Review of: "A Novel Variable Neighborhood Search Approach for Cell Clustering for Spatial Transcriptomics"

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Potential competing interests: No potential competing interests to declare.

The manuscript introduces a promising paradigm shift in spatial transcriptomics clustering, leveraging the VNS metaheuristic. The integration of gene expression and spatial coordinates for cell clustering is a substantial advancement in unraveling the intricacies of spatial transcriptomic data.

The authors adeptly demonstrate the efficacy of their approach, particularly through its superior performance compared to existing methods, as evidenced by efficiency metrics and ARI scores. Notably, the utilization of VNS in conjunction with PCA embeddings showcases robustness in capturing underlying biological structures, thus enhancing the interpretability of the generated clusters.

The comprehensive parameterization of the algorithm reflects a deep understanding of the nuances of spatial transcriptomic data analysis, allowing for adaptability to various experimental contexts. However, a more nuanced discussion on the method's generalizability across diverse datasets and its scalability to larger datasets would further strengthen the manuscript's impact.

Overall, this work significantly contributes to the bioinformatics landscape, offering a novel framework for spatial transcriptomics clustering with potential applications across various biological systems. The proposed extensions to time-series datasets and enhancements to the VNS methodology pave the way for exciting avenues of future research in this burgeoning field.