

Ni Zhao, M.D., Ph.D.

ACADEMIC APPOINTMENT	Associate Professor Department of Biostatistics, Johns Hopkins University 615 N Wolfe St, Room E3622 Baltimore, MD 21205	Aug 2016 to Present nzhao10@jhu.edu 402-955-9993
RESEARCH INTERESTS	Statistical Genetics & Genomics Metagenomics and microbiome research T/B-cell receptor sequencing studies Cancer Genomics, Collaborative Biomedical Research	
EDUCATION	Ph.D., Biostatistics, December 2013 University of North Carolina at Chapel Hill, Chapel Hill, NC. Thesis: Kernel Machine Methods for Analysis of Genomic Data from Different Sources Advisor: Michael C. Wu, Ph.D. M.S., Biostatistics, May 2012 University of North Carolina at Chapel Hill, Chapel Hill, NC. Thesis: eQTL Mapping Using RNA-seq Data Advisor: Wei Sun, Ph.D. M.S., Environmental Sciences and Engineering, Aug 2009 University of North Carolina at Chapel Hill, Chapel Hill, NC. Thesis: Genetic regulation of sex-specific gene expression in mouse liver Advisor: Ivan Rusyn, M.D., Ph.D. M.D., Preventive Medicine, July 2007 Fudan University, Shanghai, China.	
RESEARCH EXPERIENCE	Associate Professor of Biostatistics Department of Biostatistics, Bloomberg School of Public Health, Johns Hopkins University Baltimore, MD 21205	Apr 2022 to now
	Assistant Professor of Biostatistics Department of Biostatistics, Bloomberg School of Public Health, Johns Hopkins University Baltimore, MD 21205	Jul 2016 to Mar 2022
	Postdoctoral Research Fellow Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA, 98109 Supervisor: Michael C. Wu, Ph.D.	Jan 2014 to Aug 2016
	Graduate Research Assistant Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, 27599 Supervisor: D. Neil Hayes, M.D., M.S.	Jun 2009 to Dec 2013
	Graduate Research Assistant	Aug 2007 to May 2009

Department of Environmental Sciences and Engineering
University of North Carolina at Chapel Hill, Chapel Hill, NC, 27599
Supervisors: Ivan Rusyn, M.D., Ph.D.

Public Health Sciences Intern

Feb 2007 to May 2007

Shanghai Center for Disease Control and Prevention
Jing'an District, Shanghai, China

Medical Intern

Feb 2006 to Aug 2006

The Fifth People's Hospital of Shanghai,
Minhang District, Shanghai, China

PAPERS &
PUBLICATIONS

Published Peer-reviewed Papers: (* indicates corresponding author)

1. Song H., Ling, W., Zhao, N., Plantinga, A.M., Broedlow, C.A., Klatt, N.R., Hensley-McBain, T., "Accommodating Multiple Potential Normalizations in Microbiome Associations Studies". *BMC-Bioinformatics*. In Press
2. Li, M., Tyx, R.E., Rivera, A.J., Zhao, N.*, Satten, G.A.* What Can We Learn about the Bias of Microbiome Studies from Analyzing Data from Mock Communities? *Genes*, 2022, 13, 1758. <https://doi.org/10.3390/genes13101758>.
3. Ling, W., Lu, J., **Zhao, N.***, Lulla, A., Plantinga, A., Fu, W., Zhang, A., Liu, H., Song, H., Li, Z., Chen, J., Randolph, T., Koay, W.L., White, J., Launer, L.J., Fodor, A., Meyer, K., Wu, M.C.*. Batch effects removal for microbiome data via conditional quantile regression. *Nature Communication*, 13, 5418 (2022). <https://doi.org/10.1038/s41467-022-33071-9>.
4. Goedert, J., Wu, Z., Yonehara, C., Frankland, T., Sinha, R., Jones, G., Wan, Y., Ravel, J., Zhao, N., Honda, S., Reusing a prepaid health plan's fecal immunochemical tests for microbiome associations with colorectal adenoma. *Scientific Report*, 12, 14801 (2022). <https://doi.org/10.1038/s41598-022-18870-w>.
5. Mallick, H., An, L., Chen, M., Wang, P., **Zhao, N.** Methods for Single-Cell and Microbiome Sequencing Data (Editorial). *Frontiers in Genetics*, 2022. <https://doi.org/10.3389/fgene.2022.920191>.
6. Jiang, Z., He, M., Chen, J., **Zhao, N***, Zhan, X.*. MiRKAT-MC: A Distance-Based Microbiome Kernel Association Test With Multi-Categorical Outcomes. *Frontiers in Genetics*, 13:841764 (2022). doi: 10.3389/fgene.2022.841764.
7. Zhang, Y., D'Sourza, G., Fakhry, C., Bigelow, E., Usyk, M., Burk, R., **Zhao, N***. Oral HPV associated with differences in oral microbiota beta diversity and microbiota abundance. *The Journal of Infectious Diseases*. In press.
8. Mirzayi, C., Renson, A., . . . , **Zhao, N.**, . . . , Waldon L. Reporting guidelines for human microbiome research: the STORMS checklist. *Nature Medicine*. 2021. In press. <https://doi.org/10.1038/s41591-021-01552-x>.
9. **Zhao, N.**, Khamash, D., Koh, H., Voskertchian, A., Egbert, E., Mongodin, M., White, J., Hittle, L., Colantouni, E., Milstone, A. Low Diversity in Nasal Microbiome Associated with *Staphylococcus aureus* Colonization and Bloodstream Infections in Hospitalized Neonates. *Open Forum Infectious Diseases*. 2021. In press.
10. Ling, W., **Zhao, N.**, Plantinga, A. M., Launer, L., Fodor, A. A., Meyer, K., Wu, M. C. "Powerful and robust non-parametric association testing for microbiome data via a zero-inflated quantile approach (ZINQ)". *Microbiome* 9, 181. 2021. <https://doi.org/10.1186/s40168-021-01129-3>.
11. Sinha, R., **Zhao, N.**, Goedert, J., Byrd, D.A., Wan, Y., Hua, L., Hullings, A., Knight, R., Breda, S., Mathijs, k., Kok, T.M., Ward, M. "Effects of processed meat and drinking water nitrate on oral and fecal microbial populations in a controlled feeding study". *Environmental Research*, 2021 Mar 27;197:111084. doi: 10.1016/j.envres.2021.111084.

12. Koh, H., Tuddenham, S., Sears, C., **Zhao, N***. “Meta-analysis methods for multiple related markers: applications to microbiome studies with the results on multiple α -diversity indices”. *Statistics in Medicine*, 2021 Mar 25. doi: 10.1002/sim.8940.
13. Wilson, N., **Zhao, N.**, Zhan, X., Koh, H., Fu, W., Chen, J., Li, H., Wu, M. C., Plantinga, A. M. MiRKAT: Kernel machine Regression-Based global association tests for the microbiome. *Bioinformatics* . btaa951, (2020). <https://doi.org/10.1093/bioinformatics/btaa951>
14. Binka, E., **Zhao, N.**, Wood, S., Zimmerman, S., Thompson, R. “Exercise-induced Abnormalities of Regional Myocardial Deformation in Anomalous Aortic Origin of the Right Coronary Artery.” *World Journal for Pediatric and Congenital Heart Surgery*, 11(6), 712-719(2020).
15. Koh, H., **Zhao, N***. “A powerful microbial group association test based on the higher criticism analysis for sparse microbial association signals”. *Microbiome*, 8, 63 (2020).
16. Zhang, H., Ahearn, T.U., Lecarpentier, J. . . . , **Zhao, N.** . . . , “Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses”. *Nature Genetics*, 52, 572-581 (2020).
17. Zhang, H., **Zhao, N***, Mehrotra, D., Shen, J*.”Composite Kernel Association Test (CKAT) for SNP-set joint assessment of genotype and genotype-by-treatment interaction in Pharmacogenetics studies”. *Bioinformatics*, 36, 3162-3168 (2020)
18. Zhang, H., **Zhao, N.**, Ahearn, T U., Garcia-Closas., M., Chatterjee, N “A mixed model approach for powerful testing of genetic association with cancer risk incorporating tumor characteristics.” *Biostatistics*. 2020 Feb; kxz065. <https://doi.org/10.1093/biostatistics/kxz065>.
19. Zhang, J., Ji, Z., Caushi, J., Asmar, M.E., Anagnostou, V., Cottrell, T., Chan, H.Y., Suri, P., Guo, H., Merghoub, T., Chافت, J., Reuss, J., Tam, A., Blosser, R., Abu-Akeel, M., Sidhom, J., **Zhao, N.**, Ha, J., Jones, D., Marrone, K., Naidoo, J., Gabrielson, E., Taube, J., Velculescu, V., Brahmer, J., Housseau, F., Hellmann, M., Forde, P., Pardoll, D., Ji, H., Smith, K. “Compartmental analysis of T cell clonal dynamics as a function of pathologic response to neoadjuvant PD-1 blockade in resectable non-small cell lung cancer.” *Clinical Cancer Research*. 2019 Nov; DOI: 10.1158/1078-0432.CCR-19-2931.
20. Mathews, S., **Zhao, N.**, Holub, J., Lieberman, D. “Improvement in Colonoscopy Quality Metrics in Clinical Practice from 2000 to 2014.” *Gastrointestinal Endoscopy*. 2019 Oct; 90(4):651-655.e3.
21. Koh, H., Li, Y., Zhan, X., Chen, J., **Zhao, N***. (2019)“A distance-based kernel association test based on the generalized linear mixed model for correlated microbiome studies.” 458(10) *Frontiers in Genetics*. <https://doi.org/10.3389/fgene.2019.00458>
22. Lampe, J., Kim, E., Levy, L., Davidson, L., Goldsby, J., Miles, F., Navarro, S., Randolph, T., **Zhao, N.**, Ivanov, I., Kaz, A., Damman, C., Hockenbery, D., Hullar, M., Chapkin R. “Colonic mucosal and exfoliome transcriptomic profiling and fecal microbiome response to a flaxseed lignan extract intervention in humans.” *American Journal of Clinical Nutrition*. 2019 Aug; 110(2): 377-390.
23. Banerjee, K., **Zhao, N.**, Srinivasan, A., Xue, L., Hicks, S., Middleton, F., Wu, R., Zhan, X. (2019). “An adaptive multivariate two-sample test with application to microbiome differential abundance analysis.” 350(10) *Frontiers in Genetics*, <https://doi.org/10.3389/fgene.2019.00350>
24. Tuddenham, S., Koay, W., **Zhao, N.**, White J.R., Ghanem, Khalil., Sears, c., and the HIV Microbiome Re-analysis Consortium. (2019). “The Impact of HIV Infection on Gut Microbiota Alpha-Diversity: an Individual Level Meta-analysis.” *Clinical Infectious Diseases* doi:10.1093/cid/ciz258. (**media report**: www.medpagetoday.com/reading-room/idsa/general-infectious-diseases/79261)
25. **Zhao, N***, Maity. A., Wu M.C “Composite Kernel Machine Regression based on Likelihood Ratio Test and its Application on Genomic Studies.” *Biometrics*, 2018; 1-13. doi:10.1111/biom.13003
26. Zhan, X., Xue, L., Zheng, H., Planitinga, A., Wu, M C., Schaid, D J., **Zhao, N***, Chen, J.* “A small-sample kernel association test for correlated data with application to microbiome association studies.” *Genetic Epidemiology*. 2018; 42(8):772-782. doi: 10.1002/gepi.22160

27. **Zhao, N.***, Zhan, X., Guthrie, KA., Mitchell, CM., Larson, J. “Generalized Hotellings test for paired compositional data with application to human microbiome studies.” *Genetic Epidemiology*. 2018; 1-11. <https://doi.org/10.1002/gepi.22127>
28. **Zhao, N.***, Zhan, X., Huang, YT., Almli, L., Smith. A, Epstein. MP, Conneely, K., Wu M.C “Kernel Machine Methods for Integrative Analysis of Genome-Wide Methylation and Genotyping Studies.” *Genetic Epidemiology* . 2017 Dec; <https://doi.org/10.1002/gepi.22100>. (**Highlighted by IGES March 2018**)
29. Zhan,X., **Zhao, N.**, Plantinga, A., Thornton, TA., Conneely, K., Epstein, MP., Wu M.C ”Powerful Genetic Association Analysis for Common or Rare Variants with High Dimensional Structured Traits.” *Genetics*, 2017 Jun, <https://doi.org/10.1534/genetics.116.199646>
30. Zhan, X., Plantinga, A., **Zhao, N.**, Wu, M. C. ”A fast small-sample kernel independence test with application to microbiome association studies.” *Biometrics*, 2017 Mar, <https://doi.org/10.1111/biom.12684>
31. Plantinga, A., Zhan, X., **Zhao, N.**, Chen, J., Jenq, R., Wu, M. C. “MiRKAT-S: A community-level test of association between the microbiota and survival times.” *Microbiome*. 2017 Jan, DOI: 10.1186/s40168-017-0239-9
32. Zhan, X., Tong, X., **Zhao, N.**, Maity, A., Wu, M. C., Chen, J. “A small-sample multivariate kernel machine test for microbiome association studies”. *Genetic Epidemiology*, 2016 Dec, DOI: 10.1002/gepi.22030
33. Zhan, X., Girirajan, S., **Zhao, N.**, Wu, M. C., Ghosh, D.“ A novel copy number variants kernel association test with application to autism spectrum disorders studies”. *Bioinformatics*, 2016. 32 (23): 3603-3610.
34. He, Q., Cai, T., Liu, Y.,Zhao, N., Harmon, Q., Almli, L., Binder, EB., Engel, S., Ressler, K., Conneely, k., Lin, X., Wu, M C. “Prioritizing Individual Genetic Variants After Kernel Machine Testing Using Variable Selection”. *Genetic Epidemiology*, 2016 Aug 3. doi: 10.1002/gepi.21993.
35. Chen, J., Chen, W., **Zhao, N.**, Wu, M. C., Schaid D. J. “Small-Sample Kernel Association Tests for Human Genetic and Microbiome Association Studies”. *Genetic Epidemiology*, 2016 Jan;40(1):5-19. doi: 10.1002/gepi.21934.
36. Urrutia, E., Lee, S., Maity, A., **Zhao, N.**, Shen, J., Li,Y., Wu, M. C. “Rare variant testing across methods and thresholds using the multi-kernel sequence kernel association test (MK-SKAT)”. *Statistics and Its Interface*. 2015; 8(4): 495505.
37. **Zhao, N.**, Chen, J., Carroll, I. M., Ringel-Kulka, T., Epstein, M. P., Zhou, H., Zhou, J. J., Ringel Y., Li, H., Wu, M. C. (2015) “Testing in Microbiome Profiling Studies with the Microbiome Regression-based Kernel Association Test (MiRKAT)”. *American Journal of Human Genetics*, 96, 797-807.
38. Moye, V. A., Chandramouleeswaran, S., **Zhao, N.**, Muss, H. B., Weissler, M. C., Hayes, D. N., Zevallos, J. P. (2015). “Elderly Patients With Squamous Cell Carcinoma of the Head and Neck and the Benefit of Multimodality Therapy”. *The Oncologist*, 20:159-165.
39. The Cancer Genome Atlas Network: **Zhao, N.** (RNA analysis, Gene Mutation) (2015). “Comprehensive genomic characterization of head and neck squamous cell carcinomas”. *Nature*, 517, 576 - 582.
40. **Zhao, N.**, Bell, D. A., Maity, A., Staicu, A., Joubert, B. R., London, S. J., Wu, M. C., (2014). “Global Analysis of Methylation Profiles from High Resolution CpG Data”. *Genetic Epidemiology*, 39, 2, 53 - 64.
41. The Cancer Genome Atlas Network: **Zhao, N.** (miRNA analysis). (2014). “Integrated Genomic Characterization of Papillary Thyroid Carcinoma”. *Cell*, 159, 676 - 690.
42. Parfenov, M., Pedamallu, C. S., Gehlenborg, N., Freeman, S. S., Danilova, L., Bristow, C. A., Lee, S., Hadjipanayis, A. G., Ivanovab, E. V., Wilkerson, M. D., Protopopov, A., Yang, L., Seth, S., Song, X., Tang, J., Ren, X., Zhang, J., Pantazi, A., Santoso, N., Xu, A. W., Mahadeshwar, H., Wheeler, D. A., Haddad, R. I., Jung, J., Ojesina, A., Issaeva, N., Yarbrough, W. G., Hayes, N. D., Grandis, J. R., El-Naggar, A. K., Meryerson, M., Park, P. J., Chin, L., Seidman, J. G., Hammerman,

- P. S., Kucherlapati, R., The Cancer Genome Atlas Network: (**Zhao, N.**). (2014). "Characterization of HPV and host genome interactions in primary head and neck cancers". *Proceedings of the National Academy of Sciences*, 111 (43), 15544 - 15549.
43. **Zhao, N.**, Wilkerson, M. D., Shah, U., Yin, X.Y., Wang, A., Hayward, M. C., Roberts, P., Lee, C. B., Parsons, A. M., Thorne, L. B., Haithcock, B. E., Grilley-Olson, J., Stinchcombe, T. E., Funkhouser, W. K., Wong, K. K., Sharpless, N. E., Hayes, D. N. (2014). "Alterations of *LKB1* and *KRAS* and Risk of Brain Metastasis: Comprehensive Characterization by Mutation Analysis, Copy Number, and Gene Expression in Non-Small-Cell Lung Carcinoma". *Lung Cancer*, 86, 225-261.
 44. Kimes, P. K., Cabanski, C. R., Wilkerson, M. D., **Zhao, N.**, Johnson, A. R., Perou, C. M., Makowski, L., Maher, C. A., Liu, Y., Marron, J., et al. (2014). "SigFuge: single gene clustering of RNA-seq reveals differential isoform usage among cancer samples". *Nucleic Acids Research*, doi: 10.1093/nar/gku521.
 45. Patel, M. R., **Zhao, N.**, Ang, M.-K., Stadler, M. E., Fritch, K., Weissler, M. C., Zanation, A. M., Harris, S. L., Funkhouser, W. K., Olshan, A. F., Shores, C. G., Hayes, D. N. (2013). "ERCC1 protein expression is associated with differential survival in oropharyngeal head and neck squamous cell carcinoma". *Otolaryngology-Head and Neck Surgery*, doi:10.1177/0194599813496522.
 46. Walter, V., Yin, X., Wilkerson, M. D., Cabanski, C. R., **Zhao, N.**, Du, Y., Ang, M. K., Hayward, M. C., Salazar, A. H., Hoadley, K. A., et al. (2013). "Molecular subtypes in head and neck cancer exhibit distinct patterns of chromosomal gain and loss of canonical cancer genes". *PLoS one*, doi: 10.1371/journal.pone.0056823.
 47. Nakada, Y., Stewart, T. G., Peña, C. G., Zhang, S., **Zhao, N.**, Bardeesy, N., Sharpless, N. E., Wong, K.-K., Hayes, D. N., and Castrillon, D. H. (2013). "The LKB1 tumor suppressor as a biomarker in mouse and human tissues". *PLoS One*, 2013;8(9):e73449.
 48. **Zhao, N.**, Ang, M. K., Yin, X., Patel, M. R., Fritch, K., Thorne, L., Muldrew, K. L., Hayward, M. C., Sun, W., Wilkerson, M. D., Chera, B. S., Hackman, T., Zanation, A. M., Grilley-Olson, J. E., Couch, M. E., Shockley, W. W., Weissler, M. C., Shores, C. G., Funkhouser, W. K., Olshan, A. F., Hayes, D. N. (2012). "Different cellular p16^{INK4a} localisation may signal different survival outcomes in head and neck cancer". *British Journal of Cancer*, 107, 482-490.
 49. Wilkerson, M. D., Yin, X., Walter, V., **Zhao, N.**, Cabanski, C. R., Hayward, M. C., Miller, C. R., Socinski, M. A., Parsons, A. M., Thorne, L. B., Haithcock, B. E., Veeramachandani, N. K., Funkhouser, W. K., Hayes, D. N. (2012). "Differential pathogenesis of lung adenocarcinoma subtypes involving sequence mutations, copy number, chromosomal instability, and methylation". *PLoS One*, doi: 10.1371/journal.pone.0036530.
 50. Hayes, D. N., Lucas, A. S., Tanvetyanon, T., Krzyzanowska, M. K., Chung, C. H., Murphy, B. A., Gilbert, J., Mehra, R., Moore, D. T., Sheikh, A., Hoskins, J., Hayward, M. C., **Zhao, N.**, O'Connor, W., Weck, K. E., Cohen, R. B. (2012). "Phase II efficacy and pharmacogenetic study of Selumetinib (AZD6244; ARRY-142886) in iodine-131 refractory papillary thyroid carcinoma with or without follicular elements". *Clinical Cancer Research*, 18, 2056-2065.
 51. Ang, M.-K., Patel, M. R., Yin, X.-Y., Sundaram, S., Fritch, K., **Zhao, N.**, Liu, Y., Freermerman, A. J., Wilkerson, M. D., Walter, V., Weissler, M. C., Shockley, W. W., Couch, M. E., Zanation, A. M., Hackman, T., Chera, B. S., Harris, S. L., Miller, C. R., Thorne, L. B., Hayward, M. C., Funkhouser, W. K., Olshan, A. F., Shores, C. G., Makowski, L., Hayes, D. N. (2011). "High XRCC1 protein expression is associated with poorer survival in patients with head and neck squamous cell carcinoma". *Clinical Cancer Research*, 17, 6542-6552.
 52. Nelson, J. S., Allen, L. D., Parker, L. A., Hayward, M. C., **Zhao, N.**, Hayes, D. N. (2011). "Early Brain Recurrences are Potentially Detectable in Asymptomatic, Early Stage Lung Adenocarcinoma". *Clinical Oncology*, 23, 718-720.
 53. Gatti, D. M., **Zhao, N.**, Chesler, E. J., Bradford, B. U., Shabalin, A. A., Yordanova, R., Lu, L., and Rusyn, I. (2010). "Sex-specific gene expression in the BXD mouse liver". *Physiological Genomics*, 42, 456-468.

54. Huang, W., Tan, J., Kan, H., **Zhao, N.**, Song, W., Song, G., Chen, G., Jiang, L., Jiang, C., Chen, R., Chen, B. (2009). “Visibility, air quality and daily mortality in Shanghai, China”. *Science of the Total Environment*, 407, 3295–3300.
55. Cao, J., Cheng, Y., **Zhao, N.**, Song, W., Jiang, C., Chen, R., and Kan, H. (2008). “Diurnal temperature range is a risk factor for coronary heart disease death”. *Journal of Epidemiology/Japan Epidemiological Association*, 19, 328–332.

Published Book chapters: (* indicates corresponding author)

1. **Zhao, N***, Satten, G., “Log-linear model for modeling for biases in microbiome studies.” Springer 2020

PATENTS

1. Hayes, D. N., Wilkerson, M. D., Walter, V., **Zhao, N.** “Methods for Head and Neck Cancer Prognosis”, Dec. 27, 2013. WO patent App. PCT/US2013/046,136.
2. Hayes, D. N., **Zhao, N.** “*LKB1* Level and Brain Metastasis From Non-Small Cell Lung Cancer (NSCLC)” April 16, 2013. US Patent App. 13/863,842.

INVITED TALKS & PRESENTATIONS

1. “SMRmix for integrative analysis of microbiome beta diversity”. CMStatistics, London, United Kingdom. December 2022
2. “Integrative analysis of multiple microbiome studies”. Biostatistics Seminar, Fred Hutchinson Cancer Center. Seattle, USA. December 2022
3. “Integrative analysis of multiple microbiome studies”. 2nd International Congress on Spatial Life-course Health, Wuhan, China. December 2022.
4. “Gender equity in academic rewards– from a counterfactual lens”. 1st Delong International Public Health Forum, Shanghai, China. October 2022.
5. “Integrative analysis of multiple microbiome studies”. Bioinformatics Program, University of Guelph, Canada. October 2022.
6. “Integrative analysis of multiple microbiome studies”. Institute for Genome Sciences, University of Maryland, Baltimore. September 2022.
7. “Bias in microbiome sequencing studies and ways to handle it”. Department of Mathematics. University of Maryland at College Park. February 2022.
8. “What does you poop tells you and how to listen to it using statistics.” UCLA-biomathematics seminar series. October 2020.
9. “A powerful microbial group association test based on the higher criticism analysis.” virtual-JSM. August 2020.
10. “Community level association studies for microbiome data – in face of more complex study design”. ASA-BI-NESS Statistics Webinar Series. June 2020.
11. “A powerful microbial group association test based on the higher criticism analysis.” virtual-ENAR. March 2020.
12. “A benchmark study for differential abundance analysis in microbiome”. Microbiome working group, Fred Hutchinson Cancer Research Center. Seattle, WA 98109. February 2020.
13. “Kernel based approaches for microbiome association test in face of more-complex study designs”. Department of Biostatistics, Ohio State University. Columbus, OH 43210. November 2019.
14. “Kernel based approaches for microbiome association test in face of more-complex study designs”. Department of Biostatistics, Virginia Commonwealth University. Richmond, VA 23219. October 2019.
15. “A benchmark project for differential abundance testing in microbiome studies”. Banff International Research Station (BIRS) workshop. Banff, Alberta T1L 1H5, Canada. September 2019.

16. "Working with open-source Human Microbiome Project Data: Efficient Data Access and Analysis Workflow". BioC 2019 (Where Software and Biology Connect). New York City. June 2019.
17. "A robust distance-based kernel association test for correlated microbiome data." ICSA, Raleigh, NC. June 2019
18. "Generalized Higher Criticism Test for Microbiome Community Level Analysis." ENAR, Philadelphia, PA. March 2019
19. "Generalized Higher Criticism Test for Microbiome Community Level Analysis." Oncology Biostatistics/Bioinformatics Working Group. Johns Hopkins University. March, 2019.
20. "Community Level Analysis for Microbiome Data." 12th Annual Symposium on Genomics & Bioinformatics. Johns Hopkins University. Oct, 2018.
21. "MiRKAT- a Suite of Methods for Association Testing in Microbiome Profiling Studies incorporating Phylogenetic Structure." R-Ladies Baltimore. May 2018.
22. "Generalized Hotelling's Test for Paired Compositional Data", ICSA, Chicago, IL, June 2017.
23. "Analysis of Genomic Data via Likelihood Ratio Test in Composite Kernel Machine Regression", Joint Statistical Meeting, Seattle, WA, August 2015.
24. "Analysis of Genomic Data via Likelihood Ratio Test in Composite Kernel Machine Regression", ENAR, Miami, FL, March 2015.
25. "Kernel Machine Methods for Joint Testing in Genome Wide Methylation and Genotyping Studies", ICSA Applied Statistics Symposium, Portland, OR, June 2014.
26. "Global Analysis of Methylation Profiles via Kernel Machine Regression Framework", ENAR, Baltimore, MD, April 2014.

ACADEMIC ACTIVITIES

Organized Conference sessions

1. "Human Microbiome and Data Science", Modulator, AAAS 2022.
2. "Statistical Advances in Microbiome Research from Theory to Application". JSM 2020.
3. "Human Microbiome Studies: Novel Methods and New Studies". ENAR 2020.
4. "Recent Advances in Statistical Methodology for Analyzing Human Metagenomics Data", ICSA, Raleigh, NC. June 2019
5. "Human Microbiome Analysis: new study designs, novel methods, and practical considerations", ENAR, Atlanta, GA. March 2018
6. "Bugs, Bugs Everywhere - the Statistics Behind Our Microbiome", JSM, Vancouver, BC. August 2018
7. "Recent Methods and Tools in Analyzing Human Microbiome Data", JSM, Baltimore, MD. August 2017

SOFTWARE

1. Modeling microbiome biases using log-linear models (MicroBias).
 - <https://github.com/zhaoni153/MicroBias>
2. A distance-based kernel association test based on the generalized linear mixed model (GLMM-MiRKAT)
 - <https://github.com/hk1785/GLMM-MiRKAT>
3. Composite Kernel Machine Regression Based on Likelihood Ratio Test (CKLRT)
 - <https://cran.r-project.org/web/packages/CKLRT/index.html>
4. Small sample kernel association test for correlated data (SSKAT)
 - <https://github.com/jchen1981/SSKAT>
5. Microbiome regression-based kernel association test (MiRKAT)

- <https://cran.r-project.org/web/packages/MiRKAT/index.html>
6. Global analysis of methylation profiles from high resolution CpG data
- <https://research.fhrc.org/wu/en/software.html>
7. Generalized Hotelling's Test (GHT)
- <https://github.com/zhaoni153/GHT>

SERVICE

Board Member Regional Advisory Board Member, ENAR.
Chair Student paper award committee
 Statistics for Genomics and Genetics Session, ASA

Judge of

- ENAR student paper award
- JSM SGG student paper award

Review: Journals

- *American Journal of Statistical Association*
- *Genome Biology*
- *Biometrics*
- *Biostatistics*
- *Annals of Applied Statistics*
- *Genetics*
- *Genetic Epidemiology*
- *Bioinformatics*
- *PLoS-One*
- *Current Genomics*
- *Chinese Journal of Cancer*
- *BMC Genetics*
- *Theoretical Biology and Medical Modeling*
- *Cancer Biology & Medicine*
- *Frontiers in Genetics*
- *Microbiome*
- *JAMA Oncology*
- *Scientific Report*

Reviewer: Grants

- NIH ASPA study session. March 2023
- National Eye Institute. U24 "A Community Research Resource: Characterization of the Resident Ocular Microbiome." November 2022
- NIH BMRD study session (2021)
- Johns Hopkins Alzheimer's Disease Research Center Pilot Grant

Editor:

- Special issue of *Frontiers in Genetics*: "Statistical and Computational Methods for Microbiome Multi-Omics Data"
- Associate Editor of *Frontiers in Genetics*

TEACHING

- Third and Fourth Terms, 2021, 2022, 2023: Essentials of Probability and Statistical Inference III-IV (140.648-649)
- Fourth Term, 2018, 2019, 2020: Statistics for Genomics (140.688.01)
 - Received "outstanding student evaluations" in 2020.
- Fourth Term, 2018, 2020: Advanced Methods for Statistical Genetics and Genomics

CURRENT STUDENTS & POSTDOC	Mo Li (Postdoctoral fellow), Department of Biostatistics, Johns Hopkins University	Oct 2021 to Present
	Jiuyao Lu (PhD student), Department of Biostatistics, Johns Hopkins University	Aug 2021 to Present
	Runzhe Li (PhD candidate), Department of Biostatistics, Johns Hopkins University	Sep 2019 to Present
	Shuai Li (PhD student), (Joint advised with Dr. Hongkai Ji) Department of Biostatistics, Johns Hopkins University	Sep 2021 to Present
	Danwei Yao (ScM student), (Joint advised with Dr. Hongkai Ji) Department of Epidemiology, Johns Hopkins University	Sep 2021 to Present
	Debsurya De (PhD student), Applied Mathematics & Statistics Johns Hopking University	Dec 2022 to Present
PAST STUDENTS & POSTDOC	Yuehan Zhang (MHS, PhD from cancer epidemiology), – Current position: Associate at Analysis Group, Epidemiologist	August 2020 to May 2022
	Zhenyi Wu (MS, Applied Mathematics and Statistics), – Current position: PhD student, Purdue University	September 2019 to May 2020
	Mengyu He (MS, Biostatistics), – Current position: PhD student, Emory University	December 2019 to May 2021
	Hyunwook Koh (Postdoctoral Fellow) – Current position: Assistant professor of Biostatistics, State University of New York-Korea	May 2020
	Yue Cao (MS)	Graduation: May 2018
	Haoyu Zhang (PHD) – Current position: Primary investigator, Earl Stadtman Principal Investigator, National Cancer Institute.	Graduation: May 2019
	Haotian Zheng, (Undergraduate Intern) – Current position: PhD student at University of Pennsylvania	summer 2017
	Junxian Chen, (Undergraduate Intern)	summer 2018
	Yutong Li, (Undergraduate Intern)	summer 2018