

EDUCATION

University of California, Los Angeles, Fielding School of Public Health, CA
Master of Science in Biostatistics | GPA: 4.00/4.00
 Advisor: [Dr. Matteo Pellegrini](#)

Sept. 2023 – Current

Southwest University, School of Life Sciences, China
Bachelor of Science in Biological Sciences | GPA: 3.84/4.00 (Ranked 2/65)
 Outstanding Graduate
 Thesis: *Analytic Hierarchy Process for Invasive Plant Management*

Sept. 2018 – June 2022

HONORS

Warren Alpert Computational Biology and AI Network Fellow	2024-2025
Fielding Dean's Leadership Grant	2023-2025
Steve Wallace Policy Fellowship	2024
APEX Funding, UCLA Human Genetics	2024
International Research Award, Southwest University	2021
Second- and Third-Class Academic Excellence Scholarships, Southwest University	2019, 2020, 2021

RESEARCH

Influenza Vaccination: DNA Methylation and Immune Response Mechanisms Los Angeles, CA
 Supervised by [Dr. Matteo Pellegrini](#) Mar. 2024 – Current

- Established a **multivariate prediction model** with LOOCV to link targeted **bisulfite sequencing DNA methylation** profiles to sero-protection (day 0, day 28) and sero-conversion (day 28) post-influenza injection, identifying key CpG sites and **RIG-I signaling pathway** as the key regulator of vaccine-induced immunity.
- Integrated DNA methylation, bulk **RNA-seq**, and **cytokine** data through **eQTL** and co-expression analyses to uncover **regulatory mechanisms** and potential therapeutic targets.

Fast and powerful statistical method for context-specific QTL mapping in multi-context genomic studies Los Angeles, CA
 Supervised by [Dr. Brunilda Balliu](#) Mar. 2025 – Current

- Enhanced the accuracy of multiple testing correction in [FastGxC](#) by integrating [mashr](#), enabling efficient identification of tissue- and cell-type-specific eQTLs from bulk multi-tissue and single-cell RNA-seq data.

Nonlinear Aging Dynamics in Co-methylation Network Los Angeles, CA
 Graduate Student Researcher | Supervised by [Dr. Feng Gao](#) Sept. 2024 – Current

- Analyzed non-linear **DNA methylation** patterns in **aging** mice colon tissue, identifying **graph-based aDMR clusters** linked to gene expression and pathways, and uncovering age-related functional changes through gene set enrichment analysis.

Single-Cell RNA-Seq for Cell Type Annotation Los Angeles, CA
 Supervised by Dr. [Jingyi Jessica Li](#) May 2024 – June 2024

- Analyzed **single-cell RNA-seq** data from human bone marrow and pancreas to identify cell types through **Seurat**-based preprocessing, dimensional reduction, clustering, and **biomarker** identification.

Inferring Immune Histories from SARS-CoV-2 RNA-seq Data Los Angeles, CA
 Supervised by [Dr. Vanessa D. Jonsson](#) Sept. 2024 – Current

- Designed a **pipeline** integrating immune cell deconvolution, **metagenomic annotation**, TCR/BCR repertoire analysis, and HLA-epitope mapping from SARS-CoV-2 **RNA-seq** data to **infer immune histories**, validated against publicly available antibody datasets.

Statistical Analysis for Biology and Biomedicine Research Chongqing, China
 Undergraduate Research Assistant Jun. 2021 – Jan. 2023

- Modelled random walks using **MCMC** to analyze time-homogeneous, recurrent, and transient properties in biology.
- Identified significant stage-specific effects of irrigation on rice yield across five growth stages by **multivariate linear regression**.
- Applied **logistic regression** to identify dietary habits, BMI, and stress as significant factors influencing semen quality.

Lymphocyte Regeneration after Thymocyte Damage in Zebrafish Chongqing, China
 Supervised by [Dr. Li Li](#) Oct. 2019 – June 2020

- Established a zebrafish thymocyte damage model with 2 mM Metronidazole, revealing the **CXCL12/CXCR4 signaling pathway** as critical for **T-lymphocyte regeneration** through WISH, confocal microscopy, and **RT-qPCR**.
- Demonstrated that pathway inhibition with WZ811 significantly impaired lymphocyte recovery.

PUBLICATIONS

- **Ai, J.**, Pickering, H., Pellegrini, M. *et al.* Influenza Vaccination: DNA Methylation and Immune Response Mechanisms. *Genome Biology*. (forthcoming).
- **Ai, J.**, Fan, Y., Gao, F. *et al.* Nonlinear Aging Dynamics in Co-methylation Network. *Cell Reports*. (forthcoming).
- **Ai, J.** (2021) Lifestyle Does Affect Semen Quality: Factor Determination in a Statistical Way. *Lecture Notes in Medicine and Life Sciences*, 4, 163–171. [DOI: 10.23977/behdp.2021021](https://doi.org/10.23977/behdp.2021021).

CONFERENCES

2025 Computational Genomics Summer Institute (CGSI)	UCLA, Los Angeles, CA Aug. 2025
2025 Lange Symposium on Computational Statistics	UCLA, Los Angeles, CA Jan. 2025
10th Annual QCBio Retreat	UCLA, Los Angeles, CA Sept. 2024
2024 Computational Genomics Summer Institute (CGSI)	UCLA, Los Angeles, CA Aug. 2024

POSTERS & PRESENTATIONS

- “Influenza Vaccination Impact on DNA Methylation in UGA6 Cohort”, UCLA, Nov. 2024
- “Higher Education in Public Health”, Fielding School of Public Health, UCLA, Apr. 2024
- “Key Factors Linked to Depression Before Adjuvant Therapy in Breast Cancer”, UCLA, Mar. 2024
- “Lymphocyte Regeneration After Thymocyte Damage in Zebrafish”, Southwest University, June 2020

PROFESSIONAL EXPERIENCE

- Intern** at Western Biomedical Technology Inc. Mar. 2021 – June 2021
 - Designed Python and R pipelines to improve **western blot** and **ELISA** accuracy and managed experiments and biweekly reports across **immunology**, **histopathology**, and **molecular biology**.
- Office Assistant** at SWU Life Science Administrative Office Oct. 2018 – Jun. 2021
 - **Mentored** 65 students, facilitating academic advising sessions, and coordinating research opportunities.
- Volunteer** at SWU Central Library Chongqing, China | Oct. 2019 – Jan. 2020
 - Organized a **charity event** for 200+ attendees and supported library operations.

TEACHING ASSISTANT

C&S BIO M187: Research Communication (4 units)	UCLA, Los Angeles, CA Mar. 2025 – June 2025
MCD BIO 187AL: Research Immersion Laboratory in Genomic Biology (5 units)	UCLA, Los Angeles, CA June 2024 – Aug. 2024 & June 2025 – Aug. 2025

EXPERTISE

Computational & Statistical

- *Languages*: **R** (tidyverse, ggplot2, glmnet, RShiny), **Python** (NumPy, Pandas, Biopython, Scikit-learn, Pybedtools, Matplotlib), **MATLAB**, SAS, STATA, **SQL**, HTML/CSS/JavaScript, LaTeX
- *Platforms*: **Linux** scripting, **Git**/GitHub, **Hoffman2** cluster, Docker, Cloud Platforms (GCP, AWS, Azure, OCI)
- *Data Analysis & Modeling*: **ML**, **Bayesian inference**, **deep learning** (Keras, TensorFlow, PyTorch), **simulation**, **linear models**, **optimization**, graph theory
- *High-Performance Computing (HPC)*: Workflow orchestration, parallelized analysis, cluster-based computations

Bioinformatics

- *Analysis*: **GWAS**, **EWAS**, eQTL analysis, gene enrichment analysis, polygenic risk scores, Mendelian randomization, Gene Ontology analysis, multi-omics integration, genome annotation, **single-cell data analysis** (scRNA-seq, scDNA-seq)
- *Tools*: BLAST, InterProScan, PSIPRED, AlphaFold, ChimeraX, UCSC Genome Browser, Ensembl, Galaxy, Bioconductor, BEDTools, STAR, **DESeq2**, **Seurat**, edgeR, Enrichr

Mathematical

- *Core Mathematics*: Linear Algebra, Real Analysis, Probability and Statistics, Stochastic Process, Calculus, Partial Differential Equations, Discrete Mathematics, Infinite Theory

Laboratory

- *Molecular Biology*: **PCR**, qPCR, DNA/RNA extraction, **CRISPR/Cas9**, cloning, electrophoresis, next-generation sequencing (**NGS**) library preparation
- *Genomics*: RNA-seq, ChIP-seq, **single-cell RNA-seq**, bisulfite sequencing
- *Proteomics*: **Western blot**, **ELISA**, mass spectrometry, chromatin immunoprecipitation (**ChIP**)
- *Cell Biology*: Cell culture, transfection, confocal and fluorescence microscopy, immunofluorescence, **flow cytometry**