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 presents a well-structured and thoroughly evaluated framework for spatial analysis of ST data. It introduces STMSGAL, a novel framework for analyzing ST data, which incorporates graph attention autoencoder and multi-scale deep subspace clustering. With its robust performance and potential utility in advancing research, STMSGAL shows promising results to allow it as a good tool for researchers exploring cellular spatial organization and disease pathology. Specifically, I have some comments as below:1) The paper provides the evaluation of STMSGAL against five other methods using multiple datasets, demonstrating its outperformance across various evaluation metrics such as Davies-Bouldin, Calinski-Harabasz, S_Dbw, and ARI values. However, the authors lack of comparisons with most recent methods, such as STAGATE (PMID: 35365632) and SiGra (PMID: 37699885).2) When evaluating the performance of STMSGAL, the authors only include the DLPFC visium datasets and two other separate datasets. More evaluation datasets may be needed to ensure a robust, unbiased, and generalizable performance.3) STMSGAL incorporates different components in the framework, such as the graph attention autoencoder and multi-scale deep subspace clustering. Ablation study may be needed to justify the contribution and necessity of these components.4) Currently there are many tools developed for spatial domain identification, I recommend the authors to discuss the anticipated impact of STMSGAL, as well as potential points for future/further refinement of this tool.

Level of Interest

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Quality of Written English

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No competing interest.