

## Reviewer Report

**Title:** Refgenie: a reference genome resource manager

**Version:** Original Submission    **Date:** 8/26/2019

**Reviewer name:** Katherine James

### Reviewer Comments to Author:

Refgenie is a very useful tool that has several functions that are not provided by iGenomes. In particular, it allows the use of custom genomes, which will become increasingly necessary as researchers work with more diverse species following recent large genome sequencing projects, such as the International Vertebrate Sequencing Project. Refgenie would also be of particular use to groups working with multiple bacterial strains, where a large number of reference genomes may be in use.

The manuscript is extremely well written and describes the architecture and usage of Refgenie. I have four minor comments:

1. The results section introduces the three components of Refgenie: 1) command-line interface, 2) server, 3) configuration package but discusses them in the following subsections in a different order, and after the 'Genome configuration and asset organisation' section. From the readers point of view, reordering these sections to describe these three components in this order would aid clarity. Indeed, the 'command-line interface' section is likely to be of most interest to potential users of Refgenie. Additionally, as a suggestion only, combining the 'Genome configuration and asset organisation' with 'Refgenconf configuration package' would also aid clarity.
2. The 'command line interface' section provides some example commands for a download of a bowtie2 index for hg38. For better understanding of refgenie usage, it would be useful if it also had similar real world examples for the other local genome assets commands, for instance a build for a local resource.
3. In the same section, a real example of how the refgenie seek command is portable and eliminates the need for hard coded paths would aid understanding of this concept.
4. In the section, 'comparison with existing tools' the authors state that iGenomes is only available as a single archive download. However, it should be noted that there are other sources for download of indexed reference genomes. For instance pre-built indexes for model organisms are available individually from the bowtie2 website and via the command line from the linked ftp site. Additionally, the Galaxy Tool Shed provides data managers for index builds for multiple tools. This section should be expanded to highlight the unique features provided by Refgenie over existing resources for genome assets.

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