

Peer Review

Review of: "Sparse Dimensionality Reduction for Analyzing Single-Cell-Resolved Interactions"

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Thanks for the nice manuscript draft. What is missing, you can also read from the other reviewer: A thorough comparison to what related work has achieved and explaining what is specifically new in your work. You achieve dimensionality reduction in single-cell sequencing data, using a boosting autoencoder approach.

Now add a section (several pages) discussing related approaches, where you differ, and report openly and clearly where your approach is better and where you still see other approaches as better. Literature examples to compare to:

<https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2021.646936/full>

A Comparison for Dimensionality Reduction Methods of Single-Cell RNA-seq Data,

Xiang et al. *Frontiers in Genetics* (2021) <https://doi.org/10.3389/fgene.2021.646936>

Similarly, this Method

Eraslan, G., Simon, L. M., Mircea, M., Mueller, N. S., and Theis, F. J. (2019). Single-cell RNA-seq denoising using a deep count autoencoder. *Nat. Commun.* 10:390. doi: 10.1038/s41467-018-07931-2

could be a superior demonstration of your ideas, or maybe you do far better than these authors. It will only become apparent if you compare your ideas with such and related work, and then the paper quality increases strongly (e.g., to four stars or even five)

Declarations

Potential competing interests: No potential competing interests to declare.