

GENETICS, BIOINFORMATICS, AND SYSTEMS BIOLOGY COLLOQUIUM

THURSDAY FEBRUARY 16
12:00PM PST
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PASSWORD: **GENOME**

PRESENTED BY:



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"SCALABLE STATISTICAL METHODS AND SOFTWARE FOR SINGLE-CELL AND SPATIAL DATA SCIENCE"

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 some challenges in the analysis of scRNA-seq and spatially-resolved transcriptomics data and present some solutions that we have made towards addressing these challenges.