BISON: Bi-clustering of spatial omics data with feature selection

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Room BENVENUTI

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The advent of next-generation sequencing-based spatially resolved transcriptomics (SRT) techniques has reshaped genomic studies by enabling high throughput gene expression profiling while preserving spatial and morphological context. Comprehending gene functions and interactions in different spatial domains is crucial, as it can enhance our understanding of biological mechanisms, such as cancer-immune interactions and cell differentiation in various regions. This goal can be approached by clustering tissue regions into distinct domains and identifying genes with similar expression patterns within each domain, referred to as spatial-domain-marker genes. In this talk, I will present a unified Bayesian latent block model that simultaneously detects a list of informative genes contributing to spatial domain identification while clustering these informative genes and spatial locations. The efficacy of the proposed method is demonstrated through a series of simulation experiments, as well as applications to benchmark SRT datasets.

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