Reviewer Report

Title: GenPipes: an open-source framework for distributed and scalable genomic analyses

Version: Revision 2 **Date:** 1/30/2019

Reviewer name: Johannes KÃ¶ster

Reviewer Comments to Author:

I thank the authors for addressing several of my concerns. Two issues remain:
Major comments
* Regarding the feature table, the reasoning of the authors is acceptable (apart from my concern below), if the caption explicitly mentions that the table is "meant to provide the reader with an overview of the features of several tools in the field but not necessarily an exhaustive list".
* Regarding the answer "Bioconda offers a collection of packages and not an integrated system and can be quite heavy in memory requirements. Hence, we think that "package-manager-integration" is not necessarily an indication of the strength of the WMS. It is a specific choice, one that offers ease of installation but has its pitfalls as well. GenPipes does not use package managers by design. GenPipes manages its own libraries making sure there is no conflicting libraries in the process. For users who do not want to install GenPipes manually, we offer a Docker container that has also been tested with Singularity. We have updated the GenPipes' bitbucket documentation to highlight the availability of the GenPipes' Docker container.":
The way to provide the software stack for an analysis is very important for reproducibility and maintainability of a pipeline. Hence, this should definitely be a column of the feature table in any case. Certainly it is legitimate to decide against Conda or other package managerst, but in above argument I do not find any reason to hide this aspect from the user in the feature table. Why not adding a column about package manager support and let the reader decide whether they need/want this feature or not?

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