Curriculum Vitae

Jiebiao Wang

A732 Public Health
130 DeSoto Street
Pittsburgh, PA 15261

412-383-3799
jbwang@pitt.edu

https://www.sph.pitt.edu/directory/jiebiao-wang
https://randel.github.io/

Academic Interests

- Statistical genomics
- Mediation analysis
- Machine learning

Education and Training

Undergraduate

2006-2010	Renmin University of China, Beijing, China	BS, 2010	Statistics

Graduate

2010-2012	Renmin University of China, Beijing, China	MS, 2012	Statistics
2012-2017	University of Chicago, Chicago, Illinois	PhD, 2017	Biostatistics

Appointments and Positions

2017-2019	Postdoctoral Researcher	Department of Statistics and Data Science, Carnegie Mellon University, Pittsburgh, PA
2020/1- Present	Assistant Professor (Tenure Track)	Department of Biostatistics and Health Data Science, University of Pittsburgh, Pittsburgh, PA
2023/7- Present	Assistant Professor (Secondary)	Clinical and Translational Science Institute (CTSI), University of Pittsburgh, Pittsburgh, PA

Membership in Professional and Scientific Societies

2014 - Present	Member, Eastern North American Region, International Biometric Society
2013 - Present	Member, American Statistical Association

Honors

2018	Outstanding Performance Award in the Field of Public Health Sciences, Division of the Biological Sciences, University of Chicago
2023	Nominated for James L. Craig Endowed Excellence in Education Award, School of Public Health, Pitt
2024	Selected to Present at the Senior Vice Chancellor's Research Seminar ($10,000 research funding), Pitt

Professional Activities

Teaching

Courses Taught

Years Taught	Institution Program (Graduate or Undergraduate) Course Number: Title	Hours of Lecture/Credits Average Enrollment	Role in Course Primary/Coordinator
Spring 2020	BIOST 2025 (Biostatistics Seminar)	1 credit, 9 enrolled	Coordinator
Fall 2020	BIOST 2025 (Biostatistics Seminar)	1 credit, 22 enrolled	Coordinator
Spring 2021	BIOST 2025 (Biostatistics Seminar)	1 credit, 28 enrolled	Coordinator
Fall 2021	BIOST 2025 (Biostatistics Seminar)	1 credit, 27 enrolled	Coordinator
Spring 2022	BIOST 2025 (Biostatistics Seminar)	1 credit, 18 enrolled	Coordinator
Fall 2021	BIOST 2068 (Introduction to Causal Inference)	3 credits, 35 enrolled	Primary
Fall 2022	BIOST 2068 (Introduction to Causal Inference)	3 credits, 11 enrolled	Primary
Fall 2023	BIOST 2068 (Introduction to Causal Inference)	3 credits, 13 enrolled	Primary
Fall 2024	BIOST 2154 (Statistical Methods for Omics Data)	2 credits, 23 enrolled	Primary

Other Teaching (lectures, tutorials, and continuing education courses)

Date(s)	Type of Teaching	Title
Spring 2020	Guest lecture	EPID 2620: Application of Molecular Biomarkers in Epidemiology
Spring 2020	Guest lecture	HUGEN 2080: Statistical Genetics
Spring 2022	Guest lecture	HUGEN 2080: Statistical Genetics
Fall 2023	Guest lecture	BIOST 2065: Analysis of Incomplete Data
Fall 2023	Guest lecture	BIOST 2069: Statistical Methods for Omics Data

Major Advisor for Graduate Student Essays, Theses, and Dissertations

Name of Student	Degree Awarded Year	Type of Document Title	Notes
Manqi Cai	PhD, 2024	Statistical Methods for Cellular Deconvolution with Single-Cell Omics	

- Best Research Presentation Award, Graduate Student Research Conference 2022, National Institute of Statistical Sciences (NISS)
- Best PhD Poster Award, Pitt Biostatistics Research Day, 2023
- Delta Omega Dissertation Award, 2024
- Delta Omega Membership, 2024
- Dean's Service Award, 2024
- First position: Mathematical Statistician, FDA

Name of Student	Degree Awarded Year	Type of Document Title	Notes
Michelle Sun	MS, 2024	Age Related Changes in Human Circadian Rhythms	

- Best Master's Poster Award Honorable Mention, Pitt Biostatistics Research Day, 2023
- First position: Genetics, Genomics and Systems Biology PhD Program, University of Chicago

Jenny Liang   MS, 2024   Pan-Tissue Cell Deconvolution Using Single-Cell RNA-Seq References
- Outstanding Student Award, 2024
- First position: Integrative Systems Biology PhD Program, University of Pittsburgh

Chen Liu   PhD student, 2023 – Present
- Student Paper Award, Health Policy Statistics Section, American Statistical Association, 2025

Wenzhuo Lin   PhD student, 2024 – Present

As Academic/GSR Advisor

Kangyi Zhao   PhD student, 2022 - Present

Liang You   PhD student, 2025 - Present

Jinyu Wang   PhD student, 2025 - Present

Junlin Liu   MS student, 2024 – Present

Ruihan Huang   MS student, 2025 – Present

Yumeng Shao   PhD student, 2024 - 2025

Penghui Huang   PhD student, 2022 - 2024

Lingyi Peng   PhD student, 2020 - 2022

Gehui Zhang   PhD student, 2021 - 2023

Nick Heaton   MS student, 2023 - 2024

Service on Masters or Doctoral Committees

Dates Served	Name of Student	Degree Awarded	Title of Dissertation/Essay
2020	Dongjing Liu	PhD in Human Genetics	Integrated Genome-Wide Analysis of Human Facial Morphology
2021-2022	Xinjun Wang	PhD in Biostatistics	Statistical Learning and Analysis of Single-Cell Multi-Omics Data
2022-2023	Jian Zou	PhD in Biostatistics	Clustering, Biomarker and Cancer Model Selection Using Omics Data
2022-2023	Yang Ou	PhD in Biostatistics	Estimation of Causal Treatment Effect for Clustered Observational Data with Unmeasured Confounding
2022-2024	Hai-Wei Liang	PhD in Epidemiology	A Pathway Approach in Human Pregnancy to Quantify the Effects of Phthalates on Fetal Health Outcomes Mediated by Placental Function
2023-2024	Xiangning Xue	PhD in Biostatistics	Statistical Methods for Circadian Analysis on Omics Data
2023-2024	Japan Patel	MS in Biostatistics	Statistical modeling of Epstein-Barr virus infection using scRNA-Seq host expression
2023-2024	Jerry Zhou	MS in Biostatistics	Impact of COVID-19 on Adversarial Outcomes for In-Patient Congestive

			Heart Failure in the Northeast Mid Atlantic
2023-2024	Nuo Wei	MS in Biostatistics	Assessing the Impact of Metal Exposure on Chronic Kidney Disease and Hypertension: A NHANES Data Analysis
2023-Present	Rain Katz	PhD in Epidemiology	Molecular Biomarkers of Subclinical Cardiovascular Disease in the Tobago Health Study and Long Life Family Study
2024-2025	Shuangjia Xue	PhD in Environmental and Occupational Health	Impact of Air Pollution on Lung Function in Fibrotic Interstitial Lung Disease and Asthma: Insights from Geospatial Models to Gene-Environment Interactions
2024-Present	Huy Le	PhD in Statistics	Differentially methylated regions in longitudinal and multivariate DNA methylation data
2024-Present	Manuel Garcia Acosta	PhD in Statistics	An Adaptive Test for Selecting Variance Models in Multi-Omics Data with Latent Confounders
2024-Present	Yi (Emma) Lu	PhD in Environmental and Occupational Health	
2025-Present	Heqiao Ruan	PhD in Statistics	Understanding Out-of-Distribution: Hypothesis Testing and Causal Inference
2025-Present	Rick Chang	PhD in Biostatistics	Statistical and computational methods to decipher homogeneous and heterogeneous structure from multi-omics
2025-Present	Xuelin Gu	PhD in Biostatistics	Causal Inference with Intermediate Outcomes: Methods for Principal Stratum Identification and Estimation of Principal Causal Effects in Neoadjuvant Trials

Service on Comprehensive or Qualifying Committees

Dates Served	Student Population i.e. 1 PhD Biostatistics student	Type of Exam (Qualifying/Comprehensive)
2021-2022	MS Biostatistics students	Member, Master Comprehensive Exam Committee
2023-2024	MS Biostatistics students	Chair, Master Comprehensive Exam Committee

Mentoring of Early and Mid-Career Faculty

Dates	Name of Faculty	Position of Faculty Member
2021 – Present	Soyeon Kim	Research Assistant Professor of Pediatrics, University of Pittsburgh

Research and Training

Grants and Contracts Received

Principal Investigator, Multiple Principal Investigator, or Program Project Director
as listed in NIH RePORT and/or on Notice of Award

Years Inclusive	Grant Number and Title	Source	Annual Direct Costs	%Effort
2023/2-2027/11	R01AG080590 (Statistical methods for population-level cell-type-specific analyses of tissue omics data for Alzheimer's disease)	NIH	$250,000	25% + 2 GSRs
2024/12-2026/11	R21AG087057 (Heterogeneous Genetic Effects and Mediation in Alzheimer's Disease)	NIH	$ 131,350	10% + 1.5 GSRs
2022/9-2024/9	R03OD034501 (Integration of GTEx and HuBMAP data to gain population-level cell-type-specific insights)	NIH	$ 213,644	12% + 2 GSRs
2021/7-2023/6	Competitive Medical Research Fund (CMRF)	UPMC	$25,000	
2022/1-2023/12	Health Sciences Bridge Funding	Pitt	$48,720	
2022/1-2023/12	Brain Institute's Assault on Alzheimer's Seed Grant	Pitt Brain Institute	$25,000	
2022/6-2023/5	Exploring Existing Data Resources Pilot Award	Pitt Clinical and Translational Science Institute (CTSI)	$25,000	
2022/5-2023/4	Public Health Trans-Disciplinary Collaboration Pilot Award	Pitt CTSI	$45,000	

Site Principal Investigator
include grants where serving as a significant Site PI (e.g., in a large clinical study, clinical trial, consortium grant, or center grant) not identifiable in NIH RePORT

Years Inclusive	Grant Number and Title (PI: Name; Institution)	Source	Annual Direct Costs	%Effort
2020-2024	R01MH123184, Computational Methods to Integrate and Interpret the Transcriptome from Single Cell and Tissue Level Data (PI: Roeder; CMU)	NIH	$338,194	10%

Co-Investigator
include institutional grants as well as inter-institutional subcontracts for which you are officially listed as Co-Investigator (e.g., key personnel designation in NIH grant)

Years Inclusive	Grant Number and Title (PI: Name; Institution)	Source	Annual Direct Costs	%Effort
2020-2022	R37MH057881, Genetics Association in Schizophrenia and Other Disorders (PI: Devlin; Pitt)	NIH	$452,677	17%
2020-2022	MR-2020-109502 (PI: Jurczak; Pitt)	Pittsburgh Foundation	$750,000	20%
2020-2024	R01HL153058, Mucin sialylation drives epithelial cell senescence and severe asthma (PI: Wenzel; Pitt)	NIH	$543,871	10%
2020-2026	U19AG068054, Alzheimer's Biomarker Consortium - Down Syndrome (PI: Handen; Pitt)	NIH	$1,809,790	10%
2021-2023	R01ES029336, Placental origins of phthalate-induced changes in fetal reproductive development (PI: Adibi; Pitt)	NIH	$418,485	10%
2021-2023	R01AG075069, Neurodevelopmental and neurodegenerative effects of environmental	NIH	$363,431	5%

	determinants: altering neural cellular populations impacting homeostatic functions and inflammatory response (PI: Fitz; Pitt)			
2021-2022	IPA - VA Pittsburgh Healthcare System (PI: Rogal; Pitt)	VA	$34,731	25%
2022-2023	RF1AG075992, ncRNAs in plasma EVs of AD patients and their discriminatory power as biomarkers (PI: Lefterov; Pitt)	NIH	$491,681	10%
2022-2026	R01DK133454, Vinyl chloride modifies the risk for nonalcoholic fatty liver disease (PI: Beier; Pitt)	NIH	$281,631	8%
2022-2027	P01AI106684, Immune Airway-Epithelial Interactions in Steroid-Refractory Severe Asthma (PI: Wenzel; Pitt)	NIH	$325,473	10%
2023-2028	R01AI164968, Functional consequences of intergenic autoimmune disease risk variants (PI: Demirci; Pitt)	NIH	$501,801	20% + ½ GSR
2025-2030	R01CA285337, Single-cell congruence evaluation and selection of cancer models towards precision medicine (PI: Tseng and Lee; Pitt)	NIH	$585,931	8% + ½ GSR

Invited Presentations Related to Your Research

Date	Title of Presentation	Venue
2025/12	Inferring cell-type-specific co-methylation networks from single-cell DNA methylation data	13th ICSA International Conference, Taipei, Taiwan
2025/12	Inferring cell-type-specific co-methylation networks from single-cell DNA methylation data	CMStatistics, London, UK
2025/7	Inferring cell-type-specific co-methylation networks from single-cell DNA methylation data	10th International Forum on Statistics, Renmin University of China
2025/6	Inferring cell-type-specific co-methylation networks from single-cell DNA methylation data	ICSA China Conference, Zhuhai, China
2025/6	Inferring cell-type-specific co-methylation networks from single-cell DNA methylation data	WNAR, Whistler, Canada
2024/8	BLEND: Bayesian cellular deconvolution with reference selection	JSM, Portland, OR
2024/7	BLEND: Bayesian cellular deconvolution with reference selection	The 7th International Conference on Econometrics and Statistics (EcoSta), Beijing, China
2024	Integrating single-cell and tissue omics: population-level cell type-specific insights	Senior Vice Chancellor's Research Seminar, University of Pittsburgh
2024	BLEND: Bayesian cellular deconvolution with reference selection	STATGEN conference, ASA SSGG
2024	Cellular deconvolution with single-cell DNA methylation and RNA sequencing references	Biostatistics and Computational Biology Branch Seminar Series, National Institute of Environmental Health Sciences (NIEHS), NIH
2023	Accurate estimation of rare cell type fractions from tissue omics via hierarchical deconvolution	The 16th International Conference on Computational and Methodological Statistics (CMStatistics), Berlin, Germany
2023	Cellular deconvolution with single-cell DNA methylation and RNA sequencing references	Biostatistics Seminars, University of North Carolina at Chapel Hill
2023	Accurate estimation of rare cell type fractions from tissue omics data via hierarchical deconvolution	JSM, Toronto, Canada
2023	Integration of GTEx and HuBMAP data to gain population-level cell type-specific insights	Cross-Pollination Meeting, NIH Common Fund Data Ecosystem

2023	Robust and accurate estimation of cellular fractions from tissue omics data via ensemble and hierarchical deconvolution	Joint Seminar Series of CMDB (Cell, Molecular, and Developmental Biology) - GGB (Genetics, Genomics, and Bioinformatics) - MCBL (Microbiology), University of California, Riverside
2023	Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution	ENAR Spring Meeting, Nashville, TN
2023	Cellular deconvolution methods with single-cell DNA methylation and RNA-seq references	Biostatistics Research Day, University of Pittsburgh
2022	Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution	The 15th International Conference on Computational and Methodological Statistics (CMStatistics 2022), King's College London, UK
2021	Robust estimation of cell type fractions from bulk data via an ensemble of various deconvolution approaches	ICSA Applied Statistics Symposium (Virtual)
2021	Detecting cell-type-specific eQTLs Using Bayesian estimates of cell-type-specific gene expression from tissue samples with single-cell prior	ENAR Spring Meeting (Virtual)
2020	Bayesian estimation of cell-type-specific gene expression for each tissue sample with prior derived from single-cell data	Department of Statistics Seminar Series, University of Pittsburgh
2020	Gene expression deconvolution implicates cell-type-specific gene expression and co-expression in autism	The 75th Anniversary of the Society of Biological Psychiatry (SOBP) Meeting (Canceled due to COVID-19)
2019	High-dimensional mixed-effects models for multi-omics data	Department of Biostatistics Seminar Series, Pitt
2018	A random-effects model for multi-tissue deconvolution to estimate individual-level cell-type-specific gene expression	ICSA Applied Statistics Symposium
2017	High-Dimensional Multivariate Selection Models for Proteomics Data with Nonignorable Missingness	Department of Human Genetics, University of Pittsburgh
2017	A high-dimensional multivariate selection model for proteomics data with nonignorable missingness	Department of Biomedical Informatics, Arizona State University
2017	Statistical methods for genomics data with clustered structure and missingness	Division of Biostatistics, Medical College of Wisconsin
2016	A high-dimensional multivariate selection model for proteomics data with batch-level missingness	Workshop on Quantitative Research Methods in Education, Health and Social Sciences, University of Chicago

Publications

*: corresponding author
_: student
+: co-first authors

Methodological/Major Articles – Published or In Press

1. Cai M, Zhao K, Huang P, Celedón JC, McKennan C, Chen W, **Wang J***. EMixed: probabilistic multi-omics cellular deconvolution of bulk omics data. *Journal of Data Science*. 2025, 1-15.

2. Huang P, <u>Cai M</u>, Lu X, McKennan C, **Wang J***. Accurate estimation of rare cell type fractions from tissue omics data via hierarchical deconvolution. <u>*Ann. Appl. Stat*</u>. 2024 Jun;18(2): 1178-1194. doi: 10.1214/23-AOAS1829. (*An earlier version won the Research Poster Award, ICSA Applied Statistics Symposium, 2023 & Student Research Award, New England Statistics Symposium, 2023*)

3. <u>Cai M</u>, Zhou J, McKennan C, **Wang J***. scMD facilitates cell type deconvolution using single-cell DNA methylation references. <u>*Commun Biol*</u>. 2024 Jan 2;7(1):1. doi: 10.1038/s42003-023-05690-5.

4. Zhou X, <u>Cai M</u>, Yue M, Celedón J, **Wang J**, Ding Y, Chen W, Li Y. Molecular group and correlation guided structural learning for multi-phenotype prediction. *Briefings in Bioinformatics*. 2024, 25(6), bbae585.

5. Chandrashekar PB, Alatkar S, **Wang J**, Hoffman GE, He C, Jin T, Khullar S, Bendl J, Fullard JF, Roussos P, Wang D. DeepGAMI: deep biologically guided auxiliary learning for multimodal integration and imputation to improve genotype-phenotype prediction. Genome Med. 2023 Oct 31;15(1):88. doi: 10.1186/s13073-023-01248-6.

6. <u>Cai M</u>, Yue M, Chen T, Liu J, Forno E, Lu X, Billiar T, Celedón J, McKennan C, Chen W, **Wang J***. Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution. <u>*Bioinformatics*</u>. 2022 May 26;38(11):3004-3010. doi: 10.1093/bioinformatics/btac279.

7. **Wang J***, Roeder K*, Devlin B*. Bayesian estimation of cell type-specific gene expression with prior derived from single-cell data. <u>*Genome Res*</u>. 2021 Oct;31(10):1807-1818. doi: 10.1101/gr.268722.120.

8. Qiu Y, **Wang J**, Lei J, Roeder K. Identification of cell-type-specific marker genes from co-expression patterns in tissue samples. Bioinformatics. 2021 Oct 11;37(19):3228-3234. doi: 10.1093/bioinformatics/btab257.

9. Yang F, Gleason KJ, **Wang J**, Duan J, He X, Pierce BL, Chen LS. CCmed: cross-condition mediation analysis for identifying replicable trans-associations mediated by cis-gene expression. Bioinformatics. 2021 Sep 9;37(17):2513-2520. doi: 10.1093/bioinformatics/btab139.

10. <u>Tian J</u>, **Wang J**, Roeder K. ESCO: single cell expression simulation incorporating gene co-expression. Bioinformatics. 2021 Aug 25;37(16):2374-2381. doi: 10.1093/bioinformatics/btab116.

11. Chen S+, **Wang J**+, Cicek E, Roeder K, Yu H, Devlin B. De novo missense variants disrupting protein-protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. <u>*Mol Autism*</u>. 2020 Oct 8;11(1):76. doi: 10.1186/s13229-020-00386-7.

12. Satterstrom FK+, Kosmicki JA+, **Wang J**+, Breen MS, De Rubeis S, An JY, Peng M, Collins R, Grove J, Klei L, Stevens C, Reichert J, Mulhern MS, Artomov M, Gerges S, Sheppard B, Xu X, Bhaduri A, Norman U, Brand H, Schwartz G, Nguyen R, Guerrero EE, Dias C, Betancur C, Cook EH, Gallagher L, Gill M, Sutcliffe JS, Thurm A, Zwick ME, Børglum AD, State MW, Cicek AE, Talkowski ME, Cutler DJ, Devlin B, Sanders SJ, Roeder K, Daly MJ, Buxbaum JD. Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. <u>*Cell*</u>. 2020 Feb 6;180(3):568-584.e23. doi: 10.1016/j.cell.2019.12.036.

13. **Wang J**, Devlin B, Roeder K. Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. <u>*Bioinformatics*</u>. 2020 Feb 1;36(3):782-788. doi: 10.1093/bioinformatics/btz619.

14. **Wang J**, Wang P, Hedeker D, Chen LS. Using multivariate mixed-effects selection models for analyzing batch-processed proteomics data with non-ignorable missingness. *Biostatistics*. 2019 Oct 1;20(4):648-665. doi: 10.1093/biostatistics/kxy022.

15. Gibbons R, Hur K, Lavigne J, **Wang J**, Mann J. Medications and Suicide: High Dimensional Empirical Bayes Screening (iDEAS). Harvard Data Science Review. 2019 November. doi: 10.1162/99608f92.6fdaa9de.

16. **Wang J**, Liu Q, Pierce BL, Huo D, Olopade OI, Ahsan H, Chen LS. A meta-analysis approach with filtering for identifying gene-level gene-environment interactions. *Genet Epidemiol*. 2018 Jul;42(5):434-446. doi: 10.1002/gepi.22115.

17. Yang F, **Wang J**, Pierce BL, Chen LS. Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. Genome Res. 2017 Nov;27(11):1859-1871. doi: 10.1101/gr.216754.116.

18. Chen LS, **Wang J**, Wang X, Wang P. A mixed-effects model for incomplete data from labeling-based quantitative proteomics experiments. Ann Appl Stat. 2017 Mar;11(1):114-138. doi: 10.1214/16-AOAS994.

19. **Wang J**, Gamazon ER, Pierce BL, Stranger BE, Im HK, Gibbons RD, Cox NJ, Nicolae DL, Chen LS. Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. *Am J Hum Genet.* 2016 Apr 7;98(4):697-708. doi: 10.1016/j.ajhg.2016.02.020.

Collaborative Articles – Published or In Press

20. Schworer EK, Zammit MD, **Wang J**, Handen BL, Betthauser T, Laymon CM, Tudorascu DL, Cohen AD, Zaman SH, Ances BM, Mapstone M, Head E, Klunk WE, Christian BT, Hartley SL. Amyloid chronicity and tau PET timeline to symptomatic Alzheimer's disease in Down syndrome. *Lancet Neurology*. 2024 Dec;23(12):1214-1224.

21. Pyun JM, Park YH, **Wang J**, Bennett DA, Bice PJ, Kim JP, Kim S, Saykin AJ, Nho K. Transcriptional risk scores in Alzheimer's disease: From pathology to cognition. Alzheimers Dement. 2024 Jan;20(1):243-252. doi: 10.1002/alz.13406.

22. Pyun JM, Park YH, **Wang J**, Bice PJ, Bennett DA, Kim S, Saykin AJ, Nho K. Aberrant GAP43 Gene Expression Is Alzheimer Disease Pathology-Specific. Ann Neurol. 2023 May;93(5):1047-1048. doi: 10.1002/ana.26637.

23. Liang HW, Snyder N, **Wang J**, Xun X, Yin Q, LeWinn K, Carroll KN, Bush NR, Kannan K, Barrett ES, Mitchell RT, Tylavsky F, Adibi JJ. A study on the association of placental and maternal urinary phthalate metabolites. J Expo Sci Environ Epidemiol. 2023 Mar;33(2):264-272. doi: 10.1038/s41370-022-00478-x.

24. Cuddleston WH, Fan X, Sloofman L, Liang L, Mossotto E, Moore K, Zipkowitz S, Wang M, Zhang B, **Wang J**, Sestan N, Devlin B, Roeder K, Sanders SJ, Buxbaum JD, Breen MS. Spatiotemporal and genetic regulation of A-to-I editing throughout human brain development. Cell Rep. 2022 Nov 1;41(5):111585. doi: 10.1016/j.celrep.2022.111585.

25. Xu Z, Wang X, Fan L, Wang F, Lin B, **Wang J**, Trevejo-Nuñez G, Chen W, Chen K. Integrative analysis of spatial transcriptome with single-cell transcriptome and single-cell epigenome in mouse lungs after immunization. iScience. 2022 Sep 16;25(9):104900. doi: 10.1016/j.isci.2022.104900.

9

26. McKinney BC, McClain LL, Hensler CM, Wei Y, Klei L, Lewis DA, Devlin B, **Wang J**, Ding Y, Sweet RA. Schizophrenia-associated differential DNA methylation in brain is distributed across the genome and annotated to MAD1L1, a locus at which DNA methylation and transcription phenotypes share genetic variation with schizophrenia risk. Transl Psychiatry. 2022 Aug 20;12(1):340. doi: 10.1038/s41398-022-02071-0.

27. Fitz NF, **Wang J**, Kamboh MI, Koldamova R, Lefterov I. Small nucleolar RNAs in plasma extracellular vesicles and their discriminatory power as diagnostic biomarkers of Alzheimer's disease. Neurobiol Dis. 2021 Nov;159:105481. doi: 10.1016/j.nbd.2021.105481.

28. Seney ML, Kim SM, Glausier JR, Hildebrand MA, Xue X, Zong W, **Wang J**, Shelton MA, Phan BN, Srinivasan C, Pfenning AR, Tseng GC, Lewis DA, Freyberg Z, Logan RW. Transcriptional Alterations in Dorsolateral Prefrontal Cortex and Nucleus Accumbens Implicate Neuroinflammation and Synaptic Remodeling in Opioid Use Disorder. Biol Psychiatry. 2021 Oct 15;90(8):550-562. doi: 10.1016/j.biopsych.2021.06.007.

29. King CA, Brent D, Grupp-Phelan J, Casper TC, Dean JM, Chernick LS, Fein JA, Mahabee-Gittens EM, Patel SJ, Mistry RD, Duffy S, Melzer-Lange M, Rogers A, Cohen DM, Keller A, Shenoi R, Hickey RW, Rea M, Cwik M, Page K, McGuire TC, **Wang J**, Gibbons R. Prospective Development and Validation of the Computerized Adaptive Screen for Suicidal Youth. JAMA Psychiatry. 2021 May 1;78(5):540-549. doi: 10.1001/jamapsychiatry.2020.4576.

30. Piantadosi SC, McClain LL, Klei L, **Wang J**, Chamberlain BL, Springer SA, Lewis DA, Devlin B, Ahmari SE. Transcriptome alterations are enriched for synapse-associated genes in the striatum of subjects with obsessive-compulsive disorder. Transl Psychiatry. 2021 Mar 15;11(1):171. doi: 10.1038/s41398-021-01290-1.

31. Pitt JJ, Riester M, Zheng Y, Yoshimatsu TF, Sanni A, Oluwasola O, Veloso A, Labrot E, Wang S, Odetunde A, Ademola A, Okedere B, Mahan S, Leary R, Macomber M, Ajani M, Johnson RS, Fitzgerald D, Grundstad AJ, Tuteja JH, Khramtsova G, Zhang J, Sveen E, Hwang B, Clayton W, Nkwodimmah C, Famooto B, Obasi E, Aderoju V, Oludara M, Omodele F, Akinyele O, Adeoye A, Ogundiran T, Babalola C, MacIsaac K, Popoola A, Morrissey MP, Chen LS, **Wang J**, Olopade CO, Falusi AG, Winckler W, Haase K, Van Loo P, Obafunwa J, Papoutsakis D, Ojengbede O, Weber B, Ibrahim N, White KP, Huo D, Olopade OI, Barretina J. Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. Nat Commun. 2018 Oct 16;9(1):4181. doi: 10.1038/s41467-018-06616-0.

32. Chen S, Fragoza R, Klei L, Liu Y, **Wang J**, Roeder K, Devlin B, Yu H. An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. Nat Genet. 2018 Jul;50(7):1032-1040. doi: 10.1038/s41588-018-0130-z.

Referred Articles – Submitted or Preprint

33. Huang P*, Cai M, McKennan C, **Wang J***. BLEND: Probabilistic Cellular Deconvolution with Automated Reference Selection. bioRxiv. 2024:2024-08.

34. Liu C, Qin X*, Talisa VB, **Wang J***. Heterogeneous Causal Mediation Analysis with Bayesian Additive Regression Trees. (Under review). (*An earlier version won Student Paper Award, Health Policy Statistics Section, American Statistical Association, 2025*)

35. Yue M, Cai M, Zhao C, Liu J, Tao S, Hu H, Chen Y, Huang H, Celedón JC, **Wang J***, Chen W*. Multi-Omics Intermediate Fusion Network Enables Digital White Blood Cells Count Prediction. (Under Review).

36. Katz R, Cvejkus R, **Wang J**, Thyagarajan B, Barinas-Mitchell E, Carr JJ, Terry JG, Nair S, Tang WW, Miller RG, Miljkovic I, Zmuda JM, Kuipers AL. Association of cardiovascular proteins and subclinical cardiovascular disease in an Afro-Caribbean population. (Under Review).

37. Liang H, Snyder N, **Wang J**, Catov J, Barrett ES, Swan S, Sathayanarana S, Kannan K, Adibi J. An Assessment of Measurement Error when Using Maternal Urinary Phthalates as Proxies for Placental Tissue Levels in Estimation of the Association of Prenatal Phthalates and Infant Anogenital Distance. (Under Review).

38. He T, Wang J, Tumba MC, …, **Wang J**, …, Schwartz DM, Yang J, Zhou Q. Multicenter international cohort study of HA20 reveals novel genetic architecture and phenotypic evolution. (Under Review).

39. Xue S., Nouraie, M., **Wang, J**., Li, X., Meyers, D. A., Bleecker, E. R., Ortega, V. E., ... & Wenzel, S. Oxidative Stress Pathway Genotypes Interact with Environmental Pollutant Levels to Influence Gene Expression and Lung Function. (Under Review).

Published Abstracts

1. Moon M, Murali A, Bello F, **Wang J**, Jurczak MJ; 1337-P: Sex-Specific Variation in Lipid Metabolism in Response to Nutritional Stress Is Associated with Differences in NASH Progression. *Diabetes* 1 June 2022; 71 (Supplement_1): 1337–P. https://doi.org/10.2337/db22-1337-P

Non-Print Media (Software, electronic)

1. scMD: Cellular deconvolution of bulk DNA methylation data with single-cell DNA methylation references
2. HiDecon: Hierarchical cellular deconvolution
3. EnsDeconv: Ensemble Deconvolution to robustly estimate cellular fractions from bulk omics data
4. MIND: Using bulk gene expression to estimate cell-type-specific gene expression via deconvolution
5. MixRF: A random-forest-based approach for imputing clustered incomplete data
6. mvMISE: A framework for multivariate mixed-effects selection models with potential missing data
7. ofGEM: A meta-analysis approach with filtering for identifying gene-level gene-environment interactions

Service
Service to School and University

Years	Activity	Position
2024-Present	Doctoral Monitoring Committee	Member
2024-Present	MS Admissions Committee	Member
2024-Present	Planning and Budget Policies Committee, School of Public Health	Member
2023-Present	MS Student Monitoring Committee	Member
2022-Present	PhD Admissions Committee	Member
2023-2025	Competitive Medical Research Fund (CMRF) Review Committee	Member
2022	Biostatistics Department Faculty Search Committee	Member
2020-2022	Biostatistics Research Day	Organizer
2020	Biostatistics Teaching Task Force	Member
2021	Public Health Dean's Day Poster Session	Judge
2021	CTSI Quantitative Methodologies Pilot Program (QuMP)	Reviewer

Service to Field of Scholarship

Date	Organization	Position
2024-Present	Human Genetics and Genomics Advances	Editorial Board Member
2023-Present	BMC Bioinformatics	Editorial Board Member
2020-2022	Frontiers in Genetics	Guest Associate Editor
2025/1	Health Canada Genomics Research and Development Initiative	Reviewer
2025/2	NIH Neurological, Mental and Behavioral Health (NMBH) Study Section	Member
2024/3	NIH Aging, Injury, Musculoskeletal, Rheumatologic, and Dermatologic Disorders (AIMR) Study Section	Member
2023/11	NIH BBBT (Bioengineering, Biodata, and Biomodeling Technologies)-02 Bioengineering Review Panel	Member
2021/6	NIH GCAT (Genomics, Computational Biology and Technology) Study Section	Member
2024	Association for Computing Machinery Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)	Program Committee Member
2023	ENAR Poster Session	Judge
2021	ASA Pittsburgh Chapter Banquet Poster Session	Judge

Manuscript and other Documentation/Publication Review

Journal Title

Journal of the American Statistical Association
Biometrics
Biostatistics
Annals of Applied Statistics
Nature Communications
Genome Research
Genome Biology
Bioinformatics
Briefings in Bioinformatics
American Journal of Human Genetics
PLOS Genetics
PLOS Computational Biology
Science Advances
Cell Genomics
Communications Biology
Psychological Methods
American Journal of Epidemiology

Leadership in Scholarly and Professional Organizations and Honorary Societies

Date	Organization	Position
2023-2024	Local Organizing Committee, STATGEN 2024, ASA SSGG Section	Co-Chair
2025-2026	ASA Pittsburgh Chapter	President-Elect
2026-2027	ASA Pittsburgh Chapter	President