

Statistical Methods for Spatial Transcriptomics

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**ABSTRACT**

Spatial transcriptomics is a collection of groundbreaking new genomics technologies that enable the measurements of gene expression with spatial localization information on tissues or cell cultures. Here, I will discuss a few new statistical methods that our group has recently developed for analyzing spatial transcriptomics data. Specifically, I will first talk about SPARK, a method that allows for rigorous statistical analysis of spatial expression patterns in spatial transcriptomics. I will talk about a non-parametric extension of SPARK, called SPARK-X, for rapid and effective detection of spatially expressed genes in large spatial transcriptomic studies. If time allows, I will also talk about a spatially informed cell type deconvolution method, CARD, that leverages cell type specific expression information from single cell RNA sequencing for the deconvolution of spatial transcriptomics.