



181 Longwood Avenue Boston, Massachusetts 02115-5804 **Department of Medicine**Channing Division of Network Medicine

Channing Methods Seminar

February 27 (Tuesday), 2024, 9AM (ET)

MCP 5th-floor conference room & Zoom:

https://us02web.zoom.us/j/579497999?pwd=cHNIWHMzWUIFUUVJTG1EeVJmY05aQT09

Meeting ID: 579 497 999 Passcode: 844168



Jianyang Zeng Westlake University

Machine Learning for Modeling Biological Data

Abstract: Identification of molecular recognition patterns is an essential problem in biology and pharmacology. In recent years, the emerging high-throughput experimental techniques together with the massive biological data, and the advanced AI technology have provided a new opportunity to investigate molecular recognition mechanisms and

advance the drug discovery processes. In this talk, I will present several new machine learning models recently developed in my group to elucidate the molecular recognition patterns between small molecules and proteins, and inferring gene regulatory networks (GRNs) from high-throughput single-cell RNA sequencing (scRNA-seq) data, which can provide useful insights for improving the prediction of drug-target interactions and understanding the mechanisms of gene regulation and, thus advancing the drug discovery processes and biomedical researches.

Bio: Jianyang (Michael) Zeng is a full professor in the School of Engineering, and an adjunct faculty member in the School of Life Sciences, Westlake University. He was a postdoctoral associate in the Department of Computer Science at Duke University and the Duke University School of Medicine in 2011-2012. He received his PhD in Computer Science from Duke University in 2011, advised by Prof. Bruce Donald (ACM and IEEE fellows). He received his MS and BS degrees from Zhejiang University in 2002 and 1999, respectively. The research interests of the Zeng lab mainly focus on computational biology, particularly the intersection between artificial intelligence/machine learning and life sciences. He has published over 80 papers in the prominent journals and conferences of computational biology and related fields, including top conferences ISMB and RECOMB, and prestigious journals, such as Nature (as a coauthor), Nature Machine Intelligence, Nature Communications, Nature Computational Science, Cell Systems, PNAS, Nucleic Acids Research, PLOS Computational Biology and Bioinformatics. He has been awarded "The XPLORER PRIZE" in 2023 and "The National Science Fund for Distinguished Young Scholars in China" in 2021. He has been invited as a program committee (PC) member for prestigious international conferences in computational biology, including ISMB and RECOMB. He is an associate editor of IEEE/ACM Transactions on Computational Biology and Bioinformatics, and an advisory board member of Cell Systems.

Hosted by Yang-Yu Liu

