Riemannian Manifold-Coupled Joint Graphical Models for Spatial Transcriptomics

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Abstract

We propose a novel Riemannian manifold-coupled joint graphical model for spatially structured precision matrix estimation. Unlike existing Euclidean-based methods, our approach measures similarity between precision matrices of adjacent spatial regions using geodesic distances on the symmetric positive definite manifold, capturing structural deformations rather than entrywise differences.

This geometry-aware framework is particularly suited for spatial transcriptomics where regions may share dependency patterns despite scale variations. For inference, we develop an efficient alternating direction method of multipliers algorithm that decouples the region-specific likelihood and sparsity terms from manifold consensus updates and extend it with boundary-adaptive mechanisms to preserve biological discontinuities.

***Index Terms*—Riemannian geometry, joint graphical models, spatial transcriptomics, precision matrix estimation, manifold optimization, ADMM**