

BIOSTATISTICS SEMINAR



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Statistical methods for single-cell and spatial RNA-seq

In this talk, I will discuss our recent work to address challenges in single-cell and spatial RNA-seq data analysis.

Specific topics include pre-processing and normalization in droplet based single-cell RNA-seq studies. I will also discuss challenges unique to spatial RNA-seq experiments with specific focus on data from the Visium 10x Genomics platform.

Thursday March 4, 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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