Reviewer Report

Title: SciPipe - A workflow library for agile development of complex and dynamic bioinformatics pipelines

Version: Original Submission **Date:** 11/2/2018

Reviewer name: Konstantinos Krampis, PhD

Reviewer Comments to Author:

Excellent work, building a workflow system implementing the data flow paradigm for bioinformatics with a fast language (GO) as well. Some minor concerns I have are the following:
- This is obviously targeted to bioinformatics developers, but assuming there is a community that adopts it, would there be a way for someone who can do basic command line to use
it ? I am assuming that is there is a community many workflows will be published and a non developer could run it with a single command by just pointing to his / her datasets ?
- What other dependencies does it need besides GO to be installed ?
- Can it do parallelism in data chunks similar to Nextflow ? Many bioinformatics files (think for example reads) can be processed in an embarrassingly parallel way, for example if they
are split and aligned to a reference genome.
- Finally, what about Docker containers ? For example Nextflow has build in the option to pull containers "on the fly" with the tools preconfigured from repositories such as Dockstore etc
which have hundreds of pre-made containers. This is especially useful in the case of complex bioinformatics pipelines which have 10-15 different tools. Of course a developer can build a single container with all the tools pre-configured and run SciPipe from within this container, but if container support is available natively within the SciPipe implementation, developers can simply point
to available (public or internally) containers with pre-configured tools, which will be started at runtime of the workflow in order to provide the algorithms which the workflow feeds the data
for processing during each different step.
Some corrections:
Line 33, right column better to use "Fig. 1" with bold letters.
Line 36, left column missing reference.
Line 46, right column, correct as "As can be seen on lines 17, 21 and 25, Fig.1", so that we know which figure we refer to.

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No competing interesting.

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