

# ZIMO ZHU

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## EDUCATION

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### Cornell University

Ph.D. student to Dr. Frank Pugh, Computational Biology

Ithaca, NY

August 2024 – Present

### University of Washington

B.S. in Molecular, Cellular, and Developmental Biology

Minor in Data Science

Selected courses - Molecular biology, Advanced Cell biology, Quantitative Biology, Genetics, Biochemistry

- Data programming, Machine Learning, Linear Algebra, Calculus, Probability

Seattle, WA

September 2020 – June 2024

## RESEARCH EXPERIENCE

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### Boston Children's Hospital (Department of Cardiology)

Undergraduate Researcher to Dr. Kaifu Chen

Boston, MA - Remote

July 2023 - Present

#### Single-Cell RNA Sequencing Unveils Organ-Specific Human Endothelial Cell Communications

- Processed single-cell RNA sequencing data of over 20,000 cells from 16 human tissues.
- Analyzed EC heterogeneity across tissue types and subtypes using UMAP, PCA, marker gene analysis.
- Examined metabolite-mediated cell-cell communications, and identified tissue-specific metabolite-sensor pairs that might explain and regulate EC tissue specificity using LDA and hierarchical clustering.
- Presented poster at the departmental discussion and academic meeting. [*publication in progress*]

### University of Washington (Department of Biology)

Research Assistant to Dr. Neda Bagheri

Seattle, WA

October 2022 – June 2024

#### Agent-Based-Model of Lateral Root Signaling with Regulatory Mechanisms

- Analyzed relevant literature and public data to summarize cellular information to obtain initialization parameters; generated differential equations and cost functions for parameter estimation and optimization.
- Developed class functions to calculate and update circulation content to investigate hypothesized signaling cascades; implemented both continuous and discrete methods for calculations in individual cells.
- Designed user-based input module to easily customize input parameters and parse values into the model.

### University of Washington (Department of Biochemistry)

Undergraduate Researcher to Dr. Young Kwon

Seattle, WA

March 2022 – June 2023

#### Fatty Acid Oxidation and Activin Signaling in Drosophila

- Designed experiments to raise flies with target genotype by constructing genetic crosses with different markers.
- Overexpressed Activin B with Mhc gene as a driver and knocked out Smox and Tak1 TF using RNAi.
- Dissected fly muscle to collect samples and processed the sample via RNA isolation and cDNA synthesis.
- Ran qPCR with five Fatty Acid Oxidation gene primers to quantify gene expressions and analyze results.

### University of Washington

Dry Lab Member of Washington iGEM team 2022

Seattle, WA

March 2022 - October 2022

#### Quick Test-Kit Design for Early Melanoma Diagnosis

- Created a kinetic model of Lateral Flow Assay (LFA) to simulate the production of analyte-detector-receptor complex under different conditions by changing the input reagent concentrations.
- Summarized the results of the model and communicated with the wet lab to potentially choose optimal constants and concentrations of reagents to optimize LFA experimental design.
- Won the Bronze prize in 2022 International Genetically Engineered Machine competition out of 364 teams.

## SKILLS

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### Dry Lab

- Proficient in **Python** (Scanpy, Pandas, Seaborn, Scikit-Learn, PyTorch) and **R** (dplyr, topicmodels, shiny)
- GitHub for version control and collaborative coding; Slurm for cluster management and job scheduling
- AliView, BLAST, and DNASP for sequencing data analysis and polymorphism detection
- Other software/tools: LINUX, LaTeX, Markdown, Jupyter Lab/Notebook, Anaconda, Excel

### Wet Lab

- RNA interference technique; RNA isolation and cDNA synthesis; qPCR
- Cell culture operations, gel electrophoresis, and Western Blot with Gel Doc
- Fly crosses; fly gut and muscle dissections; glass slide mounting for fly gut samples

## SELECTED COURSE PROJECTS

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### **Comparing Xa21 Between Cultivated and Wild Oryza species**

*Sequencing Data Analysis & Protein Structural Analysis*

- Investigated how variations in the Xa21 receptor gene influenced Oryza species' immunological response to Xanthomonas oryza with sequence data of 7 sub-species in AliView.
- Led selection analysis and found positive selections at Leucine-rich repeat (LRR) domain using DNASP.
- Performed structural analysis on Xa21 protein and identified segments with positive selections.

### **Deep Dive into Public Sentiments: Analyzing Social Media Reception of ChatGPT on Tweeter**

*Natural Language Processing (NLP) & Machine Learning*

- Applied EDA with visualizations to summarize main characteristics of ChatGPT user profile.
- Conducted sentiment analysis with VADER, TextBlob, and RoBERTa.
- Performed topic modeling with LDA to identify top discussion topics and most frequent appeared words.

### **Fraud Detection of Bank Account Application**

*Machine Learning & Statistical Analysis*

- Preprocessed data to fill NA values and convert numeric features into either binary or categorical features.
- Identified features such as credit risk that could serve as a suitable indicator for fraud predictions.
- Built model to predict fraud application using Decision Tree and Logistic Regression with PCA; evaluated and compared model train, validation, and test accuracy to select model parameters.

## EXTRACURRICULAR ACTIVITIES

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### **Music of the Enthusiasts (MotE) Chorus**

- Performed at 10+ live houses, festivals, and formal concerts.
- Led outreach activities to collaborate with other clubs and organizations.
- Operated the official social media account, with 300+ followers, to publish our activity highlights.