spiralize: an R Package for Visualizing Data on Spirals

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Abstract

Summary: Spiral layout has two major advantages for data visualization. First, it is able to visualize data with long axes, which greatly improves the resolution of visualization. Second, it is efficient for time series data to reveal periodic patterns. Here we present the R package *spiralize* that provides a general solution for visualizing data on spirals. *spiralize* implements numerous graphics functions so that self-defined high-level graphics can be easily implemented by users. The power of *spiralize* is demonstrated by five real world datasets.
Availability and Implementation: The *spiralize* package and documentations are freely available at the Comprehensive R Archive Network (CRAN) https://CRAN.R-project.org/package=spiralize.
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Supplementary Information: Supplementary data are available at … online.

Introduction

High resolution visualization is always an urgent need for biological data and general data analysis. In a figure with a width of 1000 pixels, traditional linear visualization can only maximally distinguish 1000 data points on *x*-axis, which restricts visualization on larger datasets. There are methods aiming to improve the resolution of visualization by extending the *x*-axis into two-dimensional space by certain transformations. Circular visualization (Gu *et al.*, 2014) extends the axis to a circle, which improves the resolution by a small factor of 3.14 times, but it allows multiple tracks for simultaneously visualizing different data types. Hilbert curve (Gu *et al.*, 2016) is another type of method that densely folds the axis into two-dimensional space and it greatly improves the resolution from n to n^2, however, it is only efficient to visualize one single data type on the one-dimensional folded axis. Visualization on spirals is an alternative method that maps data to spirals (we refer to Archimedean spirals in the paper). It can visualize data with high resolutions and it also supports multi-track visualization under relatively lower resolution. These two different visualizations can be

achieved by adjusting the number of loops in the spiral. The second advantage is it is efficient to visualize time series datasets to reveal periodic patterns. In current studies, spirals were mainly used for visualizing time series datasets (Weber *et al.*, 2001; Carlis and Konstan, 1998). There was also one study that utilized spirals to visualize trees of life of more than 50000 species (Hedges *et al.*, 2015).

In polar coordinates (r, θ), Archimedean spiral has the form of $r = b\theta$. The radial distance between two neighbouring loops for a given θ is $d = 2\pi b$. This implies the radial distance is always constant regardless of the positions in the spiral, thus it is ideal to put tracks on spirals where the radial direction corresponds to the *y*-axis of the data. Spiral visualization has higher resolution than traditional linear visualization. For example, a spiral with 4 loops improves the resolution of visualization by a factor of 6.3 and a spiral with 10 loops improves by a factor of 15.7. In Supplementary File 1, we demonstrated the improvement of the resolution increases almost linearly to the number of loops in the spiral. However, users need to be cautious when selecting more loops in spiral visualization as visually there will be less space between two neighbouring loops, thus less graphics can be arranged in spirals.

In this work, we developed a new R package *spiralize*, which provides a general solution for data visualization on spirals. *spiralize* provides numerous low-level graphics functions so that user-defined complex plots can be easily constructed by combining them. We demonstrated the usefulness of *spiralize* by five examples based on real world datasets and we believe *spiralize* will greatly facilitate users for better interpretation of their data.

Implementation

spiralize supports multiple tracks along the spiral where each track serves as an independent plotting region. In each track, numerous low-level graphics functions implemented in *spiralize* can be used to add basic graphics, *e.g.*, points, lines, polygons, texts or axes, to build complex plots. *spiralize* also provides functions to draw dendrograms or phylogenetic trees with huge numbers of leaves on the spiral.

Horizon chart is a visualization method that vertically splits an area chart with uniform size, then the bands are layered on top of each other (Heer *et al.*, 2009). It reduces the height of an area chart by a factor of k times where k is the number of bands, thus it is very suitable for spiral visualization because tracks normally have small heights on spirals and it has already been applied in a previous study (Tominski and Schumann, 2008). *spiralize* specifically implements a function `spiral_horizon()` to draw horizon charts and its usage is demonstrated in Figure 1A and 1C.

spiralize supports two methods for mapping data to spirals for different scenarios of data analysis. Method "angle" linearly maps data to angles in the polar coordinate system and method "curve" linearly maps data to the length of spiral curve. Under the “angle” method, it is possible to directly compare between loops to correspond patterns at the same time points over different periods (*e.g.*, Figure 1A), thus it is more suitable for time series datasets. However, the drawback is intervals with equal bin sizes of data are visually wider in outer loops than in inner loops. As a comparison, the “curve” method does not illustrate any

periodic pattern but it keeps the interval widths consistent if they correspond to equal bin sizes in the data. (*e.g.*, Figure 1B-1E).

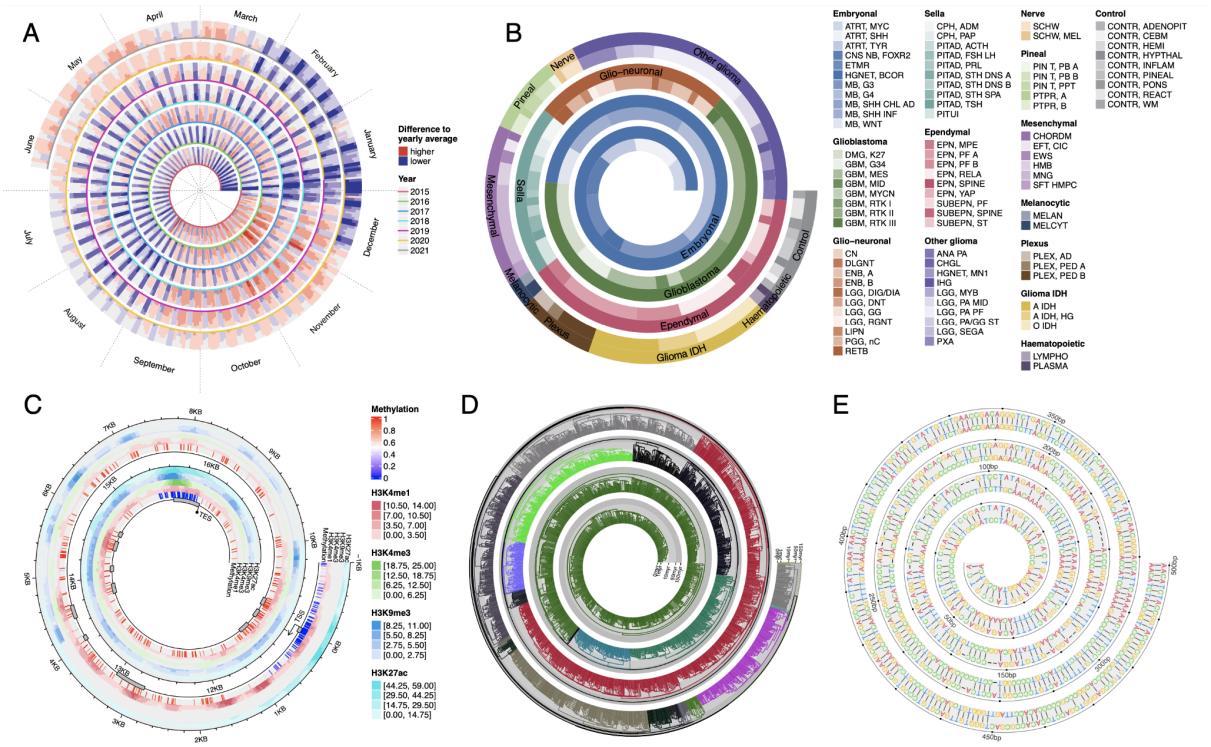

Figure 1. A) Daily downloads of the *ggplot2* package. B) 91 subtypes of central nervous system tumors from 2801 samples. C) DNA Methylation and four histone modification signals along gene BCAT2. D) Phylogenetic tree of 3738 mammals. E) Pairwise alignment of CDS of gene TP53 between human and mouse. Source code for generating all figures can be found in Supplementary File 2.

Application

Figure 1A visualizes daily downloads of the R package *ggplot2* from 2015-01-01 to 2021-06-14. Values on the plot are log2-values of the ratio between daily downloads and average downloads of the corresponding year. In Figure 1A, each loop of the spiral corresponds to 52 weeks so that the same weeks at different years can be correctly aligned and compared. Figure 1A clearly illustrates there are fewer downloads during weekends and vocation times, *e.g.*, end of December, beginning of January or in summer vocations (*i.e.*, July and August). For time series data, *spiralize* automatically calculates the start and end angles on spirals to make the position of a time point in the loop reflect its timely proportion in the corresponding period (Note the position of the end angle in Figure 1A).

Figure 1B visualizes subtype classification of central nervous system tumors (Capper *et al.*, 2018). The dataset contains 14 different tumor types that are classified into 91 subtypes based on DNA methylation from 2801 samples. On the spiral, all subtypes can be easily distinguished and the proportion of subtypes in the cohort can be visually identified by the bar widths of subtypes, which is difficult for traditional visualization methods to reveal these details.

Figure 1C visualizes DNA methylation and signals of four histone modifications along the gene BCAT2 in lung tissue, which covers a genomic range of around 18kb where BCAT2 is extended with 1kb both to upstream and downstream. The data was obtained from the GEO database with accession ID GSE16256 (Bernstein *et al.*, 2010). The plot clearly illustrates the correspondence between various epigenomics signals. The resolution of visualization can almost reach 10 base pairs per pixel in a figure with size 7 × 7 inches.

Figure 1D visualizes a phylogenetic tree of 3738 mammal species (Hedges *et al.*, 2015). The tree was cut into 26 branches and each branch was assigned a different color. On the *y*-axis, the height of the tree which corresponds to the evolutionary distance was log10-transformed. In the vignette of the *spiralize* package, we reimplemented the complete phylogenetic tree from Hedges *et al.*, 2015 which contains 50632 species.

Figure 1E visualizes pairwise alignment of coding sequence (CDS) of gene TP53 between human and mouse. The alignment was obtained by blast. Due to the space of the plot in Figure 1E, only the first 500 base pairs are shown. The full set of 1194 base pairs of the alignment can be found in the vignette of the *spiralize* package.

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Reference

Bernstein,B.E. *et al.* (2010) The NIH roadmap epigenomics mapping consortium. *Nat. Biotechnol.*, **28**, 1045–1048.

Capper,D. *et al.* (2018) DNA methylation-based classification of central nervous system tumours. *Nature*, **555**, 469–474.

Carlis,J.V. and Konstan,J.A. (1998) Interactive visualization of serial periodic data. In, *Proceedings of the 11th annual ACM symposium on User interface software and technology - UIST '98*. ACM Press, New York, USA, pp. 29–38.

Gu,Z. *et al.* (2014) circlize Implements and enhances circular visualization in R. *Bioinformatics*, **30**, 2811–2812.

Gu,Z. *et al.* (2016) HilbertCurve: an R/Bioconductor package for high-resolution visualization of genomic data. *Bioinformatics*, **32**, 2372–2374.

Hedges,S.B. *et al.* (2015) Tree of life reveals clock-like speciation and diversification. *Mol. Biol. Evol.*, **32**, 835–845.

Heer,J. *et al.* (2009) Sizing the horizon: The effects of chart size and layering on the graphical perception of time series visualizations. In, *Proceedings of the 27th international conference on Human factors in computing systems - CHI 09*. ACM Press, New York, USA, p. 1303.

Tominski,C. and Schumann,H. (2008) Enhanced Interactive Spiral Display. In, *Proceedings of the Annual SIGRAD Conference, Special Theme: Interactivity*. Linköping University Electronic Press, Stockholm, Sweden, p. 4.

Weber,M. *et al.* (2001) Visualizing Time-Series on Spirals. In, *Proceedings of the IEEE Symposium on Information Visualization 2001*, INFOVIS ’01. IEEE Computer Society, Los Alamitos, California, p. 7.