

# 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**<sup>+</sup>, “scMD: cell type deconvolution using single-cell DNA methylation references,” *bioRxiv*, 2023.
- [2] P. Huang, M. Cai, X. Lu, C. McKennan, and **J. Wang**<sup>+</sup>, “Accurate estimation of rare cell type fractions from tissue omics data via hierarchical deconvolution,” *The Annals of Applied Statistics (accepted)*, 2023.
- [3] M. Cai, M. Yue, T. Chen, J. Liu, E. Forno, X. Lu, T. Billiar, J. Celedón, C. McKennan, W. Chen<sup>+</sup>, and **J. Wang**<sup>+</sup>, “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**<sup>+</sup>, K. Roeder<sup>+</sup>, and B. Devlin<sup>+</sup>, “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] P. B. Chandrashekar, S. Alatkari, **J. Wang**, G. E. Hoffman, C. He, T. Jin, 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 genotype–phenotype prediction,” *Genome Medicine*, vol. 15, no. 1, p. 88, 2023.
- [12] 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.
- [13] 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. Tykavsky, 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.
- [14] 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.
- [15] 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.
- [16] 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.
- [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.

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## 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, 0.6 months
- 2023/3-2028/2 R01AI164968: Functional consequences of intergenic autoimmune disease risk variants (PIs: Niewold and Demerci), NIH, 1.8 months and 1/2 GSR

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## Presentations

### ***Invited Presentations***

- 2024 Biostatistics and Computational Biology Branch Seminar Series, National Institute of Environmental Health Sciences (NIEHS), NIH
- 2023 The 16th International Conference on Computational and Methodological Statistics (CMStatistics), Berlin, Germany
- 2023 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 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
- 2024 Presenter of the Senior Vice Chancellor's Research Seminar (\$10,000), University of Pittsburgh

## **Mentoring and Advising**

### ***As Ph.D. Dissertation Advisor***

- 2021-Present Manqi Cai  
*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. Academic Advisor***

- 2022-Present Penghui Huang  
*Research Poster Award, ICOSA Applied Statistics Symposium 2023*  
*Student Paper Award Honorable Mention, ICOSA 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

2021-2023 Gehui Zhang

2020-2022 Lingyi Peng

### ***As Ph.D. Dissertation Committee Member***

- 2020 Dongjing Liu (Human Genetics): Integrated Genome-Wide Analysis of Human Facial Morphology
- 2021-2022 Xinjun Wang: Statistical Learning and Analysis of Single-Cell Multi-Omics Data
- 2022-2023 Yang Ou: Estimation of Causal Treatment Effect for Clustered Observational Data with Unmeasured Confounding
- 2022-2023 Jian Zou: Clustering, Biomarker and Cancer Model Selection Using Omics Data
- 2022-Present Hai-Wei Liang (Epidemiology)
- 2023-Present Shuangjia Xue (Environmental and Occupational Health)
- 2023-Present Rain Katz (Epidemiology)
- 2023-Present Xiangning Xue
- 2023-Present Huy Le (Statistics)

### ***As MS Thesis Advisor***

- 2023-Present Michelle Sun  
*Best Master's Poster Award Honorable Mention, Pitt Biostatistics Research Day 2023*
- 2023-Present Jenny Liang

### ***As MS Academic Advisor***

- 2023-Present Nick Heaton

## **Teaching**

### ***Instructor***

- Fall 2023 BIOST 2068, Introduction to Causal Inference, 3 credits, 13 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

Fall 2023 BIOST 2065: Analysis of Incomplete 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

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**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, Genomics, Proteomics & Bioinformatics

***Grant Review***

2023/11 Reviewer, NIH BBT (Bioengineering, Biodata, and Biomodeling Technologies)-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, Section on Statistics in Genomics and Genetics, American Statistical Association
- 2023 Invited Session Organizer, ENAR (Eastern North American Region of The International Biometric Society)
- 2023 Invited Session Organizer, WNAR (Western North American Region of The International Biometric Society)
- 2017, 2023 Invited Session Organizer, ICSA Applied Statistics Symposium
- 2021, 2022 Invited Session Organizer, JSM (Joint Statistical Meetings)

### ***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 November 30, 2023.*