

Reviewer Report

Title: Galaxy as a Gateway to Bioinformatics: Multi-Interface Galaxy Hands-on Training Suite (MIGHTS) for scRNA-seq

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Reviewer name: Prashanth Suravajhala

Reviewer Comments to Author:

Gist/Summary: The authors propose a Multi-Interface Galaxy Hands-on Training Suite (MIGHTS) for single cell RNA-seq (ScRNA-seq) analysis which helps coders and as well beginners to adapt to it easily! The proposal comes up with a strong rationale mentioning the need for enhancing and developing unstandardized pipelines/iterative analysis. The authors describe the manuscript with pictorial methodology, workflows and ample datasets as an example that showcases tutorials, slide deck, video recordings, etc.. The manuscript is generally written very well and is a welcome article for the bioinformatics community in general. While the manuscript lays emphasis on unstandardized and iterative analysis, the authors could draw a strong rationale on lack of instantiation methods which is certainly the need. The tools like Scanpy/Seurat and other ecosystem tools, there is a latency and they work differently. Training-the-trainer is a very important entity as next generation sequencing (NGS) tools advances. A word or two on that would be a nice addition. While programming based and button based entities are well taken, there could be a "programming a button" section if not swapping between them. This will allow naive bioinformaticists to embrace programming. The authors may want to mention this. There could be an alternative annotation tool, viz. Annotationhub instead of Biosmart as well. Likewise vscode could be more inviting for some instead of jupyter IDE. The end user may be given a note in README file. Scores on a scale of 0-5 with 5 being the best. Language: 4.75 Novelty: 4 Brevity: 4 Scope and relevance: 4.5

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