Ziqiao Wang – Curriculum Vitae

Contact

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Education

The University of Texas MD Anderson UTHealth Graduate School (GSBS), Houston, TX   2016–2021
    Ph.D. in Biostatistics   GPA 4.0/4.0

Stony Brook University, Stony Brook, NY   2013-2015
    B. S., Double Majored in Mathematics **&** Applied Mathematics and Statistics   GPA 3.9/4.0
    Honors: Summa Cum Laude

Nanjing University, Nanjing, China   2011-2013
    B.S. in Mathematics   GPA 4.1/5.0

Professional Experience

Johns Hopkins University

- Postdoctoral Fellow, Department of Biostatistics   9/2022-

Eli Lilly and Company

- Advisor - Statistics, Statistics Data and Analytics, Early Phase Immunology   3/2022-8/2022
- Research Scientist - Statistician, Statistics Data and Analytics, Early Phase Immunology   6/2021-3/2022

The University of Texas MD Anderson Cancer Center

- Graduate Research Assistant, Department of Biostatistics   2016-2021
- Graduate Research Assistant, Department of Pathology   2018-2021

Merck & Co.

Summer Intern, Methodology Group, Biostatistics and Research Decision Science (BARDS)   5/2018-8/2018

Stony Brook University

- Teaching Assistant for Finite Mathematics Structures, Department of Applied Mathematics and Statistics
  Fall 2015
- Teaching Assistant for Data Analysis, Department of Applied Mathematics and Statistics   Summer 2015
- Peer tutor for college-level math courses, Department of Mathematics   Fall 2014-Spring 2015

Honors & Awards

- 2024-2025 Trans-Omics for Precision Medicine (TOPMed) Fellow (Award amount: $76,650)   NIH NHLBI
- 2020-2021 Andrew Sowell-Wade Huggins Scholarship in Cancer Research   GSBS
- 2020 Student Virtual Conference Award (*The American Society of Human Genetics* (**ASHG**) 2020)   GSBS
- 2020 Student Travel Award (*the Joint Statistical Meetings* (**JSM**) 2020)   QS program, GSBS
- 2019 Scholarship for Summer Institute in Statistical Genetics   University of Washington
- 2019 Student Travel Award (**JSM** 2019)   GSBS
- 2019 Student Travel Award (The International Biometric Society Eastern North American Region (**ENAR**) 2019 Spring Meeting)   QS program, GSBS
- 2018 Student Travel Award (Conference on Statistical Learning and Data Science / Nonparametric Statistics (**SLDS**) at Columbia University)   QS program, GSBS
- 2015 Outstanding Academic Achievement Award   Stony Brook University
- 2013-2015 Dean's List (Every Semester)   Stony Brook University
- 2013 Outstanding Leadership Honor   Nanjing University
- 2012 Ren Min Scholarship Academic Award   Nanjing University
- 2012 Scholarship for Outstanding Performance in Extra Curriculum Activities   Nanjing University

Peer Reviewed Publications

∗: Co-first Author.

1. **Wang, Z.**, Shi, W., Carroll, R., Chatterjee, N. (2024). Joint Modeling of Gene-Environment Correlations and Interactions Using Polygenic Risk Scores in Case-Control Studies. *American Journal of Epidemiology*. doi: 10.1093/aje/kwae081.

2. **Wang, Z.**, Lu, Y., Fornage, M., Jiao, L., Li, D., Wei, P. (2022). Identification of novel susceptibility methylation loci for pancreatic cancer in a two-phase epigenome-wide association study, *Epigenetics*. doi: 10.1080/15592294.2022.2026591.
(*Platform presentation, IGES 2019*).

3. **Wang, Z.**, Wei, P. (2020). IMIX: A Multivariate Mixture Model Approach to Association Analysis Through Multi-Omics Data Integration, *Bioinformatics*. doi:10.1093/bioinformatics/btaa1001.
(*Platform presentation, ASHG 2020*).

4. **Wang, Z.**, Chen, J. (2020). Testing for Trend in Benefit-Risk Analysis with Prioritized Multiple Outcomes. *Statistics in Biopharmaceutical Research*. doi: 10.1080/19466315.2019.1690037.

5. Xu, Y.*, **Wang, Z.***(*co-first author*), Wei, P., Gairola, R., Kelsey, K., Sikora, A., Li, G., Gu, J. (2022). Hypermethylation of nc886 in HPV-positive oropharyngeal cancer and its clinical implications: an epigenome DNA methylation profiling study. *Molecular Therapy-Nucleic Acids*, 30:596-605. doi:10.1016/j.omtn.2022.11.012.

6. Bondaruk, J.*, Jaksik, R.*, **Wang, Z.***(*co-first author*), Cogdell, D.*, Lee, S., Chen, Y., Dinh, K., Majewski, T., Zhang, L., Cao, S., Yao, H., Weinstein, J., Navai, N., Dinney, C., Gao, J., Theodorescu, D., Logothetis, C., Guo, C., Wang, W., McConkey, D., Wei, P., Kimmel, M., Czerniak, B. (2022). The origin of bladder cancer from mucosal field effects. *iScience*. doi: 10.1016/j.isci.2022.104551.

7. Yang, G.*, Bondaruk, J.*, Cogdell, D.*, **Wang, Z.***(*co-first author*), Lee S., Lee J., Zhang S., Choi W., Wang Y., Liang Y., Wang G., Wang Y., Yao H., Dadhania V., Logothetis C., Siefker-Radtke A., Kamat A., Dinney C., Theodorescu D., Kimmel M., Wei, P., Guo, C., Weinstein J., McConkey D., Czerniak, B. (2020). Urothelial-to-Neural Plasticity Drives Progression to Small Cell Bladder Cancer. *iScience*. doi: 10.1016/j.isci.2020.101201.

8. Guo, C. C., Bondaruk, J., Yao, H., **Wang, Z.**, Zhang, L., Lee, S., Lee, J. G., Cogdell, D., Zhang, M., Yang, G., Dadhania, V., Choi, W., Wei, P., Gao, J., Theodorescu, D., Logothetis, C., Dinney, C., Kimmel, M., Weinstein, J. N., McConkey, D. J., . . . Czerniak, B. (2020). Assessment of Luminal and Basal Phenotypes in Bladder Cancer. *Scientific reports*, 10(1), 9743. doi:10.1038/s41598-020-66747-7.

9. Guo, C., Majewski, T., Zhang, L., Yao, H., Bondaruk, J., Wang, Y., Zhang, S., **Wang, Z.**, Lee, J., Lee, S., Cogdell, D., Zhang, M., Wei, P., Grossman, H., Kamat, A., Duplisea, J., Ferguson, J., Huang, H., Dadhania, V., Dinney, C., Weinstein, J., Baggerly, K., McConkey, D., Czerniak, B. (2019). Dysregulation of EMT Drives the Progression to Clinically Aggressive Sarcomatoid Bladder Cancer. *Cell reports*, 27(6), 1781–1793.e4. doi:10.1016/j.celrep.2019.04.048.

10. Zhang, Y., Sturgis, E.M., Wei, P., Liu, H., **Wang, Z.**, Ma, Y., Liu, C., Gu, K.J., Wei, Q., and Li, G. (2019). A Genetic Variant within MDM4 3'UTR miRNA Binding Site is Associated with HPV16-positive Tumors and Survival of Oropharyngeal Cancer. *Molecular carcinogenesis*, 58(12), 2276–2285. doi:10.1002/mc.23116.

11. Yang, Z., Zhang, Y., Wang, X., Huang, J., Guo, W., Wei, P., Li, G., **Wang, Z.**, Huang, Z., and Zhang, L. (2019). Putative Biomarkers of Malignant Transformation of Sinonasal Inverted Papilloma into Squamous Cell Carcinoma. *The Journal of international medical research*, 47(6), 2371–2380. doi:10.1177/0300060519838385.

PREPRINTS AND PUBLICATIONS IN PROGRESS

1. **Wang, Z.**, Czerniak, B., Wei, P. (2023). Spatial IMIX: A Mixture Model Approach to Spatially Correlated Multi-Omics Data Integration. *Preprint.* doi:10.1101/2023.07.15.549148.

2. **Wang, Z.**, Ray, D., Grosvenor, L., Beaty, T., Volk, H., Ladd-Acosta, C., Chatterjee, N. (2024+). Novel Methods for Estimating Risk Parameters Associated with Polygenic Scores using Case-Parent Trio Designs.

3. **Wang, Z.**, Burk, V., Chatterjee, N., Platz, E. (2024+). Discovering plasma proteins associated with common solid cancer incidence in ARIC.

4. **Wang, Z.**, Dutta, D., Chatterjee, N. (2024+). Canonical correlation analysis and partitioned polygenic scores reveal interesting biological pathways in diseases.

5. Mathews, L., Hu, X., **Wang, Z.**, et al. (2024+). MMP7 as a Causal Factor for Incident Hypertension and its Complications Proteomic Analysis from the Atherosclerosis Risk in Communities (ARIC) Study and Mendelian Randomization Study.

6. Dzaye, O., ..., **Wang, Z.**, et al. (2024+). Polygenic Risk Scores and Extreme Coronary Artery Calcium Phenotypes in Adults > 75 Years Old: The Atherosclerosis Risk in Communities Study.

7. Alonso, D., Patel, D., Schmitz, C., **Wang, Z.**, Knorr, J., Manner, D., Datta, G., Koester, A., Na, S., Klekotka, P., Nirula, A. (2023+). Safety and efficacy of LY3454738, a novel CD200R checkpoint agonist, in a 12-week phase 1 study in atopic dermatitis.

PRESENTATIONS

Invited Talks

1. "Novel Methods for Estimating Risk Parameters Associated with Polygenic Scores using Case-Parent Trio Designs." STATGEN 2024: Conference on Statistics in Genomics and Genetics. The American Statistical Association (ASA) Section on Statistics in Genomics and Genetics (SSGG). Pittsburgh, PA. May 1-3, 2024.

2. "Risk Parameter Estimation under Polygenic Models from Case-Parent Trios and Applications on GEARs Study." GEARs seminar, Department of Epidemiology, Johns Hopkins University, Baltimore, MD. April 26, 2023.

3. "IMIX: A multivariate mixture model framework for integrative analysis of multiple types of omics data." Discovery statisticians and biologists meeting, Eli Lilly and Company, Indianapolis, IN. August 5, 2022.

4. "Testing for Trend in Benefit-Risk Analysis with Prioritized Multiple Outcomes." Dr. Anil Korkut's lab, Department of Bioinformatics & Computational Biology, The University of Texas MD Anderson Cancer Center, Houston, TX. October 12, 2018.

5. "Internship Experience at Merck." GSBS Quantitative Sciences Department Retreat, NASA Space Center, Houston, TX. September 29, 2018.

Selected Conference Talks

1. "Joint Modeling of Gene-Environment Correlations and Interactions Using Polygenic Risk Scores in Case-Control Studies." **ENAR** 2024, Baltimore, MD. March 10-13, 2024.

2. "Spatial IMIX: A Mixture Model Approach to Spatially Correlated Multi-Omics Data Integration." The Joint Statistical Meetings (**JSM**) 2022, Washington, D.C. August 7-11, 2022.

3. "IMIX: A multivariate mixture model framework for integrative analysis of multiple types of omics data." **Platform Presentation** (top 8% submitted abstracts selected), The American Society of Human Genetics (**ASHG**) 2020 Annual Meeting, virtual. October 27-30, 2020.

4. "IMIX: A multivariate mixture model framework for integrative analysis of multiple types of omics data." The Joint Statistical Meetings (**JSM**) 2020, virtual. August 2-6, 2020.

5. "A two-stage epigenome-wide association study identifies novel pancreatic cancer susceptibility loci by leveraging public controls." **Platform Presentation**, International Genetic Epidemiology Society (**IGES**) Annual Meeting, Houston, TX. October 12 - 14, 2019.

6. "Statistical methods for leveraging public controls in a two-stage epigenome-wide association study." The Joint Statistical Meetings (**JSM**) 2019, Denver, CO. July 27 - August 1, 2019.

7. "Robust and Powerful New Methods for Trend Testing of Composite Endpoints in Benefit-Risk Analysis." Merck & Co., Bards, Upper Gwynedd, PA. August 9, 2018.

Selected Conference Posters

1. "Novel Methods for Estimating Risk Parameters Associated with Polygenic Scores using Case-Parent Trio Designs." The American Society of Human Genetics (**ASHG**) 2023 Annual Meeting, Washington, D.C. November 1-5, 2023.

2. "A multivariate mixture model approach to integrative analysis of omics data." Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine (**iBRIGHT**) 2019, Houston, TX. November 11 - 13, 2019.

3. "A two-stage epigenome wide association study identifies novel pancreatic cancer susceptibility loci by leveraging public controls." The American Society of Human Genetics (**ASHG**) 2019 Annual Meeting, Houston, TX. October 15 - 19, 2019.

4. "Statistical Methods for Leveraging Public Controls in Epigenome-Wide Association Study." Conference on Statistical Learning and Data Science / Nonparametric Statistics (**SLDS**), Columbia University, New York, NY. June 4 - 6, 2018.

Academic Service and Outreach

1. Peer Reviewer: BMC Bioinformatics, Scientific Reports, Statistics in Biopharmaceutical Research, Statistics in Biosciences, Wires Computational Statistics

2. Co-founder, ASA Postdoctoral Association (ASAPA)   01/2024 - present

3. Organizer, Bi-Weekly Statistical Genetics Working Group Seminar Series, Department of Biostatistics, Johns Hopkins University   01/2023 - present

4. Executive Member, Council of Emerging and New Statisticians (CENS), ENAR of International Biometrics Society   05/2022 - 05/2024

5. Organizer, Invited Session: Paths to Success: Perspectives from Recruiters and Hiring Committees with a Focus on Fostering Inclusivity and Equity, ENAR 2024   03/2024

6. Session Chair, Contributed Papers: Genome Wide Association Studies, ENAR 2024   03/11/2024

7. Session Chair, Contributed Papers: High Dimensional Data Analysis, ENAR 2021   03/15/2021

8. Peer Mentor, GSBS Peer Mentoring Program for First-Year GSBS PhD student   08/2019 - 05/2021

9. Student Representative, GSBS Standing Committees Curriculum Committee   10/2019 - 09/2020

10. Committee Member, GSBS Quantitative Sciences Program Curriculum Committee   09/2018 - 08/2020

11. Member, Stony Brook University Environmental Club   2014-2015

12. Volunteer Teacher, AIESEC, Dare To Dream Volunteer Teaching Program, An Hui, China   Summer 2014

Research Mentorship

- Charissa Luk, Undergraduate Student in Biomedical Engineering at JHU. July 2023 - present. Project: Data preprocessing and normalization of OLINK proteomics data in the UK Biobank.

- Tryggvi McDonald, First-year PhD student from the Department of Human Genetics and Genomics, JHU. Jan - April, 2024. Project: Identifying incident cardiovascular disease and type 2 diabetes patients and PGSxE interactions in the UK Biobank.

- Sameer Gabbita, Undergraduate Student in Biomedical Engineering at JHU. Summer Internship, Bloomberg Distinguished Professor (BDP) Summer Research Program at JHU, 2024. Project: Mendelian Randomization to identify the causal relationship between LDL and Breast Cancer Survival Rates.

- Zoey Hall, Undergraduate Student from Howard University, major in Computer Science, minor in Maternal & Child health. Vivien Thomas Scholars Initiative Summer Fellow, Diversity Summer Internship Program at Johns Hopkins Bloomberg School of Public Health, 2024. Project: Polygenic scores of Attention-deficit/hyperactivity disorder (ADHD) in the Black population from the Boston Birth Cohort.

Conference Contributions

- Alonso, D., Patel, D., Schmitz, C., **Wang, Z.**, Knorr, J., Manner, D., Datta, G., Koester, A., Na, S., Klekotka, P., Nirula, A. (2022) "Safety and efficacy of LY3454738, a novel CD200R checkpoint agonist, in a 12-week phase 1 study in atopic dermatitis." ePoster, EADV Congress 2022, Milan, Italy. September 7 - 10, 2022.

- Zhao, Y., Yang, T., Zou, J., **Wang, Z.**, Niu, J., Chen, H., Wei, P. (2019) "Estimation of total mediation effect for multiple types of high-dimensional omics mediators in over 3500 individuals provides novel insight into aging-related variation in blood pressure." Platform Presentation, The American Society of Human Genetics (**ASHG**) 2019 Annual Meeting, Houston, TX. October 15 - 19, 2019.

- Shi, B., **Wang, Z.**, Huang, X., Wei, P. (2019) "Smoothed moving landmark analysis for the age-dependent effects of DNA methylation on the risk of coronary heart disease." Poster, The American Society of Human Genetics (**ASHG**) 2019 Annual Meeting, Houston, TX. October 15 - 19, 2019.

- Zhao, Y., Yang, T., Zou, J., **Wang, Z.**, Niu, J., Chen, H., Wei, P. (2019) "Estimation of total mediation effect for multiple types of high-dimensional omics mediators in over 3500 individuals provides novel insight into aging-related variation in blood pressure." Platform Presentation, International Genetic Epidemiology Society (**IGES**) Annual Meeting, Houston, TX. October 12 - 14, 2019.

- Shi, B., **Wang, Z.**, Huang, X., Wei, P. (2019) "Smoothed moving landmark analysis for the age-dependent effects of DNA methylation on the risk of coronary heart disease." Poster, International Genetic Epidemiology Society (**IGES**) Annual Meeting, Houston, TX. October 12 - 14, 2019.

Short Courses and Workshops

1. "Mendelian randomisation." Short course, Imperial College London. May 22-23, 2023.

2. "Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis." **Presentation** at Statistical Genetics Journal Club, Houston, TX. April 8, 2020.

3. "Mini Course: Academic Writing Style." Writing Support Services, UTHealth SPH, Houston, TX. March 2 - 23, 2020.

4. "PubMed for Advanced Searchers." Scientific Publications, Research Medical Library, MD Anderson Cancer Center, Houston, TX. November 14, 2019.

5. "Interactive Invited Workshop: The Michigan Imputation Server: Data Preparation, Genotype Imputation, and Data Analysis." **ASHG**, Houston, TX. October 17, 2019.

6. "Education Workshop on Mendelian Randomization." **IGES**, Houston, TX. October 12, 2019.

7. "Conversation 2: Workplace Conversations." Scientific Publications, Research Medical Library, MD Anderson Cancer Center, Houston, TX. October 2 - November 20, 2019.

8. "Making Presentations." Scientific Publications, Research Medical Library, MD Anderson Cancer Center, Houston, TX. July 29 - September 16, 2019.

9. "Literature Reviews." Scientific Publications, Research Medical Library, MD Anderson Cancer Center, Houston, TX. September 26, 2019.

10. "PubMed: The Basics." Scientific Publications, Research Medical Library, MD Anderson Cancer Center, Houston, TX. September 24, 2019.

11. "Mixed Models in Quantitative Genetics"; "Association Mapping: GWAS and Sequencing Data"; "Computational Pipeline for WGS Data." University of Washington, Seattle, WA. July 17 - 26, 2019. (**Scholarship**).

12. "Writing 2: Making your sentences flow." Scientific Publications, Research Medical Library, MD Anderson Cancer Center, Houston, TX. May 13 - June 27, 2019.

13. "An Introduction to Causal Effect Estimation with Examples Using SAS Software." **ENAR**, Philadelphia, PA. March 25 , 2019. (**Travel award**).

14. "Writing 1: Writing coherent paragraphs." Scientific Publications, Research Medical Library, MD Anderson Cancer Center, Houston, TX. March 12 - April 25, 2019.

15. "Common SNPs explain a large proportion of the heritability for human height." **Presentation** at Statistical Genetics Journal Club, Houston, TX. February 8, 2019.

16. "Writing 3: Editing your own writing." Scientific Publications, Research Medical Library, MD Anderson Cancer Center, Houston, TX. January 7 - February 21, 2019.

Professional Memberships

- American Society of Human Genetics (2019 -)
- International Genetic Epidemiology Society (2019 -)
- International Chinese Statistical Association (2019 -)
- Eastern North American Region (ENAR) / International Biometric Society (2019 -)
- American Statistical Association (2017 -)
- Institute of Mathematical Statistics (2017 -)

Research Interests

- Statistical Genetics
- Cancer Genomics
- Mixture Model
- Machine Learning and Nonparametric Methods