

Application Note

JBrowseR: An R Interface to the JBrowse 2 Genome Browser

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Abstract

Motivation: Genome browsers are an essential tool in genome analysis. Modern genome browsers enable complex and interactive visualization of a wide variety of genomic data modalities. While such browsers are very powerful, they can be challenging to configure and program for bioinformaticians lacking expertise in web development.

Results: We have developed an R package that provides an interface to the JBrowse 2 genome browser. The package can be used to configure and customize the browser entirely with R code. The browser can be deployed from the R console, or embedded in Shiny applications or R Markdown documents.

Availability: JBrowseR is available for download from CRAN, and the source code is openly available from the Github repository at

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Supplementary information: Supplementary data are available at Bioinformatics Online.

1 Introduction

The development of genome browsers is widely considered to be one of the fundamental milestones of the genomic revolution (Packer, 2007). Genome browsers provide researchers the ability to visually display and explore genomic annotations and data. Due to their widespread adoption and use, the linear display of genomic information along reference coordinates is one of the most common representations of biological data in the 21st century.

Since their original development during the advent of genome sequencing (Kent *et al.*, 2002; Birney *et al.*, 2004), genome browsers have made considerable gains in performance and sophistication. One important development has been the implementation of genome browsers in JavaScript, beginning with JBrowse (Buels *et al.*, 2016). Leveraging JavaScript makes it possible to move computation that previously took place on a server into the client browser. Another core advantage of JavaScript based browsers is that they can leverage modern web technologies such as Canvas and SVG, providing a more responsive and interactive experience for the user.

More recently, JBrowse has been rewritten using newer web technologies such as ReactJS and TypeScript to create an extensible platform for visualizing and integrating biological data called JBrowse 2. The platform can be configured and deployed with custom data and settings. This architecture enables research communities to develop and maintain curated sets of resources and data on the web, such as WormBase for the *C. elegans* community (Harris *et al.*, 2010). A new product offering of JBrowse 2 is a React component that renders a configurable genome browser, enabling researchers to embed custom browsers into existing React applications.

While the JBrowse 2 React component is powerful and extensible, it can present a steep learning curve for bioinformaticians who don't have experience with React development. On the other hand, the R programming language and environment is widely used in the bioinformatics community, as evidenced by the size and usage of efforts such as Bioconductor (Huber *et al.*, 2015). To bridge this gap, we introduce JBrowseR, an R interface to the JBrowse 2 genome browser. JBrowseR is an R package with functions for embedding a custom browser instance in a Shiny app, R Markdown document, or the R console.

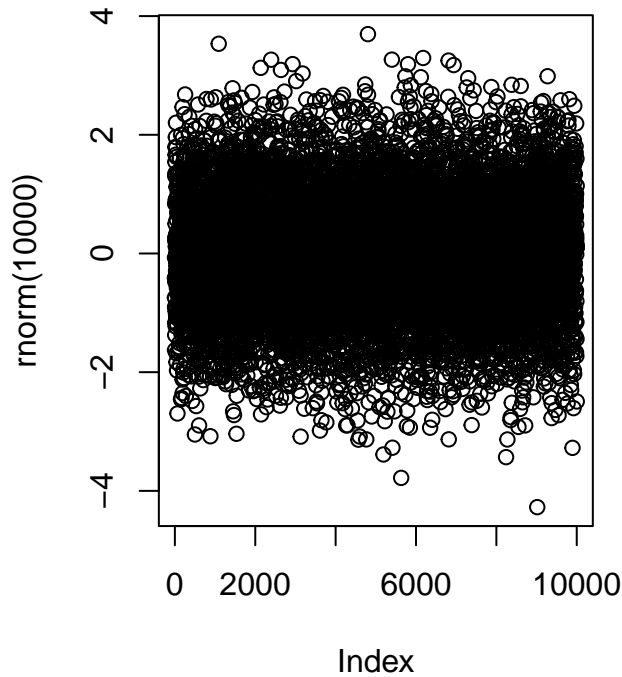


Fig. 1. Figure from an Rmd chunk.

2 Materials and Methods

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3 Methods

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5 Conclusion

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Acknowledgements

These should be included at the end of the text and not in footnotes. Please ensure you acknowledge all sources of funding, see funding section below.

Details of all funding sources for the work in question should be given in a separate section entitled ‘Funding’. This should appear before the ‘Acknowledgements’ section.

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- Multiple grant numbers should be separated by a comma as follows: ‘[grant numbers xxxx, yyyy]’
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