

Jian Zhou, Ph.D.

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RESEARCH EXPERIENCE

- 2019-Present** **Assistant Professor,**
Lupe Murchison Foundation Scholar in Medical Research,
CPRIT Scholar for Cancer Research
Lyda Hill Department of Bioinformatics, UT Southwestern Medical Center
- 2017-2019** **Flatiron Research Fellow,**
Center for Computational Biology, Simons Foundation
Advisor: Olga Troyanskaya, Ph.D.
- 2012-2017** **Graduate research assistant,**
Lewis-Sigler Institute for Integrative Genomics, Princeton University
Advisor: Olga Troyanskaya, Ph.D.

EDUCATION

- 2017** *Ph.D.*, Quantitative and computational biology, **Princeton University**, Princeton, USA
- 2011** *B.S.*, Biological Sciences, **Peking University**, Beijing, China

PUBLICATIONS

Jian Zhou*, Ignacio E. Schor*, Victoria Yao, Chandra L. Theesfeld, Raquel Marco-Ferrerres, Alicja Tadych, Eileen E. M. Furlong, Olga G. Troyanskaya (2019) Accurate genome-wide predictions of spatio-temporal gene expression during embryonic development, *PLOS Genetics* (*co-first authors)

Jian Zhou*, Christopher Park*, Chandra Theesfeld*, Yuan Yuan, Kirsty Sawicka, Jennifer Darnell, Claudia Scheckel, John Fak, Yoko Tajima, Robert Darnell[†], Olga Troyanskaya[†] (2019) “Whole-genome deep learning analysis reveals causal role of noncoding mutations in autism”, *Nature Genetics* (*co-first authors)

Jennifer Harder*, Rajasree Menon*, Edgar A. Otto*, Jian Zhou*, Sean Eddy, Noel Wys, Viji Nair, Cristina Cebrian, Jason R. Spence, Olga G. Troyanskaya, Jeffrey Hodgin, Roger Wiggins, Benjamin Freedman, Matthias Kretzler, European Renal cDNA Bank, Nephrotic Syndrome Study Network (2018) “Organoid single-cell profiling identifies a transcriptional signature of glomerular disease” *JCI Insight*, (*co-first authors)

Kathleen Chen*, Evan Cofer*, Jian Zhou, Olga Troyanskaya (2018), “Selene: a PyTorch-based deep learning library for sequence-level data”, *Nature Methods*

Jian Zhou, Chandra Theesfeld, Kevin Yao, Kathleen Chen, Aaron Wong, and Olga Troyanskaya (2018) “Deep learning sequence-based *ab initio* prediction of variant effects on expression and disease risk” *Nature Genetics*

Rajasree Menon, Edgar A. Otto, Austin Kokoruda, Jian Zhou, Zidong Zhang, Euisik Yoon, Yu-Chih Chen, Olga Troyanskaya, Jason R. Spence, Matthias Kretzler, Cristina Cebrián (2018) “Single-cell analysis of progenitor cell dynamics and lineage specification in the human fetal kidney” *Development*

Jian Zhou, Olga Troyanskaya (2016) “Probabilistic modeling of chromatin code landscape reveals functional diversity of enhancer-like chromatin states” *Nature Communications*

Jian Zhou, Olga Troyanskaya (2015) “Predicting effects of noncoding variants with deep learning-based sequence model” *Nature Methods*

Jian Zhou, Olga Troyanskaya (2014) “Global Quantitative Modeling of Chromatin Factor Interactions” *PLOS Computational Biology*

Jian Zhou, Olga Troyanskaya (2014) “Deep Supervised and Convolutional Generative Stochastic Network for Protein Secondary Structure Prediction” *International Conference of Machine Learning (ICML 2014), JMLR W&CP*

Xiaoxi Wang*, Lei Pan*, Su Wang*, Jian Zhou, William McDowell, Jungeun Park, Jeff Haug, Karen Staehling, Hong Tang, Ting Xie, (2011) “Histone H3K9 trimethylase Eggless controls germline stem cell maintenance and differentiation” *PLOS Genetics*

RESEARCH FUNDING

RR190071 (PI: Jian Zhou) \$2,000,000
Cancer Prevention and Research Institute of Texas 2019 - 2023

Endowed Scholars Program (PI: Jian Zhou) \$1,200,000
University of Texas Southwestern Medical Center 11/2019– 10/2025

HONORS AND AWARDS

2019 - present **CPRIT Scholar,**
Cancer Prevention and Research Institute of Texas

2019 - present **Lupe Murchison Foundation Scholar in Medical Research (Endowed Scholar),**
University of Texas Southwestern Medical Center

PRESENTATIONS

2019 Flash talk, NeuIPS 2020 LMRL workshop, Title: A quasilinear framework for interpretable exploratory analysis of single-cell omics data

2019 Invited Talk, Children’s Hospital of Philadelphia, Title: Learning the regulatory program of the genome: from sequence to chromatin, expression, and evolution

2019 Talk, Broad Institute of MIT and Harvard and Department of Biology, MIT, Title: Learning the regulatory program of the genome: from sequence to chromatin, expression, and evolution

2019 Talk, Department of Bioinformatics, University of Texas Southwestern Medical Center, Title: Learning the regulatory program of the genome: from sequence to chromatin, expression, and evolution

- 2018 Talk, Society of Biological Psychiatry (SoBP) Annual Meeting, Title: Decoding the Role of Noncoding Genome in Neurological Disease With Deep Learning
- 2017 Poster, CSHL NY Area Meeting in Quantitative Biology, Title: A unifying view of single cell data exploratory analysis with uncertainty estimation - statistical inference for clusters, trajectories, and surfaces
- 2016 Poster, CSHL NY Area Meeting in Quantitative Biology, Title: Predicting effects of noncoding variants with deep learning–based sequence model
- 2016 Poster, ICML workshop for computational biology, Title: On multitask learning by linear combination (co-first author)
- 2016 Oral presentation, The Allied Genetics Conference (TAGC), Title: Genome-wide spatial-temporal gene expression pattern prediction in *Drosophila melanogaster* embryonic development
- 2016 Oral presentation, ISMB, Title: Predicting effects of noncoding variants with deep learning-based sequence model
- 2014 Oral presentation, ICML, Title: Deep Supervised and Convolutional Generative Stochastic Network for Protein Secondary Structure Prediction
- 2013 Oral presentation, NIPS deep learning workshop, Title: Deep Supervised and Convolutional Generative Stochastic Network for Protein Secondary Structure Prediction

PROFESSIONAL SERVICES

Invited referee: Science, Nature Methods, Nature Communications, PLOS Computational Biology, PLOS Genetics, Nucleic Acids Research, Bioinformatics, PSB, Algorithms for Molecular Biology, Journal of Theoretical Biology, Journal of Bioinformatics and Computational Biology, Engineering Applications of Artificial Intelligence. Posters Committee: ISMB, PSB.