

Genome analysis

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

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Abstract

Summary: Creation of Circos plot is one of the most efficient approaches to visualize genomic data. However, the installation and use of existing tools to make Circos plot are challenging for users lacking of coding experiences. To address this issue, we developed an R/Shiny application shinyCircos, a graphical user interface for interactive creation of Circos plot. shinyCircos can be easily installed either on computers for personal use or on local or public servers to provide online use to the community. Furthermore, various types of Circos plots could be easily generated and decorated with simple mouse-click.

Availability and implementation: shinyCircos and its manual are freely available at <https://github.com/venyao/shinyCircos>. shinyCircos is deployed at <https://yimingyu.shinyapps.io/shinycircos/> and <http://shinycircos.ncpgr.cn/> for online use.

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1 Introduction

Data visualization is a critical element of data analysis in the era of big data. Circular visualization of genomic data with Circos plots has been widely used in various studies, which is powerful and flexible to demonstrate diverse types of genomic data (Pabinger *et al.*, 2014).

The Perl-based Circos software is the predominant tool to make Circos plots (Krzywinski *et al.*, 2009). However, its installation and use require knowledge on command-line and Perl scripts, which are challenging for users lacking of programming experiences. Several R packages including RCircos (Zhang *et al.*, 2013), omicCircos (Hu *et al.*, 2014) and circlize (Gu *et al.*, 2014) have been developed to make Circos plots, which are of great value to users familiar with R programming language. BioCircos.js is a JavaScript library to generate Circos plot (Cui *et al.*, 2016). Nevertheless, these tools still require coding efforts from users. A Java software J-Circos was developed to make Circos plots with a graphical user interface (GUI) (An *et al.*, 2015). In J-Circos, tracks are created one by one, and the radius of each track needs manual setting to avoid overlap. In addition, only limited types of plots with few options are provided by J-Circos to create Circos plots.

Here, we present shinyCircos for interactive creation of Circos plot, a GUI software developed using R and Shiny. The simplest table files with different separators are accepted as input to shinyCircos, avoiding the complex configuration of input file formats. Every detail of the output Circos plot can be fine-tuned by mouse-click based on user input.

2 Results

shinyCircos was developed by wrapping up the engine of circlize, an R package for circular visualization of genomic data with various types of Circos plots (Gu *et al.*, 2014). The construction of shinyCircos relies on Shiny, a framework to make interactive web applications using R.

The use of shinyCircos includes two steps: data input and Circos visualization. shinyCircos requires chromosome data and other data for different tracks. Chromosome data is compulsory and defines the frame of a Circos plot, which could be either chromosome ideograms or simple definition of chromosome lengths. Current version of shinyCircos allows users to upload up to ten datasets to visualize

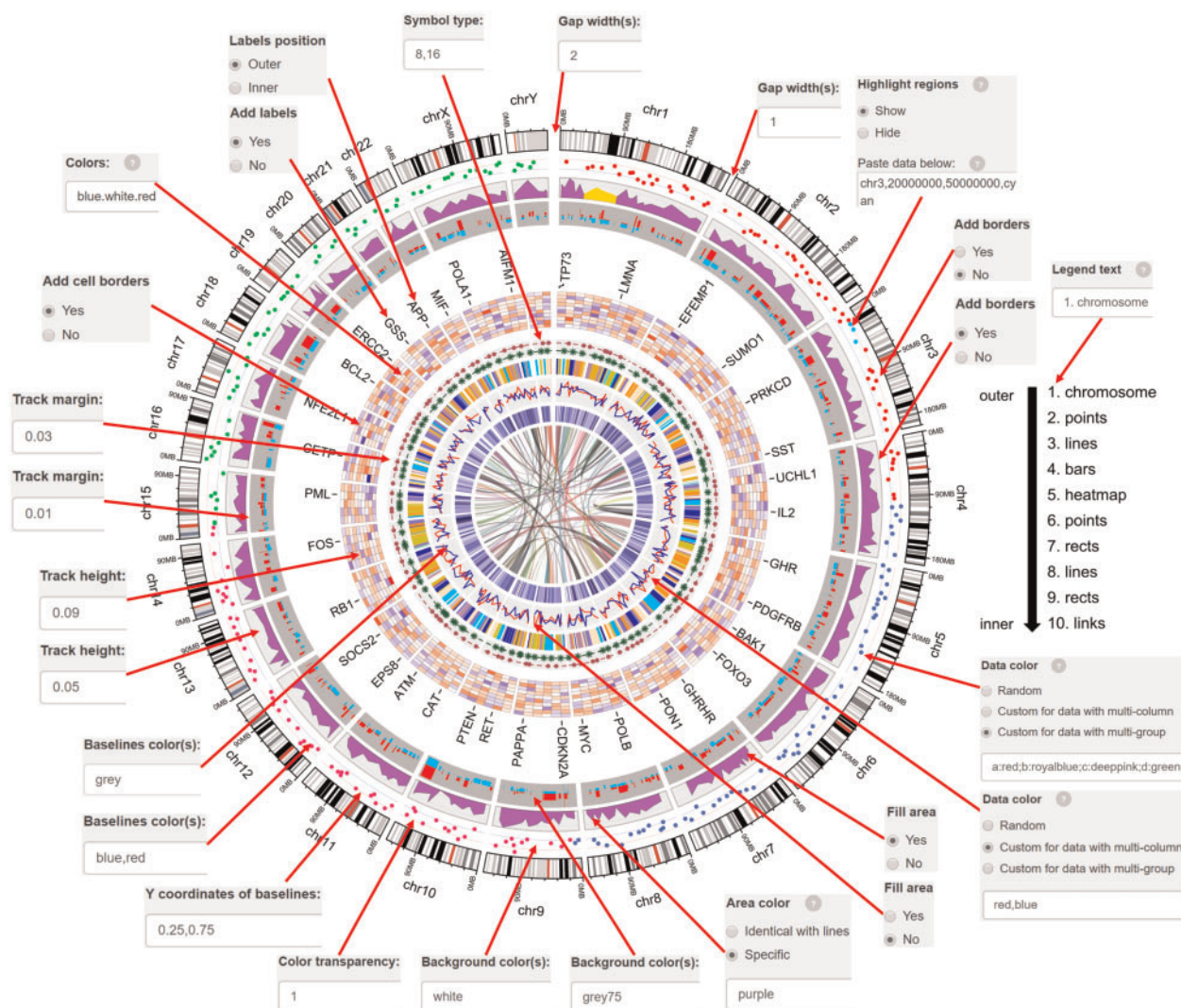


Fig. 1. An example Circos plot created with shinyCircos. Chromosome ideogram data come from the human genome. Eight tracks of simulated data are used to show the versatile of shinyCircos. Diverse available options and parameters for creating the Circos plot are indicated by red arrows

in different tracks. For each track, six types of plots can be created, including scatter plot, line plot, bar plot, rectangle, heatmap and chromosome ideogram (Fig. 1). In addition, connectors between different genomic regions can be drawn using shinyCircos.

Once the data input step is completed, a Circos plot could be created with default parameters (Fig. 1). For the generated Circos plot, various options are provided to tune the appearance of the plot. For the outermost chromosome track, the color, the labels and the axis ticks could be edited interactively. For other tracks, the color of the main plot, the height of the track, the color of the baselines and the background could be defined by the user. The baselines and shading boxes to all chromosome sectors of each track are selectable. The distances between different tracks and the distances between different chromosome sectors could be defined by the user. In addition, users can choose to highlight one or more genomic regions with specific colors. Text labels could be added on any track to mark specific genes or genomic regions. shinyCircos also provides the generation of high-quality PDF or SVG images of Circos plot with preferred size. The R scripts to reproduce any Circos plot created by shinyCircos are provided for advanced users.

3 Conclusion and outlook

shinyCircos is a lightweight Shiny application for interactive creation of Circos plot, which provides a user-friendly graphical interface for users with limited programming experiences. We deployed shinyCircos at <https://yimingyu.shinyapps.io/shinycircos/> and <http://shinycircos.ncpgr.cn/>, which enabled the use of shinyCircos online without installation. Users are encouraged to install and run shinyCircos on personal computers very easily with R installed. Advanced users can deploy shinyCircos on local or public servers to provide online use of shinyCircos to other users. Advanced users can also contribute to the development of shinyCircos, as its source code is available in GitHub.

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