

shinyCircos-V2.0: Leveraging the creation of Circos plot with enhanced usability and advanced features

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Introduction

Circos

- Display genomic data in circular format
- Demonstrate similarities or differences among genomes
- Display SNP, Indel, gene distribution, DNA methylation, etc.
- Krzywinski et al. Genome Research, 2009
- 8633 citations
- <http://circos.ca/>



The screenshot shows the Circos website interface. At the top, there is a navigation bar with links: GET HELP, GET STARTED, BEST PRACTICES, TUTORIALS, COURSE, SAMPLES, DOWNLOAD. Below this is a secondary navigation bar with links: GUIDE, IMAGES, SOFTWARE, DOCUMENTATION, PRESENTATIONS, NEWS, CITATIONS, SUPPORT, CIRCOS ONLINE. The main content area features a circular genomic plot with various tracks and a legend for CpG methylation. To the right, there is a news article snippet titled "NYT ARTICLE - MAPPING THE EPIGENOME". Below the plot, there is a section titled "DOWNLOAD CIRCOS, TUTORIALS AND TOOLS" with sub-sections for "HOW IS CIRCOS DISTRIBUTED?", "BUG REPORTS", "LICENSE", and "FILES".

Measuring CpG methylation
Bar charts indicate the average amount of CpG methylation found within the tested areas. Each chart covers 100,000 base pairs. Some charts have been shifted, shown with connecting lines.

AMOUNT OF METHYLATION
0 to 20%
20 to 80%
80 to 100% of CpG sites

NYT ARTICLE - MAPPING THE EPIGENOME
In collaboration with Jonathan Corum from the NYT, Martin Krzywinski created an illustration of data showing methylation on chromosome 22 in a variety of tissues. The illustration accompanies the article [Now: The Rest of the Genome](#), by Carl Zimmer.

DOWNLOAD CIRCOS, TUTORIALS AND TOOLS

HOW IS CIRCOS DISTRIBUTED?
Circos is distributed in three *independent* archives: Circos core, tutorials and tools. To do anything, you'll need the [Circos core code distribution](#), which contains the main code, fonts, global configuration and an example. Neither the tutorials nor tools are included in this file. To learn how to use circos, [download the tutorials](#), which contain many examples to demonstrate Circos' features. These tutorials are also [available online](#). Several, [utility add-on scripts](#) are available, such as for bundling links. These are not necessary for Circos, but helpful in carrying out common data reduction and analysis tasks. Tools are described in the [Tools Tutorial](#).

BUG REPORTS
Please direct bug reports, comments and questions to the [Circos Google group](#). To help resolve the problem faster, [send me your conf/data files](#). Do not forget to include *all* the files, including karyotype.

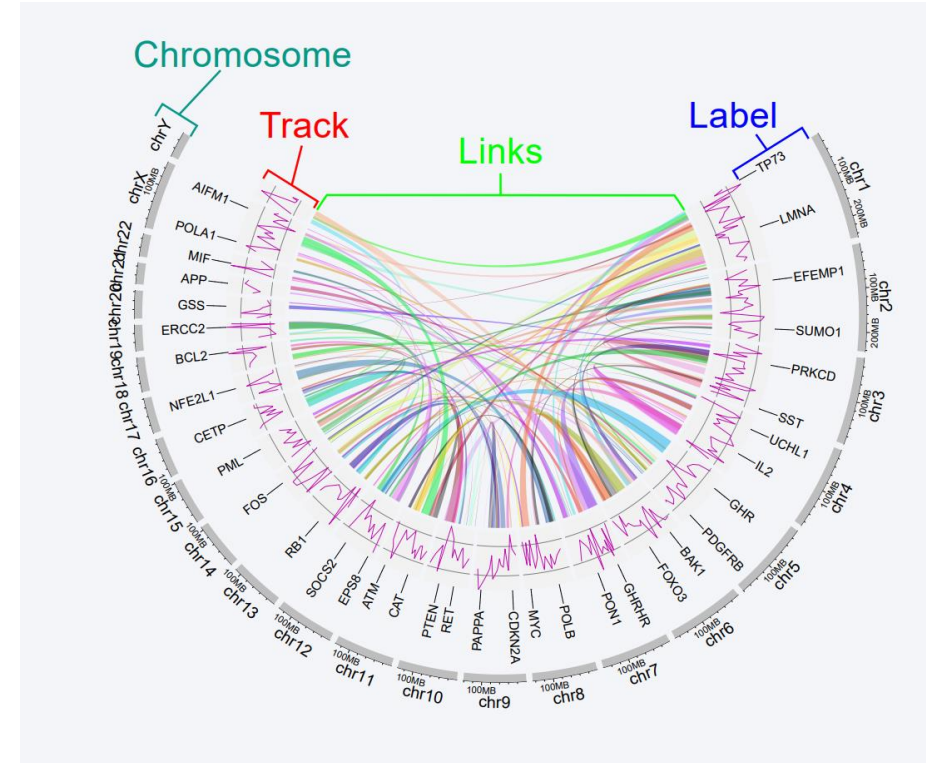
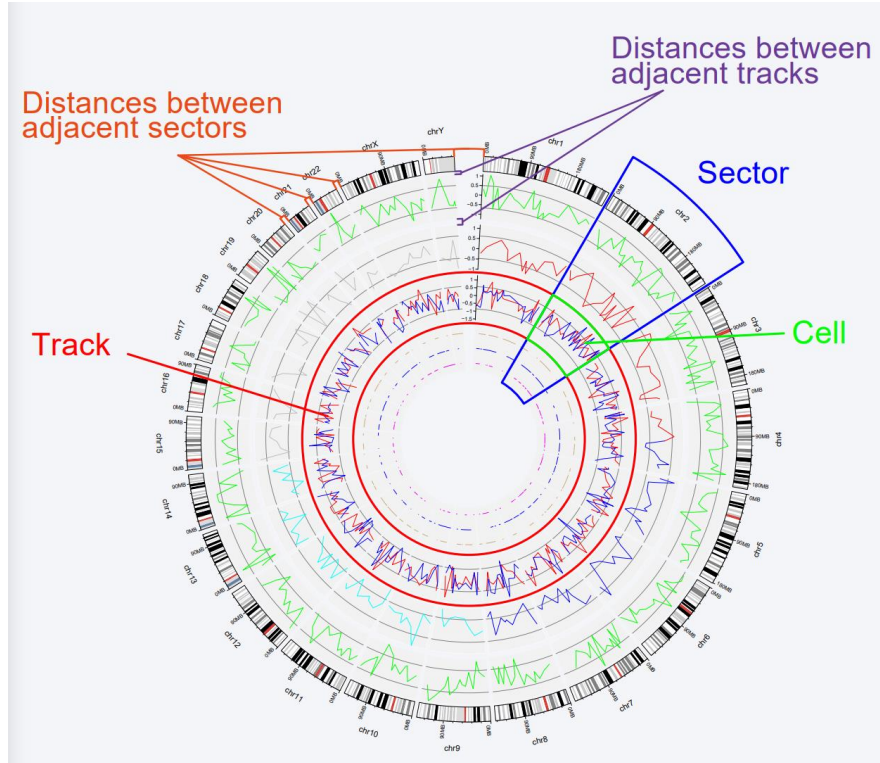
LICENSE
Circos and all associated materials are licensed under [GNU General Public License \(GPL\) v3](#).

FILES

FILE	VERSION	SIZE	DATE	COMMENT
circos-0.69-9.tgz	0.69-9	29,794,907	Wed Jul 3 09:41:16 2019	circos-0.69-9.tgz is a bug release.
circos-current.tgz				
circos-0.69-8.tgz	0.69-8	29,784,059	Sat Jun 15 20:15:18 2019	circos-0.69-8.tgz is a bug release.

Introduction

The basic structure of a Circos graph



Concepts in Circos Diagram:

- Track
- Sector
- Cell
- Links

Introduction

Circos was originally created as a command-line tool using the Perl programming language. Similar tools were developed using other programming languages.

Existing tools that can be used to make Circos diagrams:

- Circos, Perl, <http://circos.ca/>
- circlize, R, https://jokergoo.github.io/circlize_book/book/
- shinyCircos-V1, R, <https://venyao.xyz/shinyCircos-V1/>
- BioCircos.js, Javascript, <http://bioinfo.ibp.ac.cn/biocircos/index.php>
- Circleator, Perl, <https://jonathancrabtree.github.io/Circleator/>
- CIRCUS, R, <https://bmcbioinformatics.biomedcentral.com/articles/10.1186/1471-2105-15-198>
- interacCircos, R, <https://github.com/mrcuizhe/interacCircos/>
- NG-Circos, Javascript, <https://github.com/YaCui/NG-Circos>
- Galactic Circos, Javascript, <https://doi.org/10.1093/gigascience/giaa065>
- TBtools, Java, <https://github.com/CJ-Chen/TBtools>

Introduction

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

About

About Data upload Circos visualization Gallery Help

• 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. *circize: 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. Burrow, 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 (yimingyu at gmail.com). This application uses the shiny package from RStudio.

• Please cite

Yiming Yu, Yidan Ouyang, and Wen Yao. shinyCircos: an R/Shiny application for interactive creation of Circos plot. *Bioinformatics*. 2017 Nov. 24. doi:10.1093/bioinformatics/btx763



Welcome to shinyCircos-V2.0!

The Circos diagram was born in 2009, which was published by Martin Krzywinski as a visualization tool in *Genome Research* for comparative genomics. Since then, the Circos diagram has made frequent appearances in international renowned journals, including Nature, Science, Cell, etc.

shinyCircos is a web application for creation of Circos plot developed by Yu et al in 2017, which has been recognized by many users for its graphical user interface and ease of use.

shinyCircos-V2.0 is the updated version of shinyCircos. In shinyCircos-V2.0, we developed several advanced features, designed brand-new user interface, and fixed bugs detected in shinyCircos.

The structure of a Circos diagram is shown in the figure below.

The basic structure of a Circos diagram.

Different tracks of a Circos diagram.

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shinyCircos-V1

- <https://venyao.xyz/shinyCircos-V1/>
- Yu et al. *Bioinformatics*, 2018

shinyCircos-V2.0

- <https://venyao.xyz/shinyCircos/>

Optimized GUI

Home

Welcome to shinyCircos-V2.0!

The shinyCircos application is a RShiny web application that is easy to use and can be used to generate Circos plots. It is a web application that is easy to use and can be used to generate Circos plots. It is a web application that is easy to use and can be used to generate Circos plots.

The basic structure of a Circos diagram. Different tracks of a Circos diagram.

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Data Upload

Step 1. Upload input data or load example input data!

Step 2. Upload one or multiple input datasets!

Step 3. Please distribute the uploaded datasets to appropriate data groups!

Condition name	Chromosome data	Track data	Label data	Link data	Settings
	chromosome_generator	highlight_color	gene_label_color	link_color	

Step 2.1. Save uploaded data. Step 3. Submit the uploaded datasets.

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Circos Parameters

Step 4. Submit the plot parameters to render the Circos plot!

Chromosome data type: chromosome

Plot type: plot

Track index: 1

Label index: 1

Data format: use default track colors

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Circos Plot

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Gallery

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Help

Section: Introduction

Input data format

Chromosome data used to define the chromosomes of a Circos plot

chr	start	end
chr1	1	100000000
chr2	1	100000000
chr3	1	100000000
chr4	1	100000000
chr5	1	100000000
chr6	1	100000000

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About

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Further references

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Contact

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Basic steps to make a Circos plot

The first step to make a Circos plot using shinyCircos-V2.0:

- Decide whether to use a predefined reference genome
- Upload the input dataset in one go or in batches on the "Data Upload" page
- Distribute the input data correctly and click the button to save the data
- Click the Submit button to submit the data to the server



The screenshot displays the 'shinyCircos-V2.0' web application interface. On the left is a navigation menu with options: Data Upload (highlighted), Circos Parameters, Circos Plot, Gallery, Help, About, and Contact. The main content area shows a three-step process:

- Step 1. Upload input data or load example input data?** Includes a dropdown for 'Upload input data' and a toggle for 'Use a predefined reference genome?' set to 'No'.
- Step 2. Upload one or multiple input datasets:** Shows a file browser with 'links.csv' selected and an 'Upload complete' status bar.
- Step 3.1. Please distribute the uploaded datasets to appropriate data groups:** Features five input fields for data distribution: 'Candidate area' (empty), '* Chromosome data' (containing 'chromosome_general.csv'), 'Track data' (containing 'barplot.csv'), 'Label data' (containing 'gene_label.csv'), and 'Links data' (containing 'links.csv'). Below these is a 'Garbage' field.

At the bottom, there are two buttons: 'Step 2.2. Save uploaded data' and 'Step 3. Submit the uploaded datasets!'. The footer contains the copyright notice: 'Copyright © 2021 Wen Yao, College of Life Sciences, Henan Agricultural University'.

Basic steps to make a Circos plot

The second step to make a Circos plot using shinyCircos-V2.0:

- Set the plot type for individual track data
- Set the track index
- Set the drawing parameters for the track
- Set the index to draw the label and the drawing parameters of the label
- Set plotting parameters for links data
- Click the Submit button to make the Circos plot



shinyCircos-V2.0

- Data Upload
- Circos Parameters**
- Circos Plot
- Gallery
- Help
- About
- Contact

● Chromosome data (used to define the chromosomes of a Circos plot)

▶ File name ? chromosome_general.csv

▶ Chromosome data type ? general data

● Track data (to be displayed in different tracks of a Circos plot)

▶ File name ? barplot.csv

▶ Plot type ? point

▶ Track index ? 1

● Label data (used to label elements in a track)

▶ File name ? gene_label.csv

▶ Label index ? 1

● Link data (used to create links in a Circos plot)

▶ File name ? links.csv

▶ Data format ? Data without a 'color' column

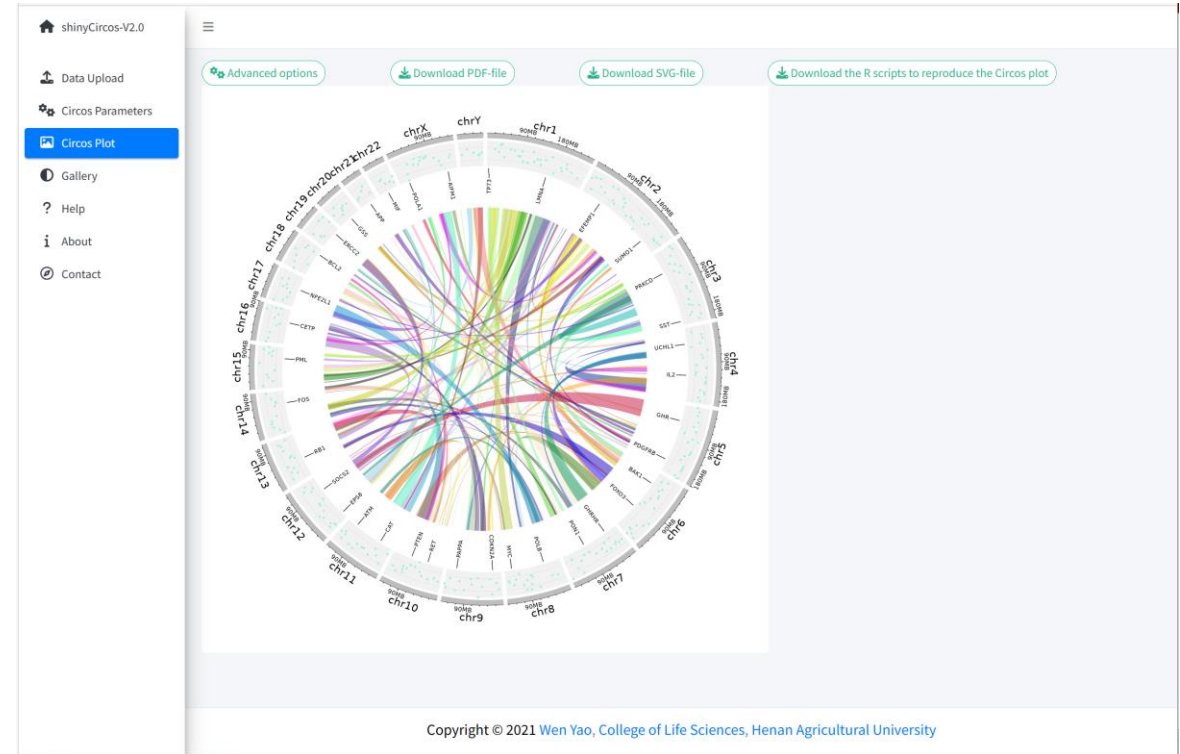
▶▶ Step 4. Submit the plot parameters to make the Circos plot!

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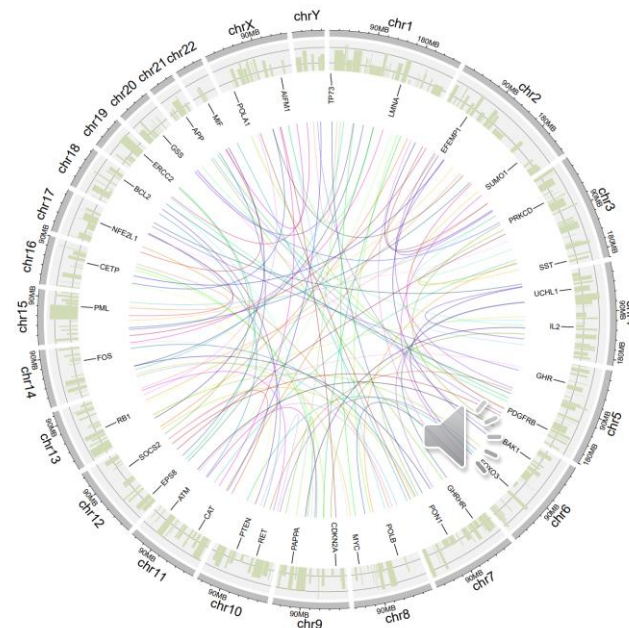
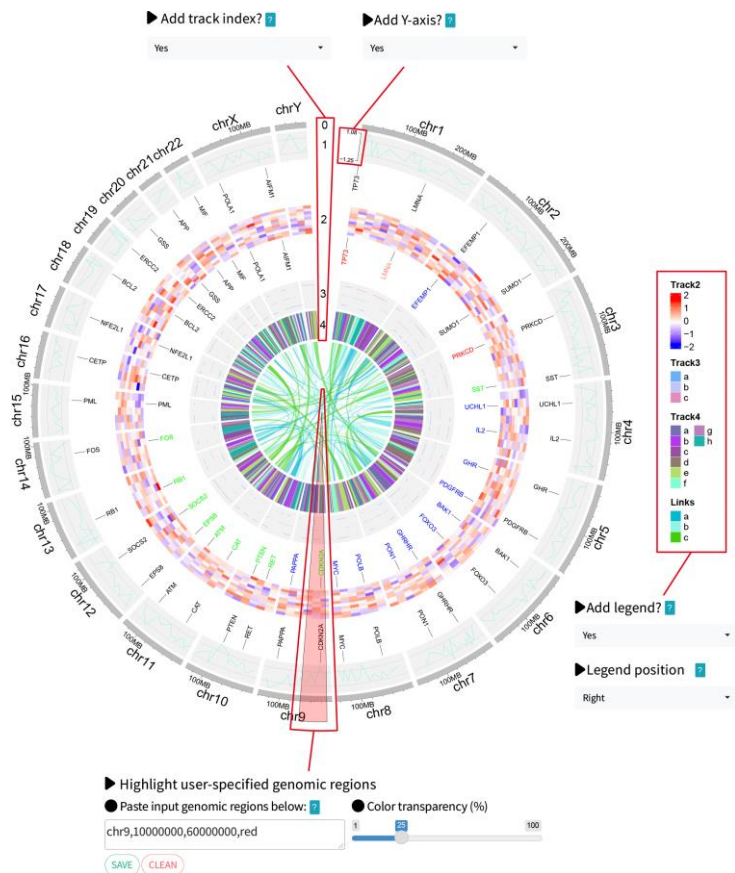
Basic steps to make a Circos plot

The third step to make a Circos plot using shinyCircos-V2.0:

- Generate a Circos graph on the "Circos Plot" page
- PDF or SVG files can be downloaded
- Advanced parameters of the Circos graph can be tuned
- R script can be downloaded



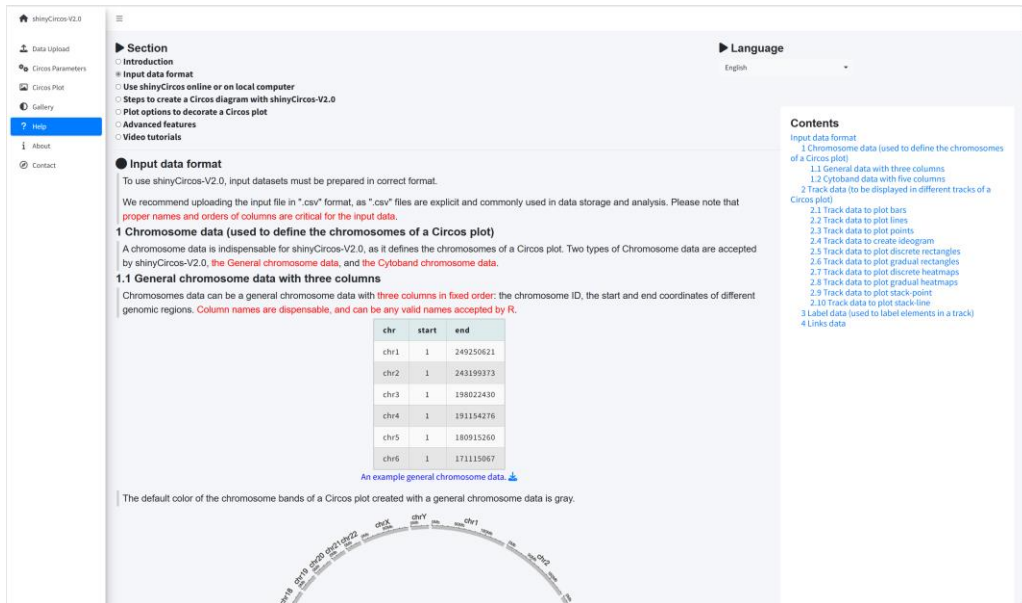
Advanced features of shinyCircos-V2.0



- Support for adding track index
- Support adding the Y axis of Track
- Support for highlighting specific areas
- Support for adding legends
- Support drawing links according to the midpoint
-

Help tutorial

Detailed help tutorial (in Chinese and English)



shinyCircos-V2.0

Section

- Introduction
- Input data format
- Steps to create a Circos diagram with shinyCircos-V2.0
- Plot options to decorate a Circos plot
- Advanced features
- Video tutorials

Language: English

Input data format

To use shinyCircos-V2.0, input datasets must be prepared in correct format.

We recommend uploading the input file in ".csv" format, as ".csv" files are explicit and commonly used in data storage and analysis. Please note that **proper names and orders of columns are critical for the input data.**

1 Chromosome data (used to define the chromosomes of a Circos plot)

A chromosome data is indispensable for shinyCircos-V2.0, as it defines the chromosomes of a Circos plot. Two types of Chromosome data are accepted by shinyCircos-V2.0, the **General chromosome data**, and the **Cytoband chromosome data**.


1.1 General chromosome data with three columns

Chromosomes data can be a general chromosome data with **three columns in fixed order**: the chromosome ID, the start and end coordinates of different genomic regions. **Column names are dispensable, and can be any valid names accepted by R.**

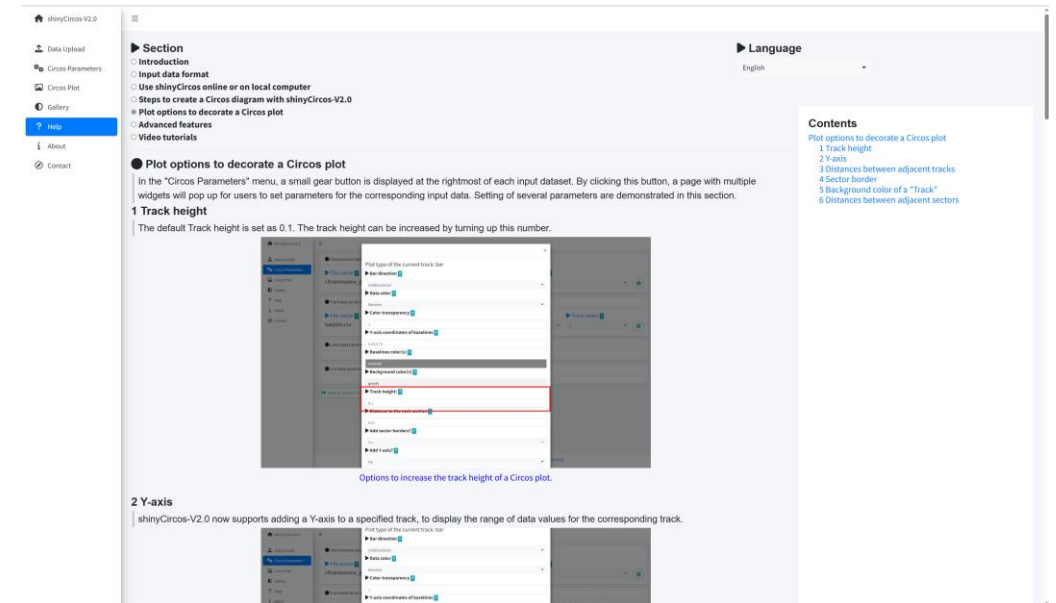
chr	start	end
chr1	1	249250621
chr2	1	243199373
chr3	1	198022430
chr4	1	191154276
chr5	1	180915260
chr6	1	171115067

An example general chromosome data. [Download](#)

The default color of the chromosome bands of a Circos plot created with a general chromosome data is gray.



Basic description of the input data format



shinyCircos-V2.0

Section

- Introduction
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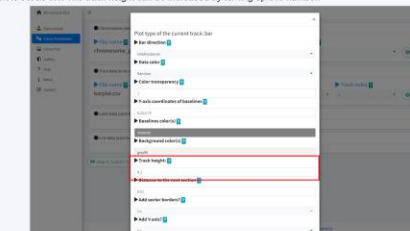
Language: English

Plot options to decorate a Circos plot

In the "Circos Parameters" menu, a small gear button is displayed at the rightmost of each input dataset. By clicking this button, a page with multiple widgets will pop up for users to set parameters for the corresponding input data. Setting of several parameters are demonstrated in this section.

1 Track height


The default Track height is set as 0.1. The track height can be increased by turning up this number.



Options to increase the track height of a Circos plot.

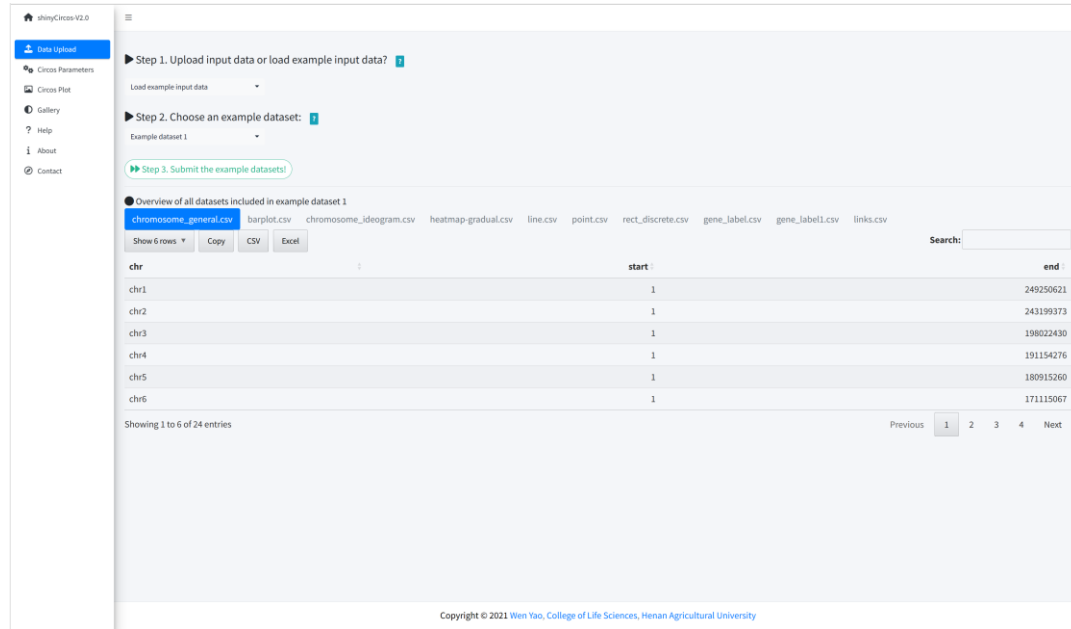
2 Y-axis

shinyCircos-V2.0 now supports adding a Y-axis to a specified track, to display the range of data values for the corresponding track.



Detailed instructions of the essential steps to make a Circos plot

Example input dataset




The screenshot shows the 'shinyCircos-V2.0' interface. The 'Data Upload' step is active, with instructions to upload input data or load example input data. Below this, there are steps for choosing an example dataset and submitting them. A table titled 'Overview of all datasets included in example dataset 1' is displayed, listing various CSV files. The 'chromosome_general.csv' file is selected, and its contents are shown in a table below.

chr	start	end
chr1	1	249250621
chr2	1	243199373
chr3	1	198022430
chr4	1	191154276
chr5	1	180915260
chr6	1	171115067

Showing 1 to 6 of 24 entries

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Ten example input datasets



The screenshot shows the 'shinyCircos-V2.0' interface with the 'Gallery' step active. It displays a grid of 30 example Circos diagrams, labeled 'Example 1' through 'Example 30'. Each diagram is accompanied by a download link for its input files. The diagrams are arranged in a 4x5 grid, with the last row containing only 6 diagrams.

30 Circos diagrams created using shinyCircos-V2.0 and their input datasets

Summary

- **Source code:** <https://github.com/YaoLab-Bioinfo/shinyCircos-V2.0>
- **Online use:** <https://venyao.xyz/shinyCircos/>
- **Online use :** <https://asiawang.shinyapps.io/shinyCircos/>
- **Contact:** gentelmanwang@gmail.com or yaowen@henau.edu.cn
- **Citation:** Wang et al. *iMeta*, 2023

Yazhou Wang, Lihua Jia, Ge Tian, Yihan Dong, Xiao Zhang, Zhengfu Zhou, Xiang Luo, Yang Li, and Wen Yao. 2023. shinyCircos-V2.0: Leveraging the creation of Circos plot with enhanced usability and advanced features. *iMeta* e109. <https://doi.org/10.1002/imt2.109>



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