

# GUAN'AO YAN

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## RESEARCH AREA

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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 enforcing education equity (reported by Forbes)

## EDUCATION

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

## AWARDS

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| JXTX+CSHL Genome Informatics 2023 Scholarship, Cold Spring Harbor Laboratory                   | 2023        |
| Don Ylvisaker Award for the Best Practice of Statistics, University of California, Los Angeles | 2023        |
| Interdisciplinary Opportunity Award, NSF-Simons Center for Multiscale Cell Fate Research       | 2022        |
| Most Promising Statistician Award, University of California, Los Angeles                       | 2022        |
| Summer Mentored Research Fellowship, 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

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†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. [Website] [Forbes article] [Podcast] (Under review at *Journal of the American Statistical Association*)

**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. (Under revision at *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.

## PATENTS

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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

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**Q-SID** An online anti-collusion proctoring system, 2022. [Website]

**scReadSim** Python package of synthetic reads simulator designed for the single-cell multiomics data, 2022. [Software]

**RA3** R package of “RA3 is a reference-guided approach for epigenetic characterization of single cells”, 2021. [Software]

## PRESENTATIONS

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### Oral Presentations

- 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

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### Teaching Assistant

- STATS 205, Hierarchical Linear Models, UCLA Spring 2024
- STATS 203, Large Sample Theory, UCLA Winter 2024
- 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

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### 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

06/2024 – 09/2024

### Research Scientist Intern

Data and Statistical Sciences  
 Product Development Department  
 Genentech

06/2023 – 09/2023

### Research Assistant

Department of Statistics  
 The Chinese University of Hong Kong  
 Advisor: Dr. Zhixiang Lin

06/2019 – 04/2020

### Undergraduate Researcher

Academy of Mathematics and Systems Science  
 Chinese Academy of Sciences  
 Advisor: Dr. Jianming Xia

06/2016 – 06/2017

## PROFESSIONAL SERVICE

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**Reviewer for Scientific Journals:**

Bioinformatics (5)

**Co-reviewer for Scientific Journals:**

Cell (2), Nature Biotechnology (1), Nature Methods (3), Nature Communications (3), Nature Machine Intelligence (1), Genome Biology (2), Bioinformatics (2), Journal of the American Statistical Association (1), Annals of Applied Statistics (1), NAR Genomics and Bioinformatics (5), Science Bulletin (1), Statistics in Medicine (1)

**Co-reviewer for Scientific Conferences:**

Research in Computational Molecular Biology (5), Intelligent Systems for Molecular Biology (5)

**PROFESSIONAL AFFILIATIONS**

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Institute of Mathematical Statistics

American Statistical Association

American Society of Human Genetics

UCLA Jonsson Comprehensive Cancer Centers

International Indian Statistical Association