Chong Wu

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RESEARCH INTERESTS

Statistical genomics (TWAS, PWAS, GWAS, multi-omics, integrative analysis, polygenic risk score)
Machine learning (unsupervised learning, supervised learning, DNA foundation model)
Causal inference (Mendelian randomization, instrumental variables regression)

EMPLOYMENT

Assistant Professor Sept. 2022–Present
Department of Biostatistics, The University of Texas MD Anderson Cancer Center

Adjunct Assistant Professor Sept. 2022–Present
Department of Statistics, Florida State University

Adjunct Assistant Professor April. 2023–Present
Department of Biostatistics and Data Science, UTHealth School of Public Health

Adjunct Assistant Professor July. 2023–Present
Department of Statistics, Rice University

Assistant Professor Aug. 2018–Aug. 2022
Department of Statistics, Florida State University

EDUCATION

University of Minnesota Minneapolis, MN
Ph.D., Biostatistics Jun. 2018
Advisors: Drs. Weihua Guan & Wei Pan
Thesis: Statistical methods for high-dimensional genetic and genomic data

Huazhong University of Science & Technology Wuhan, China
B.S., Applied Mathematics Jun. 2013
Advisor: Dr. Xiaoyang Zhou

PEER-REVIEWED ARTICLES

Google Scholar: `https://scholar.google.com/citations?user=sWUsT2UAAAAJ&hl=en`.
Citations: over 1,400; h-index: 19

* Corresponding author; † Co-first author; ‡ Students or Postdocs advised by C Wu; ¶ Co-senior author

—Theory & Methods

1. King, A.‡, & **Wu, C.** (2024). Integrative Multi-Omics Approach for Improving Causal Gene Identification. *Genetic Epidemiology*. Accepted.

2. Meng, Z.‡, Wang, J., Lin, L.*, & **Wu, C.*** (2024). Sensitivity analysis with iterative outlier detection for systematic reviews and meta-analyses. *Statistics in Medicine*, 43(8), 1549–1563.
3. Zhao, C., Su, K. J., **Wu, C.**, Cao, X., Sha, Q., Li, W., ...& Deng, H. W. (2024). Multi-scale variational autoencoder for imputation of missing values in untargeted metabolomics using whole-genome sequencing data. *Computers in Biology and Medicine*, 179, 108813.
4. Melton, H.J.‡, Zhang, Z.‡, Deng, H.W., Wu, L.*, & **Wu, C.*** (2024). MIMOSA: a resource consisting of improved methylome prediction models increases power to identify DNA methylation-phenotype associations. *Epigenetics*, 19(1), 2370542.
5. Lyu, Y., **Wu, C.**, Sun, W., & Li, Z. (2024). Regional analysis to delineate intrasample heterogeneity with RegionalST. *Bioinformatics*, 40(4), btae186.
6. Melton, H.J.‡, Zhang, Z.‡, & **Wu, C.*** (2024). SUMMIT-FA: A new resource for improved transcriptome imputation using functional annotations. *Human Molecular Genetics*, 33(7), 624–635.
7. Wei, W., Laan, M., **Wu, C.***, & Wang, J.* (2023). Efficient targeted learning of treatment effects for multiple subgroups in observational studies. *Biometrics*, 79(3), 1934-1946.
   (An earlier version won the Best Presentation and Best Student Paper Awards, Nonparametric Statistics Section, American Statistics Association.)
8. Guo, X., Wei, W., Liu, M., Cai, T., **Wu, C.**, & Wang, J. (2023). Assessing heterogeneous risk of type 2 diabetes associated with statins usage: Evidence from electronic health record data. *Journal of the American Statistical Association*, 118 (543), 1488-–1499.
9. Ma, X., Wang, J., & **Wu, C.** (2023). Breaking the winner's curse in Mendelian randomization: Rerandomized inverse variance weighted estimator. *Annals of Statistics*, 51(1), 211-232.
   (Alphabetical order)
10. Song, M., Greenbaum, J., IV J., Zhou, W. **Wu, C.**, ..., Deng, HW., Zhang, C. (2022). An autoencoder-based deep learning method for genotype imputation. *Frontiers in Artificial Intelligence*, 5:1028978.
    (Highlights from the MCBIOS 2022 Conference.)
11. Zhang, Z.‡, Bae, Y.‡, Bradley, J., Wu, L, & **Wu, C.*** (2022). SUMMIT: An integrative approach for better transcriptomic data imputation improves causal gene identification. *Nature Communications*, 13, 6336.
    (An earlier version won a poster talk (top 10% of all posters) and Reviewers' Choice at ASHG 2021).
12. He, Y., Xu, G., **Wu, C.**, & Pan, W. (2021). Asymptotically independent U-statistics in high-dimensional testing. *Annals of Statistics*, 49(1), 154–181.
13. **Wu, C.***, Bradley, J., Li, Y., Wu, L., & Deng, H. (2021). A gene-level methylome-wide association analysis identifies novel Alzheimer's disease genes. *Bioinformatics*, 37(14), 1933–1940.
14. Bae Y.‡, Wu, L., & **Wu, C.*** (2021). InTACT: An adaptive and powerful framework for joint-tissue transcriptome-wide association studies. *Genetic Epidemiology*, 45(8), 848–859.
    (Editor's pick paper for Issue 8)
15. **Wu, C.***, Xu, G., Shen, X., & Pan, W.* (2020). A regularization-based adaptive test for high-dimensional generalized linear models. *Journal of Machine Learning Research*, 21, 1–67.
    (An earlier version won the 2019 ENAR Distinguished Student Paper Award.)
16. Xue, H., **Wu, C.**, & Pan, W. (2020). Leveraging existing GWAS summary data to improve power for a new GWAS. *Genetic Epidemiology*, 44(7), 717–732.

17. **Wu, C.** (2020). Multi-trait genome-wide analyses of the brain imaging phenotypes in UK Biobank. *Genetics*, 215(4), 947–958.
    (This paper won a platform presentation at the American Society of Human Genetics (ASHG) 2019 Annual Meeting; highlighted in *Genetics* August issue)
18. Yang, T., **Wu, C.**, Wei, P., & Pan, W. (2020). Integrating DNA sequencing and transcriptomic data for association analyses of low-frequency variants and lipid traits. *Human Molecular Genetics*, 29(3), 515–526.
19. Yang, T., Kim, J., **Wu, C.**, Ma, Y., Wei, P., & Pan, W. (2020). An adaptive test for meta-analysis of rare variant association studies. *Genetic Epidemiology*, 44(1), 104–116.
20. **Wu, C.***, & Pan, W.* (2020). A powerful fine-mapping method for transcriptome-wide association studies. *Human Genetics*, 139, 199–213.
21. **Wu, C.***, & Pan, W.* (2019) Integration of methylation QTL and enhancer-target gene maps with schizophrenia GWAS summary results identifies novel genes. *Bioinformatics*, 35(19), 3576–3583.
22. **Wu, C.***, Xu, G., & Pan, W.* (2019). An adaptive test on high dimensional parameters in generalized linear models. *Statistica Sinica*, 29, 2163–2186.
23. **Wu, C.**, & Pan, W. (2018). Integration of enhancer-promoter interactions with GWAS summary results identifies novel schizophrenia-associated genes and pathways. *Genetics*, 209(3), 699–709.
24. **Wu, C.**, & Pan, W. (2018). Integrating eQTL data with GWAS summary statistics in pathway-based analysis. *Genetic Epidemiology*, 42(3), 303–316.
    (Highlighted by International Genetic Epidemiology Society (IGES). This paper won a poster talk at the ASHG 2017 Annual Meeting.)
25. Park, J.Y., **Wu, C.**, Basu, S., McGue, M., & Pan, W. (2018). Adaptive SNP set association testing in generalized linear mixed models with application to family studies. *Behavior Genetics*, 48(1), 55–66.
26. Xu, Z., **Wu, C.**, Wei, P., & Pan, W. (2017). A powerful framework for integrating eQTL and GWAS summary data. *Genetics*, 207(3), 893–902.
27. Liu, B., **Wu, C.**, Shen, X., & Pan, W. (2017). A novel and efficient algorithm for de novo discovery of mutated driver pathways. *Annals of Applied Statistics*, 11(3), 1481–1512.
28. Xu, Z., **Wu, C.**, Pan, W., & Alzheimer's Disease Neuroimaging Initiative (ADNI). (2017). Imaging-wide association study: Integrating imaging endophenotypes in GWAS. *NeuroImage*, 159, 159–169.
    (This paper won a platform presentation at the ASHG 2017 Annual Meeting.)
29. **Wu, C.**[†], Kwon, S.[†], Shen, X., & Pan, W. (2016). A new algorithm and theory for penalized regression-based clustering. *Journal of Machine Learning Research*, 17(188), 1–25.
30. **Wu, C.**, Chen, J., Kim, J., & Pan, W. (2016). An adaptive association test for microbiome data. *Genome Medicine*, 8(1), 1–12.
    (This paper won the 2016 Joint Statistical Meetings (JSM) Distinguished Student Paper Award on Statistics in Genomics and Genetics Section.)
31. **Wu, C.**, Demerath, E. W., Pankow, J. S., Bressler, J., Fornage, M., Grove, M. L., Chen, W., & Guan, W. (2016). Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. *Epigenetics*, 11(2), 132–139.

—Applications & Collaborations

32. Yu, J., Zhu, J., Zhong, H., Zhang, Z., Liu, J., Lin, X., Zeng, G., Zhang, M., **Wu, C.**, Deng, Y., Sun, Y., ... & Wu, L. 2024. Age-Related Hearing Impairment: Genome and Blood Methylome Data Integration Reveals Candidate Epigenetic Biomarkers. *OMICS: A Journal of Integrative Biology*, 28(12), pp.620-631.
33. Liu, S., Zhu, J., Green, D., Zhong, H., Long, Q., **Wu, C.**, ... & Wu, L. (2024). Integrating Multi-Omics Data to Uncover Prostate Tissue DNA Methylation Biomarkers and Target Genes for Prostate Cancer Risk. *Molecular Carcinogenesis*. Accepted.
34. Lin, W., Ji, J., Su, K. J., Qiu, C., Tian, Q., ... **WU, C.**, ... & Deng, H. (2024). omicsMIC: a comprehensive benchmarking platform for robust comparison of imputation methods in mass spectrometry-based omics data. *NAR Genomics and Bioinformatics*, 6(2).
35. Liu, Y., Meng, X. H., **Wu, C.**, Su, K. J., Liu, A., Tian, Q., ... & Deng, H. W. (2024). Variability in performance of genetic-enhanced DXA-BMD prediction models across diverse ethnic and geographic populations: A risk prediction study. *PLoS Medicine*, 21(8), e1004451.
36. Liu, S., Zhu, J., Zhong, H., **Wu, C.**, Xue, H., Darst, B. F., ... & Wu, L. (2024). Identification of proteins associated with type 2 diabetes risk in diverse racial and ethnic populations. *Diabetologia*, 1-17.
37. Zhu, J., Wu, K., Liu, S., Masca, A., Zhong, H., Yang, T., ...**Wu C.¶**, Wu, Y.¶, & Wu, L.¶ (2024). Proteome-wide association study and functional validation identify novel protein markers for pancreatic ductal adenocarcinoma. *GigaScience*, 13, giae012.
38. Zhu, J., Liu, S., Walker, K. A., Zhong, H., Ghoneim, D. H., Zhang, Z., ... **Wu, C.*** & Wu, L.* (2024). Associations between genetically predicted plasma protein levels and Alzheimer's disease risk: a study using genetic prediction models. *Alzheimer's Research & Therapy*, 16(1), 8.
39. Meng, Z.‡, **Wu, C.***, & Lin, L*. (2023). The effect direction should be taken into account when assessing small-study effects. *Journal of Evidence-Based Dental Practice*, 23(1), 101830.
40. Liu, D.†, Bae, Y.E. †‡, Zhu, J., Zhang, Z., Sun, Y.,..., **Wu, C.***, & Wu, L.* (2023). Splicing transcriptome-wide association study to identify splicing events for pancreatic cancer risk *Carcinogenesis*, bgad069.
41. Zhong, X., Xu, X., Zhu, J., Ghoneim, D., Surendran, P., Fahle, S., Butterworth, A., **Wu, C.¶**, & Wu, L¶. (2023). Identification of genetically predicted blood protein biomarkers associated with prostate cancer risk using genetic prediction models: analysis of over 140,000 subjects. *Human Molecular Genetics*, 32(22), 3181-3193.
42. Sun, Y.†, Bae, Y. E. †‡, Zhu, J., Zhang, Z., Zhong, H., Cheng, C., ... **Wu, C.*** & Wu, L.* (2023). A splicing transcriptome-wide association study identifies candidate altered splicing for prostate cancer risk. *OMICS: A Journal of Integrative Biology*, 27(8), 372-380.
43. Sun, Y.†, Bae, Y. E. †‡, Zhu, J., Zhang, Z., Zhong, H., Yu, J., ... **Wu, C.*** & Wu, L.* (2023). A splicing transcriptome-wide association study identifies novel altered splicing for Alzheimer's disease susceptibility. *Neurobiology of Disease*, 106209.
44. Sun, Y., Zhu, J., Yang, Y., Zhang, Z., Zhong, H., Zeng, G., ..., **Wu, C.** & Wu, L. (2023). Identification of candidate DNA methylation biomarkers related to Alzheimer's disease risk by integrating genome and blood methylome data. *Translational Psychiatry*, 13(1), 387.
45. King, A.‡, Wu, L., Deng, HW., & **Wu, C.*** (2022). Polygenic risk score improves the accuracy of a clinical risk score for coronary artery disease. *BMC Medicine*, 20, 385.
46. Sun, Y., Zhou, D., Rahman, M.R., Zhu, J., Ghoneim, D., Cox, N.J., ...**Wu, C.**, Gamazon E.R.,

& Wu, L. (2022). A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimer's disease risk. *Human Molecular Genetics*, 31(2), 289-299.

47. Liu, D., Zhu, J., Zhou, D., ..., **Wu, C.**, ..., & Wu, L. (2022). A transcriptome-wide association study identifies novel candidate susceptibility genes for prostate cancer risk. *International Journal of Cancer*, 150(1), 80-90.
48. Xie, T., Xu, C., Shi, X., **Wu, C.**, Meng, R., Meng, X., Yu, G., Wang, K., Xiao, H., & Deng, H. (2021). Accurate recognition of colorectal cancer with semi-supervised deep learning on pathological images. *Nature Communications*, 12, 6311.
49. **Wu, C.***, Zhu, J., King, A.[‡], Tong, X., Lu, Q., Park, J. Y., ... & Wu, L.* (2021). Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation data: a multi-phased study of prostate cancer. *Cancer Communications*, 1–11.
50. Wu, L.*, Zhu, J., Liu, D., Sun, Y., & **Wu, C.*** (2021). An integrative multiomics analysis identifies putative causal genes for COVID-19 severity. *Genetics in Medicine*, 1–11.
51. **Wu, C.***, Wu, L., Wang, J., Lin, L., Li, Y., Lu, Q., & Deng, H. (2021). Systematic identification of modifiable risk factors and drug repurposing options for Alzheimer's disease: Mendelian randomization analyses. *Alzheimer's Dement*, 7:e12148.
52. Sun, Y., Zhou, D., Rahman, R., **Wu, C.**, Zhu, J., Cox NJ., Beach TG., Wu, C., Gamazon, ER., & Wu, L. (2021). A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimer's disease risk. *Human Molecular Genetics*, ddab229.
53. Sun, Y., Zhu, J., Zhou, D., Canchi, S., **Wu, C.**, Cox NJ., Rissman, RA. Gamazon, ER., & Wu, L. (2021). A transcriptome-wide association study of Alzheimer's disease using prediction models of related tissues identifies novel candidate susceptibility genes. *Genome Medicine*, 13(1), 1–11.
54. Wang, K. S., Yu, G., Xu, C., ..., **Wu, C.**, ... & Deng, H. W. (2021). Accurate diagnosis of colorectal cancer based on histopathology images using artificial intelligence. *BMC Medicine*, 19(1), 1–12.
55. Zhu, J., **Wu, C.**, & Wu, L. (2021). Associations between genetically predicted protein levels and COVID-19 severity. *The Journal of Infectious Diseases*, 223(1), 19–22.
56. Liu, D., Zhou, D., Sun, Y., Zhu, J., Ghoneim, D., **Wu, C.**, Yao, Q., Gamazon, E.R., Cox, N.J., & Wu, L. (2020). A transcriptome-wide association study identifies candidate susceptibility genes for pancreatic cancer risk. *Cancer Research*, 80(20), 4346–4354.
57. Wu L., Yang Y., Guo X., ..., **Wu C.**, ..., & Long, J., The Practical Consortium (2020). An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. *Nature Communications*, 11(1), 1–11.
58. Song, M., Greenbaum, J., Luttrell IV, J., Zhou, W., **Wu, C.**, Shen, H., Gong P., Zhang C., & Deng, H. W. (2020). A review of integrative imputation for multi-omics datasets. *Frontiers in Genetics*, 11.
59. Zhu, J., Shu, X., Guo, X., ..., **Wu, C.**, ..., & Wu L. (2020). Associations between genetically predicted blood protein biomarkers and pancreatic cancer risk. *Cancer Epidemiology, Biomarkers & Prevention*, 29(7), 1501–1508.
60. Zhu, L., Li, Y., Chen, Y., Carrera, C., **Wu, C.**, & Fork, A. (2018). Comparison between two post-dentin bond strength measurement methods. *Scientific Reports*, 8(1), 2350.
61. Bose, M., **Wu, C.**, Pankow, J. S., Demerath, E. W., Bressler, J., Fornage, M., Grove, M. L.,

Mosley, T. H., Hicks, C., North, K., Kao, W. H., Zhang, Y., Boerwinkle, E., & Guan, W. (2014). Evaluation of microarray-based DNA methylation measurement using technical replicates: the Atherosclerosis Risk In Communities (ARIC) Study. *BMC Bioinformatics*, 15(1), 1–10.

—Peer-reviewed Proceedings

61. Park, J. Y., **Wu, C.**, & Pan, W. (2018). An adaptive gene-level association test for pedigree data. *BMC Genetics*, 19(1), 68.
62. **Wu, C.**, Park, J.Y., Guan, W., & Pan, W. (2018). A powerful gene-based test for methylation data. *BMC Proceedings*, 12(9), 60.

—Book Chapter

63. **Wu, C.** (2022). Using R for Cell-Type Composition Imputation in Epigenome-Wide Association Studies. In *Epigenome-Wide Association Studies* (pp. 49-56). Humana, New York, NY.

GRANTS

—Undergoing

- Uncovering Causal Protein Markers to Characterize Pancreatic Cancer Etiology and Improve Risk Prediction (Wu, L and Wu, C) **U01**
  NIH, NCI 09/18/2024–08/31/2029
  Role: **MPI** 15% efforts in Years 1–2, 20% efforts in Years 3–5
- Uncovering causal protein markers to improve prostate cancer etiology understanding and risk prediction in Africans and Europeans (Wu, L and Wu, C) **R01**
  NIH, NCI 07/01/2022–06/31/2027
  Role: **MPI** 15% efforts in Years 1–2, 20% efforts in Years 3–5
- Various Co-Investigator (Co-I) grants supporting my research efforts, including grants from the NIH and CPRIT.

—Completed

- Novel statistical methods for multi-omics data integration in Alzheimer's disease (Wu, C and Bradley, J) R03
  NIH, NIA 01/01/21–12/31/22
  Role: **Contact PI** 20% efforts
- Trans-omics integration of multi-omics studies for osteoporosis: Administrative supplement for COVID-19 studies (Deng, HW) U19
  NIH 09/10/2021–07/31/2022
  Role: Subcontract PI 5% efforts

SOFTWARE & PLATFORM

- Owner and maintainer for the following R packages:
  - prclust: Penalized Regression-Based Clustering Methods; 21K downloads
  - MiSPU: Microbiome Based Sum of Powered Score (MiSPU) Tests; 21K downloads
  - aSPU2: A New Version of Adaptive Sum of Powered Score (aSPU) Test;
  - GLMaSPU: Adaptive Tests on High Dimensional Parameters in GLMs; 19K downloads
  - glmtlp: Truncated Lasso Regularized Generalized Linear Models; 14K downloads

- Global Causal Biomarker Hub: `https://gcbhub.org` (Developed by Zichen Zhang; co-advised by Bingxin Zhao and Chong Wu)
- Online software tutorial: `http://wuchong.org/software.html`
- Lab GitHub Repo: `https://github.com/ChongWuLab`

TEACHING EXPERIENCE

- STA 4321/5323 Introduction to Mathematical Statistics
  - Instructor, Department of Statistics, Florida State University Jan. 2021–April. 2021
  - Instructor, Department of Statistics, Florida State University Jan. 2020–May 2020
  - Instructor, Department of Statistics, Florida State University Aug. 2019–Dec. 2019
  - Instructor, Department of Statistics, Florida State University Jan. 2019–May 2019
  - Instructor, Department of Statistics, Florida State University Aug. 2018–Dec. 2018
- STA 5934 Statistical Genetics (Topic course, redesigned by Wu, C)
  - Instructor, Department of Statistics, Florida State University Aug. 2020–Dec. 2020
  - Instructor, Department of Statistics, Florida State University Aug. 2021–Dec. 2021
- PUBH 6451 Biostatistics (Instructor: Dr. William Thomas)
  - Lab Instructor, Division of Biostatistics, University of Minnesota Jan. 2014–May 2014
- PUBH 6414 Biostatistical Methods (Instructor: Dr. Ann M. Brearley)
  - Teaching Assistant, Division of Biostatistics, University of Minnesota Sept. 2013–Dec. 2013

STUDENTS

Alumni:

PhD Students:

- Shengjie Jiang Florida State University
  - Current Position: Assistant Professor at The University of Texas at Dallas Graduated: 2022
- Ye Eun Bae (co-advised with Xufeng Niu) Florida State University
  - Current Position: Sr. Biostatistician at Beckman Coulter Graduated: 2023
- Zichen Zhang (co-advised with Jonathan Bradley) Florida State University
  - Current Position: Postdoc at MD Anderson Graduated: 2023
- Meng Zhuo (co-advised with Xufeng Niu) Florida State University
  - Current Position: Postdoc at Florida State University Graduated: 2023
- Austin King (co-advised with Chao Huang)
  - Current Position: Biostatistician at CDC Graduated: 2023
- Hunter Melton (co-advised with Jonathan Bradley) Florida State University
  - Current Position: Postdoc at Dartmouth College Graduated: 2024

Current lab members:

- Haonan Feng (Co-advised with Peng Wei) UT MD Anderson Cancer Center
- Wanheng Zhang UT Health
- Zichen Zhang (Postdoc) UT MD Anderson Cancer Center

Rotation students at MD Anderson GSBS program:

- Xiaohan Chi and Shuyue Wang 2023

- Yan Zhang 2024

PRESENTATIONS

Many of my presentation slides can be found at `https://wuchong.org/talks.html`.

- "An adaptive association test for microbiome data"
  - Presentation at Eastern North American Region (ENAR) 2016 Spring Meeting
    Austin, TX Mar. 2016
  - Presentation at 2016 Joint Statistical Meetings (JSM)
    Chicago, IL Aug. 2016
- "Iterative PCA in epigenome-wide association studies"
  - Poster presented at American Society of Human Genetics (ASHG) 2016 Annual Meeting
    Vancouver, BC, Canada Oct. 2016
- "A gene-level adaptive association test for methylation data"
  - Presentation at Genetic Analysis Workshop (GAW) 20
    San Diego, CA Mar. 2017
- "An adaptive test on high dimensional parameters in GLMs"
  - Presentation at ENAR 2017 Spring Meeting
    Washington, DC Mar. 2017
  - Poster presented at MSI Research Exhibition
    Minneapolis, MN Apr. 2017
  - Presentation at 2017 JSM
    Baltimore, MD Aug. 2017
- "Imaging-wide association study: Integrating imaging endophenotypes in GWAS"
  - Invited presentation at 2017 JSM (On behalf of Dr. Wei Pan)
    Baltimore, MD Aug. 2017
  - Invited presentation at Third Annual Kliakhandler Conference (On behalf of Dr. Wei Pan)
    Houghton, MI Aug. 2017
- "Integrating eQTL data with GWAS summary statistics in pathway-based analysis"
  - Poster talk at ASHG 2017 Annual Meeting
    Orlando, FL Oct. 2017
- "Integration of methylation QTL and enhancer-target gene maps with schizophrenia GWAS summary results identifies novel genes"
  - Oral presentation at IGES 27th Annual Meeting
    San Diego, CA Oct. 2018
- "An adaptive test for high-dimensional generalized linear models with application to detect gene-environment interactions"
  - Presentation at ENAR 2019 Spring Meeting
    Philadelphia, PA Mar. 2019
- "Complex disease risk prediction via a deep learning method"
  - Presentation at JSM 2019
    Denver, CO Jul. 2019
- "Multi-trait genome-wide analyses of the brain imaging phenotypes in UK Biobank"
  - Platform presentation at ASHG 2019
    Huston, TX Oct. 2019

- "A powerful fine-mapping method for transcriptome-wide association studies"
  - Invited Presentation at JSM 2020
    Virtual Aug. 2020
- "Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation: a multi-phased study of prostate cancer"
  - Department seminar at Florida State University School of Medicine
    Virtual Sep. 2020
  - Invited presentation at International Indian Statistical Association (IISA) 2021
    Virtual May 2021
- "A gene-level methylome-wide association analysis identifies novel Alzheimer's disease genes"
  - Poster presented at ASHG 2020
    Virtual Oct. 2020
- "A regularization-based adaptive test for high-dimensional generalized linear models"
  - Department seminar at Shanghai University of Finance and Economics, Statistics
    Virtual Dec. 2020
  - Department seminar at Washington University School of Medicine, Biostatistics
    Virtual Dec. 2020
- "Accounting for winner's curse and pleiotropy in two-sample Mendelian randomization"
  - Department seminar at Tulane Unveristy, Biomedical Informatics & Genomics Center
    Virtual Dec. 2021
  - Department seminar at the Chinese University of Hong Kong, Statistics
    Virtual Dec. 2021
  - Invited talk at UC Berkeley (Causal inference working group)
    Virtual Jan. 2022
  - Invited presentation at The ICSA 2022 Applied Statistics Symposium
    Gainesville, FL Jun. 2022
- "SUMMIT: An integrative approach for better transcriptomic data imputation improves causal gene identification"
  - Invited presentation at New Investigator in AD and AFAR Grantee Conference
    Virtual Oct. 2021
  - Invited presentation at 2023 ICSA Applied Statistics Symposium
    Ann Arbor, MI Jun., 2023
  - Invited presentation at The 12th ICSA International Conference
    Hong Kong, China Jul., 2023
  - Invited presentation at University of Hawaii Cancer Center
    Honolulu, HI Mar., 2023
  - Invited talk at Indiana University School of Medicine (Biostatistics)
    Virtual Mar. 2023
  - Invited talk at UTHealth Houston School of Public Health (Human Genetics Center)
    Houston, TX Sept. 2023
  - Invited talk at University of Chicago (Statistical genetics/genomics Journal club)
    Virtual Jun. 2023
  - Invited talk at University of Arizona (Epidemiology and Biostatistics)
    Virtual Sept. 2023

- "An iterative method for detecting outlying studies in meta-analysis"
  - Invited presentation at WNAR 2023
    Anchorage, AK Jun. 2023
- "Large-scale imputation models for multi-ancestry proteome-wide association analysis"
  - Invited presentation at MidSouth Computational Biology and Bioinformatics Society (MCBIOS) 2024
    Atlanta, GA Mar. 2024
  - Invited presentation at Vanderbilt University
    Virtual Mar. 2024
  - Invited presentation at ICSA 2024 China Conference
    Wuhan, China Jun. 2024
  - Contributed presentation at 2024 Joint Statistical Meetings
    Portland, OR Aug. 2024
  - Invited presentation at Association of Chinese Americans in Cancer Research(ACACR) summer seminar
    Virtual Aug. 2024

HONORS & AWARDS

- Dean's Faculty Travel Award Apr. 2020
  - Florida State University
- ENAR Distinguished Student Paper Award Mar. 2019
  - Eastern North American Region International Biometric Society
- James R. Boen Student Achievement Award May 2018
  - Division of Biostatistics, University of Minnesota
- Pre-Doctoral Trainee Award Oct. 2017
  - Association of Chinese Geneticists in America (ACGA)
- Poster Award May 2017
  - University of Minnesota Chapter of Sigma Xi
- Elected to Delta Omega (Public Health Honorary Society) May 2017
  - University of Minnesota
- Elected to Sigma Xi (The Scientific Research Society) May 2017
  - University of Minnesota
- Distinguished Student Paper Award, Genomics and Genetics Section Aug. 2016
  - 2016 Joint Statistical Meetings
- Doctoral Dissertation Fellowship 2016–2017
  - University of Minnesota
- Travel Award, Computational Neuroscience Summer School Jul. 2015
  - Statistical and Applied Mathematical Sciences Institute
- Dean's Ph.D. Scholarship Sept. 2013
  - University of Minnesota
- Honorable Mention in Mathematical Contest in Modeling Apr. 2012
  - Consortium for Mathematics and Its Application
- National Scholarship Sept. 2011

  - Ministry of Education, China

PROFESSIONAL ACTIVITIES

Manuscript Reviewer

- Statistics/Biostatistics: Annals of Statistics, Biometrics, Journal of the American Statistical Association, Journal of Machine Learning Research, Statistics in Medicine, Electronic Journal of Statistics, Statistical Applications in Genetics and Molecular Biology, Statistics in Biosciences, Journal of Theoretical Biology, Biometrical Journal, Computational Statistics and Data Analysis
- Genetics/Genomics/Medicine/Bioinformatics: Genetic Epidemiology, Bioinformatics, Genome Biology, Frontiers in Genetics, Alzheimer's & Dementia, Briefings in Bioinformatics, PLOS Computational Biology, Nature Genetics, Cell Genomics, American Journal of Human Genetics
- Epidemiology: American Journal of Epidemiology
- Multidisciplinary: Nature Communications, PLOS One, Scientific Reports

Guest Editor, *Frontiers in Genetics*
Associate Editor, *BMC Genomics*

Education Officer, Mental Health Statistics Section (MHSS), American Statistical Association (ASA) 2020–2023
Program Chair, Mental Health Statistics Section, American Statistical Association (ASA) 2024–2025

Program Committee Member, IEEE BIBM 2022

Invited Session Chair & Organizer

- Recent Advances of Causal Inferences in Human Genetics, JSM 2021 (with Dr. Jingshen Wang)
- Recent Advances in Mendelian randomization, 2022 ICSA Applied Statistics Symposium
- Recent Advances in Statistical Genetics, 2023 ICSA Applied Statistics Symposium

Grant Reviewer (ad hoc)

- NIA Special Emphasis panel, ZAG ZIJ-P J2, Functional genomics 2020
- NCI Informatics Technology for Cancer Research (ITCR) study section 2020
- NCI ITCR study section, ZCA1 TCRB-Q (M1) 2022
- Lifestyle and Health Behaviors (LHB) study section 2022
- NINDS Special Emphasis Panel ZNS1 SRB-S (15) 2023
- Swiss National Science Foundation 2023
- Lifestyle and Health Behaviors study (LHB) section 2023
- Aging, Injury, Musculoskeletal, Rheumatologic, and Dermatologic disorders (AIMR) Study Section; served **twice** 2024

Last updates: Nov 2024