数学与系统科学研究院

计算数学所学术报告

报告人： **Dr. Shuxiong Wang**

（ ***Department of Mathematics, University of California, Irvine*** ）

报告题目：

Optimization Methods for high-dimensional Transcriptomics Data Analysis

邀请人： 刘亚锋 副研究员

报告时间：**2020 年 1 月 8 日（周三）**

下午 16:00-17:00

报告地点： 科技综合楼三层

311 报告厅

Abstract:

The rapid development of single-cell RNA-seq sequencing technologies in recent years enables the studies of complex biological systems at an unprecedented resolution. As more datasets are generated, various computational methods have been proposed to reveal the heterogeneity of cells, infer gene-regulatory networks, and reconstruct the trajectories of cell lineages in development. In this talk, we intend to introduce the scRNA-seq approaches, review the typical scRNA-seq data analysis (including quality control, normalization, feature selection, dimensionality reduction, and clustering etc.), and illustrate the recent advances for multi-omics data analysis. In addition, we will present an optimization-based method for high-dimensional transcriptomics data analysis. Via benchmarking the proposed approach against the state-of-the-art methods on multiple datasets, we show the efficiency and scalability of optimization techniques for large-scale problems.

欢迎大家参加！