

shinyCircos-V2.0:易用性提高和功能 增强的Circos图绘制工具

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Circos

- 环形格式展示基因组数据
- 展示基因组特征的相似性或差异性
- 展示SNP、Indel、基因分布、DNA甲基化等
- Krzywinski et al. Genome Research, 2009
- 8633 citations
- <http://circos.ca/>

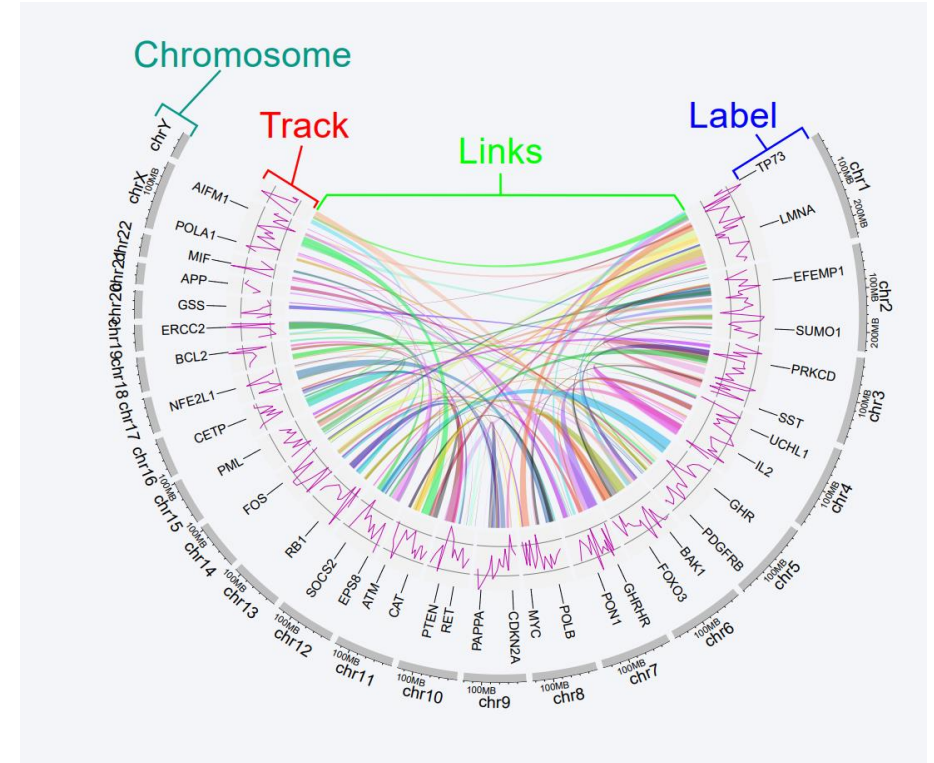
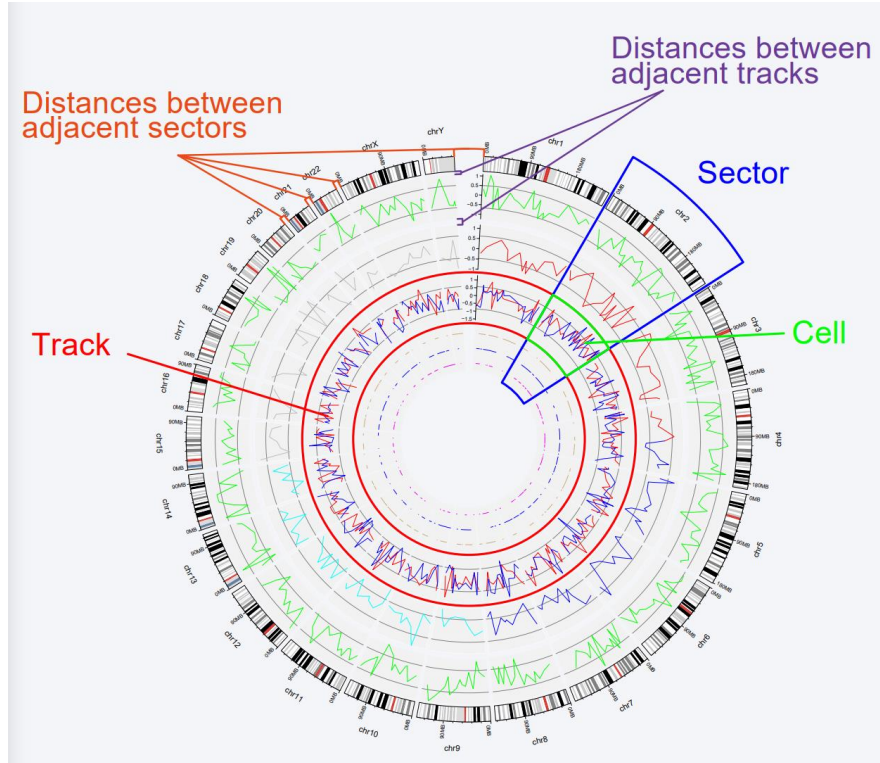


The screenshot shows the Circos website interface. At the top, there is a navigation bar with links for GET HELP, GET STARTED, BEST PRACTICES, TUTORIALS, COURSE, SAMPLES, and DOWNLOAD. Below this is a secondary navigation bar with links for GUIDE, IMAGES, SOFTWARE, DOCUMENTATION, PRESENTATIONS, NEWS, CITATIONS, SUPPORT, and CIRCOS ONLINE. The main content area features a large circular genome plot with various tracks, including CpG methylation levels. A legend indicates the amount of methylation from 0 to 100%. To the right of the plot is a news article titled "NYT ARTICLE - MAPPING THE EPIGENOME" with a sub-headline "Measuring CpG methylation". Below the plot and article, there is a section titled "DOWNLOAD CIRCOS, TUTORIALS AND TOOLS" which includes information about how to distribute Circos, where to find tutorials, and how to report bugs. At the bottom, there is a table listing available files for download.

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	29,784,039	Sat Jun 15 20:15:18 2019	circos-0.69-8.tgz is a bug release.

背景介绍

Circos图的基本结构



Circos图中的基本概念:

- Track (轨道)
- Sector (扇区)
- Cell (单元格)
- Links (连接)

背景介绍

Circos最初是使用Perl编程语言创建的命令行工具，后逐渐发展到其他编程语言。

现有的可用于绘制Circos图的工具：

- 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>

背景介绍

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/>

优化的图形界面

Home

Welcome to shinyCircos-V2.0!

The shinyCircos application is a RShiny web application, which is established by [RStudio](#) as a [cross-platform based browser interface](#) for computer graphics. Here, the Circos diagram track program supports operational interaction, including [Web-based Circos Diagram](#).

shinyCircos-V2.0 is an application for creation of Circos plot developed by [Yao et al. \(2017\)](#), which has been recognized by many users for its practical user interface and ease of use.

shinyCircos-V2.0 is the upgraded version of [shinyCircos](#). In shinyCircos-V2.0, we developed several advanced features, designed from new user interface, and added help document to 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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Data Upload

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

Upload input data:

Step 2. Upload one or multiple input datasets!

Chromosome:

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

Condition name	Chromosome data	Track data	Label data	Link data	Category
	<input type="text" value="Chromosome-general.Chr"/>	<input type="text" value="Sample1.Chr"/>	<input type="text" value="gene_label.Chr"/>	<input type="text" value="Site.Chr"/>	<input type="text" value="Category"/>

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Circos Parameters

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

Chromosome data type:

Plot type:

Track index:

Label index:

Data format:

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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
- General chromosome data with three columns

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

Software references

1. RStudio: an IDE for R. [RStudio Team](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
2. Shiny: web application framework for R. [RStudio Team](#). 2015.
3. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
4. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
5. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
6. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
7. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
8. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
9. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
10. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
11. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
12. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
13. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
14. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
15. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.
16. [RStudio](#). [RStudio: an IDE for R](#). [RStudio Team](#). 2015.

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Contact

Contact us

- If you have any questions or suggestions about this tool, please do not hesitate to contact us.
- E-mail: zhouwen@hainan.edu.cn or genedev@hainan.edu.cn
- QQ group: 484267662
- Wechat group: <https://www.weixin.com/q/484267662>

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绘制Circos图基本步骤

使用shinyCircos-V2.0绘制Circos图的第一步:

- 选择输入数据的类型
- 选择是否使用预定义的参考基因组
- 在“Data Upload”页面一次性或分批上传输入数据集
- 将数据正确分组并点击保存数据
- 点击Submit按钮将数据提交到服务器

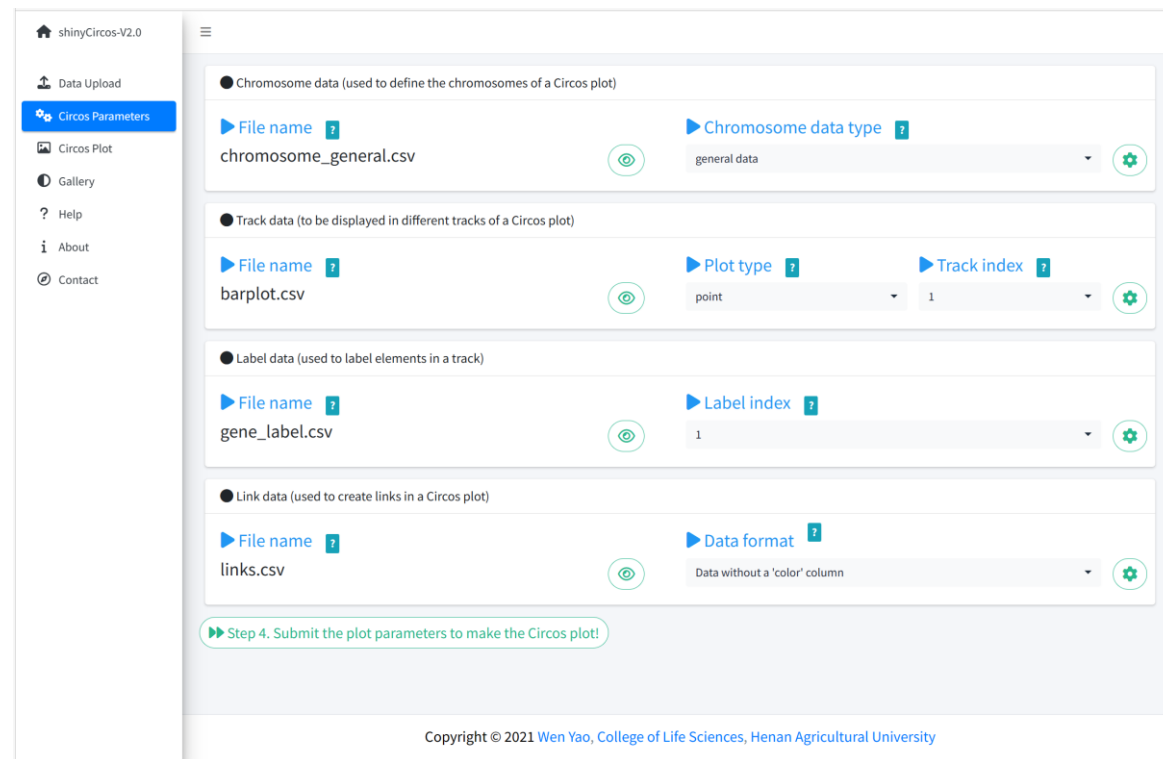


The screenshot displays the 'shinyCircos-V2.0' web application interface. On the left is a navigation sidebar with options: Data Upload (selected), Circos Parameters, Circos Plot, Gallery, Help, About, and Contact. The main content area is titled 'Step 1. Upload input data or load example input data?'. It includes a dropdown for 'Upload input data', a toggle for 'Use a predefined reference genome?' set to 'No', and a 'Step 2. Upload one or multiple input datasets:' section with a 'Browse...' button and a file named 'links.csv' selected. Below this is a 'Step 3.1. Please distribute the uploaded datasets to appropriate data groups:' section with five input fields: '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'). A 'Garbage' field is also present. 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'.

绘制Circos图基本步骤

使用shinyCircos-V2.0绘制Circos图的第二步:

- 设置染色体数据的绘图类型及染色体的绘图参数
- 设置各个轨道数据的绘图类型 (Plot type)
- 设置轨道的索引 (Track index)
- 设置轨道的绘图参数
- 设置绘制标签的索引及标签的绘图参数 (Label data)
- 指定连接数据的数据类型 (Link data)
- 设置连接数据的绘图参数 (Link data)
- 点击绘图按钮绘图



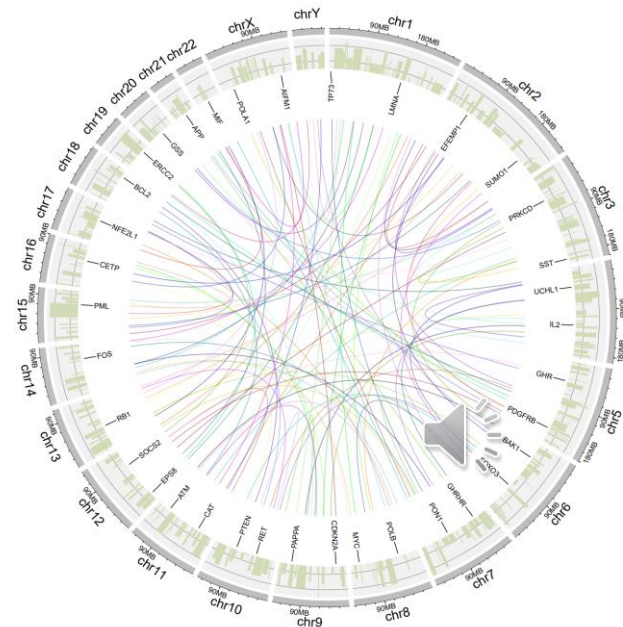
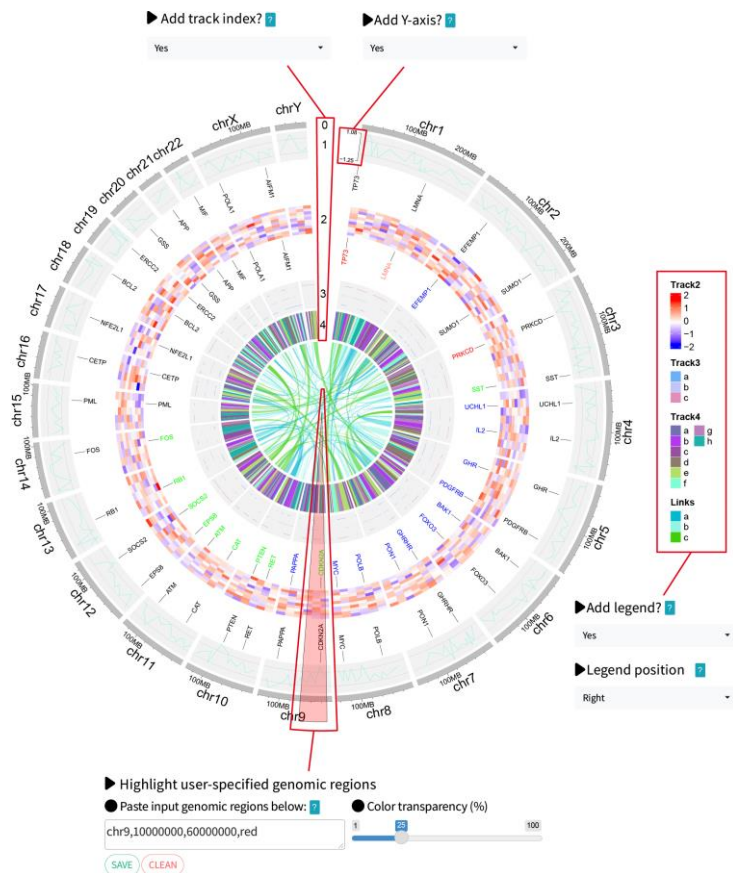
绘制Circos图基本步骤

使用shinyCircos-V2.0绘制Circos图的第三步：

- 在“Circos Plot”页面生成Circos图
- 可以下载PDF或SVG文件
- 可以调整Circos图的高级参数
- 下载R script, 方便用户修改更多细节



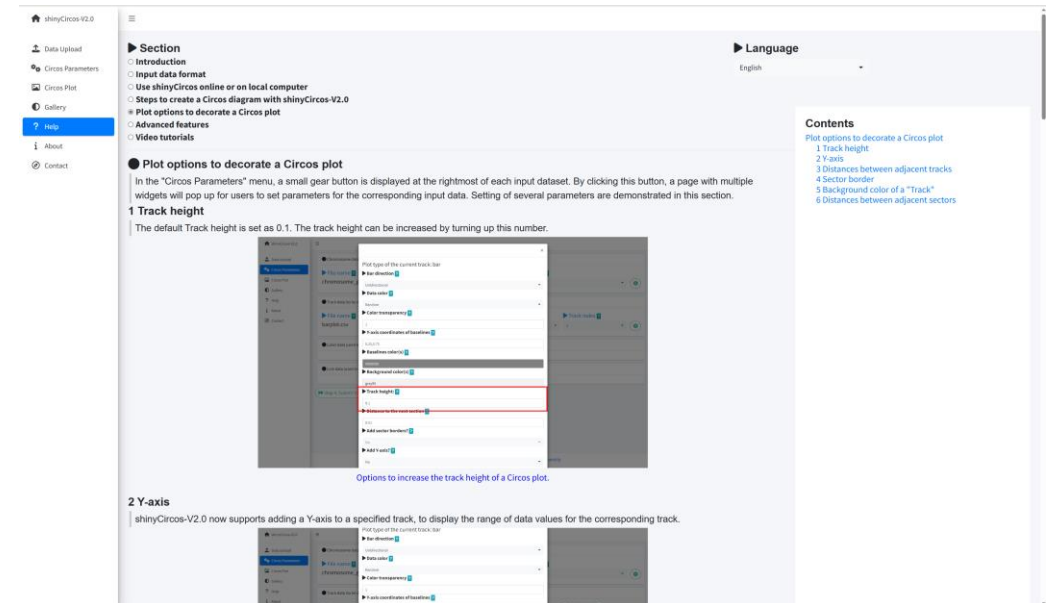
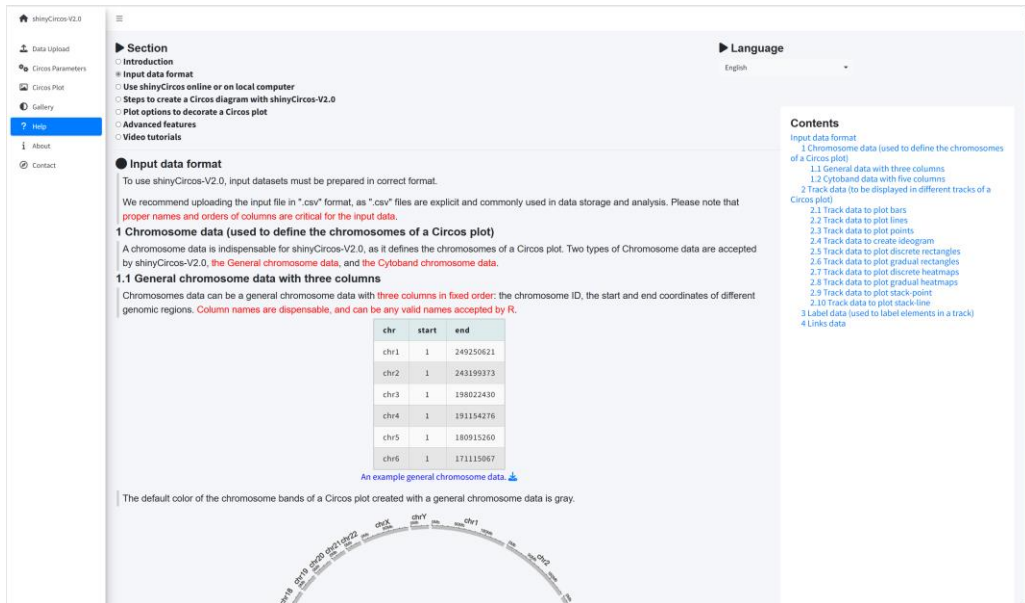
shinyCircos-V2.0的高级功能



- 支持添加轨道索引
- 支持添加轨道的Y坐标轴
- 支持高亮特定区域
- 支持添加图例
- 支持按照中点绘制连接线
-

帮助文档

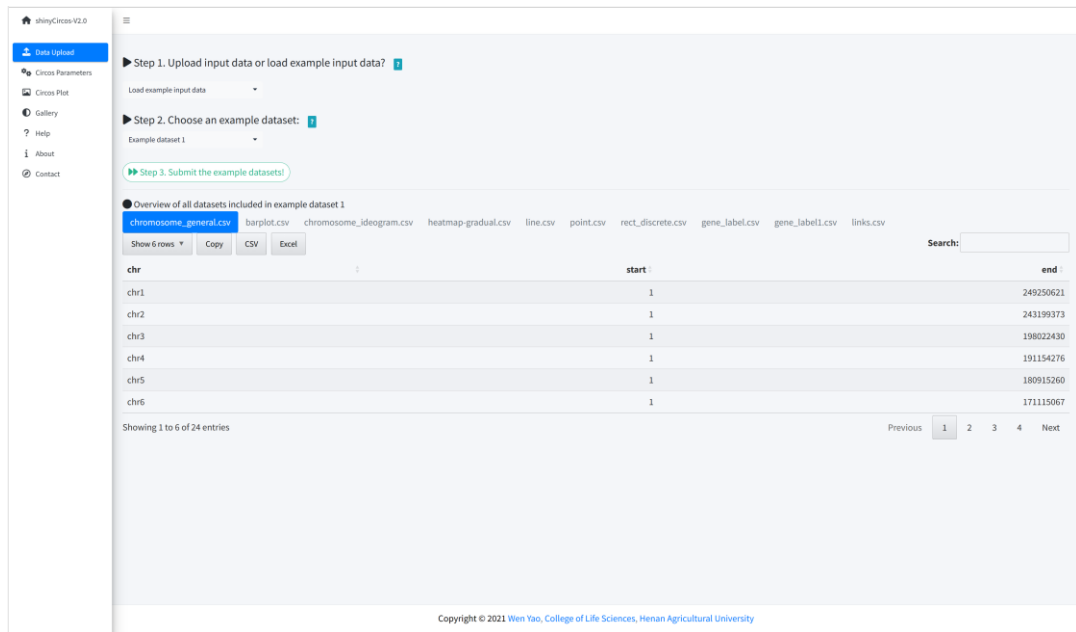
详细的帮助文档（中英文双语）



输入数据格式的基本说明

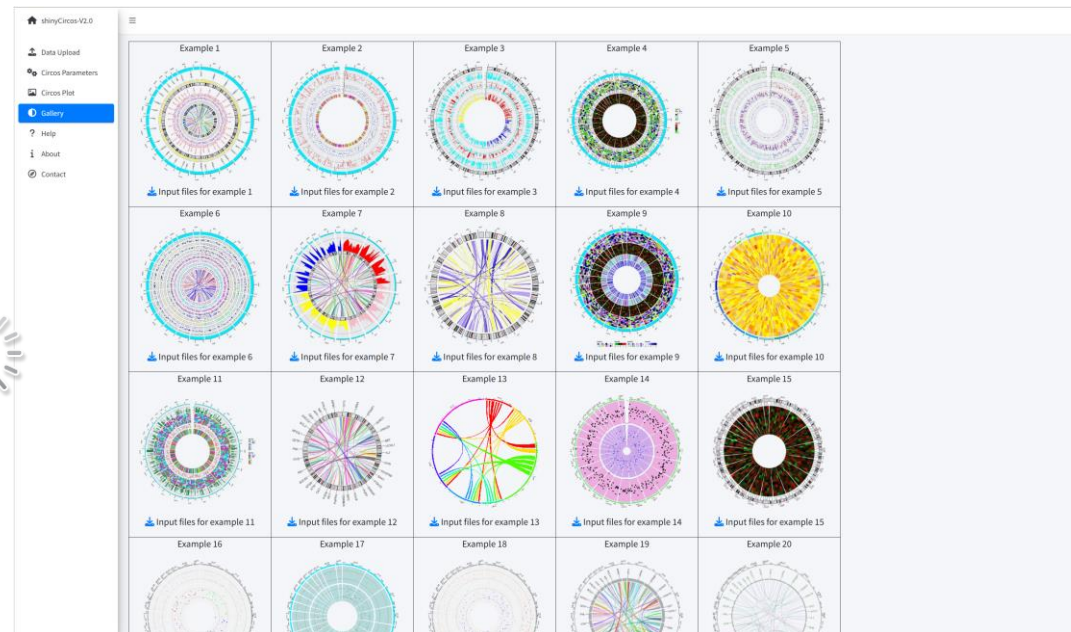
绘图步骤的详细说明

示例输入数据集



The screenshot shows the 'Data Upload' step of the shinyCircos-V2.0 interface. It includes a sidebar with navigation options like 'Data Upload', 'Circos Parameters', 'Circos Plot', 'Gallery', 'Help', 'About', and 'Contact'. The main content area has three steps: 'Step 1. Upload input data or load example input data?', 'Step 2. Choose an example dataset:', and 'Step 3. Submit the example datasets!'. Below the steps is an 'Overview of all datasets included in example dataset 1' section, which contains a table of input files and a table of chromosome data.

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



The screenshot shows the 'Gallery' view of the shinyCircos-V2.0 interface. It displays a grid of 20 example Circos plots, labeled 'Example 1' through 'Example 20'. Each plot is accompanied by a download link for its input files, such as 'Input files for example 1' through 'Input files for example 20'. The plots show various data visualizations on a circular genome map.

十个示例输入数据集

30个用shinyCircos-V2.0绘制的Circos图及其输入数据集

总结

- 源代码: <https://github.com/YaoLab-Bioinfo/shinyCircos-V2.0>
- 在线使用: <https://venyao.xyz/shinyCircos/>
- 在线使用: <https://asiawang.shinyapps.io/shinyCircos/>
- 联系: gentelmanwang@gmail.com or yaowen@henau.edu.cn
- 引用: 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>



“*iMeta*”由威立、肠菌分会和华人科学家出版的开放获取期刊，主编由中科院微生物所刘双江和荷兰格罗宁根大学傅静远教授共同担任。目的是发表原创研究、方法和综述以促进宏基因组学、微生物组和生物信息学发展。目标是发表前10%(IF > 15)的高影响力论文。期刊特色包括视频投稿、可重复分析、图片打磨、青年编委、前3年免出版费、50万用户的社交媒体宣传等。2022年的三月、六月、九月和十二月期已正式在线出版发行，相继被Google Scholar、PubMed(部分)、DOAJ、Scopus等数据库收录！



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