Jiebiao Wang, PhD

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Education

2012–2017	Ph.D., Biostatistics, University of Chicago, Chicago, Illinois
2010–2012	Master, Statistics, Renmin University of China, Beijing, China
2006–2010	Bachelor, Statistics, Renmin University of China, Beijing, China

Appointments and Positions

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

Publications/Preprints

+: corresponding author; *: co-first author; _: PhD advisee

[1] M. Cai, J. Zhou, C. McKennan, and **J. Wang**+, "scMD: cell type deconvolution using single-cell DNA methylation references," *bioRxiv*, 2023.

[2] P. Huang, M. Cai, X. Lu, C. McKennan, and **J. Wang**+, "Accurate estimation of rare cell type fractions from tissue omics data via hierarchical deconvolution," *bioRxiv*, 2023.

[3] M. Cai, M. Yue, T. Chen, J. Liu, E. Forno, X. Lu, T. Billiar, J. Celedón, C. McKennan, W. Chen+, and **J. Wang**+, "Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution," *Bioinformatics*, vol. 38, no. 11, pp. 3004–3010, 2022.

[4] **J. Wang**+, K. Roeder+, and B. Devlin+, "Bayesian estimation of cell type–specific gene expression with prior derived from single-cell data," *Genome research*, vol. 31, no. 10, pp. 1807–1818, 2021.

[5] **J. Wang**, B. Devlin, and K. Roeder, "Using multiple measurements of tissue to estimate subject-and cell-type-specific gene expression," *Bioinformatics*, vol. 36, no. 3, pp. 782–788, 2020.

[6] K. Satterstrom*, J. Kosmicki*, **J. Wang***, M. S. Breen, S. De Rubeis, J.-Y. An, M. Peng, R. Collins, J. Grove, L. Klei, C. Stevens, J. Reichert, M. S. Mulhern, M. Artomov, S. Gerges, B. Sheppard, X. Xu, A. Bhaduri, U. Norman, H. Brand, G. Schwartz, R. Nguyen, E. E. Guerrero, C. Dias, Autism Sequencing Consortium, iPSYCH-Broad Consortium, C. Betancur, E. H. Cook, L. Gallagher, M. Gill, J. S. Sutcliffe, A. Thurm, M. E. Zwick, A. D. Børglum, M. W. State, A. E. Cicek, M. E. Talkowski, D. J. Cutler, B. Devlin, S. J. Sanders, K. Roeder, M. J. Daly, and J. D. Buxbaum, "Large-scale

exome sequencing study implicates both developmental and functional changes in the neurobiology of autism," *Cell*, vol. 180, no. 3, pp. 568–584.e23, 2020.

[7] S. Chen*, **J. Wang***, E. Cicek, K. Roeder, H. Yu, and B. Devlin, "De novo missense variants disrupting protein–protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types," *Molecular autism*, vol. 11, no. 1, pp. 1–16, 2020.

[8] **J. Wang**, P. Wang, D. Hedeker, and L. S. Chen, "Using multivariate mixed-effects selection models for analyzing batch-processed proteomics data with non-ignorable missingness," *Biostatistics*, vol. 20, no. 4, pp. 648–665, 2019.

[9] **J. Wang***, Q. Liu*, B. Pierce, D. Huo, O. Olopade, H. Ahsan, and L. Chen, "A meta-analysis approach with filtering for identifying gene-level gene-environment interactions," *Genetic epidemiology*, vol. 42, no. 5, pp. 434–446, 2018.

[10] **J. Wang**, E. R. Gamazon, B. L. Pierce, B. E. Stranger, H. K. Im, R. D. Gibbons, N. J. Cox, D. L. Nicolae, and L. S. Chen, "Imputing gene expression in uncollected tissues within and beyond GTEx," *The American Journal of Human Genetics*, vol. 98, no. 4, pp. 697–708, 2016.

[11] J.-M. Pyun, Y. H. Park, **J. Wang**, P. J. Bice, D. A. Bennett, J. P. Kim, S. Kim, A. J. Saykin, and K. Nho, "Transcriptional risk score in alzheimer's disease: from pathology to cognition," *Alzheimer's & Dementia*, 2023.

[12] H.-W. Liang, N. Snyder, **J. Wang**, X. Xun, Q. Yin, K. LeWinn, K. N. Carroll, N. R. Bush, K. Kannan, E. S. Barrett, R. T. Mitchell, F. Tylavsky, and J. J. Adibi, "A study on the association of placental and maternal urinary phthalate metabolites," *Journal of exposure science & environmental epidemiology*, vol. 33, no. 2, pp. 264–272, 2023.

[13] J.-M. Pyun, Y. H. Park, **J. Wang**, P. J. Bice, D. A. Bennett, S. Kim, A. J. Saykin, and K. Nho, "Aberrant GAP43 gene expression is alzheimer disease pathology-specific," *Annals of Neurology*, vol. 93, no. 5, pp. 1047–1048, 2023.

[14] W. H. Cuddleston, X. Fan, L. Sloofman, L. Liang, E. Mossotto, K. Moore, S. Zipkowitz, M. Wang, B. Zhang, **J. Wang**, N. Sestan, B. Devlin, K. Roeder, S. J. Sanders, J. D. Buxbaum, and M. S. Breen, "Spatiotemporal and genetic regulation of A-to-I editing throughout human brain development," *Cell Reports*, vol. 41, no. 5, p. 111585, 2022.

[15] Z. Xu, X. Wang, L. Fan, F. Wang, B. Lin, **J. Wang**, G. Trevejo-Nuñez, W. Chen, and K. Chen, "Integrative analysis of spatial transcriptome with single-cell transcriptome and single-cell epigenome in mouse lungs after immunization," *iScience*, p. 104900, 2022.

[16] P. Chandrashekar, **J. Wang**, G. E. Hoffman, C. He, T. Jin, S. Alatkar, S. Khullar, J. Bendl, J. F. Fullard, P. Roussos, and D. Wang, "DeepGAMI: Deep biologically guided auxiliary learning for multimodal integration and imputation to improve phenotype prediction," *bioRxiv*, 2022.

[17] B. C. McKinney, L. L. McClain, C. M. Hensler, Y. Wei, L. Klei, D. A. Lewis, B. Devlin, **J. Wang**, Y. Ding, and R. A. Sweet, "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," *Translational psychiatry*, vol. 12, no. 1, pp. 1–12, 2022.

[18] J. Tian, **J. Wang**, and K. Roeder, "ESCO: single cell expression simulation incorporating gene co-expression," *Bioinformatics*, vol. 37, no. 16, pp. 2374–2381, 2021.

[19] Y. Qiu, **J. Wang**, J. Lei, and K. Roeder, "Identification of cell-type-specific marker genes from co-expression patterns in tissue samples," *Bioinformatics*, vol. 37, no. 19, pp. 3228–3234, 2021.

[20] F. Yang, K. Gleason, **J. Wang**, J. Duan, X. He, B. L. Pierce, and L. S. Chen, "CCmed: cross-condition mediation analysis for identifying replicable trans-associations mediated by cis-gene expression," *Bioinformatics*, vol. 37, no. 17, pp. 2513–2520, 2021.

[21] S. C. Piantadosi, L. L. McClain, L. Klei, **J. Wang**, B. L. Chamberlain, S. A. Springer, D. A. Lewis, B. Devlin, and S. E. Ahmari, "Transcriptome alterations are enriched for synapse-associated genes in the striatum of subjects with obsessive-compulsive disorder," *Translational psychiatry*, vol. 11, no. 1, pp. 1–11, 2021.

[22] C. A. King, D. Brent, J. Grupp-Phelan, T. C. Casper, J. M. Dean, L. S. Chernick, J. A. Fein, E. M. Mahabee-Gittens, S. J. Patel, R. D. Mistry, S. Duffy, M. Melzer-Lange, A. Rogers, D. M. Cohen, A. Keller, R. Shenoi, R. W. Hickey, M. Rea, M. Cwik, K. Page, T. C. McGuire, **J. Wang**, R. Gibbons, and Pediatric Emergency Care Applied Research Network, "Prospective development and validation of the computerized adaptive screen for suicidal youth," *JAMA psychiatry*, vol. 78, no. 5, pp. 540–549, 2021.

[23] M. L. Seney, S.-M. Kim, J. R. Glausier, M. A. Hildebrand, X. Xue, W. Zong, **J. Wang**, M. A. Shelton, B. N. Phan, C. Srinivasan, A. R. Pfenning, G. C. Tseng, D. A. Lewis, Z. Freyberg, and R. W. Logan, "Transcriptional alterations in dorsolateral prefrontal cortex and nucleus accumbens implicate neuroinflammation and synaptic remodeling in opioid use disorder," *Biological Psychiatry*, vol. 90, no. 8, pp. 550–562, 2021.

[24] N. F. Fitz, **J. Wang**, M. I. Kamboh, R. Koldamova, and I. Lefterov, "Small nucleolar RNAs in plasma extracellular vesicles and their discriminatory power as diagnostic biomarkers of alzheimer's disease," *Neurobiology of Disease*, vol. 159, p. 105481, 2021.

[25] R. Gibbons, K. Hur, J. Lavigne, **J. Wang**, and J. J. Mann, "Medications and Suicide: High Dimensional Empirical Bayes Screening (iDEAS)," *Harvard Data Science Review*, vol. 1, no. 2, 2019.

[26] S. Chen, R. Fragoza, L. Klei, Y. Liu, **J. Wang**, K. Roeder, B. Devlin, and H. Yu, "An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders," *Nature genetics*, vol. 50, no. 7, pp. 1032–1040, 2018.

[27] J. Pitt, M. Riester, Y. Zheng, T. Yoshimatsu, A. Sanni, O. Oluwasola, A. Veloso, E. Labrot, S. Wang, A. Odetunde, A. Ademola, B. Okedere, S. Mahan, R. Leary, M. Macomber, M. Ajani, R. Johnson, D. Fitzgerald, J. Grundstad, J. Tuteja, G. Khramtsova, J. Zhang, E. Sveen, B. Hwang, W. Clayton, C. Nkwodimmah, B. Famooto, E. Obasi, V. Aderoju, M. Oludara, F. Omodele, O. Akinyele, A. Adeoye, T. Ogundiran, C. Babalola, K. MacIsaac, A. Popoola, M. Morrissey, L. S. Chen, **J. Wang**, C. O. Olopade, A. G. Falusi, W. Winckler, K. Haase, P. V. Loo, J. Obafunwa, D. Papoutsakis, O. Ojengbede, B. Weber, N. Ibrahim, K. P. White, D. Huo, O. I. Olopade, and J. Barretina, "Characterization of nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features," *Nature communications*, vol. 9, no. 1, p. 4181, 2018.

[28] F. Yang, **J. Wang**, The GTEx Consortium, B. L. Pierce, and L. S. Chen, "Identifying cis-mediators for trans-eqtls across many human tissues using genomic mediation analysis," *Genome research*, vol. 27, no. 11, pp. 1859–1871, 2017.

[29] L. S. Chen, **J. Wang**, X. Wang, and P. Wang, "A mixed-effects model for incomplete data from labeling-based quantitative proteomics experiments," *The annals of applied statistics*, vol. 11, no. 1, pp. 114–138, 2017.

Funding

As Principal Investigator

2023/2-2027/11	**R01AG080590** (Role: **Contact PI**), NIH, "Statistical methods for population-level cell-type-specific analyses of tissue omics data for Alzheimer's disease", Total: $1,891,625
2022/9-2024/9	**R03OD034501** (Role: **Contact PI**), NIH, "Integration of GTEx and HuBMAP data to gain population-level cell-type-specific insights", $314,739
2021/7-2023/6	Competitive Medical Research Fund (CMRF) (Role: PI), UPMC, $25,000
2022/1-2023/12	Health Sciences Bridge Funding (Role: PI), University of Pittsburgh Schools of Health Sciences, $48,720
2022/1-2023/12	Brain Institute's Assault on Alzheimer's Seed Grant (Role: PI), University of Pittsburgh Brain Institute, $25,000
2022/6-2023/5	Exploring Existing Data Resources Pilot Award (Role: PI), University of Pittsburgh Clinical and Translational Science Institute (CTSI), $25,000
2022/5-2023/4	Public Health Trans-Disciplinary Collaboration Pilot Award (PIs: Wang and Talisa), Pitt CTSI, "Precision Health Methods for Alzheimer's Disease", $45,000

As Co-Investigator/Subcontract PI

2020/5-2024/2	R01MH123184: Computational methods to integrate and interpret the transcriptome from single cell and tissue level data (PI: Roeder), NIH, 1.2 months support per year
2020/7-2025/6	R01HL153058: Mucin sialylation drives epithelial cell senescence and severe asthma (PI: Wenzel), NIH, 1.2 months
2020/10-2025/8	U19AG068054: Alzheimer's Biomarker Consortium - Down Syndrome (ABC-DS) (PI: Handen), NIH, 1.2 months
2022/4-2027/4	P01AI106684: Immune airway-epithelial interactions in steroid-refractory severe asthma (PIs: Ray and Wenzel), NIH, 1.2 months
2022/7-2026/4	R01DK133454: Vinyl chloride modifies the risk for nonalcoholic fatty liver disease (PI: Beier), NIH, 1.2 months
2023/3-2028/2	R01AI164968: Functional consequences of intergenic autoimmune disease risk variants (PIs: Niewold and Demerci), NIH, 1.86 months and 1/2 GSR

Presentations

Invited Presentations

2023	The 16th International Conference on Computational and Methodological Statistics (CMStatistics 2023), Berlin, Germany
2023	Biostatistics Seminar, 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	Cross-Pollination Meeting, NIH Common Fund Data Ecosystem
2023	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	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 ensemble of various deconvolution approaches. ICSA Applied Statistics Symposium

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

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, University of Pittsburgh

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

Contributed Presentations

2020   Bayesian Subject-Level Bulk Expression Deconvolution and Application to Cell-Type-Specific Differential Expression Analysis, Joint Statistical Meetings (JSM)

2019   An empirical Bayes method for deconvolving multi-measure bulk gene expression, JSM

2018   Using multi-tissue gene expression to estimate individual- and cell-type-specific expression via deconvolution, American Society of Human Genetics (ASHG) Annual Meeting (Platform talk)

2017   A High-Dimensional Multivariate Selection Model for Proteomics Data with Batch-Level Missingness, JSM

2016   A multivariate selection model for cluster-level outcome-dependent missing data, JSM

2016   Mixed-effects models for multivariate clustered data with nonignorable missing outcomes, ENAR Spring Meeting

2015   Imputing the transcriptome in inaccessible tissues in and beyond the GTEx project, JSM

2015   A mixed-effects model for incomplete data with experiment-level abundance-dependent missing-data mechanism, ENAR Spring Meeting

Honors and Awards

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, University of Pittsburgh |

Mentoring and Advising

As Ph.D. Dissertation Advisor

2021-Present	Manqi Cai: won **Best Research Presentation Award**, Graduate Student Research Conference 2022, National Institute of Statistical Sciences; **Best PhD Poster Award**, Pitt Biostatistics Research Day 2023

As Ph.D. Dissertation Committee Member

2020	Dongjing Liu (Human Genetics)
2021-2022	Xinjun Wang
2022-2023	Yang Ou
2022-2023	Jian Zou
2022-Present	Hai-Wei Liang (Epidemiology)
2023-Present	Shuangjia Xue (Environmental and Occupational Health)
2023-Present	Rain Katz (Epidemiology)

As Ph.D. Academic Advisor

2020-2022	Lingyi Peng
2021-Present	Gehui Zhang
2022-Present	Penghui Huang: won **Research Poster Award & Student Paper Award Honorable Mention**, ICSA Applied Statistics Symposium 2023; **Student Research Award**, New England Statistics Symposium 2023; **Best PhD Poster Award**, Pitt Biostatistics Research Day 2023
2023-Present	Chen Liu

As MS Academic Advisor

2022-Present	Michelle Sun: won Best Master's Poster Award Honorable Mention, Pitt Biostatistics Research Day 2023
2023-Present	Nick Heaton

Teaching

Instructor

Fall 2023	BIOST 2068, Introduction to Causal Inference, 3 credits, 11 enrolled
Fall 2022	BIOST 2068, Introduction to Causal Inference, 3 credits, 11 enrolled
Fall 2021	BIOST 2068, Introduction to Causal Inference, 3 credits, 35 enrolled

Guest Lecturer

Fall 2023	BIOST 2069: Statistical Methods for Omics Data
Spring 2022	HUGEN 2080: Statistical Genetics
Spring 2020	HUGEN 2080: Statistical Genetics
Spring 2020	EPID 2620: Application of Molecular Biomarkers in Epidemiology

Coordinator

Spring 2022	BIOST 2025, Biostatistics Seminar, 1 credit, 18 enrolled
Fall 2021	BIOST 2025, Biostatistics Seminar, 1 credit, 27 enrolled
Spring 2021	BIOST 2025, Biostatistics Seminar, 1 credit, 28 enrolled
Fall 2020	BIOST 2025, Biostatistics Seminar, 1 credit, 22 enrolled

Spring 2020   BIOST 2025, Biostatistics Seminar, 1 credit, 9 enrolled

Service

Journal Editorship

2023-Present   Editorial Board Member, BMC Bioinformatics

2020-2022   Guest Associate Editor, Statistical Genetics and Methodology, Frontiers in Genetics

2022-Present   Review Editor, Behavioral and Psychiatric Genetics, Frontiers in Genetics & Frontiers in Psychiatry

Manuscript Review

2014-Present   Journal of the American Statistical Association, Biometrics, Biostatistics, Annals of Applied Statistics, Nature Communications, Genome Research, Genome Biology, Bioinformatics, American Journal of Human Genetics, PLOS Genetics, PLOS One, PLOS Computational Biology, Psychological Methods, Statistics and Computing, American Journal of Epidemiology, Briefings in Bioinformatics, Genetic Epidemiology, Human Genetics and Genomics Advances, Science Advances, Statistics in Biosciences, Annals of Surgical Oncology, Biometrical Journal, F1000Research, Frontiers in Genetics, Frontiers in Psychiatry, Neurobiology of Aging, PeerJ, Psychological Medicine, Theranostics, Frontiers in Aging Neuroscience, Schizophrenia Bulletin, Communications Biology, Health Services and Outcomes Research Methodology, Journal of Biopharmaceutical Statistics, BMC Bioinformatics, npj Systems Biology and Applications, NAR Genomics and Bioinformatics

Grant Review

2023/11   Reviewer, NIH BBBT-02 Bioengineering Review Panel

2021/6   Reviewer, NIH GCAT (Genomics, Computational Biology and Technology) Study Section

2021   Grant Reviewer, CTSI Quantitative Methodologies Pilot Program (QuMP), University of Pittsburgh

2022   Grant Reviewer, Department of Psychiatry, University of Pittsburgh

2023   Member, Competitive Medical Research Fund (CMRF) Review Committee, University of Pittsburgh

International Organizations

2023-2024   Co-Chair, Local Organizing Committee, STATGEN 2024: Conference on Statistics in Genomics and Genetics, ASA SSGG

2023   Invited Session Organizer, ENAR

2023   Invited Session Organizer, WNAR

2017, 2023   Invited Session Organizer, ICSA Applied Statistics Symposium

2021, 2022   Invited Session Organizer, JSM

Department Committees

2022-Present   Member, PhD Admissions Committee

2023-Present   Chair, Master Comprehensive Exam Committee

2022   Member, Search Committee for Tenure Stream Faculty

2021-2022   Member, Master Comprehensive Exam Committee

2020-2022   Organizer, Biostatistics Research Day

2020   Member, Biostatistics Teaching Task Force

Other Services

2021-Present   Member, Scholarly Oversight Committee, Pitt Department of Pediatrics

2023   Judge, ENAR Poster Session
2021   Judge, Public Health Dean's Day Poster Session, University of Pittsburgh
2021   Judge, ASA Pittsburgh Chapter Banquet Poster Session

Last updated on August 26, 2023.