OXFORD

Application Note

JBrowseR: An R Interface to the JBrowse 2 Genome Browser

Elliot Hershberg [1], Garrett Stevens [1], Colin Diesh [1], Peter Xie [1], Teresa De Jesus Martinez [1], Rob Buels [1], Lincoln Stein [2], Ian Holmes [1*],

[1]Department of Bioengineering, University of California, Berkeley, Berkeley, CA 94720, USA
[2]Ontario Institute for Cancer Research, Toronto, ON M5G 0A3, Canada

*To whom correspondence should be addressed. E-mail: ihh@berkeley.edu
Associate Editor: XXX

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
Contact:ihh@berkeley.edu
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 represenations 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 and usage of efforts such as Bioconductor (Huber *et al.*, 2015). To bridge this gap, we introduce JBrowseR, an R interface 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.
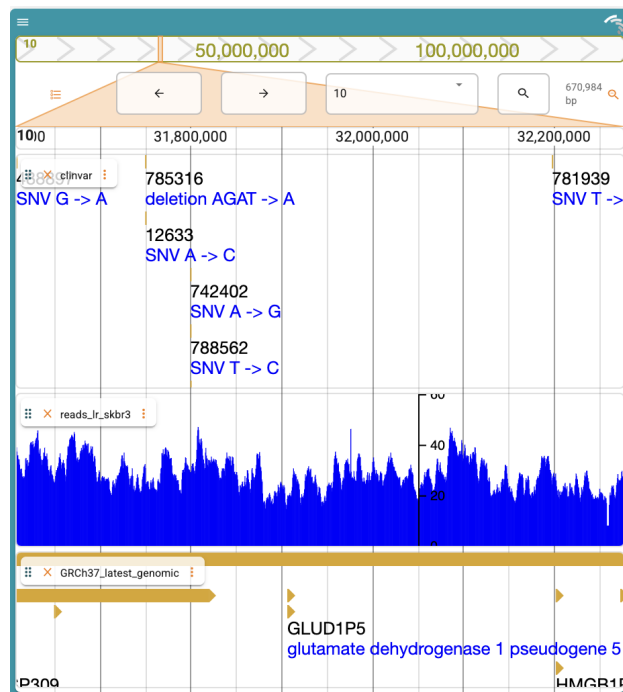
Fig. 1. A custom JBrowse 2 genome browser generated using JBrowseR.

2 Materials and Methods

JBrowseR is implemented as an R package and distributed on CRAN. The package was built according to R best practices, leveraging the devtools package. The core rendering methods of the library rely on the htmlwidgets framework, which can be used to embed JavaScript visualization tools in R Shiny apps, as well as R Markdown documents. Htmlwidgets can also can be used from an R interactive console. Using the reactR package, JBrowseR renders the JBrowse 2 widget inside of a root HTML element in an htmlwidget.

The interface of JBrowseR enables users to generate JBrowse 2 configuration for their own data using simple R functions. The configuration values can be composed together to create an arbitrarily complex custom browser. The majority of major genomic data types displayed in genome browsers are supported. JBrowseR also includes a HTTP server for serving local data that is configured with the necessary settings and features for working with genome browsers such as JBrowse and IGV.js (Robinson *et al.*, 2011, 2017).

The source code for JBrowseR is hosted on GitHub, and is automatically tested using continuous integration running on the Windows, MacOS and Linux operating systems. Automated tests for the package are implemented using the testthat R package.

3 Results and discussion

In order to demonstrate the utility of JBrowseR, several Shiny apps were built and included along with the package source code on GitHub. One of the included apps demonstrates adding CRAM, VCF, GFF3, and bigWig data (fig. 1), as well as setting a custom color palette for the browser. Another one of the provided demo apps illustrates how JBrowseR can also be configured with a JSON file like the other JBrowse 2 products by loading the Sars-CoV-2 reference genome and NCBI annotations from a JBrowse 2 configuration file. Finally, we have provided an example deployment of JBrowseR in an app with interactions connected to other

R shiny UI components at https://elliothershberg.shinyapps.io/sars-cov-2-spike-mutations/.

One of the core strengths of JBrowseR is its versatility. It considerably lowers the level of web development expertise required to create a genomics application with a fast and flexible genome browser. However, applications are not the only available target point for the rendering functions. JBrowseR can embed a genome browser into R Markdown, which is a flexible documentation format that is widely used to write scientific articles. We anticipate that as platforms such as eLife's "reproducible article" (Maciocci *et al.*, 2019) mature and become more widely adopted, it will be possible for genomics articles to contain interactive genome browsers such as JBrowseR displaying their data.

4 Availability

The JBrowseR is freely available for download from CRAN, and the source code is publicly available at https://github.com/elliothershberg/JBrowseR/. The package reference guide and tutorials can be found at https://elliothershberg.github.io/JBrowseR/.

References

Birney, E., Andrews, T. D., Bevan, P., Caccamo, M., Chen, Y., Clarke, L., Coates, G., Cuff, J., Curwen, V., Cutts, T., *et al.* (2004). An overview of ensembl. *Genome research*, **14**(5), 925–928.

Buels, R., Yao, E., Diesh, C. M., Hayes, R. D., Munoz-Torres, M., Helt, G., Goodstein, D. M., Elsik, C. G., Lewis, S. E., Stein, L., *et al.* (2016). Jbrowse: a dynamic web platform for genome visualization and analysis. *Genome biology*, **17**(1), 1–12.

Harris, T. W., Antoshechkin, I., Bieri, T., Blasiar, D., Chan, J., Chen, W. J., De La Cruz, N., Davis, P., Duesbury, M., Fang, R., *et al.* (2010). Wormbase: a comprehensive resource for nematode research. *Nucleic acids research*, **38**(suppl_1), D463–D467.

Huber, W., Carey, V. J., Gentleman, R., Anders, S., Carlson, M., Carvalho, B. S., Bravo, H. C., Davis, S., Gatto, L., Girke, T., *et al.* (2015). Orchestrating high-throughput genomic analysis with bioconductor. *Nature methods*, **12**(2), 115.

Kent, W. J., Sugnet, C. W., Furey, T. S., Roskin, K. M., Pringle, T. H., Zahler, A. M., and Haussler, D. (2002). The human genome browser at ucsc. *Genome research*, **12**(6), 996–1006.

Maciocci, G., Aufreiter, M., and Bentley, N. (2019). Introducing elife's first computationally reproducible article. *eLife Labs [Internet]*, **20**.

Packer, A. (2007). The clickable genome. *Nature Reviews Genetics*, **8**(1), S17–S17.

Robinson, J. T., Thorvaldsdóttir, H., Winckler, W., Guttman, M., Lander, E. S., Getz, G., and Mesirov, J. P. (2011). Integrative genomics viewer. *Nature biotechnology*, **29**(1), 24–26.

Robinson, J. T., Thorvaldsdóttir, H., Wenger, A. M., Zehir, A., and Mesirov, J. P. (2017). Variant review with the integrative genomics viewer. *Cancer research*, **77**(21), e31–e34.