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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

Contact: ihh@berkeley.edu

Supplementary information: Supplementary data are available at Bioinformatics Online.

1 Introduction

Cite others using bracket notation (Pepe, 2003). Can also cite with Zou and Hastie (2005).

Instructions for authors are available online.

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2 Approach

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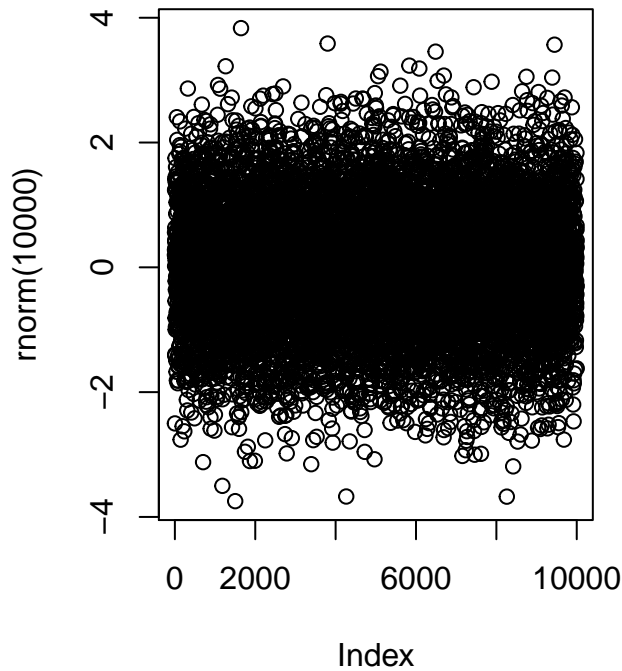
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Fig. 1. Figure from an Rmd chunk.

3 Methods

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5 Conclusion

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