

Reviewer Report

Title: Deciphering spatial domains from spatially resolved transcriptomics with Siamese Graph Autoencoder

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Reviewer Comments to Author:

This paper introduces SGAE, a novel method designed for the detection of spatial domains in spatial transcriptomics (ST). The authors utilize various public datasets and demonstrate that SGAE enhances representation discrimination, outperforming other spatial transcriptomics clustering software in clustering index evaluations. The study holds significant interest, as the application of SGAE has the potential to offer profound insights into complex biological systems. While the authors effectively showcase the efficacy and robustness of SGAE across various real datasets, it would be intriguing to assess SGAE's performance and compare it with other ST methods under different sequencing depths and clustering parameters. Additionally, a comparative analysis of maximum memory usage and runtime among various ST methods could provide valuable insights. In the "Results" section, enhancing the data description would contribute to a more compelling presentation. Please provide the explanations of error bars in the figure legends. Furthermore, it is recommended to standardize specialized terms, such as 'F-score,' for consistency throughout the paper.

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