

# BIOSTATISTICS SEMINAR



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## **More (single-cell) data, more (statistical) problems**

Single-cell RNA-Seq (scRNA-seq) is the most widely used high-throughput technology to measure genome-wide gene expression at the single-cell level. However, single-cell data present unique challenges that have required the development of specialized methods and software infrastructure to successfully derive biological insights. Compared to bulk RNA-seq, there is an increased scale of the number of observations (or cells) that are measured and there is increased sparsity of the data, or fraction of observed zeros. Furthermore, as single-cell technologies mature, the increasing complexity and volume of data require fundamental changes in data access, management, and infrastructure alongside specialized methods to facilitate scalable analyses. I will discuss these challenges and present some solutions that we have made towards addressing these challenges.

**Thursday February 13, 2020**

**3:30 pm - 4:30 pm**

**Blue Cross and Blue Shield of North Carolina Foundation Auditorium**



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