# Xilin Shen

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## EDUCATION

**Tianjin Medical University**, China, Ph.D., Medical Biochemistry and Molecular Biology, 2024

**Tianjin Medical University**, China, M.Sc., Medical Biochemistry and Molecular Biology, 2021

**Hebei Medical University**, China, B.Sc., Medical Examination Technology, 2019

## ACADEMIC EXPERIENCE

**Bioinformatics, Medical Biochemistry and Molecular Biology, Tianjin Medical University,** Ph.D, 2021-2024

- Committed to the application of large language models in bioinformatics, spanning single-cell and nucleic acid sequence analyses. Developed a foundational model for nucleotide sequences spanning diverse tissues.

- Designed a deep learning tool for characterizing protein-RNA interactions. Collaborating with other researchers to experimentally validate the pathogenic mutation discovered by the method.

- Collaborating with "wet-lab" members and offer bioinformatics evidence complementing wet-lab experiments. Assist in mentoring researches in wet-lab research projects related to bioinformatics.

**Bioinformatics, Medical Biochemistry and Molecular Biology, Tianjin Medical University,** M.Sc, 2019-2021

- Developed deep learning tools for integrating millions of single-cell transcriptomes; Contribute to the development of methods that represent large-scale single-cell transcriptomes by exploring gene ranking.

- Dedicate in applying deep learning methodologies to unravel biomarkers and regulatory mechanisms in immune-oncology within the realm of bioinformatics analysis.

## RESEARCH INTERESTS

Artificial intelligence for science;

Single-cell analysis, large-scale single-cell integration and representation;

Bioinformatics, high-throughput sequencing data analysis;

Deep learning, nature language processing, large language model

## TECHNICAL EXPERTISE

- **Scientific Programming Languages:** Proficient in Python, R, and Shell scripting.
- **Single-cell Analysis:** Proficient in integration and representation of single-cell trasncriptomes. Experience in the analysis and interpretation of single-cells, including cell clustering, pseudo-time analysis and cell-cell communication analysis.
- **Bioinformatics Skills:** Experience in the analysis of high-throughput sequencing data, including RNA-seq, ChIP-seq and Hi-C. Familiar with tools for genomics, epigenomics, proteomics analysis and other tools written in R and Python.
- **Deep Learning Approaches:** Stay up-to-date with the latest advancements in deep learning, including large language models, natural language processing, and computer vision. Stay well-versed in applying transformer models, including pre-training, fine-tuning and feature representation. Proficient in exploring and interpreting gene correlation and sequence interaction based on attention mechanisms. Experiences in the implemention and remould of deep learning models such as MoCo, VAE and CNN. Proficiency in deep learning frameworks including PyTorch.
- **Large-scale Datasets Analysis:** Experience in integration and analysis of large-scale nucleotide sequence data, such as sequence element discovery, pathogenic mutation mining and phylogenetic analysis.

## PUBLICATIONS

### Lead Author

**Xilin Shen**, Hongru Shen, Dan Wu, et al.. Scalable batch-correction approach for integrating large-scale single-cell transcriptomes. *Briefings in Bioinformatics*. 2022 Sep 20;23(5):bbac327. doi: 10.1093/bib/bbac327.

**Key words: Single-cell transcriptomes; deep learning; batch correction; large-scale.**

**Xilin Shen**, Lei Shi, Xiangchun Li. OmniNA: A foundation model for nucleotide sequences. (Under review)

**Key words: Foundation model; nucleotide sequence; deep learning; generative model.**

**Xilin Shen**, Yayan Hou, Chunyong Zhang, et al.. Reformer: Deep learning model for characterizing protein-RNA interactions from sequence at single-base resolution. (Under review in *Genome Research*).

**Key words: protein-RNA interaction; deep learning; transformer.**

Kaiwen Bao[*], Yanhui Ma[*], Yuan Li[*], **Xilin Shen**[*], et al.. A Di-Acetyl-Decorated Chromatin Signature Couples Liquid Condensation to Suppress DNA End Synapsis. (In press in *Molecular Cell*).

**Key words: Di-Acetyl-Decorated Chromatin, Liquid Condensation, DNA End Synapsis**

**Xilin Shen**, Xiangchun Li. Deep-learning methods for unveiling large-scale single-cell transcriptomes. (In press in *Cancer Biology & Medicine*).
**Key words: Single-cell; deep learning; large-scale.**

Hongru Shen[*], **Xilin Shen**[*], Mengyao Feng[*], et al.. A universal approach for integrating super large-scale single-cell transcriptomes by exploring gene rankings. *Briefings in Bioinformatics*. 2022 Mar 10;23(2):bbab573. doi: 10.1093/bib/bbab573.
**Key words: Single-cell; deep learning; gene ranking; large-scale.**

**Xilin Shen**, Xiaoli Wang, Hongru Shen, et al.. Transcriptomic Analysis Identified Two Subtypes of Brain Tumor Characterized by Distinct Immune Infiltration and Prognosis. *Frontiers in Oncology*. 2021 Oct 15;11:734407. doi: 10.3389/fonc.2021.734407.
**Key words: brain tumor; immune subtypes; biomarkers.**

**Contributing Author**

Hongru Shen[*], Jianghua Wu[*], **Xilin Shen**, et al.. An efficient context-aware approach for whole-slide image classification. *iScience*. 2023 Oct 12;26(12):108175. doi: 10.1016/j.isci.2023.108175.

Hongru Shen[*], Jilei Liu[*], Jiani Hu[*], **Xilin Shen**, et al.. Generative pretraining from large-scale transcriptomes for single-cell deciphering. *iScience*. 2023 Apr 20;26(5):106536. doi: 10.1016/j.isci.2023.106536.

Hongru Shen, Yang Li, Mengyao Feng, **Xilin Shen**, et al. Miscell: An efficient self-supervised learning approach for dissecting single-cell transcriptome. *iScience*. 2021 Oct 2;24(11):103200. doi: 10.1016/j.isci.2021.103200.

Dan Wu, Mengyao Feng, Hongru Shen, **Xilin Shen**, et al. Prediction of Two Molecular Subtypes of Gastric Cancer Based on Immune Signature. *Frontiers in Genetics*. 2022 Jan 17;12:793494. doi: 10.3389/fgene.2021.793494.

Hongru Shen, **Xilin Shen**, Dan Wu, et al.. An immunomodulatory signature of responsiveness to immune checkpoint blockade therapy. *Clinical and Translation Medicine*. 2020 Dec;10(8):e238. doi: 10.1002/ctm2.238.