DISSECTING SPATIOTEMPORAL SINGLE-CELL TRANSCRIPTOMICS DATA BY COMBINING DYNAMICAL MODELS AND GENERATIVE AI

Speaker: Peijie Zhou (Peking University)

Time：Mon., August 25th, 14:00
Venue: Room 102, SCMS

Abstract: Reconstructing cellular dynamics from sparsely sampled single-cell sequencing data is a major challenge in biology. Classical dynamical models, despite their superior interpretability and predictive power for perturbation analysis, meet with challenges due to the curse of dimensionality and insufficient continuous-time observations. Can we revitalize models in the era of single-cell data science, by taking advantage of Artificial Intelligence?

In this talk, I will introduce our recent efforts to dynamically integrate sampled cell state distributions, combining dynamical systems models and generative AI. I will begin by presenting a framework that employs flow-based generative models to uncover the underlying dynamics (i.e. PDEs) of scRNA-seq data, and demonstrate the development of a dimensionless solver capable of inferring continuous cell-state transitions, as well as proliferation and apoptosis, from real datasets. For spatial transcriptomics, we have further extended this framework by developing stVCR, which addresses the critical challenge of aligning snapshots collected from (1) different biological replicates and (2) distinct temporal stages. stVCR enables interpretable reconstruction and simulation of cell differentiation, growth, and migration in physical space, aligning spatial coordinates from transcriptomic snapshots—effectively generating a "video" of tissue development from limited static "images." This approach will be illustrated through applications in axolotl brain regeneration and 3D Drosophila embryo development. To further infer stochastic dynamics from static data, we explore a regularized unbalanced optimal transport (RUOT) framework and its theoretical connections to the Schrödinger Bridge and diffusion models. I will also introduce how to incorporate cellular interactions in such models, and discuss the design of efficient generative deep-learning solvers designed with applications in single-cell transcriptomic data analysis.

Bio: 周沛劼，北京大学前沿交叉学科研究院国际机器学习研究中心和定量生物学中心研究员、博士生导师，博雅青年学者，国家级青年人才。2014 年和 2019 年在北京大学数学科学学院获得计算数学学士和博士学位，导师为李铁军教授，获北京大学优秀博士论文奖。2020-2023 年任美国加州大学尔湾分校数学系访问助理教授，合作导师为聂青教授。研究领域为计算系统生物学，主要科研兴趣为单细胞数据和人工智能方法驱动的复杂生物系统建模与计算，研究成果发表在 Nature Methods, Nature Climate Change, Nature Communications, Nature Machine Intelligence, Nature Genetics, Physical Review X, Molecular Systems Biology, Advanced Science 等交叉学科期刊，并担任 Nature Methods, PNAS, Nature Communications 等多个期刊审稿人。