

# Daiwei (David) Zhang

Department of Biostatistics, Epidemiology and Informatics  
Perelman School of Medicine, University of Pennsylvania  
423 Guardian Drive, Philadelphia, PA 19104  
[daiwei.zhang@pennmedicine.upenn.edu](mailto:daiwei.zhang@pennmedicine.upenn.edu)

## Research Interests

Methodology: machine learning, vision-language models, generative AI

Applications: spatial multi-omics, computational pathology, medical imaging

## Education and Training

Postdoctoral Training in Biostatistics, University of Pennsylvania, Philadelphia, PA    2021 – Present

Advisor: Mingyao Li

Ph.D. in Biostatistics and Scientific Computing, University of Michigan, Ann Arbor    2016 – 2021

Thesis: Novel statistical learning methods for  
high-dimensional complex biomedical data analysis

Advisors: Jian Kang & Seunggeun Lee

M.S. in Biostatistics, University of Michigan, Ann Arbor    2016 – 2019

Budapest Semester in Mathematics, Hungarian Academy of Sciences    2014

B.S. in Mathematics (with Honors), Calvin College, Grand Rapids, MI    2012 – 2016

## Research Experience

Research Associate in Biostatistics    2022 – Present

Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA

Postdoctoral Researcher in Biostatistics    2021 – 2022

Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA

Research Assistant in Biostatistics    2016 – 2021

University of Michigan, Ann Arbor, MI

Research Assistant in Mathematics    2013 – 2016

Calvin College, Grand Rapids, MI

## Teaching Experience

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| Teaching Assistant (Calculus, Differential Equations)<br>Department of Mathematics, Calvin College, Grand Rapids, MI                         | 2013 – 2014 |
| Teaching Assistant (Introduction to Programming, Information Technology)<br>Department of Computer Science, Calvin College, Grand Rapids, MI | 2012 – 2013 |

## Awards

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|--|-------------|
| Penn Conference on Big Data in Biomedical and Population Health Sciences Best Poster Award   | 2022        |
| International Biometric Society ENAR Distinguished Student Paper Award                       | 2021        |
| Michigan Student Symposium for Interdisciplinary Statistical Sciences Best Oral Presentation | 2021        |
| Rackham Conference Travel Grant  | 2018, 2020  |
| William Rinck Memorial Prize (for the best graduating mathematics major)                     | 2016        |
| W. L. Putnam Mathematical Competition (ranked top 9% internationally)                        | 2013        |
| William Rinck Memorial Scholarship (for outstanding mathematics majors)                      | 2013 – 2016 |
| Trustee Scholarship (full tuition coverage)  | 2012 – 2016 |

## Professional Service

### JOURNAL REFEREE

- Journal of Machine Learning Research
- Journal of the American Statistical Association
- Biometrics
- Statistics in Medicine
- Annals of Applied Statistics
- Biostatistics

## Publications

\*Equal contribution or alphabetical authorship

### JOURNAL ARTICLES

1. **D. Zhang**, A. Schroeder, H. Yan, H. Yang, J. Hu, M. Y. Y. Lee, K. S. Cho, K. Susztak, G. X. Xu, M. D. Feldman, E. B. Lee, E. E. Furth, L. Wang, and M. Li. Inferring super-resolution tissue architecture by integrating spatial transcriptomics with histology. *Nature Biotechnology*, in press, 2023.
2. **D. Zhang**, L. Li, C. Sripada, and J. Kang. Image response regression via deep neural networks. *Journal of the Royal Statistical Society Series B: Statistical Methodology*, page qkad073, 2023.
3. **D. Zhang**, T. Liu, and J. Kang. Density regression and uncertainty quantification with bayesian deep noise neural networks. *Stat*, 12(1):e604, 2023.
4. J. Hu, K. Coleman, **D. Zhang**, E. B. Lee, H. Kadara, L. Wang, and M. Li. Deciphering tumor ecosystems at super resolution from spatial transcriptomics with TESLA. *Cell Systems*, 14(5):404–417, 2023.
5. **D. Zhang** and J. Kang. Discussion of “LESA: Longitudinal elastic shape analysis of brain subcortical structures”. *Journal of the American Statistical Association*, 118(541):22–24, 2023.
6. X. Yin, L. S. Chan, D. Bose, A. U. Jackson, P. VandeHaar, A. E. Locke, C. Fuchsberger, H. M. Stringham, R. Welch, K. Yu, L. Fernandes Silva, S. K. Service, **D. Zhang**, E. C. Hector, E. Young, L. Ganel, I. Das, H. Abel, M. R. Erdos, L. L. Bonnycastle, J. Kuusisto, N. O. Stitziel, I. M. Hall, G. R. Wagner, J. Kang, J. Morrison, C. F. Burant, F. S. Collins, S. Ripatti, A. Palotie, N. B. Freimer, K. L. Mohlke, L. J. Scott, X. Wen, E. B. Fauman, M. Laakso, and M. Boehnke. Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. *Nature Communications*, 13(1):1644, March 2022.
7. L. G. Fritzsche, Y. Ma, **D. Zhang**, M. Salvatore, S. Lee, X. Zhou, and B. Mukherjee. On cross-ancestry cancer polygenic risk scores. *PLOS Genetics*, 17(9):e1009670, September 2021.
8. **D. Zhang**, R. Dey, and S. Lee. Fast and robust ancestry prediction using principal component analysis. *Bioinformatics*, 36(11):3439–3446, 2020.
9. S. Auyeung\*, J. Ruiter\*, and **D. Zhang\***. An algebraic characterization of highly connected 2n-manifolds. *Rose-Hulman Undergraduate Mathematics Journal*, 17(2):5, 2016.
10. C. Blom\*, T. DeVries\*, A. Hayes\*, and **D. Zhang\***. Analytic extension and conformal mapping in the dual and the double planes. *Rose-Hulman Undergraduate Mathematics Journal*, 14(2):9, 2013.

### UNDER REVIEW

11. K. Coleman, **D. Zhang**, J. Hu, and M. Li. Integrating gene expression and histology images for spatial domain detection in spatial transcriptomics. *Nature Communications*, under review.

12. G. Pei, V. Branchi, J. Min, K. I. Rajapakshe, D. Sadeghian, **D. Zhang**, Y. Liu, K. S. Cho, Y. Chu, E. Dai, G. Han, M. Li, C. Yee, P. M. Grandgenett, M. A. Hollingsworth, P. A. Guerrero, L. Wang, and A. Maitra. Spatial mapping of transcriptomic and lineage diversity in metastatic pancreatic cancer. *Nature*, under review.
13. Y. Liu, Y. Zhang, **D. Zhang**, G. Han, J. Min, G. Pei, K. S. Cho, E. Dai, Y. Chu, J. Jiang, R. Wang, P. A. Guerrero, A. Sinjab, J. Fujimoto, L. M. S. Soto, A. Serrano, J. A. Ajani, C. Yee, P. Mazur, A. J. Lazar, K. Lu, H. Kadara, M. Li, C. Friedman, W. H. Friedman, A. A. Jazaeri, A. Maitra, and L. Wang. Conserved cellular neighborhoods of cancer-associated fibroblasts revealed by high-plex pan-cancer single-cell spatial imaging analysis. *Cancer Cell*, under review.
14. **D. Zhang\***, J. Jiang\*, K. S. Cho\*, Y. Liu, J. Chen, R. L. Segura, X. Yan, G. Pei, L. M. S. Soto, Y. Chu, A. F. Sinjab, C. Yee, S. Kopetz, A. Maitra, A. A. Jazaeri, A. Futreal, H. Kadara, A. Lazar, J. Gao, M. Li, and L. Wang. iStarTLS: Advanced detection and phenotyping of tertiary lymphoid structures. *Cancer Cell*, under review.
15. **D. Zhang**, B. Gao, Q. Feng, A. Manichaikul, G. M. Peloso, R. P. Tracy, P. Durda, K. D. Taylor, Y. Liu, W. C. Johnson, S. Gabriel, N. Gupta, J. D. Smith, F. Aguet, K. G. Ardlie, T. W. Blackwell, R. E. Gerszten, S. S. Rich, J. I. Rotter, L. J. Scott, X. Zhou, and S. Lee. Proteome-wide association studies for blood lipids and comparison with transcriptome-wide association studies. *bioRxiv*, 10.1101/2023.08.17.553749, 2023.
16. E. C. Hector\*, **D. Zhang\***, X. Yin, M. Laakso, T. Xu, Y. Bai, M. Boehnke, J. Kang, and T. Yu. A dmGWAS approach to understanding genetic regulators of metabolic networks. Under review.

#### IN PREPARATION

17. A. Schroeder, **D. Zhang**, M. Loth, C. Luo, S. Piya, H.-H. Thai, B. Zhang, and M. Li. Predicting super-resolution gene expression in large tissues with iStarXL. In preparation.
18. J. Hu, K. Coleman, **D. Zhang**, E. Peyster, A. Janowczyk, and M. Li. Heart quality prediction by integrating histology with proteomics. In preparation.
19. M. Li\*, **D. Zhang\***, Y. Guo, and J. Kang. Neural network-guided independent component analysis with application to neuroimaging. In preparation.

#### Patents

1. **D. Zhang** and M. Li. Inferring super-resolution tissue architecture by integrating spatial transcriptomics with histology. US Patent, 2023.

#### Presentations

##### INVITED

1. **D. Zhang**, A. Schroeder, H. Yan, H. Yang, J. Hu, M. Y. Y. Lee, K. S. Cho, K. Susztak, G. X. Xu, M. D. Feldman, E. B. Lee, E. E. Furth, L. Wang, and M. Li. *Inferring super-resolution tissue architecture by integrating spatial transcriptomics with histology*. Joint Statistical Meetings, Portland, OR, 2024.

2. **D. Zhang**, L. Li, C. Sripada, and J. Kang. *Image-on-Scalar Regression via Deep Neural Networks*. Distinguished Student Paper Award Presentation, Spring Meeting, ENAR, International Biometric Society, Virtual Event, 2021.
3. **D. Zhang**, R. Dey, and S. Lee. *Fast and robust ancestry prediction with FRAPOSA*. Tools and Technology Seminar, Department of Internal Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI, 2020.

## CONTRIBUTED

4. **D. Zhang**, A. Schroeder, H. Yan, H. Yang, J. Hu, M. Y. Y. Lee, K. S. Cho, K. Susztak, G. X. Xu, M. D. Feldman, E. B. Lee, E. E. Furth, L. Wang, and M. Li. *Inferring super-resolution tissue architecture by integrating spatial transcriptomics with histology*. Annual Meeting, American Society of Human Genetics, Washington, DC, 2023.
5. **D. Zhang**, L. Li, C. Sripada, and J. Kang. *Image-on-Scalar Regression via Deep Neural Networks*. Michigan Student Symposium for Interdisciplinary Statistical Sciences, Virtual Event, 2021.
6. **D. Zhang**, Y. Guo, and J. Kang. *Neural network-guided independent component analysis with application to neuroimaging*. Spring Meeting, ENAR, International Biometric Society, Nashville, TN, 2020.
7. **D. Zhang**, R. Dey, and S. Lee. *Fast and robust ancestry inference using principal component analysis*. Annual Meeting, American Society of Human Genetics, San Diego, CA, 2018.