Xiang Zhan

Contact Information

Beijing International Center for Mathematical Research
& Department of Biostatistics, School of Public Health
Peking University
81 Jingchunyuan Suite, 5 Yiheyuan Rd, Haidian District
Beijing, China 100871
Phone: +86 10-6274-4100
E-mail: zhanxiang@bicmr.pku.edu.cn
Website: `https://bicmr.pku.edu.cn/ zhanxiang/`

Education & Training

Fred Hutchinson Cancer Research Center (FHCRC), Seattle, WA, USA

Postdoctoral Scholar, August 2015 – July 2017

Pennsylvania State University (PSU), University Park, PA, USA

Ph.D. in Statistics, August 2015

Peking University (PKU), Beijing, China

B.S. in Statistics (School of Mathematical Sciences/SMS), July 2010

B.A. in Economics (China Center for Economic Research/CCER), July 2010

Academic Positions

Associate Professor 2021.09–present
Beijing International Center for Mathematical Research (BICMR), PKU

Associate Professor 2021.09–present
Department of Biostatistics, School of Public Health, PKU

Affiliate Faculty 2021.09–present
Center for Statistical Science (CSS), PKU

Adjunct Associate Professor 2021.07–2022.06
Div of Biostatistics and Bioinformatics, Dept of Public Health Sciences,
College of Medicine, PSU

Visiting Associate Professor 2021.07–2021.09
Beijing International Center for Mathematical Research, PKU

Assistant Professor 2017.07–2021.06
Div of Biostatistics and Bioinformatics, Dept of Public Health Sciences,
College of Medicine, PSU

Affiliate Faculty 2018.01–2021.06
Bioinformatics and Genomics (BG) Program,
Huck Institutes of Life Sciences, PSU

Affiliate Faculty 2018.01–2021.06
Microbiome Center,
Huck Institutes of Life Sciences, PSU

Honors & Awards

Article selected by *Biometrics* as one of “Top Cited Article 2021–2022”
February 2023

Best Student Paper Award in Applied Statistics, May 2021
International Indian Statistical Association (IISA)

JSM David P. Byar Early Career Paper Award, Jan 2021
American Statistical Association (ASA), Biometrics Section

Article selected by *Biometrics* as one of "Top Downloaded Article 2017–2018"
June 2019

Travel award selected by the ENAR2019 workshop for junior Biostatistician
March 2019

Nominee of Program Chair-Elect, March 2018
American Statistical Association (ASA), Statistics in Genomics and Genetics Section
[**In AMSTATNEWS**]

JSM David P. Byar Young Investigator Travel Award, Jan 2017
American Statistical Association (ASA), Biometrics Section [**Webpage**]

ENAR Distinguished Student Paper Award, Mar 2016
International Biometric Society, East North America Region (IBS–ENAR)

Special Commendation for Highest Performance in Ph.D Qualifying Exam, Jan 2012
Department of Statistics, PSU

PEER-REVIEWED PUBLICATIONS

#Alphabetical order; *Corresponding author; †Equal contribution; **Group Member/Trainee**.

1. Li, C., Li, R., Wen, J.*, Yang, S.*, and **Zhan, X.**#(2023+). Regularized Linear Programming Discriminant Rule with Folded Concave Penalty for Ultrahigh-dimensional Data. ***Journal of Computational and Graphical Statistics, in press***.
   Preprint available at `https://doi.org/10.1080/10618600.2022.2143785`.
2. Rou, L., **Zhan, X.***, and Wang, T.* (2023). A Flexible Zero-inflated Poisson-Gamma Model with Application to Microbiome Sequence Count Data ***Journal of the American Statistical Association***, **118**, 792-804.
3. Li, D.†, Srinivasan, A.†, Xue, L.*, and **Zhan, X.*** (2023). Robust Shape Matrix Estimation for High-Dimensional Compositional Data with Application to Microbial Inter-Taxa Analysis. ***Statistica Sinica***, **33**, 1577-1602.
4. Srinivasan, A., Xue, L.*, and **Zhan, X.*** (2023). Identification of microbial features in multivariate regression under false discovery rate control. ***Computational Statistics & Data Analysis***, **181**:107621.
5. Jiang, Z., Zhang, H., Aheran, T.U., Garcia-Closas, M., Chatterjee, N., Zhu, H., **Zhan, X.***, and Zhao, N.* (2023). Sequence kernel association test with multi-categorical outcomes with application to breast cancer genome-wide association studies. ***Genetic Epidemiology***, **47(6)**, 432-449.
6. Li, Y.†, Hu, Y.†, **Zhan, X.**†, Song, Y., Xu, M., Wang, S., Huang, X., and Xu, Z.Z.* (2023). Meta-analysis reveals Helicobacter pylori mutual exclusivity and reproducible gastric microbiome alterations during gastric carcinoma progression. ***Gut Microbes***, **15**:2197835.
   [**Journal 2022 IF: 12.2, ranked 11/135 in Microbiology**]
7. Liu, H., Ling, W., Hua, X., Moon, J. Y., Williams-Nguyen, J. S.,**Zhan, X.**, ... & Wu, M. C. (2023). Kernel-based genetic association analysis for microbiome

phenotypes identifies host genetic drivers of beta-diversity. ***Microbiome***, **11:**80.
[Journal 2022 IF: 15.5, ranked 7/135 in Microbiology]

8. Schneider A, Nolan Z, Banerjee K, Paine A, Cong Z, Gettle S, Longenecker A, **Zhan X**, Agak G., Nelson A* (2023). Evolution of the facial skin microbiome during puberty in normal and acne skin. ***Journal of the European Academy of Dermatology and Venereology***, **37(1)**, 166–175.
[Journal 2022 IF: 9.2, ranked 4/70 in Dermatology]

9. Zachary T. Nolan, Kalins Banerjee, Zhaoyuan Cong, Samantha L. Gettle, Amy L. Longenecker, Yuka I. Kawasawa, Andrea L. Zaenglein, Diane M. Thiboutot, George W. Agak, **Xiang Zhan**, Amanda M. Nelson* (2023). Treatment response to isotretinoin correlates with specific shifts in Cutibacterium acnes strain composition within the follicular microbiome. ***Experimental Dermatology***. **32(7)**, 955-964.

10. Banerjee, K.*, Chen, J., and **Zhan, X.*** (2022). An adaptive test for microbiome association studies via feature selection. ***NAR Genomics and Bioinformatics***, **4(1)**, lqab120.
[**An earlier version won the first author a JSM 2021 Biometrics Section paper award** (In PSU News)]
[**An earlier version won the first author a Best Student Paper Competition Award in IISA 2021 May Virtual Conference**]

11. Wang, T. Lin, W., Plangtinga, A. M., Wu, M. C. and **Zhan, X.*** (2022). Testing microbiome association using integrated quantile regression models. ***Bioinformatics***, **38(2)**, 419–425. [R Software]

12. Jiang., Z., He, M., Chen, J., Zhao, N.* and **Zhan, X.*** (2022). MiRKAT-MC: a distance-based kernel association test for microbiome studies with multi-categorical outcomes. ***Frontiers in Genetics***, **13**:841764.

13. Cho, Y.*, **Zhan, X.*** and Ghosh, D. (2022). Nonlinear predictive directions in clinical trials. ***Computational Statistics & Data Analysis***, **174**:107476.

14. Chen, H.†, Ji, T.†, **Zhan, X.**, Liu, X., Yu, G., Wang, W., Jiang, Y.*, and Zhou X-H* (2022). Seizures Prediction and Epileptogenic Focus Localization via Dynamic Functional Brain Connectivity View from Scalp EEG. ***Computational Intelligence and Neuroscience***, **2022:** 2183562.

15. Colello, J., Ptasinski, A., **Zhan, X.**, Kaur, S., and Craig, T. J.* (2022). Assessment of Patient Perspectives and Barriers to Self-Infusion of Augmentation Therapy for Alpha-1 Antitrypsin Deficiency During the COVID-19 Pandemic. ***Pulmonary Therapy***, **8**, 95-103.

16. Srinivasan, A., Xue, L.*, and **Zhan, X.*** (2021). Compositional knockoff filter for high-dimensional regression analysis of microbiome data. ***Biometrics***, **77(3)**, 984–995.
[**Selected as a top cited article in Biometrics 2021-2022**]

17. **Zhan, X.***, Banerjee, K., and Chen, J.* (2021). Variant-Set Association Test for Generalized Linear Mixed Model. ***Genetic Epidemiology***, **45(4)**, 402–412.

18. Jiang, L., Liu, X., He, X., Jin, Y., Cao, Y., **Zhan, X.**, Griffine, C.H., Gragnoli, C., and Wu, R.* (2021). A behavioral model for mapping the genetic architecture of gut-microbiota networks. ***Gut Microbes***, **13:** e1820847.
[Journal 2020 IF: 10.245]

19. Wilson, N., Zhao, N., **Zhan, X.**, Koh, H., Fu, W., Chen, J., Li, H., Wu, M.C. and Plantinga, A. M.* (2021). MiRKAT: Kernel Machine Regression-Based Global Association Tests for the Microbiome. ***Bioinformatics***, **37(11)**, 1595–1597. [R Software]

20. Carney, M. C., **Zhan, X.**, Rangnekar, A., Chroneos, M. Z., Craig, S. J., Makova, K. D., Paul, I. M. and Hicks, S. D.* (2021). Associations between stool micro-transcriptome, gut microbiota, and infant growth. ***Journal of Developmental Origins of Health and Disease***, **12(6)**, 876-882.

21. Bagley, J. J., Piazza, B., Lazarus, M. D., Fox E. J.*, **Zhan, X.** (2021). Resident Training and the Assessment of Orthopaedic Surgical Skills. ***JBJS Open Access*** **6(4)**, e20.00173.

22. Yang S., Wen, J., Eckert S.T., Wang, Y., Liu, D., Wu, R., Li, R., and **Zhan, X.*** (2020). Prioritizing genetic variants in GWAS using permutation-assisted lasso tuning. ***Bioinformatics***, **36(12)** 3811–3817. [R Software].

23. Agarwal, A., Wen, T.*, Chen, A., Zhang, A. Y., Niu, X., **Zhan, X.**, Xue, L.* and Brantley, S. L. (2020). Assessing Contamination of Stream Networks near Shale Gas Development Using a New Geospatial Tool. ***Environmental Science & Technology***, **54(14)**, 8632–8639.
[Journal 2019 IF: 7.864]

24. Schneider, A. M., Cook, L. C., **Zhan, X.**, Banerjee, K., Cong, Z., Imamura-Kawasawa, Y., Gettle, S.L., Longenecker, A.L., Kirby, J.S., and Nelson, A. M.* (2020). Loss of skin microbial diversity and alteration of bacterial metabolic function in Hidradenitis Suppurativa. ***Journal of Investigative Dermatology***, **140(3)**, 716-720.
[Journal 2019 IF: 7.143]

25. Schneider, A. M., Cook, L. C., **Zhan, X.**, Banerjee, K., Cong, Z., Imamura-Kawasawa, Y., Gettle, S.L., Longenecker, A.L., Kirby, J.S., and Nelson, A. M.* (2020). Response to Ring: *In silico* predictive metagenomic analyses highlight key metabolic pathways impacted in the HS skin microbiome. ***Journal of Investigative Dermatology***, **140(7)**, 1476-1479.
[Journal 2019 IF: 7.143]

26. Gandhi C.*, Patel, J. and **Zhan, X.** (2020). Trend of influenza vaccine Facebook posts in last four years: a content analysis. ***American Journal of Infection Control***, **48(4)**, 361-367.

27. Patel, V. A., Dunklebarger, M., Banerjee, K., Shokri, T., **Zhan, X.**, and Isildak, H.* (2020). Surgical Management of Vestibular Schwannoma: Practice Pattern Analysis via NSQIP. ***Annals of Otology, Rhinology & Laryngology***, **129(3)**, 230-237.

28. Ruzieh, M., Rogers, A. M., Banerjee, K., Soleymani, T., **Zhan, X.**, Foy, A. J., and Peterson, B. R.* (2020). Safety of bariatric surgery in patients with coronary artery disease. ***Surgery for Obesity and Related Diseases***, **16(12)**, 2031-2037.

29. **Banerjee, K.**, Zhao, N., **Srinivasan, A.**, Xue, L., Steven, D. H., Middleton, F. A., Wu, R. and **Zhan, X.*** (2019). An adaptive multivariate two-sample test with application to microbiome differential abundance analysis. ***Frontiers in Genetics***, **10**: 350. [R Software].
[**An earlier version won the first author a top-5 finalist of Best Student Paper Competition in IISA 2019 December Conference in Mumbai India**]

30. **Zhan, X.*** (2019). Relationship between MiRKAT and coefficient of determination in similarity matrix regression. ***Processes***, **7(2)**, 79.

31. Yang, S., Wen, J., **Zhan, X.**, and Kifer, D. (2019). ET-Lasso: A New Efficient Tuning of Lasso-type Regularization for High-Dimensional Data. In Proceedings of the 25th ACM SIGKDD International Conference on Knowledge Discovery & Data Mining (pp. 607-616). ACM.
    [KDD2019 Research track oral acceptance rate ≈ 110/1200 = 9.17%]

32. Wang, Q., Liu, X., Jiang, L., Cao, Y., **Zhan, X.**, Griffin, C.H., and Wu, R.* (2019). Interrogation of Internal Workings in Microbial Community Assembly: Play a Game through a Behavioral Network? ***mSystems***, **4(5)**, e00550-19.
    [Journal 2018 IF: 6.519]

33. Koh, H., Li, Y., **Zhan, X.**, Chen, J., and Zhao, N.* (2019). An adaptive distance-based kernel association test based on the generalized linear mixed effect model for correlated microbiome studies. ***Frontiers in Genetics***, **10**: 458.

34. Ozdemir, T., Bowers, D., **Zhan, X.**, Ghosh, D., Brown J.L.* (2019). Identification of Key Signaling Pathways Orchestrating Substrate Topography Directed Osteogenic Differentiation Through High-Throughput siRNA Screening. ***Scientific Reports***, **9**, 1001.

35. **Zhan, X.*** and Wu, M. C.* (2018). A note on testing and estimation in marker-set association study using semiparametric quantile regression kernel machine. ***Biometrics***, **74**, 764–766.

36. **Zhan, X.**, Xue, L., Zheng, H., Plantinga, A., Wu, M.C., Schaid, D.J., Zhao, N.* and Chen, J.* (2018). A small-sample kernel association test for correlated data with application to microbiome association studies. ***Genetic Epidemiology***, **42**, 772–782. [R Software].

37. Zhao, N.*, **Zhan, X.**, Guthrie, K.A., Mitchell, C.M. and Larson, J. (2018). Generalized Hotelling's test for paired compositional data with application to human microbiome studies. ***Genetic Epidemiology***, **42**, 459–469.

38. Zhao, N.*, **Zhan, X.**, Huang, Y. T., Almli, L., Smith, A., Ressler, K., Binder, E., Epstein, M. P., Conneely, K. and Wu, M. C.* (2018). Kernel machine methods for integrative analysis of genome-wide methylation and genotyping studies. ***Genetic Epidemiology***, **42**, 156–167.
    [**Highlight paper of the March 2018 issue of *Genetic Epidemiology* selected by The International Genetic Epidemiology Society (IGES)** (Twitter link)]

39. **Zhan, X.***, Plantinga, A., Zhao, N. and Wu, M. C.* (2017). A fast small-sample kernel independence test for microbiome community-level association analysis. ***Biometrics***, **73**, 1453–1463.
    [**An earlier version won a JSM 2017 Biometrics Section Young Investigator Paper Award**]
    [**Selected as a top downloaded article in Biometrics 2017-2018**]

40. **Zhan, X.**, Zhao, N., Plantinga, A., Thornton, T., Conneely, K., Epstein, M. P. and Wu, M. C.* (2017). Powerful genetic association analysis for common or rare variants with high dimensional structured traits. ***Genetics***, **206**, 1779–1790. [R Software]
    [**Highlight paper of the August 2017 issue of *Genetics* selected by The Genetics Society of America (GSA)** (Paper link)]
    [**An earlier version won an ENAR 2016 Distinguished Student Paper Award**]

41. **Zhan, X.**†, Tong, X.†, Zhao, N., Maity, A., Wu, M. C.* and Chen, J.* (2017). A small-sample multivariate kernel machine test for microbiome association studies. ***Genetic Epidemiology***, **41**, 210-220. [R Software]

42. Plantinga, A., **Zhan, X.**, Zhao, N., Chen, J., Jenq, R. R. and Wu, M. C.* (2017). MiRKAT-S: a community-level test of association between the microbiota and survival times. ***Microbiome***, **5:**17. [R Software]
    [Journal 2016 IF: 8.496]

43. Mitchell, C.*, Srinivasan, S., **Zhan, X.**, Wu, M. C., Reed, S., Guthrie, K., LaCroix, A., Fiedler, T., Munch, M., Liu, C., Hoffman, N., Blair, I., Newton, K., Freeman, E., Joffe, H., Cohen, L., Fredricks. D. (2017). Vaginal microbiota and genitourinary symptoms of menopause: A cross sectional analysis. ***Menopause***, **24**, 1160-1166.
    [**Featured as a Researcher Highlight by the Fred Hutchinson Cancer Research Center** (In The News)]

44. **Zhan, X.***, Girirajan, S., Zhao, N., Wu, M. C., and Ghosh, D.* (2016). A novel copy number variants kernel association test with application to autism spectrum disorders studies. ***Bioinformatics***, **32**, 3603–3610. [R Software]

45. **Zhan, X.*** and Ghosh, D. (2016). A novel power-based approach to Gaussian kernel selection in the kernel-based association test. ***Statistical Methodology***, **33**, 180-191.

46. **Zhan, X.**, Patterson, A. D. and Ghosh, D.* (2015). Kernel approaches for differential expression analysis of mass spectrometry-based metabolomics data. ***BMC Bioinformatics***, **16:**77. [R Software]

47. **Zhan, X.*** and Ghosh, D. (2015). Incorporating auxiliary information for improved prediction using combination of kernel machines. ***Statistical Methodology***, **22**, 47-57.

48. **Zhan, X.***, Epstein, M. and Ghosh, D. (2015). An adaptive genetic association test using double kernel machines. ***Statistics in Biosciences***, **7**, 262–281.

Pending preprints which have been submitted:

49. Rios, N.*, Xue. L.*, and **Zhan, X.*** (2024+). A latent variable mixture model for composition-on-composition regression with application to chemical recycling. ***Revision under Annals of Applied Statistics***. Preprint available at
    `http://faculty.bicmr.pku.edu.cn/ zhanxiang/preprint1.pdf`.

50. Deng, Y., Wang, Y., and **Zhan, X.**, and Zhou, X-H* (2024+). Separable Pathway Effects of Semi-Competing Risks via Multi-State Models. ***Submitted***. Preprint available at
    `http://faculty.bicmr.pku.edu.cn/ zhanxiang/preprint2.pdf`.

51. Li, R., Mu, J., Yang, S., Ye, C., and **Zhan, X.*** (2024+). Compositional variable selection in quantile regression for microbiome data with false discovery rate control. ***Submitted***. Preprint available at
    `http://faculty.bicmr.pku.edu.cn/ zhanxiang/preprint3.pdf`.

52. Yang, S., Yang, H., **Zhan, X.***, and Li, R. (2024+). A nonconvex partial compositional Dantzig selector for high-dimensional microbiome mediation analysis ***Submitted***.

Other publications/preprints without peer review:

53. Poulsen, A., Jang, D., Khan, M., Al-Mohtaseb, Z. N., Chen, M., **Zhan, X.**, Banerjee, K., Scott, I. U. and Pantanelli, S. M. (2020). Repeatability of a Dual-Scheimpflug Placido Disc Corneal Tomographer/Topographer in Eyes with Keratoconus. medRxiv. https://doi.org/10.1101/2020.05.13.20067710.

RESEARCH SUPPORT

Current support:

1. **Title:** National Key Technology Research and Development Program For Early Stage Investigators (ESI)
   Source: Ministry of Science and Technology of China-2022YFA1305400
   Role: Co-I (PI: Xiang L. of Wuhan University)
   Period: 12/01/2022 – 11/30/2027
   Awarded: CNY 5,000,000 (my sub-award amount is CNY 500,000)
   Purpose: This project supports an ESI to build an independent research program in the area of biomacromolecule and microbiology.
2. **Title:** Novel statistical methods and theories for high-dimensional microbiome compositional data analysis
   Source: NSFC-12371287
   Role: PI
   Period: 01/01/2024 – 12/31/2027
   Amount: CNY 435,000 (direct cost)
   Purpose: This project aims to develop new statistical methods and theories for high-dimensional microbiome compositional data analysis.

Previous support:

1. **Title:** Novel statistical methods for controlled variable selection of microbiome data
   Source: NIH-R21AI144765
   Role: PI
   Period: 03/01/2020 – 02/28/2022 (my part terminated on June 30, 2021)
   Awarded: $ 412,329
   Purpose: This project aims to identify microbial features that are associated with outcomes of interest with finite-sample performance guarantee.
2. **Title:** Collaborative Research: New Methods, Theory and Applications for Nonsmooth Manifold-Based Learning
   Source: NSF-DMS1953189
   Role: Co-PI (Multiple-PIs: Xue and Zhan)
   Period: 06/01/2020 – 05/31/2023 (my part terminated on June 30, 2021)
   Awarded: $200,000
   Purpose: This project aims to develop new methods and theories for analysis of complex and large modern data sets.
3. **Title:** Data Coordinating Center for the Type 1 Diabetes in Acute Pancreatitis Consortium (T1DAPC)
   Source: NIH-U01DK127384
   Role: Co-I (PI: Chinchilli)
   Period: 09/17/2020 – 07/31/2025 (my part terminated on June 30, 2021)
   Awarded: $11,426,874
   Purpose: The DCC provides biostatistical leadership, scientific coordination, data management, computer infrastructure, and data quality assurance for the T1DAPC.

SELECTED ORAL PRESENTATIONS

Departmental Seminars:

1. “Statistical methods for microbiome data sciences”
   Academy of Mathematics and Systems Science, Chinese Academy of Sciences, Beijing, China (November 3, 2022)
2. “From microbiome-wide association analysis to causal microbial feature identification”
   Webinar for Microbiome Research-In-Progress Working Group, University of Colorado, Denver, USA (April 26, 2022)
3. “Statistical methods for microbiome association analysis”
   — Center for Statistical Science, Tsinghua University, Beijing, China. (December 6, 2021)
   — Center for Statistical Science, Peking University, Beijing, China. (November 11, 2021)
   — Institute of Statistics and Big Data, Renmin University of China, Beijing, China. (October 29, 2021)
4. “Opportunities and limits of microbiome data analysis”
   Webinar for the Spring 2021“Recent Topics in Research methods Seminar Series” of Penn State University Park Clinical and Translational Science Institute (March 30, 2021).
5. “Statistical methods and computational tools for analysis of next-generation omics data”
   Webinar at the Department of Biostatistics, Peking University. (January 7, 2021)
6. “Big data, Big challenges and Big opportunities”
   Webinar at the School of Health Sciences, Wuhan University. (December 8, 2020)
7. “Next-Generation Statistical Variable Selection with Application to Microbiome Data Analysis”
   Webinar at the Microbiome Working Group in Department of Biostatistics at the Johns Hopkins University. (March 12, 2020)
8. “Next-Generation Statistical Methods for Association Analysis of Now-Generation Sequencing Studies”
   — Department of Statistics and Data Science, Southern University of Science and Technology (SUSTech), ShenZhen. (January 5, 2020)
   — College of Biological Sciences and Technology, Beijing Forestry University (BFU). Beijing. (December 26, 2019)
9. “Fine-Mapping the Microbiome with Confidence”
   2019 Annual Bioinformatics and Genomics Retreat, Huck Institutes of the Life Sciences, University Park, PA. (September 27, 2019)
10. “An Introduction to Microbiome Data Analysis”
    Biostatistics, Epidemiology and Research Design (BERD) Seminar Series, Penn State Clinical and Translational Science Institute (CTSI), Hershey, PA. (December 11, 2018)
11. “Statistical Methods for Microbiome Association Analysis: from Global to Local”
    Penn State Microbiome Center, University Park, PA. (October 26, 2018)
12. “Statistical Methods for Inference in “Omics” Data”
    — Department of Biostatistics and Epidemiology, College of Public Health, University of Oklahoma Health Sciences Center, Oklahoma City, OK. (April 18, 2017)
    — Department of Epidemiology and Biostatistics, School of Public Health, SUNY, Albany, NY. (April 12, 2017)

— Department of Public Health Sciences, College of Medicine, the Pennsylvania State University, Hershey, PA. (March 29, 2017)
— Biostatistics Shared Resource, University of New Mexico Comprehensive Cancer Center. Albuquerque, NM. (March 21, 2017)

13. "A fast small-sample kernel independence test with application to microbiome data"
— Department of Mathematics & Statistics , University of Nevada, Reno, NV. (February 21, 2017)
— Department of Mathematical Sciences, Michigan Technological University, Houghton, MI. (February 16, 2017)

14. "Statistical methods for multivariate association analysis of microbiome community data"
Division of Biostatistics, Medical College of Wisconsin, Milwaukee, WI. (February 3, 2017)

15. "Kernel methods for high-dimensional omics data"
ATME (Analysis Tools and MEthods for high-throughput genomic data) Affinity Group, Fred Hutchinson Cancer Research Center, Seattle, WA. (October 27, 2016)

16. "Measuring and testing independence by KRV coefficient with application to genome-wide association studies"
Department of Statistics, Pennsylvania State University, University Park, PA. (February 21, 2016)

17. "Kernel machine approaches in association analysis of '-omics' data"
Department of Mathematics and Statistics, Texas Tech University, Lubbock, TX. (February 10, 2015)

18. "Kernel machines: an overview and applications to high-throughput data"
The Jackson Laboratory & University of Connecticut Health Center, Farmington, CT. (January 6, 2015)

Conference Presentations:

1. "Compositional Variable Selection in Quantile regression for microbiome data with FDR control"
Invited presentation at 2023 ICSA China Conference, Chengdu, China (July 1,2023)

2. "Novel Statistical Methods for High-dimensional Microbiome Compositional Data Analysis"
–Invited presentation at the High-dimensional Statistics Branch of Chinese Association for Applied Statistics 2023 meeting, Changsha, China (May 21, 2023)
–Invited presentation at 2023 Statistics and Data Science Frontiers Forum by Tianyuan Mathematical Center in Southeast China, Xiamen, China (July 30, 2023)
–Invited presentation at the Statistical Interdisciplinary Branch of Chinese Association for Applied Statistics 2023 meeting, Kunming, China (August 9, 2023)

3. "Statistical methods for microbiome data sciences"
Invited presentation at PKU 2022 Statistical Sciences Forum. (November 12, 2022)

4. "Variable Selection Analysis for Finite-Sample Microbiome Compositional Data"
–Invited presentation at 2022 National Conference of Computational Biology and

Bioinformatics (NCCBB), Guangzhou, China (July 23, 2022)
–Invited presentation at 2022 ICSA China Conference, Xi'an, China (July 3, 2022)

5. "Compositional knockoff filter for high–dimensional regression analysis of microbiome data"
   – Invited presentation at ICSA Applied Statistics Symposium virtual meeting (September 12, 2021)
   – Topic-contributed presentation at JSM virtual meeting (August 12, 2021)
   – Invited presentation at ENAR virtual meeting (March 17, 2021)

6. "Powerful adaptive microbiome differential abundance analysis"
   Invited presentation at ICSA Applied Statistics Symposium, Raleigh, NC. (June 9, 2019)

7. "An Adaptive Multivariate Two-Sample Test with Application to Microbiome Differential Abundance Analysis"
   ENAR, Philadelphia, PA. (March 24, 2019)

8. "A fast small-sample kernel independence test with application to microbiome community-level association analysis"
   Topic contributed presentation at JSM, Baltimore, MD. (August 2, 2017).

9. "Associating microbiome community composition to multivariate complex outcomes"
   Invited presentation at ICSA Applied Statistics Symposium, Chicago, IL. (June 27, 2017)

10. "A novel kernel-based CNV association analysis with application to autism spectrum disorders studies"
    Invited presentation at 2016 International Conference for Japanese Society of Computational Statistics (JSCS) 30th Anniversary, Seattle, WA. (October 16, 2016)

11. "MMiRKAT: kernel-based association test on microbiome profiling studies with multiple outcomes"
    Topic contributed presentation at JSM, Chicago, IL. (August 2, 2016)

12. "KRV-based association analysis for genome-wide association studies with complex multivariate traits"
    ENAR, Austin, TX. (March 9, 2016)

13. "A Kernel Machine Approach for Metabolomics"
    JSM, Boston, MA. (August 5, 2014).

14. "Adaptive Double Least Squares Kernel Machine Score Test for Genetic Pathway Effect"
    ENAR, Baltimore, MD. (March 17, 2014)

15. "Incorporating auxiliary information using combinations of kernel machines"
    JSM, Montreal, Quebec, Canada. (August 7, 2013)

SELECTED BIOMEDICAL ABSTRACTS & POSTERS

1. Nolan, Z., Banerjee, K.,Cong, Z., Gettle, S., Longenecker, A., **Zhan, X.**,, Imamura, Y., Zaenglein, A., Thiboutot, D., and Nelson, A. "Isotretinoin Disrupts Skin Microbiome Composition and Metabolic Function After 20 Weeks of Therapy". Society for Investigative Dermatology (SID) 2021 Virtual Meeting (May 3–8, 2021).

2. Peterson, B., Banerjee, K., **Zhan, X.**, and Foy, A. “Patients With Prior Myocardial Infarction or Prior Percutaneous Coronary Intervention Have Increased Perioperative Mortality and Adverse Cardiac Events Following Bariatric Surgery”. American Heart Association (AHA) 2019 Scientific Sessions, Philadelphia, PA. (November 16–17, 2019).
3. Scipioni, A., **Zhan, X.**, Hicks, S. D., Ornstein R. M. “Salivary microbiome in adolescents with anorexia nervosa”. Society for Adolescent Health and Medicine (SAHM) 2019 Annual Meeting, Washington, DC (March 6–9, 2019).
4. Schneider, AM., Cook., LC., **Zhan, X.**, Banerjee, K., Cong, Z., Imamura-Kawasawa, I., Gettle, S., Longenecker, A., Kirby, JS., Nelson AM. “Microbiome of Hidradenitis”. International Investigative Dermatology (IID) 2018 Annual Meeting, Orlando FL (May 16–19, 2018).
5. Mitchell, C., Srinivasan, S., **Zhan, X**., Wu, M., Reed, S., Guthrie, K., LaCroix, A., Fiedler, T., Munch, M., Liu, C., Hoffman, N., Blair, I., Newton, K., Freeman, E., Joffe, H., Cohen, L., Fredricks. D. “Associations Between Serum Estrogen, Vaginal Microbiota and Vaginal Glycogen in Postmenopausal Women”. Infectious Diseases Society for Obstetrics and Gynecology (IDSOG) 2016 Annual Meeting. Annapolis, MD (August 11–13, 2016).

Teaching Experience

Department of Statistics, Eberly College of Science, PSU
(**SRTE**=**S**tudent **R**ating of **T**eaching **E**ffectiveness)

- STAT 301 (Statistical Analysis I), Fall 2014 (Role: Sole-Instructor)
  Enrollment: 34 Undergraduate students from various disciplines, SRTE Course: 6.22/7, Instructor: 5.67/7

Department of Public Health Sciences, College of Medicine, PSU

- PHS 520 (Principles of Biostatistics), Multiple Semesters (Role: Sole-Instructor)
  – (Fall 2017) Enrollment: 12 PhD/DrPH/MD students from various disciplines, SRTE Course: 6.00/7, Instructor: 6.33/7
  – (Fall 2018) Enrollment: 4 PhD/DrPH/MD students from various disciplines, SRTE Course: 5.33/7, Instructor: 6.00/7

- PHS 520 (Principles of Biostatistics–online class), Fall 2019 (Role: Sole-Instructor)
  Enrollment: 20 students from the Integrated Undergraduate-Graduate (IUG) BS-MPH Program of various disciplines, SRTE Course: 4.33/7, Instructor: 4.22/7

- PHS 523 (Multivariate analysis), Fall 2020 (Role: Sole-Instructor)
  Enrollment: 4 students from the Biostatistics PhD Program, SRTE Course: 5.25/7, Instructor: 5.5/7

Health Science Center, PKU

- 89330044 (Biostatistics), Fall 2022 (Role: Sole-Instructor)
  Enrollment: 14 Undergraduate students from various medical disciplines, SRTE Course: 96/100, Instructor: 99/100

- 89330045 (Advanced Biostatistics), Spring 2023 (Role: Sole-Instructor)
  Enrollment: 14 Undergraduate students from various medical disciplines, SRTE Course: pending, Instructor: pending

STUDENT ADVISING

Doctoral Dissertation Directed or Co-Directed:

- Kalins Banerjee, PSU Biostatistics, Fall 2018– Summer 2021 (Placement: Postdoc researcher in Department of Biostatistics at University of Michigan)
- Yicong Mao, PKU Biostatistics, Fall 2022–present

Doctoral Dissertation Committee Served:

- Amal Agarwal, Statistics, Summer 2017–Summer 2020 (Advisor: Xue L.)
- Arun Srinivasan, Statistics, Fall 2018– Spring 2022 (Advisor: Xue L.)
- Lin Qiu, Biostatistics, Fall 2018– Spring 2021 (Advisors: Chinchilli V. and Lin L.)
- Chixiang Chen, Biostatistics, Summer 2019–Summer 2020 (Advisors: Wu R. and Wang M.)
- Zachary Nolan, Dermatology, Fall 2019– Spring 2022 (Advisor: Nelson A.)
- Bipin Rimal, Bioinformatics and Genomics, Summer 2020– Summer 2021 (Advisor: Patterson A.)

Lab Rotation Students ($\geq$ 3 months):

- Kalins Banerjee, Biostatistics PhD student, Spring 2018
- Arun Srinivasan, Statistics PhD student, Summer 2018
- Bingyuan Liu, Statistics PhD student, Summer 2018
- Jun Tao, Statistics PhD student, Summer 2019
- Amal Agarwal, Statistics PhD student, Summer 2019
- Zhiwen (Owen) Jiang, Biostatistics Master student, Fall 2020 and Spring 2021

Other Educational Programs and Outreach:

Integrative Analysis of Metabolic Phenotypes (IAMP) Predoctoral Training Program: This is a graduate research program supported by NIH (T32DK120509, PIs: Patterson and Perdew of PSU), aiming at building a new graduate program in metabolomics, genomics and bioinformatics within the Huck Institutes of Life Sciences at the Penn State University (my role in this program is Training Faculty 06/01/2020-06/30/2022).

SERVICE

Penn State University

Outreach:
Consultant, PSU Statistics Consulting Service, 6 consultees helped (2012-2013)
Consultant, PSU Biostatistics Consulting Service, 20 consultees helped (2017-2021)

Administrative Services:
Biostatistics PhD Admissions Committee: 2017–2018
Biostatistics Student Rotations Committee: 2017–2018
PHS Curriculum Peer Review Task Force: 2019 Fall
Faculty Recruitment: 2020 Spring

Peking University

Outreach:
Teaching Faculty, 3+X discussion class for undergraduates in SMS, 2022 Spring

Administrative Services:
Organizer, Weekly Seminar Series in Dept. of Biostatistics at PKU: 2022 Spring–present

External

Funding Agency Services:
Mail Reviewer, NIH institutional KL2 Program, 2020 March

Editorial Services:
Associate Editor: Biostatistics & Epidemiology (The Official Journal of IBS-China) (2021-present)
Editorial Board: Frontier in Genetics, Section of Statistical Genetics and Methodology (2020-present)

Referee Services:
Annals of Applied Statistics
Bioinformatics (3), Biometrics (4), Biometrika (2), Biostatistics, Biostatistics & Epidemiology (10), BMC Bioinformatics (4)
Computational and Structural Biotechnology Journal, Current Pharmaceutical Design
Frontiers in Genetics (3)
Genetic Epidemiology (3)
JASA, Journal of Molecular Biology
Nature Communications, Nucleic Acids Research (2)
PeerJ (2), PLOS Genetics, PLOS ONE
Scientific Reports (3), Statistics in Biosciences (2), Statistics in Medicine
The Pharmacogenomics Journal

Professional Community Services:

- Chair, Contributed Session #667 “Statistics in Genomics and Genetics”. JSM 2017, Baltimore, MD
- Organizer, Invited Session #214 “Novel statistical methods for analysis of microbiome data”. ENAR 2019, Philadelphia, PA

- Chair, Invited Session #251 “Statistical advances in microbiome research from theory to application”. JSM 2020, Philadelphia, PA (moving virtual due to COVID-19)
- Organizer, Invited Session “Statistical Methods for Large-scale Omics Data”. ENAR 2021, Baltimore, MD (moving virtual due to COVID-19)
- Organizer, Topic-Contributed Session “Novel statistical methods for microbiome data analysis”. JSM 2021, Seattle, WA (moving virtual due to COVID-19)
- Judge (2 times), Best Student Paper Award Competition for China Annal Conference of Biostatistics (CACB) 2021-2022
- Judge (3 times), Section on Statistics in Genomics and Genetics (SGG) Student Paper Award Competition for JSM 2021-2023
- Committee Member, The Conference Advisory Committee of International Biometric Society (IBS), 2022-2025.
- Vice Secretary, Statistical Interdisciplinary Branch of Chinese Association for Applied Statistics (SIB-CAAS), 2023-present.

Professional Affiliations

American Statistician Association (ASA):	2010–present.
Chinese Mathematical Society, Section of Mathematics in Medicine:	2021–present.
Chinese Association for Applied Statistics (CAAS):	2024–present.
International Biometric Society, China Region:	2021–present.
International Biometric Society, East North America Region (ENAR):	2013–present.
International Chinese Statistician Association (ICSA):	2017–present.

Last updated on August 27, 2023