



Department of Data Science

香港城市大學
City University of Hong Kong

DS SEMINAR

Scalable Representation Learning for Multi-View, Multi-Condition Single-Cell Data

Date: 22 January 2026 (Thursday)

Time: 9:30am - 10:30am

Zoom: <https://cityu.zoom.us/j/87571482634>

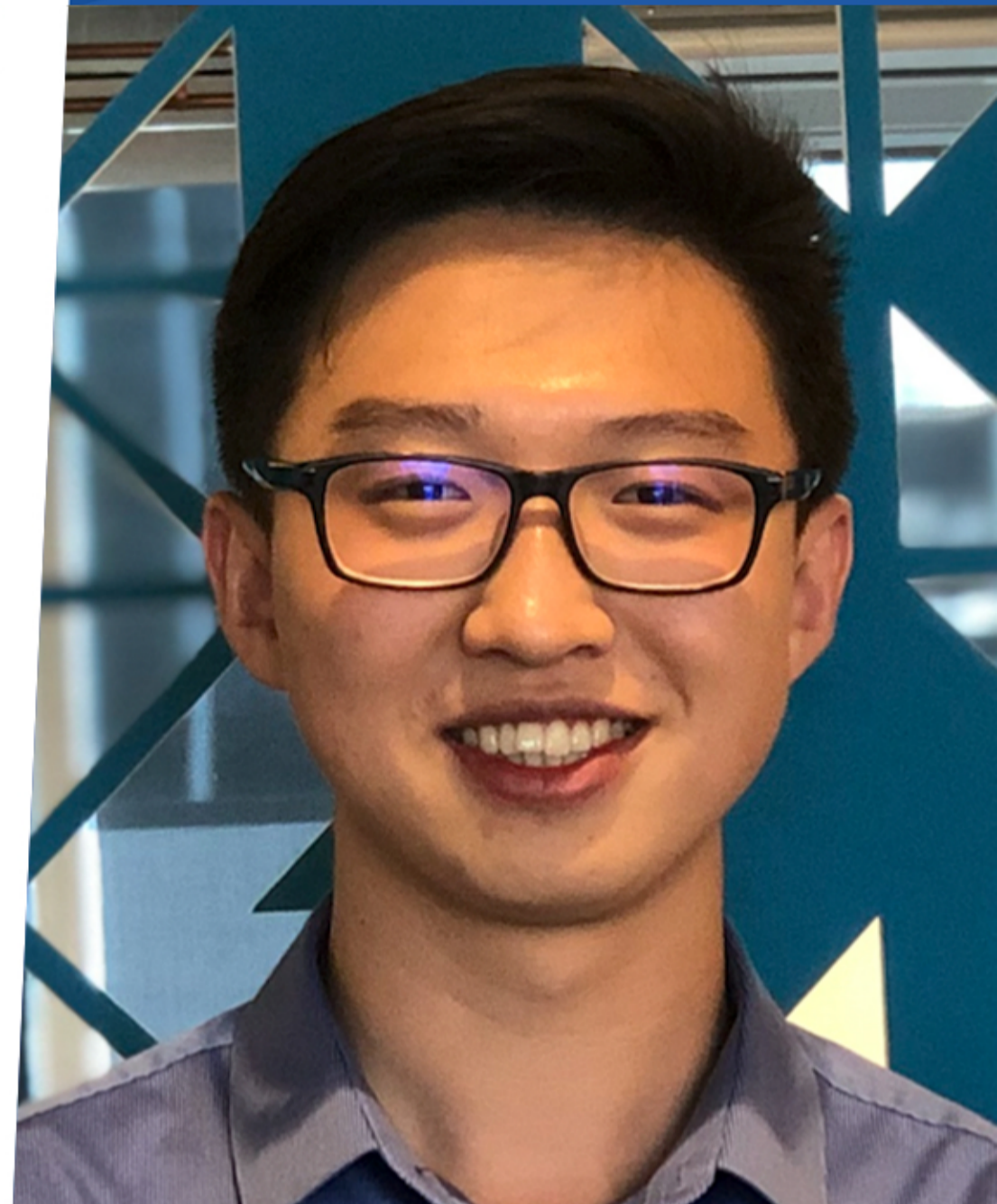


ABSTRACT

Single-cell sequencing technology produces large-scale, high-dimensional, multi-view datasets that measure molecules (e.g., mRNA, proteins) across each target cell within the bio-sample of interest. These data are noisy, sparse, and heterogeneous, presenting core data-science challenges in representation learning and knowledge transfer across domains and conditions.

In this talk I present my machine-learning solutions to address these computational challenges. First, I introduce my approach for learning robust cell representations by integrating information across multiple data domains. Next, I describe my method for modeling multi-conditional data and predicting cellular responses to external stimuli. In the end, I extend these ideas to large-scale data atlases and introduce an efficient single-cell foundation model that leverages pretraining on massive single-cell datasets to achieve improved generalization and strong performance across a wide range of downstream tasks.

I close by outlining future directions toward clinical impact: modeling heterogeneity at the levels of cells, cell types, and patients, and using pretrained, interpretable models to predict patient-level responses to treatments. Collectively, these methods advance general techniques for multi-view learning, domain adaptation, and learning from structured, high-dimensional data.



Dr. Ziqi ZHANG

GUEST SPEAKER'S PROFILE

Ziqi ZHANG received his Ph.D. from the School of Computational Science and Engineering at the Georgia Institute of Technology, where he was advised by Xiuwei ZHANG. His research focuses on developing machine-learning methods to study cellular mechanisms using high-throughput, multi-modal single-cell data. His work has been published in leading computational biology journals, including Nature Communications, Nature Methods, and Genome Biology, and has been supported by the U.S. National Science Foundation (NSF) and the National Institutes of Health (NIH). Ziqi has also collaborated closely with wet-lab researchers at Emory University and gained industry experience at Genentech, Inc., where he conducted computational cancer data analysis and translated methodological advances into real-world clinical applications.

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All are welcome