

# Michael Cheng

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## SKILLS

**Programming Languages:** Python, R, C++, Bash, SQL, Cypher, HTML, CSS, JavaScript, PHP

**Programming Frameworks:** PyTorch, HuggingFace, LangChain, Pandas, NumPy, Matplotlib, Seaborn, Scanpy, ggplot2, ComplexHeatmap, dplyr, Seurat, JQuery/AJAX, Bootstrap

**Concepts:** Deep Learning, Graph Neural Networks, Git, Docker, High Performance Computing, Bioinformatics, Genomics, Biological Network Modeling

## RESEARCH EXPERIENCE

**Ph.D. Researcher, Advisor: Professor Xia Yang**

April 2022 - Present

**UCLA Bioinformatics Interdepartmental Program**

Los Angeles, CA

Multimomics machine learning for drug target discovery and precision medicine.

- **Machine Learning:** Developed gradient boosting model to infer gene regulation networks from scRNA-seq data with 0.5 AUROC improvement over existing methods in drug effect prediction on gene expression. Published in *iScience*.
- **Graph Neural Networks:** Training graph attention networks on spatial transcriptomics and scRNA-seq data for cell communication inference.
- **Data Engineering:** Created and deployed the first cell type-specific gene network database across millions of cells from public scRNA-seq data repositories for network biology research using LAMP stack, Neo4j, and Jenkins. Presented at *RECOMB/ICSB* and *Cell Symposia* Conferences 2023.
- **Precision Medicine:** Integrated scRNA-seq with genome wide association studies (GWAS) to identify genetic causes of memory deficits in traumatic brain injury and calculated polygenic risk scores to improve patient stratification and diagnosis. Submitted to *PLOS Genetics* and *bioRxiv* and presented at *Western Neurotrauma Conference* 2024.
- **Drug Target Discovery:** Integrated scRNA-seq gene networks and drug signature databases to discover and validate 4 drug targets that weaken cancer resistance to immunotherapy. Submitted to *Nature Communications* and *bioRxiv*.

**Bioinformatics Researcher, Advisor: Professor Hilary Collier**

September 2020 – October 2023

**UCLA Department of Molecular Biology**

Los Angeles, CA

Multimomics representation learning of cancer heterogeneity. Published in *Communications Biology* and featured by *UCLA Health* and the *National Cancer Institute*.

- **Representation Learning:** Performed nonnegative matrix factorization on RNA-seq and methylation data of 24 cancer types in The Cancer Genome Atlas to identify latent epigenomic features that correlate with cancer survival.
- **Neural Networks:** Trained neural network to predict log hazard of cancer patients from RNA-seq data, which significantly stratified testing cohort into high and low survival groups.

## PROJECTS

**GeneRegRAG:** Created multi-agent RAG/GraphRAG system that incorporates gene interaction knowledgebase with biomedical fine-tuned LLMs to assist with bioinformatics research.

## FEATURED PUBLICATIONS

**Cheng, M., Mitra, M. & Collier, H.** Pan-cancer landscape of epigenetic factor expression predicts tumor outcome. *Communications Biology*. (2023).

Littman, R., **Cheng, M.**, Wang, N., Peng, C. & Yang, X. SCING: Inference of robust, interpretable gene regulatory networks from single cell and spatial transcriptomics. *iScience*. (2023).

## EDUCATION

**University of California, Los Angeles (UCLA)**

Los Angeles, CA

*Ph.D., Bioinformatics* | Overall GPA: 4.0/4.0

Anticipated June 2026

• Relevant Coursework: Natural Language Processing, Machine Learning and Statistical Methods in Bioinformatics

*B.S., Molecular Biology, Bioinformatics* | Overall GPA: 3.919/4.0

June 2021

• Relevant Coursework: Data Science, Machine Learning, Algorithms and Data Structures

## HONORS AND AWARDS

**Hyde Fellowship Award – UCLA Department of Integrative Biology and Physiology**

2024

- Received \$42,600 to support my dissertation research in multimomics machine learning methods development.