

## Reviewer Report

**Title:** Comparative Analysis of common alignment tools for single cell RNA sequencing

**Version:** Revision 2      **Date:** 11/29/2021

**Reviewer name:** Hirak Sarkar

### Reviewer Comments to Author:

I have one more comment about this version of the manuscript. I think that since alevin exposes multiple ways to run the alignment phase upstream of alevin-fry, including the sketch mode, a more apt performance comparison is either to include the alevin-fry pipeline in sketch mode, or if this isn't done, to make clear in the manuscript that this configuration is not included.

I would like to refer authors to Figure 6A of STAR-solo manuscript (<https://www.biorxiv.org/content/10.1101/2021.05.05.442755v1.full.pdf>) which exposes such a comparison, and which finds alevin-fry with sketch based alignment to be the fastest configuration overall. As such, drawing conclusion about the speed of the tools presented, without mentioning that certain configurations that optimize for speed have not been included, might be misleading to general readers who are not otherwise aware of the configurability of these tools.

## Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

## Conclusions

Are the conclusions adequately supported by the data shown? Choose an item.

## Reporting Standards

Does the manuscript adhere to the journal's guidelines on [minimum standards of reporting?](#) Choose an item.

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## Quality of Written English

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