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Application Note

JBrowseR: An R Interface to the JBrowse 2 Genome Browser

Elliot Hershberg¹, Garrett Stevens¹, Colin Diesh¹, Peter Xie¹, Teresa De Jesus Martinez¹, Rob Buels¹, Lincoln Stein², Ian Holmes^{1*},

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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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$$= (x+y)(x^2 + 2xy + y^2)$$
$$= x^3 + 3x^2y + 3xy^3 + x^3.$$

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¹Department of Bioengineering, University of California, Berkeley, Berkeley, CA 94720, USA

²Ontario Institute for Cancer Research, Toronto, ON M5G 0A3, Canada

^{*}To whom correspondence should be addressed. E-mail: ihh@berkeley.edu





2 FirstAuthorLastName et al.

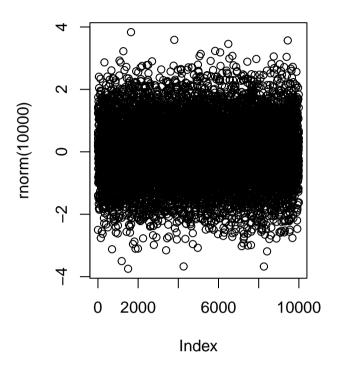


Fig. 1. Figure from an Rmd chunk

3 Methods

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3.1 Sub-Method

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4 Discussion

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5 Conclusion

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JBrowseR: R Interface to JBrowse 2

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Acknowledgements

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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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- The full official funding agency name should be given, i.e. 'National Institutes of Health', not 'NIH' (full RIN-approved list of UK funding agencies)
- Grant numbers should be given in brackets as follows: '[grant number xxxx]'
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Zou, H. and Hastie, T. (2005). Regularization and variable selection via the elastic net. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, **67**(2), 301–320.



