

Reviewer Report

Title: SMIntegration: A Web Tool for Comprehensive Spatial Metabolomics and Transcriptomics Integrated Analysis and Visualization

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Reviewer name: Reviewer 2

Reviewer Comments to Author:

In this manuscript, the authors built with R/Shiny and deployed using Docker containerization, providing a complete analytical workflow from data preprocessing to functional annotation. They used adjacent mouse brain coronal sections (Stereo-seq transcriptomics and AFADESI-MS metabolomics) as an example, and identified both the periaqueductal gray and subcommissural organ. This web-tool seems to be interesting and useful. However, the next concerns should be addressed before acceptance for publication.[1] The authors should explain more detailed for cell type analysis of their algorithm. How to figure out the association between astrocyte enriched GABA metabolism and Slc6a11?[2] Due to resolution difference, which algorithm has been utilized or developed for integration of spatial transcriptomics and spatial metabolomics in the web-tool?

Level of Interest

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