Jingtian Zhou
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Education

University of California, San Diego
Ph.D. in Bioinformatics and Systems Biology   09/2016 – 12/2022
Advisor: Dr. Joseph Ecker
Research: Epigenetic diversity of mammalian brain

Tsinghua University
B.S. in Pharmaceutical Sciences   08/2012 – 07/2016

Stanford University
Visiting Student Researcher in Genetics   07/2015 – 09/2015
Advisor: Dr. Michael Snyder
Research: Genomic variants in complex human disease

Selected Publications (* denotes equal contribution)

1. **Zhou J***, Zhang Z*, ..., Ecker JR, Callaway EM. (2023). Brain-wide Correspondence Between Neuronal Epigenomics and Long-Distance Projections. *bioRxiv*.
2. Heffel MG*, **Zhou J***, Zhang Y*, Lee DS*, Hou K*, ..., Paredes MF, Luo C. (2022). Epigenomic and chromosomal architectural reconfiguration in developing human frontal cortex and hippocampus. *bioRxiv*.
3. Tian W*, **Zhou J***, …, Ecker JR. (2022). Epigenomic complexity of the human brain revealed by single-cell DNA methylomes and 3D genome structures. *bioRxiv*.
4. Liu H*, **Zhou J***, …, Ecker JR. (2021). DNA methylation atlas of the mouse brain at single-cell resolution. *Nature, 598*(7879), 120-128.
5. Zhang Z*, **Zhou J***, …, Ecker JR, Callaway EM. (2021). Epigenomic diversity of cortical projection neurons in the mouse brain. *Nature 598*(7879), 167-173.
6. BICC Network. (2021). A multimodal cell census and atlas of the mammalian primary motor cortex. *Nature, 598*(7879), 86.
7. Lee DS*, Luo C*, **Zhou J***, …, Dixon JR, Ecker JR. (2019). Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. *Nature methods*, *16*(10), 999-1006.
8. **Zhou J***, Ma J*, Chen Y*, …, Ecker JR. Robust single-cell Hi-C clustering by convolution- and random-walk-based imputation. (2019). *Proceedings of the National Academy of Sciences*, *116*(28), 14011-14018.
9. Zhang S*, Hu H*, **Zhou J***, …, Zeng J. (2017). Analysis of ribosome stalling and translation elongation dynamics by deep learning. *Cell systems*, *5*(3), 212-220.
10. Luo Y*, Zhao X*, **Zhou J***, …, Chen L, Zeng J. (2017). A network integration approach for drug-target interaction prediction and computational drug repositioning from heterogeneous information. *Nature communications*, *8*(1), 1-13. 7.
11. Zhang S, **Zhou J***, Hu H*, …, Cheng C, Zeng J. (2016). A deep learning framework for modeling structural features of RNA-binding protein targets. *Nucleic acids research*, *44*(4), e32-e32.

Other Publications (* denotes equal contribution)

1. Liu H, Zeng Q, **Zhou J**, ..., Ecker JR. (2022). Single-cell DNA Methylome and 3D Multi-omic Atlas of the Adult Mouse Brain. *bioRxiv*.
2. Zemke NR*, Armand EJ*, Wang W, Lee S, **Zhou J**, ..., Ren B. (2023). Comparative single cell epigenomic analysis

of gene regulatory programs in the rodent and primate neocortex. *bioRxiv*.

3. Nobori T, Monell A, Lee TA, **Zhou J**, Nery J, Ecker, J. R. (2023). Time-resolved single-cell and spatial gene regulatory atlas of plants under pathogen attack. *bioRxiv*.
4. Luo C*, Liu H*, Xie F*, ..., Mukamel EA, Ecker JR. (2022). Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. *Cell genomics, 2*(3), 100107.
5. Shu H, **Zhou J**, …, Zeng J, Ma J. (2021). Modeling gene regulatory networks using neural network architectures. *Nature computational science 1*(7), 491-501.
6. Luo C, Rivkin A, **Zhou J**, …, Ecker JR. (2018). Robust single-cell DNA methylome profiling with snmC-seq2. *Nature communications*, *9*(1), 1-6.
7. Luo C*, Keown CL*, Kurihara L, **Zhou J**, …, Mukamel EA, Behrens MM, Ecker JR. (2017). Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. *Science*, *357*(6351), 600-604.
8. Pan Y, Dong Y, **Zhou J**, …, Zeng J, Xu W. (2016). cOSPREY: a cloud-based distributed algorithm for large-scale computational protein design. *Journal of computational biology*, *23*(9), 737-749.

Honors and Awards

College Graduate Excellence Award of Beijing	07/2016
Qualcomm Scholarship	06/2016
Outstanding Academic and Innovation Scholarship of Tsinghua University	09/2015
First Prize in Beijing "Challenge Cup"	05/2015
Outstanding Academic and Research Scholarship of Tsinghua University	09/2014

Conference Presentations and Invited Talks

A single-cell multi-omic view of the brain.
Salk Featured Fellows   05/2023

Deciphering cell-type specific 3D genome structures with single-cell analyses.
Single-Cell 3D Genomics in Neuroscience and the BRAIN Initiative (Webinar hosted by Arima Genomics)   12/2022

Brain-wide Correspondence Between Neuronal Epigenomics and Long-Distance Projections.
Annual Meeting of Society of Neuroscience   11/2022

Simultaneously profiling of 3D genome structure and DNA methylation in single cells.
Annual Meeting of Advanced Genomic Technology Development   07/2022

Brain-wide Correspondence Between Neuronal Epigenomics and Long-Distance Projections. (Poster)
HHMI Science Meeting: Cellular and Molecular Neuroscience   05/2022

Single-cell Multiomic Study of Mammalian Brain.
Annual Meeting of International Society of Minimally Invasive Neurosurgery (ISMINS)   12/2021

DNA Methylation Atlas of the Mouse Brain at Single-Cell Resolution.
Duke Single Cell Initiative Seminar   11/2021

Single-cell multi-omic profiling of DNA methylation and 3D genome structure in primary motor cortex of human and mouse.
Annual Meeting of BRAIN Initiative Cell Census Network   06/2021

Epigenomic diversity of cortical projection neurons in the mouse brain.
Annual Meeting of BRAIN Initiative Cell Census Network   06/2020

HiCluster: A Robust Single-Cell Hi-C Clustering Method Based on Convolution and Random Walk. (Poster)
Keystone Conference for 3D Genome: Gene Regulation and Disease   03/2019