

# Curriculum Vitae

Zuoheng (Anita) Wang

April, 2024

## CONTACT INFORMATION

Department of Biostatistics  
Yale School of Public Health  
60 College Street, LEPH 200  
New Haven, CT 06510

Phone: (203) 737-2672  
Fax: (203) 785-6912  
Email: zuoheng.wang@yale.edu

## RESEARCH INTERESTS

Longitudinal data analysis; Varying coefficient models; Mixed effects models; Kernel machine methods; Mediation analysis; Machine learning methods; Network analysis; Whole genome sequencing; Bulk and single-cell RNA sequencing; Spatial transcriptomics; Biomarker studies; Electronic health records

## EDUCATION

University of Science & Technology of China, Hefei, Anhui, China  
B.S. in Biology, July 2001

University of Florida, Gainesville, FL  
M.S. in Statistics, August 2004

University of Chicago, Chicago, IL  
Ph.D. in Statistics, August 2009

## PROFESSIONAL POSITIONS

- Assistant Professor, Department of Biostatistics, Yale School of Public Health, 2009–2016
- Associate Professor, Department of Biostatistics, Yale School of Public Health, 2016–present
- Affiliated Faculty, Computational Biology and Bioinformatics, Yale School of Medicine, 2012–present
- Affiliated Faculty, Biomedical Informatics and Data Science, Yale School of Medicine, 2024–present
- Member, Center for Biomedical Data Science, Yale School of Medicine, 2019–present
- Member, Genomics, Genetics, and Epigenetics Program, Yale Cancer Center, 2020–present
- Member, Center for Brain and Mind Health, Yale School of Medicine, 2023–present

## HONORS AND AWARDS

- Yale School of Public Health Faculty Marshal, University Commencement, 2022.
- Elected Member, International Statistical Institute, 2015.
- Institute of Mathematical Statistics New Researchers Conference Travel Award, 2013.
- Yale Center for Clinical Investigation Scholar Award, 2012.
- Eastern North American Region Junior Investigator Workshop Travel Award, 2012.
- International Genetic Epidemiology Society Meeting Travel Award, 2007.
- Paul Meier Fellowship, Department of Statistics, University of Chicago, 2004.
- Member, Mu Sigma Rho National Statistics Honorary Society, 2004
- International Student Academic Award, Office of International Studies and Programs, University of Florida, 2004.
- William Mendenhall Award for outstanding first year graduate student, Department of Statistics, University of Florida, 2003.
- International Student Academic Award, Office of International Studies and Programs, University of Florida, 2003.

## **BIBLIOGRAPHY**

### **Peer-Reviewed Original Research**

1. Lou X.Y., Todhunter R.J., Lin M., Lu Q., Liu T., **Wang Z.**, Bliss S.P., Casella G., Acland G.M., Lust G., Wu R., (2003) The extent and distribution of linkage disequilibrium in a multi-hierarchic outbred canine pedigree. *Mammalian Genome*, 14:555-564.
2. Wu R., Ma C.X., Lin M., **Wang Z.**, Casella G., (2004) Functional mapping of quantitative trait loci underlying growth trajectories using a transform-both-sides logistic model. *Biometrics*, 60:729-738.
3. Gong Y.\*, **Wang Z.\***, Liu T., Zhao W., Zhu Y., Johnson J.A., Wu R., (2004) A statistical model for functional mapping of quantitative trait loci regulating drug response. *The Pharmacogenomics Journal*, 4:315-321. \*Joint first author.
4. **Wang Z.**, Wu R., (2004) A statistical model for high-resolution mapping of quantitative trait loci determining HIV dynamics. *Statistics in Medicine*, 23:3033-3051.
5. Wu R., **Wang Z.**, Zhao W., Cheverud J.M., (2004) A mechanistic model for genetic machinery of ontogenetic growth. *Genetics*, 168:2383-2394.
6. **Wang Z.**, Hou W., Wu R., (2006) A statistical model to analyse quantitative trait locus interactions for HIV dynamics from the virus and human genomes. *Statistics in Medicine*, 25:495-511.
7. **Wang Z.**, Li Y., Li Q., Wu R., (2009) Joint functional mapping of quantitative trait loci for HIV-1 and CD4<sup>+</sup> dynamics. *The International Journal of Biostatistics*, Vol. 5: Iss. 1, Article 9.
8. **Wang Z.**, McPeck M.S., (2009) An incomplete-data quasi-likelihood approach to haplotype-based genetic association studies on related individuals. *Journal of the American Statistical Association*, 104:1251-1260.

9. **Wang Z.**, McPeck M.S., (2009) ATRIUM: Testing untyped SNPs in case-control association studies with related individuals. *American Journal of Human Genetics*, 85:667-678.
10. Huang J., Detterbeck F.C., **Wang Z.**, Loehrer P.J. Sr., (2010) Standard outcome measures for thymic malignancies. *Journal of Thoracic Oncology*, 5:2017-2023.
11. **Wang Z.**, (2011) Direct assessment of multiple testing correction in case-control association studies with related individuals. *Genetic Epidemiology*, 35:70-79.
12. Wang K., Li W.D., Zhang C.K., **Wang Z.**, Glessner J.T., Grant S.F.A., Zhao H., Hakonarson H., Price R.A., (2011) A genome-wide association study on obesity and obesity-related traits. *PLoS One*, 6(4):e18939.
13. Wu C., DeWan A., Hoh J., **Wang Z.**, (2011) A comparison of association methods correcting for population stratification in case-control studies. *Annals of Human Genetics*, 75:418-427.
14. Huang J., Detterbeck F.C., **Wang Z.**, Loehrer P.J. Sr., (2011) Standard outcome measures for thymic malignancies. *Journal of Thoracic Oncology*, 6:S1691-S1697. *\*This article was translated in Chinese and published at Chinese Journal of Lung Cancer, 2014, 17:122-129.*
15. Muralidaran A., Detterbeck F.C., Boffa D.J., **Wang Z.**, Kim A.W., (2011) Long-term survival after lung resection for non-small cell lung cancer with circulatory bypass: a systematic review. *Journal of Thoracic and Cardiovascular Surgery*, 142:1137-1142.
16. Wu C., Walsh K.M., DeWan A.T., Hoh J., **Wang Z.**, (2011) Disease risk prediction with rare and common variants. *BMC Proceedings*, 5:S61.
17. Kim A.W., Boffa D.J., **Wang Z.**, Detterbeck F.C., (2012) An analysis, systematic review, and meta-analysis of the perioperative mortality after neoadjuvant therapy and pneumonectomy for non-small cell lung cancer (NSCLC). *Journal of Thoracic and Cardiovascular Surgery*, 143:55-63.
18. Zhang C.K., Stein P.B., Liu J., **Wang Z.**, Yang R., Cho J.H., Gregersen P.K., Aerts J.M., Zhao H., Pastores G.M., Mistry P.K., (2012) Genome-wide association study of N370S homozygous Gaucher disease reveals the candidacy of CLN8 gene as a genetic modifier contributing to extreme phenotypic variation. *American Journal of Hematology*, 87:377-383.
19. Ahmad U., **Wang Z.**, Bryant A.S., Kim A.W., Kukreja J., Mason D.P., Bermudez C.A., Detterbeck F.C., Boffa D.J., (2012) Outcomes for lung transplantation for lung cancer in the united network for organ sharing registry. *The Annals of Thoracic Surgery*, 94:935-941.
20. Hou W., Sui Y., Wang Z., Wang Y., Wang N., Liu J., Li Y., Goodenow M., Yin L., **Wang Z.**, Wu R., (2012) Systems mapping of HIV-1 infection. *BMC Genetics*, 13:91.
21. Wang Z., **Wang Z.**, Wang J., Sui Y., Zhang J., Liao D., Wu R., (2012) A quantitative genetic and epigenetic model of complex traits. *BMC Bioinformatics*, 13:274.
22. Wang C., Li H., Wang Z., Wang Y., Wang N., **Wang Z.**, Wu R., (2012) A maximum likelihood approach to functional mapping of longitudinal binary traits. *Statistical Applications in Genetics and Molecular Biology*, Vol. 11: Iss. 6, Article 2.

23. **Wang Z.**, Luo J., Fu G., Wang Z., Wu R., (2013) Stochastic modeling of systems mapping in pharmacogenomics. *Advanced Drug Delivery Reviews*, 65:912-917.
24. Kuzmik G.A., Detterbeck F.C., Decker R.H., Boffa D.J., **Wang Z.**, Oliva I.B., Kim A.W., (2013) Pulmonary resections following prior definitive chemoradiation therapy are associated with acceptable survival. *European Journal of Cardio-Thoracic Surgery*, 44:e66-e70.
25. **Wang Z.**, Liu X., Yang B.Z., Gelernter J., (2013) The role and challenges of exome sequencing in studies of human diseases. *Frontiers in Genetics: Statistical Genetics and Methodology*, Vol. 4: Article 160.
26. Liu X., Han S., **Wang Z.**, Gelernter J., Yang B.Z., (2013) Variant callers for next-generation sequencing data: a comparison study. *PLoS One*, 8(9):e75619.
27. Zhu S., Wang Z., Wang J., Wang Y., Wang N., **Wang Z.**, Xu M., Su X., Wang M., Zhang S., Huang M., Wu R., (2013) A quantitative model of transcriptional differentiation driving host-pathogen interactions. *Briefings in Bioinformatics*, 14:713-723.
28. Wang Z., Wang Y., Wang N., Wang J., **Wang Z.**, Vallejos C.E., Wu R., (2014) Towards a comprehensive picture of the genetic landscape of complex traits. *Briefings in Bioinformatics*, 15:30-42.
29. Wang Z., Pang X., Wu W., Wang J., **Wang Z.**, Wu R., (2014) Modeling phenotypic plasticity in growth trajectories: A statistical framework. *Evolution*, 68:81-91.
30. Sui Y., Wu W., Wang Z., Wang J., **Wang Z.**, Wu R., (2014) A case-control design for testing epigenetic effects on complex diseases. *Briefings in Bioinformatics*, 15:319-326.
31. Law T.D., Boffa D.J., Detterbeck F.C., **Wang Z.**, Park H.S., Kim A.W., (2014) Lethality of cardiovascular events highlights the variable impact of complication type between thoracoscopic and open pulmonary lobectomies. *The Annals of Thoracic Surgery*, 97:993-999.
32. Moreno A.C., Morgensztern D., Boffa D.J., Decker R.H., Yu J.B., Detterbeck F.C., **Wang Z.**, Rose M.G., Kim A.W., (2014) Treating locally advanced disease: an analysis of very large, hilar lymph node positive non-small cell lung cancer using the National Cancer Data Base. *The Annals of Thoracic Surgery*, 97:1149-1155.
33. Zhou L., Shen Y., Wu W., **Wang Z.**, Hou W., Zhu S., Wu R., (2014) A model for computing genes governing marital dissolution through sentimental dynamics. *Journal of Theoretical Biology*, 353:24-33.
34. Zhang H., Wang F., Kranzler H.R., Yang C., Xu H., **Wang Z.**, Zhao H., Gelernter J., (2014) Identification of methylation quantitative trait loci (mQTLs) influencing promoter DNA methylation of alcohol dependence risk genes. *Human Genetics*, 133:1093-1104.
35. Wang W., Feng Z.Z., Bull S.B., **Wang Z.**, (2014) A 2-step strategy for detecting pleiotropic effects on multiple longitudinal traits. *Frontiers in Genetics: Statistical Genetics and Methodology*, Vol. 5: Article 357.
36. Li X., Sui Y., Liu T., Wang J., Li Y., Lin Z., Hegarty J., Koltun W.A., **Wang Z.**, Wu R., (2014) A model for family-based case-control studies of genetic imprinting and epistasis. *Briefings in Bioinformatics*, 15:1069-1079.

37. Sartor C.E., **Wang Z.**, Xu K., Kranzler H.R., Gelernter J., (2014) The joint effects of ADH1B variants and childhood adversity on alcohol-related phenotypes in African-American and European-American women and men. *Alcoholism: Clinical and Experimental Research*, 38:2907-2914.
38. Assi R., Wong D.J., Boffa D.J., Detterbeck F.C., **Wang Z.**, Chupp G.L., Kim A.W., (2015) Hospital readmission after pulmonary lobectomy is not affected by surgical approach. *The Annals of Thoracic Surgery*, 99:393-398.
39. Xu K., Krystal J.H., Ning Y., Chun D.C., He H., Wang D., Ke X., Zhang X., Ding Y., Liu Y., Gueorguieva R., **Wang Z.**, Limoncelli D., Pietrzak R.H., Petrakis I.L., Zhang X., Fan N., (2015) Preliminary analysis of positive and negative syndrome scale in ketamine-associated psychosis in comparison with schizophrenia. *Journal of Psychiatric Research*, 61:64-72.
40. Wang Y., Tong C., Wang Z., **Wang Z.**, Mauger D., Tantisira K.G., Israel E., Szeffler S.J., Chinchilli V.M., Boushey H.A., Lazarus S.C., Lemanske R.F., Wu R., (2015) Pharmacodynamic genome-wide association study identifies new responsive loci for glucocorticoid intervention in asthma. *The Pharmacogenomics Journal*, 15:422-429.
41. DeLuzio M.R., Moores C., Dhamija A., **Wang Z.**, Cha C., Boffa D.J., Detterbeck F.C., Kim A.W., (2015) Resection of oligometastatic lung cancer to the pancreas may yield a survival benefit in select patients - A systematic review. *Pancreatology*, 15:456-462.
42. Liu J., Hancock J.G., Moreno A.C., **Wang Z.**, Boffa D.J., Detterbeck F.C., Kim A.W., (2016) Evaluating the fate of patients who undergo resections of very large, node-negative lung cancers using the National Cancer DataBase. *European Journal of Cardio-Thoracic Surgery*, 49:596-601.
43. Sandler B.J., **Wang Z.**, Hancock J.G., Boffa D.J., Detterbeck F.C., Kim A.W., (2016) Gender, age, and comorbidity status predict improved survival with adjuvant chemotherapy following lobectomy for non-small cell lung cancers larger than 4 cm. *Annals of Surgical Oncology*, 23:638-645.
44. Xu M., Liu S., Xuan L., Huang M., **Wang Z.**, (2016) Isolation and characterization of a poplar D-type cyclin gene associated with the SHORT-ROOT/SCARECROW network. *Trees*, 30:255-263.
45. Jean R.A., DeLuzio M.R., Kraev A.I., Wang G., Boffa D.J., Detterbeck F.C., **Wang Z.**, Kim A.W., (2016) Analyzing risk factors for morbidity and mortality after lung resection for lung cancer using the NSQIP database. *Journal of the American College of Surgeons*, 222:992-1000.
46. Jawitz O.K., Boffa D.J., Detterbeck F.C., **Wang Z.**, Kim A.W., (2016) Estimating the annual incremental cost of several complications following pulmonary lobectomy. *Seminars in Thoracic and Cardiovascular Surgery*, 28:531-540.
47. Rosen J.E., Salazar M.C., **Wang Z.**, Yu J.B., Decker R.H., Kim, A.W., Detterbeck F.C., Boffa D.J., (2016) Lobectomy versus stereotactic body radiotherapy in healthy patients with stage I lung cancer. *Journal of Thoracic and Cardiovascular Surgery*, 152:44-54.

48. DeLuzio M.R., Keshava H.B., **Wang Z.**, Boffa D.J., Detterbeck F.C., Kim A.W., (2016) A model for predicting prolonged length of stay in patients undergoing anatomic lung resection: a National Surgical Quality Improvement Program (NSQIP) database study. *Interactive Cardiovascular and Thoracic Surgery*, 23:208-215.
49. Han L., Cai Q., Tian D., Kong D.K., Gou X., Chen Z., Strittmatter S.M., **Wang Z.**, Sheth K.N., Zhou J., (2016) Targeted drug delivery to ischemic stroke via chlorotoxin-anchored, lexiscan-loaded nanoparticles. *Nanomedicine: Nanotechnology, Biology, and Medicine*, 12:1833-1842.
50. Zhang X., Justice A.C., Hu Y., **Wang Z.**, Zhao H., Wang G., Johnson E.O., Emu B., Sutton R.E., Krystal J.H., Xu K., (2016) Epigenome-wide differential DNA methylation between HIV-infected and uninfected individuals. *Epigenetics*, 11:750-760.
51. Jawitz O.K., **Wang Z.**, Boffa D.J., Detterbeck F.C., Blasberg J.D., Kim A.W., (2017) The differential impact of preoperative comorbidity on perioperative outcomes following thoroscopic and open lobectomies. *European Journal of Cardio-Thoracic Surgery*, 51:169-174.
52. Wang Z., Xu K., Zhang X., Wu X., **Wang Z.**, (2017) Longitudinal SNP-set association analysis of quantitative phenotypes. *Genetic Epidemiology*, 41:81-93.
53. Husain Z.A., Chen T., Corso C.D., **Wang Z.**, Park H., Judson B., Yarbrough W., Desphande H., Mehra S., Kuo P., Decker R.H., Burtness B.A., (2017) A comparison of prognostic ability of staging systems for human papillomavirus-related oropharyngeal squamous cell carcinoma. *JAMA Oncology*, 3:358-365.
54. Bellin M.D., Clark P., Usmani-Brown S., Dunn T.B., Beilman G.J., Chinnakotla S., Pruett T.L., Ptacek P., Hering B.J., **Wang Z.**, Gilmore T., Wilhelm J.J., Hodges J.S., Moran A., Herold K.C., (2017) Unmethylated insulin DNA is elevated after total pancreatectomy with islet autotransplantation: assessment of a novel beta cell marker. *American Journal of Transplantation*, 17:1112-1118.
55. Salazar M.C., Rosen J.E., **Wang Z.**, Arnold B.N., Thomas D.C., Herbst R.S., Kim A.W., Detterbeck F.C., Blasberg J.D., Boffa D.J., (2017) Association of delayed adjuvant chemotherapy with survival after lung cancer surgery. *JAMA Oncology*, 3:610-619.
56. Fragoso C.A., Moreno M., **Wang Z.**, Heffelfinger C., Arbelaez L.J., Aguirre J.A., Franco N., Romero L.E., Labadie K., Zhao H., Dellaporta S.L., Lorieux M., (2017) Genetic architecture of a rice nested association mapping population. *G3: Genes, Genomes, Genetics*, 7:1913-1926.
57. Lu L., Bai Y., **Wang Z.**, (2017) Elevated T cell activation score is associated with improved survival of breast cancer. *Breast Cancer Research and Treatment*, 164:689-696.
58. Zhang X., Hu Y., Justice A.C., Li B., **Wang Z.**, Zhao H., Krystal J.H., Xu K., (2017) DNA methylation signatures of illicit drug injection and hepatitis C are associated with HIV frailty. *Nature Communications*, 8:2243.
59. Xu K., Zhang X., **Wang Z.**, Hu Y., Sinha R., (2018) Epigenome-wide association analysis revealed that SOCS3 methylation influences the effect of cumulative stress on obesity. *Biological Psychology*, 131:63-71.

60. Salinas Y.D., **Wang Z.**, DeWan A.T., (2018) Statistical analysis of multiple phenotypes in genetic epidemiologic studies: from cross-phenotype associations to pleiotropy. *American Journal of Epidemiology*, 187:855-863.
61. Wang Z., Wang N., Wu R., **Wang Z.**, (2018) *f*GWAS: An R package for genome-wide association analysis with longitudinal phenotypes. *Journal of Genetics and Genomics*, 45:411-413.
62. Arnold B.N., Thomas D.C., Bhatnagar V., Blasberg J.D., **Wang Z.**, Boffa D.J., Detterbeck F.C., Kim A.W., (2019) Defining the learning curve in robot-assisted thoracoscopic lobectomy. *Surgery*, 165:450-454.
63. Shan N., **Wang Z.**<sup>#</sup>, Hou L.<sup>#</sup>, (2019) Identification of trans-eQTLs using mediation analysis with multiple mediators. *BMC Bioinformatics*, 20(Suppl 3):126. <sup>#</sup>Joint corresponding author.
64. Lu L., Huang H., Zhou J., Ma W., Mackay S., **Wang Z.**, (2019) BRCA1 mRNA expression modifies the effect of T cell activation score on patient survival in breast cancer. *BMC Cancer*, 19:387.
65. Fu L., Wang M., **Wang Z.**, Song X., Tang S., (2019) Maximum likelihood estimation of nonlinear mixed-effects models with crossed random effects by combining first-order conditional linearization and sequential quadratic programming. *International Journal of Biomathematics*, 12:1950040.
66. Chen C., Jiang L., Fu G., Wang M., Wang Y., Shen B., Liu Z., **Wang Z.**, Hou W., Berceli S.A., Wu R., (2019) An omnidirectional visualization model of personalized gene regulatory networks. *npj Systems Biology and Applications*, 5:38.
67. Rowe B., Chen X., **Wang Z.**, Chen J., Amei A., (2019) Biological and practical implications of genome-wide association study of schizophrenia using Bayesian variable selection. *npj Schizophrenia*, 5:19.
68. Wu W., Wang Z., Xu K., Zhang X., Amei A., Gelernter J., Zhao H., Justice A.C., **Wang Z.**, (2019) Retrospective association analysis of longitudinal binary traits identifies important loci and pathways in cocaine use. *Genetics*, 213:1225-1236.
69. Shan N., Li N., Dai Q., Hou L., Yan X., Amei A., Lu L., **Wang Z.**, (2020) Interplay of tRNA-derived fragments and T cell activation in breast cancer patient survival. *Cancers*, 12:2230.
70. Shu C., Justice A.C., Zhang X., **Wang Z.**, Hancock D.B., Johnson E.O., Xu K., (2020) DNA methylation mediates the effect of cocaine use on HIV severity. *Clinical Epigenetics*, 12:140.
71. Dai Q., Wu W., Amei A., Yan X., Lu L., **Wang Z.**, (2021) Regulation and characterization of tumor-infiltrating immune cells in breast cancer. *International Immunopharmacology*, 90:107167.
72. Salinas Y.D., **Wang Z.**, DeWan A.T., (2021) Discovery and mediation analysis of cross-phenotype associations between asthma and body mass index in 12q13.2. *American Journal of Epidemiology*, 190:85-94.
73. Li N., Shan N., Lu L., **Wang Z.**, (2021) tRFtarget: a database for transfer RNA-derived fragment targets. *Nucleic Acids Research*, 49:D254-D260.

74. Ramaswamy A., Brodsky N.N., Sumida T.S., Comi M., Asashima H., Hoehn K.B., Li N., Liu Y., Shah A., Ravindra N.G., Bishai J., Khan A., Lau W., Sellers B., Bansal N., Guerrierio P., Unterman A., Habet V., Rice A.J., Catanzaro J., Chandnani H., Lopez M., Kaminski N., Dela Cruz C.S., Tsang J.S., **Wang Z.**, Yan X., Kleinstein S.H., van Dijk D., Pierce R.W., Hafler D.A., Lucas C.L., (2021) Immune dysregulation and autoreactivity correlate with disease severity in SARS-CoV-2-associated multisystem inflammatory syndrome in children. *Immunity*, 54:1083-1095.
75. Wu W., Liu Y., Dai Q., Yan X., **Wang Z.**, (2021) G2S3: A gene graph-based imputation method for single-cell RNA sequencing data. *PLoS Computational Biology*, 17:e1009029.
76. Li W., Amei A., Bui F., Norouzifar S., Lu L., **Wang Z.**, (2021) Impact of neoantigen expression and T-cell activation on breast cancer survival. *Cancers*, 13:2879.
77. Cheng C., Spiegelman D., **Wang Z.**, Wang M., (2021) Testing gene-environment interactions in the presence of confounders and mismeasured environmental exposures. *G3: Genes, Genomes, Genetics*, 11:jkab236.
78. Shan N., Xie Y., Song S., Jiang W., **Wang Z.**<sup>#</sup>, Hou L.<sup>#</sup>, (2021) A novel transcriptional risk score for risk prediction of complex human diseases. *Genetic Epidemiology*, 45:811-820. <sup>#</sup>Joint corresponding author.
79. Zhang B., Wang S., Mei X., Han Y., Wang R., Fang H.-B., Chiu C.-Y., Ding J., **Wang Z.**, Wilson A.F., Bailey-Wilson J.E., Xiong M., Fan R., (2022) Stochastic functional linear models for gene-based association analysis of quantitative traits in longitudinal studies. *Statistics and Its Interface*, 15:181-196.
80. Unterman A., Sumida T.S., Nouri N., Yan X., Zhao A.Y., Gasque V., Schupp J.C., Asashima H., Liu Y., Cosme C. Jr., Deng W., Chen M., Raredon M.S.B., Hoehn K.B., Wang G., **Wang Z.**, Deluliis G., Ravindra N.G., Li N., Castaldi C., Wong P., Fournier J., Bermejo S., Sharma L., Casanovas-Massana A., Vogels C.B.F., Wyllie A.L., Grubaugh N.D., Melillo A., Meng H., Stein Y., Minasyan M., Mohanty S., Ruff W.E., Cohen I., Raddassi K., The Yale IMPACT research team, Niklason L.E., Ko A.I., Montgomery R.R., Farhadian S.F., Iwasaki A., Shaw A.C., van Dijk D., Zhao H., Kleinstein S.H., Hafler D.A., Kaminski N., Dela Cruz C.S., (2022) Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. *Nature Communications*, 13:440.
81. Xiao X., **Wang Z.**, Kong Y., Lu H., (2023) Deep learning-based morphological feature analysis and the prognostic association study in colon adenocarcinoma histopathological images. *Frontiers in Oncology*, 13:1081529.
82. Weinschutz Mendes H., Neelakantan U., Liu Y., Fitzpatrick S.E., Chen T., Wu W., Pruitt A., Jin D.S., Jamadagni P., Carlson M., Lacadie C.M., Enriquez K.D., Li N., Zhao D., Ijaz S., Sakai C., Szi C., Rooney B., Ghosh M., Nwabudike I., Gorodezky A., Chowdhury S., Zaheer M., McLaughlin S., Fernandez J.M., Wu J., Eilbott J.A., Vander Wyk B., Rihel J., Papademetris X., **Wang Z.**, Hoffman E.J., (2023) High-throughput functional analysis of autism genes in zebrafish identifies convergence in dopaminergic and neuroimmune pathways. *Cell Reports*, 42:112243.

83. Li Z., **Wang Z.**, Chen Z., Voegeli H., Lichtman J.H., Smith P., Liu J., DeWan A.T., Hoh J., (2023) Systematically identifying genetic signatures including novel SNP-clusters, nonsense variants, frame-shift INDELs, and long STR expansions that potentially link to unknown phenotypes existing in dog breeds. *BMC Genomics*, 24:302.
84. Liu Y., Zhao J., Adams T.S., Wang N., Schupp J.C., Wu W., McDonough J.E., Chupp G.L., Kaminski N., **Wang Z.**<sup>#</sup>, Yan X.<sup>#</sup>, (2023) iDESC: identifying differential expression in single-cell RNA sequencing data with multiple subjects. *BMC Bioinformatics*, 24:318. <sup>#</sup>Joint corresponding author.
85. Cheng Y., Justice A., **Wang Z.**, Li B., Hancock D.B., Johnson E.O., Xu K., (2023) Cis-meQTL for cocaine use-associated DNA methylation in an HIV-positive cohort show pleiotropic effects on multiple traits. *BMC Genomics*, 24:556.
86. Jin D.S., Neelakantan U., Lacadie C.M., Chen T., Rooney B., Liu Y., Wu W., **Wang Z.**, Papademetris X., Hoffman E.J., (2023) Brain registration and evaluation for zebrafish (BREEZE)-mapping: a pipeline for whole-brain structural and activity analyses. *STAR Protocols*, 4:102647.
87. Liu Y., Rajeevan H., Simonov M., Lee S., Wilson F.P., Desir G.V., Vinetz J.M., Yan X., **Wang Z.**, Clark B.J., Possick J.D., Price C., Lutchmansingh D.D., Ortega H., Zaeh S., Gomez J.V.-L., Cohn L., Gautam S., Chupp G.L., (2023) Differences in mortality among patients with asthma and COPD hospitalized with COVID-19. *The Journal of Allergy and Clinical Immunology: In Practice*, 11:3383-3390.
88. Xiao X., Kong Y., Li R., **Wang Z.**, Lu H., (2024) Transformer with convolution and graph-node co-embedding: an accurate and interpretable vision backbone for predicting gene expressions from local histopathological image. *Medical Image Analysis*, 91:103040.
89. Li N., Yao S., Yu G., Lu L., **Wang Z.**, (2024) tRFtarget 2.0: expanding the targetome landscape of transfer RNA-derived fragments. *Nucleic Acids Research*, 52:D345-D350.
90. Xu G., Amei A., Wu W., Liu Y., Shen L., Oh E.C., **Wang Z.**, (2024) Retrospective varying coefficient association analysis of longitudinal binary traits: application to the identification of genetic loci associated with hypertension. *The Annals of Applied Statistics*, 18:487-505.
91. Zhang X., Hu Y., Vandenhoudt R.E., Yan C., Marconi V.C., Cohen M.H., **Wang Z.**, Justice A.C., Aouizerat B.E., Xu K., (2024) Computationally inferred cell-type specific epigenome-wide DNA methylation analysis unveils distinct methylation patterns among immune cells for HIV infection in three cohorts. *PLoS Pathogens*, 20:e1012063.
92. Zhuang X., Xu G., Amei A., Cordes D., **Wang Z.**, Oh E.C., Alzheimer's Disease Neuroimaging Initiative, (2024) Detecting time-varying genetic effects in Alzheimer's disease using a longitudinal GWAS model. *Alzheimer's & Dementia: Diagnosis, Assessment & Disease Monitoring*, accepted.
93. Zhang B., Wang S., Luo Y., Chiu C.-Y., Xu G., Ding J., Amei A., **Wang Z.**, Wilson A.F., Bailey-Wilson J.E., Xiong M., Fan R., (2024) Stochastic generalized functional linear models for gene-based association analysis of binary traits in longitudinal studies. *Statistics and Its Interface*, accepted.

## Chapters, Books, and Reviews

94. **Wang Z.**, Yan X., (2022) Computational and statistical methods for single-cell RNA sequencing data. In: Lu H.H.-S., Schölkopf B., Wells M.T., Zhao H., (eds), Handbook of Statistical Bioinformatics, 2nd Ed., Springer Handbooks of Computational Statistics. Springer, Berlin, Heidelberg. pp 3-35.

## Invited Editorials and Commentaries

95. Wu R., **Wang Z.**, (2013) Mathematical modeling of systems pharmacogenomics towards personalized drug delivery. *Advanced Drug Delivery Reviews*, 65:903-904.
96. **Wang Z.**, (2017) Integrating evolutionary game theory into epigenetic study of embryonic development: 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*, 20:164-165.

## Article Under Review/Revision

1. Shen L., Amei A., Liu B., Liu Y., Xu G., Oh E.C., **Wang Z.**, Detection of interactions between genetic marker sets and environment in a genome-wide study of hypertension. <https://doi.org/10.1101/2023.05.28.542666>
2. Liu Y., Li N., Qi J., Xu G., Zhao J., Wang N., Huang X., Jiang W., Wei H., Justet A., Adams T.S., Homer R., Amei A., Rosas I.O., Kaminski N., **Wang Z.**<sup>#</sup>, Yan X.<sup>#</sup>, A hybrid machine learning and regression method for cell type deconvolution of spatial barcoding-based transcriptomic data. <sup>#</sup>Joint corresponding author. <https://doi.org/10.1101/2023.08.24.554722>
3. Huang X., Arora J., Erzurumluoglu A.M., Lam D., Boehringer Ingelheim-GCBDS, Zhao H., Ding Z., **Wang Z.**<sup>#</sup>, de Jong J.<sup>#</sup>, Enhancing patient representation learning from electronic health records through predicted family relations. <sup>#</sup>Joint corresponding author. <https://doi.org/10.1101/2024.03.12.24304163>
4. Wang S., Luo Y., Chiu C.-Y., Xu G., Amei A., Zhang J., **Wang Z.**, Fang H.-B., Wilson A.F., Bailey-Wilson J.E., Fan R., Bivariate stochastic functional linear models for gene-based association analysis of quantitative traits in longitudinal studies.
5. Kay S., Rajeevan H., Son M., Kwah J., Ramirez M., Liu Y., **Wang Z.**, Yan X., Nino G., Britto C., Chupp G., Gomez J.L., Sex-biased gene expression underlies immune dysfunction in asthma.
6. Korutla L., Hu R., Liu Y., Romano C., Habbertheuer A., Abedi P., Wang H., Molugu S., Rostami S., Naji A., Marguiles K., Nuqali A., Beasley M., Maulion C., Hahn S., Ahmad T., **Wang Z.**, Sen S., Vallabhajosyula P., Circulating tissue specific extracellular vesicles as biomarkers of acute cellular rejection in clinical heart transplantation.

## PRESENTATIONS

### Invited Talks

- Joint Statistical Meetings (JSM), Portland, OR. A doubly robust machine learning method for causal inference in the presence of measurement error in the exposure of interest and confounders. August 2024.

- New England Statistics Symposium (NESS), Storrs, CT. Enhancing patient representation learning from electronic health records through predicted family relations. May 2024.
- VA Connecticut Healthcare System, Cooperative Studies Program Clinical Epidemiology Research Center Strategic Retreat, West Haven, CT. Representation learning on electronic health records using pedigree-based graph attention networks. October 2023.
- Joint Statistical Meetings (JSM), Toronto, ON, Canada. Graphical generative model for identification of disease associated perturbations to intercellular communications in single-cell RNA sequencing data. August 2023.
- Banff International Research Station (BIRS) Workshop on Data Science Challenges in Single-Cell Research, Banff, AB, Canada. Graphical generative model for identification of disease associated perturbations to intercellular communications in single-cell RNA sequencing data. July 2023.
- ICSA China Conference, Chengdu, Sichuan, China. A hybrid machine learning and regression method for cell type deconvolution in spatial transcriptomics. July 2023.
- New England Statistics Symposium (NESS), Boston, MA. A hybrid machine learning and regression method for cell type deconvolution in spatial transcriptomics. June 2023.
- Joint Statistical Meetings (JSM), Washington, DC. A hybrid machine learning and regression method for cell type deconvolution in spatial transcriptomics. August 2022.
- ICSA China Conference, online. Retrospective varying coefficient association analysis of longitudinal binary traits. July 2022.
- Boehringer Ingelheim, online. Statistical methods for correlated data: application in genetics and genomics. January 2022.
- Joint Statistical Meetings (JSM), online. Variant-set retrospective association tests for longitudinal phenotypes. August 2020.
- University of Nevada, Department of Mathematical Sciences, Las Vegas, NV. Gene graph-based imputation for scRNA-seq data. November 2019.
- ICSA China Conference, Tianjin, China. Retrospective association testing for longitudinal binary outcomes. July 2019.
- Tsinghua University, Center for Statistical Science, Beijing, China. Retrospective association testing for longitudinal binary outcomes. June 2019.
- International Conference on Econometrics and Statistics (EcoSta), Taichung, Taiwan. Identification of trans-eQTLs using mediation analysis with multiple mediators. June 2019.
- International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Raleigh, NC. Identification of trans-eQTLs using mediation analysis with multiple mediators. June 2019.
- New England Statistics Symposium (NESS), Hartford, CT. Identification of trans-eQTLs using mediation analysis with multiple mediators. May 2019.

- University of North Texas, Department of Mathematics, Denton, TX. Retrospective association testing for longitudinal binary outcomes. December 2018.
- Huazhong University of Science and Technology, Wuhan, Hubei, China. Genome-wide association analysis with longitudinal phenotypes. May 2018.
- Shanghai Jiao Tong University, SJTU-Yale Joint Center for Biostatistics, Shanghai, China. Kernel machine association testing in longitudinal studies. April 2018.
- Tsinghua University, Center for Statistical Science, Beijing, China. Mathematical modeling of dendritic cell population dynamics in the immune system. December 2017.
- Beijing University of Technology, Department of Probability and Statistics, Beijing, China. Joint statistical modeling of multiple phenotypes in samples with related individuals. December 2017.
- Johns Hopkins University, Research Program in Quantitative Sciences, Division of Biostatistics & Bioinformatics at the SKCCC. Baltimore, MD. Kernel machine association testing in longitudinal studies. September 2017.
- ICSA China Conference: with focus on lifetime data. Jilin, Changchun, China. GEE-based kernel machine association testing in longitudinal studies. July 2017.
- International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Chicago, IL. Kernel machine association testing in longitudinal studies. June 2017.
- Conference on Lifetime Data Science: Data Science, Precision Medicine, and Risk Analysis with Lifetime Data. Storrs, CT. Kernel machine association testing in longitudinal studies. May 2017.
- Hong Kong Baptist University, Department of Mathematics, Hong Kong, China. Kernel machine association testing in longitudinal studies. April 2017.
- Pennsylvania State University, Department of Public Health Sciences, Hershey, PA. Kernel machine association testing in longitudinal studies. March 2017.
- The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, Shanghai, China. Longitudinal SNP-set association analysis of quantitative phenotypes. December 2016.
- Tsinghua University, Center for Statistical Science, Beijing, China. Joint statistical modeling of multiple phenotypes in related samples. December 2016.
- International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Atlanta, GA. Kernel machine association testing for longitudinally-measured quantitative phenotypes. June 2016.
- University of Connecticut, Department of Statistics, Storrs, CT. Longitudinal SNP-set association analysis of quantitative phenotypes. February 2016.
- International Symposium on Frontiers of Genetics and Genomics, Shenzhen, Guangdong, China. Genome-wide and epigenome-wide association study in an HIV cohort. December 2015.

- VA Connecticut Healthcare System, Cooperative Studies Program Biostatistics Seminar, West Haven, CT. Kernel methods for association testing in longitudinal genetic study of alcohol use disorder in a veteran cohort. November 2015.
- University of Nevada, Department of Mathematical Sciences, Las Vegas, NV. Mathematical modeling of dendritic cell population dynamics in the immune system. October 2015.
- 4th Annual Thomas Ten Have Symposium on Statistics in Psychiatry, New York, NY. A kernel-machine statistical approach to association testing in longitudinal genetic study of alcohol use disorder in a veteran cohort. May 2015.
- Beijing Forestry University, Center for Computational Biology, Beijing, China. Longitudinal exome-focused GWAS of alcohol use disorder in a veteran cohort. December 2014.
- University of Pennsylvania, Department of Biostatistics & Epidemiology, Philadelphia, PA. Kernel methods for association testing in longitudinal genetic study of alcohol use disorder in a veteran cohort. November 2014.
- International Chinese Statistical Association-Korean International Statistical Society (ICSA-KISS) Joint Applied Statistics Symposium, Portland, OR. Longitudinal exome-focused GWAS of alcohol use disorders in a veteran cohort. June 2014.
- Institute of Mathematical Statistics (IMS) New Researchers Conference, Montreal, QC, Canada. A powerful model for family-based case-control studies of genetic imprinting. August 2013.
- Tongji Medical College, Wuhan, Hubei, China. VACS exome chip data analysis. July 2013.
- 4th Institute of Mathematical Statistics (IMS)-China International Conference, Chengdu, Sichuan, China. Joint statistical modeling of multiple phenotypes in related samples. July 2013.
- Huazhong University of Science and Technology, Wuhan, Hubei, China. Stochastic modeling of systems mapping in pharmacogenomics. June 2013.
- The Western North American Region of the International Biometric Society (WNAR) Annual Meeting, Los Angeles, CA. Joint statistical modeling of multiple phenotypes in related samples. June 2013.
- Stony Brook University, Stony Brook, NY. Joint statistical modeling of multiple phenotypes in related samples. May 2013.
- 2nd Annual Thomas Ten Have Symposium on Statistics in Psychiatry, New York, NY. Joint statistical modeling of multiple phenotypes in related samples. May 2013.
- University of Guelph, Department of Mathematics & Statistics, Guelph, ON, Canada. Direct assessment of multiple testing correction in genetic association studies with related individuals. November 2012.
- International Symposium on Mapping the Genetic Regulation of Forest Ecosystems, Beijing, China. Joint statistical modeling of multiple phenotypes in related samples. October 2012.

- Zhejiang A & F University, Lin'an, Hangzhou, Zhejiang, China. A powerful association test of ordinal traits in samples with related individuals. July 2012.
- Beijing Forestry University, Center for Computational Biology, Beijing, China. Quasi-likelihood methods and association analysis with related samples. July 2012.
- Beijing Computing Institute, Beijing, China. Genome-wide association studies and assessment of the risk of disease. July 2012.
- 2nd Joint Biostatistics Symposium, Beijing, China. Joint statistical modeling of multiple phenotypes in related samples. July 2012.
- International Conference and Exhibition on Biometrics & Biostatistics, Omaha, NE. A powerful model for family-based case-control studies of genetic imprinting. March 2012.
- Beijing Computing Institute, Beijing, China. Genome-wide association studies, disease risk prediction, and application in biology and medicine. August 2011.
- International Symposium on Genome-Wide Association Studies, Beijing, China. Direct assessment of multiple testing correction in case-control association studies with related individuals. August 2011.
- Beijing University of Technology, Department of Probability and Statistics, Beijing, China. Direct assessment of multiple testing correction in case-control association studies with related individuals. July 2011.
- International Chinese Statistical Association (ICSA) Applied Statistics Symposium, New York, NY. A powerful association test of ordinal traits in samples with related individuals. June 2011.
- France Chicago Collaborating in the Sciences (FACCTS) Workshops, Chicago, IL. Haplotype-based case-control association testing with related individuals: application to analysis of untyped SNPs. May 2009.
- University of Minnesota, Division of Biostatistics, Minneapolis, MN. Testing untyped SNPs in case-control association studies with related individuals. April 2009.
- Columbia University, Department of Biostatistics, New York City, NY. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- Genentech, Inc, South San Francisco, CA. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- University of California at Riverside, Department of Statistics, Riverside, CA. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- St. Jude Children's Research Hospital, Department of Biostatistics, Memphis, TN. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- University of Chicago, Department of Human Genetics, Chicago, IL. Haplotype-based case-control association testing with related individuals. February 2009.
- Yale University, Department of Epidemiology and Public Health, New Haven, CT. Testing untyped SNPs in case-control association studies with related individuals. February 2009.

- Michigan Technological University, Department of Mathematical Sciences, Houghton, MI. Testing untyped SNPs in case-control association studies with related individuals. January 2009.

### **Peer-reviewed Talks**

- Asia Pacific Bioinformatics Conference (APBC), Wuhan, Hubei, China. Identification of trans-eQTLs using mediation analysis with multiple mediators. January 2019.
- Joint Statistical Meetings (JSM), Chicago, IL. Kernel machine statistical approaches to genetic association testing in longitudinal studies. August 2016.
- Joint Statistical Meetings (JSM), Seattle, WA. A novel kernel-based statistical approach to testing association with body mass index in a longitudinal genetic study. August 2015.
- Joint Statistical Meetings (JSM), Montreal, QC, Canada. Stochastic modeling of systems mapping in pharmacogenomics. August 2013.
- Joint Statistical Meetings (JSM), San Diego, CA. Improved statistical methods for allele frequency estimation in sequencing data. July 2012.
- Joint Statistical Meetings (JSM), Vancouver, BC, Canada. Multiple testing correction method in genetic association studies with related individuals. August 2010.
- The Eastern North American Region of the International Biometric Society (ENAR) Meeting, New Orleans, LA. Association analysis of ordinal traits on related individuals. March 2010.
- The Eastern North American Region of the International Biometric Society (ENAR) Meeting, Arlington, VA. An incomplete-data quasi-likelihood framework with application to genetic association studies on related individuals. March 2008.
- Genentech, Inc, South San Francisco, CA. Designing a single arm phase II clinical trial with time to event endpoint. August 2004.
- The Eastern North American Region of the International Biometric Society (ENAR) Meeting, Pittsburgh, PA. A unifying model for fine mapping of quantitative trait loci affecting CD4<sup>+</sup> T cell and HIV-1 dynamics under highly active antiretroviral therapy. March 2004.

### **Posters**

- American Society of Human Genetics (ASHG) Annual Meeting, Washington, DC. GATEHR: representation learning on electronic health records using pedigree-based graph attention networks. November 2023.
- American Society of Human Genetics (ASHG) Annual Meeting, Los Angeles, LA. A hybrid machine learning and regression method for cell type deconvolution of spatial barcoding-based transcriptomic data. October 2022.
- American Society of Human Genetics (ASHG) Annual Meeting, Houston, TX. Longitudinal variant-set retrospective association test. October 2019.
- International Genetic Epidemiology Society (IGES) Annual Meeting, Houston, TX. Identification of trans-eQTLs using mediation analysis with multiple mediators. October 2019.

- American Society of Human Genetics (ASHG) Annual Meeting, San Diego, CA. Retrospective association tests for longitudinal binary outcomes in GWAS. October 2018.
- International Genetic Epidemiology Society (IGES) Annual Meeting, Cambridge, UK. Joint statistical modeling of multiple phenotypes in related samples. September 2017.
- International Genetic Epidemiology Society (IGES) Annual Meeting, Baltimore, MD. Kernel machine association testing for longitudinally-measured quantitative phenotypes. October 2015.
- 37th Annual Research Society on Alcoholism (RSA) Scientific Meeting, San Antonio, TX. A novel kernel-based statistical approach to testing association with body mass index in a longitudinal genetic study. June 2015.
- International Genetic Epidemiology Society (IGES) Annual Meeting, Vienna, Austria. Longitudinal exome-focused GWAS of alcohol use disorder in a veteran cohort. August 2014.
- American Society of Human Genetics (ASHG) Annual Meeting, San Francisco, CA. Joint statistical modeling of multiple phenotypes in samples with related individuals. November 2012.
- American Society of Human Genetics (ASHG) Annual Meeting, Montreal, QC, Canada. A powerful model for family-based case-control studies of genetic imprinting. October 2011.
- 2nd Midwest Statistics Research Colloquium, Chicago, IL. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- 1st Midwest Statistics Research Colloquium, Chicago, IL. An incomplete-data quasi-likelihood framework with application to genetic association studies on related individuals. March 2008.
- International Genetic Epidemiology Society (IGES) Annual Meeting, York, England, UK. Haplotype-based case-control association studies with related individuals: a quasi-likelihood score test approach. September 2007.
- SNPs, Haplotypes, and Cancer: Applications in Molecular Epidemiology Meeting, AACR, Key Biscayne, FL. A dynamic model for genetic control of tumor growth. September 2003.

## **PROFESSIONAL SERVICE**

### **Peer Review Groups/Grant Study Sections**

- NSF Molecular and Cellular Biosciences review panel, 2024
- Grant Reviewer, Ministry of Health, Singapore, 2022
- Mail-in Reviewer, National Science Centre, Poland, 2020
- NSF joint DMS/NIGMS review panel, 2019
- Grant Reviewer, Nebraska Research Initiative, 2017
- Mail-in Reviewer, Israel Science Foundation, 2016

### **Editorial Service**

- Associate Editor, *Frontiers in Integrative Genetics and Genomics*, 2023–present
- Associate Editor, *BMC Genomics*, 2020–present
- Associate Editor, *BMC Genetics*, 2012–2020
- Review Editor, *Frontiers in Integrative Genetics and Genomics*, 2021–2023
- Theme Co-Editor, Mathematical modeling of systems pharmacogenomics, special issue of *Advanced Drug Delivery Reviews*, 2012
- Review Editor, *Frontiers in Genetic Architecture*, 2011–present
- Review Editor, *Frontiers in Statistical Genetics and Methodology*, 2011–present
- Editorial Board Member, *Journal of Biometrics & Biostatistics*, 2011–present

### **Journal Referee**

*American Journal of Human Genetics, Annals of Applied Statistics, Atherosclerosis, Bioinformatics, Biostatistics, BMC Genetics, Briefings in Bioinformatics, Cell Reports Methods, Frontiers in Bioscience, Frontiers in Statistical Genetics and Methodology, Genetic Epidemiology, Genetics, Genomics, Human Genetics, Human Heredity, Human Molecular Genetics, Infection, Genetics and Evolution, International Journal of Data Mining and Bioinformatics, Journal of Biometrics & Biostatistics, Journal of Biopharmaceutical Statistics, Journal of Computational Biology, Journal of the American Statistical Association, Ornamental Plant Research, Pharmacogenomics, Plant Biotechnology Journal, PLoS Computational Biology, PLoS Genetics, PLoS One, Quantitative Biology, Scientific Reports, Statistical Applications in Genetics and Molecular Biology, Statistics and Its Interface, Statistics in Biosciences, Statistics in Medicine, Theranostics, International Conference on Research in Computational Molecular Biology (RECOMB 2020)*

### **Society Activities**

- Member, Organizing Committee, Thomas R. Ten Have Symposium on Statistics in Mental Health, 2022–present
- Member, Communications Committee, International Genetic Epidemiology Society (IGES), 2019–present
- Organizer, Recent Developments in Statistics and Machine Learning for Electronic Health Records Data and Precision Medicine Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2024
- Member, Nomination Committee in Bioinformatics, Frontiers of Science Award (FSA), International Congress of Basic Science (ICBS), 2024
- Organizer, Recent Advances in Analysis of Large-Scale Omics Data Session, Joint Statistical Meetings (JSM), 2023
- Organizer, Statistical and Machine Learning Methods in Omics Data Analysis, New England Statistics Symposium (NESS), 2023
- Organizer, Statistical Advance and Computational Challenges in Omics Studies Session, International Chinese Statistical Association (ICSA) China Conference, 2019

- Organizer, Statistical Advances in Genetics, Genomics and Bioinformatics Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2019
- Organizer, Recent Advance in Bioinformatics and Computational Biology Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2017
- Reviewer, Student Paper Competition, Section on Statistics in Genomics and Genetics, American Statistical Association (ASA), 2017
- Organizer, Advance in Statistical Genomics and Computational Biology Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2016
- Organizer, Recent Advances in Genetic Epidemiology Session, New England Statistics Symposium (NESS), 2016
- Reviewer, Student Paper Competition, Section on Statistics in Genomics and Genetics, American Statistical Association (ASA), 2016
- President, American Statistical Association (ASA), Connecticut Chapter, 2014–2015
- Chair, Challenging Statistical Issues in Functional Neuroimaging Modeling Session, 4th Institute of Mathematical Statistics (IMS)-China international conference, 2013
- Organizer, Statistical Challenges in Large Scale Genetic Studies of Complex Diseases Session, The Eastern North American Region of the International Biometric Society (ENAR) Meeting, 2013
- Chair, Statistical Genomics Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2011

### **Yale University Services**

- Chair, Qualifying Exam Committee, Department of Biostatistics, Yale School of Public Health, 2021–present
- COVID-19 Safety Officers, Yale School of Public Health, 2020
- Chair, Colin White Memorial Scholarship Committee, Department of Biostatistics, Yale School of Public Health, 2019–2022
- Member, Qualifying Exam Committee, Department of Biostatistics, Yale School of Public Health, 2019–2020
- Member, Selection Committee on YSPH Associate Dean for Diversity, Equity and Inclusion, Yale School of Public Health, 2019
- Member, MPH Admissions Committee, Yale School of Public Health, 2017–2022
- Member, Practicum Advisory Committee (PAC), Yale School of Public Health, 2015–2017
- Chair, Master Thesis Prize Committee, Department of Biostatistics, Yale School of Public Health, 2013–present
- Member, Faculty Search Committee, Department of Biostatistics, Yale School of Public Health, 2013, 2022
- Member, Colin White Memorial Scholarship Committee, Department of Biostatistics, Yale School of Public Health, 2012–2018

- Member, Committee on Academic and Professional Integrity (CAPI), Yale School of Public Health, 2012–2015
- Seminar Organizer, Department of Biostatistics, Yale School of Public Health, 2009–2010, 2012

## **TEACHING ACTIVITIES**

- BIS691, Generalized Linear Models  
Department of Biostatistics, Yale School of Public Health  
Spring 2020–2024
- BIS625, Categorical Data Analysis  
Department of Biostatistics, Yale School of Public Health  
Fall 2011–2017, Spring 2019
- Applied Data Science  
Department of Biological Sciences, Shanghai Jiao Tong University  
Spring 2023
- Longitudinal and Multilevel Data Analysis  
Department of Biological Sciences, Shanghai Jiao Tong University  
Spring 2017, 2018, 2021
- Generalized Linear Models  
Department of Biological Sciences, Shanghai Jiao Tong University  
Spring 2017
- Short course on Categorical Data Analysis  
Beijing Forestry University  
October 2012
- Short course on Nonparametric Statistics  
Beijing Forestry University  
October 2012
- STAT 220, Statistical Methods and Applications  
Department of Statistics, University of Chicago  
Spring 2008

## **MENTORING ACTIVITIES**

- Postdoctoral/Research Associate Mentor
  - Zhong Wang (2013–2014, Professor at Dalian University of Technology)
  - Xinyu Zhang (2014–2015, Research Scientist at Yale University)
  - Xiayuan Huang (2022–present)
  - Gang Xu (2023–present)
  - Siming Zheng (2023–2024)
- PhD Dissertation Advisor
  - Weimiao Wu (Biostatistics, 2016–2021, First job: Meta Platforms, Inc.)

- Ningshan Li (Bioinformatics & Biostatistics, Shanghai Jiao Tong University, 2019–2022, Postdoc at the Chinese University of Hong Kong, Shenzhen & Longgang District People’s Hospital of Shenzhen)
- Yunqing Liu (Biostatistics, 2018–2023, First job: Food and Drug Administration)
- Yi Dai (Biostatistics, 2022–present)
- Xiao Xiao (Biostatistics, 2023–present)
- Master Thesis Advisor
  - Gongyi Wang (Biostatistics MS, 2013, First job: Michael Allen Co.)
  - Yun Huang (Biostatistics MS, 2014)
  - Xiyang Dou (Biostatistics MS, 2015, First job: HSBC)
  - Bingbing Lu (Biostatistics MS, 2015, First job: State Street Co.)
  - Siwan Huang (Biostatistics MS, 2016, First job: PwC)
  - Tiange Chen (Biostatistics MPH, 2016, **BIS master thesis award**, First job: IBM Research China)
  - Yuhao Qian (Environmental Health Sciences MPH, 2016, First job: Haoyue Capital)
  - Yunqing Liu (Biostatistics MS, 2018, **BIS master thesis award**, PhD student at Yale University)
  - Ningya Wang (Biostatistics MS, 2022, PhD student at Rutgers University)
  - Yi Dai (Biostatistics MPH, 2022, **BIS master thesis award**, PhD student at Yale University)
  - Nating Wang (Biostatistics MPH, 2023, PhD student at Cornell University)
- PhD Dissertation Committee
  - Jieming Chen (Computational Biology and Bioinformatics, 2015)
  - Josefa Martinez (Chronic Disease Epidemiology, 2016)
  - Qiongshi Lu (Biostatistics, 2017)
  - Christopher Fragoso (Computational Biology and Bioinformatics, 2017)
  - Qian Wang (Computational Biology and Bioinformatics, 2017)
  - Yasmmyn Salinas (Chronic Disease Epidemiology, 2019)
  - Mo Li (Biostatistics, 2020)
  - Boyang Li (Biostatistics, 2022)
  - Xing Wu (Molecular, Cellular and Developmental Biology, 2022)
  - Hongyu Li (Biostatistics, 2023)
  - Yuhan Xie (Biostatistics, 2023)
  - Zicheng Li (Chronic Disease Epidemiology, 2023)
  - Paulina Tolosa-Tort (Chronic Disease Epidemiology, expected in 2024)
  - Youshu Cheng (Biostatistics, expected in 2025)
  - Zihan Dong (Biostatistics, expected in 2025)
  - Chen Lin (Biostatistics, expected in 2025)

- Esther Kang (Chronic Disease Epidemiology, expected in 2027)
- PhD Dissertation Reader
  - Gregory Ryslik (Biostatistics, 2014)
  - Qing Zhao (Biostatistics, 2015)
  - Zhixuan Fu (Biostatistics, 2016)
  - Tianqi Liu (Biostatistics, 2017)
  - Jiehuan Sun (Biostatistics, 2017)
  - Yiyi Liu (Biostatistics, 2018)
  - Li Zeng (Biostatistics, 2018)
  - Kyaw Sint (Biostatistics, 2019)
  - Megan Cahill (Epidemiology of Microbial Diseases, 2019)
  - Xiaoxuan Cai (Biostatistics, 2020)
  - Xiaochen Wang (Biostatistics, 2020)
  - Ming Chen (Biostatistics, 2021)
  - Wenxuan Deng (Biostatistics, 2021)
  - Daiwei Tang (Biostatistics, 2021)
  - Yaqing Xu (Biostatistics, 2021)
  - Huangdi Yi (Biostatistics, 2021)
  - Yiliang Zhang (Biostatistics, 2022)
  - Wei Dai (Biostatistics, 2023)
  - Chang Su (Biostatistics, 2023)
  - Shiyang Wang (Biostatistics, 2023)
  - Yuge Wang (Biostatistics, 2023)
  - Chi Zhang (Biostatistics, 2024)
- PhD Qualifying Oral Exam Committee
  - Ming Chen (Biostatistics, 2018)
  - Boyang Li (Biostatistics, 2018)
  - Hongyu Li (Biostatistics, 2020)
  - Chang Su (Biostatistics, 2020)
  - Yuhan Xie (Biostatistics, 2020)
  - Youshu Cheng (Biostatistics, 2022)
  - Zihan Dong (Biostatistics, 2022)
  - Biqing Zhu (Computational Biology and Bioinformatics, 2022)
  - Wangjie Zheng (Biostatistics, 2023)
  - Zexiang Li (Biostatistics, 2024)
  - Xinning Shan (Biostatistics, 2024)
- Master Thesis Reader
  - Motao Sun (Chronic Disease Epidemiology MPH, 2016)

- Yi Jin (Chronic Disease Epidemiology MPH, 2020)
- Research Assistants Supervised
  - Lu Wang (Biostatistics MS, Summer 2013, PhD student at University of Pennsylvania)
  - Zhaolong Yu (Computational Biology & Bioinformatics, Spring 2017)
  - Shiyu Wang (Biostatistics MS, 2018–2019, PhD student at Emory University)
  - Qile Dai (Biostatistics MS, 2018–2020, PhD student at Emory University)
  - Ran Tu (Biostatistics MPH, 2020–2021, PhD student at Georgetown University)
  - Gang Xu (Statistics, University of Nevada, Las Vegas, 2018–2022)
  - Wenhao Jiang (Biostatistics MS, 2021–2023, PhD student at the University of Massachusetts Amherst)
  - Ji Qi (Biostatistics MS, 2021–2023, PhD student at the Chinese University of Hong Kong)
  - Jiayi Zhao (Biostatistics MS, 2021–2023, Postgraduate Associate at Yale University)
  - Linchuan Shen (Statistics, University of Nevada, Las Vegas, 2018–present)
  - Yihan Liu (Biostatistics MS, 2023–present)
  - Annie Jiang (Biostatistics MPH, 2023–present)
  - Shanshan Gao (Biostatistics MS, 2023–present)
- Visiting Scholar Mentor
  - Lihong Zhao (Visiting PhD Student, Beijing University of Chinese Medicine, 2012–2013)
  - Meng Xu (Visiting Associate Professor, Nanjing Forestry University, 2014–2015)
  - Yisha Tang (Undergraduate, University of Science & Technology of China, Summer 2018)
  - Nayang Shan (Visiting PhD Student, Tsinghua University, 2019–2020)
  - Huanhuan Wei (Visiting PhD Student, Shanghai Jiao Tong University, 2022–2023)