

## Reviewer Report

**Title: Machado: open source genomics data integration framework**

**Version: Original Submission**    **Date: 6/28/2020**

**Reviewer name: Daniel Cook**

### Reviewer Comments to Author:

The authors present Machado, which is a python-based framework for browsing genomic datasets. The software itself is of very high quality. It is version controlled, conforms to formatting standards, is easy to read, is well commented, and critically - it includes excellent documentation. These are attributes common to successful scientific software.

There are some additional features the authors should consider adding.

- The export icons for TSV/FASTA are identical. This is a UX issue that should be addressed.
- To facilitate deployment/usage, it may be beneficial to create a Dockerfile that can read a configuration and allow users to immediately test Machado on their existing Chado database.
- documentation for the API appears to be lacking. When I go to [https://www.machado.cnptia.embrapa.br/demo\\_machado/api/](https://www.machado.cnptia.embrapa.br/demo_machado/api/) I get 'undefined' for some queries, and it is unclear how to use the API.

Within the manuscript, there were some minor wording issues the authors should consider revising. For example, it is unclear what a "public wide database" is. There are also a handful of grammatical errors in the manuscript that need to be fixed. Also, the first github link appears to be broken.

Overall, I believe Machado is of high quality and worthy of publications. The authors should consider revising their manuscript for grammatical errors and consider the software suggestions above.

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