

Reviewer Report

Title: ASaiM: a Galaxy-based framework to analyze microbiota data

Version: Original Submission **Date: 10/4/2017**

Reviewer name: Efthymios Ladoukakis, Ph.D

Reviewer Comments to Author:

Some spelling errors: line 56: blocking scientist -> blocking scientists line 124 an web-interface -> a web-interfaceline 135: visualization -> visualizations line 135: such Phyloviz -> such as Phyloviz line 157 Figure 2): we -> Figure2) and we line 175-176: We integrate then also a workflow -> We also integrated them in a workflow in report (supp. material) targeted abundances may be not reflect -> targeted abundances may not reflect-----

-----Further remarks: 1)The title is a bit lacking in context. ASAIM is clearly dedicated only towards the taxonomic and functional analysis of metagenomic data (either from amplicon sequencing or from shotgun sequencing). It would be beneficial for the reader to deduce that from the title. 2)It's not quite clear the innovative part of the platform. Besides collecting all those preexisting tools in an organized manner under Galaxy's umbrella what was the added contribution of ASAIM's team? Did you develop new wrapper/parser scripts for some/all of these tools in order to integrate them with Galaxy? What is the added value of the 3 new tools you developed? The GO slim term tool seems to be one of the final tools (purple) in your workflow (is that correct?). What about the other two for searching EBI and ENA databases? Are they part of one of the workflows or just additional standalone tools? 3)The comparison between ASAIM and EBI analysis seems rather trivial. It's not a comparison of the two platforms rather than a comparison of the two different tools they are using (QIIME and Metaphlan). It would make much more sense a comparison between EBI's workflow run in the exact same way as an ASAIM/Galaxy workflow with the same tools. 4)The same goes for functional analysis (where you mention comparison is not feasible). You just present results derived from two different methods with no comparable points. 5)In line 200 the command you state docker run -d -p 8080:80 quay.io/bebatut/asaim is different than the one stated in your webpage where the installation instructions are: docker run -d -p 8080:80 quay.io/bebatut/asaim-framework while the "asaim" command doesn't work (not authorized error) the "asaim-framework" seems to work 6)In supplementary material report page 3 contains a table that is not well displayed 7)Installation was not succesful so actual testing of the tool was not possible. Installation in a new CentOS distribution (3.10.0-514) under a Virtuabox engine failed. It could be useful to mention in your docs how to install and start the docker engine before attempting to download the ASAIM package especially for those with little or no command line knowledge. At some point during the installation process there was an error saying: "failed to register layer: ApplyLayer exit status 1 stdout: stderr: write /tool_deps/_conda/envs/__picrust@1.1.1/lib/python2.7/site-packages/mpl4py/MPI.so: no space left on device." Not sure how that's possible with 34GB available free space. Does ASAIM include databases that take up more space than that? If that's the case you should probably include that in the Requirements section in your webpage and inform the reviewers as well in order for us to be able to succesfully install and properly test it.

Level of Interest

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Quality of Written English

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