

# CURRICULUM VITAE

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Department of Biostatistics  
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## EDUCATION and TRAINING

### Undergraduate

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

### Graduate

2010-2012 Renmin University of China Master, 2010 Statistics  
Beijing, China

2012-2017 University of Chicago Ph.D., 2017 Biostatistics  
Chicago, IL

### Post-Graduate

2017-2019 Carnegie Mellon University Postdoctoral researcher Statistics  
Pittsburgh, PA

## APPOINTMENTS and POSITIONS

### Academic

2020 - Present University of Pittsburgh Assistant Professor (Tenure Stream)  
Pittsburgh, PA Department of Biostatistics

2017 - 2019 Carnegie Mellon University Postdoctoral Researcher  
Pittsburgh, PA Department of Statistics and Data Science

2013 - 2017 University of Chicago Research Assistant  
Chicago, IL Department of Public Health Sciences

## MEMBERSHIP in PROFESSIONAL and SCIENTIFIC SOCIETIES

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

## HONORS and AWARDS

- 2018 Outstanding Performance Award in the Field of Public Health Sciences,  
Division of the Biological Sciences, University of Chicago
- 2018 Trainee Award Honorable Mention, Association of Chinese Geneticists in America

## PUBLICATIONS

[Google Scholar Profile](#)

[GitHub Profile](#)

+: corresponding/senior author

\*: co-first author

\_: PhD advisee

### Statistical Papers (from independent methodological research)

1. **Wang, J.**, Gamazon, E. R., Pierce, B. L., Stranger B. E., Im, H. K., Gibbons, R. D., Cox, N. J., Nicolae, D. L., Chen, L. S. (2016). Imputing gene expression in uncollected tissues within and beyond GTEx. *American Journal of Human Genetics*, 98(4), 697-708.
2. Chen, L. S., **Wang, J.**, Wang, X., Wang, P. (2017). A mixed-effects model for incomplete data from labeling-based quantitative proteomics experiments. *Annals of Applied Statistics*, 11(1), 114-138.
3. Yang, F., **Wang, J.**, the GTEx consortium, Pierce, B. L., Chen, L. S. (2017). Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. *Genome Research*, 27(11), 1859-1871.
4. **Wang, J.\***, Liu, Q.\*, Pierce, B. L., Huo, D., Olopade, O. I., Ahsan, H., Chen, L. S. (2018). A meta-analysis approach with filtering for identifying gene-level gene-environment interactions. *Genetic Epidemiology*, 42(5): 434-446.
5. **Wang, J.**, Wang, P., Hedeker, D., Chen, L. S. (2019). Using multivariate mixed-effects selection models for analyzing batch-processed proteomics data with non-ignorable missingness. *Biostatistics*, 20(4), 648–665.
6. Gibbons R. D., Kwan Hur, Lavigne J., **Wang J.**, Mann J. J. (2019). Medications and suicide high dimensional empirical Bayes screening (iDEAS). *Harvard Data Science Review*, 1(2).
7. **Wang, J.**, Devlin, B., Roeder, K. (2020). Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. *Bioinformatics*, 36(3), 782-788. (Selected as a Platform Talk at American Society of Human Genetics 2018 Annual Meeting)
8. Tian, J., **Wang, J.**, & Roeder, K. (2021). ESCO: single cell expression simulation incorporating gene co-expression. *Bioinformatics*.
9. Yang, F., Gleason, K. J., **Wang, J.**, Duan, J., He, X., Pierce, B. L., & Chen, L. S. (2021). CCmed: Cross-condition mediation analysis for identifying replicable trans-associations mediated by cis-gene expression. *Bioinformatics*.
10. **Wang, J.\***, Roeder, K.\*, Devlin, B.\* (2021). Bayesian estimation of cell type-specific gene expression with prior derived from single-cell data. *Genome Research* (Accepted).

### Collaborative Papers (from interdisciplinary collaborative research)

11. Chen, S., Fragoza, R., Klei, L., Liu, Y., **Wang, J.**, Roeder, K., Devlin, B., Yu H. (2018). An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. *Nature Genetics*, 50, 1032-1040.
12. Pitt, J. J., Riester, M., Zheng, Y., Yoshimatsu, T. F., Sanni, A., Oluwasola, O., Artur Veloso, Emma Labrot, Shengfeng Wang, Abayomi Odetunde, Adeyinka Ademola, Babajide Okedere, Scott Mahan,

- Rebecca Leary, Maura Macomber, Mustapha Ajani, Ryan S. Johnson, Dominic Fitzgerald, A. Jason Grundstad, Jigyasa H. 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 P. Morrissey, Lin S. Chen, **Wang, J.**, Christopher O. Olopade, Adeyinka G. Falusi, Wendy Winckler, Kerstin Haase, Peter Van Loo, John Obafunwa, Dimitris Papoutsakis, Oladosu Ojengbede, Barbara Weber, Nasiru Ibrahim, Kevin P. White, Dezheng Huo, Olufunmilayo I. Olopade & Jordi Barretina (2018). Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. *Nature Communications*, 9(1), 4181.
13. Satterstrom, F. K.\* , Kosmicki, J. A.\* , **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, S. J., Roeder, K., Buxbaum, J. D., Daly, M. J. (2020). Large-scale exome sequencing study implicates both developmental and functional changes in the neurobiology of autism. *Cell*, 180(3), 568-584.
  14. Chen, S.\* , **Wang, J.\*** , Cicek, E., Roeder, K., Yu, H., Devlin, B. (2020). 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*. 11(1):76.
  15. Cheryl A. King, David Brent, Jacqueline Grupp-Phelan, T. Charles Casper, J. Michael Dean, Lauren Chernick, Joel A. Fein, MPH, E. Melinda Mahabee-Gittens, M.S., Shilpa J. Patel, MPH, Rakesh D. Mistry, M.S., Susan Duffy, Marlene Melzer-Lange, Alexander Rogers, Daniel M. Cohen, Allison Keller, Rohit Sheno, Robert W. Hickey, Margaret Rea, Kent Page, **Wang, J.**, Robert Gibbons, and the Pediatric Emergency Care Applied Research Network. (2021). Prospective Development and Validation of the Computerized Adaptive Screen for Suicidal Youth. *JAMA Psychiatry*.
  16. Piantadosi S, McClain L, Klei L, **Wang J**, Chamberlain B, Springer S, Lewis D, Devlin B, Ahmari S. (2021). Transcriptome alterations are enriched for synapse-associated genes in the striatum of subjects with obsessive-compulsive disorder. *Translational Psychiatry* 11(1):171.

### Manuscripts under Revision/Review

17. Qiu Y, **Wang J.**, Lei J, Roeder K. Identification of cell-type-specific marker genes from co-expression patterns in tissue samples. *Bioinformatics* (under revision). 2021
18. McKinney B, Hensler C, Wei Y, Lewis D, **Wang J.**, Ding Y, Sweet R. Schizophrenia-associated differential DNA methylation in the superior temporal gyrus is distributed to many sites across the genome and annotated by the risk gene MAD1L1. medRxiv. 2020
19. Seney M, Moon-Kim S, Glausier J, Hildebrand M, Xue X, Zong W, **Wang J.**, Shelton M, Phan B, Srinivasan C, Pfenning A, Tseng G, Lewis D, Freyberg Z, Logan R. Transcriptional alterations in opioid use disorder reveal an interplay between neuroinflammation and synaptic remodeling. bioRxiv. 2020
20. Nicholas F. Fitz, **Wang J.**, Florent Letronne, Kyong Nyon Nam, M. Ilyas Kamboh, Radosveta Koldamova, Iliya Lefterov. Small nucleolar RNAs in plasma extracellular vesicles and their discriminatory power as diagnostic biomarkers for Alzheimer's disease. 2020
21. Ryn Cuddleston, Enrico Mossotto, Laura Sloofman, Lindsay Liang, Xuijana Fan, Minghui Wang, Bin Zhang, **Wang J.**, Nenad Sestan, Bernie Devlin, Kathryn Roeder, Joseph D. Buxbaum, Stephan J. Sanders, Michael S. Breen. Expansion of RNA sequence diversity and RNA editing rates throughout human cortical development. 2021

## RESEARCH

### Co-Investigator / Subcontract PI

#### Current research support

Years/Months	Grant and/or Contract Number and Title	Source	Effort
2020/5-2024/2	R01MH123184: Computational Methods to Integrate and Interpret the Transcriptome from Single Cell and Tissue Level Data (PI: Roeder)	NIH	10%
2020/7-2025/6	R01HL153058: Mucin sialylation drives epithelial cell senescence and severe asthma (PI: Wenzel)	NIH	10%
2020/10-2025/8	U19AG068054: Alzheimer's Biomarker Consortium - Down Syndrome (ABC-DS) (PI: Handen/ Christian/ Head/ Mapstone)	NIH	10%
2020/5-2021/4	R37MH057881-22S1: Genetic Association in Schizophrenia and Other Disorders (PI: Devlin)	NIH	16.7%
2020/3-2022/2	MR2020-109502: Overcoming insulin deficiency and resistance to reduce diabetes risk (PI: Jurczak)	Pittsburgh Foundation	20%

#### Upcoming research support

2021/5-2023/4	R01ES029336: Placental origins of phthalate-induced changes in fetal reproductive development (PI: Adibi)	NIH	10%
2021/8-2022/7	W81XWH1810284: Controlled trial of the emotion awareness (PI: Mazefsky)	DOD	20%

## INVITED PRESENTATIONS

1. Detecting Cell-type-specific eQTLs Using Bayesian Estimates of Cell-type-specific Gene Expression from Tissue Samples with Single-cell Prior. ENAR, 2021.
2. Bayesian estimation of cell-type-specific gene expression for each tissue sample with prior derived from single-cell data. Department of Statistics, University of Pittsburgh, 2020.
3. Gene expression deconvolution implicates cell-type-specific gene expression and co-expression in autism. 75th Anniversary of the Society of Biological Psychiatry (SOBP) Meeting (canceled due to COVID-19), 2020.
4. High-dimensional mixed-effects models for multi-omics data. Department of Biostatistics, University of Pittsburgh, 2019.
5. A random-effects model for multi-tissue deconvolution to estimate individual-level cell-type-specific gene expression. ICSA Applied Statistics Symposium, 2018
6. High-Dimensional Multivariate Selection Models for Proteomics Data with Nonignorable Missingness. Department of Human Genetics, University of Pittsburgh, 2017.
7. A high-dimensional multivariate selection model for proteomics data with nonignorable missingness. Dept of Biomedical Informatics, Arizona State University, 2017.
8. Statistical methods for genomics data with clustered structure and missingness. Division of Biostatistics, Medical College of Wisconsin, 2017.
9. 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, 2016.

## OTHER PRESENTATIONS

10. Joint Statistical Meetings, Bayesian Subject-Level Bulk Expression Deconvolution and Application to Cell-Type-Specific Differential Expression Analysis, Virtual, 2020
11. Joint Statistical Meetings, An empirical Bayes method for deconvolving multi-measure bulk gene expression, Denver, CO, 2019
12. American Society of Human Genetics Annual Meeting, Using multi-tissue gene expression to estimate individual- and cell-type-specific expression via deconvolution, San Diego, CA, 2018 (Platform talk)
13. Joint Statistical Meetings, A High-Dimensional Multivariate Selection Model for Proteomics Data with Batch-Level Missingness, Washington, DC, 2017
14. Joint Statistical Meetings, A multivariate selection model for cluster-level outcome-dependent missing data, Chicago, IL, 2016
15. ENAR Spring Meeting, Mixed-effects models for multivariate clustered data with nonignorable missing outcomes, Austin, TX, 2016
16. Joint Statistical Meetings, Imputing the transcriptome in inaccessible tissues in and beyond the GTEx project, Seattle, WA, 2015
17. ENAR Spring Meeting, A mixed-effects model for incomplete data with experiment-level abundance-dependent missing-data mechanism, Miami, FL, 2015

## TEACHING

### Graduate Courses

Year(s)	Course Number & Title	Role	Credit & Class Size
2021 Fall	BIOST 2068, Introduction to Causal Inference	Primary instructor	Upcoming
2021 Spring	BIOST 2025, Biostatistics Seminar	Coordinator	1 credit, 28 enrolled
2020 Fall	BIOST 2025, Biostatistics Seminar	Coordinator	1 credit, 22 enrolled
2020 Spring	BIOST 2025, Biostatistics Seminar	Coordinator	1 credit, 9 enrolled
2020 Spring	HUGEN 2080: Statistical Genetics	Guest lecturer	
2020 Spring	EPID 2620: Application of Molecular Biomarkers in Epidemiology	Guest lecturer	

## MENTORING AND ADVISING

### Doctoral Students

#### Part A: as PhD Dissertation Committee Member

Year(s)	Student's Name (Department), Dissertation	Role
2020	Dongjing Liu (Human Genetics), Integrated genome-wide analysis of normal-range facial variation	Dissertation Committee Member

#### Part B: as PhD Academic Advisor

Year(s)	Student's Name (Department)	Role
2020-	Lingyi Peng (Biostatistics)	Academic Advisor

## SERVICE

### Department Committees

2020 – Present Member, Biostatistics Research Day Organization Committee  
2020 – Present Member, Biostatistics Teaching Task Force  
2021 – Present Member, MS Comprehensive Exam Committee

### Other Service

2021 Judge, Dean's Day Poster Session

### Journal Editorial Board

2020 – Present Guest Associate Editor Frontiers in Genetics

### Manuscript Reviewer

#### [Publons Profile](#)

2021 Annals of Surgical Oncology  
2020 Journal of the American Statistical Association  
2020 Briefings in Bioinformatics  
2020- Science Advances  
2020 Statistics in Biosciences  
2020 Genetic Epidemiology  
2020 Frontiers in Genetics  
2019 Biostatistics  
2019- PLOS Genetics  
2019- PLOS Computational Biology  
2019- Psychological Methods  
2019 Theranostics  
2018- Biometrics  
2018 American Journal of Epidemiology  
2018 PeerJ  
2017- The American Journal of Human Genetics  
2015- Bioinformatics  
2014- PLOS One

### International Organizations

2017 Invited Session Organizer, Applied Statistics Symposium,  
International Chinese Statistical Association (ICSA)  
2021 Invited Session Organizer, JSM (Joint Statistical Meetings)