Yuehua Cui

CONTACT INFORMATION

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EDUCATION

Ph. D.	Statistics (2005) Department of Statistics, University of Florida, Gainesville, FL
M.S.	Plant Biology (1998) College of Biological Science, China Agricultural University, Beijing, China

ACADEMIC POSITIONS

Professor	2015 – pres, Department of Statistics & Probability, Michigan State University
Graduate Director	2019 – 2025, Department of Statistics & Probability, Michigan State University
Associate Professor	2010 – 2015, Department of Statistics & Probability, Michigan State University
Assistant Professor	2005 – 2010, Department of Statistics & Probability, Michigan State University
Research Scientist	1998 – 2000, Institute of Botany, Chinese Academy of Sciences

Other MSU Affiliations:

Faculty Member of MSU Genetics and Genome Sciences Program
Faculty Member of MSU BioMolecular Science Gateway Program
Faculty Member of MSU Ecology, Evolution and Behavior (EEB) Program
Faculty Member of MSU Center for Research on Autism, Intellectual and other Neurodevelopmental Disabilities (C-RAIND) Program

RESEARCH INTERESTS

- Statistical genetics/genomics: gene-gene and gene-environment interactions, multi-omics data integration, causal mediation analysis, Mendelian randomization, scRNA-seq and spatial transcriptomics
- Applied functional/longitudinal data analysis, semi- and non-parametric models, high-dimensional data analysis, statistical machine learning
- Statistical applications in public health and biological sciences

ACADEMIC AWARDS AND HONORS

2022	Elected Fellow, American Statistical Association (ASA)
2010	Elected member, International Statistics Institute (ISI)
2008	Junior Faculty Meritorious Research Award, Sigma Xi Scientific Research Society, Michigan State University Chapter
2008-	Sigma Xi full membership, the Sigma Xi Scientific Research Society
2007	William L. Harkness Instructional Innovation Award, Department of Statistics & Probability, Michigan State University
2003	Mu Sigma Rho, Statistics Honor Society
2002-2004	Superfund Graduate Fellow, Superfund Basic Research Program, Center for Environmental & Human Toxicology, University of Florida

EDITORIAL SERVICES

Senior Editorial Board: *BMC Genomic Data* (2021-)

Academic Editor:

- *PLoS Genetics* (2026-)
- *PLoS Computational Biology* (2025-)

Associate Editor:

- *Statistical Applications in Genetics and Molecular Biology* (2026-)
- *Computational and Structural Biotechnology Journal* (2023-)
- *Frontiers in Systems Biology - Integrative Genetics and Genomics* (2021-)
- *Statistics and Probability Letters* (2015-2026)
- *BMC Genetics* (2010-2016)

Deputy Section Editor: *BMC Genetics*, Section on Statistical and Computational Genetics (2016-2020)

Editorial Board Member:

- *Mathematics (Math Biology section board member)* (2023-)
- *Journal of Computational Systems Biology* (2014-)
- *Computational and Structural Biotechnology Journal* (2021-2023)
- *The Scientific World Journal*, Computational Biology Domain (2011-2017)
- *Recent Patents on Biotechnology* (2010-2014)

Review Editor:

- *Frontiers in Genetics - Statistical Genetics and Methodology* (2011-)
- *Frontiers in Bioinformatics – Network Bioinformatics* (2020-)

Guest Editor: *Recent Patents on Biotechnology* (2011)

Guest Associate Editor

- Special issue on “Design and analysis of genome-wide association and next generation sequencing data in cancer pharmacogenomics”, *Frontier in Genetics - Statistical Genetics and Methodology* (2014-2015)
- Special issue on “The Development and Application of Multi-Omics Integration Approaches to Dissecting Complex Traits in Plants”, *Frontier in Genetics – Plant Genomics* (2021)
- Special Issue on “Network-Based Statistical Methods and Applications in Transcriptome-Wide Association Studies (TWAS)”, *Frontier in Genetics – Computational Genomics* (2021)
- Special Issue on “Algorithms for Single Cell Data Analyses”, *Frontiers in Systems Biology – Integrative Genetics and Genomics* (2022)

RESEARCH GRANTS

Active

2025-2029	(Co-I, with D. Vendramini (PI)) “Endoplasmic Reticulum Stress in the activation and pro-tumor functions of fibroblasts in pancreatic cancer”, NIH/NCI R01CA295509 Total Award Amount: $2,709,577 (0.6 summer) Total Award Period Covered: 01/01/2025-12/31/2029
2024-2027	(Co-I, with L. Wang (PI) and C. Hong). “Genetic polymorphisms as predisposed risk for apparent treatment-resistant hypertension in CKD”, AHA 24TPA1288424 Total Award Amount: $300,000 (1.3 summer) Total Award Period Covered: 07/01/2024-06/30/2027

Completed

2024-2025	(Co-PI, with Knickmeyer R and Sadler R), “Understanding gene-environment interactions in neurodevelopment using a global, multicohort study”, MSU Tetrad Initiative Award Total Award Amount: $30,000 (only student RA support) Total Award Period Covered: 09/01/2024-12/31/2025

2023-2025 (PI) “Statistical analysis of pancreatic cancer spatial transcriptomics data”, subcontract from Henry Ford Health System
Total Award Amount: $76,616 (only student RA support)
Total Award Period Covered: 05/15/2023-05/15/2025

2023-2025 (Co-I, with B. Chen (PI)) “AI center for drug discovery (AID)”, MSU Strategic Partnership Grants, MSU Research Foundation
Total Award Amount: $240,000 (only student RA support)
Total Award Period Covered: 09/01/2023-08/31/2025

2024-2024 (Co-I, with B. Chen (PI)) “Interrogating the phenotype and function of γδT cells in pancreatic cancer liver metastasis”, MSU+Henry Ford Health Integrative Grant
Total Award Amount: $21,846 (only student RA support)
Total Award Period Covered: 01/01/2024-12/31/2024

2018-2024 (Co-PI, With J. Wang (PI) and E. Andrechek) “Statistical modeling of long-range chromatin interactions on gene regulation and underlying molecular mechanisms”, NIH R01GM131398.
Total Award Amount: $1,300,004 (1 calendar)
Total Award Period Covered: 09/01/2018-05/31/2024

2019-2022 (PI, with P. Zhong, A. Burt and K. Klump) “Novel methods for longitudinal study of synergistic gene-environment interactions in complex diseases”. NIH R21HG010073.
Total Award Amount: $422,646.00
Total Award Period Covered: 05/01/2019-04/30/2022

2019-2022 (Co-I, with H-S Wu), “Effects of bright light on co-occurring cancer-related symptoms in breast cancer survivors: A personalized intervention”. National Inst. of Nursing Research, NR016828.
Total Award Amount: $323,837.55 (10% effort)
Total Award Period covered: 09/01/2019-08/31/2022

2012-2016 (PI, with P-S Zhong), “Statistical inference for gene regulation with genetical genomic data”, NSF (DMS-1209112), $208,688

2012-2017 (Co-PI, with CR Buell, J Jiang, D Douches and RE Veilleux) “Unraveling the Heterozygosity, Allelic Composition, and Copy Number Variation of Potato”, NSF (IOS-1237969).
Total Award Amount: $5,774,862.00 (My portion: $567,256.00)
Total Award Period Covered: 10/01/2012-09/30/2017

2011-2017 (Co-PI, with N Jiang, CR Buell, J Jiang), “The Impact of Pack-MULEs on Plant Genome Evolution and Mechanisms of Sequence Acquisition”, NSF (MCB-1121650), $1,490,000 (my portion: $144,011)
Total Award Period Covered: 09/01/2011-08/31/2017

2009-2017 (Major participant), “The dynamic response of plants to a changing environment”, International Research Training Grant, Deutsche Forschungs Gemeinschaft (DFG) of Germany, Partnership between the University of Dusseldorf and Michigan State University.

2013-2015 (Co-PI, with R Freed and D Douches) “SNP Marker Identification for Pre-harvest Sprouting Resistance in Wheat”. Michigan GREEN project, $69,482 (no personal effort, student support).

2010-2011 (Statistician, with D. DellaPenna), “Advancing Drug Development from Medicinal Plants using Transcriptomics and Metabolomics”, NIH, $1,451,717 (10% effort and one ½ time RA)

2007-2011 (sole PI), “Statistical methods for mapping imprinted genes underlying complex traits”, National Science Foundation, (DMS-0707031), $116,817.

2010-2010 (sole PI), “Statistical methods to identify genetic conflicts associated with pregnancy complications”, NIH/NICHD subcontract, $55,932.

2006-2007	(Co-PI, with Wenjiang Fu), “Genetic association study of complications of pregnant women”, NIH subcontract, $492,968 (40% effort).
2006-2008	(sole PI), “Dissecting genomic imprinting and maternal effect underlying triploid endosperm development through genetic mapping”, MSU Intramural Research Grants Program (06-IRGP-789), $38,062.

PUBLICATIONS

Research Highlight: Our work on Gene-centric genetic association study (Cui et al. 2008, *Genetics*) was highlighted in *Nature Reviews Genetics* Vol. 9 No. 6 (2008).

Peer-referred Journal Articles (#equal contribution; ✉senior corresponding author)

1. Vo, P. and **Y.H. Cui**✉. (2026) Spatially informed reference-free cell type deconvolution for spatial transcriptomics with SpatialCD. *Genome Research* (accepted in principle)
2. Zhang, Z., M. Zhu, R. Guo, F. Chen, H. Dong, **Y.H. Cui**✉, H. Yang✉. （2026）Nonlinear kernel-based high-dimensional inference for set-based genetic association studies. *Briefings in Bioinformatics* (accepted)
3. Cao H.✉, Z. Xu, S. Lin, G. Du, T. Wang, J. Wang, X. Yang, R. Fang, Y. Luo, P. Zeng, H. Yu, Y. Zhang, **Y.H. Cui**✉. (2026) CEDR: Robust consensus cancer subtyping with multi-omics data via ensemble dimensionality reduction. *Briefings in Bioinformatics* (in press)
4. Wang, Z., Y. Li, Y. Li, **Y.H. Cui**, and X. Liu. (2026) Subgroup testing in threshold quantile regression model. *Stat*. https://doi.org/10.1002/sta4.70134 (in press)
5. Cao, H✉, G. Liu, J. Xia, R. Chen, T. Wang, X. Yang, R. Fang, Y. Luo, P. Zeng, H. Yu, Y. Zhang, and **Y.H. Cui**✉. (2026) SpatialESD: Spatial ensemble domain detection in spatial transcriptomics. *Advanced Science*, e20912.
6. Wu, H., M. Boehnke, **Y.H. Cui**, X. Liang, A.I. Vazquez, and G. de los Campos. (2026) Improving Polygenic Score Prediction for Underrepresented Groups Through Transfer Learning. *Nature Communications* 17, 1973.
7. Zhang, J., X. Liu, H. Wang and **Y.H. Cui**✉. (2026) Functional varying-index coefficient model for dynamic gene-environment interactions. *Statistics in Biosciences*, 18: 111-130.
8. Xie, A. and **Y.H. Cui**✉. (2026) gnSPADE: reference-free deconvolution incorporating gene network structures in spatial transcriptomics. *Advanced Intelligent System*, e202500639.
9. Miao, R, D. Fan, H. Wu, J. Du, H. Wang, **Y.H. Cui**, T. Cheng, Q. Zhang, and L Sun. (2026) Identification of DEAD-box RNA Helicase Genes in Prunus mume Reveals the Role of PmDDX39 in Cold Stress Tolerance. *Horticultural Plant Journal* 12(2): 431-446.
10. Cao, H.✉, T. Wang, Z. Xu, X. Zhao G. Liu, X. Yang, R. Fang, Y. Luo, P. Zeng, H. Yu, Y. Zhang, and **Y.H. Cui**✉. (2025) Interactive multi-kernel learning for integrating multi-omics data in cancer subtyping. *Briefings in Bioinformatics* 26 (6), bbaf687.
11. Xie, A., N.G. Steele and **Y.H. Cui**✉. (2025) gwSPADE: gene-frequency weighted reference-free deconvolution in spatial transcriptomics. *Nucleic Acids Research* 53 (18), gkaf966.
12. Yao, X., T. Wang, Q. Yang, J. Wang, Y. Qi, T. Xu, Z. Wei, **Y.H. Cui**, H. Cao, and K. Yun. (2025) Multi-omics data integration for improved cancer subtyping via denoising autoencoder-based multi-kernel learning. *Genes* 16 (11), 1246.
13. Das Adhikari, S., N.G. Steele, B. Theisen, J. Wang*, and **Y.H. Cui**✉. (2025) SPACE: Spatially variable gene clustering adjusting for cell type effect for improved spatial domain detection. *Nucleic Acids Research* 53(18): gkaf936.
14. Su, H. and **Y.H. Cui**✉. (2025) Rotation-invariance is essential for accurate detection of spatially variable genes in spatial transcriptomics. *Nature Communications* 16(1), 7122.
15. Su, H., Y. Wu, B. Chen, **Y.H. Cui**✉. (2025) STANCE: a unified statistical model to detect cell-type-specific

spatially variable genes in spatial transcriptomics. *Nature Communications* 16(1): 1793.

16. Guan, S., X. Liu and **Y.H. Cui**✉. (2025) Variable selection for generalized single-index varying-coefficient models with applications to synergistic G× E interactions. *Mathematics* 13 (3): 1-23.
17. Zhang, J., H. Wang and **Y.H. Cui**✉. (2025) Generalized functional varying-index coefficient model for dynamic synergistic gene-environment interactions. *PloS One* 20 (1), e0318103.
18. Loveless, I., S. Kemp, K. Hartway, J. Mitchell, Y. Wu, S. Zwernik, D. Salas-Escabillas, S. Brender, M. George, Y. Makinwa, T. Stockdale, K. Gartrelle, R. Reddy, D. Long, A. Wombwell, J. Clark, A. Levin, D. Kwon, L. Huang, R. Francescone, D. Barbosa Vendramini-Costa, B. Stanger, A. Alessio, A. Waters, **Y.H. Cui**, E. Fertig, L. Kagohara, B. Theisen, H. Crawford, N. Steele. (2025) Human pancreatic cancer single cell atlas reveals association of CXCL10+ fibroblasts and basal subtype tumor cells. *Clinical Cancer Research* 31(4):756-772.
19. **Cui, Y.H.** ✉ (2025) GLMY homology theory meets idopNetwork: Dissecting soil microbiota resilience under forest thinning and climate change. Comment on "Topological change of soil microbiota networks for forest resilience under global warming" by Gong et al. *Physics of Life Reviews* 52: 44-45.
20. Liyanage, J. S. S., J.H. Estepp, K. Srivastava, S. R. Rashkin, J. S. Hankins, C. M. Takemoto, Y. Li, **Y.H. Cui**, M. Mori, M. J. Weiss, and G. Kang. (2024) A Novel Mendelian Randomization Approach for Count Outcome Robust to Correlated and Uncorrelated Pleiotropic Effects. *Genetic Epidemiology* 49: e22602.
21. Jia, C., T. Wang, G. Liu, Y. Tian, D. Cui, Z. Xu, R. Fang, H. Yu, Y. Zhang, **Y.H. Cui**✉ and H. Cao✉. (2024) Multi-omics data integration for subtype identification of renal cell carcinoma: a metagene-based similarity network fusion approach. *Briefings in Bioinformatics* 25: bbae606.
22. Liu, Y., B. Thyreau, **Y.H. Cui**, Y. Zhang, Y. Tatewaki and Y. Taki. (2024) Influence of Intergenerational Social Mobility On Brain Structure and Global Cognition: Findings From the Whitehall II Study Across 20 Years. *Age and Aging* 53(10): afae221.
23. Tan, X., X. Zhang, **Y.H. Cui**, X. Liu. (2024) Uncertainty quantification in high-dimensional linear models incorporating graphical structures with applications to gene set analysis. *Bioinformatics*, 40(9): btae541.
24. Yang, H., X. Wang, Z. Zhang, F. Chen, H. Cao, L. Yan, X. Gao, H. Dong, **Y.H. Cui**✉. (2024) A high-dimensional omnibus test for set-based association analysis. *Briefings in Bioinformatics* 25: bbae456.
25. Cao, D.Q., S.C. Lei, H. Liu, Y. Jin, Y.F. Wu, **Y.H. Cui**, R. Wu. (2024) Reverse Solute Diffusion Enhances Sludge Dewatering in Dead-End Forward Osmosis. *Membranes* 14(9): 196.
26. Shi, R., L. Wang, S. Burgess and **Y.H. Cui**✉. (2024) MR-SPLIT: a novel method to address selection and weak instrument bias in one-sample Mendelian randomization studies. *PloS Genetics* 20: e1011391.
27. Das Adhikari, S., J. Yang, **Y.H. Cui**✉, and J. Wang✉. (2024) BayesKAT: Bayesian optimal kernel-based test for genetic association studies reveals joint genetic effects in complex diseases. *Briefings in Bioinformatics* 25 (3): bbae182
28. Cao, H, Z. Li, H. Yang, R. Fang, Y. Zhang, B. Wang and **Y.H. Cui**✉. (2024) Multi-omics data integration identified novel cancer subtypes with weighted multi-kernel learning. *British Journal of Cancer* 130: 1001-1012.
29. Yang, J., SD. Adhikari, H. Wang, B. Huang, W. Qi, **Y.H. Cui** and J. Wang. (2024) De novo prediction of functional effects of genetic variants from DNA sequences based on context-specific molecular information. *Front. Syst. Biol. - Integrative Genetics and Genomics* 4: 1402664.
30. Das Adhikari, S., J. Yang, J. Wang✉, and **Y.H. Cui**✉. (2024) Recent advances in detecting spatially variable genes for spatial transcriptomics. *Computational and Structural Biotechnology Journal* 23: 883-891.
31. He, T., P-S. Zhong, **Y.H. Cui,** and V. Mandrekar. (2023) Unified tests for nonparametric functions in RKHS with kernel selection and regularization. *Statistica Sinica* 33: 919-944.
32. Guan, S.$^{\#}$, M. Zhao$^{\#}$ and **Y.H. Cui**✉. (2023) Variable selection in varying multi-index coefficient models for synergistic gene-environment interactions. *Electronic Journal of Statistics* 17(1): 823-857.
33. Wei, Y-F., X. Zhao, L. Li, H. Yang, H. Cao✉ and **Y.H. Cui**✉. (2023) Cancer subtyping with multi-omics data via multi-kernel learning. *Briefings in Bioinformatics* 24(1), bbac488.

34. Liu, Y., Liu, Y., **Cui, Y.**, Thyreau, B., Zhang, Y., Taki, Y., Chen, H. (2023), Intergenerational Social Mobility, Brain Structure, and Cognitive Trajectory: Findings from the Whitehall II Study. *Alzheimer's Dement.*, 19: e071978.
35. Liyanage, J.S.S., J.H. Estepp, K. Srivastava, S.R. Rashkin, V.A. Sheehan, J.S. Hankins, C.M. Takemoto, Y. Li, **Y.H. Cui**, M. Mori, S. Burgess, M.R. DeBaun and G. Kang. (2022) A Versatile and Efficient Novel Approach for Mendelian Randomization Analysis with Application to Assess the Causal Effect of Fetal Hemoglobin on Anemia in Sickle Cell Anemia. *Mathematics*, 10(20): 3743.
36. Wang, J†, Y. Miao†, L. Li, Y. Wu, Y. Ren*, **Y.H. Cui**✉ and H Cao✉. (2022) Multi-omics data integration for hepatocellular carcinoma subtype identification with multi-kernel learning. *Frontiers in Genetics-Computational Genomics* 13: 962870. (†contributed equally to this work)
37. Li, L-M., G. Shi, Y. Wei, H. Yang, Z. Li, R. Fang, H. Cao✉ and **Y.H. Cui**✉. (2022) Multi-omics data integration for subtype identification of Chinese lower-grade gliomas: A joint similarity network fusion approach. *Computational and Structural Biotechnology Journal* 20: 3482-3492.
38. Wang, H.L., J.Y. Zhang, K.L. Klump, S.A. Burt and **Y.H. Cui**✉. (2022) Multivariate partial linear varying-coefficients model for gene-environment interactions with multiple longitudinal traits. *Statistics in Medicine* 41: 3643-3660.
39. Qu, J. and **Y.H. Cui**✉. (2022) Gene set association analysis with graph embedded kernel association test. *Bioinformatics* 38(6): s1560-1567.
40. Zheng, X., **Y.H. Cui**, Y. Xue, L. Shi, Y. G, F. Dong, C. Zhang. (2022) Adverse childhood experiences in depression and the mediating role of multimorbidity in mid-late life: A nationwide longitudinal study. *Journal of Affective Disorders* 301:217-224.
41. Shen, X., Y. Wen, **Y.H. Cui** and Q. Lu. (2022) A conditional autoregressive model for genetic association analysis accounting for genetic heterogeneity. *Statistics in Medicine* 41: 517-542.
42. Zhao, M., Y. Gao and **Y.H. Cui**✉. (2022) Variable selection for longitudinal varying coefficient errors-in-variables models. *Communications in Statistics: Theory and Method* 51(11): 3713-3738.
43. Liu, Y., Y. Gao, R. Fang, H. Cao, J. Sa, J. Wang, H. Liu, T. Wang and **Y.H. Cui**✉. (2021) Identifying complex gene-gene interactions: a mixed kernel omnibus testing approach. *Briefings in Bioinformatics* 22(6): bbab305.
44. Fang, R., H. Yang, Y. Gao, H. Cao, E.L. Goode and **Y.H. Cui**✉. (2021) Gene-based mediation analysis in epigenetic studies. *Briefings in Bioinformatics* 22(3): bbaa113.
45. Yang, H., X. Li, H. Cao, **Y.H. Cui**, Y. Luo, J. Liu and Y. Zhang. (2021) Using machine learning methods to predict hepatic encephalopathy in cirrhotic patients with unbalanced data. *Computer Methods and Programs in Biomedicine* 211: 106420.
46. Zhou, L., Z. Guo, B. Wang, Y. Wu, Z. Li, H. Yao, R. Fang, H. Yang, H. Cao✉ and **Y.H. Cui**✉. (2021) Risk prediction in Heart Failure with Preserved Ejection Fraction patients with gene expression data using machine learning. *Frontier in Genetics: Statistical Genetics and Methodology* 12: 412.
47. Wu, Y., H. Wang, Z. Li, J. Cheng, R. Fang, H. Cao✉ and **Y.H. Cui**✉. (2021) Subtypes identification on heart failure with preserved ejection fraction via network enhancement fusion using multi-omics data. *Computational and Structural Biotechnology Journal* 19: 1567-1578.
48. Liu, X., P-S. Zhong and **Y.H. Cui**✉. (2020) Joint test of parametric and nonparametric effects in partial linear models for gene-environment interaction. *Statistica Sinica* 30: 325-346.
49. Sun, H., **Y.H. Cui**, H, Wang, H. Liu and T. Wang. (2020) Comparison of methods for the detection of outliers and associated biomarkers in mislabeled omics data. *BMC Bioinformatics* 21: 1-23.
50. Wang, H., Y. Wu, R. Fang, J. Sa, Z. Li, H. Cao and **Y.H. Cui**✉. (2020) Time-varying gene network analysis of human prefrontal cortex development. *Frontiers in Genetics*: *Computational Genomics* 11: 1409.
51. Deng, Y., T. He, R. Fang, S. Li, H. Cao, and **Y.H. Cui**✉. (2020) Genome-wide gene-based multi-trait analysis. *Frontiers in Genetics: Statistical Genetics and Methodology* 11: 437.
52. Kao, T-S. A., J. Ling, M. Dalaly, L.B. Robbins, **Y.H. Cui**. (2020) Parent-Child Dyad's Collective Family Efficacy and Risky Adolescent Health Behaviors. *Nursing Research* 69(6): 455-465.

53. Zhang, H., W. Bi, **Y.H. Cui,** H. Chen, J. Chen, Y. Zhao, and G. Kang. (2020) Extreme-value sampling design is cost-beneficial only with a valid statistical approach for exposure–secondary outcome association analyses. *Statistical Methods in Medical Research* 29: 466-480.
54. Yang, H., H. Cao, T. He, T. Wang and **Y.H. Cui**✉. (2020) Multi-level heterogeneous omics data integration with kernel fusion. *Briefings in Bioinformatics* 21: 156-170.
55. Sun, H.W., **Y.H. Cui**, Q. Gao, and T. Wang. (2020) Trimmed LASSO Regression Estimator for Binary Response. *Statistics and Probability Letters* 159: 108679.
56. Jing, L.W., **Y.H. Cui**, Q. Lu, and H. Yu. (2020) Multiplier method estimates of the population of men who have sex with men: the effect of privacy protection. *Journal of Public Health* 42: 429-434.
57. Gao, B., X. Liu, H. Li and **Y.H. Cui**✉. (2019) Integrative analysis of genetical genomics data incorporating network structures. *Biometrics* 75(4): 1063-1075.
58. Gao, Y., H. Yang, R. Fang, Y. Zhang, E. L. Goode and **Y.H. Cui**✉. (2019) Testing mediation effects in high-dimensional epigenetic studies. *Frontiers in Genetics: Epigenomics and Epigenetics* 10: 1195.
59. He, T., S. Li, P-S. Zhong* and **Y.H. Cui**✉. (2019) An optimal kernel-based method for gene set association analysis. *Genetic Epidemiology* 43: 137-149.
60. Kang, Y., I. Torres-Jerez, Z. An, V. Greve, D. Huhman, N. Krom, **Y.H. Cui** and M. Udvardi. (2019) Genome-wide association analysis of salinity responsive traits in Medicago truncatula. *Plant, Cell & Environment*.13508 42: 1513–1531.
61. Wu, C., P-S. Zhong and **Y.H. Cui**✉. (2018) Additive varying-coefficient model for nonlinear gene-environment interactions. *Statistical Applications in Genetics and Molecular Biology* 17(2).
62. Wang, H.L., P-S. Zhong and **Y.H. Cui**. (2018) Empirical likelihood ratio tests for coefficients in high dimensional heteroscedastic linear models. *Statistica Sinica* 28: 2409-2433.
63. Wu, C., Y. Jiang, J. Ren, **Y.H. Cui** and S. Ma. (2018) Dissecting gene-environment interactions: a penalized robust approach accounting for hierarchical structures. *Statistics in Medicine* 37(3): 437-456.
64. Wang, H.L., P-S. Zhong, **Y.H. Cui** and Y. Li. (2018) Unified empirical likelihood ratio tests for functional concurrent linear models and the phase transition from sparse to dense functional data. *Journal of the Royal Statistical Society B*. 80(2): 343-364.
65. Jing, L., Q. Lu, **Y.H. Cui**, H. Yu and T. Wang. (2018) Combining the randomized response technique and the network scale-up method to estimate the female sex worker population size: an exploratory study. *Public Health* 160:81-86.
66. Zhao, D., J.P. Hamilton, B. Vaillancourt, W. Zhang, G.C. Eizenga, **Y.H. Cui**, J. Jiang, C.R. Buell, and N. Jiang. (2018) The unique epigenetic features of Pack-MULEs and their impact on chromosomal base composition and expression spectrum. *Nucleic Acids Research* 46: 2380-2397.
67. Wu, D., H. Yang, S.J. Winham, Y. Natanzon, D.C. Koestler, T. Luo, B.L. Fridley, E.L. Goode, Y.B. Zhang and **Y.H. Cui**✉. (2018) Mediation analysis of alcohol consumption, DNA methylation, and epithelial ovarian cancer. *Journal of Human Genetics* 63: 339-348.
68. Yang, H., S. Li, H. Cao, C. Zhang and **Y.H. Cui**✉. (2017) Predicting disease trait with genomic data: A composite kernel approach. *Briefings in Bioinformatics* 18(4):591–601.
69. Cao, H.Y., Z. Li, H. Yang, **Y.H. Cui**✉ and Y. Zhang✉. (2017) Longitudinal next-generation sequencing data analysis for rare variants detection with penalized quadratic inference function. *Scientific Reports* 7(1): 650.
70. Zhao, J., S. Li, L. Wang, L. Jiang, R. Yang✉ and **Y.H. Cui**✉. (2017) Genome-wide random regression analysis for parent-of-origin effects of body composition allometries in mouse. *Scientific Reports* 7: 45191.
71. Liu, X., B. Gao and **Y.H. Cui**✉. (2017) Generalized partial linear varying-index coefficient model for gene-environment interactions. *Statistical Applications in Genetics and Molecular Biology* 16(1): 59-74.
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73. Ren, Yan, J. Jia, J. Sa, L-X. Qiu, **Y. Cui**, Y-A. Zhang, H. Yang, G-F. Liu. (2017) Association between N-terminal proB-type natriuretic peptide and depressive symptoms in patients with acute myocardial infarction. *Chinese Medical Journal* 130(5): 542-548.

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Conference Proceedings

151. Ma D., W. Bu, **Y.H. Cui**, Y. Xie, and X. Wu. (2018) Learning Collaborative Model for Visual Tracking. *24th International Conference on Pattern Recognition (ICPR)*, 2582-2587.
152. Ma D., W. Bu, Y. Xie, **Y.H. Cui**, and X. Wu. (2018) Segmentation-Guided Tracking with Prior Map Decision. *2018 24th International Conference on Pattern Recognition (ICPR)*, 2014-2019.

Invited Book Chapters

153. Liu, T., C. Tong, J.S. Wu, B. Zhang, **Y.H. Cui**, Y. Li, Y. Zeng and R.L. Wu. (2011) Haplotype Analysis of Complex Traits in Outcrossing Tree Species: Allele Discovery of Quantitative Trait Loci. In: *Genetics, Genomics and Breeding of Poplar* (C.P. Joshi, S.P. DiFazio, and C. Kole eds.) Science Publishers, Northants, UK.
154. **Cui, Y.H.**✉**,** G.X. Li, S.Y. Li and R.L. Wu. (2010) Designs for Linkage Analysis and Association Studies of Complex Diseases. In: *Statistical Methods in Molecular Biology* (Eds.: H. Bang, X.K. Zhou, H.L. Van Epps and M. Mazumdar) Humana Press.

Book Review

155. **Cui, Y.H.** (2022) "Multivariate Data Integration Using R: Methods and Applications with the mixOmics Package" by Kim-Anh LeCao, Zoe Marie Welham. *Biometrics*.
156. **Cui, Y.H.** (2015) "Statistical methods for QTL mapping" by Z. Chen. *Journal of the American Statistical Association*.
157. **Cui, Y.H.** (2009) "Multivariate Statistics: Exercises and Solutions" by W. Hardle and Z. Hlavka. *Journal of the American Statistical Association* 104(488): 1722.

Papers under review/revision

158. Wu, Y.$^{\#}$, D. Såłas-Escabillas$^{\#}$, A. Xie$^{\#}$, I. M. Loveless, K. Hartway, R. Shankar, M. George, A. Wombwell, J.M. Clark, D. Kwon, B. Chen, R. Francescone, D.B. Vendramini-Costa, B. Theisen, L. Huang, **Y.H. Cui**✉, H.C. Crawford✉, N.G. Steele✉. Spatial transcriptomics on a diverse pancreatic cancer cohort reveals Black African Americans display reduced classical and increased intermediate tumor subtype ($^{\#}$equal contribution). *Cancer Research* (revision submitted)
159. Wu, Y., H. Su and **Y.H. Cui**✉. Decoding cell-cell communication in spatial transcriptomics: mechanistic insights, modeling constraints, and analytical caveats. *Briefings in Bioinformatics* (under revision)
160. Guan, S.J., and **Y.H. Cui**✉. Quantile varying multi-index coefficient model for synergistic gene-environment interactions. *Statistics Innovation* (under revision)
161. Gao, Y., N. Qiao, L. Yang, Y. Liu, R. Fang, N. Shen, Y. Zhang, G. Wang, Y. Li✉ and **Y. Cui**✉. Gene-set mediation analysis in high-dimensional epigenetic studies. *Briefings in Bioinformatics* (under revision)
162. Xie, A. and **Y.H. Cui**✉. CASTLE: Cell-type Aware SpaTial domain detection via contrastive Learning Embedding. *PLoS Genetics* (under review)
163. Liu, X., Y. Liu, X. Zhang, J. Huang, **Y.H. Cui**, X. Shi. Multi-omics data integration with multi-view learning via composed tensors. *Science China: Mathematics* (under review)
164. Qu, J., K. Klump and **Y.H. Cui**✉. Causal inference in longitudinal studies with time-varying confounding: a Mendelian randomization approach. *Data Analytics and Topology* (under review)
165. Chen, F., R. Yin, Z. Zhang, Z. Zhao, **Y.H. Cui**✉, and H. Yang✉. Scalable continuous functional tensor modeling of spatial transcriptomics with ASTER. *Nature Communications* (submitted)
166. Wu, Y., H. Su, N. Steele, Y. Xie, and **Y.H. Cui**✉. TESSA: trajectory-preserved spatially variable gene detection in spatial transcriptomics. *Communications Biology* (submitted)

PROFESSIONAL SERVICE ACTIVITIES

Panelist and Ad hoc Reviewer for Grant Proposals

- University of Sharjah Research Funding Department, 2022
- NSF Panelist, 2016, 2022
- Ad hoc NSF Reviewer, 2009, 2011, 2020
- Netherlands Genomics Initiative Reviewer, 2009
- National Natural Science Foundation of China Reviewer, 2018, 2019
- Intramural Funding Program Reviewer, the Office of the Vice President for Research and Graduate Studies, Michigan State University, 2009
- Michigan AgBio Research Program Reviewer, 2012
- UK Medical Research Council Reviewer, 2017
- Hong Kong Research Grants Council Reviewer, 2019

NIEHS/NIH Program Review (May 5-6, 2025)

Book proposal reviewer for Prentice-Hall and Springer

Reviewer for *Mathematical Reviews*

Journal referee services for the following journals (>300 papers)

Statistics related journals

1. *Annals of Applied Statistics*
2. *Biometrics*
3. *Biometrical Journal*
4. *Biostatistics*
5. *Communications in Statistics – T&M*
6. *Computational Statistics and Data Analysis*
7. *Journal of the American Statistical Association*
8. *Journal of Biopharmaceutical Statistics*
9. *Journal of Business & Economic Statistics*
10. *Journal of Multivariate Statistics*
11. *Journal of the Royal Statistical Society B*
12. *Journal of the Royal Statistical Society C*
13. *Journal of Statistical Planning and Inference*
14. *Journal of Statistical Software*
15. *Scandinavian Journal of Statistics*
16. *Science China Mathematics*

17. *Stat*
18. *Statistica Sinica*
19. *Statistical Applications in Genetics and Molecular Biology*
20. *Statistics and Its Interface*
21. *Statistics and Probability Letters*
22. *Statistics in Medicine*

Statistical Genetics and Bioinformatics journals

23. *American Journal of Human Genetics*
24. *Annals of Human Genetics*
25. *Bioinformatics*
26. *BMC Bioinformatics*
27. *BMC Genetics*
28. *BMC Genomics*
29. *BMC Medicine*
30. *Briefings in Bioinformatics*
31. *Communications in Information and Systems*
32. *Computational and Structural Biotechnology Journal*
33. *Communications Biology*
34. *Frontiers in Genetics, Statistical Genetics and Methodology*
35. *Genetics*
36. *Genetic Epidemiology*
37. *Genetics Research*
38. *Genomics*
39. *Genome Biology*
40. *Genome Research*
41. *Heredity*
42. *Human Genetics*
43. *Human Genetics and Genomics Advances*
44. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
45. *IEEE Transactions on Neural Networks and Learning Systems*
46. *Journal of Chemical Information and Modeling*
47. *Journal of Computational Biology*
48. *Journal of Neuroscience methods*
49. *Journal of Theoretical Biology*
50. *Mathematical Biosciences and Engineering*
51. *Methods in Ecology and Evolution*
52. *Nature Biomedical Engineering*
53. *Nature Computational Science*
54. *Nature Communications*
55. *Nature Genetics*
56. *Nucleic Acids Research*
57. *PLoS Computational Biology*
58. *PLoS Genetics*
59. *Theoretical and Applied Genetics*
60. *Theoretical Biology and Medical Modeling*

Natural Science and Public Health journals

61. *African Journal of Biotechnology*
62. *BioMed Research International*
63. *Biomolecules*
64. *BMC Plant Biology*
65. *British Journal of Psychiatry*
66. *Cancer Medicine*
67. *Cellular and Molecular Life Sciences*
68. *Current Genomics*
69. *Drug Discovery*
70. *eFood*
71. *Environmental Science and Pollution Research*
72. *Environmental International*
73. *Euphytica*
74. *European Journal of Public Health*
75. *Food Science and Technology*
76. *Frontiers in Cardiovascular Medicine*
77. *Frontiers in Public Health*
78. *Gene*
79. *G3: Genes, genomics, Genetics*
80. *Genetica*
81. *Health Expectations*
82. *Horticulture Research*
83. *Hypertension*
84. *International Journal of Obesity*
85. *Journal of Affective Disorders*
86. *Journal of Hazardous Materials*
87. *Journal of Internal Medicine*
88. *Journal of King Saud University*
89. *Journal of Molecular Endocrinology*
90. *Journal of Nutrition Education and Behavior*
91. *Journal of Public Health*
92. *Journal of Sleep Research*
93. *Mammalian Genome*
94. *Marine Biotechnology*
95. *Molecular Genetics and Genomics*
96. *Molecular Plant*
97. *Nutrition, Metabolism and Cardiovascular Diseases*
98. *Plant Cell*
99. *Plant Journal*
100. *Plant Physiology*
101. *Plants*
102. *PloS One*
103. *Proceedings of the National Academy of Sciences (PNAS)*
104. *Public Health Nutrition*
105. *Science in China*
106. *Scientific Reports*
107. *Scientific World Journal*
108. *Translational Psychiatry*

CONFERENCE ACTIVITIES

Organizing Committee for Conferences

- *14th International Conference on Intelligent Biology and Medicine (ICIBM 2026)*, Buffalo, NY, (August 2-5, 2026) (Workshop Committee)
- *DahShu 2024 Data Science Symposium*, East Lansing, MI (May 16-18, 2024) (co-chair)
- *International Symposium in Graduate Research on Data Sciences and Technology* by Dokuz Eylul University, Türkiye (Dec. 2, 2023)
- *9th International Forum on Statistical Genetics and Genomics*, Jinan, China (July 2-July 4, 2023) (co-chair)
- *The Data Science Section of the First International Symposium on Graduate Research* by Dokuz Eylul University, Türkiye (Dec. 2-3, 2022) (as a member of both the Organizing Committee and Scientific Committee)
- *5th International Workshop on Statistical Genetics and Genomics*, Jinan, China (June 30-July 2, 2018) (co-chair)
- *4th International Workshop on Statistical Genetics and Genomics*, Taiyuan, China (June 21-23, 2017) (as chair)
- Program Committee member, *2017 ICSA Applied Statistics Symposium*, Chicago, IL
- *3rd International Workshop on Statistical Genetics and Genomics*, Taiyuan, China (June 20-23, 2016) (as chair)
- *2nd International Workshop on Statistical Genetics and Genomics*, Taiyuan, China (June 23-24, 2015) (as chair)
- *1st International Workshop on Statistical Genetics and Genomics*, Taiyuan, China (June 24-25, 2014) (as chair)
- *2nd International Conference on Epidemiology & Evolutionary Genetics*, Beijing, China (Aug 18-19, 2014)
- International Year of Statistics: Statistics in Applications Forum, MSU (October 1, 2013)
- *Statistical Genetics and Genomics Workshop*, East Lansing, MI (May, 2008) (as chair)

Conference Invited Session Organizer/Chair:

- "Statistical, Computational, and AI Innovations for Spatial Single-Cell and Multi-Omics", *ICIBM 2026*, Buffalo, NY (August 2-6, 2026)
- "Recent Methodological Advances in Spatial Omics in an AI-Augmented Era", *2026 ENAR Spring Meeting*, Indianapolis, IN (March 15-18, 2026)
- "Recent Statistical Advances in Complex Genetic and Genomic Data Analysis", *2025 ICSA-China Conference*, Zhuhai, China (June 28-30, 2025)
- "Recent Methodological Advances in Single-Cell and Spatial Multi-omics", *STATGEN 2025: Conference on Statistics in Genomics and Genetics*, Minneapolis, MN (May 21-23, 2025)
- "Advancing Statistical and Machine Learning Models for Single-Cell and Spatial Omics", *MCBIOS 2025: Data-Driven Discovery: Harnessing the power of AI to transform health*, University of Utah, Salt Lake City (March 27-29, 2025)
- "Statistical and computational advances for complex biological data analysis", *2024 ICSA-China Conference*, Wuhan, China (June 28-30, 2024)
- "Recent Advances in Mendelian Randomization for Causal Inference", *STATGEN 2024: Conference on Statistics in Genomics and Genetics*, Pittsburgh, PA (May 1-3, 2024)
- "Unraveling Intricate Molecular Pathways in Complex Diseases: Insights from Recent Statistical and Computational Advances", *MCBIOS 2024: From Codes to Cells to Care, Transforming Health Care with AI*, University of Emory, Atlanta (March 22-24, 2024)
- "*Statistical advances in Mendelian randomization for causal inference*", *The 16th International Conference of the ERCIM WG on Computational and Methodological Statistics (CMStatistics 2023)*, Berlin, Germany (December 16-18, 2023)

- "*Statistical innovations in scRNA-seq and spatial transcriptomics analysis*", *The 16th International Conference of the ERCIM WG on Computational and Methodological Statistics (CMStatistics 2023)*, Berlin, Germany (December 16-18, 2023)
- "Recent statistical advances for complex multi-omics data analysis", *The 2023 ICSA China Conference*, Chengdu, China (June 30-July 3, 2023)
- "Statistical advances for biomedical data with complex structures", *The 2023 ICSA Applied Symposium*, Ann Arbor, MI (June 14-16, 2023)
- "Recent advances in statistical methods for complex genetic/genomic data", *15th International Conference of the ERCIM WG on Computational and Methodological Statistics (CMStatistics 2022)*, London, UK (December 17-19, 2022)
- "Statistical advances for genetic data analysis", 2021 *ICSA Applied Statistics Symposium*, Washington DC (Sept 12-15, 2021)
- "Statistical methods for complex human genetic data", 2020 *ICSA Applied Statistics Symposium*, Houston, TX (Dec 17-20, 2020)
- "Recent advances in high-dimensional genomic data analysis", *The 3rd International Conference on Econometrics and Statistics (EcoSta 2019)*, Taichung, Taiwan (June 25-27, 2019)
- "Recent advances in statistical analysis of genetic/genomic data", 2018 *ICSA China Statistics Conference, Qingdao, China (July 2-5, 2018)*
- "Recent advances in statistical analysis of genetic/genomic data", 2017 *ICSA Applied Statistics Symposium*, Chicago, IL (June 25-28, 2017)
- "Novel statistical methods for genetic data analysis", 2017 *ICSA Applied Statistics Symposium*, Chicago, IL (June 25-28, 2017)
- "Recent advances in statistical analysis of genetic data", *2016 ICSA China Statistics Conference*, Qingdao, China (June 24-25, 2016)
- "Statistical advances for the detection of gene-environment interactions", *Joint Statistical Meeting*, Seattle, WA (August 8-13, 2015)
- "Statistical advances for genetic data analysis", *Joint 24th ICSA Applied Statistics Symposium and 13th Graybill Conference*, Fort Collins, CO (June 14-17, 2015)
- "Recent advances in statistical genetics: methods and applications", *The 3rd Biostatistics Symposium*, Chengdu, China (June 27-28, 2014)
- "Recent advances in statistical analysis of high-dimensional genetic data", *The 4th IMS-China International Conference on Statistics and Probability*, Chengdu, China (June 30-July 4, 2013)
- "Public Health Genomics", *BIT's 3rd World DNA and Genome Day-2012*, Xi'an, China (April 25-28, 2012)
- "New statistical challenges and advancements in eQTL mapping studies", *XXVth International Biometric Conference*, Florianópolis-SC, Brazil (December 5-10, 2010)
- "Statistical genetics: challenges, advances and prospects", *First Joint Biostatistics Symposium*, Beijing, China (July 1-3, 2010)
- "Recent advances and statistical challenges in genetical genomics analysis", *ICSA Applied Statistics Symposium*, Indianapolis, IN (June 20-23, 2010)

CONFERENCE AND DEPARTMENTAL SEMINAR PRESENTATIONS

Invited Plenary Talks

1. "Advancing spatial transcriptomics through statistical innovation", *2025 International Congress of Basic Science*, Beijing, China (July 13-25, 2025)
2. "A unified model to detect trajectory-preserved and spatially variable genes in spatial transcriptomics", *The 11th International Forum on Statistical Genetics and Genomics*, Xi'an, China (July 4-July 5, 2024)
3. "From Association to Causation: Causal Inference with Mendelian Randomization in Biomedical Studies", *2024 International Congress of Basic Science*, Beijing, China (July 14-26, 2024)

4. "A unified statistical model to detect cell-type-specific spatially variable genes in spatial transcriptomics", *The 10th International Forum on Statistical Genetics and Genomics*, Wuhan, China (June 30-July 2, 2024)
5. "Dealing with weak instruments in Mendelian randomization: an adaptive data splitting approach", *The 9th International Statistical Genetics and Genomics* (*ISGG*) *Forum*, Jinan, China (July 3, 2023)
6. "Genome-wide gene-based multi-trait analysis", *The 6th International Symposium on Statistical Genetics/Genomics*, Nanjing, China (June 29-July 1, 2019)
7. "Network-constrained genetical genomics analysis with nonlinear environmental modification", *The Third Annual Kliakhandler Conference on Bayesian Inference in Statistics and Statistical Genetics*, Michigan Technological University, Houghton, MI (Aug 16–20, 2017)
8. "Statistics in post genomic era: challenges and opportunities", *Marrakesh International conference on Probability and Statistics* 2016, Marrakech, Morocco (April 25-28, 2016)

Invited Conference and Workshop Presentations (V=virtual)

1. "Multi-sample integration enables robust spatially variable gene detection in spatial transcriptomics", *2026 Joint Statistical Meeting*, Boston, MA (August 1-6, 2026)
2. "Spatially-informed reference-free deconvolution for spatial transcriptomics with SpatialCD", *ICIBM 2026*, Buffalo, NY (August 2-6, 2026)
3. "Spatially-informed reference-free cell type deconvolution with SpatialCD" *2026 ICSA-China Conference*, Shenzhen, China (June 26-29, 2026)
4. "Spatially-informed reference-free cell type deconvolution with SpatialCD", *STATGEN 2026: Conference on Statistics in Genomics and Genetics*, Atlanta, MI (May 18-20, 2026)
5. "Making sense of spatial transcriptomics: from statistical foundations to biological insights", *2nd International Conference on Data Analytics and Topology*, Sanya, China (Feb. 2-6, 2026)
6. (V)"Spatial deconvolution and cell type-specific spatially variable gene detection in spatial transcriptomics", *19th International Joint Conference on Computational and Financial Econometrics (CFE) and Computational and Methodological Statistics (CMStatistics), CFE-CMStatistics 2025*, London, UK (Dec. 13-15, 2025)
7. "Addressing some challenges in spatial transcriptomics: spatial deconvolution, gene variability, and domain detection", *Banff International Research Station (BIRS) Workshop: Foundation Models and their Biomedical Applications*, Banff, Canada (August 17-22, 2025).
8. "A unified model to detect spatially-variable and trajectory-preserved genes in spatial transcriptomics", *2025 Joint Statistical Meeting*, Nashville, TN (August 2-7, 2025)
9. "Spatial deconvolution and cell type-specific spatially variable gene detection in spatial transcriptomics", *2025 ICSA-China Conference*, Zhuhai, China (June 28-30, 2025)
10. "Spatial deconvolution and cell type-specific spatially variable gene detection in spatial transcriptomics", *STATGEN 2025: Conference on Statistics in Genomics and Genetics*, Minneapolis, MI (May 21-23, 2025)
11. "A unified model for cell-type-specific spatially variable gene detection in spatial transcriptomics", *MCBIOS 2025: Data-Driven Discovery: Harnessing the power of AI to transform health*, Salt Lake City (March 27-29, 2025)
12. "Spatially informed trajectory-based differential expression analysis for spatial transcriptomics", *2024 Joint Statistical Meeting*, Portland, OR (August 3-8, 2024)
13. "MR-SPLIT: a novel method to deal with weak instruments in one-sample Mendelian randomization studies", *ICSA China 2024*, Wuhan, China (June 28-30, 2024)
14. "Mendelian randomization for causal inference with MR-SPLIT", *STATGEN 2024: Conference on Statistics in Genomics and Genetics*, Pittsburgh, PA (May 1-3, 2024)
15. "From association to causation: causal inference with Mendelian randomization in biomedical studies", *WDD 2024*, Nagoya, Japan (April 22-24, 2024).
16. "Causal inference with MR-SPLIT", *MICOBIO*, University of Emory, Atlanta (March 22-24, 2024)

17. (V)“Addressing weak instruments in one sample MR analysis with MR-SPLIT”, *16th International Conference of the ERCIM WG on Computational and Methodological Statistics* (CMStatistics 2023), Berlin, GA (Dec. 18, 2023)
18. “Dealing with weak instruments in Mendelian randomization: an adaptive data splitting approach”, *The 9th International Statistical Genetics/Genomics Forum*, Jinan, China (July 3-4, 2023)
19. “Gene set analysis with graph embedded kernel association test”, *2023 ICSA applied statistics symposium*, Ann Arbor, MI (June 11-14, 2023)
20. “FDR control in high-dimensional mediation analysis”, *2023 New England Statistics Symposium*, Boston, MA (June 3-6, 2023)
21. “Causal inference with Mendelian randomization for longitudinal traits”, *Advances in Statistical and Computational Methods for Analysis of Biomedical, Genetic, and Omics Data* (in celebrating Prof. Shili Lin’s 60th birthday), The University of Texas at Dallas, Richardson, TX (March 17-19, 2023)
22. (V)“Mendelian randomization for causal inference on longitudinal traits”, Frontier in Mathematical Science at Tsinghua-Sanya International Mathematics Forum (TSIMF), Sanya, Hainan Province, China (Dec 22 to Dec 29, 2022)
23. (V)“Causal inference with Mendelian randomization for longitudinal traits”, *15th International Conference of the ERCIM WG on Computational and Methodological Statistics* (CMStatistics 2022), London, UK (December 17-19, 2022)
24. (V)“Recent developments in causal inference”, *International Symposium on Statistical Theory and Methods*, Anhui University of Finance and Economics, China (December 11, 2022)
25. (V)“Causal inference with Mendelian randomization for longitudinal traits”, *The 8th International Symposium on Statistical Genetics/Genomics*, Taiyuan, China (Nov 26-27, 2022)
26. (V)“Variable selection in varying multi-index coefficient model for synergistic gene-environment interactions”, *2022 ENAR Spring Meeting*, Houston, TX (March 27-30, 2022)
27. (V)“Multi-omics data integration with kernel learning”, *2020 ICSA applied statistics symposium*, Houston, TX (Dec 17-20, 2020)
28. (V)“Multivariate partial linear varying-coefficient model for G×E studies with longitudinal traits”, *2020 JSM Meeting*, Philadelphia, PA (Aug. 1-6, 2020)
29. (V)“Nonlinear moderated mediation analysis with genetical genomics data”, *2020 ENAR Meeting*, Nashville, TN (March 22-25, 2020)
30. “High-dimensional mediation analysis in (epi)genomics studies”, *2019 CoCoH Symposium on Computational Systems Biology*, Grand Rapids, MI (Aug. 27, 2019)
31. “Nonlinear moderated mediation analysis with genetical genomics data”, *2019 ICSA China Statistics Conference*, Tianjin, China (July 1-4, 2019)
32. “Functional partial linear varying-index coefficients model for gene-environment interaction”, *The 3rd International Conference on Econometrics and Statistics (EcoSta 2019)*, Taichung, Taiwan (June 25-27, 2019)
33. “Omics data integration with kernel fusion”, *San Francisco Bay area chapter of ASA*, San Francisco, CA (Oct. 26, 2018)
34. “Statistics in post-genomic era: challenges and opportunities”, *Western Meeting of AMS*, San Francisco, CA (Oct. 27-28, 2018)
35. “Integrative genetical genomics analysis incorporating network structures”, *2018 ICSA China Statistics Conference*, Qingdao, China (July 2-5, 2018)
36. “Gene selection in big data era: biologically guided statistical treatment”, *The 5th International Symposium on Statistical Genetics/Genomics*, Jinan, China (June 30-July 2, 2018)
37. “Embracing the complexity of genomic data: some statistical challenges and solutions”, *Symposium on Big Data and the Future of Statistics*, Shanxi University of Finance and Economics, Taiyuan, China (Dec. 16-18, 2017)
38. “An optimal kernel-based method for gene set association analysis”, 2017 *IMS-China International Conference on Statistics and probability*, Nanning, China (June 28-July 2, 2017)
39. “Gene selection with nonlinear instrumental regression incorporating network structures”, *The 10th R Conference*, Taiyuan University of Technology, Taiyuan, China (June 24-25, 2017)
40. “An optimal kernel-based method for gene set association analysis”, 4th *International Workshop on*

Statistical Genetics/Genomics, Taiyuan, China (June 22-23, 2017)

41. "Integrative genetical genomics analysis incorporating network structures", Biostatistics workshop, *Statistical Inference for Biomedical Big Data*, Gainesville, FL (April 7-8, 2017)
42. "Integrative analysis of genetical genomics data incorporating network structures", *Joint Statistical Meeting*, Chicago, IL (July 30-August 4, 2016)
43. "Integrative genetical genomics analysis incorporating network structures", *The 4th International Symposium on Biostatistics*, Shanghai, China (July 2-3, 2016)
44. "Integrative genetical genomics analysis incorporating network structures", *2016 ICSA China Statistics Conference*, Qingdao, China (June 24-25, 2016)
45. "Integrative analysis of gene-environment interactions", 3rd *International Workshop on Statistical Genetics/Genomics*, Taiyuan, China (June 21-22, 2016)
46. "Integrative genetical genomics analysis incorporating network structures", *HDDA-VI: The 6th International Workshop on the Perspectives on High-Dimensional Data Analysis*, Toronto, Canada (May 25-27, 2016)
47. "Integrative analysis of gene-environment interactions". *Joint Statistical Meeting*, Seattle, WA (August 7-13, 2015)
48. "Integrative genetical genomics analysis incorporating network structures", *ICSA-China Statistics Conference*, Shanghai, China (July 6-7, 2015)
49. "Integrative genetical genomics analysis incorporating network structures", *IMS-China International Conference on Statistics and Probability*, Kunming, Yunnan, China (July 1-4, 2015)
50. "Integrative genetical genomics analysis incorporating network structures", *2nd International Workshop on Statistical Genetics/Genomics*, Taiyuan, China (June 22-24, 2015)
51. "Econometrics in the age of big data: the opportunities, challenges and prospects", *The 2nd Innovation and Global Industrial Development Forum：2015 International Symposium on Innovation Creating New Competitive Advantage*, Wuhan, China (June 3, 2015)
52. "Statistical genetics: current status and perspectives", *Statistics in Applications Symposium* East Lansing, MI (October 2, 2014)
53. "Partial linear models for integrative gene-environment interactions", *3rd International Biostatistics Symposium*, Chengdu, China (June 27-28, 2014)
54. "Challenges and strategies in gene-environment interactions", *1st International Workshop on Statistical Genetics/Genomics*, Taiyuan, China (June 24-25, 2014)
55. "Novel strategies in high-dimensional genetic data analysis", *The 4th IMS-China International Conference on Statistics and Probability*, Chengdu, China (June 30-July 4, 2013)
56. "Linear or Non-linear: how genes respond to environmental stimuli", International *Symposium on Mapping the Genetic Regulation of Forest Ecosystems*, Beijing, China, (Oct. 6-13, 2012)
57. "Varying coefficient model for nonlinear gene-environment interaction", *The 8th Purdue Symposium on Statistics*, Lafayette, IN (June 20-24, 2012)
58. "Statistical identification of gene-gene and gene-environment interactions for complex disease", Epigenetics and the Elucidation of Complex Genetic Traits and Diseases section, *BIT's 3rd World DNA and Genome Day-2012*, Xi'an, China (April 25-29, 2012).
59. "Gene-centric gene-gene interaction", Statistical Genomics Workshop, *Plant and Animal Genome XX Conference*, San Diego, CA (January 15-17, 2012)
60. "eQTL mapping: the added value in complex trait dissection", *iGRAD-Plant Symposium/Retreat*, Henrich Heine University, Düsseldorf, Germany (September 12-17, 2011)
61. "Gene-centric gene-gene interaction in genome-wide association studies", *International workshop on statistical and computational genetics*, Beijing Forestry University, China, (August 4-5, 2011)
62. "Statistical dissection of genetic conflicts associated with pregnancy complications", (Session title 'Design and Analysis Issues for Assessing Complex Joint Maternal-Fetal Genetic Effects"), *Joint Statistical Meeting* (JSM), Vancouver, Canada (August 1-5, 2010)
63. "Gene-based genome-wide association studies", *Summer Workshop on Statistical & Computational Genetics*, Beijing Forest University, Beijing, China (July 19, 2010)
64. "eQTL mapping: the added value in complex trait dissection", *First Joint Biostatistics Symposium*, Beijing, China, (July 15-18, 2010).
65. "Enriching our knowledge in network regulation in eQTL mapping: a combined p-value approach",

Statistical Genomics Workshop, *Plant and Animal Genome XVIII Conference*, San Diego, CA, (January 9-13, 2010).

66. "A statistical variance components framework for mapping imprinted quantitative trait loci underlying endosperm traits in flowering plant", *Joint Conference of the Society for Mathematical Biology and the Chinese Society for Mathematical Biology*, Hangzhou, China, (June 14-17, 2009).
67. "Functional mapping genomic imprinting underlying developmental characteristics", *Fall Conference on Statistics in Biology*, Ames, IA, (October 13-15, 2008).
68. "Large-scale genome-wide association studies via entropy test", *Workshop on Multiscale Modeling, Analysis and Simulations*, East Lansing, MI, (October 10-11, 2008).
69. "Understanding the genetic architecture of genomic imprinting by Functional QTL Mapping", *Midwest Conference on System Biology*, East Lansing, MI, (October 27-28, 2007).
70. "Sequencing complex diseases with penalized logistic regression", *Interdisciplinary bioinformatics workshop*, the University of Michigan, (November 3, 2006).
71. "Binary Trait Nucleotides Mapping Complex Disease With HapMap", *ICSA applied statistics symposium*, Storrs, CT, (June 14-17, 2006).

Contributed Conference Talks

72. "Gene-gene and gene-environment interactions: beyond the traditional linear models". *ENAR Spring Meeting*, Orlando, FL, March 2013.
73. "Nucleotide mapping complex diseases and the limiting distribution of the likelihood ratio test", *ENAR Spring Meeting*, San Antonio, TX, March 2009.
74. "A statistical approach for genomewide scanning and testing imprinted quantitative trait loci", *Joint Statistical Meeting*, Seattle, WA, August 2006.
75. "Functional mapping for genetic control of programmed cell death: a semiparametric model", *ENAR Spring Meeting*, Tampa, FL, March 2006.
76. "Dissecting plant development through genetic mapping", *Fifth Annual IFAS graduate research symposium*, University of Florida, FL, April 2005.
77. "A two-stage hierarchical model for detecting the epistatic control of maternal-offspring QTL over endosperm development", *ENAR Spring Meeting*, Pittsburgh, PA, March 2004.

Invited Department Colloquium/Seminar Talks

1. Tsinghua University, Department of Statistics and Data Science (6/22/2026)
2. East China Normal University, School of Statistics (5/9/2026)
3. Shanghai University of Finance and Economics, School of Statistics (5/9/2026)
4. Peking University, Guanghua School of Management (4/9/2026)
5. Hong Kong University of Science and Technology, Department of Mathematics (3/19/2026)
6. Chinese University of Hong Kong, Department of Statistics and Data Science (3/17/2026)
7. Michigan State University, Genetics & Genome Sciences (GGS) Research Forum, (11/06/2025)
8. Case Western Reserve University, Department of Mathematics, Applied Mathematics and Statistics (10/22/2025)
9. University of Texas at Arlington, Department of Mathematics (10/17/2025)
10. University of Texas at San Antonio, Department of Management Science and Statistics (4/18/2025)
11. (V)Texas Tech University, Department of Mathematics & Statistics (3/10/2025)
12. Zhejiang University, College of Agriculture and Biotechnology, China (7/4/2024)
13. Zhengzhou University, School of Public Health, China (7/7/2023)
14. Tsinghua University, Yau Mathematical Sciences Center, China (6/26/2023)
15. Shanxi Medical University, School of Public Health, China (6/20/2023)
16. (V)Indiana University and Purdue University at Indianapolis (IUPUI), Department of Mathematical Science (4/4/2023)
17. (V)Anhui University of Finance and Economics, School of Statistics, China (12/10/2022)
18. (V)Shanghai University of Finance and Economics, School of Statistics, China (12/7/2022)
19. (V)University of Illinois at Chicago, Department of Math, Stat, & Comp Sci (10/26/2022)

20. (V)University of Georgia, Department of Statistics (10/29/2020)
21. University of Florida, Department of Biostatistics (03/14/2019)
22. Michigan State University, Department of Statistics and Probability (1/22/2019)
23. University of Notre Dame, Department of Applied and Computational Mathematics and Statistics (11/16/2018)
24. Zhengzhou University (China), School of Public Health, China (05/28/2018)
25. Anhui University of Finance and Economics, School of Statistics, China (06/05/2018)
26. University of Minnesota, Division of Biostatistics (04/07/2017)
27. University of Notre Name, Department of Applied and Computational Mathematics and Statistics (9/26/2016)
28. Beijing Academy of Agriculture and Forestry Sciences (China) (07/13/2016)
29. Taiyuan University of Technology (China), School of Mathematics (06/03/2016)
30. Western Michigan University, Department of Statistics (02/12/2016)
31. Stony Brook University, Department of Applied Mathematics and Statistics (11/20/2015)
32. University of Alabama at Birmingham, Section on Statistical Genetics, Department of Biostatistics (09/25/2014)
33. Wuhan University (China), School of Mathematics and Statistics (05/26/2014)
34. Wright State University, Department of Mathematics and Statistics (04/11/2014)
35. Zhengzhou University China), School of Public Health (06/24/2013)
36. St. Jude Children’s Research Hospital, Department of Biostatistics (01/08/2013)
37. Chinese Academy of Sciences, Beijing Institute of Botany (05/21/2012)
38. Wuhan University of Science and Technology (China), College of Science (05/07/2012).
39. Xi’an Jiaotong University (China), College of Mathematics and Statistics (04/28/2012)
40. Beijing Forestry University (China), College of Biological Sciences and Biotechnology (04/24/2012)
41. Yale University, Division of Biostatistics (11/8/2011)
42. Michigan State University, Department of Statistics and Probability (10/17/2011)
43. Shanxi Medical University (China), School of Public Health (6/15/2011)
44. Haerbin Medical University (China), College of Bioinformatics and Technology (6/10/2011)
45. Virginia Tech, Department of Statistics (09/30/2010)
46. University of Connecticut, Department of Statistics (04/19/2010)
47. UT Southwestern Medical Center, Department of Clinical Science (04/15/2010)
48. University of South Carolina, Department of Epidemiology and Biostatistics (04/07/2010)
49. Georgia State University, Department of Mathematics and Statistics (03/31/2010)
50. Saint Louis University, Division of Biostatistics (03/19/2010)
51. University of Nebraska Medical Center, Department of Biostatistics (03/17/2010)
52. Indiana University, Department of Medical and Molecular Genetics (03/09/2010)
53. Emory University, Department of Biostatistics and Bioinformatics (02/18/2010)
54. Marquette University, Department of Mathematics and Statistics, and Computer Science (02/14/2010)
55. MSU Computational Biology Group kick-off seminar (02/10/2010)
56. Michigan State University, Department of Statistics & Probability (02/02/2010)
57. Ohio State University, Department of Statistics (01/28/2010)
58. Indiana University and Purdue University at Indianapolis, Department of Mathematical Science (01/25/2010)
59. National Center for Integrative Biomedical Informatics (NCIBI) (08/13/2009)
60. Kansas State University, Department of Statistics (05/08/2008)
61. Ohio State University, Department of Statistics (01/15/2008)
62. Michigan State University, Genetics Research Forum (11/12/2007)
63. Michigan State University, Department of Statistics & Probability (09/04/2007)

64. University of Michigan, Department of Biostatistics (11/03/2006)
65. Michigan State University, Department of Statistics & Probability (02/21/2006)
66. The Perinatology Research Branch, NICHD/NIH (01/25/2006)
67. University of Florida, Department of Statistics graduate student seminar (04/19/2005)
68. University of Florida, Institute of Food and Agricultural Sciences-Statistics (03/11/2005)
69. Tulane University, Department of Epidemiology (03/14/2005)
70. University of Minnesota, Department of Biostatistics (03/092005)
71. University of Alabama, Department of Biostatistics (02/22/2005)
72. Wake Forest University, Department of Public Health (02/14/2005)
73. Michigan State University, Department of Statistics and Probability (02/04/2005)
74. Michigan State University, Department of Plant Biology (02/02/2005)
75. University of Florida, Superfund Basic Research Program Center for Environmental & Human Toxicology (Dec. 2003)
76. University of Florida, Superfund Basic Research Program Center for Environmental & Human Toxicology (June 2003).

STUDENTS ADVISING

Current Ph.D. students

1.	Siling Liu	Ph.D.	Ongoing
2.	Naijia Wang	Ph.D.	Ongoing
3.	Wei (Alice) Lai	Ph.D.	Ongoing
4.	Siyue Nie	Ph.D. (co-advised with Yue Xing)	Ongoing
5.	Zun Wang	Ph.D. (co-advised with Hao Zhang)	Ongoing
6.	Haohao Su	Ph.D.	Ongoing
7.	Yuesong Wu	Ph.D. (co-advised with Yuying Xie)	Ongoing
8.	Phuong Vo	Ph.D.	Ongoing

Past PhD students, their thesis title, and job placement

As advisor

9. Aoqi Xie, Ph.D. in Statistics, degree conferred in 12/2025

   Thesis title: “Statistical and deep learning methods to decode tissue architecture in spatial transcriptomics: cell type deconvolution and spatial domain detection”
   1st job: Innovation Scientist, Huawei Technologies Co., Ltd., China

10. Ruxin Shi, Ph.D. in Statistics, degree conferred in 08/2025

    Thesis title: “Robust Statistical Methods for Causal Discovery in One-sample Mendelian Randomization Studies”
    1st job: Research Scientist, Huawei Technologies Co., Ltd., China

11. Sikta Das Adhikari (joint with Jianrong Wang from CMSE), Dual Ph.D. in Statistics and Computational Mathematics, degree conferred in 08/2024

    Thesis title: “Advanced Statistical and Computational Techniques for Genomic Data Analysis”
    1st job: Statistician, FDA, Washington DC

12. Jialin Qu, Ph.D. in Statistics, degree conferred in 08/2022

    Thesis title: “Causal Inference with Mendelian Randomization for Longitudinal Data”
    1st job: Statistician, Moderna Inc., Boston

13. Shunjie Guan, Ph.D. in Statistics, degree conferred in 08/2017

    Thesis title: “Variable selection in varying multi-index coefficient models with applications to gene-environmental interactions”
    1st job: Senior Research Statistician, AbbVie; Currently Director, Statistician at Pfizer

14. Jingyi Zhang, Ph.D. in Statistics, degree conferred in 08/2017
    Thesis title: "Functional varying index coefficient model for gene-environment interactions with longitudinal data"
    1st job: Statistician, Wells Fargo; Currently Applied Scientist, Amazon Lab126
15. Tao He, (joint with Ping-Shou Zhong) Dual Ph.D. in Statistics and Quantitative Biology, degree conferred in 08/2015
    Thesis title: "Kernel-based Nonparametric Testing in High-dimensional Data with Applications to Gene Set Analysis".
    1st job: Assistant Professor, Department of Mathematics, San Francisco State University
    Currently Associate Professor, Department of Mathematics, San Francisco State University
16. Honglang Wang, (joint with Ping-Shou Zhong) Dual Ph.D. in Statistics and Quantitative Biology, degree conferred in 08/2015
    Thesis title: "Empirical likelihood based functional data analysis and high dimensional inference with applications in biology".
    1st job: Assistant Professor, Department of Mathematical Sciences, IUPUI
    Currently Associate Professor, Department of Mathematical Sciences, Indiana University Indianapolis
17. Bin Gao, Ph.D. in Statistics, degree conferred in 08/2015
    Thesis title: "Graph estimation and network constrained regularization with application in genetical genomics"
    1st job: Senior Statistician, Janssen Research & Development, LLC; Currently Principal Scientist II Biostatistics, Johnson & Johnson Innovative Medicine
18. Cen Wu, Dual Ph.D. in Statistics and Quantitative Biology, degree conferred in 08/2013
    Thesis title: "High-dimensional statistical methods for gene-environment interactions".
    1st job: Postdoc, Department of Biostatistics, Yale University.
    Currently Associate Professor, Department of Statistics, Kansas State University
19. Shaoyu Li, Dual Ph.D. in Statistics and Quantitative Biology, degree conferred in 08/2011
    Thesis title: "Statistical issues and novel strategies for eQTL mapping".
    1st job: Assistant member, Department of Biostatistics, St. Jude Children's Research Hospital.
    Currently Professor, Department of Mathematics and Statistics, University of North Carolina at Charlotte
20. Gengxin Li, Dual Ph.D. in Statistics and Quantitative Biology, degree conferred in 08/2010
    Thesis title: "Variance component models in mapping imprinted genes: statistical theory and applications".
    1st job: Postdoc, Department of Biostatistics, Yale University.
    Currently Associate Professor, Dept. of Mathematics and Statistics, University of Michigan at Dearborn.

As co-chair

21. Shan Zhang, Ph.D. in Statistics (joint with Qing Lu from Biostat/UF), degree conferred in 2021
    Thesis title: "Neural networks models with applications to genetic studies"
    1st job: Statistician, FDA.
22. Jinghang Lin, Ph.D. in Statistics (joint with Qing Lu from Biostat/UF), degree conferred in 2021
    Thesis title: "A neural network-based method with genetic data analysis of complex diseases".
    1st job: Postdoc, Department of Biostatistics, Yale University; Currently, Quantitative analytics specialist, Wells Fargo
23. Xiaoxi Shen, Ph.D. in Statistics (joint with Q. Lu from Epi/Biostat), degree conferred in 08/2019
    Thesis title: "Statistical Analysis for Network-Based Models with Application to Genetic Association Tests and Predictions".
    1st job: Postdoc, Department of Biostatistics, University of Florida; Currently Assistant Professor, Dept of Mathematics, Texas State University

24. Daewoo Pak, Ph.D. in Statistics (joint with C. Li from Epi/Biostat), degree conferred in 08/2018
    Thesis title: "Analysis of complex life-history data and variable selection in survival analysis under interval censoring".
    1st job: Postdoc, MD Anderson Cancer Center; Currently Associate Professor, Yonsei University, South Korea
25. Wei-Wen Hsu, Ph.D. in Statistics (joint with D. Todem from Epi/Biostat), degree conferred in 08/2011
    Thesis title: "Tests of homogeneity in two-component mixture models".
    1st job: Assistant Professor, Department of Statistics, Kansas State University; Currently Associate Professor, Division of Biostatistics and Bioinformatics, University of Cincinnati
26. Yanwei Zhang, Ph.D. in Statistics (joint with D. Todem from Epi/Biostat), degree conferred in 05/2008
    Thesis title: "A hierarchical Bayesian approach to model spatially correlated binary data with applications to dental research".
    1st job: Statistician, Pfizer; Currently Senior Director, Statistical & Quantitative Sciences, Takeda

Past postdocs and their current position

27. Hongyan Cao, Postdoctoral Fellow, 2019-2021
    Currently Associate Professor, School of Public Health, Shanxi Medical University, China
28. Haitao Yang, Postdoctoral Fellow, 2016-2017 (supported by NSF IOS-1237969)
    Currently Professor, School of Public Health, Hebei Medical University, China
29. Xu Liu, Postdoctoral Fellow, 2013-2016 (supported by NSF IOS-1237969)
    Currently Professor with tenure, School of Statistics and Management, Shanghai University of Finance and Economics, China.
30. Guolian Kang, Postdoctoral Fellow, 2006-2007 (supported by MSU 06-IRGP-789)
    Currently Full Member, Department of Biostatistics, St. Jude Children's Research Hospital.

Past MS students and their 1st position

1. Hanyu Yang, M.Sc., degree conferred in 5/2024, PhD student in Biostatistics, MSU
2. Di Zhang, M.Sc., degree conferred in 5/2020, PhD student at National University of Singapore
3. Ze Meng, M.Sc., degree conferred in 5/2020, Statistician, Henry Ford Health, Detroit
4. Yimin Wu, M.Sc., degree conferred in 12/2017, Statistician, DTE Energy, Ann Arbor
5. Ran Cao, M.Sc., degree conferred in 05/2013, Statistician, i360 at Washington DC
6. Chenyang Gu, M.Sc., degree conferred in 05/2012, Ph.D. student, Department of Biostatistics, Brown University
7. Chunyu Chen, M.Sc., degree conferred in 05/2012, Ph.D. student, Department of Animal Science, Michigan State University
8. Wenzhao Yang, M.Sc., degree conferred in 08/2008. She obtained her Ph.D. degree at Michigan State University in 2014.
9. Guanghui Liu, M.Sc., degree conferred in 12/2006, currently Biostatistician, Mayo Clinic

Guidance Committee for MSU Ph.D. Students

Name	Department	Time thesis defended
1. Jialin Li	Dept. of Statistics and Probability	ongoing
2. Yue Di	Dept. of Counseling, Educational Psychology and Special Education	ongoing
3. Kenia Seguraaba	Genetics and Genome Sciences Program	ongoing
4. Wenzhuo Tang	Dept. of Statistics and Probability	ongoing
5. Pengfei He	Dept. of Computer Science and Engineering	ongoing

6.	Harold Wu	Dept. of Epidemiology and Biostatistics	04/2026
7.	Jianrui Zhang	Dept. of Statistics and Probability	11/2025
8.	Meiqi Liu	Dept. of Statistics and Probability	11/2025
9.	Arash Yunesi	Dept. of Statistics and Probability	08/2025
10.	Dali Liu	Dept. of Statistics and Probability	07/2025
11.	Jiachen Liu	Dept. of Counseling, Educational Psychology and Special Education	06/2025
12.	Fei Zhang	Dept. of Animal Science	12/2024
13.	Liang Wang	Dept. of Epidemiology and Biostatistics	07/2024
14.	Sang Kyu Lee	Dept. of Statistics and Probability	07/2024
15.	Jiaxin Yang	Dept. of Computational Mathematics, Science and Engineering	05/2024
16.	Zichun Cao	Dept. of Epidemiology and Biostatistics	07/2023
17.	Andriana Manousidaki	Dept. of Statistics & Probability	07/2023
18.	Wenjie Qi	Dept. of Computational Mathematics, Science and Engineering	08/2022
19.	Sanket Jantre	Dept. of Statistics and Probability	08/2022
20.	Nilanjan Chakraborty	Dept. of Statistics and Probability	07/2022
21.	Di Wu	Dept. of Epidemiology and Biostatistics	06/2022
22.	Runze Su	Dept. of Statistics and Probability	06/2022
23.	Hao Wang	Dept. of Computational Mathematics, Science and Engineering	05/2022
24.	Binbin Huang	Dept. of Computational Mathematics, Science and Engineering	12/2021
25.	Ningyu Sha	Dept. of Computational Mathematics, Science and Engineering	07/2021
26.	Bixi Zhang	Dept. of Counseling, Educational Psychology and Special Education	06/2021
27.	Xiaoran Tong	Dept. of Epidemiology and Biostatistics	04/2020
28.	Yuning Hao	Dept. of Statistics and Probability	12/2019
29.	Bing Tong	Dept. of Counseling, Educational Psychology and Special Education	08/2019
30.	Shawn Santo	Dept. of Statistics and Probability	12/2018
31.	Yaohui Ding	Dept. of Computer Science and Engineering	01/2018
32.	Sneha Jadhav	Dept. of Statistics and Probability	07/2017
33.	Chunyu Chen	Dept. of Animal Science	08/2017
34.	Ashwini Maurya	Dept. of Statistics and Probability	05/2016
35.	Keyin Wang	Dept. of Counseling, Educational Psychology and Special Education	08/2016
36.	Jikai Lei	Dept. of Computer Science	07/2015
37.	Aritro Nath	The Genetics Program	05/2015
38.	Changshuai Wei	Dept. of Epidemiology and Biostatistics	05/2014
39.	Wenzhao Yang	Dept. of Animal Science	04/2014
40.	Yvonne Badke	Dept. of Animal Science	08/2013
41.	Greg Habing	Center for Comparative Epidemiology	08/2012
42.	Xuechun Zhou	Dept. of Counseling, Educational Psychology and Special Education	08/2012
43.	Ming Wu	Dept. of Computer Sciences and Engineering	08/2012
44.	Shannon Bell	Dept. of Biochemistry & Molecular Biology	04/2012
45.	Ming Li	Division of Biostatistics, Dept. of Epidemiology	05/2011
46.	Shujie Ma	Dept. of Statistics and Probability	07/2011
47.	Qiongxia Song	Dept. of Statistics and Probability	07/2010
48.	Nora Bello	Dept. of Animal Science	07/2010
49.	Menghan Liu	Dept. of Crop & Soil Science	03/2010

50. Young Gui Kim	Dept. of Economics	07/2009
51. Tianshu Pan	Dept. of Counseling, Educational Psychology and Special Education	10/2008
52. Lan Xiao	Dept. of Animal Science	08/2007

Lab rotation student

- Shubham Koirala (fall 2023), BioMolecular Science Program, MSU

Undergraduate Students Advised:

- Ning Jiang (2019-2020), exchange student from Xi'an Jiaotong University
- Ruobing Jia (2017-2018), exchange student from Jilin University
- Joseph Xiao (1/2016-5/2016), exchange student from Nankai University
- Yuchen Guo (2015-2016), Regression analysis of DNA methylation data
- Supervised undergraduate Sebastian Raschka from biochemistry for a project titled “Statistical Identification of Potential CLAVATA2 Interactors by Fluorescence Resonance Energy Transfer Analysis” to participate in the online OpenIntro Student Project Competition. He was one of the students in my STT421 class in fall 2011. The work was published in http://www.openintro.org/stat/.

TEACHING EXPERIENCES

Graduate Level

- STT843 – Multivariate Analysis
- STT847 – Survival Data Analysis
- STT855 – Statistical Genetics
- STT863 – Statistics Methods I (Linear Regression)
- STT864 – Statistics Methods II (Generalized Linear Model)
- STT890 – Statistical Problems
- HRT892/GEN800 – Quantitative Genetics Seminar

Undergraduate Level

- STT481 – Issues in Statistical Practice
- STT442 – Probability & Statistics II (Statistics)
- STT421 – Statistics I
- STT351 – Probability and Statistics for Engineering
- STT315 – Intro Prob & Stat for Business
- STT231 – Statistics for Scientists
- STT200 – Statistical Methods

COMMITTEE SERVICES

Professional Societies

International Congress of Basic Science (ICBS)

2025	Manager for the Bioinformatics and AI for Life Sciences section, Frontier of Science Award (FSA)
2024	Chair of the Nomination Committee and Selection Committee for the Bioinformatics and AI for Life Sciences section, Frontier of Science Award (FSA)

American Statistical Association (ASA) Committee

2021-2023	ASA Archives and Historical Materials Committee
2020-2022	Membership Engagement Committee, ASA Section on Statistics in Genomics and Genetics

Department Committee

2024-2025	Faculty Search Committee (as chair)
2023-2025	Major Curriculum Committee (as chair)
2023-2024	Dept Bylaws Committee

2022-2025	Reappoint, Promotion and Tenure (RPT) Committee (as chair)
2022-2023	Junior Faculty Search Committee (as chair)
2021-2023	Faculty Advisory Committee (as chair)
2020-2021	Mentoring Policy Committee (as chair)
2020-2021	Prelim Policy Committee (as chair)
2019-2025	Graduate Support Committee (as chair)
2019-2025	Master Support Committee
2019-2022	Major Curriculum Committee (as chair from 2019-2021)
2018-2019	Committee of the Whole (as President)
2018-2019	Department Tenure & Promotion Committee
2017-2018	Faculty Search Committee (as chair)
2016-2017	Data Science Master Program Committee
2014-2015	Faculty Search Committee for the joint CMSE-STT faculty search (as chair)
2014-2016	Department Advisory Committee
2014-2015	Committee of the Whole (as President)
2014-2015	Graduate Support Committee
2014-2015	Master Admissions Committee (as chair)
2014-2017	Committee on Responsible Conduct for Research training
2012-2013	Colloquium Committee (as chair)
2005-pres	Committee of the Whole
2010-2011	Internal Review Committee
2009-2011	Major Curriculum Committee (as chair)
2010-2011	Service Course Committee
2007-2008	Faculty Search Committee
2007-2008	Graduate Support Committee
2006-2009	Colloquium Committee
2005-2007	Secretary of the Advisory Committee
2005-2006	Computer Committee

College and University Committee

2025-2027	NatSci Faculty Advisory Council
2023-2025	University Honors College Committee
2019-2025	NatSci College Graduate Committee
2016-2019	CMSE Undergraduate Data Science Major Committee
2016-2018	Committee on University Student-Faculty Judiciaries
2016-2017	Faculty Search Committee for Quantitative/Statistical/Computational Genomics faculty hire
2015-2017	Faculty Search Committee for CMSE data science faculty hire
2014-2015	Umbrella Committee (committee for the new CMSE department)
2013-2015	Executive Committee, Quantitative Biology Program
2009-2011	Faculty Advisory Council, College of Natural Science
2009	All-University Awards Committee, College of Natural Science
2009	Awards Committee, MSU chapter of Sigma Xi Scientific Research Society
2009-2011	Genetics Program Executive Committee
2009	Dean’s Representative, College of Social Science
2007-2008	Faculty Search Committee in Human Statistical Genetics, Genetics Program
2006-2007	Faculty Search Committee in quantitative genetics/genomics, Departments of Animal Science, and Fishery and Wildlife

Other Committee Service

2020-2021	President of MSU Chinese Faculty Club
2018-pres	Executive Committee and Advisory Board, MSU Chinese Faculty Club

PROFESSIONAL MEMBERSHIPS

- American Association for the Advancement of Science (AAAS) (2018-)
- Institute of Mathematical Society (IMS) (2024-)
- American Statistical Association (ASA) (lifetime member)
- International Chinese Statistical Association (ICSA) (lifetime member)
- Sigma Xi full membership, The Scientific Research Society (2008-)