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 Comments to Author:

The authors present a set of training materials in the Galaxy Training Network dedicated to scRNA-seq, They provide button based and programming based material to suit different level of skill and goals. This is a great work of making bioinformatic analyses accessible to everyone, regardless of learning trajectories.SpellingAs access to computationally driven domains of biology continue[s] to growblending skills across disciplines is not without challenge[s]"MIGHTS demonstrates the use of many frequently used data types and packages for scRNA-seq analyses (Table 2), preparing users with research[-]relevant skills.""Workflows for each tutorial topic are shown -below- in Figure 4.""Workflow is demonstrated -below- in Figure 8" (remove the belows)Figures and tables1. Figure 1 is too small to read, and it would be interesting to compare the BB method and the PE method to get the same images.2. Table 1 and 2 are redundant, use only table 2.3. Figure 4: Too small to see the stars.4. Figure 4,5,6,7: Add the significance of colored boxes in the legend. (too small to read the box titles). Overall, these figures are hard to read and are difficult to link with the text. Maybe in the text about tutorials, mention which step corresponds to which box color, or move these figure to supplemental material with more detailed legends.5. Figure 9: what does each letter correspond to? It looks like it is showing the same information than figure 1.Text1. "MIGHTS demonstrates the use of many frequently used data types and packages for scRNA-seq analyses (Table 2), preparing users with research relevant skills. " : Discuss a bit more which skills are deemed "research-relevant". I agree that both the biological skills and coding skills are important, but in that sentence I am not sure why it's linked to the datatypes and packages.2. Tutorials:- Intro: Give some information about the type of information these tutorial provide in the end: is it the growth rate for each cell type in the fetus? What are the main steps that each tutorial provide?- Overall, add a little bit more high-level information about what each tutorial does, for people who are not already familiar with scRNA-seq.3. It would be nice to be able to find this set of tutorials by searching MIGHTS in the GTN.4. The Single cell subpage contains more than the MIGHTS material, are they all supported the same way by the community with the same revision rate than described in table 3?5. It would be nice to have separate learning paths for BB and PE, so that users who want to focus on developing one set of skill find them more easily.6. In the Discussion: Do you have advice to give to people who want to develop similar material in their field?

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