

To the editor,

We are grateful for the time that the reviewers took to review our JBrowseR manuscript and would like to submit what we view as a considerably improved manuscript revision. In this document, we summarize the changes we have made in response to the reviewers.

Reviewer 1

Comments to the Author

General: JBrowseR looks to be a very useful package that couples a powerful genomic visualization with the computational facilities of R. JBrowseR is joining a family of many other R/browser integrations, which would be good to acknowledge. Better integration with other bioinformatics infrastructure in R would benefit the user.

We appreciate the reviewer's positive reception of JBrowseR and are excited to contribute to the strong history of R/browser tools in genomics. As we will detail, we have made an effort to better acknowledge existing other packages in this space, and to add new functionality to JBrowseR to better integrate with the powerful computational tools available in R for bioinformatics.

Major:

- Instead of citing Bioconductor, cite packages in Bioconductor that do similar things, like epivizr, igvR, and rtracklayer (UCSC). epivizr is probably closest as it integrates with Shiny through htmlwidgets. There is also an igvShiny package in GitHub that does the same thing for igv.js.

We thank the reviewer for calling to our attention a better way to cite prior work. Based on this request, we have significantly restructured the introduction of our manuscript to cite these tools and describe what they do. We would like to clarify that epivizr does not use the htmlwidgets framework but provides an interface between epivizr and R using WebSockets.

We also appreciate the reviewer mentioning igvShiny. In researching this project, it appears to also be based on htmlwidgets but we have decided not to discuss it in the paper because it is not publicly downloadable from CRAN or Bioconductor, lacks documentation and testing, and does not appear to be actively maintained or developed.

- The package could integrate with other bioinformatics packages in R, particularly Bioconductor (strange for it to be cited but ignored from this perspective). For example, it would be very convenient for someone generating results in R to pass those results as a track object (like a GRanges object) to the browser. Behind the scenes, it could write the data to disk (for example using rtracklayer), potentially using BiocFileCache to make that efficient. This could be done via Suggests so as not to introduce a strong dependency on Bioconductor.

We thank the reviewer for providing this very thoughtful and useful feature suggestion. JBrowseR is actively developed and maintained, and this feature has been a high priority on our project roadmap. We are excited to say that we have implemented this feature (available in most recent CRAN release), and users can now create tracks from R data frames. We chose to focus on data frames as they are a core data structure in the base R language. There are existing tools for converting between data frames and GRanges objects in R and in keeping the implementation general by focusing on data frames, this feature also supports integration with the fuzzyjoin and tidygenomics CRAN packages.

We have added a description of this new feature to the Materials and Methods section.

Minor:

- Would be nice to know what types of interactions the widget can send back to Shiny.

We appreciate another thoughtful consideration about the package functionality from the reviewer. This is another feature that has been on our roadmap that we have recently implemented (available in most recent CRAN release). We use the Shiny messaging system to send data from JavaScript back to R. We have added an example app that creates a data frame of bookmarked features from the browser. This is an area that we are actively expanding, and welcome feature suggestions from users.

We have added a description of this new feature to the Materials and Methods section.

Reviewer 2

Comments to the Author

The app note by Hershberg, et al. describes an R library which provides access to the popular and powerful JBrowse software for genome viewing. The authors describe the functionality in the paper and include good documentation and vignettes to show users how to use the software. A nice addition is the ability to run Browse from the R environment (e.g. RStudio) or as a standalone Shiny app.

We thank the reviewer for taking the time to review our JBrowseR manuscript. We appreciate the acknowledgement of our documentation, as we have made a considerable effort to provide a comprehensive reference for all functions in the package, as well as providing tutorials and a continually growing set of example apps. We believe that this work has made our package more readily adopted, as we have grown to roughly 800 downloads a month since our initial release.