

Yichen, Zhu

Email: : yiczhu@umich.edu | Tel: +1 858-232-3247

Address: 2033 Medford Rd APT 292, Ann Arbor, MI, 48104

EDUCATION

-
- University of Michigan, MI** 09/2024 - 05/2026
- MS Bioinformatics (Expected) GPA: 3.533/4.0
 - Core modules: Programming Laboratory in Bioinformatics; Probability & Distribution Theory; Molecular, Cellular, and Organismal Genetics; Bioinformatics Concepts and Algorithms; Molecular Genomic & Epigenomic Data Analysis; Biostatistics Inference; Mathematics of Biological Networks; Introduction to Signal Processing and Machine Learning in Biomedical Sciences; Machine Learning in Computational Biology
- University of California, San Diego, CA** 09/2020 - 06/2024
- Bachelor of Science
 - Major: Molecular and Cell Biology GPA: 3.424/4.0
 - Minor: Computer Science
 - Awards: **Provost Honors** (Fall 2020, Spring 2022, Fall 2022, Winter 2023, Winter 2024)

RESEARCH INTERESTS

-
- Computational cancer genomics; spatial transcriptomics; tumor phylogeography; multi-omics integration; statistical modeling

RESEARCH EXPERIENCE

-
- **Research Assistant in Professor Cong Ma's Lab** 01/2025 - Present
Advisor: Assistant Professor Cong Ma, Department of Computational Medicine & Bioinformatics, University of Michigan
 - Develop computational methods for allele-specific copy-number alteration (CNA) inference from spatial transcriptomics data using heterozygous SNPs and B-allele frequency (BAF) signals, enabling resolution of copy-number changes on maternal vs. paternal alleles
 - Designed and implemented an EM algorithm for SNP phasing, enabling estimation of single-cell allele-specific profiles across genomic regions
 - Built Python pipelines for BAF signal processing, visualization, and per-clone allele quantification to support downstream clonal analysis
 - Integrated EM-derived latent variables with observed BAF deviations and CNA calls to characterize tumor clonal architecture
 - Processed 10x Visium datasets using Space Ranger and constructed reproducible workflows with Snakemake for scalable analysis
 - Developed an anomaly-detection module for CalicoST using per-spot deviance scoring to identify rare or previously undetected tumor clones, by comparing observed BAF likelihoods with inferred clone-specific copy-number profiles
 - **The Application of Biology Cutting-edge Technology in Clinical and Scientific Research** 07/2022 - 08/2022
Advisor: Prof. Shibin Cheng, Medical School, Brown University
 - Learned the basic concept about Endoplasmic Reticulum (ER) Homeostasis (such as structure, ER stress, unfolding protein response, and ER in human disease);
 - Developed a deep understanding of cell death modes and diseases apoptosis, necrosis, pyroptosis, and necroptosis;
 - Grasped the autophagy-Lysosomal degradation machinery;
 - Mastered the basic concepts regarding Structure and function of ER, ER stress, ER quality control and the ubiquitin-proteasome pathway and how those concepts related to disease like Alzheimer.
 - **Effects of Three Polysaccharides on CAFs (Cancer-Associated Fibroblasts)** 06/2019 - 07/2019
Team Leader *Institute of Biophysics, Chinese Academy of Sciences*
 - Investigated the effects of three polysaccharides (Lentinan, MPSSS, Sargassum fusiforme) on cancer-associated fibroblasts (CAF) and normal bone marrow and spleen cells

- Performed cell viability assays using MTT and flow cytometry to evaluate differential cellular responses
- Isolated primary splenocytes and bone marrow cells and conducted in vitro cell culture
- Led a small team in designing and executing experimental protocols and data collection

PROFESSIONAL EXPERIENCE

- **Intern**, BGI Genomics Co., Ltd. 07/2023 - 09/2023
 - Applied pseudo-time series analysis to investigate endosperm development in *Arabidopsis thaliana*
 - Performed single-cell RNA-seq analysis using Seurat, including preprocessing and standard PBMC3K workflow benchmarking
 - Conducted co-expression network analysis using hdWGCNA to support gene regulatory studies in *Arabidopsis* seeds
 - Utilized SCENIC to infer gene regulatory networks and identify potential transcriptional regulators in *Arabidopsis thaliana* seed development
 - Gained exposure to machine learning methods, including support vector machines (SVM), in genomic data analysis
- **Intern**, Department of Biology, Jacobio Pharmaceuticals Co., Ltd. 08/2021 - 09/2021
 - Supported preclinical cancer drug development by conducting cellular activity assays and evaluating treatment responses
 - Performed in vitro cell culture and viability assays, including cell growth analysis and CellTiter-Glo assays
 - Assisted in protein detection and basic molecular biology experiments to support drug evaluation studies
- **Intern**, Lhasa Guangming Ophthalmic Rehabilitation Hospital 08/2019
 - Learned about the application of hospital equipment, for example, how to test intraocular pressure using medical equipment, and how to confirm whether a patient suffered from glaucoma using equipment to observe his corneas;
 - Observed the therapeutic process of glaucoma surgery, including disinfection of operating room, tools preparation, anesthesia, and treatment method, namely by changing intraocular lens to make sure patient remeasured eyesight;
 - Attended doctors' lectures about the development of ophthalmology in Tibet, which is a high-risk region of glaucoma and acute conjunctivitis; learned about the public health issues, as well as the treatment methods, process, and cost of ophthalmic diseases;
 - Followed nurses to engage in the therapeutic process of acute conjunctivitis for patients.

EXTRACURRICULAR ACTIVITIES

- **Volunteer** in Tibetan Orphanage 7/2019 - 9/2019
 - Educated children on basic health topics, including ophthalmic diseases and common conditions such as glaucoma and conjunctivitis
 - Delivered interactive sessions on general health awareness, including cancer and infectious diseases
 - Organized educational activities and games to promote engagement and learning

SKILLS

- **Programming:** Python, R (Seurat), Java, C, Bash
- **Bioinformatics & Tools:** Seurat, SCENIC, hdWGCNA, Space Ranger, Snakemake
- **Methods:** EM algorithms, statistical modeling, single-cell & spatial transcriptomics, gene regulatory network inference
- **Laboratory Techniques:** Cell culture, PCR, gel electrophoresis, Western blotting, cell viability assays
- **Languages:** Mandarin (native), English (proficient)
- **Interests:** Tennis, cooking