

# GUAN'AO YAN

Contact: (+1) 213-469-7747 ◊ [gayan@g.ucla.edu](mailto:gayan@g.ucla.edu) ◊ <https://www.guanaoy.com>  
520 Portola Plaza, Room 8911, Los Angeles, CA 90095

## RESEARCH AREA

---

My research interests lie in developing new statistical methods for understanding real-world data. Specific research topics include

- Statistical Bioinformatics
  - Statistical methods for analyzing high-dimensional single-cell and spatial omics data
  - Using synthetic data to enhance the statistical rigor in single-cell and spatial omics data analysis
- General Statistical Methodologies: High-dimensional model inference and variable selection
- Statistics in Education: Statistical methods for promoting education equity (reported by Forbes)

## EDUCATION

---

<b>University of California, Los Angeles</b>	09/2020 - Present
Ph.D. Candidate in Statistics Advisor: Dr. Jingyi Jessica Li	
<b>Zhejiang University</b>	09/2017 - 03/2020
M.Sc in Probability and Mathematical Statistics Advisor: Dr. Yi Zhang	
<b>Shandong University</b>	09/2013 - 06/2017
B.Sc in Mathematics and Applied Mathematics B.Ec in Economics	

## GRANTS & AWARDS

---

Dissertation Year Fellowship (\$38,000), University of California, Los Angeles	2024
JXTX+CSHL Genome Informatics 2023 Scholarship (\$2,000), Cold Spring Harbor Laboratory	2023
Don Ylvisaker Award for the Best Practice of Statistics, University of California, Los Angeles	2023
Interdisciplinary Opportunity Award (\$10,000), NSF-Simons CMCF	2022
Most Promising Statistician Award, University of California, Los Angeles	2022
Summer Mentored Research Fellowship (\$6,000), University of California, Los Angeles	2021
China National Scholarship	2018
Merit Graduate Student Award, Zhejiang University	2018
Outstanding Student Award, Shandong University	2014 - 2016
Hua Loo-Keng Talent Scholarship, Chinese Academy of Sciences	2015

## PUBLICATIONS & MANUSCRIPTS

---

†*Indicating co-first author*

**G. Yan**, J.J. Li and M. Biggin (2024). Question-Score Identity Detection (Q-SID): A statistical algorithm to detect collusion groups with error quantification from exam question scores. *arXiv*, 2407.07420. (Under review at *Journal of the American Statistical Association*) [Website] [Forbes article] [Podcast]

**G. Yan**, S. Hua and J.J. Li (2024). Categorization of 31 computational methods to detect spatially variable genes from spatially resolved transcriptomics data. *arXiv*, 2405.18779. (Accepted by *Nature Communications*)

J. Zhao, F. Lao, **G. Yan** and Y. Zhang (2024). How data heterogeneity affects innovating knowledge and information in gene identification: A statistical learning perspective. *Journal of Innovation & Knowledge*, 9-3.

**G. Yan**, D. Song and J.J. Li (2023). scReadSim: a single-cell RNA-seq and ATAC-seq read simulator. *Nature Communications*, 14(1), 7428. [Software] [Website]

D. Song, Q. Wang, **G. Yan**, T. Liu and J.J. Li (2023). scDesign3 generates realistic in silico data for multimodal single-cell and spatial omics. *Nature Biotechnology*, 1-6. [Software]

Z. Li, Z. M. Patel, D. Song, **G. Yan**, J. J. Li and L. Pinello (2023). Benchmarking computational methods to identify spatially variable genes and peaks. *bioRxiv*, 2023-12. (Under review at *Nature Methods*)

S. Tang, H. Wang, **G. Yan**, L. Zhang (2022). Empirical likelihood based tests for detecting the presence of significant predictors in marginal quantile regression. *Metrika*, 1-31.

S. Chen<sup>†</sup>, **G. Yan**<sup>†</sup>, W. Zhang, J. Li, R. Jiang and Z. Lin (2021). RA3 is a reference-guided approach for epigenetic characterization of single cells. *Nature Communications*, 12(1), 1-13. [Software]

J. Zhao, **G. Yan** and Y. Zhang (2021). Robust estimation and shrinkage in ultrahigh dimensional expectile regression with heavy tails and variance heterogeneity. *Statistical Papers*, 1-28.

J. Zhao<sup>†</sup>, **G. Yan**<sup>†</sup> and Y. Zhang (2019). Semiparametric expectile regression for high-dimensional heavy-tailed and heterogeneous data. *arXiv*, 1908.06431. (Accepted at *Applied Mathematics-A Journal of Chinese Universities*)

## PATENTS

---

M. Biggin, J.J. Li, **G. Yan**. Systems and methods for detecting collusion in student testing using graded scores or answers for individual questions (Serial No. 17/450,984; US Patent 11,915,615 B2)

## SOFTWARE

---

**Q-SID** An online anti-collusion proctoring system [Website]

**scReadSim** Python package of synthetic read simulator designed for the single-cell multiomics data [Software]

**RA3** R package of “RA3 is a reference-guided approach for epigenetic characterization of single cells” [Software]

## PRESENTATIONS

---

### Oral Presentations

- NHGRI Genome Tech Dev Working Group, Jackson Laboratory, USA 1/2025
- Department of Statistics and Data Sciences, University of California, Los Angeles, USA 11/2024
- Department of Mathematical Sciences, New Jersey Institute of Technology, USA 11/2024
- Joint Statistical Meetings, Portland, USA 08/2024
- Institute for Computational and Experimental Research in Mathematics, Providence, USA 12/2023
- Jonsson Comprehensive Cancer Center Gene Regulation Seminar, Los Angeles, USA 11/2023
- Institute for Quantitative and Computational Biosciences Research Seminar, Los Angeles, USA 12/2022
- NSF-Simons Center for Multiscale Cell Fate 5th Annual Symposium, Irvine, USA 10/2022

- The 7th International Conference on Statistics and Probability, IMS-China, Dalian, China 07/2019

### Poster Presentations

- Cold Spring Harbor Laboratory Genome Informatics Conference, New York, USA 12/2023
- RECOMB/ISCB Conference on Regulatory & Systems Genomics, Los Angeles, USA 11/2023
- Chan Zuckerberg Initiative Single-Cell Biology 2023 Annual Meeting, Carlsbad, USA 11/2023
- ISMB/ECCB, Lyon, France 07/2023
- Los Angeles Bioscience Ecosystem Summit, Los Angeles, USA 05/2023
- Jonsson Comprehensive Cancer Center Retreat Poster Session, Los Angeles, USA 05/2023
- Institute for Quantitative and Computational Biosciences Poster Session, Los Angeles, USA 09/2022

## TEACHING & MENTORING

---

### Teaching Assistant

- STATS 205, Hierarchical Linear Models, UCLA Spring 2024
- STATS 203, Large Sample Theory, UCLA Winter 2024
- Statistical Science with Applications to Epidemiology, ElevatePro Summer 2021
- MATH 1001, Advanced Mathematics, Zhejiang University Fall 2019
- MATH 1001, Advanced Mathematics, Zhejiang University Fall 2018

### Workshop Instructor

- Coordinator & Presenter, QCBio Workshop, UCLA May 2022  
*“Statistical Methods for Enhancing the Rigor in Single-cell RNA-seq Data Analysis”*

### Guest Lecturer

- STATS 205, Hierarchical Linear Models, UCLA Spring 2024
- BIOINFO 229, Current Topics in Bioinformatics, UCLA Winter 2024

### Undergraduate Student Mentor

- Weijian Wang, Zhejiang University 12/2022 - Present
- Zhiyin Liu, Hong Kong University of Science and Technology 12/2022 - Present
- Shuo Hua, Tsinghua University 06/2022 - 12/2022

## PROFESSIONAL EXPERIENCE

---

### Graduate Student Reseracher

Department of Statistics & Data Science  
 University of California, Los Angeles  
 Advisor: Dr. Jingyi Jessica Li

09/2021 – Present

### Research Scientist Intern

Data and Statistical Sciences  
 Product Development Department  
 Genentech, Inc.

06/2024 – 09/2024

*“Enhancing Statistical Practice in Recurrent Event Endpoint Data Analysis”*

### Research Scientist Intern

Data and Statistical Sciences  
 Product Development Department  
 Genentech, Inc.

06/2023 – 09/2023

*“Dynamic Monitoring of Ongoing Clinical Trials for Early Decision Making”*

**Research Assistant**

06/2019 – 04/2020

Department of Statistics

The Chinese University of Hong Kong

Advisor: Dr. Zhixiang Lin

**Undergraduate Researcher**

06/2016 – 06/2017

Academy of Mathematics and Systems Science

Chinese Academy of Sciences

Advisor: Dr. Jianming Xia

**ASSISTANCE WITH GRANT PROPOSALS**

---

**Single-Cell Biology Data Insights Grant**

07/01/2022 – 12/31/2023

Chan-Zuckerberg Initiative

\$200,000

*“Enhancing Rigor and Reliability of Single-Cell Data Science”* (PI: Dr. Jingyi Jessica Li)**R35 GM140888**

06/01/2021 – 05/31/2026

NIH / NIGMS MIRA for established investigators

\$1,848,665

*“Statistical methods for elucidating regulatory mechanisms and functional impacts of transcriptome variation at population and single-cell scales”* (PI: Dr. Jingyi Jessica Li)**PROFESSIONAL SERVICE**

---

**Statistical Consulting Services**

Jonsson Comprehensive Cancer Center

**Reviewer for Scientific Journals** (# papers in parentheses)

Nature Communications (1), Bioinformatics (5)

**Co-reviewer for Scientific Journals**

Cell (2), Nature Biotechnology (1), Nature Methods (4), Nature Communications (3), Nature Machine Intelligence (1), Genome Biology (2), Genome Research (1), Bioinformatics (2), Journal of the American Statistical Association (1), Annals of Applied Statistics (1), NAR Genomics and Bioinformatics (8), Science Bulletin (1), Statistics in Medicine (1)

**Co-reviewer for Scientific Conferences**

Research in Computational Molecular Biology (5), Intelligent Systems for Molecular Biology (5), National Council on Measurement in Education (8)

**PROFESSIONAL AFFILIATIONS**

---

Institute of Mathematical Statistics

2023 - Present

American Statistical Association

2022 - Present

American Society of Human Genetics

2022 - 2023

UCLA Jonsson Comprehensive Cancer Centers

2022 - Present

International Indian Statistical Association

2022 - 2023