BIOSTATISTICS SEMINAR

Statistical and Computational Methods for Single-Cell Integrative Genomics

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Over the past decade, single-cell technologies have enabled a new era of high-resolution interrogation of cell-type diversity, vastly expanding our understanding of the role that cell types play in development and disease. In our pursuit of these opportunities, we are hampered by the lack of rigorous statistical methods and scalable computational algorithms. In this talk, I will present statistical and computational methods for single-cell integrative genomics from two perspectives. (i) Genome-wide association studies (GWAS) have yielded genetic variants associated with various complex traits, yet the specific cell types leading to the risk are usually unknown. I will first describe a framework that integrates GWAS summary statistics with single-cell transcriptomic/epigenomic data to prioritize trait-relevant cell types and thus elucidate disease etiology. (ii) Single-cell multiomic experiments that sequence RNA and ATAC from the same cells directly enable joint modeling of a cell's gene expression and chromatin accessibility. In the second half of the talk, I will discuss how this data can be best harnessed using a nonparametric approach to interrogate cell-type-specific transcriptional regulatory mechanism

Thursday, March 2, 2023, 3:30-4:30 PM Eastern

133 Rosenau Hall

Virtual using link and info below.

https://unc.zoom.us/j/91249030964?pwd=UXloTWlHajdQbkRqd1d5TnRaMitYdz09

Meeting ID: 912 4903 0964

Passcode: 884852