



JOHNS HOPKINS  
BLOOMBERG  
SCHOOL of PUBLIC HEALTH

*Department of Biostatistics*

## BIostatISTICS SEMINAR

### On Methods for Normalizing Single-Cell RNA-Seq Data

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#### **Abstract:**

High levels of technical variability and artifacts in single-cell RNA-sequencing data (scRNA-seq) present challenges for accurately conducting downstream analyses. In this talk, I will illustrate the motivations for the considerable efforts devoted to overcoming these challenges including methods for normalization. I will introduce SCnorm - a quantile regression framework that enables accurate normalization for scRNA-seq data and establishes a novel evaluation criterion. Finally, I will discuss our ongoing efforts to develop normalization methods that are scalable, robust, and applicable to all scRNA-seq platforms.

Johns Hopkins Bloomberg School of Public Health, Department of Biostatistics  
Monday, October 7, 2019, Room W2008 (Refreshments 12:00pm)

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