

BIOSTATISTICS SEMINAR



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Statistical analysis of spatial expression pattern for spatially resolved transcriptomic studies

Identifying genes that display spatial expression patterns in spatially resolved transcriptomic studies is an important first step towards characterizing the spatial transcriptomic landscape of complex tissues. Here, we developed a statistical method, SPARK, for identifying such spatially expressed genes in data generated from various spatially resolved transcriptomic techniques. SPARK directly models spatial count data through the generalized linear spatial models. It relies on newly developed statistical formulas for hypothesis testing, providing effective type I error control and yielding high statistical power. With a computationally efficient algorithm based on penalized quasi-likelihood, SPARK is also scalable to data sets with tens of thousands of genes measured on tens of thousands of samples. In four published spatially resolved transcriptomic data sets, we show that SPARK can be up to ten times more powerful than existing methods, revealing new biology in the data that otherwise cannot be revealed by existing approaches.

Thursday March 18, 2021

3:30 pm - 4:30 pm

Zoom meeting: Please also find a link in the email invite, with the password.
<https://uncsph.zoom.us/j/95116832073?pwd=TnV4QUtGLzMwaFRBTlRsd2xmTjVMQT09>



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