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Tilted-CCA: Quantifying Common and Distinct Information in Multi-Modal Single-Cell Data via Matrix Factorization

Wednesday, September 27, 2023

3:30 pm – 4:30 pm

Room 1140

Hybrid Seminar (Dr. Lin will present virtually from Seattle)

Zoom Link: <https://mcgill.zoom.us/j/88354140659>

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.

Bio: Kevin Lin is a current assistant professor at the University of Washington's Biostatistics department. He was formerly a post-doctoral researcher at the University of Pennsylvania's Wharton Department of Statistics & Data Science with Dr. Nancy Zhang and completed his Ph.D. at Carnegie Mellon University's Department of Statistics & Data Science under Dr. Kathryn Roeder and Dr. Jing Lei. His research focuses on studying cellular mechanisms from single-cell data. He develops novel methods using ideas from matrix factorization, network modeling, and changepoint detection to derive new theoretical and biological insights. Link to website: <https://linnykos.github.io/>