Shanghai Institute for Mathematics and Interdisciplinary Sciences

MATHEMATICS AND INTERDISCIPLINARY SCIENCES

Summer Seminar Series in Shanghai

Deep Learning Methods for Single-Cell Data Analyses

10:30 am, June 10, Tuesday

SPEAKER: Fei He

Fei He is currently pursuing a second Ph.D. in the Department of Electrical Engineering and Computer Science at the University of Missouri. Prior to this, he joined the School of Information Science and Technology at Northeast Normal University, China, in Fall 2015, where he now serves as an Associate Professor. He earned his first Ph.D. in Engineering with a specialization in Bioinformatics from Jilin University in 2015. With a strong foundation in both bioinformatics and computer science. He is passionate about developing interdisciplinary methodologies that leverage artificial intelligence and foundation models to tackle complex challenges in biology and medicine. To date, he has authored over 50 peer-reviewed publications in leading journals and conferences. His work has earned more than 1,200 citations, with an h-index of 18 and an i10-index of 28 on Google Scholar.

ABSTRACT

The rapid evolution of single-cell sequencing technologies has generated high-dimensional and heterogeneous datasets at unprecedented scales. This presents both exciting opportunities and significant computational challenges. In this talk, we will showcase graph-based models such as scGNN, which leverage cell-to-cell topologies for representation learning and imputation, as well as RESEPT, a deep learning pipeline designed for spatial transcriptomics visualization. Moving into the multimodal space, we will examine the integration of scRNA sequencing, scATAC sequencing, and histopathological images using heterogeneous graph transformers and attention-based embeddings. A central focus will be the development and adaptation of large-scale single-cell foundation models, also known as scLLMs. We introduce scPEFT, a parameter-efficient fine-tuning framework that enables effective domain adaptation while preserving pre-trained knowledge. Applications include cell type classification, cross-species transfer learning, batch correction, and gene perturbation prediction, all with significantly reduced computational cost. This talk offers a technical exploration of scalable deep learning strategies for single cell data, aiming to bridge advanced machine learning methods with impactful biomedical discovery.

Schedule & Detail:

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Zoom ID: 881 0309 9426
Password: 540575
Link: nus-sg.zoom.us/j/85183632572?pwd=iHArat2VZHuPtuBncpzCYxWgs0TtJY.1

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