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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) China Agricultural University, Beijing, China
B. S. Agronomy (1995) Shanxi Agricultural University, Shanxi, China

ACADEMIC APPOINTMENTS

- Professor** 2015 – present, Department of Statistics & Probability, Michigan State University
Professor 2018 – present, College of Nursing, 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 08/1998 – 05/2000, Institute of Botany, Chinese Academy of Sciences

Other Academic Affiliation:

- Faculty Member of MSU **Genetics** Program
- Faculty Member of MSU **System Biology** Program
- Faculty Member of MSU **Quantitative Biology Initiative** (QBI) Program
- Faculty Member of MSU **Ecology, Evolutionary Biology, and Behavior** (EEBB) Program

RESEARCH INTERESTS

- Statistical genetics: (e)QTL mapping, Genome-wide association study, Gene-gene and gene-environment interactions;
- Statistical genomics: Microarray data analysis, RNA-seq data analysis, Pathway analysis, Gene network inference;
- Bioinformatics, Systems Biology, Computational biology, Next-generation sequencing data analysis;
- Applied functional and longitudinal data analysis, Mixture model;
- Statistical applications in life science.

HONORS AND AWARDS

- 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
- 2000 University Fellowship, The Ohio State University

RESEARCH GRANTS

Active

- 2019-2021 (PI, with P. Zhong, A. Burt and K. Klump) “Novel methods for longitudinal study of synergistic gene-environment interactions in complex diseases”. NIH 1R21HG010073-01A1.
Total Award Amount: \$422,646.00
Total Award Period Covered: 05/01/2019-04/30/2021
- 2018-2022 (Co-PI, With J. Wang (PI) and E. Andrechek) “Statistical modeling of long-range chromatin interactions on gene regulation and underlying molecular mechanisms”, NIH 1R01GM131398.
Total Award Amount: \$1,300,004.00
Total Award Period Covered: 09/01/2018-05/31/2022

Finished

- 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.

- 2012-2016 (PI, with Co-PI P-S Zhong), “Statistical inference for gene regulation with genetical genomic data”, NSF ([DMS-1209112](#)), \$208,688
- 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; PI: 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.

EDITORIAL SERVICES

Deputy Section Editor: *BMC Genetics*, Section on Statistical and Computational Genetics (2010-)

Associate Editor:

Statistics and Probability Letters (2015-)

BMC Genetics (2010-2016)

Editorial Board:

Journal of Computational Systems Biology (2014-)

The Scientific World Journal, Computational Biology Domain (2011-2017)

Recent Patents on Biotechnology (2010-2014)

Review Editorial Board: *Frontier in Statistical Genetics and Methodology* (2011-)

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

Co-editor: Special issue on “Design and analysis of genome-wide association and next generation sequencing data in cancer pharmacogenomics”, *Frontier in Statistical Genetics and Methodology* (2014-2015)

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 (*corresponding author; Trainees)

Methodology Papers

1. Gao, B., X. Liu, H. Li and **Y. Cui***. (2019) Integrative analysis of genetical genomics data incorporating network structures. *Biometrics* (in press)
2. Zhang, H., Bi, W., **Cui, Y.H.**, Chen, H., Chen, J., Zhao, Y., Kang, G. (2019) Extreme-value sampling design is cost-beneficial only with a valid statistical approach for exposure–secondary outcome association analyses. *Statistical Methods in Medical Research* (in press)
3. Yang, H.T., H. Cao, T. He, T. Wang and **Y.H. Cui***. (2019) Multi-level heterogeneous omics data integration with kernel fusion. *Briefings in Bioinformatics* (in press)
4. Liu, X., P-S. Zhong and **Y.H. Cui***. (2019) Joint test of parametric and nonparametric effects in partial linear models for gene-environment interaction. *Statistica Sinica* (in press)
5. 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.
6. 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).
7. 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.
8. 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.
9. 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.
10. 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.
11. 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.
12. 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 Report* 7: 45191.
13. 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.
14. 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.
15. 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.

16. 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.
17. 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.
18. 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).
19. 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.
20. Gao, B. and **Y.H. Cui***. (2015) Learning directed acyclic graphical structures with genetical genomics data. *Bioinformatics* 31(24): 3953-60.
21. 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.
22. 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.
23. 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.
24. 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.
25. 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.
26. 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.
27. 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.
28. 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.
29. 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.
30. 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.

31. 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.
32. 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.
33. Yang, R., X. Wang and **Y.H. Cui***. (2012) Bayesian inference for genomic imprinting underlying developmental characteristics. *Briefings in Bioinformatics* 13(5): 555-568.
34. 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.
35. Wu, C., G.X. Li, J. Zhu and **Y.H. Cui***. (2011) Function mapping with robust t-distribution. *PloS One* 6(9): e24902.
36. 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.
37. 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.
38. 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.
39. 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.
40. Li, M., R. Romero, W.J. Fu and **Y.H. Cui***. (2010) Mapping haplotype-haplotype interactions with adaptive LASSO. *BMC Genetics* 11:79.
41. 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.
42. 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.
43. 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.
44. 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.
45. 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.

46. **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.
47. **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.
48. 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.
49. **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.
50. **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.
51. 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.
52. **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.
53. **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.
54. **Cui, Y.H.*** (2007) A statistical framework for genome-wide scanning and testing imprinted quantitative trait loci. *Journal of Theoretical Biology* 244: 115-126.
55. 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.
56. **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.
57. **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.
58. **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 F₂ design. *Genomics* 87: 543-551.
59. **Cui, Y.H.**, J. Zhu, and R.L. Wu. (2006) Functional mapping for genetic control of programmed cell death. *Physiological Genomics* 25: 458-469.
60. **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.
61. **Cui, Y.H.** and R.L. Wu. (2005) Mapping genome-genome epistasis: a high-dimensional model. *Bioinformatics* 21(10): 2447-2455.

62. **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.
63. 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.

Application Papers

64. Jing, LW, **Y.H. Cui**, Q. Lu, and H. Yu. (2019) Multiplier method estimates of the population of men who have sex with men: the effect of privacy protection. *Journal of Public Health* (in press)
65. 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* 42: 1513-1531.
66. 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.
67. 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.
68. 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.
69. 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.
70. 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.
71. 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.
72. 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.
73. 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.
74. 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.

75. 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.
76. 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.
77. 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.
78. 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.
79. Humphries, Brock, Z. Wang, A. Oom, T. Fisher, D. Tan, **Y.H. Cui**, Y. Jiang, and C. Yang. (2014) nMicroRNA-200b targets protein kinase C α and impairs triple negative breast cancer cell migration and tumor metastasis. *Carcinogenesis* 35(10): 2254-2263.
80. 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 G \times E interaction. *BMC Proceedings* 8(Suppl 1): S61.
81. 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.
82. Dang, M-T., C. Gu, J.I. Klavarian, 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.
83. Kang, G.L., B. Jiang and **Y.H. Cui**. (2013) Gene-based genome-wide association analysis: a comparison study. *Current Genomics* 14: 4.
84. 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.
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. 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.
87. 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.
88. 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.

89. Sun, K.L., **Y.H. Cui** and B. Hauser. (2005) Changes in gene expression during ovule abortion in *Arabidopsis*. *Planta* 222: 632-642.
90. 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
91. **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.
92. **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.
93. 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.
94. 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

95. **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>.
96. Wu, C., S. Li and **Y.H. Cui***. (2012) Genetic association studies: an information content perspective. *Current Genomics* 13(7): 566-573.
97. 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.

Invited Book Chapters

98. 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.
99. **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.

Conference Proceedings

100. Ma D., W. Bu, **Y. Cui**, Y. Xie and X. Wu. (2018) Learning Collaborative Model for Visual Tracking. *Proceedings on International Conference in Pattern Recognition 2018*

101. Ma D., W. Bu, Y. Xie, **Y. Cui** and X. Wu. (2018) Segmentation-Guided Tracking with Prior Map Decision. *Proceedings on International Conference in Pattern Recognition 2018*

Book Review

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

103. **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. Jing, LW, **Y.H. Cui**, and Q. Lu. Use of the multiplier method to estimate the size of populations most at risk of HIV infection in China: a systematic review. *Public Health*
2. Sun, H., **Y.H. Cui** and T. Wang. Robust Penalized Logistic Regression through Maximum Trimmed Likelihood Estimator. *Statistics and Probability Letters*
3. He, T., P-S. Zhong, **Y.H. Cui** and V. Mandrekar. Tests for high-dimensional nonparametric functions with kernel regularization.
4. Sun, H., **Y.H. Cui**, H. Wang, H. Liu, and T. Wang. Comparison of methods for the detection of outliers and associated biomarkers in mislabeled omics data. *BMC Bioinformatics*
5. Gao, Y., H. Yang, R. Fang, Y. Zhang and **Y.H. Cui***. Testing mediation effects in high-dimensional epigenetic studies. *Frontiers in Genetics*

SERVICE TO PROFESSION

Invited session organizer/chair:

- "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, 2010)
- “Statistical genetics: challenges, advances and prospects”, *First Joint Biostatistics Symposium*, Beijing, China (July, 2010)
- “Recent advances and statistical challenges in genetical genomics analysis”, *ICSA Applied Statistics Symposium*, Indianapolis, IN (June, 2010)

Organizing Committee:

- *The 5th International Workshop on Statistical Genetics and Genomics*, Jinan, China (June 30-July 2, 2018)
- *The 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)
- *The 4th International Conference & exhibition on Biometrics & Biostatistics*, San Antonio, TX (Nov 16-18, 2015)
- *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)
- *International Conference and Exhibition on Biometrics & Biostatistics*, Omaha, USA (March 05-07, 2012)
- *Statistical Genetics and Genomics Workshop*, East Lansing, MI (May, 2008) (as chair)

Panelist and Ad hoc Reviewer for Grant Proposals

- UK Medical Research Council
- NSF BIGDATA panelist, 2016
- Netherlands Genomics Initiative
- National Science Foundation
- Intramural Funding Program, the Office of the Vice President for Research and Graduate Studies, Michigan State University
- Michigan AgBioResearch Program

China Chang-Jiang Scholar Program External Expert Reviewer (2016)

Book proposal reviewer for Prentice-Hall

Reviewer for *Mathematical Reviews* (2010-)

Journal referee services for the following journals (>150 times)

Statistics related journals

1. *Annals of Applied Statistics*
2. *Biometrics*
3. *Biostatistics*
4. *Communications in Statistics – T&M*
5. *Journal of Biopharmaceutical Statistics*
6. *Journal of Business & Economic Statistics*
7. *Journal of Statistical Planning and Inference*
8. *Journal of Statistical Software*
9. *Scandinavian Journal of Statistics*
10. *Statistical Applications in Genetics and Molecular Biology*
11. *Statistics and Its Interface*
12. *Statistics and Probability Letters*
13. *Statistics in Medicine*

Statistical Genetics and Bioinformatics related journals

14. *American Journal of Human Genetics*
15. *Annals of Human Genetics*
16. *Bioinformatics*
17. *BMC Bioinformatics*
18. *BMC Genetics*
19. *BMC Genomics*
20. *Briefings in Bioinformatics*
21. *Communications in Information and Systems*
22. *Current Genomics*
23. *Frontiers in Statistical Genetics and Methodology*
24. *G3: Genes, genomics, Genetics*
25. *Genetica*
26. *Genetics*
27. *Genetic Epidemiology*
28. *Genetics Research*
29. *Genomics*
30. *Heredity*
31. *Human Genetics*
32. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
33. *Journal of Neuroscience methods*
34. *Journal of Theoretical Biology*
35. *Methods in Ecology and Evolution*
36. *PloS Computational Biology*
37. *PloS One*
38. *Theoretical and Applied Genetics*
39. *Theoretical Biology and Medical Modeling*
40. *Scientific Report*
41. *Scientific World Journal*

Natural Science and Public Health journals

42. *African Journal of Biotechnology*
43. *BioMed Research International*
44. *BMC Plant Biology*
45. *Cellular and Molecular Life Sciences*
46. *Drug Discovery*
47. *Euphytica*
48. *Food Science and Technology*
49. *Gene*
50. *Health Expectations*
51. *Journal of Affective Disorder*
52. *Journal of Nutrition Education and Behavior*
53. *Journal of Public Health*
54. *Mammalian Genome*
55. *Marine Biotechnology*
56. *Methods in Ecology and Evolution*
57. *Molecular Genetics and Genomics*
58. *Plant Cell*
59. *Plant Journal*
60. *Plant Physiology*
61. *Science in China*

CONFERENCE AND DEPARTMENTAL SEMINAR PRESENTATIONS

Invited Plenary Talks

1. "Genome-wide multi-trait analysis", *The 6th International forum on statistical genetics and genomics*, Nanjing, China (June 29-30, 2019)
2. "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)
3. "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

1. "Nonlinear moderated mediation analysis with genetical genomic data", *2019 ICSA Conference*, Tianjin, China (July 1-5, 2019)
2. "Nonlinear moderated mediation analysis with genetical genomic data", *The 3rd International Conference on Econometrics and Statistics (EcoSta 2019)*, Taichung, Taiwan (June 25-27, 2019)
3. "Omics data integration with kernel fusion", *San Francisco Bay area chapter of ASA*, San Francisco, CA (Oct. 26, 2018)
4. "Statistics in post genomic era: challenges and opportunities", *Western Meeting of AMS*, San Francisco, CA (Oct. 27-28, 2018)
5. "Integrative genetical genomics analysis incorporating network structures", *2018 ICSA China Statistics Conference*, Qingdao, China (July 2-5, 2018)
6. "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)
7. "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)
8. "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)
9. "Gene selection with nonlinear instrumental regression incorporating network structures", *The 10th R Conference*, Taiyuan University of Technology, Taiyuan, China (June 24-25, 2017)
10. "An optimal kernel based method for gene set association analysis", *4th International Workshop on Statistical Genetics/Genomics*, Taiyuan, China (June 22-23, 2017)
11. "Integrative genetical genomics analysis incorporating network structures", *Biostatistics workshop, Statistical Inference for Biomedical Big Data*, Gainesville, FL (April 7-8, 2017)

12. "Integrative analysis of genetical genomics data incorporating network structures", *Joint Statistical Meeting*, Chicago, IL (July 30-August 4, 2016)
13. "Integrative genetical genomics analysis incorporating network structures", *The 4th International Symposium on Biostatistics*, Shanghai, China (July 2-3, 2016)
14. "Integrative genetical genomics analysis incorporating network structures", *2016 ICSA China Statistics Conference*, Qingdao, China (June 24-25, 2016)
15. "Integrative analysis of gene-environment interactions", *3rd International Workshop on Statistical Genetics/Genomics*, Taiyuan, China (June 21-22, 2016)
16. "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)
17. "Integrative analysis of gene-environment interactions". *Joint Statistical Meeting*, Seattle, WA (August 7-13, 2015)
18. "Integrative genetical genomics analysis incorporating network structures", *ICSA-China Statistics Conference*, Shanghai, China (July 6-7, 2015)
19. "Integrative genetical genomics analysis incorporating network structures", *IMS-China International Conference on Statistics and Probability*, Kunming, Yunnan, China (July 1-4, 2015)
20. "Integrative genetical genomics analysis incorporating network structures", *2nd International Workshop on Statistical Genetics/Genomics*, Taiyuan, China (June 22-24, 2015)
21. "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)
22. "Statistical genetics: current status and perspectives", *Statistics in Applications Symposium* East Lansing, MI (October 2, 2014)
23. "Partial linear models for integrative gene-environment interactions", *3rd International Biostatistics Symposium*, Chengdu, China (June 27-28, 2014)
24. "Challenges and strategies in gene-environment interactions", *1st International Workshop on Statistical Genetics/Genomics*, Taiyuan, China (June 24-25, 2014)
25. "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)
26. "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)
27. "Varying coefficient model for nonlinear gene-environment interaction", *The 8th Purdue Symposium on Statistics*, Lafayette, IN (June 20-24, 2012)
28. "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).

29. "Gene-centric gene-gene interaction", Statistical Genomics Workshop, *Plant and Animal Genome XX Conference*, San Diego, CA (January 15-17, 2012)
30. "eQTL mapping: the added value in complex trait dissection", *iGRAD-Plant Symposium/Retreat*, Henrich Heine University, Düsseldorf, Germany (September 12-17, 2011)
31. "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)
32. "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)
33. "Gene-based genome-wide association studies", *Summer Workshop on Statistical & Computational Genetics*, Beijing Forest University, Beijing, China (July 19, 2010)
34. "eQTL mapping: the added value in complex trait dissection", *First Joint Biostatistics Symposium*, Beijing, China, (July 15-18, 2010).
35. "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).
36. "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).
37. "Functional mapping genomic imprinting underlying developmental characteristics", *Fall Conference on Statistics in Biology*, Ames, IA, (October 13-15, 2008).
38. "Large-scale genome-wide association studies via entropy test", *Workshop on Multiscale Modeling, Analysis and Simulations*, East Lansing, MI, (October 10-11, 2008).
39. "Understanding the genetic architecture of genomic imprinting by Functional QTL Mapping", *Midwest Conference on System Biology*, East Lansing, MI, (October 27-28, 2007).
40. "Sequencing complex diseases with penalized logistic regression", *Interdisciplinary bioinformatics workshop*, University of Michigan, (November 3, 2006).
41. "Binary Trait Nucleotides Mapping Complex Disease With HapMap", *ICSA applied statistics symposium*, Storrs, CT, (June 14-17, 2006).

Invited Departmental Seminars and Colloquium Talks

1. University of Florida, Department of Biostatistics (3/16/2019)
2. Michigan State University, Department of Statistics & Probability (01/22/2019)
3. University of Notre Dame, Department of Applied and Computational Mathematics and Statistics (11/16/2018)
4. Zhengzhou University (China), School of Public Health China (05/28/2018)
5. Anhui University of Finance and Economics (China), College of Statistics and Applied Math

(06/05/2018)

6. University of Minnesota, Division of Biostatistics (04/07/2017)
7. University of Notre Dame, Department of Applied and Computational Mathematics and Statistics (9/26/2016)
8. Beijing Academy of Agriculture and Forestry Sciences (China) (07/13/2016)
9. Taiyuan University of Technology (China), School of Mathematics (06/03/2016)
10. Western Michigan University, Department of Statistics (02/12/2016)
11. Stony Brook University, Department of Applied Mathematics and Statistics (11/20/2015)
12. University of Alabama at Birmingham, Section on Statistical Genetics, Department of Biostatistics (09/25/2014)
13. Wuhan University (China), School of Mathematics and Statistics (05/26/2014)
14. Wright State University, Department of Mathematics and Statistics (04/11/2014)
15. Zhengzhou University (China), School of Public Health (06/24/2013)
16. St. Jude Children's Research Hospital, Department of Biostatistics (01/08/2013)
17. Chinese Academy of Sciences, Beijing Institute of Botany (05/21/2012)
18. Wuhan University of Science and Technology (China), College of Science (05/07/2012).
19. Xi'an Jiaotong University (China), College of Mathematics and Statistics (04/28/2012)
20. Beijing Forestry University (China), College of Biological Sciences and Biotechnology (04/24/2012)
21. Yale University, Division of Biostatistics (11/8/2011)
22. Michigan State University, Department of Statistics and Probability (10/17/2011)
23. Shanxi Medical University (China), School of Public Health (6/15/2011)
24. Haerbin Medical University (China), College of Bioinformatics and Technology (6/10/2011)
25. Virginia Tech, Department of Statistics (09/30/2010)
26. University of Connecticut, Department of Statistics (04/19/2010)
27. UT Southwestern Medical Center, Department of Clinical Science (04/15/2010)
28. University of South Carolina, Department of Epidemiology and Biostatistics (04/07/2010)
29. Georgia State University, Department of Mathematics and Statistics (03/31/2010)
30. Saint Louis University, Division of Biostatistics (03/19/2010)
31. University of Nebraska Medical Center, Department of Biostatistics (03/17/2010)
32. Indiana University, Department of Medical and Molecular Genetics (03/09/2010)
33. Emory University, Department of Biostatistics and Bioinformatics (02/18/2010)
34. Marquette University, Department of Mathematics and Statistics, and Computer Science (02/14/2010)
35. MSU Computational Biology Group kick-off seminar (02/10/2010)
36. Michigan State University, Department of Statistics & Probability (02/02/2010)

37. Ohio State University, Department of Statistics (01/28/2010)
38. Indiana University and Purdue University at Indianapolis, Department of Mathematical Science (01/25/2010)
39. National Center for Integrative Biomedical Informatics (NCIBI) (08/13/2009)
40. Kansas State University, Department of Statistics (05/08/2008)
41. Ohio State University, Department of Statistics (01/15/2008)
42. Michigan State University, Genetics Research Forum (11/12/2007)
43. Michigan State University, Department of Statistics & Probability (09/04/2007)
44. University of Michigan, Department of Biostatistics (11/03/2006)
45. Michigan State University, Department of Statistics & Probability (02/21/2006)
46. The Perinatology Research Branch, NICHD/NIH (01/25/2006)
47. University of Florida, Department of Statistics graduate student seminar (04/19/2005)
48. University of Florida, Institute of Food and Agricultural Sciences-Statistics (03/11/2005)
49. Tulane University, Department of Epidemiology (03/14/2005)
50. University of Minnesota, Department of Biostatistics (03/09/2005)
51. University of Alabama, Department of Biostatistics (02/22/2005)
52. Wake Forest University, Department of Public Health (02/14/2005)
53. Michigan State University, Department of Statistics and Probability (02/04/2005)
54. Michigan State University, Department of Plant Biology (02/02/2005)
55. University of Florida, Superfund Basic Research Program Center for Environmental & Human Toxicology (Dec. 2003)
56. University of Florida, Superfund Basic Research Program Center for Environmental & Human Toxicology (June 2003).

STUDENTS ADVISING

Past postdocs and their current position

1. Haitao Yang, Postdoctoral Fellow, 10/2016-04/2017
Associate Professor, School of Public Health, Hebei Medical University, China
2. Xu Liu, Postdoctoral Fellow, 08/2013-06/2016
Assistant Professor, School of Statistics and Management, Shanghai University of Finance and Economics, China.
3. Guolian Kang, Postdoctoral Fellow, 02/07-07/07
Associate Member, Department of Biostatistics, St. Jude Children's Research Hospital.

Past PhD students, their thesis title and current position

4. Daewoo Pak, Ph.D. in Statistics (co-advisor, major advisor: C.X. Li and D. Todem 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".

Postdoc, MD Anderson Cancer Center.

5. 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"

Senior Research Statistician, AbbVie

6. 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"

Statistician, Wells Fargo

7. 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".

Assistant Professor, Department of Mathematics, San Francisco State University

8. 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".

Assistant Professor, Department of Mathematical Sciences, IUPUI

9. Bin Gao, Ph.D. in Statistics, degree conferred in 08/2015

Thesis title: "Graph estimation and network constrained regularization with application in genetical genomics"

Senior Statistician, Johnson & Johnson

10. Cen Wu, Ph.D. in Statistics and Quantitative Biology, degree conferred in 08/2013

Thesis title: "High-dimensional statistical methods for gene-environment interactions".

Assistant Professor, Department of Statistics, Kansas State University

11. Shaoyu Li, Ph.D. in Statistics and Quantitative Biology, degree conferred in 08/2011

Thesis title: "Statistical issues and novel strategies for eQTL mapping".

Assistant Professor, Department of Mathematics and Statistics, University of North Carolina at Charlotte (2014-)

Assistant Member, Department of Biostatistics, St. Jude Children's Research Hospital (2011-2014)

12. Wei-Wen Hsu, Ph.D. in Statistics (co-advisor, major advisor: D. Todem), degree conferred in 08/2011

Thesis title: "Tests of homogeneity in two-component mixture models".

Assistant Professor, Department of Statistics, Kansas State University

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”.

Associate Professor, Dept. of Mathematics and Statistics, Wright State University

MS students and current position

1. Yimin Wu, M.Sc., degree conferred in 12/2017, Statistician, DTE Energy, Ann Arbor
2. Ran Cao, M.Sc., degree conferred in 05/2013, Statistician, i360 at Washington DC
3. Chenyang Gu, M.Sc., degree conferred in 05/2012, Ph.D. student, Department of Biostatistics, Brown University
4. Chunyu Chen, M.Sc., degree conferred in 05/2012, Ph.D. student, Department of Animal Science, Michigan State University
5. Wenzhao Yang, M.Sc., degree conferred in 08/2008. She obtained her Ph.D. degree at Michigan State University in 2014.
6. 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
Binbin Huang	Dept. of Computational Mathematics, Science and Engineering	ongoing
Ningyu Sha	Dept. of Computational Mathematics, Science and Engineering	ongoing
Xiaoran Tong	Dept. of Epidemiology and Biostatistics	ongoing
Bing Tong	Dept. of Counseling, Educational Psychology and Special Education	07/2019
Shawn Santo	Dept. of Statistics and Probability	12/2018
Yaohui Ding	Dept. of Computer Science and Engineering	01/2018
Sneha Jadhav	Dept. of Statistics and Probability	07/2017
Chunyu Chen	Dept. of Animal Science	08/2017
Ashwini Maurya	Dept. of Statistics and Probability	05/2016
Jikai Lei	Dept. of Computer Science	07/2015
Keyin Wang	Dept. of Counseling, Educational Psychology and Special Education	08/2016
Aritro Nath	The Genetics Program	05/2015
Changshuai Wei	Dept. of Epidemiology and Biostatistics	05/2014
Wenzhao Yang	Dept. of Animal Science	04/2014
Yvonne Badke	Dept. of Animal Science	08/2013
Greg Habing	Center for Comparative Epidemiology	08/2012
Xuechun Zhou	Dept. of Counseling, Educational Psychology and Special Education	08/2012
Ming Wu	Dept. of Computer Sciences and Engineering	08/2012
Shannon Bell	Dept. of Biochemistry & Molecular Biology	04/2012
Ming Li	Division of Biostatistics, Dept. of Epidemiology	05/2011
Shujie Ma	Dept. of Statistics and Probability	07/2011

Qiongxia Song	Dept. of Statistics and Probability	07/2010
Nora Bello	Dept. of Animal Science	07/2010
Menghan Liu	Dept. of Crop & Soil Science	03/2010
Young Gui Kim	Dept. of Economics	07/2009
Tianshu Pan	Dept. of Counseling, Educational Psychology and Special Education	10/2008
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/>.

COMMITTEE SERVICES

Department Committee

2018-2019	Committee of the Whole (as chair)
2018-2019	Department Tenure & Promotion Committee
2017-2018	Faculty Search Committee (as chair)
2016-2017	Faculty Search Committee for Quantitative/Statistical/Computational Genomics faculty hire
2016-2017	Committee member on Master in Data Science committee
2016-2019	Committee member on CMSE Undergraduate Major in Data Science
2015-2017	Faculty Search Committee for CMSE data science faculty hire
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 chair)
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)
2005-2012	Faculty Advisory Committee
2012-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

2016-2018	Committee on University Student-Faculty Judiciaries
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 Wild Life

TEACHING EXPERIENCES (BY COURSE)

COURSE NAME	SCHEDULE	# OF STUDENTS ENROLLED
STT843 – MULTIVARIATE ANALYSIS	SPRING 2008	35
	SPRING 2009	29
STT847 – SURVIVAL DATA ANALYSIS	SPRING 2007	25
STT855 – STATISTICAL GENETICS	FALL 2009	25
	FALL 2011	16
	FALL 2013	14
	FALL 2015	11
	FALL 2017	19
	FALL 2019	
STT863 – STATISTICS METHODS I (LINEAR REGRESSION)	FALL 2016	32
STT864 – APPLIED STATISTICS METHODS II (GLM)	SPRING 2011	35
STT890 – STATISTICAL PROBLEMS	FALL 2007	22
HRT892/GEN800 – QUANTITATIVE GENETICS SEMINAR	SPRING 2013	9
STT481 – ISSUES IN STATISTICAL PRACTICE	SPRING 2008	10
STT442 – PROBABILITY & STATISTICS II (STATISTICS)	SPRING 2017	39
	SPRING 2017	33
	SPRING 2018	34
	SPRING 2018	25
STT421 – STATISTICS I	FALL 2008	18
	SPRING 2009	22
	FALL 2010	49
	SPRING 2011	40
	FALL 2011	43

STT351 – PROBABILITY AND STATISTICS FOR ENGINEERING	FALL 2012	32
STT315 – INTRO PROB & STAT FOR BUSINESS	SPRING 2015	333
	SPRING 2015	350
	SPRING 2016	321
STT231 – STATISTICS FOR SCIENTISTS	FALL 2005	65
	SPRING 2006	80
	SPRING 2007	128
	FALL 2009	156
	FALL 2012	149
STT200 – STATISTICAL METHODS	SPRING 2014	213

Guest lecturer for QB826 (fall 2012), Quantitative Biology Program, MSU

Guest lecturer for STT890 (spring 2006), Dept. of Statistics and Probability, MSU

Guest lecturer for EPI950 (fall 2006), Department of Epidemiology, MSU

Teaching Assistant, Department of Statistics, University of Florida (2001)

PROFESSIONAL MEMBERSHIPS

- American Statistical Association (ASA) (2005-)
- International Biometric Society (IBS) (2004-)
- International Chinese Statistical Association (ICSA) (lifetime member)
- International Statistics Institute (ISI) (2010-)
- Sigma Xi full membership, The Scientific Research Society (2008-)