[BIOINFO 2025]

Leveraging Self-Similarity to Enhance Mass Spectrometry Imaging-based Biomolecular Mapping

Jae Min Kim[1,*], Jae Kyoo Lee[1,2,3]

[1]Department of Applied Bioengineering, Graduate School of Convergence Science and Technology, Seoul National University, Seoul, Korea

[2]Research Institute for Convergence Science, Seoul National University, Seoul, Korea

[3]Interdisciplinary Program in Artificial Intelligence, Seoul National University, Korea

*Corresponding author: kimjaemin99@snu.ac.kr

Traditional medical imaging techniques such as X-ray, CT, and MRI enable non-invasive visualization of anatomy and function but cannot capture molecular-level information which is essential for understanding biological processes. Among molecular imaging approaches, mass spectrometry imaging (MSI) overcome this challenge by directly mapping spatial distributions of various molecular species, including metabolites, lipids, and proteins, without staining or labeling. Despite its advantages, acquiring high-quality MSI data remains time-consuming and labor-intensive, making it difficult to build large-scale MSI datasets. This poses challenges for developing deep learning-based super-resolution (SR) methods, which typically require abundant paired training data. To overcome this limitation, we propose a self-similarity-based super-resolution framework for MSI (SSS-MSI), which utilizes recurring structural and molecular patterns within each MSI image to reconstruct high-resolution data in a data-efficient manner. Unlike conventional deep learning methods, SSS-MSI achieves high-fidelity super-resolution with only 30 MSI training datasets, thereby substantially reducing data dependency. This approach also demonstrate strong generalization performance to unseen tissue types through fine-tuning with the same limited data. Additionally, SSS-MSI converges faster in iterative training compared to existing methods, while maintaining superior perceptual and structural fidelity. This is reflected in improved LPIPS (Learned Perceptual Image Patch Similarity) and DISTS (Deep Image Structure and Texture Similarity) scores. By enhancing the spatial resolution of molecular and medical images to the single-cell level, SSS-MSI enables more precise analysis of spatial cellular heterogeneity, which is a critical factor in understanding tissue organization and disease progression, thereby opening new avenues for improved MSI-based biomedical research and diagnosis.