复旦大学数学科学学院
数学综合报告会

报告题目：SCOPE: A generative model for decoding cellular evolution from unpaired single-cell transcriptomic snapshots

报告人：明静思 (华东师范大学)

时间：2025-12-06 星期六 11:00-12:00

地点：光华楼东主楼1801

报告摘要：

The dynamic evolution of cell fate is a fundamental scientific question in developmental biology, disease modeling, and regenerative medicine. While single-cell RNA-sequencing provides high-resolution snapshots of cellular states, the destructive nature of the technology means that longitudinal tracking of individual cells is often impossible, resulting in unpaired temporal data. This poses a significant hurdle for reconstructing developmental trajectories. Here, we introduce SCOPE, a novel generative model that learns the evolutionary dynamics from these unpaired snapshots by formulating it in a generalized version of Schrödinger Bridge framework. We validate SCOPE on multiple datasets to show that SCOPE can generate complete and high-resolution trajectories, interpolate missing time points, and predict shifts in cell fate through gene perturbation. Our results establish SCOPE as a powerful and flexible framework for generating continuous and reliable cellular trajectories from discrete scRNA-seq data, opening new avenues for dissecting the mechanisms of cell fate determination.

非线性数学模型与方法教育部重点实验室
中法应用数学国际联合实验室
上海市现代应用数学重点实验室
复旦大学数学研究所