JIACHEN AI

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EDUCATION

University of California, Los Angeles, Fielding School of Public Health, CA — Sept. 2023 – Dec. 2025
Master of Science in **Biostatistics** | GPA: 4.00/4.00

Southwest University, School of Life Sciences, China — Sept. 2018 – June 2022
Bachelor of Science in **Biological Sciences** | GPA: 3.84/4.00 (Ranked 2/65) |Outstanding Graduate

PUBLICATIONS

- Li, J., **Ai, J**.*, Wong, W. K. Clinical Utility Index in Pharmaceutical Decision-Making: A Review and Optimization of the Index Using Optimal Design Strategies via Particle Swarm Optimization. *Computer Methods and Programs in Biomedicine*. (CMPB-D-25-06848)
- Yen, P., **Ai, J.***, & Wong, W. K. Desirability Functions and Applications in the Biosciences. *Statistical Methods in Medical Research*. (SMM-25-0705)
- **Ai, J.**, Pickering, H., Pellegrini, M. *et al*. Influenza Vaccination: DNA Methylation and Immune Response Mechanisms. *Genome Biology*.
- **Ai, J.**, Fan, Y., Gao, F. *et al*. Nonlinear Aging Dynamics in Co-methylation Network. *Aging Cells*.
- **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

Optimal Design and Desirability Functions — Los Angeles, CA
Supervised by Dr. Weng Kee Wong — June 2025 – Current
- Co-authored a review on optimal dose design using the Emax Clinical Utility Index model and developed the first Shiny app (https://jiachenai.shinyapps.io/c-optimal_by_PSO/) for efficient CUI-based dose selection.
- Co-authored a review paper and contributed the software and metaheuristics sections, detailing the practical application of Particle Swarm Optimization for non-smooth desirability function.

Cell Type Specific eQTLs for Inflammatory Bowel Disease — Los Angeles, CA
Supervised by Dr. David Casero — June 2025 – Current
- Deconvolved bulk RNA-seq into cell-type specific expression with CIBERSORTx and 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
- 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 Medical Center	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

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