



THE UNIVERSITY OF
CHICAGO

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STATISTICS COLLOQUIUM

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Statistical Approaches for Single Cell Technologies

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Via Zoom

ABSTRACT

I will start the talk by describing general statistical challenges in high-throughput genomics related to batch effects and systematic errors. Then I will describe some of our recent work related to single cell RNA-Seq (scRNA-Seq) including spatial transcriptomics. Specifically, I will describe how a relatively simple GLM based approach can reduce systematic errors and greatly reduce false positives that result when using the default procedures.

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