

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 – Dec. 2025

Southwest University, School of Life Sciences, China
Bachelor of Science in Biological Sciences | GPA: 3.84/4.00 (Ranked 2/65)
 Outstanding Graduate

Sept. 2018 – June 2022

PUBLICATIONS

- Yen, P., **Ai, J.**, & Wong, W. K. Desirability Functions and Applications in the Biosciences. *Statistical Methods in Medical Research*. (submitted).
- Ai, J.**, Pickering, H., Pellegrini, M. *et al.* Influenza Vaccination: DNA Methylation and Immune Response Mechanisms. *Genome Biology*. (submitted).
- Ai, J.**, Fan, Y., Gao, F. *et al.* Nonlinear Aging Dynamics in Co-methylation Network. *Aging Cells*. (submitted).
- Ai, J.** Lifestyle does affect semen quality: factor determination in a statistical way. *Lecture Notes in Medicine and Life Sciences*. 2021;4:163–171. doi:10.23977/behdp.2021021

RESEARCH**Desirability Functions and Applications in the Biosciences**

Los Angeles, CA

Supervised by [Dr. Weng Kee Wong](#)

June 2025 – Current

- Co-authored the review and contributed the software landscape and metaheuristics sections, detailing practical R/JMP/Minitab workflows and Genetic Algorithms/Particle Swarm Optimization for non-smooth desirability surfaces, validated on MIMIC-IV.

Cell Type Specific eQTLs for Bowel Inflammatory Disease

Los Angeles, CA

Supervised by [Dr. David Casero](#)

June 2025 – Current

- Deconvolved bulk RNA-seq into cell-type specific expression (CIBERSORTx, bMIND) and mapped cell-type specific eQTLs with FastGxC in rectum and ileum biopsies from inflammatory bowel disease patients.

Influenza Vaccination: DNA Methylation and Immune Response Mechanisms

Los Angeles, CA

Supervised by [Dr. Matteo Pellegrini](#)

Mar. 2024 – June 2025

- Modeled DNA methylation to predict vaccine responsiveness, mapped response-associated CpGs to target genes, and tested cis-regulatory and transcription-factor mediated pathways connecting methylation to gene expression.

FastGxC: 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 – June 2025

- Integrated mashr and benchmarked hierarchical FDR (TreeQTL/TreeBH) within FastGxC to improve multiple-testing accuracy and enable efficient detection of context-specific and shared eQTLs in bulk and single-cell RNA-seq.

Nonlinear Aging Dynamics in Co-methylation Network

Los Angeles, CA

Supervised by [Dr. Feng Gao](#)

Aug. 2024 – May 2025

- Constructed age-stratified co-methylation networks from aDMRs in mice to characterize nonlinear aging dynamics, mapped topology shifts to GO pathways, and externally validated a DMR-summary random-forest aging clock (AUROC = 0.998).

Single-Cell RNA-Seq for Cell Type Annotation

Los Angeles, CA

Supervised by [Dr. Jingyi Jessica Li](#)

May 2024 – June 2024

- Annotated cell types in human bone marrow and pancreas scRNA-seq using Seurat (QC, dimensionality reduction, clustering, marker discovery).

Inferring Immune Histories from SARS-CoV-2 RNA-seq Data

Los Angeles, CA

Supervised by [Dr. Vanessa D. Jonsson](#)

Sept. 2024 – Mar. 2025

- Built and validated a SARS-CoV-2 RNA-seq immunoprofiling pipeline (cell deconvolution, metagenomics, TCR/BCR repertoire, HLA-epitope mapping) to infer immune histories using public 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

- Built a 2 mM metronidazole zebrafish thymocyte damage model and showed, using WISH, confocal imaging, and RT-qPCR, that CXCL12/CXCR4 drives T-cell regeneration; WZ811 blockade markedly reduced recovery.

PROFESSIONAL EXPERIENCE

Research Intern at Cedars-Sinai	July 2025 – Current
TA for C&S BIO M187: Research Communication (4 units) at UCLA	Mar. 2025 – June 2025
TA for MCD BIO 187AL: Research Immersion Laboratory in Genomic Biology (5 units) at UCLA	June 2024 – Aug. 2024 & June 2025 – Aug. 2025
Graduate Student Researcher at UCLA	Sept. 2024 – Mar. 2025
Immunology Intern at Western Biomedical Technology Inc.	Mar. 2021 – June 2021

FELLOWSHIPS

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

CONFERENCES

2024 Computational Genomics Summer Institute (CGSI)	UCLA, Los Angeles, CA Aug. 2024
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POSTERS & PRESENTATIONS

- “Influenza Vaccination Impact on DNA Methylation in UGA6 Cohort”, UCLA, May 2025
- “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