-group

black

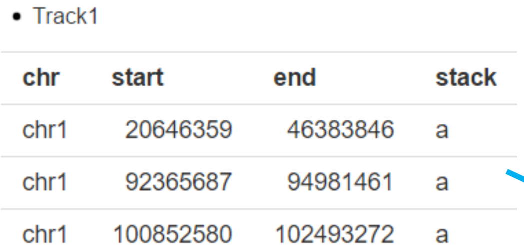
**Color transparency:**

0.5

**Background color(s):**

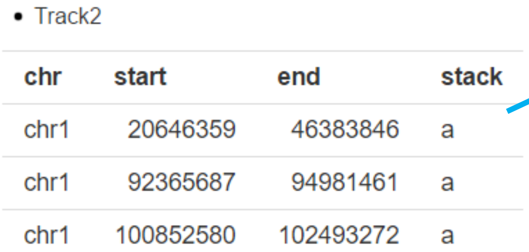
# Example 2

## Data format



- Track1

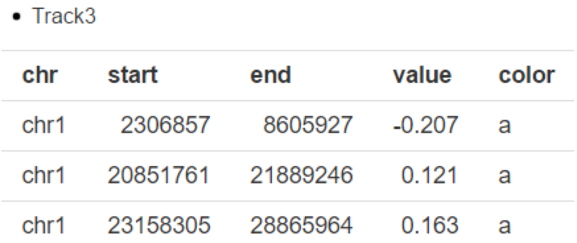
| chr | start | end | stack |
|---|---|---|---|
| chr1 | 20646359 | 46383846 | a |
| chr1 | 92365687 | 94981461 | a |
| chr1 | 100852580 | 102493272 | a |



- Track2

| chr | start | end | stack |
|---|---|---|---|
| chr1 | 20646359 | 46383846 | a |
| chr1 | 92365687 | 94981461 | a |
| chr1 | 100852580 | 102493272 | a |

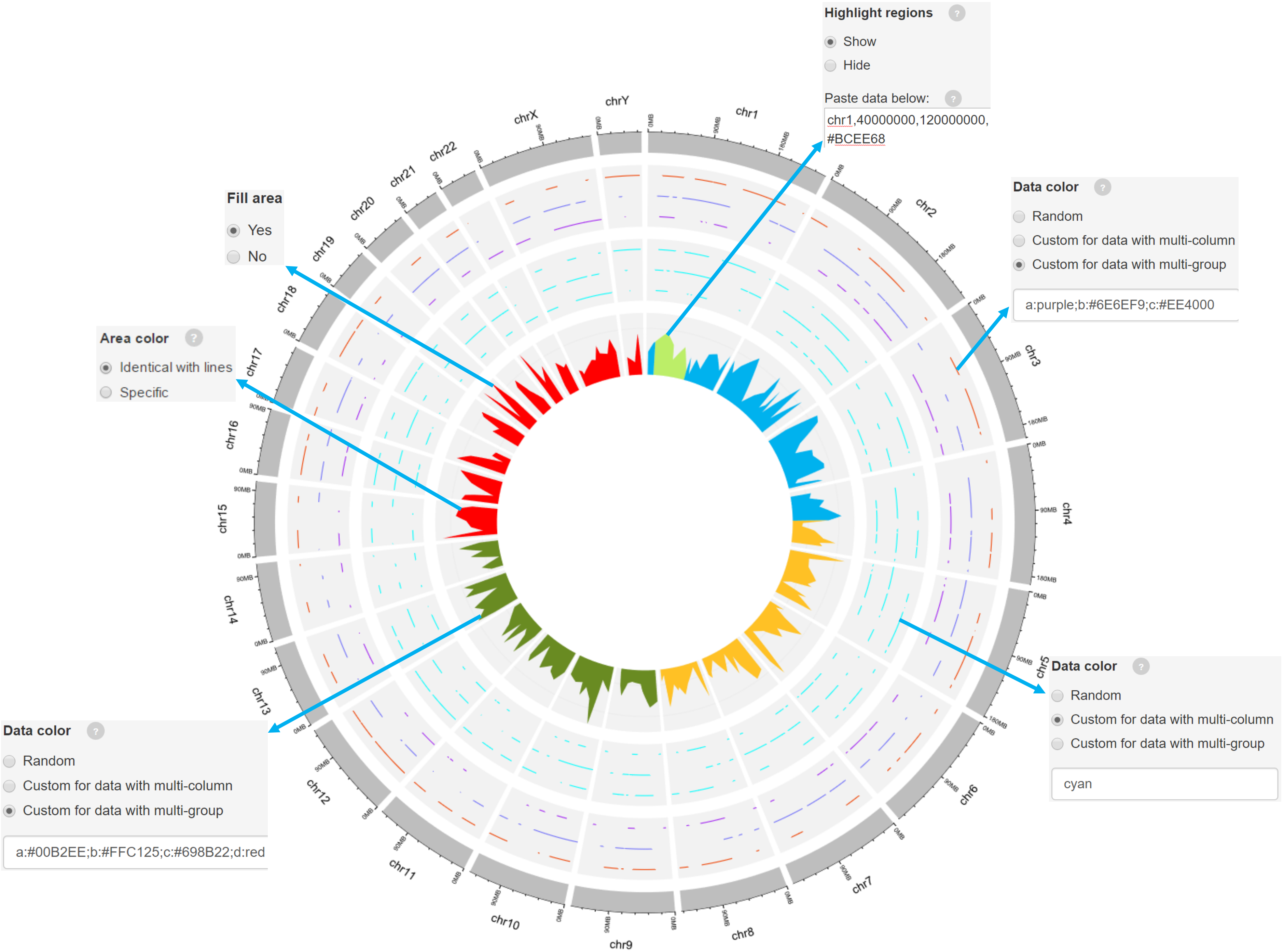
stack_line.csv



- Track3

| chr | start | end | value | color |
|---|---|---|---|---|
| chr1 | 2306857 | 8605927 | -0.207 | a |
| chr1 | 20851761 | 21889246 | 0.121 | a |
| chr1 | 23158305 | 28865964 | 0.163 | a |

line_color.csv



**Highlight regions**

● Show
○ Hide

Paste data below:

chr1,40000000,120000000,#BCEE68

**Fill area**

● Yes
○ No

**Data color**

○ Random
○ Custom for data with multi-column
● Custom for data with multi-group

a:purple;b:#6E6EF9;c:#EE4000

**Area color**

● Identical with lines
○ Specific

**Data color**

○ Random
● Custom for data with multi-column
○ Custom for data with multi-group

cyan

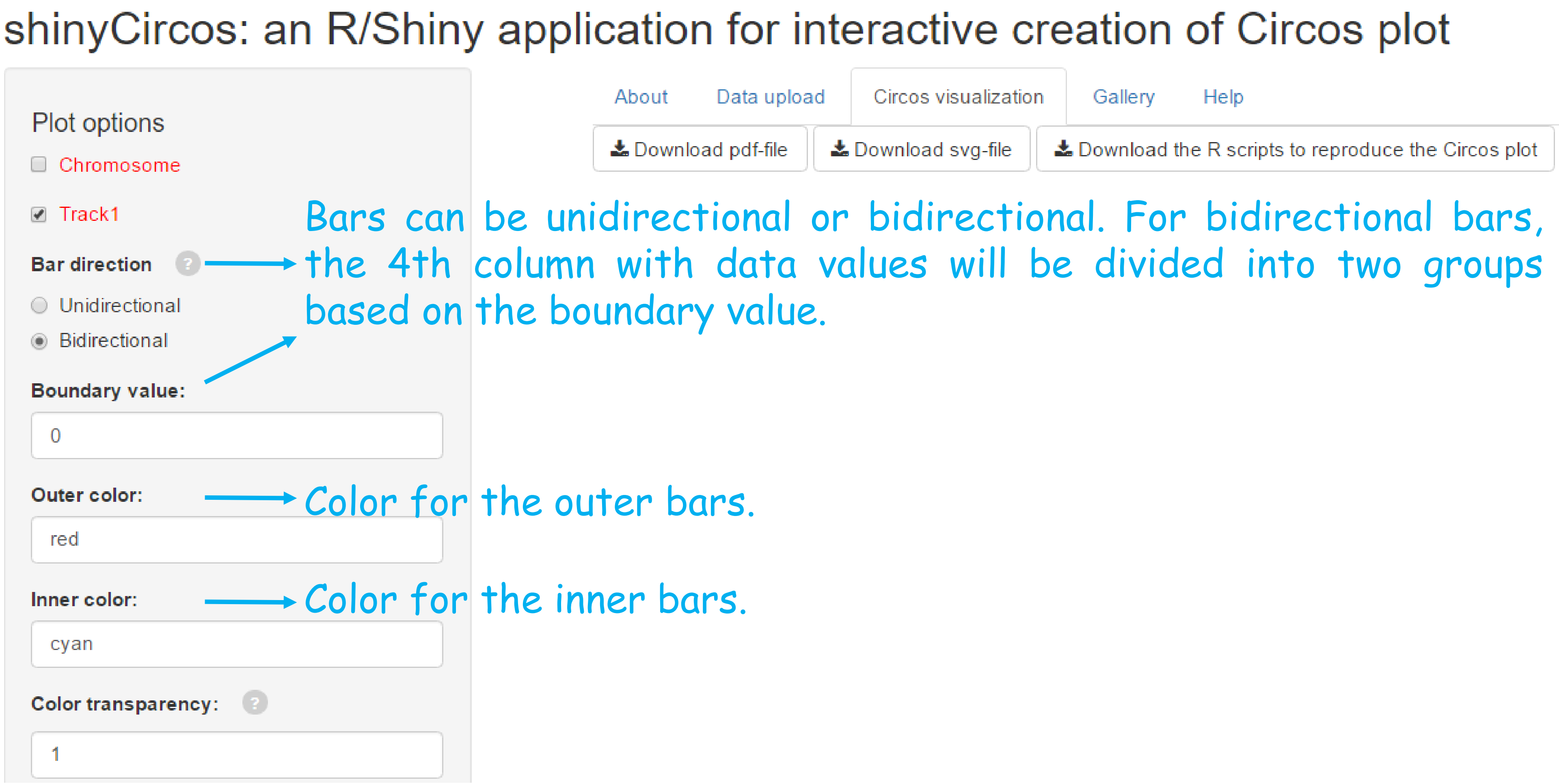
**Data color**

○ Random
○ Custom for data with multi-column
● Custom for data with multi-group

a:#00B2EE;b:#FFC125;c:#698B22;d:red

# 2.4 Plot bars

# Options



shinyCircos: an R/Shiny application for interactive creation of Circos plot

☐ Chromosome

☑ Track1

**Bar direction**

○ Unidirectional

● Bidirectional

**Boundary value:** 0

**Outer color:** red

**Inner color:** cyan

**Color transparency:** 1

Bars can be unidirectional or bidirectional. For bidirectional bars, the 4th column with data values will be divided into two groups based on the boundary value.

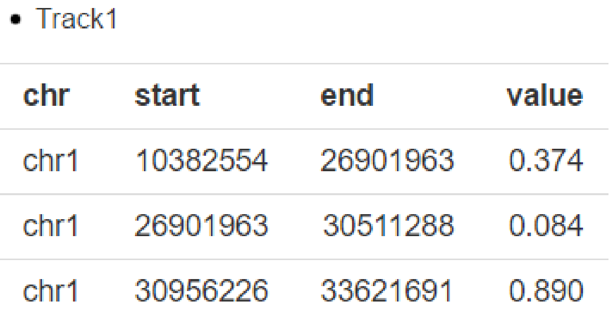
Color for the outer bars.

Color for the inner bars.

- See section 2.2 for more plot options.

# Example 1

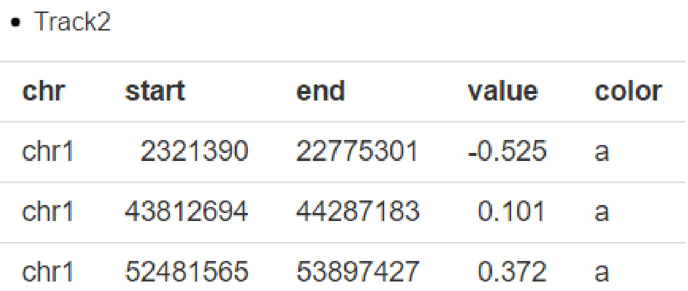
## Data format



- Track1

| chr | start | end | value |
|---|---|---|---|
| chr1 | 10382554 | 26901963 | 0.374 |
| chr1 | 26901963 | 30511288 | 0.084 |
| chr1 | 30956226 | 33621691 | 0.890 |

barplot.csv



- Track2

| chr | start | end | value | color |
|---|---|---|---|---|
| chr1 | 2321390 | 22775301 | -0.525 | a |
| chr1 | 43812694 | 44287183 | 0.101 | a |
| chr1 | 52481565 | 53897427 | 0.372 | a |

barplot_color.csv

- Data for bar plot generally includes 4 columns.
- The 4th column is a numeric vector.
- A “color” column can be added to assign color to different bars.

**Data color**

○ Random

○ Custom for data with multi-column

● Custom for data with multi-group

a:dodgerblue2;b:red;c:gold2;d:tan

**Data color**

○ Random

● Custom for data with multi-column

○ Custom for data with multi-group

forestgreen

**Highlight regions**

● Show

○ Hide

Paste data below:

chr2,40000000,90000000,purple
chr5,20000000,70000000,cyan

**Highlight regions**

● Show

○ Hide

Paste data below:

chr12,40000000,70000000,#FF00FF

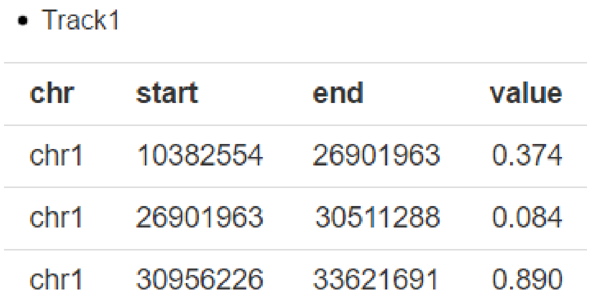
**Bar direction**

● Unidirectional

○ Bidirectional

# Example 2

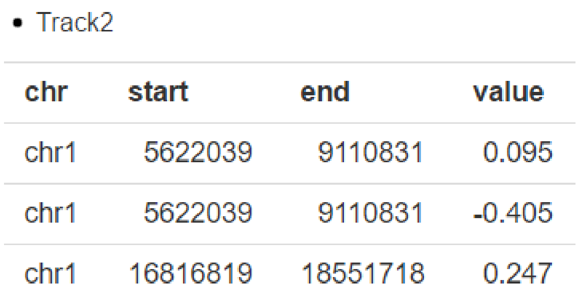
## Data format



- Track1

| chr | start | end | value |
|---|---|---|---|
| chr1 | 10382554 | 26901963 | 0.374 |
| chr1 | 26901963 | 30511288 | 0.084 |
| chr1 | 30956226 | 33621691 | 0.890 |

barplot.csv

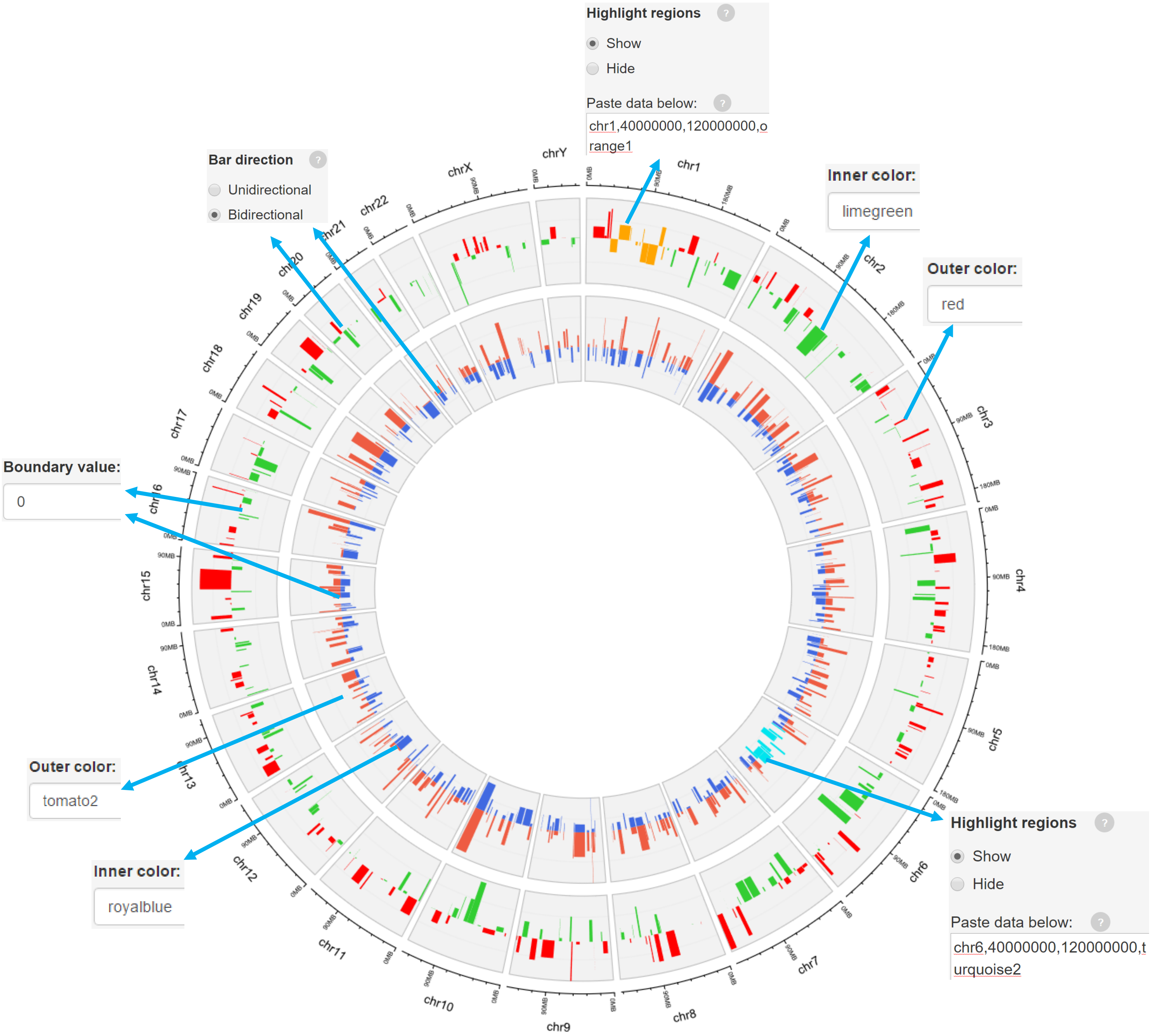


- Track2

| chr | start | end | value |
|---|---|---|---|
| chr1 | 5622039 | 9110831 | 0.095 |
| chr1 | 5622039 | 9110831 | -0.405 |
| chr1 | 16816819 | 18551718 | 0.247 |

barplot_bidirectional.csv

- For bidirectional bars, each genomic region corresponds to one or two values.



**Highlight regions**

● Show

○ Hide

Paste data below:

chr1,40000000,120000000,orange1

**Bar direction**

○ Unidirectional

● Bidirectional

**Inner color:** limegreen

**Outer color:** red

**Boundary value:** 0

**Outer color:** tomato2

**Inner color:** royalblue

**Highlight regions**

● Show

○ Hide

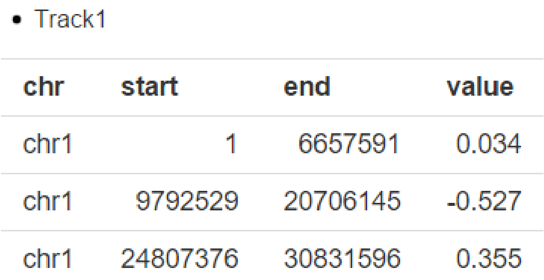
Paste data below:

chr6,40000000,120000000,turquoise2

# 2.5 Plot rects

# Upload rect data

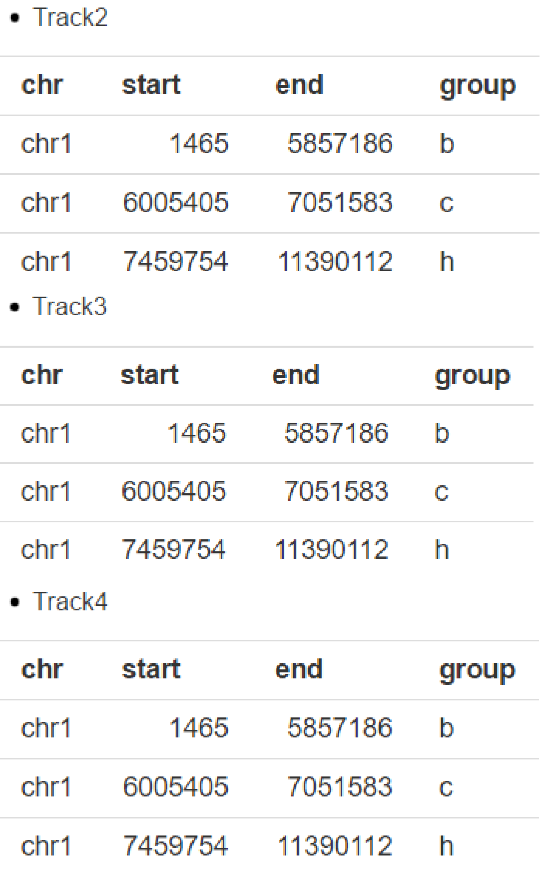
## Data format



- Track1

| chr | start | end | value |
|---|---|---|---|
| chr1 | 1 | 6657591 | 0.034 |
| chr1 | 9792529 | 20706145 | -0.527 |
| chr1 | 24807376 | 30831596 | 0.355 |

rect_gradual.csv



- Track2

| chr | start | end | group |
|---|---|---|---|
| chr1 | 1465 | 5857186 | b |
| chr1 | 6005405 | 7051583 | c |
| chr1 | 7459754 | 11390112 | h |

- Track3

| chr | start | end | group |
|---|---|---|---|
| chr1 | 1465 | 5857186 | b |
| chr1 | 6005405 | 7051583 | c |
| chr1 | 7459754 | 11390112 | h |

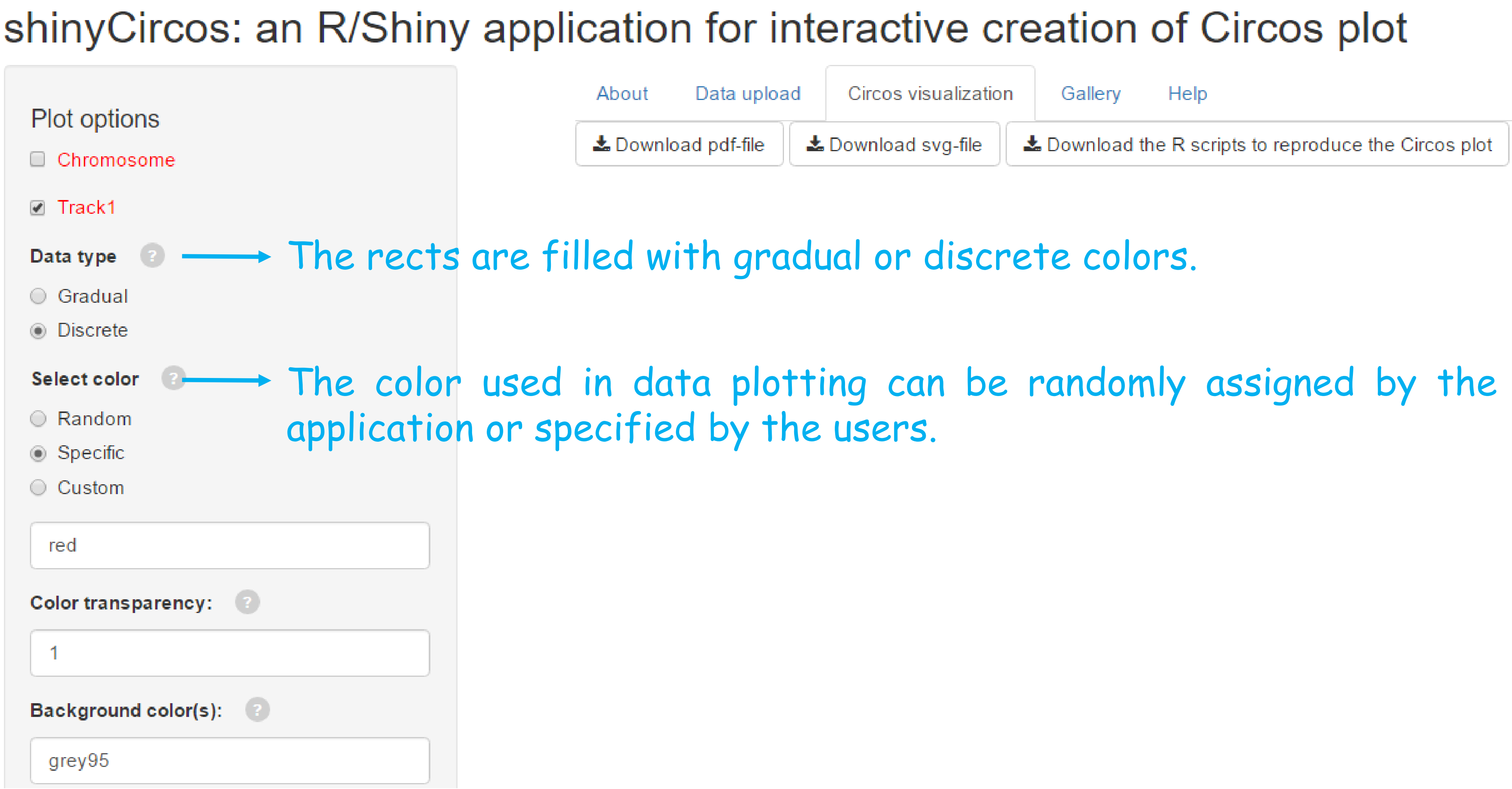
- Track4

| chr | start | end | group |
|---|---|---|---|
| chr1 | 1465 | 5857186 | b |
| chr1 | 6005405 | 7051583 | c |
| chr1 | 7459754 | 11390112 | h |

rect_discrete.csv

- Data for rect plot generally includes four columns.
- The last column should be a numeric vector representing gradual values or a character vector representing discrete variables.

# Options



Plot options

☐ Chromosome

☑ Track1

**Data type**

○ Gradual

● Discrete

**Select color**

○ Random

● Specific

○ Custom

red

**Color transparency:**

1

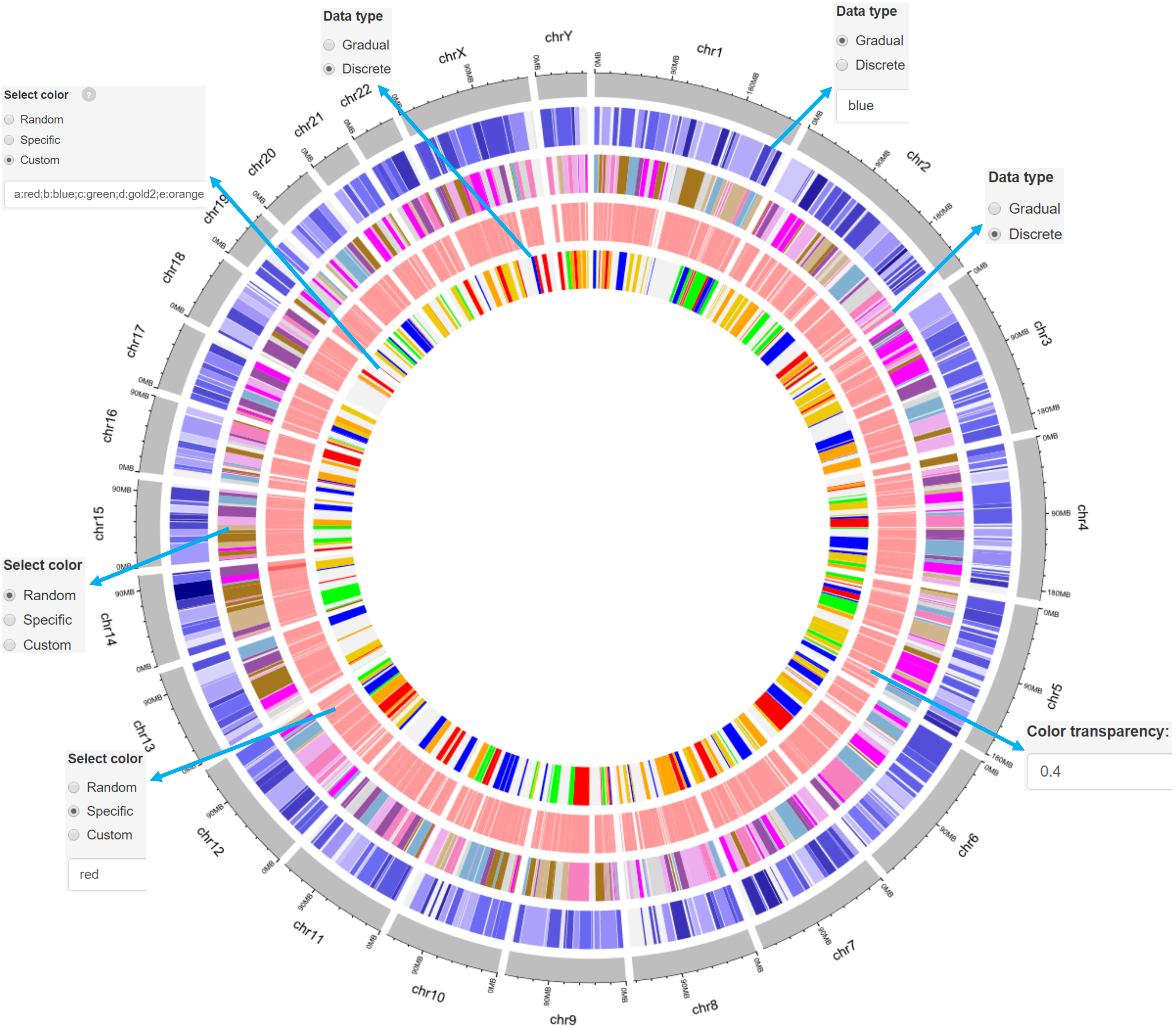
**Background color(s):**

grey95

Data type → The rects are filled with gradual or discrete colors.

Select color → The color used in data plotting can be randomly assigned by the application or specified by the users.

- See section 2.2 for more plot options.



**Select color**

○ Random
○ Specific
● Custom

a:red;b:blue;c:green;d:gold2;e:orange

**Data type**

○ Gradual
● Discrete

**Data type**

● Gradual
○ Discrete

blue

**Data type**

○ Gradual
● Discrete

**Select color**

● Random
○ Specific
○ Custom

**Select color**

○ Random
● Specific
○ Custom

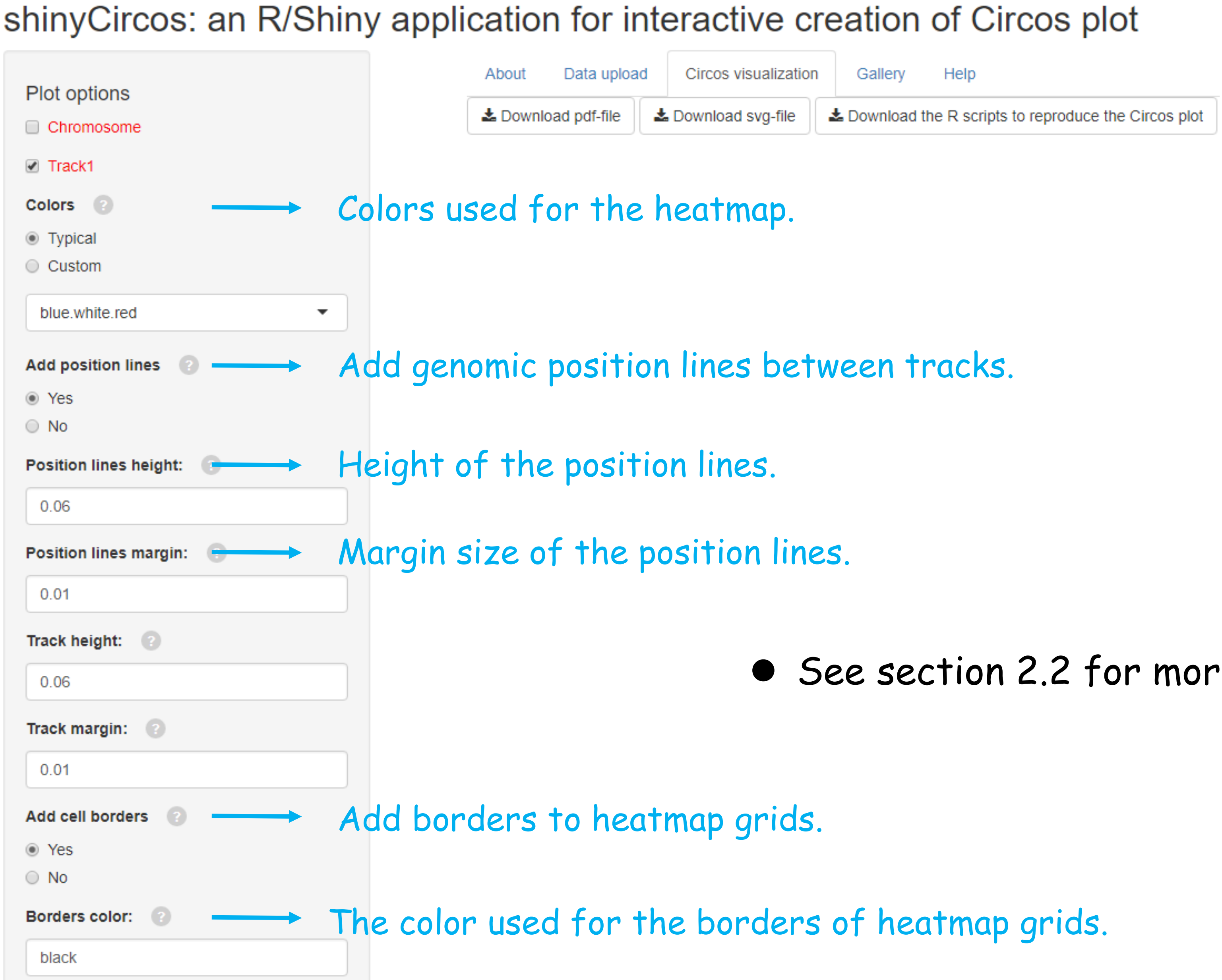
red

**Color transparency:**

0.4

# 2.6 Plot heatmaps

# Options



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☐ Chromosome

☑ Track1

**Colors**

● Typical

○ Custom

blue.white.red

**Add position lines**

● Yes

○ No

**Position lines height:** 0.06

**Position lines margin:** 0.01

**Track height:** 0.06

**Track margin:** 0.01

**Add cell borders**

● Yes

○ No

**Borders color:** black

Colors → Colors used for the heatmap.

Add position lines → Add genomic position lines between tracks.

Position lines height → Height of the position lines.

Position lines margin → Margin size of the position lines.

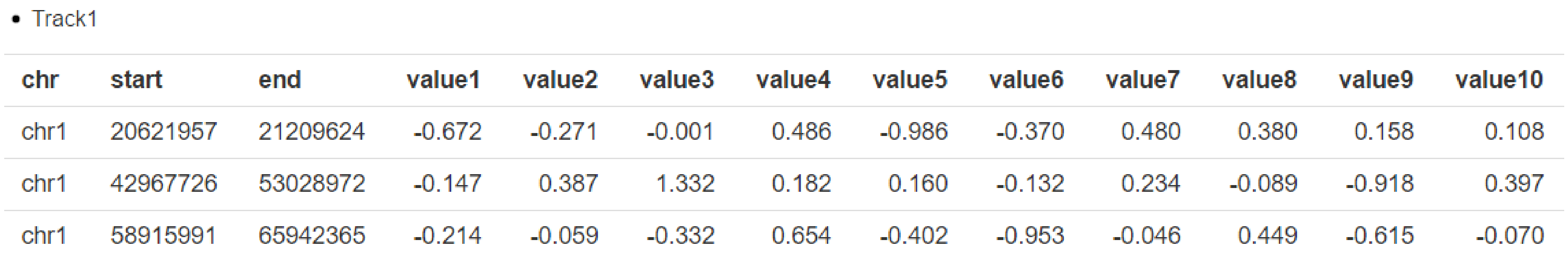
- See section 2.2 for more plot options.

Add cell borders → Add borders to heatmap grids.

Borders color → The color used for the borders of heatmap grids.

# Upload heatmap data

## Data format

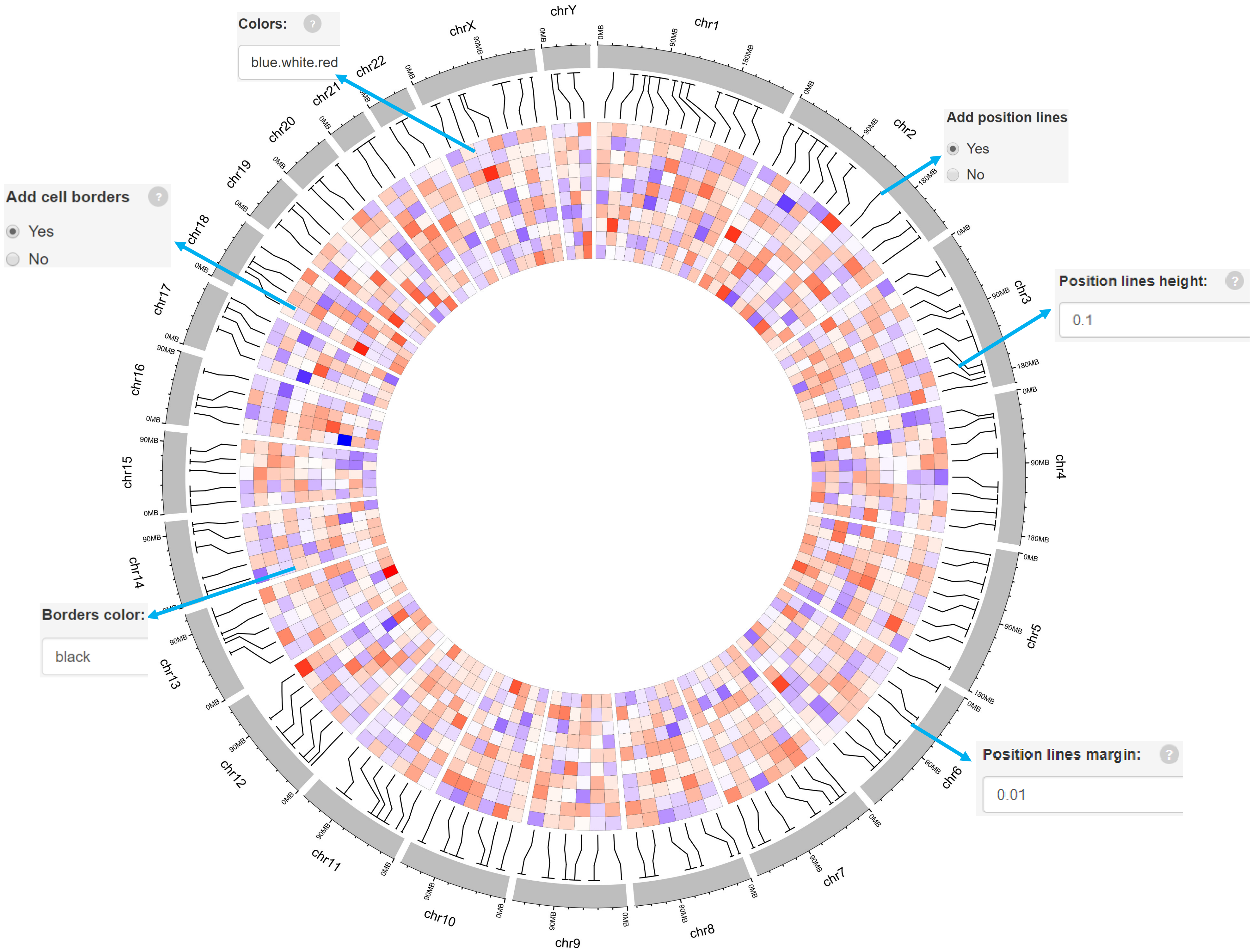


- Track1

| chr | start | end | value1 | value2 | value3 | value4 | value5 | value6 | value7 | value8 | value9 | value10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 20621957 | 21209624 | -0.672 | -0.271 | -0.001 | 0.486 | -0.986 | -0.370 | 0.480 | 0.380 | 0.158 | 0.108 |
| chr1 | 42967726 | 53028972 | -0.147 | 0.387 | 1.332 | 0.182 | 0.160 | -0.132 | 0.234 | -0.089 | -0.918 | 0.397 |
| chr1 | 58915991 | 65942365 | -0.214 | -0.059 | -0.332 | 0.654 | -0.402 | -0.953 | -0.046 | 0.449 | -0.615 | -0.070 |

heatmap.csv

- Apart from the first three columns, other columns are numeric vectors representing different values.



**Colors:**
blue.white.red

**Add position lines**
● Yes
○ No

**Position lines height:**
0.1

**Position lines margin:**
0.01

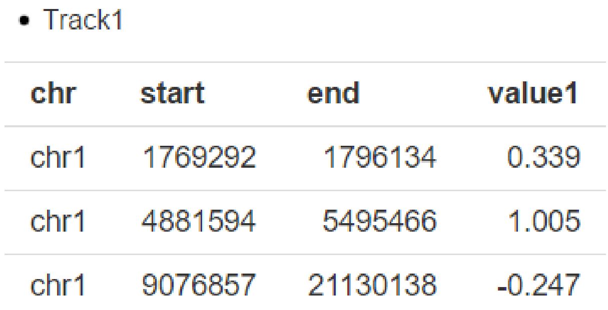
**Add cell borders**
● Yes
○ No

**Borders color:**
black

# 2.7 Plot ideogram

# Upload ideogram data

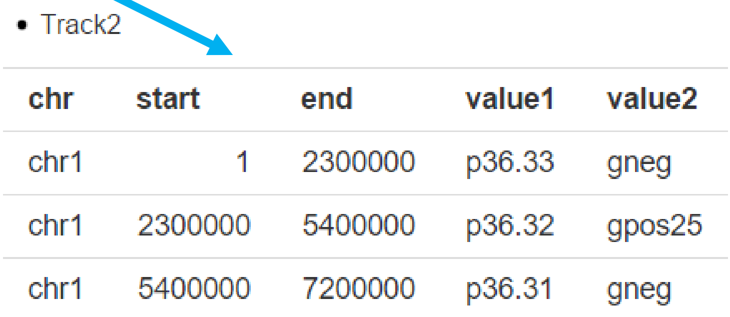
Data format



- Track1

| chr | start | end | value1 |
|---|---|---|---|
| chr1 | 1769292 | 1796134 | 0.339 |
| chr1 | 4881594 | 5495466 | 1.005 |
| chr1 | 9076857 | 21130138 | -0.247 |

point.csv

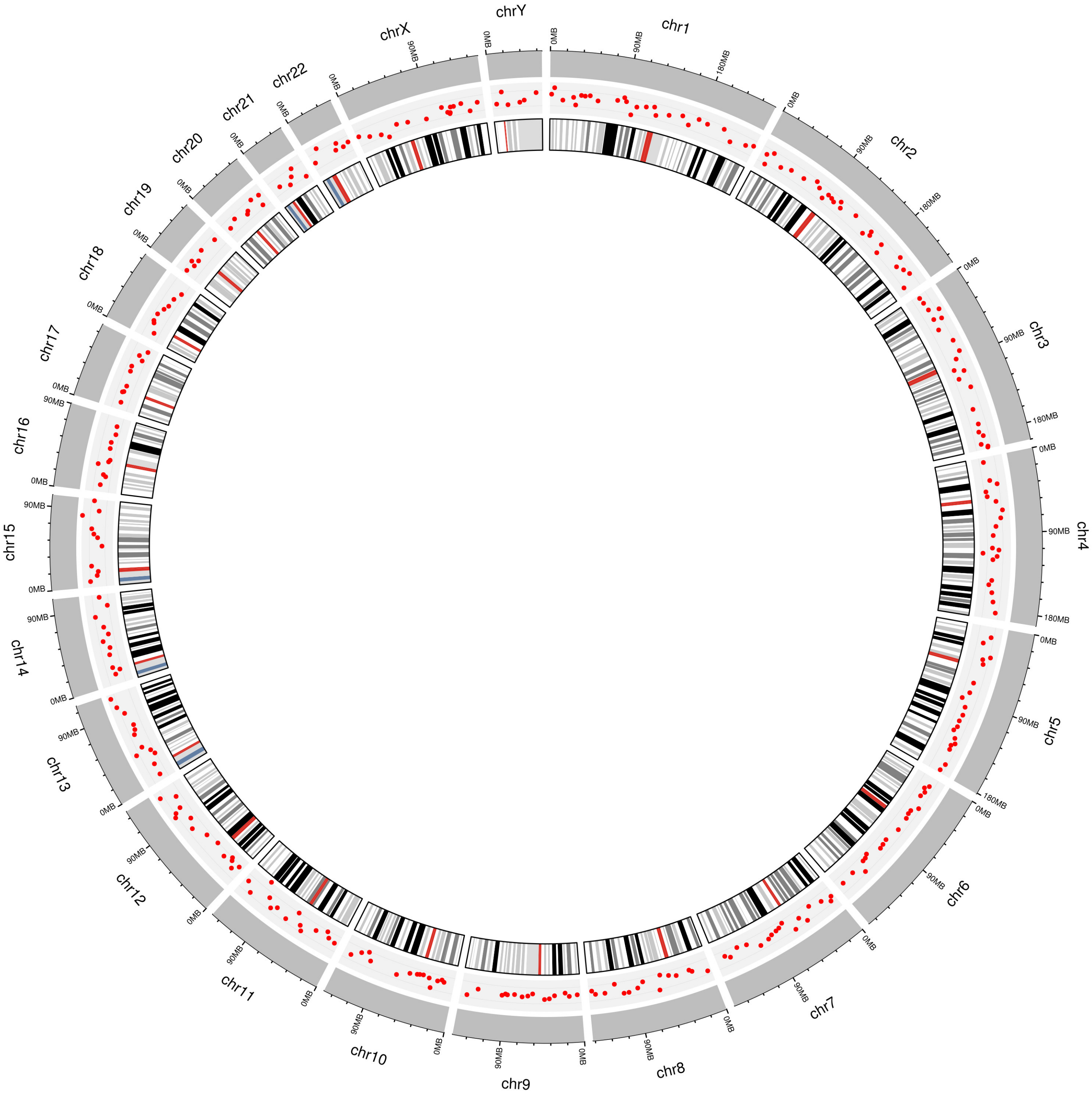


- Track2

| chr | start | end | value1 | value2 |
|---|---|---|---|---|
| chr1 | 1 | 2300000 | p36.33 | gneg |
| chr1 | 2300000 | 5400000 | p36.32 | gpos25 |
| chr1 | 5400000 | 7200000 | p36.31 | gneg |

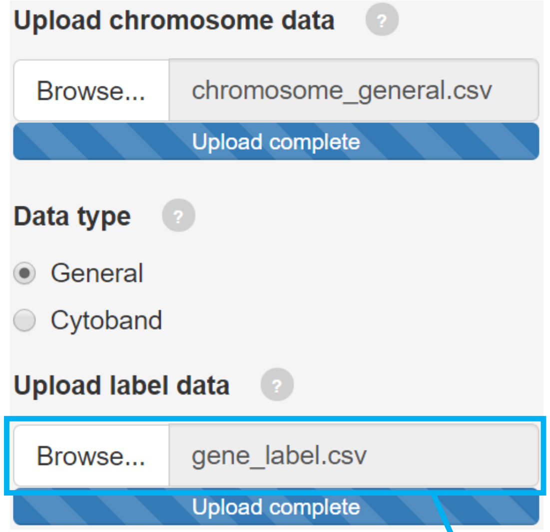
chromosome_ideogram.csv

- Data to plot ideogram is the same as “chromosome_cytoband.csv”.
- Ideogram plot can be generated in any track.


chr1
0MB
90MB
180MB
chr2
0MB
90MB
180MB
chr3
0MB
90MB
180MB
chr4
0MB
90MB
180MB
chr5
0MB
90MB
180MB
chr6
0MB
90MB
chr7
0MB
90MB
chr8
0MB
90MB
chr9
0MB
90MB
chr10
0MB
90MB
chr11
0MB
90MB
chr12
0MB
90MB
chr13
0MB
90MB
chr14
0MB
90MB
chr15
0MB
90MB
chr16
0MB
90MB
chr17
0MB
chr18
0MB
chr19
0MB
chr20
0MB
chr21
0MB
chr22
0MB
chrX
0MB
90MB
chrY
0MB

# 2.8 Plot labels

# Upload label data



**Upload chromosome data**

Browse... chromosome_general.csv

Upload complete

**Data type**

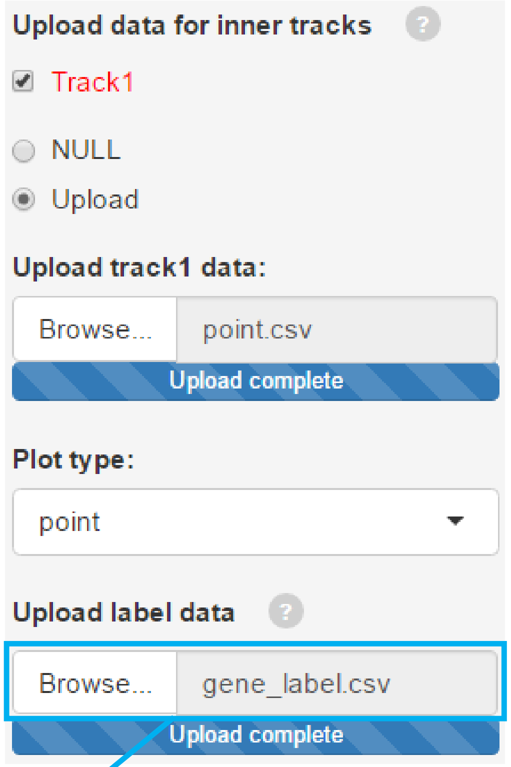
● General

○ Cytoband

**Upload label data**

Browse... gene_label.csv

Upload complete



**Upload data for inner tracks**

☑ Track1

○ NULL

● Upload

**Upload track1 data:**

Browse... point.csv

Upload complete

**Plot type:**

point

**Upload label data**

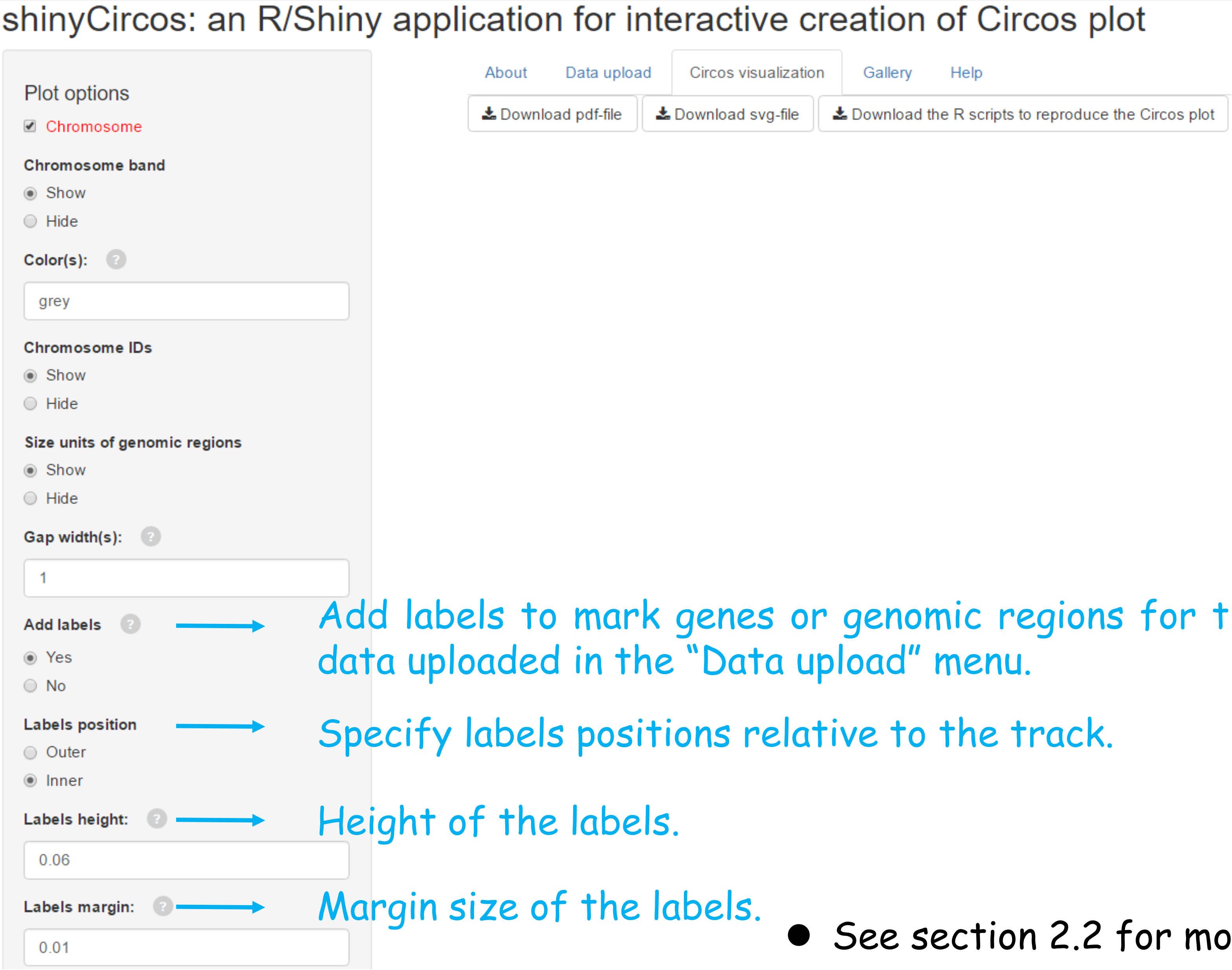
Browse... gene_label.csv

Upload complete

- Label

| chr | start | end | label |
|---|---|---|---|
| chr1 | 3698046 | 3736201 | TP73 |
| chr1 | 156114670 | 156140089 | LMNA |
| chr2 | 202206180 | 202238599 | SUMO1 |

# Options



Plot options

☑ Chromosome

**Chromosome band**
- ● Show
- ○ Hide

**Color(s):** grey

**Chromosome IDs**
- ● Show
- ○ Hide

**Size units of genomic regions**
- ● Show
- ○ Hide

**Gap width(s):** 1

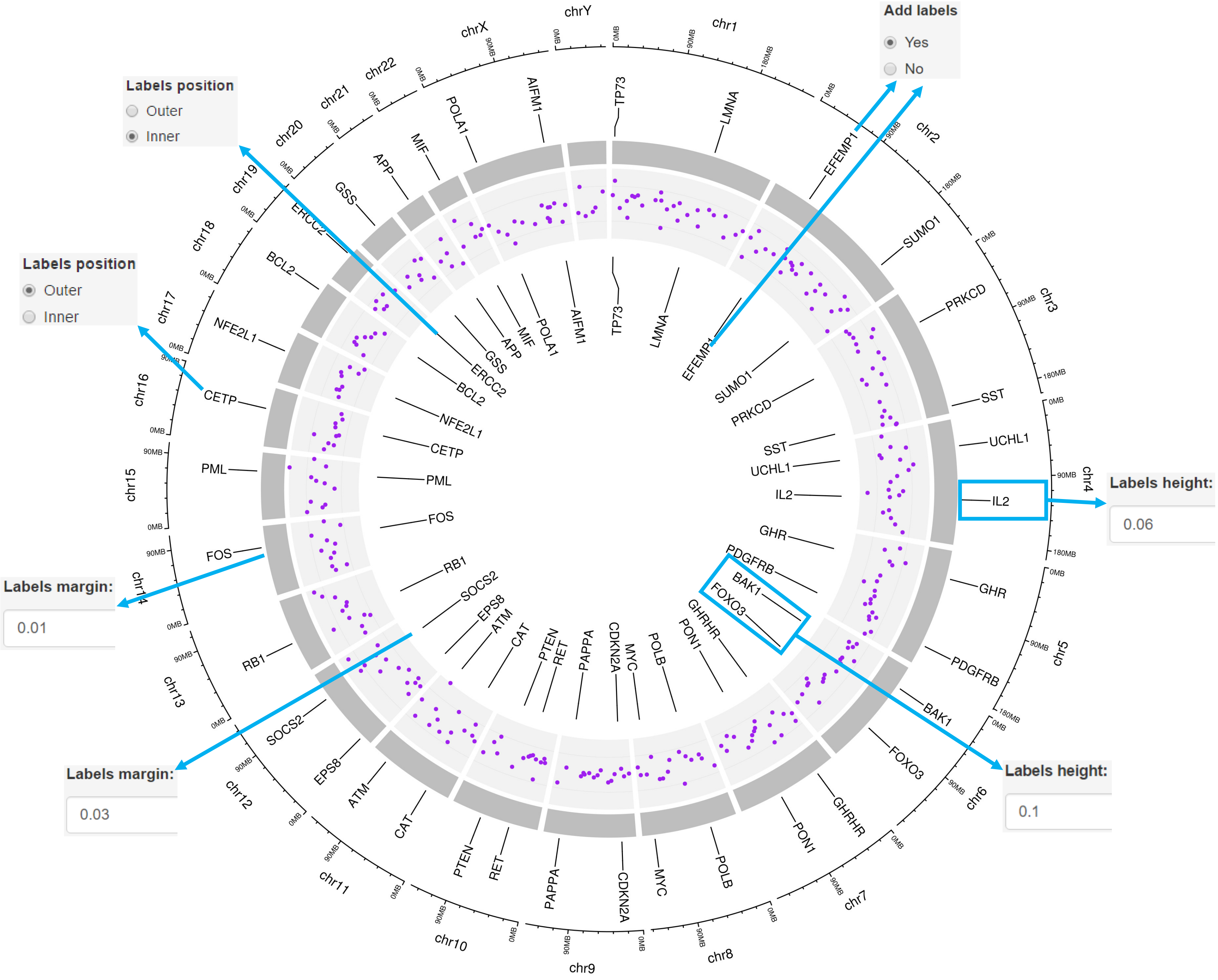
**Add labels** → Add labels to mark genes or genomic regions for this track using data uploaded in the "Data upload" menu.
- ● Yes
- ○ No

**Labels position** → Specify labels positions relative to the track.
- ○ Outer
- ● Inner

**Labels height:** 0.06 → Height of the labels.

**Labels margin:** 0.01 → Margin size of the labels.

- See section 2.2 for more plot options.



**Add labels**
● Yes
○ No

**Labels position**
○ Outer
● Inner

**Labels position**
● Outer
○ Inner

**Labels height:**
0.06

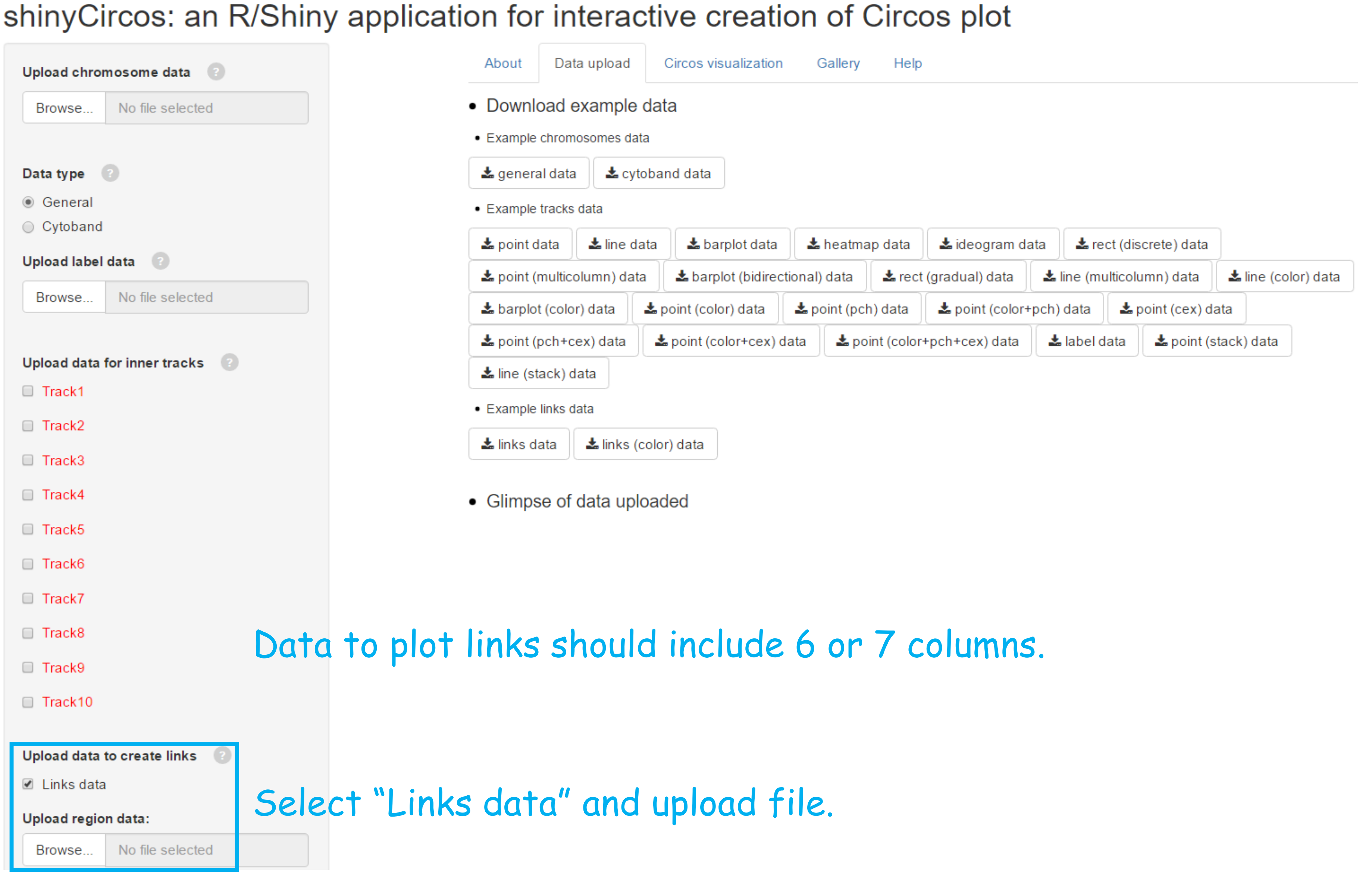
**Labels height:**
0.1

**Labels margin:**
0.01

**Labels margin:**
0.03

# 2.9 Plot links

# Upload links data



shinyCircos: an R/Shiny application for interactive creation of Circos plot

**Upload chromosome data**

Browse... No file selected

**Data type**

● General

○ Cytoband

**Upload label data**

Browse... No file selected

**Upload data for inner tracks**

☐ Track1

☐ Track2

☐ Track3

☐ Track4

☐ Track5

☐ Track6

☐ Track7

☐ Track8

☐ Track9

☐ Track10

**Upload data to create links**

☑ Links data

**Upload region data:**

Browse... No file selected

- Download example data
  - Example chromosomes data

  - Example tracks data

  - Example links data

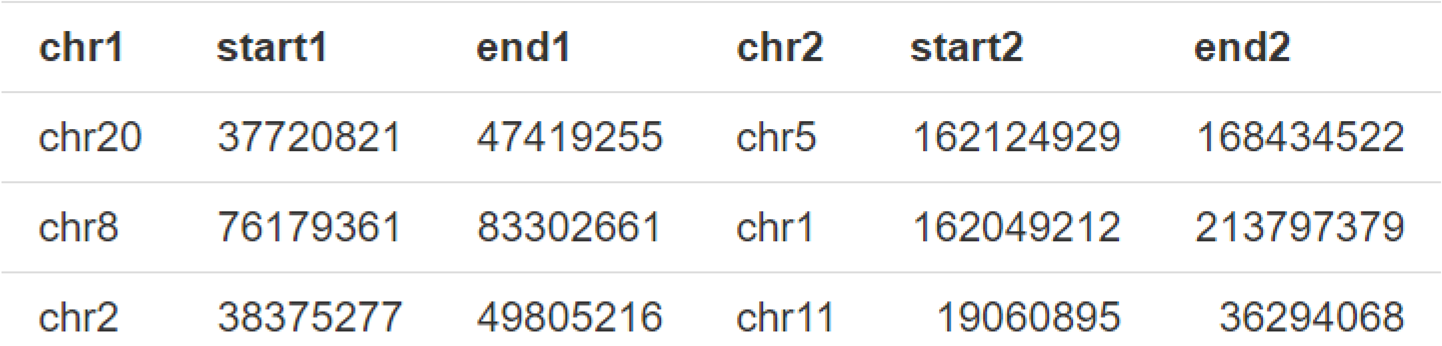
- Glimpse of data uploaded

Data to plot links should include 6 or 7 columns.

Select “Links data” and upload file.

# Example 1

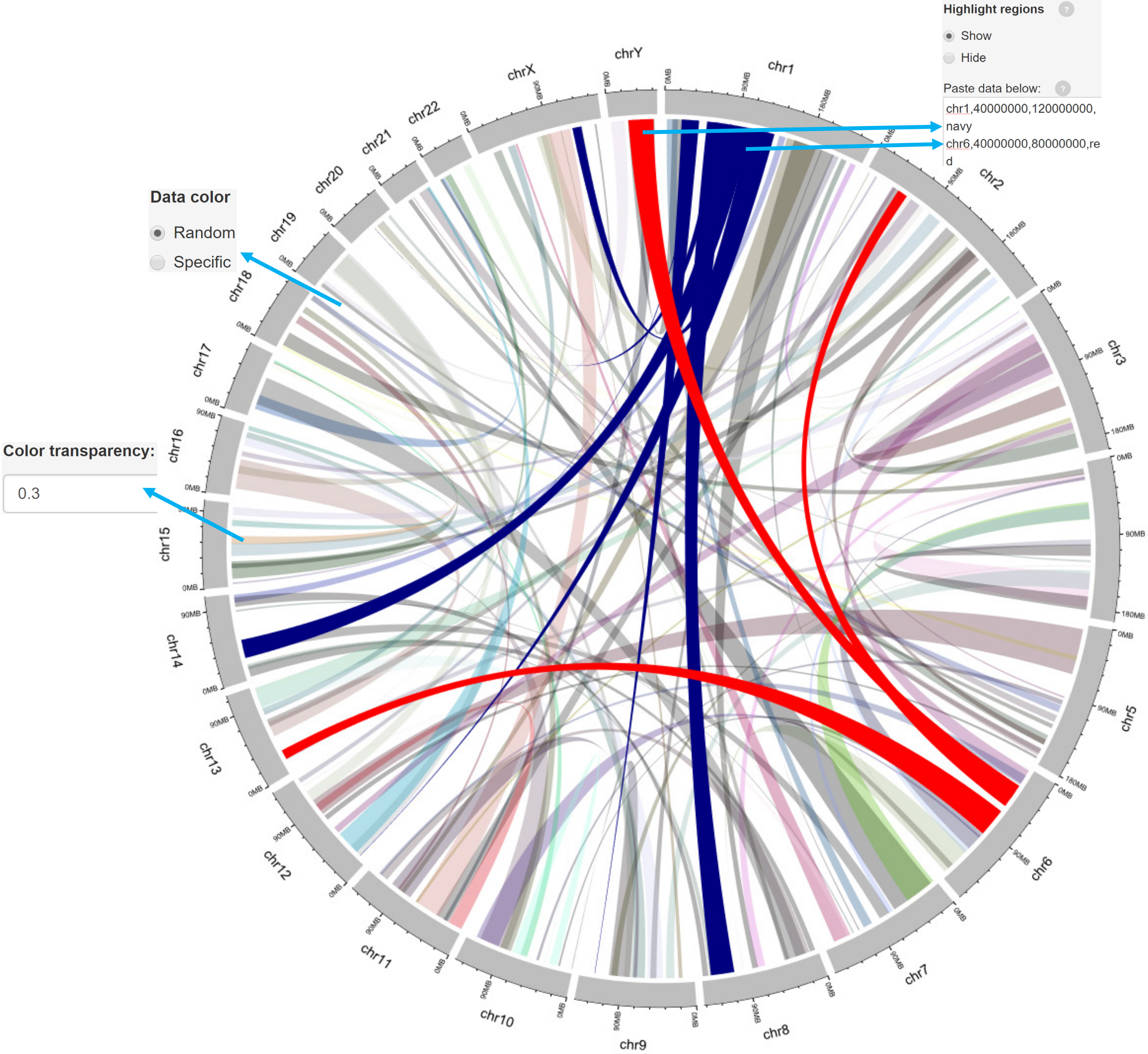
## Data format



| chr1 | start1 | end1 | chr2 | start2 | end2 |
|---|---|---|---|---|---|
| chr20 | 37720821 | 47419255 | chr5 | 162124929 | 168434522 |
| chr8 | 76179361 | 83302661 | chr1 | 162049212 | 213797379 |
| chr2 | 38375277 | 49805216 | chr11 | 19060895 | 36294068 |

links.csv

- Data with 6 columns.
- Columns 1-3 and columns 4-6 represent the two ends of connectors respectively.



**Highlight regions**

● Show

○ Hide

Paste data below:

```
chr1,40000000,120000000,navy
chr6,40000000,80000000,red
```

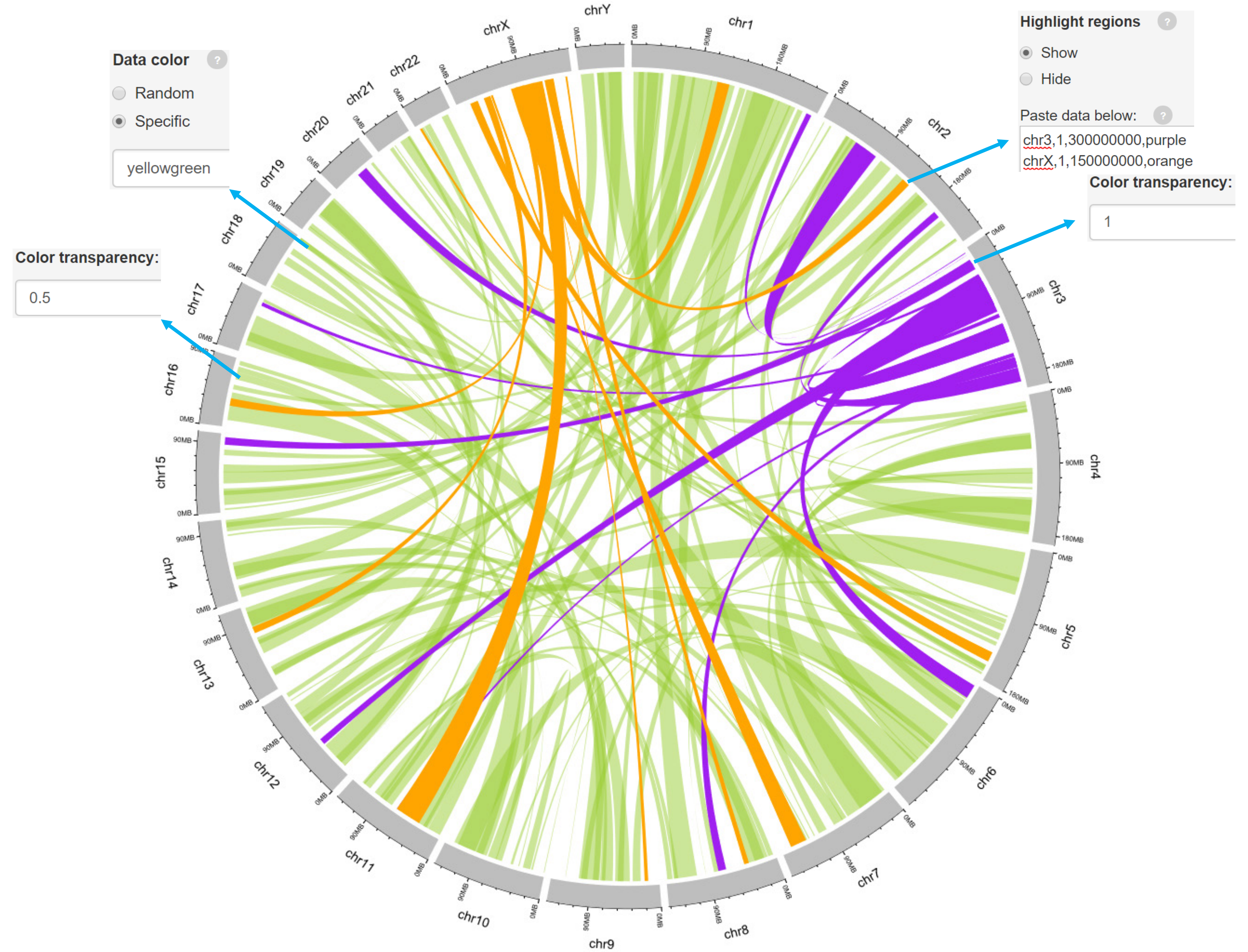
**Data color**

● Random

○ Specific

**Color transparency:**

0.3



**Data color**

○ Random
● Specific

yellowgreen

**Color transparency:**

0.5

**Highlight regions**

● Show
○ Hide

Paste data below:

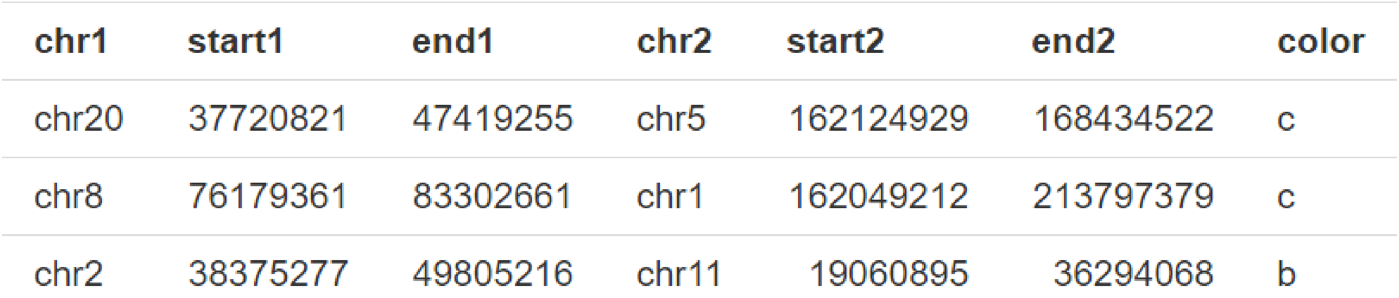
```
chr3,1,300000000,purple
chrX,1,150000000,orange
```

**Color transparency:**

1

# Example 2

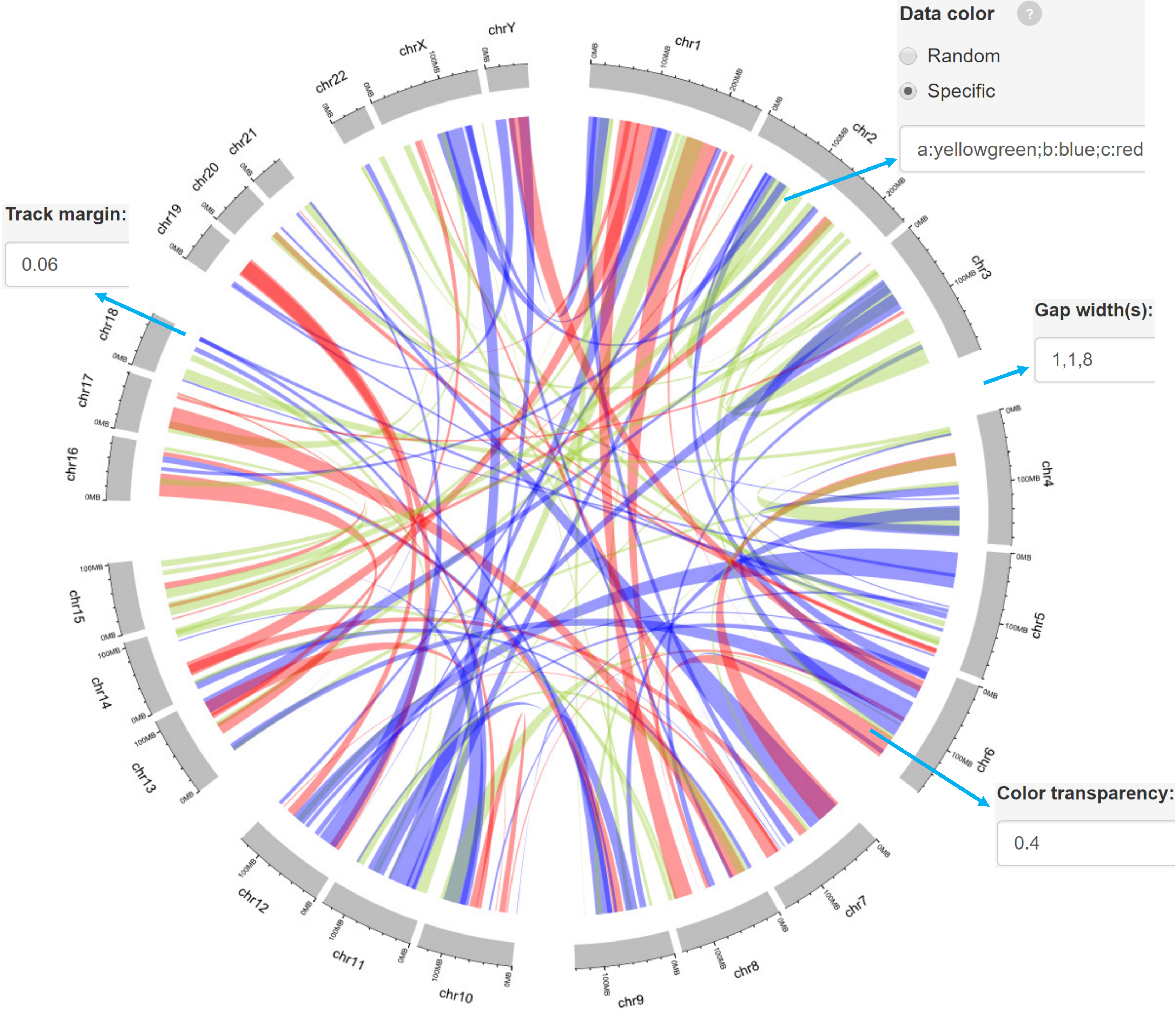
## Data format



| chr1 | start1 | end1 | chr2 | start2 | end2 | color |
|---|---|---|---|---|---|---|
| chr20 | 37720821 | 47419255 | chr5 | 162124929 | 168434522 | c |
| chr8 | 76179361 | 83302661 | chr1 | 162049212 | 213797379 | c |
| chr2 | 38375277 | 49805216 | chr11 | 19060895 | 36294068 | b |

links_color.csv

- Data with 7 columns.
- A “color” column representing different groups of data with differing colors can be added.



**Data color**

○ Random

● Specific

a:yellowgreen;b:blue;c:red

**Track margin:**

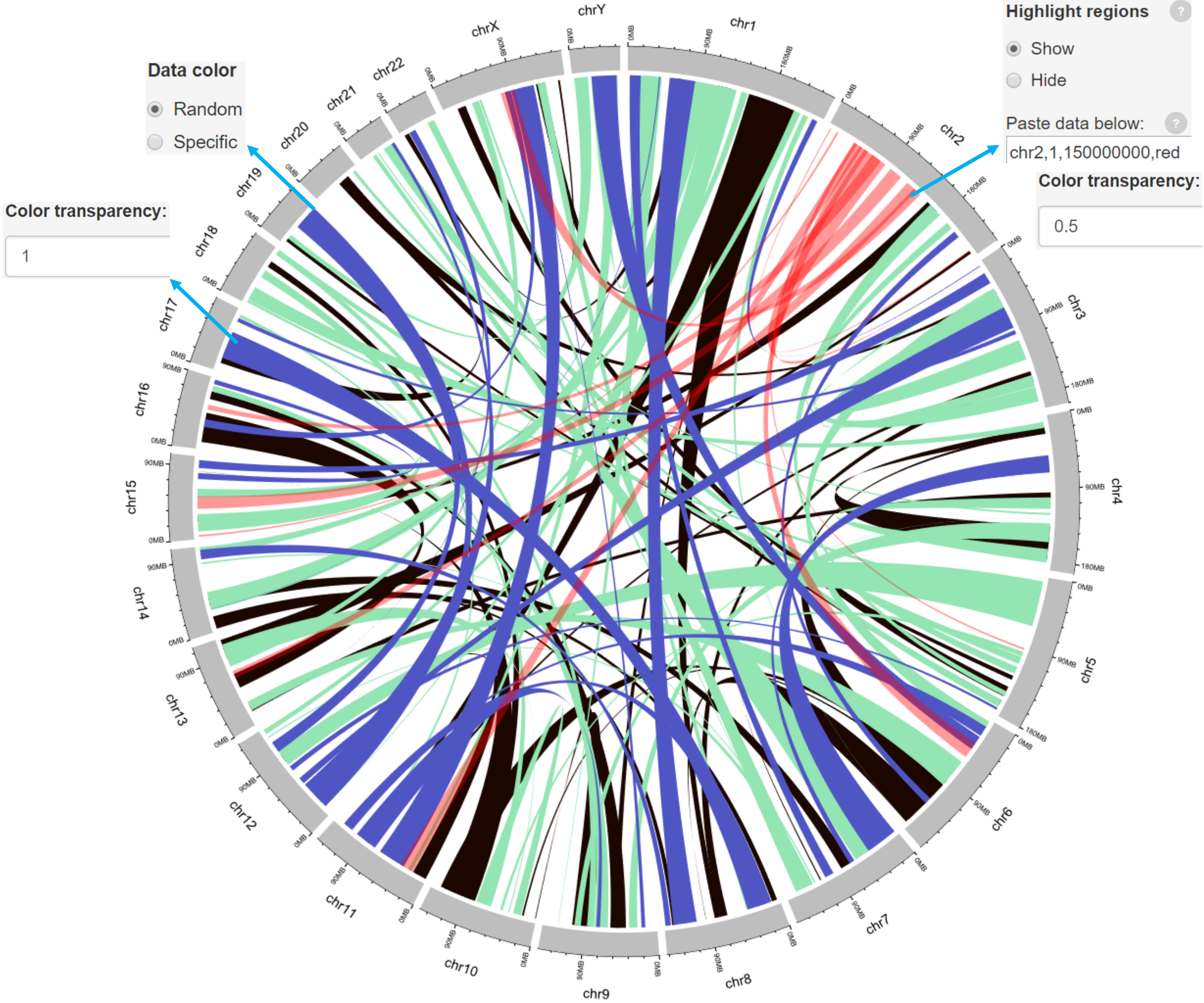
0.06

**Gap width(s):**

1,1,8

**Color transparency:**

0.4



**Data color**

● Random

○ Specific

**Color transparency:**

1

**Highlight regions**

● Show

○ Hide

Paste data below:

chr2,1,150000000,red

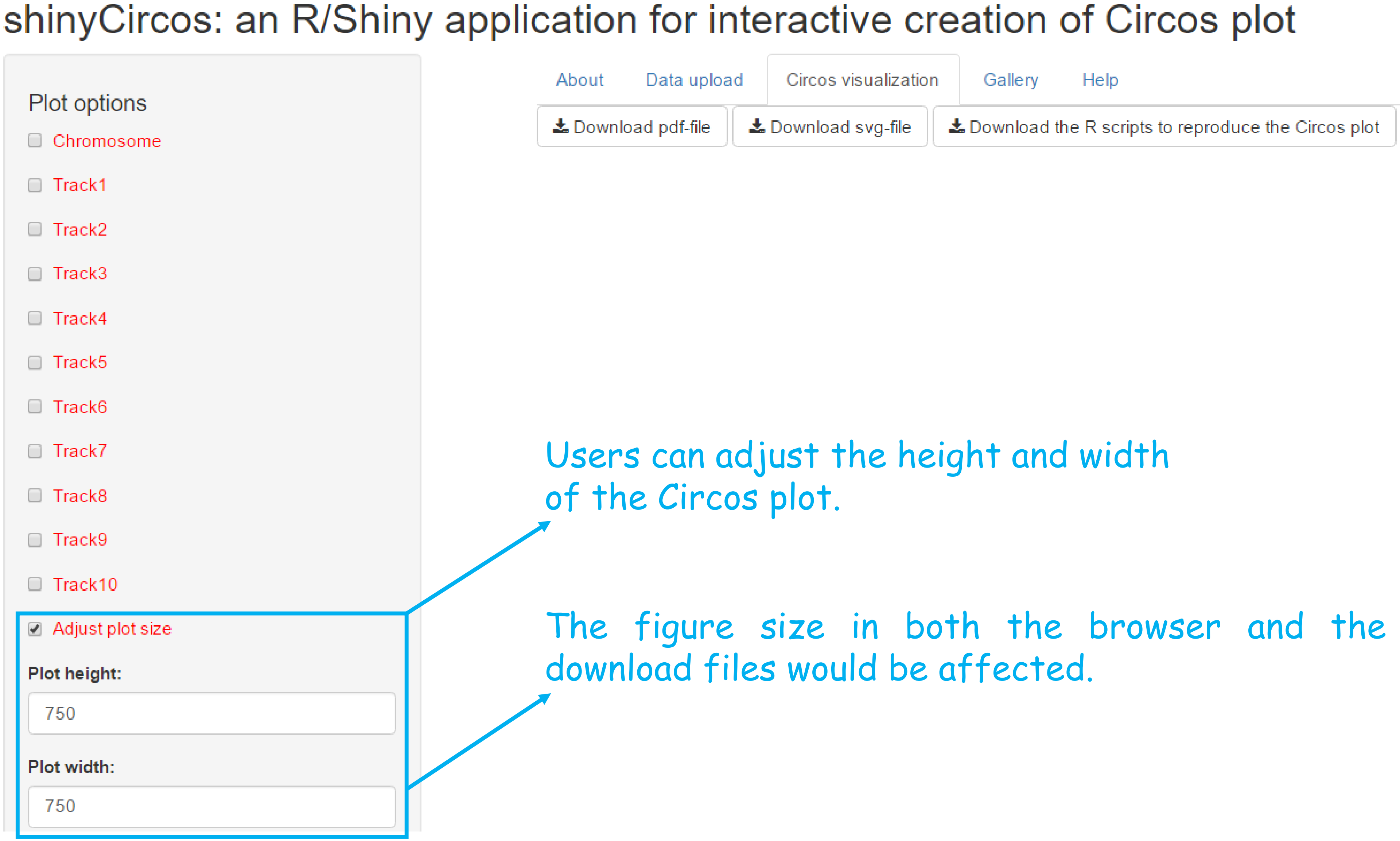
**Color transparency:**

0.5

# 3. Other features

# 3.1 Figure size

# Options



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

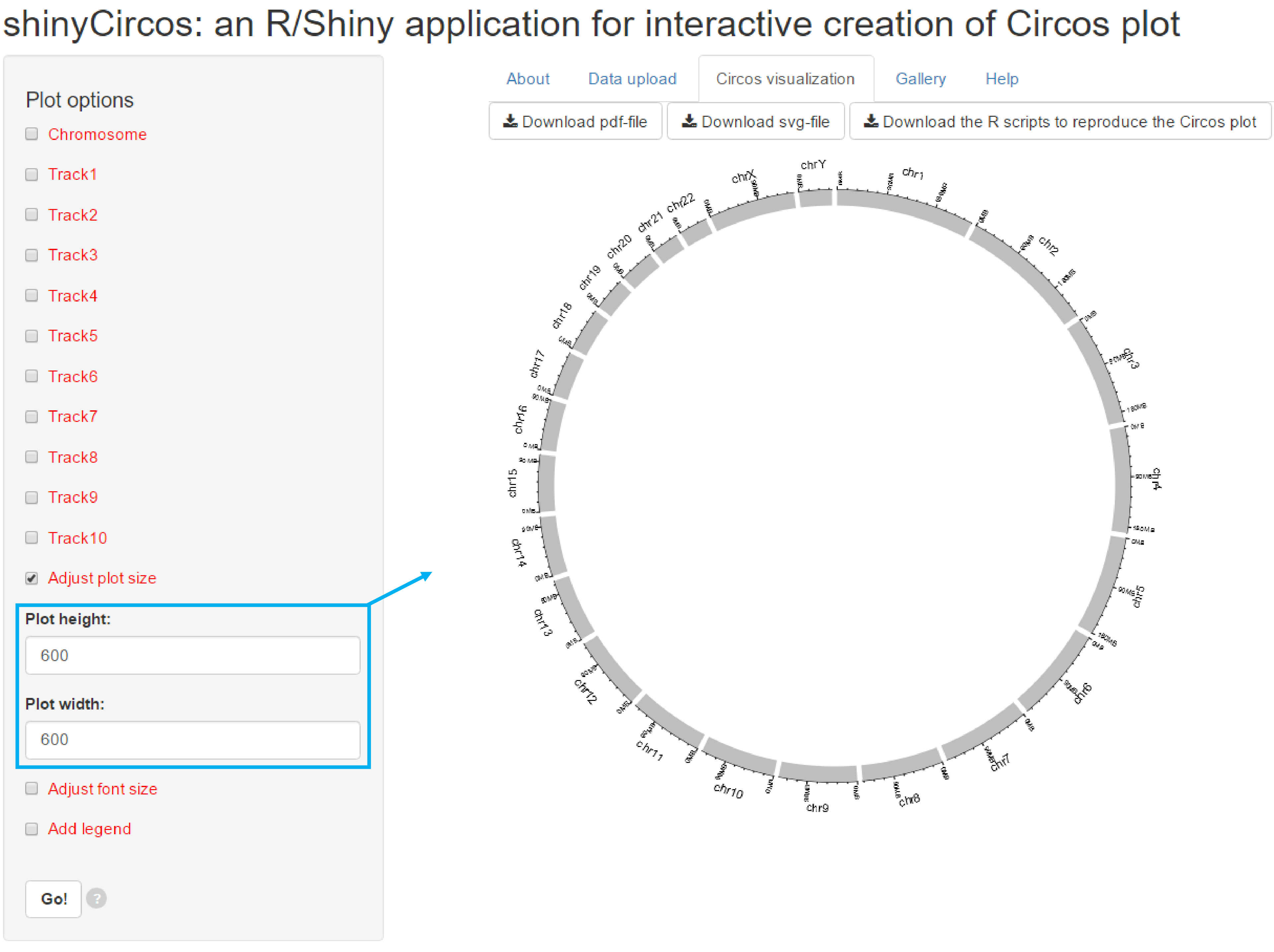
- ☐ Chromosome
- ☐ Track1
- ☐ Track2
- ☐ Track3
- ☐ Track4
- ☐ Track5
- ☐ Track6
- ☐ Track7
- ☐ Track8
- ☐ Track9
- ☐ Track10
- ☑ Adjust plot size

**Plot height:** 750

**Plot width:** 750

Users can adjust the height and width of the Circos plot.

The figure size in both the browser and the download files would be affected.



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☐ Chromosome

☐ Track1

☐ Track2

☐ Track3

☐ Track4

☐ Track5

☐ Track6

☐ Track7

☐ Track8

☐ Track9

☐ Track10

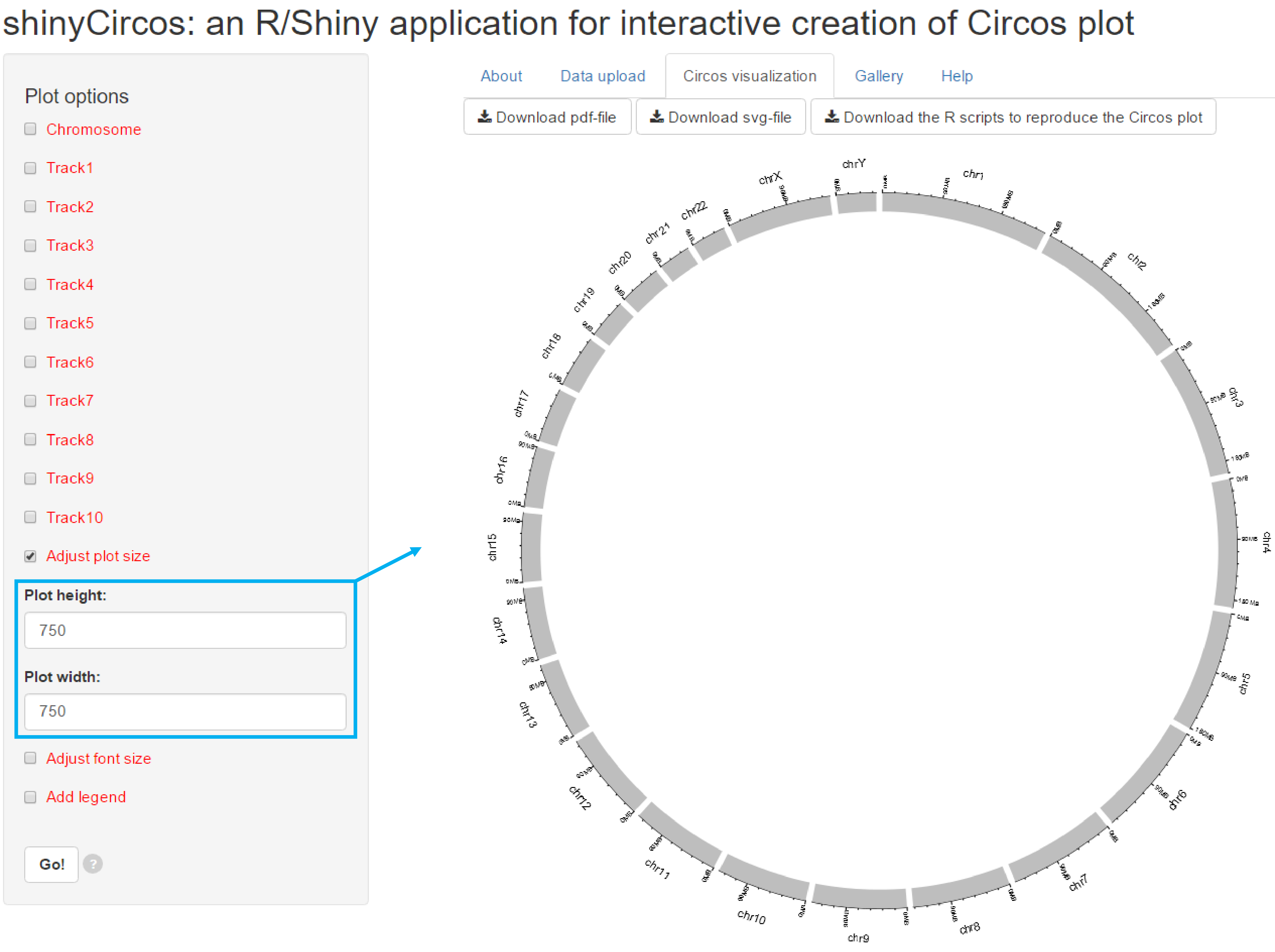
☑ Adjust plot size

**Plot height:** 600

**Plot width:** 600

☐ Adjust font size

☐ Add legend



# shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☐ Chromosome

☐ Track1

☐ Track2

☐ Track3

☐ Track4

☐ Track5

☐ Track6

☐ Track7

☐ Track8

☐ Track9

☐ Track10

☑ Adjust plot size

**Plot height:** 750

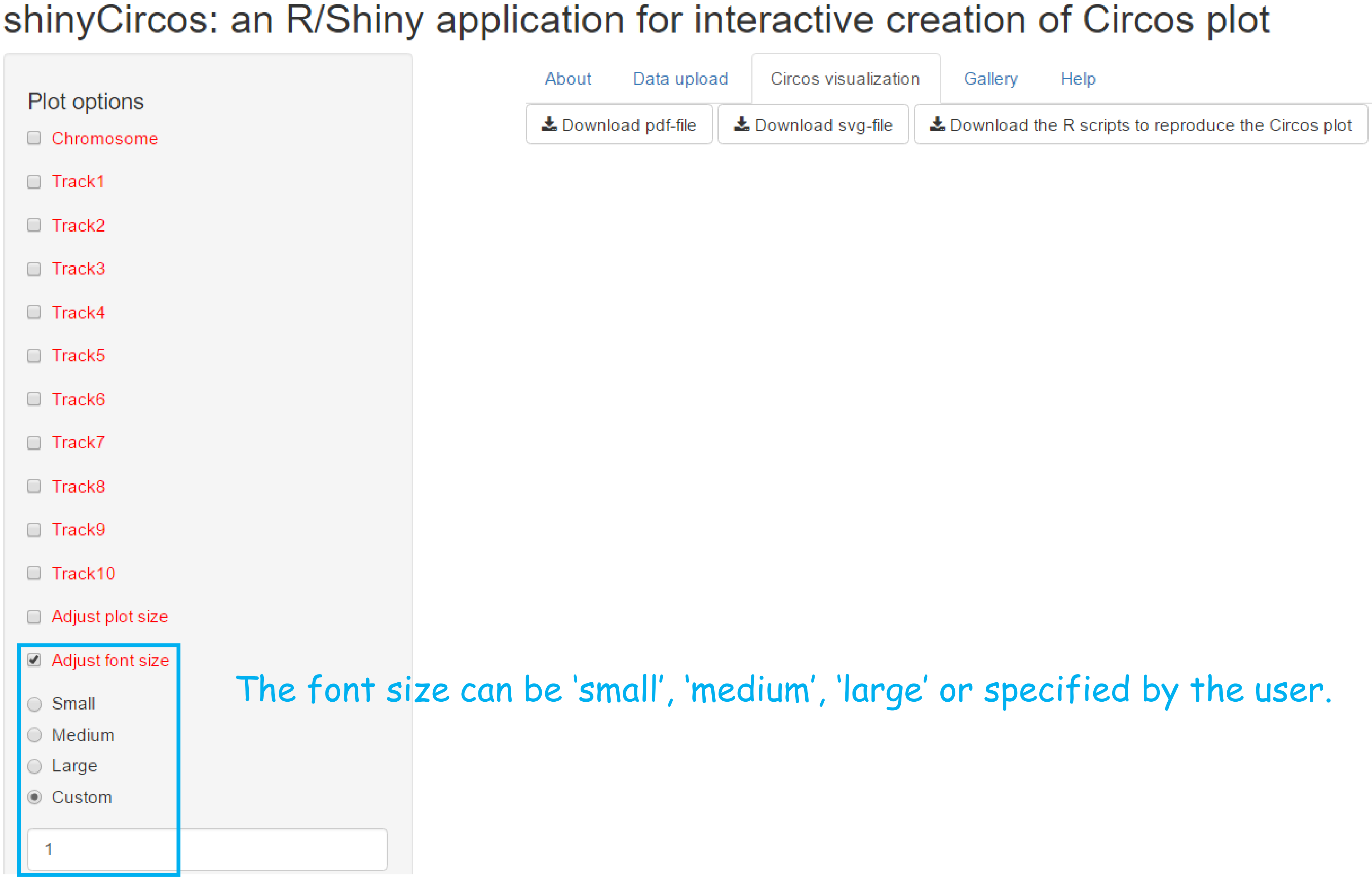
**Plot width:** 750

☐ Adjust font size

☐ Add legend

## 3.2 Font size

# Options



Plot options

☐ Chromosome

☐ Track1

☐ Track2

☐ Track3

☐ Track4

☐ Track5

☐ Track6

☐ Track7

☐ Track8

☐ Track9

☐ Track10

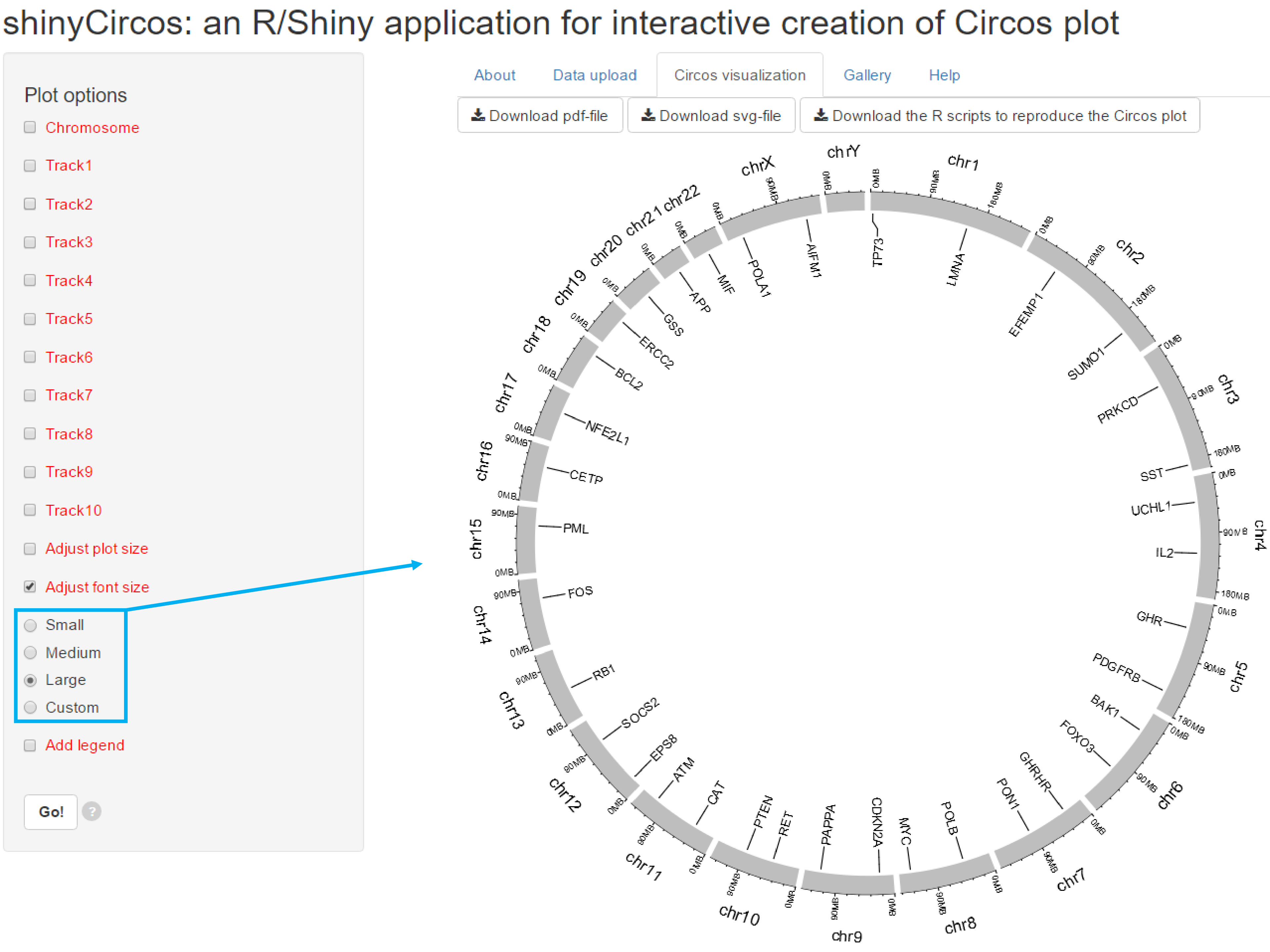
☐ Adjust plot size

☑ Adjust font size

○ Small
○ Medium
○ Large
● Custom

1

The font size can be 'small', 'medium', 'large' or specified by the user.



# shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☐ Chromosome

☐ Track1

☐ Track2

☐ Track3

☐ Track4

☐ Track5

☐ Track6

☐ Track7

☐ Track8

☐ Track9

☐ Track10

☐ Adjust plot size

☑ Adjust font size

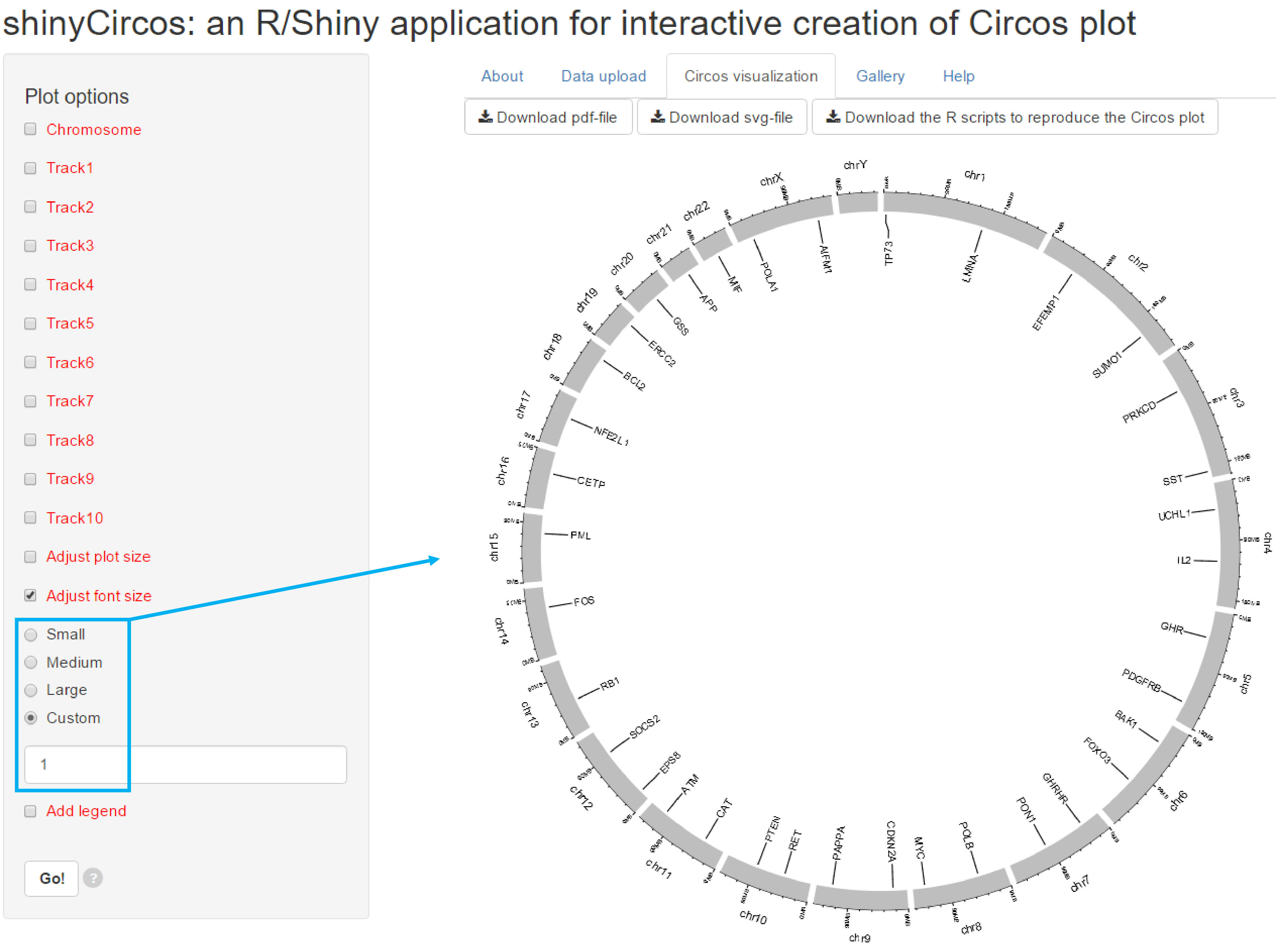
○ Small

○ Medium

● Large

○ Custom

☐ Add legend



# shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

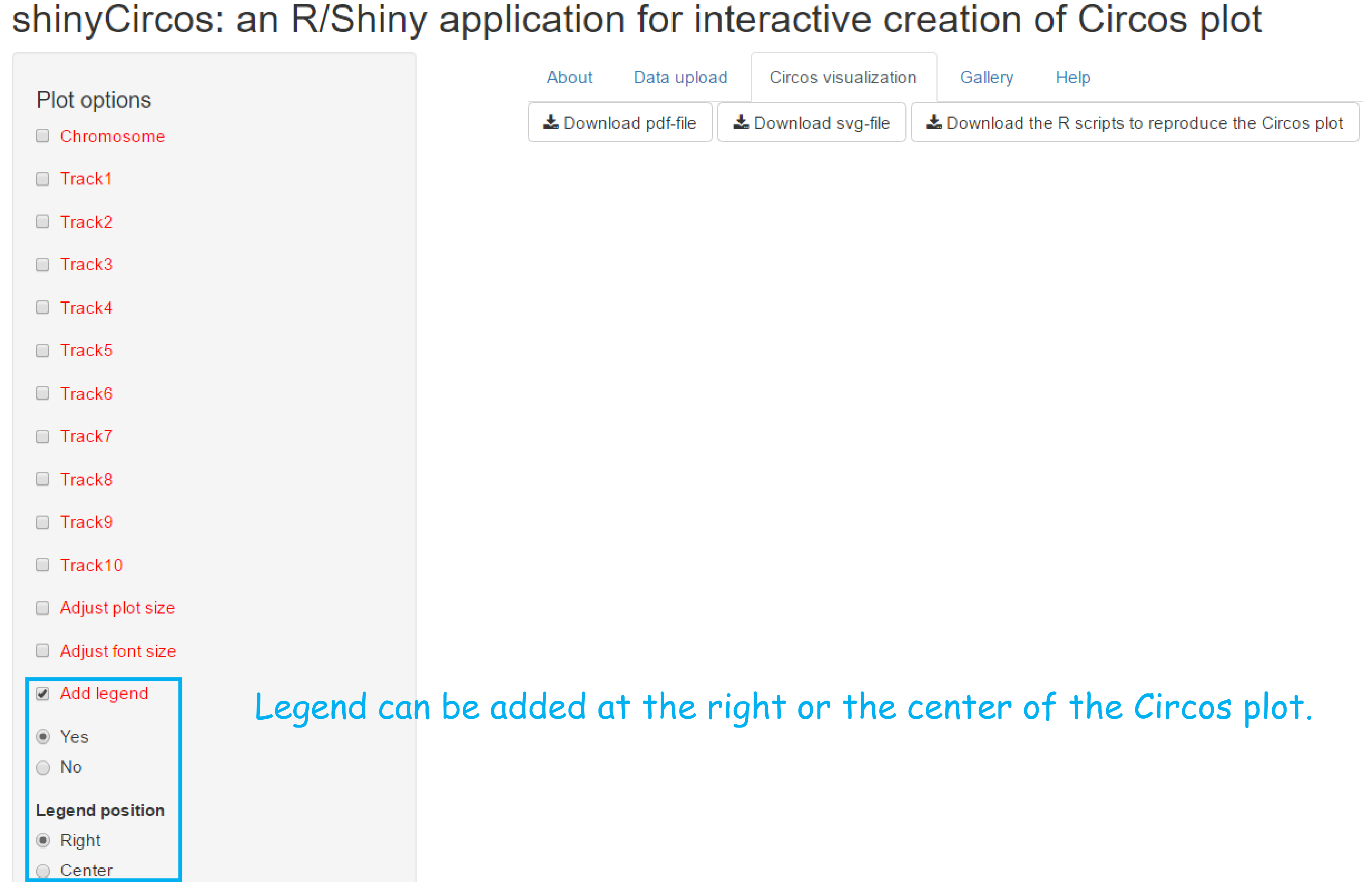
- ☐ Chromosome
- ☐ Track1
- ☐ Track2
- ☐ Track3
- ☐ Track4
- ☐ Track5
- ☐ Track6
- ☐ Track7
- ☐ Track8
- ☐ Track9
- ☐ Track10
- ☐ Adjust plot size
- ☑ Adjust font size
  - ○ Small
  - ○ Medium
  - ○ Large
  - ● Custom

1

- ☐ Add legend

# 3.3 Legend

# Options



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☐ Chromosome

☐ Track1

☐ Track2

☐ Track3

☐ Track4

☐ Track5

☐ Track6

☐ Track7

☐ Track8

☐ Track9

☐ Track10

☐ Adjust plot size

☐ Adjust font size

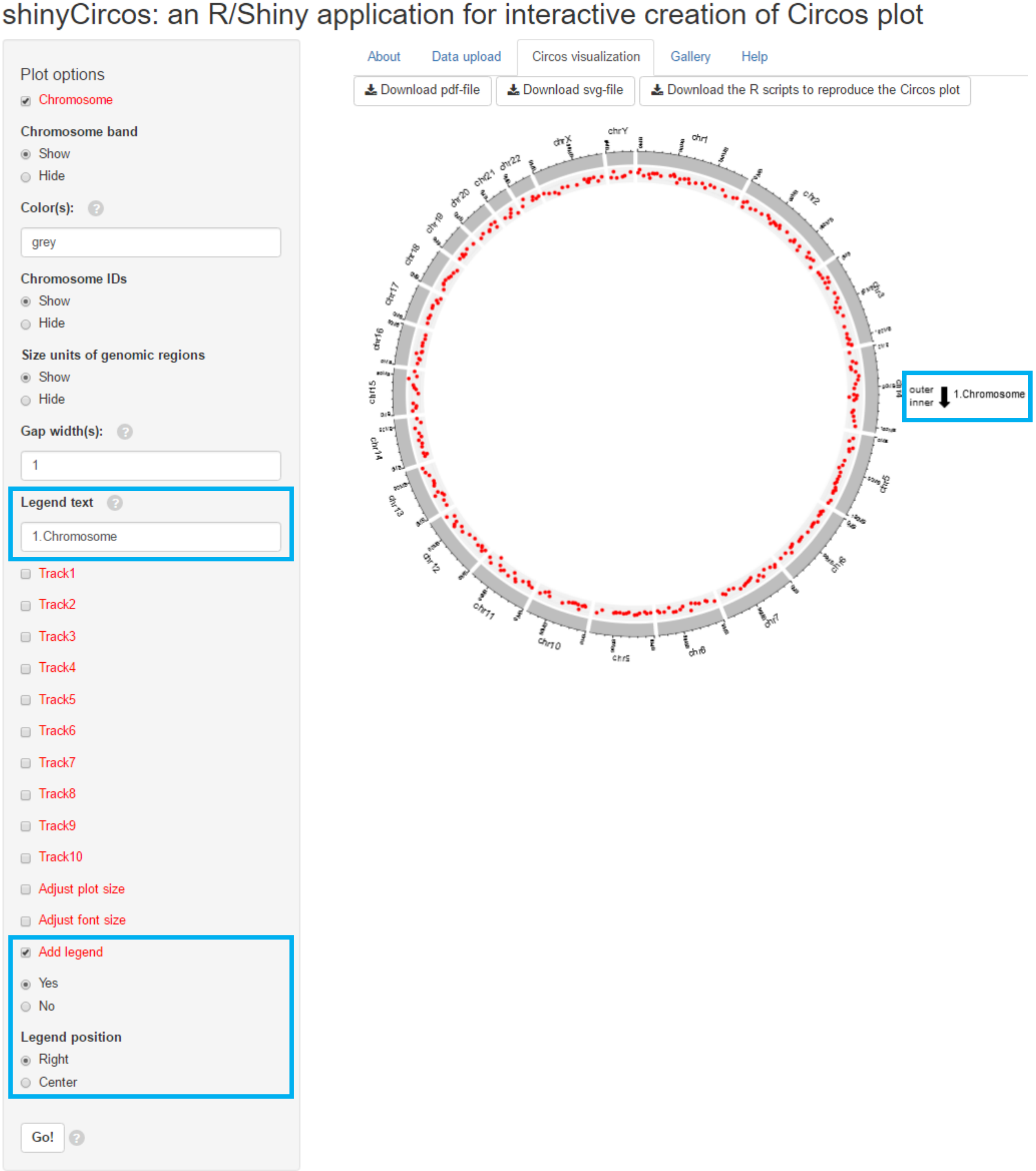
☑ Add legend

● Yes
○ No

**Legend position**

● Right
○ Center

Legend can be added at the right or the center of the Circos plot.



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☑ Chromosome

Chromosome band
● Show
○ Hide

Color(s):
grey

Chromosome IDs
● Show
○ Hide

Size units of genomic regions
● Show
○ Hide

Gap width(s):
1

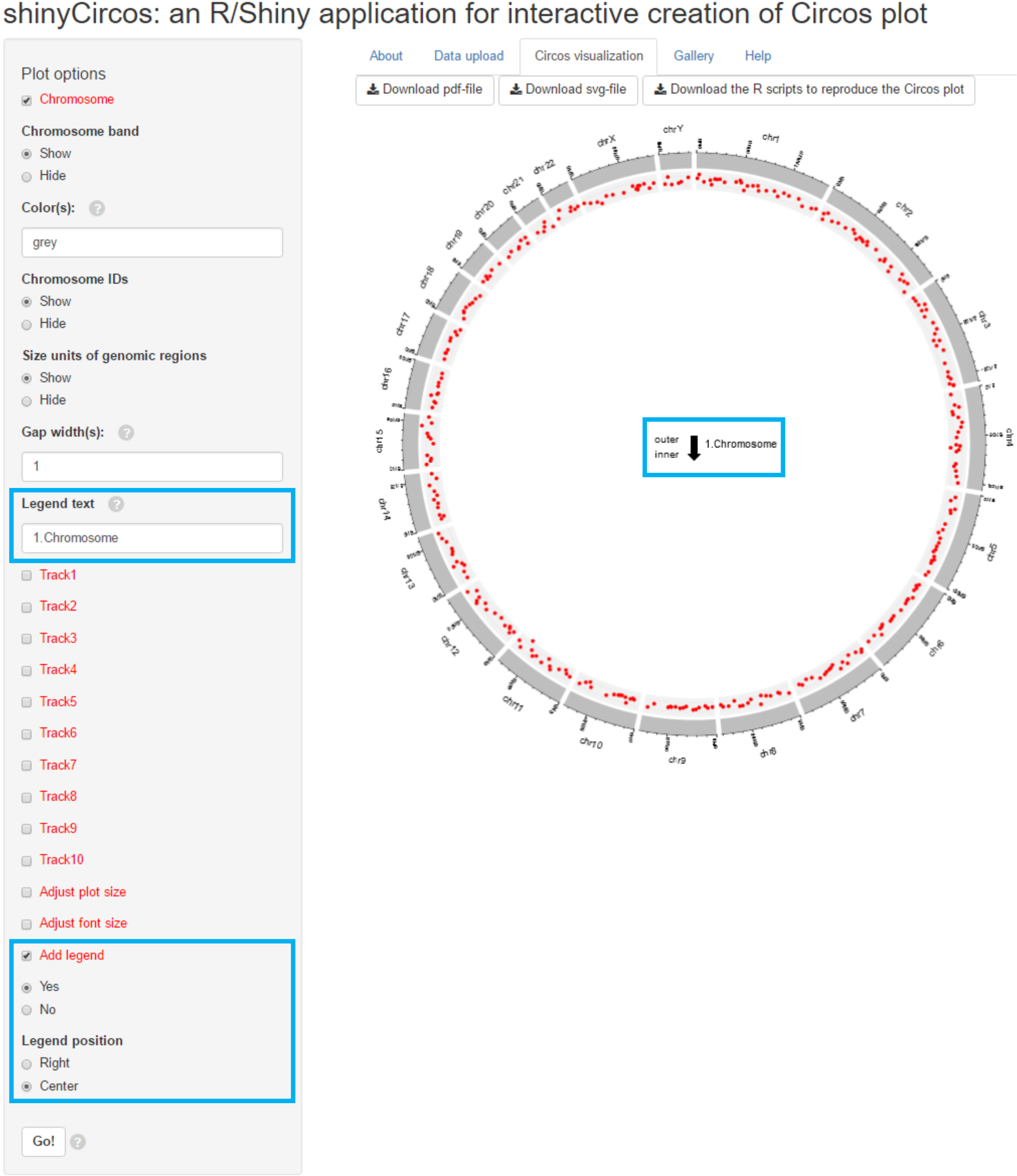
Legend text
1.Chromosome

☐ Track1
☐ Track2
☐ Track3
☐ Track4
☐ Track5
☐ Track6
☐ Track7
☐ Track8
☐ Track9
☐ Track10
☐ Adjust plot size
☐ Adjust font size
☑ Add legend
● Yes
○ No

Legend position
● Right
○ Center

Input legend text

Legend option



shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

☑ Chromosome

Chromosome band
● Show
○ Hide

Color(s): grey

Chromosome IDs
● Show
○ Hide

Size units of genomic regions
● Show
○ Hide

Gap width(s): 1

Legend text: 1.Chromosome

☐ Track1
☐ Track2
☐ Track3
☐ Track4
☐ Track5
☐ Track6
☐ Track7
☐ Track8
☐ Track9
☐ Track10
☐ Adjust plot size
☐ Adjust font size

☑ Add legend
● Yes
○ No

Legend position
○ Right
● Center

Input legend text

Legend option