Yuehua Cui
Curriculum Vitae

CONTACT INFORMATION

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EDUCATION

Ph. D.	Statistics (2005) Department of Statistics, University of Florida, Gainesville, FL
M. Stat.	Statistics (2002) Department of Statistics, University of Florida, Gainesville, FL
M.S.	Plant Biology (1998) College of Biological Science, China Agricultural University
B.S.	Agronomy (1995) Department of Agronomy, Shanxi Agricultural University

ACADEMIC POSITIONS

Graduate Director	2019 – pres, Department of Statistics & Probability, Michigan State University
Professor	2015 – pres, 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 Affiliation:

Professor (2018 – 2020), College of Nursing, Michigan State University

Faculty Member of MSU Genetics and Genome Sciences Program

Faculty Member of MSU Quantitative Biology Initiative (QBI) 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: GWAS, gene-gene and gene-environment interactions, causal mediation analysis, Mendelian randomization
- Statistical genomics: gene network analysis, multi-omics data integration, gene expression data analysis, single cell RNA-seq and spatial transcriptomics data analysis
- Functional/longitudinal data analysis, semi- and non-parametric models, high-dimensional inference, 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-)

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

Associate Editor:
- *Statistics and Probability Letters* (2015-)
- *BMC Genetics* (2010-2016)
- *Frontiers in Systems Biology - Integrative Genetics and Genomics* (2021-)

Editorial Board Member:
- *Computational and Structural Biotechnology Journal* (2021-)
- *Journal of Computational Systems Biology* (2014-)
- *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)

RESEARCH GRANTS

2018-2023	(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: $1.3M Total Award Period Covered: 09/01/2018-05/31/2023
2019-2022	(Co-I, with PI 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
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

2012-2016   (PI, with Co-PI 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, supported one graduate student).

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 (*senior corresponding author)

1. 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* (in press)

2. 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.

3. Wei, Y-F., X. Zhao, L. Li, H. Yang, H. Cao* and **Y.H. Cui***. (2023) Cancer subtyping with multi-omics data via multikernel learning. *Briefings in Bioinformatics* 24 (1), bbac488.

4. 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.

5. 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)

6. 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 (IF=7.3).

7. 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.

8. Qu, J. and **Y.H. Cui***. (2022) Gene set association analysis with graph embedded kernel association test. *Bioinformatics* 38(6): s1560-1567.

9. 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.

10. 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.

11. 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.

12. 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 (impact factor=11.6)

13. 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.

14. 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.

15. 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.

16. 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. (IF=7.3)

17. 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.

18. 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.

19. 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.

20. 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.

21. 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.

22. 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.

23. 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.

24. 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.

25. 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.

26. 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.

27. 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.

28. 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* doi: 10.1111/pce.13508 42: 1513–1531.

29. 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).

30. 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.

31. 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.

32. 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.

33. 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.

34. 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.

35. 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.

36. 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.

37. 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.

38. 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.

39. 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.

40. Cao, HY, P. Zeng, Z. Li, **Y.H. Cui** and Y.B. Zhang. (2017) The application of penalized generalized estimating equations in genetic association with longitudinal data. *Chinese Journal of Health Statistics* 34(4): 534-537.

41. 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.

42. Zhao, D., J. Hamilton, M. Hardigan, D. Yin, T. He, B. Vaillancourt, M. Reynoso, G.G. Pauluzzi, S. Funkhouser, **Y. Cui**, J. Bailey-Serres, J. Jiang, C.R. Buell and N. Jiang. (2017) Analysis of ribosome-associated mRNAs in rice reveals the importance of transcript size and GC content in translation. *G3* 7(1): 203-219.

43. Li, G.X. and **Y.H. Cui***. (2016) Assessing statistical significance in variance components linkage analysis: a theoretical justification. *Journal of Statistical Planning and Inference* 178: 70-83.

44. Liu, X., H. Wang and **Y.H. Cui***. (2016) Statistical identification of gene-gene interactions triggered by nonlinear environmental modulation. *Current Genomics* 17(5): 388-395.

45. Liu, X., **Y.H. Cui*** and R. Li. (2016) Partial linear varying multi-index coefficient model for integrative gene-environment interactions. *Statistica Sinica* 26: 1037-1060.

46. Li, Z., H.Y. Cao, **Y.H. Cui***, Y.B. Zhang*. (2016) Extracting DNA Words Based on the Sequence Features: Non-uniform Distribution and Integrity. *Theoretical Biology and Medical Modelling* 13:2 (DOI 10.1186/s12976-016-0028-3).

47. Luo, T., X. Liu and **Y. Cui***. (2016) A genome-wide association analysis in four populations reveals strong genetic heterogeneity on birth weight. *Current Genomics* 17(5): 416-426.

48. Sa, J., X. Liu, T. He, G. Liu* and **Y.H. Cui***. (2016) A nonlinear model for gene-based gene-environment interaction. *International Journal of Molecular Sciences* 17(6): 882; doi:10.3390/ijms17060882.

49. Wu, C., X. Shi, **Y.H. Cui** and S.G. Ma. (2015) A penalized robust semi-parametric approach for gene-environment interactions. *Statistics in Medicine* 34(30):4016-30.

50. Gao, B. and **Y.H. Cui***. (2015) Learning directed acyclic graphical structures with genetical genomics data. *Bioinformatics* 31(24): 3953-60.

51. Li, G., **Y.H. Cui** and H.Y. Zhao (2015) An Empirical Bayes risk prediction model using multiple traits for sequencing data. *Statistical Applications in Genetics and Molecular Biology* 14(6): 551-73.

52. Bi, W., G. Kang, Y. Zhao, **Y.H. Cui**, S. Yan, Y. Li, C. Cheng, S.B. Pounds, M.J. Borowitz, M.V. Relling, J.J. Yang, C-H. Pui, S.P. Hunger, C.M. Hartford, W. Leung and J-F. Zhang. (2015) SVSI: fast and powerful set-valued system identification approach to identifying rare variants in sequencing studies for ordered categorical traits. *Annals of Human Genetics* 79(4): 294-309.

53. Cao, H.Y., X. Wei, X. Guo, C. Song, Y. Luo, **Y. Cui**, X. Hu, and Y. Zhang. (2015) Screening high-risk clusters for developing birth defects in mothers in Shanxi Province, China: application of latent class cluster analysis. *BMC Pregnancy and Childbirth* 15: 343.

54. Habing, G.G., S. Manning, C. Bolin, **Y.H. Cui**, J. Rudrik, S. Dietrich and J.B. Kaneene. (2015) Within-farm changes in dairy farm associated Salmonella subtypes and comparison to human clinical isolates in Michigan, USA, 2000-2001 and 2009. *Applied and Environmental Microbiology* 81(17): 5724-35.

55. Manrique-Carpintero, N. C., J.J. Coombs, **Y.H. Cui**, R.E. Veilleux, C. R. Buell, and D. Douches. (2015) Genetic map and QTL analysis of agronomic traits in a diploid potato population using SNP markers. *Crop Science* 55(16): 2566-2579.

56. Ren Y, **Cui Y.H.**, Li X, Wang B, Na L, Shi J, Wang L, Qiu L, Zhang K, Liu G, Xu Y. (2015) A co-expression network analysis reveals lncRNA abnormalities in peripheral blood in early-onset schizophrenia. *Progress in Neuro-psychopharmacology & Biological Psychiatry* 63:1-5.

57. Wu, C., **Y.H. Cui** and S.G. Ma. (2014) Integrative analysis of gene-environment interactions under a multi-response partially linear varying coefficient model. *Statistics in Medicine* 33: 4988-4998.

58. He, T., P-S. Zhong and **Y.H. Cui***. (2014) Gene set association test identifies sex-specific pathways associated with type 2 diabetes. *Frontiers in Genetics: Statistical Genetics and Methodology* 5: 395.

59. Li*, S., **Y.H. Cui*** and R. Romero. (2014) Entropy-based selection for maternal-fetal genotype incompatibility with application to preterm pre-labor rupture of membranes. *BMC Genetics* 15: 66.

60. He, T., J. Sa, P-S. Zhong and **Y.H. Cui***. (2014) Statistical dissection of cyto-nuclear epistasis subject to genomic imprinting in line crosses. *PloS One* 9(3): e91702.

61. Wu, C., and **Y.H. Cui***. (2014) Boosting signals in gene-based association studies via efficient SNP selection. *Briefings in Bioinformatics* 15(2):279-291.

62. Dai, H.Y., T. Srivastava and **Y.H. Cui**. (2014) A modified generalized fisher method for combining probabilities from dependent tests. *Frontiers in Genetics: Evolution and Population Genetics* 5:23.

63. Bi, W., G. Kang, **Y. Cui**, Y. Li, C.M. Hartford, W. Leung, J.F. Zhang. (2014) A new set-valued system identification approach to identifying rare genetic variants for ordered categorical phenotype. *BMC Bioinformatics* 15(Suppl 10): P29.

64. Li Z., **Y.H. Cui** and Y.B. Zhang. (2014) Quantification of the differences in genome sequence distribution. *Chinese Journal of Health Statistics* 31(4): 554-558.

65. Humphries, Brock, Z. Wang, A. Oom, T. Fisher, D. Tan, **Y.H. Cui**, Y. Jiang, and C. Yang. (2014) nMicroRNA-200b targets protein kinase Cα and impairs triple negative breast cancer cell migration and tumor metastasis. *Carcinogenesis* 35(10): 2254-2263.

66. Wang, H.L., T. He, C. Wu, P-S. Zhong, and **Y.H. Cui***. (2014) A powerful statistical method identifies novel loci associated with diastolic blood pressure triggered by nonlinear GxE interaction. *BMC Proceedings* 8(Suppl 1): S61.

67. Jing, L., C. Qu, H. Yu, T. Wang and **Y.H. Cui**. (2014) Estimating the sizes of populations at high risk for HIV: A comparison study. *PloS One* 9(4): e95601.

68. Wu, C., and **Y.H. Cui***. (2013) A novel method for identifying nonlinear gene-environment interactions in case-control association studies. *Human Genetics* 132: 1413-1425.

69. Fu, W.J., M. Li, K.L. Sun, **Y.H. Cui**, M.P. Qian, and R. Romero. (2013) Testing maternal-fetal genotype incompatibility with mother-offspring pair data. *Journal of Proteomics and Genomics Research* 1:39-60.

70. Kim, D.-Y., **Y.H. Cui** and O. Zhao. (2013) Asymptotic test in mixture model with applications to QTL mapping. *Journal of Statistical Planning and Inference* 143: 1320-1329.

71. Dang, M-T., C. Gu, J.I. Klavanian, K.A. Jernigan, K.H. Friderici, **Y.H. Cui**, M. Molina-Molina, J. Ancochea, A. Xaubet, and B.D. Uhal. (2013) Angiotensinogen promoter polymorphisms predict low diffusing capacity in U.S. and Spanish idiopathic pulmonary fibrosis cohorts. *Lung* 191(4):353-360.

72. Kang, G.L., B. Jiang and **Y.H. Cui**. (2013) Gene-based genome-wide association analysis: a comparison study. *Current Genomics* 14: 4.

73. Geu-Flores, F., N.H. Sherden, V. Courdavault, V. Burlat, W.S. Glenn, C. Wu, E. Nims, **Y.H. Cui**, and S.E. O'Connor. (2012) An alternative route to cyclic terpenes by reductive cyclization in iridoid biosynthesis. *Nature* 492: 138-142.

74. Li, S.Y., and **Y.H. Cui*.** (2012) Gene-centric gene-gene interaction: a model-based kernel machine method. *The Annals of Applied Statistics* 6(3): 1134-1161.

75. Yang, R., X. Wang and **Y.H. Cui***. (2012) Bayesian inference for genomic imprinting underlying developmental characteristics. *Briefings in Bioinformatics* 13(5): 555-568.

76. Li, G.X., C. Wu, C. Coelho, R. Wu, B.A. Larkins and **Y.H. Cui***. (2012) A bivariate variance components model for mapping imprinted quantitative trait loci underlying endosperm traits. *Frontiers in Bioscience* (Elite Ed) 4: 2464-2475.

77. Wu, C., G.X. Li, J. Zhu and **Y.H. Cui***. (2011) Functional mapping with robust t-distribution. *PloS One* 6(9): e24902.

78. Ye, C.Y., **Y.H. Cui**, R.C. Elston, J. Zhu, and Q. Lu. (2011) A novel non-parametric method for building predictive genetic tests, with an application to rheumatoid arthritis. *Human Heredity* 71: 161–170.

79. Li, S.Y., B. Williams and **Y.H. Cui***. (2011) A combined p-value approach to infer pathway regulations in eQTL mapping. *Statistics and Its Interface* 4(3): 389-402.

80. Ma, S.J., L.J. Yang, R. Romero, and **Y.H. Cui***. (2011) Varying coefficient model for gene-environment interaction: a non-linear look. *Bioinformatics* 27(15): 2119-2126.

81. Li, G.X. and **Y.H. Cui*.** (2010) A general statistical framework for dissecting parent-of-origin effects underlying endosperm traits in flowering plants. *Annals of Applied Statistics* 4: 1214-1233.

82. Li, M., R. Romero, W.J. Fu and **Y.H. Cui***. (2010) Mapping haplotype-haplotype interactions with adaptive LASSO. *BMC Genetics* 11:79.

83. Li, S.Y., Q. Lu and **Y.H. Cui*.** (2010) A systems biology approach for identifying novel pathway regulators in eQTL mapping. *Journal of Biopharmaceutical Statistics* 20(2): 373–400.

84. Lu, Q, **Y.H. Cui**, C. Ye, C. Wei and R.C. Elston. (2010) A bagging optimal ROC curve method for predictive genetic tests with an application to rheumatoid arthritis. *Journal of Biopharmaceutical Statistics* 20(2): 401-414.

85. Lu, Q, Y. Song, X.F. Wang, S. Won, **Y.H. Cui** and R.C. Elston. (2009) The effect of multiple genetic variants in predicting the risk of Type 2 Diabetes. *BMC Proceedings* (Suppl 7): S49.

86. Wan, L. K. Sun, Q. Ding, **Y.H. Cui**, M. Li, Y. Wen, R. Elston, M. Qian, W.J. Fu. (2009) Hybridization modeling of oligonucleotide SNP arrays for accurate DNA copy number estimation. *Nucleic Acids Research* 37(17): e117.

87. Li, S.Y., Q. Lu, W. Fu, R. Romero and **Y.H. Cui***. (2009) A regularized regression approach for dissecting genetic conflicts that increase disease risk in pregnancy. *Statistical Applications in Genetics and Molecular Biology* Vol. 8: Iss. 1, Article 45.

88. Li, G.X. and **Y.H. Cui***. (2009) A statistical variance components framework for mapping imprinted quantitative trait loci in experimental crosses. *Journal of Probability and Statistics* vol. 2009, Article ID 689489.

89. **Cui, Y.H.*** and W.Z. Yang. (2009) Zero inflated generalized Poisson regression mixture model for mapping quantitative trait loci underlying count trait with many zeros. *Journal of Theoretical Biology* 256: 276-285.

90. **Cui, Y.H.***, G.L. Kang, K.L. Sun, R. Romero, M. Qian, and W.J. Fu. (2008) Gene-centric genome-wide association study via entropy. *Genetics* 179: 637-650.

91. Ma, C-X., Q. Yu, A. Berg, D. Drost, E. Novaes, G. Fu, J.S. Yap, A. Tan, M. Kirst, **Y.H. Cui** and R.L. Wu. (2008) A statistical model for testing the pleiotropic control of phenotypic plasticity for a count trait. *Genetics* 179: 627-636.

92. **Cui, Y.H.***, S.Y. Li, and G.X. Li. (2008) Functional mapping imprinted quantitative trait loci underlying developmental characteristics. *Theoretical Biology and Medical Modeling* 5:6.

93. **Cui, Y.H.***, R.L. Wu, G. Casella, and J. Zhu. (2008) Nonparametric functional mapping quantitative trait loci underlying programmed cell death. *Statistical Applications in Genetics and Molecular Biology* 7(1): Article 4.

94. Kang G.L., W. Yue, J. Zhang, **Y.H. Cui**, Y. Zuo and D. Zhang. (2008) An entropy-based approach for testing genetic epistasis underlying complex diseases. *Journal of Theoretical Biology* 250: 362-374.

95. **Cui, Y.H.***, W. Fu, K.L. Sun, R. Romero, and R. Wu. (2007) Mapping nucleotide sequences that encode complex binary disease traits with Hapmap. *Current Genomics* 8(5): 307-322.

96. **Cui, Y.H.***, J.M. Cheverud and R.L. Wu. (2007) A statistical model for dissecting genomic imprinting through genetic mapping. *Genetica* 130: 227-239.

97. **Cui, Y.H**.* (2007) A statistical framework for genome-wide scanning and testing imprinted quantitative trait loci. *Journal of Theoretical Biology* 244: 115-126.

98. Wu, J.S., B. Zhang, **Y.H. Cui**, W. Zhao, L. Xu, Huang, Y. Zeng, and R. Wu. (2007) Genetic determination of developmental instability: design, model and algorithm. *Genetics* 176: 1187-1196.

99. Cintia, M.C., S, Wu, Y. Li, B. Hunter, R.A. Dante, **Y.H. Cui**, R.L. Wu, and B.A. Larkins. (2007) Identification of quantitative trait loci that affect endoreduplication in maize endosperm. *Theoretical and Applied Genetics* 115:1147–1162.

100. Rice, L., R. Handayani, **Y.H. Cui**, T. Medrano, Von G. Samedi, H.V. Baker, N.J. Szabo, and K. Shiverick. (2007) Effects of soy isoflavone concentrate on gene expression profiles in LNCaP human prostate cancer cells. *Journal of Nutrition* 137: 964-972.

101. Handayani, R., L. Rice, **Y.H. Cui**, T. Medrano, V.G. Samedi, H. Baker, N.J. Szabo and K. Shiverick. (2006) Soy isoflavones alter expression of genes associated with cancer progression, including IL-8, in androgen-independent PC-3 human prostate cancer cells. *Journal of Nutrition* 136: 75-82.

102. **Cui, Y.H.***, D.-Y. Kim, and J. Zhu. (2006) On the generalized Poisson regression mixture model for mapping quantitative trait loci with count data. *Genetics* 174: 2159–2172.

103. **Cui, Y.H.**, J. G. Wu, C.H. Shi, J. Zhu, R.C. Littell and R.L. Wu. (2006) Modeling epistatic effects of embryo and endosperm QTL on seed quality traits. *Genetical Research* 87: 61-71.

104. **Cui, Y.H.**, Q. Lu, J.M. Cheverud, R.C. Littell and R.L. Wu. (2006) Model for mapping imprinted quantitative trait loci in an inbred F_2 design. *Genomics* 87: 543-551.

105. **Cui, Y.H.,** J. Zhu, and R.L. Wu. (2006) Functional mapping for genetic control of programmed cell death. *Physiological Genomics* 25: 458-469.

106. **Cui, Y.H.** and R. L. Wu. (2005) A statistical model for characterizing epistatic control of triploid endosperm triggered by maternal and offspring QTL. *Genetical Research* 86: 65-76.

107. **Cui, Y.H.** and R.L. Wu. (2005) Mapping genome-genome epistasis: a high-dimensional model. *Bioinformatics* 21(10): 2447-2455.

108. Sun, K.L., **Y.H. Cui** and B. Hauser. (2005) Changes in gene expression during ovule abortion in Arabidopsis. *Planta* 222: 632-642.

109. **Cui, Y.H.**, G. Casella and R.L. Wu. (2004) Mapping Quantitative trait locus interactions from the maternal and offspring genomes. *Genetics* 167: 1017-1026.

110. Lu, Q., **Y.H. Cui** and R.L. Wu. (2004) A multilocus likelihood approach to joint modeling of linkage, parental diplotype and gene order in a full-sib family. *BMC Genetics* 5: 20.

111. Sun, K.L., M. Wang and **Y.H. Cui**. (2000) Study on the primary vascular system of the seedling of *Nelumbo Nucifera* Gaertn. *Acta Botanica Yunnanica*, 22(3): 286-290

112. **Cui, Y.H.**, M. Wang and K.L. Sun. (1999) Study on the heterogeneity of endosperm cell development in *Eucommia ulmoides* Oliv. *Journal of Agricultural Biotechnology* 7(1): 89-93.

113. **Cui, Y.H.**, M. Wang and K.L. Sun. (1999) Morphology of gutta-containing cells in *Eucommia ulmoides* Oliv. *Chinese Bulletin of Botany* 16(4): 439-443.

114. Wang, M., **Y.H. Cui** and K.L. Sun. (1999) Study on the programmed cell death in the process of

endosperm degeneration in *Eucommia ulmoides* Oliv. *Bulletin of Botanical Research* 19(4): 401-406.

115. Zhao, Y.J., W. Zhang, G. C. Li, T. Wang and **Y.H. Cui**. (1998) Genetic Studies on several morphological index of columnar apple trees. *Journal of China Agricultural University* Vol. 3, supplement: 96-98.

Review and Comment Papers

116. **Cui, Y.H.*** and H. Yang. (2017) Dissecting genomic imprinting and genetic conflict from a game theory prospective: Comment on: "Epigenetic game theory: How to compute the epigenetic control of maternal-to-zygotic transition" by Qian Wang et al. *Physics of Life Reviews* http://dx.doi.org/10.1016/j.plrev.2017.01.028.

117. Wu, C., S. Li and **Y.H. Cui***. (2012) Genetic association studies: an information content perspective. *Current Genomics* 13(7): 566-573.

118. Wu, R.L., W. Hou, **Y.H. Cui**, H.Y.Li, T. Liu, S.Wu, C-X. Ma, and Y. Zeng. (2007) Modeling the genetic architecture of complex traits with molecular markers. *Recent Patents on Nanotechnology* 1: 41-49.

Conference Proceedings

119. Ma D., W. Bu, **Y. Cui**, Y. Xie and X. Wu. (2018) Learning Collaborative Model for Visual Tracking. *24th International Conference on Pattern Recognition (ICPR)*, 2582-2587.

120. Ma D., W. Bu, Y. Xie, **Y. 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

121. 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.

122. **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

123. **Cui, Y.H.** (2022) "Multivariate Data Integration Using R: Methods and Applications with the mixOmics Package" by Kim-Anh LeCao, Zoe Marie Welham. *Biometrics*.

124. **Cui, Y.H.** (2015) "Statistical methods for QTL mapping" by Z. Chen. *Journal of the American Statistical Association*.

125. **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

1. Tan, X., X. Zhang, **Y.H. Cui**, and X. Liu. Confidence intervals in high-dimensional linear models incorporating graphical structures.

2. Zhang, J-Y., X. Liu, H. Wang and **Y.H. Cui***. Functional varying-index coefficient model for dynamic gene-environment interactions.

3. Zhang, J-Y., H. Wang and **Y.H. Cui***. Generalized functional varying-index coefficient model for dynamic synergistic gene-environment interactions.

4. Cao, H, Z. Li, H. Yang, R. Fang, Y. Zhang, B. Wang and **Y.H. Cui***. Multi-omics data integration identified novel cancer subtypes with weighted multi-kernel learning.

PROFESSIONAL ACTIVITIES

Invited session organizer/chair:

- "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)

Organizing Committee:

- *The Data Science Section of the First International Symposium on Graduate Researches* by Dokuz Eylul University, Türkiye (Dec. 2, 2022) (as a member of both Organizing Committee and Scientific Committee)
- *5th International Workshop on Statistical Genetics and Genomics*, Jinan, China (June 30-July 2, 2018) (as 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)

Panelist and Ad hoc Reviewer for Grant Proposals

- University of Sharjah Research Funding Department, 2022
- NSF Review 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

Book proposal reviewer for Prentice-Hall and Springer

Reviewer for *Mathematical Reviews* (2010-)

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 American Statistical Association*
8. *Journal of Biopharmaceutical Statistics*
9. *Journal of Business & Economic Statistics*
10. *Journal of Statistical Planning and Inference*
11. *Journal of Statistical Software*
12. *Scandinavian Journal of Statistics*
13. *Statistica Sinica*
14. *Statistical Applications in Genetics and Molecular Biology*
15. *Statistics and Its Interface*
16. *Statistics and Probability Letters*
17. *Statistics in Medicine*

Statistical Genetics and Bioinformatics related journals

18. *American Journal of Human Genetics*
19. *Annals of Human Genetics*
20. *Bioinformatics*
21. *BMC Bioinformatics*
22. *BMC Genetics*
23. *BMC Genomics*
24. *BMC Medicine*
25. *Briefings in Bioinformatics*
26. *Communications in Information and Systems*

27. *Computational and Structural Biotechnology Journal*
28. *Current Genomics*
29. *Frontiers in Genetics, Statistical Genetics and Methodology*
30. *G3: Genes, genomics, Genetics*
31. *Genetica*
32. *Genetics*
33. *Genetic Epidemiology*
34. *Genetics Research*
35. *Genomics*
36. *Heredity*
37. *Human Genetics*
38. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
39. *Journal of Chemical Information and Modeling*
40. *Journal of Neuroscience methods*
41. *Journal of Theoretical Biology*
42. *Mathematical Biosciences and Engineering*
43. *Methods in Ecology and Evolution*
44. *Nucleic Acid Research*
45. *PloS Computational Biology*
46. *PloS Genetics*
47. *Theoretical and Applied Genetics*
48. *Theoretical Biology and Medical Modeling*

Natural Science and Public Health journals

49. *African Journal of Biotechnology*
50. *BioMed Research International*
51. *BMC Plant Biology*
52. *British Journal of Psychiatric*
53. *Cellular and Molecular Life Sciences*
54. *Drug Discovery*
55. *Environmental Science and Pollution Research*
56. *Environmental International*
57. *Euphytica*
58. *European Journal of Public Health*
59. *Food Science and Technology*
60. *Frontiers in Cardiovascular Medicine*
61. *Frontiers in Publish Health*
62. *Gene*
63. *Health Expectations*
64. *Journal of Affective Disorder*
65. *Journal of Internal Medicine*
66. *Journal of Public Health*
67. *Journal of Nutrition Education and Behavior*
68. *Mammalian Genome*
69. *Marine Biotechnology*
70. *Molecular Genetics and Genomics*
71. *Molecular Plant*
72. *Nutrition, Metabolism and Cardiovascular Diseases*
73. *Plant Cell*
74. *Plant Journal*
75. *Plant Physiology*
76. *Plants*
77. *PloS One*
78. *Public Health Nutrition*
79. *Science in China*
80. *Scientific Reports*
81. *Scientific World Journal*
82. *Translational Psychiatry*

STUDENTS ADVISING

Current Ph.D. students in statistics (as advisor/co-advisor)

1.	Ruxin Shi	Ph.D. (advisor)	Ongoing
2.	Sikta Dasadhikari	Ph.D. (co-advisor, joint with Jianrong Wang in CMSE)	Ongoing
3.	Aoqi Xie	Ph.D. (advisor)	Ongoing
4.	Yuesong Wu	Ph.D. (co-advisor, joint with Yuying Xie)	Ongoing

Past PhD students, their thesis title and job placement

As major (co)advisor

5. 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

6. 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 manager at Pfizer

7. 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 statistician at Amazon

8. Tao He, (joint with Ping-Shou Zhong) 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

9. Honglang Wang, (joint with Ping-Shou Zhong) 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

10. 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, Johnson & Johnson

11. Cen Wu, 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

12. Shaoyu Li, 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 Associate Professor, Department of Mathematics and Statistics, University of North Carolina at Charlotte

13. Gengxin Li, 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-advisor

14. 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.

15. 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.

16. 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

17. 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.

18. 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, Department of Statistics, Kansas State University

19. 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

20. Haitao Yang, Postdoctoral Fellow, 2016-2017
Currently Professor, School of Public Health, Hebei Medical University, China

21. Xu Liu, Postdoctoral Fellow, 2013-2016
Currently Associate Professor with tenure, School of Statistics and Management, Shanghai University of Finance and Economics, China.

22. Guolian Kang, Postdoctoral Fellow, 2006-2007
Currently Full Member, Department of Biostatistics, St. Jude Children's Research Hospital.

Past MS students and position

1. Di Zhang, M.Sc., degree conferred in 5/2020, Statistician, WeGene, China

2. Ze Meng, M.Sc., degree conferred in 5/2020, Statistician, Henry Ford Health, Detroit

3. Yimin Wu, M.Sc., degree conferred in 12/2017, Statistician, DTE Energy, Ann Arbor

4. Ran Cao, M.Sc., degree conferred in 05/2013, Statistician, i360 at Washington DC

5. Chenyang Gu, M.Sc., degree conferred in 05/2012, Ph.D. student, Department of Biostatistics, Brown University

6. Chunyu Chen, M.Sc., degree conferred in 05/2012, Ph.D. student, Department of Animal Science, Michigan State University

7. Wenzhao Yang, M.Sc., degree conferred in 08/2008. She obtained her Ph.D. degree at Michigan State University in 2014.

8. Guanghui Liu, M.Sc., degree conferred in 12/2006, currently Biostatistician, Mayo Clinic

Other MSU Ph.D. Students (as a member of the Guidance Committee)

Name	Department	Time thesis defended
1. Dali Liu	Dept. of Statistics and Probability	ongoing
2. Jianrui Zhang	Dept. of Statistics and Probability	ongoing

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

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

Undergraduate Student Advising:

- 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 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

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

2022-2023	Junior Faculty Search Committee (as chair)
2022-pres	Reappoint, Promotion and Tenure Committee
2021-2023	Faculty Advisory Committee (as chair)
2020-2021	Mentoring Policy Committee (as chair)
2020-2021	Prelim Policy Committee (as chair)
2019-pres	Graduate Support Committee (as chair)
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	Comupter Committee

College and University Committee

2019-pres	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 Scentifit 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 Wild Life

Other Committee Service

2020-2021	President of MSU Chinese Faculty Club
2018-2022	Member of Executive Committee, MSU Chinese Faculty Club

PROFESSIONAL MEMBERSHIPS

- American Association for the Advancement of Science (AAAS) (2018-)
- American Statistical Association (ASA) (2005-)
- International Biometric Society (IBS) (2004-)
- International Chinese Statistical Association (ICSA) (lifetime member)
- Sigma Xi full membership, The Scientific Research Society (2008-)