

Reviewer Report

Title: A Single-cell RNA-seq Training and Analysis Suite using the Galaxy Framework

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Reviewer name: Efthymios Ladoukakis, Ph.D

Reviewer Comments to Author:

Small typos:

Other Approaches. The pre-processing workflow for these -> Other Approaches. The pre-processing workflows for these

A missing parenthesis in the "Downstream Workflows" section of the manuscript (two of which are shown in Figure 2, each -> (two of which are shown in Figure 2), each

Suggestions:

In the "Pre-processing Workflows" section of the manuscript I suggest you make the name and availability of each published workflow clearer, perhaps by introducing it in the appropriate paragraph's title. e.g.

Quantification with STARsolo -> Quantification with "10x STARsolo" workflow

Flexible Pre-processing -> Flexible Pre-processing with "CelSeq2: Single Batch mm10" workflow

I suggest you do the same in the "Downstream Workflows" section e.g.

Scater-based Quality Control -> Quality Control with "Single-Cell Quality Control with Scater" Workflow (I suggest the same for the rest of the workflows)

In the "Downstream Workflows" section of the manuscript you mention that there are five main stages of downstream scRNA-seq analysis but in the following paragraph it is not very clear which of the three workflows contain them. It becomes quite clear (the 2 after the pre-analysis workflow) in the next page from the Figure 2. explanation but I suggest that you mention it during the description of each workflow. e.g.

stage is complete, the full downstream analysis can be performed -> stage is complete, the full downstream analysis (comprising the five stages mentioned above) can be performed

Overall this is a very well written paper that verifies once more Galaxy's huge potential in -omic data analysis and specifically focuses on single cell transcriptomic data to prove that point.

Level of Interest

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Quality of Written English

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