

Gene Regulation, Single-Cell Genomics, Computational Biology, and Machine Learning

A joint recruitment postdoctoral position is available in the laboratories of [Dr. Jian Xu](#) at Children's Research Institute and [Dr. Jian Zhou](#) at Lyda Hill Department of Bioinformatics, UT Southwestern Medical Center, to study the gene regulation and genomics using computational biology and machine learning. This position leverages two experienced mentors with complementary expertise in wet-lab (cancer genetics and genomics) and dry-lab (machine learning and bioinformatics), providing a **unique opportunity for training in a collaborative and multidisciplinary setting.**

[Dr. Jian Xu's lab](#) focuses on the intersection of gene regulation with stem cell biology and cancer. We study the genetic, epigenetic and metabolic programs that control stem cell development, and how these processes go awry in cancer progression. Our laboratory is equipped with cutting-edge genomics and molecular biology platforms, and has access to many shared facilities including an in-house illumina sequencer, 10xGenomics single-cell technologies, and metabolomics. Since the lab was established in 2014, our team has published many impactful papers, which include:

- Development of a dCas9-based affinity purification approach ('CAPTURE') for in situ analysis of chromatin interactions that regulate genomic enhancers (*Cell* 170:1028, 2017)
- Mitochondrial biogenesis and metabolism are regulated by post-transcriptional through mTOR-mediated effects on protein synthesis during erythropoiesis (*Nature Cell Biology* 19:626, 2017)
- Reported an integrative pipeline to identify pathogenic non-coding variants connecting enhancer dysregulation with nuclear receptor signaling in leukemia (*Cancer Discovery* 10:724, 2020)
- Discovered that the epigenetic silencing of LINE-1 retrotransposons is a selective dependency of myeloid leukemia (*Nature Genetics* 2021, *in press*)

[Dr. Jian Zhou's lab](#) studies computational genomics with machine learning and statistical approaches. Understanding how the genome operates at the sequence level is a primary focus of the lab. We develop computational methods, especially deep learning-based methods, for extracting regulatory programs encoded in the gene sequence, and apply them to study the roles of genetic dysregulation of regulatory genome in human diseases. Our lab has access to state-of-the-art high-performance computing facilities including cutting-edge GPU computing servers. Dr. Jian Zhou has published many influential papers, which include:

- Predicting effects of noncoding variants with deep learning-based sequence model (*Nature Methods*, 2015)
- Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk (*Nature Genetics*, 2018)
- Whole-genome deep learning analysis identifies contribution of noncoding mutations in autism (*Nature Genetics*, 2019)

Candidates must hold a Ph.D. and/or M.D. degree with a strong background in computational biology, gene regulation, genomics, or a related field. The ideal candidate will exhibit independence, flexibility and creativity with a record of scientific productivity. Previous experience in cancer genomics, machine learning, single-cell genomics or hematology-oncology is strongly preferred.

Interested individuals should send a CV, a short summary of research statement, and a list of three references to:

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Information on our postdoctoral training program and benefits can be found in our [Postdoc Handbook](#) or at [UT Southwestern's Postdoctoral Scholars page](#).

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