Jiebiao Wang, PhD

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Education

2012–2017   PhD, 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-Present   Assistant Professor (Tenure Track), Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA

2023-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

Major/statistical work

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

2023   Huang, Penghui, Cai, Manqi, Xinghua Lu, Chris McKennan, and **Wang, Jiebiao**[+]. Accurate estimation of rare cell type fractions from tissue omics data via hierarchical deconvolution. *bioRxiv*, 2023.

2022   Cai, Manqi, Molin Yue, Tianmeng Chen, Jinling Liu, Erick Forno, Xinghua Lu, Timothy Billiar, Juan Celedón, Chris McKennan, Wei Chen[+], and **Wang, Jiebiao**[+]. Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution. *Bioinformatics*, volume 38, pages 3004–3010, 2022.

2022   Pramod Chandrashekar, **Wang, Jiebiao**, Gabriel E Hoffman, Chenfeng He, Ting Jin, Sayali Alatkar, Saniya Khullar, Jaroslav Bendl, John F. Fullard, Panos Roussos, and Daifeng Wang. DeepGAMI: Deep biologically guided auxiliary learning for multimodal integration and imputation to improve phenotype prediction. *bioRxiv*, 2022.

2021   Fan Yang, Kevin Gleason, **Wang, Jiebiao**, Jubao Duan, Xin He, Brandon L Pierce, and Lin S Chen. CCmed: cross-condition mediation analysis for identifying replicable trans-associations mediated by cis-gene expression. *Bioinformatics*, volume 37, pages 2513–2520, 2021.

2021   Tian, Jinjin, **Wang, Jiebiao**, and Kathryn Roeder. ESCO: single cell expression simulation incorporating gene co-expression. *Bioinformatics*, volume 37, pages 2374–2381, 2021.

2021   **Wang, Jiebiao**[+], Kathryn Roeder[+], and Bernie Devlin[+]. Bayesian estimation of cell type–specific gene expression with prior derived from single-cell data. *Genome research*, volume 31, pages 1807–1818, 2021.

2021 Yixuan Qiu, **Wang, Jiebiao**, Jing Lei, and Kathryn Roeder. Identification of cell-type-specific marker genes from co-expression patterns in tissue samples. *Bioinformatics*, volume 37, pages 3228–3234, 2021.

2020 **Wang, Jiebiao**, Bernie Devlin, and Kathryn Roeder. Using multiple measurements of tissue to estimate subject-and cell-type-specific gene expression. *Bioinformatics*, volume 36, pages 782–788, 2020.

2020 Kyle Satterstrom*, Jack Kosmicki*, **Wang, Jiebiao***, Michael S Breen, Silvia De Rubeis, Joon-Yong An, Minshi Peng, Ryan Collins, Jakob Grove, Lambertus Klei, et al. Large-scale exome sequencing study implicates both developmental and functional changes in the neurobiology of autism. *Cell*, volume 180, pages 568–584, 2020.

2020 Siwei Chen*, **Wang, Jiebiao***, Ercument Cicek, Kathryn Roeder, Haiyuan Yu, and Bernie 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*, volume 11, pages 1–16, 2020.

2019 **Wang, Jiebiao**, Pei Wang, Donald Hedeker, and Lin S Chen. Using multivariate mixed-effects selection models for analyzing batch-processed proteomics data with non-ignorable missingness. *Biostatistics*, volume 20, pages 648–665, 2019.

2019 Robert Gibbons, Kwan Hur, Jill Lavigne, **Wang, Jiebiao**, and J. John Mann. Medications and Suicide: High Dimensional Empirical Bayes Screening (iDEAS). *Harvard Data Science Review*, volume 1, 2019. https://hdsr.mitpress.mit.edu/pub/18lm7jrp.

2018 **Wang, Jiebiao***, Qianying Liu*, Brandon Pierce, Dezheng Huo, Olufunmilayo Olopade, Habibul Ahsan, and Lin Chen. A meta-analysis approach with filtering for identifying gene-level gene-environment interactions. *Genetic epidemiology*, volume 42, pages 434–446, 2018.

2017 Fan Yang, **Wang, Jiebiao**, The GTEx Consortium, Brandon L Pierce, and Lin S Chen. Identifying cis-mediators for trans-eqtls across many human tissues using genomic mediation analysis. *Genome research*, volume 27, pages 1859–1871, 2017.

2017 Lin S Chen, **Wang, Jiebiao**, Xianlong Wang, and Pei Wang. A mixed-effects model for incomplete data from labeling-based quantitative proteomics experiments. *The annals of applied statistics*, volume 11, pages 114–138, 2017.

2016 **Wang, Jiebiao**, Eric R Gamazon, Brandon L Pierce, Barbara E Stranger, Hae Kyung Im, Robert D Gibbons, Nancy J Cox, Dan L Nicolae, and Lin S Chen. Imputing gene expression in uncollected tissues within and beyond GTEx. *The American Journal of Human Genetics*, volume 98, pages 697–708, 2016.

Collaborative articles

2023 Jung-Min Pyun, Young Ho Park, **Wang, Jiebiao**, Paula J. Bice, David A. Bennett, SangYun Kim, Andrew J. Saykin, and Kwangsik Nho. Aberrant GAP43 gene expression is alzheimer disease pathology-specific. *Annals of Neurology*, volume 93, pages 1047–1048, 2023.

2022 Zhongli Xu, Xinjun Wang, Li Fan, Fujing Wang, Becky Lin, **Wang, Jiebiao**, Giraldina Trevejo-Nuñez, Wei Chen, and Kong Chen. Integrative analysis of spatial transcriptome with single-cell transcriptome and single-cell epigenome in mouse lungs after immunization. *iScience*, page 104900, 2022.

2022 Brandon C McKinney, Lora L McClain, Christopher M Hensler, Yue Wei, Lambertus Klei, David A Lewis, Bernie Devlin, **Wang, Jiebiao**, Ying Ding, and Robert 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*, volume 12, pages 1–12, 2022.

2022 Hai-Wei Liang, Nathaniel Snyder, **Wang, Jiebiao**, Xiaoshuang Xun, Qing Yin, Kaja LeWinn, Kecia N Carroll, Nicole R Bush, Kurunthachalam Kannan, Emily S Barrett, et al. A study on the association of placental and maternal urinary phthalate metabolites. *Journal of Exposure Science & Environmental Epidemiology*, pages 1–9, 2022.

2022 Winston H. Cuddleston, Xuanjia Fan, Laura Sloofman, Lindsay Liang, Enrico Mossotto, Kendall Moore, Sarah Zipkowitz, Minghui Wang, Bin Zhang, **Wang, Jiebiao**, and et al. Spatiotemporal and genetic regulation of A-to-I editing throughout human brain development. *Cell Reports*, volume 41, page 111585, 2022.

2021 Marianne Seney, Sam-Moon Kim, Jill Glausier, Mariah Hildebrand, Xiangning Xue, Wei Zong, **Wang, Jiebiao**, Micah Shelton, BaDoi Phan, et al. Transcriptional alterations in dorsolateral prefrontal cortex and nucleus accumbens implicate neuroinflammation and synaptic remodeling in opioid use disorder. *Biological Psychiatry*, volume 90, pages 550–562, 2021.

2021 Sean C Piantadosi, Lora L McClain, Lambertus Klei, **Wang, Jiebiao**, Brittany L Chamberlain, Sara A Springer, David A Lewis, Bernie Devlin, and Susanne E Ahmari. Transcriptome alterations are enriched for synapse-associated genes in the striatum of subjects with obsessive-compulsive disorder. *Translational psychiatry*, volume 11, pages 1–11, 2021.

2021 Cheryl A. King, David Brent, Jacqueline Grupp-Phelan, T. Charles Casper, J. Michael Dean, Lauren S. Chernick, Joel A. Fein, E. Melinda Mahabee-Gittens, Shilpa J. Patel, Rakesh D. Mistry, Susan Duffy, Marlene Melzer-Lange, Alexander Rogers, Daniel M. Cohen, Allison Keller, Rohit Shenoi, Robert W. Hickey, Margaret Rea, Mary Cwik, Kent Page, Taylor C. McGuire, **Wang, Jiebiao**, Robert Gibbons, and Pediatric Emergency Care Applied Research Network. Prospective development and validation of the computerized adaptive screen for suicidal youth. *JAMA psychiatry*, volume 78, pages 540–549, 2021.

2021 Nicholas F Fitz, **Wang, Jiebiao**, M Ilyas Kamboh, Radosveta Koldamova, and Iliya Lefterov. Small nucleolar RNAs in plasma extracellular vesicles and their discriminatory power as diagnostic biomarkers of alzheimer's disease. *Neurobiology of Disease*, volume 159, page 105481, 2021.

2018 Jason Pitt, Markus Riester, Yonglan Zheng, Toshio Yoshimatsu, Ayodele Sanni, Olayiwola Oluwasola, Artur Veloso, Emma Labrot, Shengfeng Wang, Abayomi Odetunde, Adeyinka Ademola, Babajide Okedere, Scott Mahan, Rebecca Leary, Maura Macomber, Mustapha Ajani, Ryan Johnson, Dominic Fitzgerald, Jason Grundstad, Jigyasa Tuteja, Galina Khramtsova, Jing Zhang, Elisabeth Sveen, Bryce Hwang, Wendy Clayton, Chibuzor Nkwodimmah, Bisola Famooto, Esther Obasi, Victor Aderoju, Mobolaji Oludara, Folusho Omodele, Odunayo Akinyele, Adewunmi Adeoye, Temidayo Ogundiran, Chinedum Babalola, Kenzie MacIsaac, Abiodun Popoola, Michael Morrissey, Lin S. Chen, **Wang, Jiebiao**, et al. Characterization of nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. *Nature communications*, volume 9, pages 1–12, 2018.

2018 Siwei Chen, Robert Fragoza, Lambertus Klei, Yuan Liu, **Wang, Jiebiao**, Kathryn Roeder, Bernie Devlin, and Haiyuan Yu. An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. *Nature genetics*, volume 50, pages 1032–1040, 2018.

Research

As Principal Investigator

2022/9-2023/9	**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

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	Joint Seminar Series of Genetics, Genomics, and Bioinformatics, University of California, Riverside
2023	Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution. ENAR Spring Meeting, Nashville, TN
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

Software Packages

EnsDeconv Ensemble Deconvolution to robustly estimate cellular fractions from bulk omics data: https://github.com/randel/EnsDeconv

MIND Using bulk gene expression to estimate cell-type-specific gene expression via deconvolution: https://github.com/randel/MIND

MixRF A random-forest-based approach for imputing clustered incomplete data: https://github.com/randel/MixRF

mvMISE A general framework for multivariate mixed-effects selection models with potential missing data: https://github.com/randel/mvMISE

ofGEM A meta-analysis approach with filtering for identifying gene-level gene-environment interactions: https://github.com/randel/ofGEM

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 Craig Excellence in Education Award, School of Public Health, University of Pittsburgh

Mentoring and Advising

As PhD 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 PhD 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 (EOH)

2023-Present   Xiangning Xue

2023-Present   Rain Katz (Epidemiology)

As PhD Academic Advisor

2020-2022   Lingyi Peng

2021-Present   Gehui Zhang

2022-Present   Penghui Huang: won **Best PhD Poster Award**, Pitt Biostatistics Research Day 2023

As MS Academic Advisor

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

Teaching

Instructor

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

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

2020-2022	Guest Associate Editor, Frontiers in Genetics
2022-Present	Review Editor, 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

Study Section

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

International Organizations

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	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	Member, Competitive Medical Research Fund (CMRF) Review Committee, Pitt
2023	Judge, ENAR Poster Session
2022	Grant Reviewer, Department of Psychiatry, University of Pittsburgh
2021	Grant Reviewer, CTSI Funding Competition, University of Pittsburgh
2021	Judge, Pitt Public Health Dean's Day Poster Session
2021	Judge, ASA Pittsburgh Chapter Banquet Poster Session

Last updated on May 3, 2023.