Reviewer Report

Title: Unveiling Patterns in Spatial Transcriptomics Data: A Novel Approach Utilizing Graph Attention Autoencoder and Multi-Scale Deep Subspace Clustering Network

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Reviewer Comments to Author:

This paper introduces a tool, STMSGAL that generates spatial context-aware embeddings for spots in spatial transcriptomics data. The tool mainly contains three components, a cell type-aware neighborhood graph, a graph attention network, and a subspace clustering network. The tool is tested on some 10X Visium and STARmap data and compared to several existing methods.Specific points:1. Many parts of the proposed method, except the multi-scale deep subspace clustering part, seem to largely resemble STAGATE, which uses a cell type-aware spatial graph and a graph attention autoencoder. While STAGATE is briefly mentioned in Introduction, the differences and relations should be clarified in detail in the Methods section as well.2. The neural network part looks very similar to the method described in reference [51]. It is mentioned in "Latent embedding feature learning" section, that this approach is inspired by [51]. It should be clarified if the approach utilizes the method described in [51] or is it a novel extension inspired by [51].3. Due to the previous concerns, the contribution of STMSGAL is rather unclear given the current benchmark and comparison results. On the benchmark side, there are many different technologies but only two (Visium and STARmap) are used here. Regarding comparison, STAGATE should at least be added to the compared methods due to the similarity in approaches. A recent work (Yuan, Zhiyuan, et al. "Benchmarking spatial clustering methods with spatially resolved transcriptomics data." Nature Methods (2024): 1-11.) systematically benchmarked a collection of clustering methods for spatial transcriptomics data. I suggest the authors to use some of the datasets in this benchmark paper to extend the current benchmark to more technologies, and add comparisons to the top performers according to the benchmark paper.4. Why the clustering results from the multi-scale deep subspace clustering is not directly used for identifying spatial domains instead of performing clustering again using Leiden/Louvain/mclust? Also, could the authors explain the rationale of using different clustering methods for different datasets?5. It would be helpful to perform some ablation analysis to clarify what are the major contributors to the better performance compared to other methods. I suggest adding results 1) without the additional optimization step on DLPFC dataset and 2) without the clustering module in the graph neural network.

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