Department of Biostatistics and Bioinformatics Seminar
Faculty Candidate

R. Randall Rollins Building, Auditorium, L20
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Tilted-CCA: Quantifying common and distinct information in multi-modal single-cell data via matrix factorization

ABSTRACT

Paired multi-modal single-cell data profile multiple modalities for each cell simultaneously, such as the transcriptome alongside either the surface antibodies or epigenome. This new type of data has been growing in popularity in many areas of biomedical research and provides new opportunities to learn how different modalities coordinate within each cell. In this talk, we develop the Tilted-CCA to learn this coordination via dimension reduction. This novel method estimates low-dimensional embeddings that separate the axes of variation shared between both modalities (i.e., the "common geometry," capturing the coordination between both modalities) from the axes of variation unique to a particular modality (i.e., the "distinct geometry"). This task fundamentally differs from existing methods, which capture all the axes of variation from either modality instead. Methodologically, Tilted-CCA combines ideas from Canonical Correlation Analysis (CCA) and density clustering. Our method first uses the nearest-neighbor graphs from each modality to infer the common geometry between both modalities and decomposes the canonical scores from CCA to approximate this geometry. Biologically, we demonstrate that Tilted-CCA can enable many downstream analyses for CITE-seq (measuring the transcriptome alongside surface antibodies) and 10x Multiome (measuring the transcriptome alongside accessible chromatin regions) datasets on various biological systems. We focus on one particular analysis in this talk, showing that Tilted-CCA can unveil cellular dynamics in developmental systems based on the proportion of variation between the common and distinct embeddings.

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