

Jia Zhao

Tenure-track Associate Professor, School of Mathematical Sciences, Shanghai Jiao Tong University

Email: jia.zhao@sjtu.edu.cn

Website: <https://jiazhao97.github.io/>

[Google scholar](#)

EMPLOYMENT

- **Shanghai Jiao Tong University** Shanghai, China
Tenure-track Associate Professor, School of Mathematical Sciences 2026 – Present
- **Yale University** New Haven, CT, United States
Postdoctoral Associate in Biostatistics 2023 – 2026
Advisors: Professor Hongyu Zhao and Professor Rui Chang

EDUCATION

- **The Hong Kong University of Science and Technology** Hong Kong, China
Ph.D. in Mathematics 2019 – 2023
Advisor: Professor Can Yang
Dissertation: *Computational and statistical methods for data integration and causal inference*
- **Beijing Normal University** Beijing, China
B.S. in Mathematics & Applied Mathematics 2015 – 2019

SELECTED PUBLICATIONS

Note: (*) denotes equal-contribution first authorship.

1. **Zhao, J.**, Zhang, X., Wang, G., Lin, Y., Liu, T., Chang, R. B., and Zhao, H. (2026). Interpretable, flexible and spatially aware integration of multiple spatial transcriptomics datasets from diverse sources. *Nature Genetics*, 58(5), 1138-1150. url: <https://www.nature.com/articles/s41588-026-02579-x>.
2. Hsu, I. U., **Zhao, J.**, Lin, Y., Guo, Y., Xu, Q. J., Shao, Y., Wang, R. L., Yin, D., Ghoshal, K., Mourad, R., Pozzi, A., Halabi, C. M., Young, L. H., Zhao, H., Zhang, L., and Chang, R. B. (2026). Lineage and organ signals sequentially build organ intrinsic nervous systems. *Nature*. url: <https://www.nature.com/articles/s41586-026-10490-y>.
3. Wang, G. (*), **Zhao, J. (*)**, Yan, Y., Wang, Y., Wu, A. R., and Yang, C. (2023). Construction of a 3D whole organism spatial atlas by joint modelling of multiple slices with deep neural networks. *Nature Machine Intelligence*, 5(11), 1200-1213. url: <https://www.nature.com/articles/s42256-023-00734-1>.
4. **Zhao, J. (*)**, Wang, G. (*), Ming, J., Lin, Z., Wang, Y., **The Tabula Microcebus Consortium** (†), Wu, A. R., and Yang, C. (2022). Adversarial domain translation networks for integrating large-scale atlas-level single-cell datasets. *Nature Computational Science*, 2(5), 317-330. url: <https://www.nature.com/articles/s43588-022-00251-y>.
5. Hu, X. (*), **Zhao, J. (*)**, Lin, Z., Wang, Y., Peng, H., Zhao, H., Wan, X., and Yang, C. (2022). Mendelian randomization for causal inference accounting for pleiotropy and sample structure using genome-wide summary statistics. *Proceedings of the National Academy of Sciences*, 119(28), e2106858119. url: <https://www.pnas.org/doi/10.1073/pnas.2106858119>.

6. **Zhao, J.**, Ming, J., Hu, X., Chen, G., Liu, J., and Yang, C. (2020). Bayesian weighted Mendelian randomization for causal inference based on summary statistics. *Bioinformatics*, 36(5), 1501-1508. url: <https://academic.oup.com/bioinformatics/article/36/5/1501/5583736>.

OTHER PUBLICATIONS (REVERSE CHRONOLOGICAL ORDER)

Note: **(*)** denotes equal-contribution first authorship. **(†)** denotes consortium membership.

1. Guo, Y., **Zhao, J.**, Chang, R. B., and Zhao, H. (2026). scGPD: single-cell informed gene panel design for targeted spatial transcriptomics. *Briefings in Bioinformatics*, 27(2), bbag160. url: <https://academic.oup.com/bib/article/27/2/bbag160/8658477>.
2. Xu, L., Zheng, W., Hu, J., Lin, Y., **Zhao, J.**, Wang, G., Liu, T., and Zhao, H. (2025). Improving polygenic risk prediction performance through integrating electronic health records by phenotype embedding. *The American Journal of Human Genetics*, 112(12), 3030-3045. url: [https://www.cell.com/ajhg/abstract/S0002-9297\(25\)00431-8](https://www.cell.com/ajhg/abstract/S0002-9297(25)00431-8).
3. **The Tabula Microcebus Consortium (†)**, Ezran, C. (*), Liu, S. (*), Chang, S. (*), ..., **Zhao, J.**, ..., Quake, S. R., Krasnow, M. A. (2025). A molecular cell atlas of mouse lemur, an emerging model primate. *Nature*, 644(8075), 173-184. url: <https://www.nature.com/articles/s41586-025-09113-9>.
4. Ezran, C. (*), Liu, S. (*), Chang, S. (*), ..., **The Tabula Microcebus Consortium (†)**, ..., Quake, S. R., Krasnow, M. A. (2025). Mouse lemur cell atlas informs primate genes, physiology and disease. *Nature*, 644(8075), 185-196. url: <https://www.nature.com/articles/s41586-025-09114-8>.
5. Liu, T., **Zhao, J.**, and Zhao, H. (2025). SuperGLUE facilitates an explainable training framework for multi-modal data analysis. *Cell Reports Methods*, 5(9). url: [https://www.cell.com/cell-reports-methods/fulltext/S2667-2375\(25\)00203-6](https://www.cell.com/cell-reports-methods/fulltext/S2667-2375(25)00203-6).
6. Zhang, X., Wang, L., **Zhao, J.**, and Zhao, H. (2025). Knockoff procedure improves susceptibility gene identifications in conditional transcriptome-wide association studies. *The American Journal of Human Genetics*, 112(10), 2476-2492. url: [https://www.cell.com/ajhg/fulltext/S0002-9297\(25\)00317-9](https://www.cell.com/ajhg/fulltext/S0002-9297(25)00317-9).
7. Wang, G., **Zhao, J.**, Lin, Y., Liu, T., Zhao, Y., and Zhao, H. (2025). scMODAL: a general deep learning framework for comprehensive single-cell multi-omics data alignment with feature links. *Nature Communications*, 16(1), 4994. url: <https://www.nature.com/articles/s41467-025-60333-z>.
8. Liu, S., Ezran, C., ..., **The Tabula Microcebus Consortium (†)**, ..., Krasnow, M. A., Ferrell Jr, J. E. (2024). An organism-wide atlas of hormonal signaling based on the mouse lemur single-cell transcriptome. *Nature Communications*, 15(1), 2188. url: <https://www.nature.com/articles/s41467-024-46070-9>.
9. Ming, J., **Zhao, J.**, and Yang, C. (2023). scPI: a scalable framework for probabilistic inference in single-cell RNA-sequencing data analysis. *Statistics in Biosciences*, 15, 633-656. url: <https://link.springer.com/article/10.1007/s12561-022-09335-9>.
10. Ming, J. (*), Lin, Z. (*), **Zhao, J.**, Wan, X., **The Tabula Microcebus Consortium (†)**, Yang, C., and Wu, A. R. (2022). FIRM: Flexible integration of single-cell RNA-sequencing data for large-scale multi-tissue cell atlas datasets. *Briefings in Bioinformatics*, bbac167. url: <https://academic.oup.com/bib/article/23/5/bbac167/6585621>.

PREPRINTS

1. **Zhao, J.**, Shan, X., Wang, G., Chu, T., Lin, C., Chang, R. B., and Zhao, H. (2026+). Spatial co-expression and cell-cell communication inference from spatially resolved transcriptomics with

CONCISE. bioRxiv preprint: [10.64898/2026.06.22.733860](https://doi.org/10.64898/2026.06.22.733860). *Submitted*.

- Wang, G., Liu, T., **Zhao, J.**, Cheng, Y., and Zhao, H. (2026+). Modeling and predicting single-cell multi-gene perturbation responses with scLAMBDA. bioRxiv preprint: [10.1101/2024.12.04.626878](https://doi.org/10.1101/2024.12.04.626878). *Under revision at Nature Genetics*.

SOFTWARES

Python Packages

INSPIRE	GitHub , Website , Paper link
Portal	GitHub , Paper link
STitch3D	GitHub , Website , Paper link

R Packages

CONCISE	GitHub , Website , Paper link
BWMR	GitHub , Paper link
MR-APSS	GitHub , Paper link

TALKS AND POSTERS

Invited Talks

- INSPIRE: interpretable, flexible and spatially-aware integration of multiple spatial transcriptomics datasets from diverse sources. 2025
Conference on Statistics in Genomics and Genetics Minneapolis, MN
- scPI: A scalable framework for probabilistic inference in single-cell RNA-sequencing data analysis. 2024
ICSA Applied Statistics Symposium Nashville, TN
- Adversarial domain translation networks for fast and accurate integration of large-scale atlas-level single-cell datasets. 2023
Capital of Statistics Remote

Contributed Talk

- Interpretable integration of multiple spatial transcriptomics datasets with INSPIRE. 2025
Joint Statistical Meetings Nashville, TN

Poster

- INSPIRE: interpretable, flexible and spatially-aware integration of multiple spatial transcriptomics datasets from diverse sources. 2024
18th Annual PQG Conference: AI for Genomics & Health Boston, MA

HONORS

- STATGEN Travel Award** 2025
Conference on Statistics in Genomics and Genetics
- Statistics in Biosciences Best Paper Award** 2024
Statistics in Biosciences
- Hong Kong PhD Fellowship (HKPFS) Extra Funding Award for Outstanding Academic and Research Performance** 2023
School of Science, The Hong Kong University of Science and Technology (HKUST)
- RedBird Academic Excellence Award** 2022
HKUST

- **Best Teaching Assistant for the Din-Yu Hsieh Teaching Award** 2022
Department of Mathematics, HKUST
For teaching assistance in MATH 3423 Statistical Inference, and MATH 2421 Probability
- **Best Teaching Assistant for the Din-Yu Hsieh Teaching Award** 2021
Department of Mathematics, HKUST
For teaching assistance in MATH 2411 Applied Statistics, and MATH 2431 Honors Probability
- **Epsilon Fund Award** 2021
Department of Mathematics, HKUST
- **HKUST Excellent Research Award** 2019
HKUST
- **Hong Kong PhD Fellowship** 2019 – 2023
Research Grants Council, University Grants Committee (Hong Kong)
- **Beijing Outstanding Graduate** 2019
Beijing Municipal Commission of Education & Beijing Normal University
- **National Scholarship** 2019
Ministry of Education of PRC

TEACHING

- **MATH 2411 Applied Statistics** Spring 2020, Fall 2020, Fall 2022
Teaching Assistant, Department of Mathematics, The Hong Kong University of Science and Technology (HKUST)
- **MATH 2421 Probability** Spring 2022
Teaching Assistant, Department of Mathematics, HKUST
- **MATH 2431 Honors Probability** Spring 2021
Teaching Assistant, Department of Mathematics, HKUST
- **MATH 3423 Statistical Inference** Fall 2021
Teaching Assistant, Department of Mathematics, HKUST

PROFESSIONAL SERVICES

Journal Reviewer

*Cell, Nature Computational Science,
Genome Research, Annals of Applied Statistics,
Journal of Translational Medicine, Computational and Structural Biotechnology Journal,
Human Genomics, Bioinformatics Advances*

REFERENCES

Hongyu Zhao

Ira V. Hiscock Professor of Biostatistics
Professor of Genetics and Professor of Statistics and Data Science
Yale University
New Haven, CT, United States
Email: hongyu.zhao@yale.edu

Rui Chang

Associate Professor
Department of Neuroscience
Department of Cellular and Molecular Physiology
Yale University

New Haven, CT, United States
Email: rui.chang@yale.edu

Can Yang

Professor
Department of Mathematics
The Hong Kong University of Science and Technology
Clear Water Bay, Kowloon, Hong Kong, China
Email: macyang@ust.hk

Angela Ruohao Wu

Associate Professor
Division of Life Science
Department of Chemical and Biological Engineering
The Hong Kong University of Science and Technology
Clear Water Bay, Kowloon, Hong Kong, China
Email: angelawu@ust.hk