Daiwei (David) Zhang

Assistant Professor (Tenure-Track)
Department of Biostatistics
Department of Genetics
University of North Carolina
3107E Mcgavran-Greenberg Hall, Chapel Hill, NC 27599
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Research Interests

Methodology: computer vision, language models, generative AI

Applications: spatial omics, computational pathology, medical imaging

Education and Training

Postdoctoral Training, University of Pennsylvania, Philadelphia, PA   2021 – 2024
   Mentor: 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
   Mentors: 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

Assistant Professor (Tenure-Track) in Biostatistics and Genetics   2024 – Present
University of North Carolina, Chapel Hill, NC

Research Associate in Biostatistics   2022 – 2024
University of Pennsylvania, Philadelphia, PA

Postdoctoral Researcher in Biostatistics   2021 – 2022
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

Teaching Assistant (Calculus, Differential Equations) 2013 – 2014
Department of Mathematics, Calvin College, Grand Rapids, MI

Teaching Assistant (Introduction to Programming, Information Technology) 2012 – 2013
Department of Computer Science, Calvin College, Grand Rapids, MI

Awards

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

Publications

*Equal contribution or alphabetical authorship

JOURNAL ARTICLES

1. E. C. Hector*, **D. Zhang***, L. Tian*, J. Feng*, X. Yin, T. Xu, , M. Laakso, Y. Bai, J. Xiao, J. Kang, and T. Yu. Dissecting genetic regulation of metabolic coordination. *Briefings in Bioinformatics*, in press.

2. **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. *Human Genetics and Genomics Advances*, 6(1), 2024.

3. K. Coleman, A. Schroeder, M. Loth, **D. Zhang**, J. H. Park, J.-Y. Sung, N. Blank, A. J. Cowan, X. Qian, J. Chen, and others. Resolving tissue complexity by multimodal spatial omics modeling with miso. *Nature Methods*, pages 1–9, 2025.

4. Z. Bai*, D. Zhang *, Y. Gao*, B. Tao*, **D. Zhang***, S. Bao*, A. Enninful, Y. Wang, H. Li, G. Su, X. Tian, N. Zhang, Y. Xiao, Y. Liu, M. Gerstein, M. Li, Y. Xing, J. Lu, M. L. Xu, and R. a. Fan. Spatially exploring RNA biology in archival formalin-fixed paraffin-embedded tissues. *Cell*, 187(23):6760–6779, 2024.

5. **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*, pages 1–6, 2024.

6. **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.

7. **D. Zhang**, T. Liu, and J. Kang. Density regression and uncertainty quantification with bayesian deep noise neural networks. *Stat*, 12(1):e604, 2023.

8. 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.

9. **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.

10. 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.

11. L. G. Fritsche, 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.

12. **D. Zhang**, R. Dey, and S. Lee. Fast and robust ancestry prediction using principal component analysis. *Bioinformatics*, 36(11):3439–3446, 2020.

13. S. Auyeung*, J. Ruiter*, and **D. Zhang***. An algebraic characterization of highly connected 2n-manifolds. *Rose-Hulman Undergraduate Mathematics Journal*, 17(2):5, 2016.

14. 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

15. A. Schroeder, M. Loth, C. Luo, **D. Zhang**, S. Piya, E. Plowey, W. Hu, S. J. Chan, T. L. Reynolds, T. Carlile, P. Cullen, H.-H. Tsai, B. Zhang, and M. Li. Scaling up spatial transcriptomics for large-sized tissues: uncovering cellular-level tissue architecture beyond conventional platforms with iSCALE. *Nature Methods*, under review.

16. 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.

17. 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. Fridman, W. H. Fridman, 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.

Patents

1. **D. Zhang** and M. Li. Inferring super-resolution tissue architecture by integrating spatial transcriptomics with histology. 2025. US Patent App. 18/764,858.

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. *A journey in oncology through artificial intelligence and its impact on patients*. AstraZeneca Oncology Summit 2024, Mexico City, Mexico, 2024.

2. **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.

3. **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.

4. **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

5. **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.

6. **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.

7. **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.

8. **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.

Professional Service

JOURNAL REFEREE

Scientific journals

Nature Methods

American Journal of Human Genetics

Nature Communications

Nature Communications Biology

Genome Biology

Cell Reports Methods

Statistical journals

Journal of the Royal Statistical Society Series B: Statistical Methodology

Biometrics

Statistics in Medicine

Annals of Applied Statistics

Biostatistics

Precision Medicine: Theory, Methods and Applications