Hao Feng

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Mailing address	1930 Old Spanish Trail, PHB 710.07 Houston, TX 77054
Email	hao.feng@uth.tmc.edu
Google Scholar	Link to Google scholar
Official Website	Link to Official Website
Lab Website	https://hfenglab.org/

Academic Appointment

- **Associate Professor (tenure-track)** 2025.07-present
  Department of Biostatistics & Data Science
  School of Public Health
  The University of Texas Health Science Center at Houston (UTHealth)
- **Faculty Member** 2025.07-present
  Center for Spatial Temporal Modeling for Applications in Population Sciences
  School of Public Health
  The University of Texas Health Science Center at Houston (UTHealth)

Education

- **Ph.D. in Biostatistics and Bioinformatics** 2014-2019
  Emory University, Laney Graduate School
  — Advisor: Dr. Hao Wu
  — Dissertation committee members: Dr. Zhaohui Steve Qin, Dr. Peng Jin, Dr. Karen Conneely
  — Dissertation: *Statistical Methods for High-throughput Epigenomics Data.*
  [** Michael Kutner Distinguished Doctoral Student Award **]
- **MSPH in Biostatistics and Bioinformatics** 2011-2013
  Emory University, Rollins School of Public Health
  — Advisors: Hao Wu, Karen Conneely
  — Thesis: *A Hierarchical Bayesian Approach to Detect Differentially Methylated Loci from Bisulfite Sequencing Data*
  [** Charles C. Shepard Award finalist**]
- **B.S. in Biosciences** 2007-2011
  University of Science and Technology of China (USTC)

Past Professional Experience

- **Assistant Professor (tenure-track)** 2019.08-2025.06
  Department of Population & Quantitative Health Sciences
  Case Western Reserve University School of Medicine, Cleveland, Ohio
- **Member** 2019.08-2025.06
  Case Comprehensive Cancer Center
  Case Western Reserve University, Cleveland, Ohio

- **Statistician/Full-Time Summer Intern** 2017.05-2017.08
  Global Research & Development
  Pfizer Inc, La Jolla, California
- **Data Analyst** 2013.06-2014.04
  Department of Human Genetics, School of Medicine,
  Emory University, Atlanta, Georgia.

Research Interests

- Statistical Methodology: Biostatistics, Bioinformatics, Computational methods in high-throughput -*omics* data, Signal deconvolution, Single-cell DNA methylation.
- Applications: Cancer epigenetics/epigenomics, computational biology, cell-free DNA, biomarker discovery, neurodegenerative diseases, PTSD.

Publications

Google Scholar citation statistics (as of October 2026): All citations: 2575. h-index: 19. i10-index: 23.

† = These authors contributed equally to this work.
* = Corresponding author.
underline = lab member.

Biostatistics Methodology Publications

1. Daoyu Duan, Wenjing Ma, Wen Tang, Hao Wu, Liangliang Zhang*, **Hao Feng***. *mist: a hierarchical Bayesian framework for detecting differential DNA methylation dynamics in single-cell data.* (2026) **Nature Communications**.
2. Daxuan Deng, Lijun Zhang, **Hao Feng**, Vernon M Chinchilli, Chixiang Chen, Ming Wang. *Improving estimation efficiency for survival data analysis by integrating a coarsened time-to-event outcome from an external study.* (2025) **Biometrics**.
3. Shilin Yu†, Guanqun Meng†, Wen Tang, Wenjing Ma, Rui Wang, Xiongwei Zhu, Xiaobo Sun, **Hao Feng***. *cypress: an R/Bioconductor package for cell-type-specific differential expression analysis power assessment.* (2024) **Bioinformatics**.
4. Kaichen Xu, Yan Lu, Suyang Hou, Kainan Liu, Yihang Du, Mengqian Huang, **Hao Feng**, Hao Wu, Xiaobo Sun. *Detecting anomalous anatomic regions in spatial transcriptomics with STANDS.* (2024) **Nature Communications**.
5. Guanqun Meng, Yue Pan, Wen Tang, Lijun Zhang, Ying Cui, Fredrick R. Schumacher, Ming Wang, Rui Wang, Sijia He, Jeffrey Krischer, Qian Li*, **Hao Feng***. *imply: improving cell-type deconvolution accuracy using personalized reference profiles.* (2024) **Genome Medicine**.
6. Daxuan Deng, Vernon M Chinchilli, **Hao Feng**, Chixiang Chen, Ming Wang. *Robust integration of secondary outcomes information into primary outcome analysis in the presence of missing data.* (2024) **Statistical Methods in Medical Research**.
7. Zhenxing Guo†, Daoyu Duan†, Wen Tang, Julia Zhu, William S. Bush, Liangliang Zhang, Xiaofeng Zhu, Fulai Jin, **Hao Feng***. *magpie: a power evaluation method for differential RNA methylation analysis in N6-methyladenosine sequencing.* (2024) **PLOS Computational Biology**.

8. **Hao Feng***, Guanqun Meng, Tong Lin, Hemang Parikh, Ziyi Li, Jeffery Krischer, Qian Li*. *ISLET: individual-specific reference panel recovery improves cell-type-specific inference.* (2023) **Genome Biology**.
9. Daoyu Duan, Wen Tang, Runshu Wang, Zhenxing Guo*, **Hao Feng***. *Evaluation of epitranscriptome-wide N6-methyladenosine differential analysis methods.* (2023) **Briefings in Bioinformatics**.
10. Guanqun Meng, Wen Tang, Emina Huang, Ziyi Li, **Hao Feng***. *A comprehensive assessment of cell type-specific differential expression methods in bulk data.* (2023) **Briefings in Bioinformatics**.
11. Daoyu Duan, Sijia He, Emina Huang, Ziyi Li*, **Hao Feng***. *NeuCA web server: a neural network-based cell annotation tool with web-app and GUI.* (2022) **Bioinformatics**.
12. Ziyi Li*, **Hao Feng***. *A neural network-based method for exhaustive cell label assignment using single cell RNA-seq data.* (2022) **Scientific Reports**.
13. **Hao Feng**, Hao Wu. *Differential methylation analysis for bisulfite sequencing using DSS.* (2019) **Quantitative Biology**.
14. **Hao Feng**, Peng Jin, Hao Wu. *Disease prediction by cell-free DNA methylation.* (2018) **Briefings in Bioinformatics**.
15. Weiwei Zhang†, **Hao Feng**†, Hao Wu, Xiaoqi Zheng. *Accounting for tumor purity improves cancer subtype classification from DNA methylation data.* (2017) **Bioinformatics**.
16. Hao Wu, Tianlei Xu, **Hao Feng**, Li Chen, Ben Li, Bing Yao, Zhaohui Steve Qin, Peng Jin, Karen N. Conneely. *Detection of differentially methylated regions from whole-genome bisulfite sequencing data without replicates.* (2015) **Nucleic Acids Research**.
17. **Hao Feng**, Karen N. Conneely, Hao Wu. *A Bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data.* (2014) **Nucleic Acids Research**.

Book Chapter

18. **Hao Feng**, Karen Conneely, Hao Wu. *Differential Methylation Analysis for Bisulfite Sequencing (BS-Seq) Data.* (2022) **Epigenome-Wide Association Studies**. Methods in Molecular Biology book series. Humana Press, Springer.

Team Science Publications

19. Ming Wang, Hongke Wu, Aaron Bonner-Jackson, Yiming Chen, Wen Tang, **Hao Feng**, Lijun Zhang, Chixiang Chen, James B Leverenz, Jagan A Pillai. *Early Behavioral and Cognitive Changes in Patients With Pathologically Confirmed Alzheimer Disease, Lewy Body Dementia, and Mixed Dementia.* (2026) Neurology Open Access.
20. Aditi Singh, Ximena Lu Ruden, Wen Tang, Awoniyi Olumide Awonuga, Douglas Mark Ruden, Steven James Korzeniewski, Elizabeth Ella Puscheck, **Hao Feng**, Daniel Allen Rappolee. *Novel kinetic and developmental transcriptomic pan-stress responses by embryonic stem cells.* (2025) Scientific Reports.

21. Yiqian Zhang, Jonas Schluter, Lijun Zhang, Xuan Cao, Robert R. Jenq, **Hao Feng**, Jonathan Haines, Liangliang Zhang. *Review and revamp of compositional data transformation: A new framework combining proportion conversion and contrast transformation.* (2024) Computational and Structural Biotechnology Journal.

22. Ximena L Ruden, Aditi Singh, Teya Marben, Wen Tang, Awoniyi O Awonuga, Douglas M Ruden, Elizabeth E Puscheck, **Hao Feng**, Steven J Korzeniewski, Daniel A Rappolee. *A Single Cell Transcriptomic Fingerprint of Stressed Premature, Imbalanced Differentiation of Embryonic Stem Cells.* (2024) Birth Defects Research.

23. Moeez Rathore, Kimberly Curry, Wei Huang, Daniel Martin, Jiyeon Baek, Derek Taylor, Masaru Miyagi, Wen Tang, **Hao Feng**, Yamu Li, Zhenghe Wang, Hallie Graor, Joseph Willis, Elizabeth Bryson, Christina S Boutros, Omkar Desai, Bianca Islam, Lee M Elis, Stephen E Moss, Jordan M Winter, John Greenwood, Rui Wang. *Leucine-Rich Alpha-2-Glycoprotein 1 Promotes Metastatic Colorectal Cancer Growth Through Human Epidermal Growth Factor Receptor 3 Signaling.* (2024) Gastroenterology.

24. Wenzhang Wang, Fanpeng Zhao, Yubing Lu, Sandra L. Siedlak, Hisashi Fujioka, **Hao Feng**, George Perry, Xiongwei Zhu. *Damaged Mitochondria Coincide with Presynaptic Vesicle Loss and Abnormalities in Alzheimer's Disease Brain.* (2023) Acta Neuropathologica Communications.

25. Moeez Rathore, Wei Zhang, Michel'le Wright, Mehrdad Zarei, Ali Vaziri-Gohar, Omid Hajihassani, Ata Abbas, **Hao Feng**, Jonathan Brody, Sandy D. Markowit, Jordan Winter, Rui Wang. *Liver Endothelium Microenvironment Promotes HER3-mediated Cell Growth in Pancreatic Ductal Adenocarcinoma.* (2022) Journal of Cancer Science and Clinical Therapeutics.

26. Grace E Weber, Maria Khrestian, Elizabeth D Tuason, Yvonne Shao, Jagan Pillai, Stephen Rao, **Hao Feng**, Yadi Zhou, Feixiong Cheng, Tara M DeSilva, Shaun Stauffer, James B Leverenz, Lynn M Bekris. *Peripheral sTREM2-Related Inflammatory Activity Alterations in Early-Stage Alzheimer's Disease.* (2022) The Journal of Immunology.

27. Grace E Weber, Maria Khrestian, Elizabeth D Tuason, Yvonne Shao, Jagan A Pillai, Stephen M Rao, **Hao Feng**, Tara M DeSilva, Shaun Stauffer, James B Leverenz, Lynn M Bekris. *Older adults with Alzheimer's disease exhibit an altered relationship between plasma sTREM2 and inflammatory markers.* (2021) Alzheimer's & Dementia.

28. Yunhee Kang, Ying Zhou, Yujing Li, Yanfei Han, Jie Xu, Weibo Niu, Ziyi Li, Shiying Liu, **Hao Feng**, Wen Huang, Ranhui Duan, Tianmin Xu, Nisha Raj, Feiran Zhang, Juan Dou, Chongchong Xu, Hao Wu, Gary J Bassell, Stephen T Warren, Emily G Allen, Peng Jin, Zhexing Wen. *A human forebrain organoid model of fragile X syndrome exhibits altered neurogenesis and highlights new treatment strategies.* (2021) Nature Neuroscience.

29. Bin Jiao, Mengli Wang, **Hao Feng**, Han Bao, Feiran Zhang, Hao Wu, Junling Wang, Beisha Tang, Peng Jin, Lu Shen. *Downregulation of TOP2 modulates neurodegeneration caused by GGGGCC expanded repeats.* (2021) Human Molecular Genetics.

30. Samaneh K Sarvestani, Steven Signs, Bo Hu, Yunku Yeu, **Hao Feng**, Ying Ni, David R Hill, Robert C Fisher, Sylvain Ferrandon, Reece K DeHaan, Jennifer Stiene, Michael Cruise, Tae Hyun Hwang, Xiling Shen, Jason R Spence, Emina H Huang. *Induced organoids derived from patients with ulcerative colitis recapitulate colitic reactivity.* (2021) Nature Communications.

31. E. M. Kennedy, D. R. Powell, Z. Li, J. S. K. Bell, B. G. Barwick, **Hao Feng**, M. R. McCrary, B. Dwivedi, J. Kowalski, W. S. Dynan, K. N. Conneely, P. M. Vertino. *Galactic Cosmic Radiation Induces Persistent Epigenome Alterations Relevant to Human Lung Cancer.* (2018) Scientific Reports.

32. Yufang Qin, **Hao Feng**, Ming Chen, Hao Wu, Xiaoqi Zheng. *InfiniumPurify: An R package for estimating and accounting for tumor purity in cancer methylation research.* (2018) Genes & Diseases.

33. Lynn M Almli, Adriana Lori, Jacquelyn L Meyers, Jaemin Shin, Negar Fani, Adam X Maihofer, Caroline M Nievergelt, Alicia K Smith, Kristina B Mercer, Kimberly Kerley, Jennifer M Leveille, **Hao Feng**, Duna Abu-Amara, Janine D Flory, Rachel Yehuda, Charles R Marmar, Dewleen G Baker, Bekh Bradley, Karestan C Koenen, Karen N Conneely, Kerry J Ressler. *Problematic alcohol use associates with sodium channel and clathrin linker 1 (SCLT1) in trauma-exposed populations.* (2017) Addiction Biology.

34. Feiran Zhang, Christy Hammack, Sarah C Ogden, Yichen Cheng, Emily M Lee, Zhexing Wen, Xuyu Qian, Ha Nam Nguyen, Yujing Li, Bing Yao, Miao Xu, Tianlei Xu, Li Chen, Zhiqin Wang, **Hao Feng**, Wei-Kai Huang, Ki-jun Yoon, Chao Shan, Luoxiu Huang, Zhaohui Qin, Kimberly M Christian, Pei-Yong Shi, Mingjiang Xu, Menghang Xia, Wei Zheng, Hao Wu, Hongjun Song, Hengli Tang, Guo-Li Ming, Peng Jin. *Molecular signatures associated with ZIKV exposure in human cortical neural progenitors.* (2016) Nucleic Acids Research.

35. E Kennedy, DR Powell, Z Li, JSK Bell, **Hao Feng**, W Dynan, B Dwivedi, J Kowalski, KN Conneely, PM Vertino. *Space radiation exposure induces stable epigenome alterations relevant to human lung cancer.* (2016) Cancer Research.

36. Lynn M Almli, Richard Duncan, **Hao Feng**, Debashis Ghosh, Elisabeth B Binder, Bekh Bradley, Kerry J Ressler, Karen N Conneely, Michael P Epstein. *Correcting systematic inflation in genetic association tests that consider interaction effects: application to a genome-wide association study of posttraumatic stress disorder.* (2014) JAMA Psychiatry.

37. Lynn M Almli, Amita Srivastava, Negar Fani, Kimberly Kerley, Kristina B Mercer, **Hao Feng**, Bekh Bradley, Kerry J Ressler. *Follow-up and Extension of a Prior Genome-wide Association Study of Posttraumatic Stress Disorder: Gene × Environment Associations and Structural Magnetic Resonance Imaging in a Highly Traumatized African-American Civilian Population.* (2014) Biological Psychiatry.

38. Lynn M Almli, Kristina B Mercer, Kimberly Kerley, **Hao Feng**, Bekh Bradley, Karen N Conneely, Kerry J Ressler. *ADCYAP1R1 genotype associates with post-traumatic stress symptoms in highly traumatized African-American females.* (2013) American Journal of Medical Genetics Part B: Neuropsychiatric Genetics.

Funding Support

Grants as Principal Investigator (PI)

- **1R35GM154862** (PI: Hao Feng) 09/01/2024 — 06/30/2029
  NIH/NIGMS
  Personalized genomics signal deconvolution to improve cell-type level inference
  Direct cost: $1,250,000. Total cost: $1,925,620.

Role: PD/PI
Effort level: 6.6 calendar month
Status: active

- **58005** (PI: Hao Feng) 01/01/2026 — 12/31/2026
  University of Texas Health Science Center at Houston, Office of the President
  Dementia Prevention and Research Institute of Texas (DPRIT) Seed Funding Program
  Cell-Type-Specific Genomics Risk Models for Parkinson's Disease
  Total cost: $10,000.
  Role: PD/PI
  Status: active

- **IRG-16-186-21** (PI: Hao Feng) 08/01/2022 — 07/31/2023
  American Cancer Society — Institutional Research Grants (ACS-IRG) pilot award, through Case Comprehensive Cancer Center
  Jointly Profiling Microbiome and Transcriptome in Pancreatic Cancer Metastasis
  Direct cost: $50,000.
  Role: PD/PI
  Effort level: 2.4 calendar month
  Status: completed

- **CASE60007** (PI: Hao Feng) 01/01/2022 — 12/31/2022
  Corinne L. Dodero Foundation for the Arts and Sciences
  Data Harmonizing and Cell Label Prediction Methods in Autism Single-cell RNA-seq Data
  Direct cost: $25,000.
  Role: PD/PI
  Effort level: 1.2 calendar month
  Status: completed

Grants as subcontract site-PI

- R01CA237304 (PD: Emina Huang; site-PI: Hao Feng) 03/01/2019 — 02/29/2023
  NIH/NCI
  The miR-20/c-Myc/E2F Regulatory Axis is Critical for the Tumor Promoting Activity of Inflammatory Fibroblasts in Colitis-Associated Cancer
  Role: Subcontract site-PI, Biostatistician
  Effort level: 1.8 calendar month
  Status: completed

Grants as co-Investigator

- 1R01CA264320 (PI: Zhenghe Wang) 07/01/2021 — 04/30/2025
  NIH/NCI
  Mechanisms of PIK3CA helical domain mutations driving colorectal tumorigenesis
  Role: Biostatistician
  Effort level: 0.6 calendar month
  Status: completed

- 1R01HD105892 (PI: Adonis Hijaz) 08/20/2021 — 01/31/2025
  NIH/NICHD
  Patient-Centered Outcomes of Sacrocolpopexy versus Uterosacral Ligament Suspension for the Treatment of Uterovaginal Prolapse

Role: Biostatistician
Effort level: 0.6 calendar month
Status: completed

- P30AG072959 (PI: Jonathan Haines) 09/01/2021 — 01/31/2025
NIH/NIA
Cleveland Alzheimers Disease Research Center (CADRC) Data Management and Statistics Core(DMSC)
Role: Biostatistician
Effort level: 1.8 calendar month
Status: completed

- R37CA227865 (PI: Jordan Winter) 09/01/2018 — 06/30/2025
NIH/NCI
Targeting pancreatic cancer's metabolic addiction to HuR
Role: Biostatistician
Effort level: 0.6 calendar month
Status: completed

- PA220063 – GRANT13720187 (PIs: Jordan Winter, Rui Wang) 08/01/2023 — 06/30/2025
Department of Defense(DoD)/Congressionally Directed Medical Research Programs (CDMRP)
Leveraging the tumor microenvironment in primary and metastatic pancreatic cancer
Role: Biostatistician
Effort level: 0.6 calendar month
Status: completed

- R37CA278982 (PI: Rui Wang) 02/01/2024 — 06/30/2025
NIH/NCI
Role of LRG1 in colorectal tumorigenesis
Role: Biostatistician
Effort level: 0.6 calendar month
Status: completed

- 2U01NS100610 (PI: James Leverenz) 09/01/2022 — 06/30/2025
NIH/NINDS
Dementia with Lewy Bodies Consortium
Role: Lead Biostatistician
Effort level: 1.2 calendar month
Status: completed

- 1RF1AG083811 (PI: Xiongwei Zhu) 09/01/2023 — 06/30/2025
NIH/NIA
Role of Mettl3-dependent RNA m6A dysregulation in Alzheimer's disease
Role: Biostatistician
Effort level: 0.6 calendar month
Status: completed

- 2T32NS077888 (PI: Xiongwei Zhu) 08/15/2024 — 06/30/2025
NIH/NINDS
Training in Neurodegenerative Diseases
Role: Biostatistician faculty trainer

Effort level: 1.2 calendar month (exceptionally budgeted)
Status: completed

- ID: 605146 (PI: Alex Huang) 11/01/2018 — 10/30/2021
  St. Baldrick's Foundation
  High Impact Research for Pediatric Osteosarcoma
  Targeting myeloid and lymphoid immune tolerance in metastatic osteosarcoma
  Role: Biostatistician
  Effort level: 0.6 calendar month
  Status: completed
- 1R01AG066526 (PI: Wen-Cheng Xiong) 09/15/2020 — 08/31/2024
  NIH/NIA
  LRP4 deficiency in Alzheimer's disease development
  Role: Biostatistician
  Effort level: 0.6 calendar month
  Status: completed
- W81XWH2110804 (PI: Mei Zhang) 09/01/2021 — 08/31/2024
  Department of Defense(DoD)/Congressionally Directed Medical Research Programs (CDMRP)
  BG34-200 Triggers Myeloid Recruitment and M1 Reprogramming to Enhance Immunotherapy for Pediatric and AYA Osteosarcoma
  Role: Biostatistician
  Effort level: 0.6 calendar month
  Status: completed

Honors and Awards

- **UCITE Learning Fellowship Award**, 2021
- **Senior Ph.D. Student Presentation Award**, 2018
- **ENAR Distinguished Student Paper Award**, 2017
- **Michael Kutner Distinguished Doctoral Student Award**, 2017
- **SAMSI trave award** for epigenetics workshop, 2015
- Finalist for the **Charles C. Shepard Award**, 2013
  — The best master's thesis of the Rollins School of Public Health
- **Outstanding Student Scholarship** from USTC Overseas Alumni Foundation, 2007

Software Packages

- **mist**: methylation inference for single-cell along trajectory. It is the first method to identify genomic features with significant methylation changes along pseudotime, and performs Differential Methylation (DM) analysis along pseudotime across phenotypical groups. Available on Bioconductor: https://bioconductor.org/packages/mist/.
- **tapas**: a method to evaluate and quantify the confidence of cell type annotation by large language models (LLMs). Available on GitHub: https://github.com/wxt175/tapas.

- **ISLET**: Individual-Specific cell type referencing tool. An R/Bioconductor package deconvolute mixture samples and obtain the individual-specific and cell-type-specific reference panels. Available on Bioconductor: https://bioconductor.org/packages/ISLET/.
- **magpie**: This package aims to perform power analysis for the MeRIP-seq study. It calculates FDR, FDC, power, and precision under various study design parameters. Available on Bioconductor: https://bioconductor.org/packages/magpie/.
- **NeuCA**: Neural network-based cell type annotation tool. Available at https://bioconductor.org/packages/NeuCA/.
- **cypress**: (cell-type-specific differential expression power assessment) is the first experimental design and statistical power evaluation tool in cell-type-specific Differential Expression analysis. This tool can reliably model purified cell-type-specific (CTS) profiles, cell-type compositions, biological and technical variations, to help researchers optimize experimental design and conduct power analysis. Available at https://www.bioconductor.org/packages/cypress/.
- **DSS**: Dispersion Shrinkage for Sequencing. An R/Bioconductor package for differential analysis from high-throughput sequencing data, including differential expression for RNA-seq and differential methylation for bisulfite-sequencing data. Available at https://bioconductor.org/packages/DSS/.
- **InfiniumPurify**: A comprehensive R package for estimating and accounting for tumor purity based on DNA methylation Infinium 450k array data. 'InfiniumPurify' provides functionalities for tumor purity estimation. In addition, it can perform differential methylation detection and tumor sample clustering with the consideration of tumor purities. Available at https://cran.r-project.org/web/packages/InfiniumPurify/index.html.
- **cfDNAMethy**: Reference-free and reference-based methods for disease prediction by cell-free DNA methylation. Available at https://github.com/haoharryfeng/cfDNAmethy.

Presentations

Invited

- Departmental Seminar at Michigan State University, Department of Statistics and Probability. East Lansing, Michigan. September, 2026.
  — Computational methods for single-cell DNA methylation data.
- The 43rd Korean International Statistical Society(KISS) Webinar. Online. May, 2026.
  — Computational methods for single-cell DNA methylation data.
- STATGEN 2026: Conference on Statistics in Genomics and Genetics, Atlanta, Georgia. May, 2026.
  — Computational methods for single-cell DNA methylation data.
- The 11th Workshop on Biostatistics and Bioinformatics, Atlanta, Georgia. May, 2026.
  — Computational methods for single-cell DNA methylation data.
- Advances in Genome Biology and Technology (AGBT) 2026 General Meeting, Orlando, Florida. February, 2026.
  — Computational methods for single-cell DNA methylation data.

- International Chinese Statistical Association (ICSA) International Conference, Taipei, Taiwan. December, 2025.
  — Computational methods for single-cell DNA methylation data.
- The 19th International Joint Conference on Computational and Financial Econometrics (CFE) and Computational and Methodological Statistics (CMStatistics), CFE-CMStatistics 2025, Birkbeck, University of London, United Kingdom. December, 2025.
  — Computational methods for single-cell DNA methylation data.
- Biostatistics and Bioinformatics seminar at The University of Illinois at Chicago Cancer Center. September, 2024.
  — Personalized cell-type-specific omics profile deconvolution.
- International Statistical Genetics and Genomics (ISGG) meeting, Wuhan, China. July, 2024.
  — Personalized cell-type-specific omics profile deconvolution and inference.
- International Chinese Statistical Association (ICSA) 2024, Wuhan, China. June, 2024.
  — Personalized cell-type-specific omics profile deconvolution and inference.
- MidSouth Computational Biology and Bioinformatics Society (MCBIOS) 2024, Atlanta GA. March, 2024.
  — Personalized cell-type-specific omics profile deconvolution and inference.
- Departmental Seminar Series, Wayne State University, Center for Urban Responses to Environmental Stressors (CURES), Detroit MI. November, 2023.
  — Personalized cell-type-specific omics profile deconvolution and inference.
- Joint Statistical Meetings (JSM), Toronto, Ontario, Canada. August, 2023.
  — Individual-specific and cell-type-specific gene expression reference panel deconvolution.
- International Chinese Statistical Association (ICSA) International Conference, Hong Kong SAR, China. July, 2023.
  — Individual-specific and cell-type-specific gene expression reference panel deconvolution.
- International Biometric Society (IBS) — the Western North American Region (WNAR), Anchorage, AK. June, 2023.
  — Individual-specific and cell-type-specific gene expression reference panel deconvolution.
- Case Comprehensive Cancer Center seminar series. April, 2023.
  — Signal deconvolution methods development in *-omics* data.
- Departmental Seminar Series, University of Pittsburgh. Pittsburgh, PA. December, 2022.
  — Individual-specific and cell-type-specific gene expression reference panel deconvolution.
- Departmental Seminar Series, University of South Carolina Statistics Department. Columbia, SC. October, 2022.
  — Individual-specific and cell-type-specific gene expression reference panel deconvolution.
- Bioconductor Asia 2021, Tokyo, Japan. November, 2021.
  — NeuCA: a neural network-based method for exhaustive cell label assignment using single cell RNA-seq data.
- Joint Biostatistics Symposium 2021, Columbus, OH. May, 2021.
  — NeuCA: a neural network-based method for exhaustive cell label assignment using single cell RNA-seq data.
- University Hospitals Seidman Cancer Center, Cleveland, OH. November, 2020.
  — Omics data in cancer research.

- The University of Alabama at Birmingham, Birmingham, AL. March, 2019.
  — Statistical methods for high-throughput epigenomics data.
- Case Western Reserve University, Cleveland, OH. March, 2019.
  — Statistical methods for high-throughput epigenomics data.
- University of Missouri – Columbia, Columbia, MO. January, 2019.
  — Statistical methods for high-throughput epigenomics data.

Topic-contributed, Contributed, and others

- The 33rd International Biometric Conference (IBC) 2026, Seoul, South Korea. July, 2026.
  — Computational methods for single-cell DNA methylation data.
- JSM 2024, Portland, OR. August, 2024.
  — Personalized cell-type-specific omics profile deconvolution and inference.
- STATGEN 2024, Pittsburgh, PA. May, 2024.
  — Personalized cell-type-specific omics profile deconvolution and inference.
- JSM 2022, Washington DC, USA. August, 2022
  — NeuCA: a neural network-based method for exhaustive cell label assignment using single cell RNA-seq data.
- ENAR 2022, Houston, TX, USA. March, 2022
  — NeuCA: a neural network-based method for exhaustive cell label assignment using single cell RNA-seq data.
- Affordable Cancer Technology 2021 (ACT 2021), Virtual, USA. October, 2021
  — NeuCA: a neural network-based method for exhaustive cell label assignment using single cell RNA-seq data.
- Senior Ph.D. students presentation competition, Emory University, Atlanta, GA. September, 2018
  — Statistical methods for high-throughput epigenomics data.
- Pfizer Global Research and Development, La Jolla, CA. August, 2017
  — A Bayesian method in tumor growth inhibition study.
- JSM 2017, Chicago, IL. August, 2017
  — Accounting for tumor purity improves cancer subtype classification from DNA methylation data.
- ENAR 2017 Spring meeting, Washington, DC. March, 2017
  — Accounting for tumor purity improves cancer subtype classification from DNA methylation data.
  [** ENAR Distinguished Student Paper Award **]
- Statistical and Applied Mathematical Sciences Institute (SAMSI) workshop, Research Triangle Park, NC. March, 2015
  — A Bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data.
- American Society of Human Genetics (ASHG) 63^{rd} annual meeting, Boston, MA. October, 2013
  — A Bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data.

Teaching

Instructor

- PH 1910: **Probability and Distribution Theory**. [3 credits] (2025 – current). Department of Biostatistics & Data Science, The University of Texas Health Science Center at Houston (UTHealth), School of Public Health.
- PH 1999: **Individual Study in Biostatistics**. [varied credits] (2025 – current). Department of Biostatistics & Data Science, The University of Texas Health Science Center at Houston (UTHealth), School of Public Health.
- PH 9997: **Practicum**. [varied credits] (2025 – current). Department of Biostatistics & Data Science, The University of Texas Health Science Center at Houston (UTHealth), School of Public Health.
- PHD 9999: **Dissertation Research**. [varied credits] (2025 – current). Department of Biostatistics & Data Science, The University of Texas Health Science Center at Houston (UTHealth), School of Public Health.
- PHM 9998: **Integrative Learning (Thesis Research)**. [varied credits] (2025 – current). Department of Biostatistics & Data Science, The University of Texas Health Science Center at Houston (UTHealth), School of Public Health.
- PQHS 471: **Machine Learning and Data Mining**. [3 credits] (2021 – 2025). Department of Population & Quantitative Health Sciences, Case Western Reserve University School of Medicine.
- PQHS 701: **Ph.D. Dissertation Research**. [varied credits] (2023 – 2025). Department of Population & Quantitative Health Sciences, Case Western Reserve University School of Medicine.
- PQHS 499: **Independent Study on Modern Regression Methods**. [6 credits] (2022 – 2023). Department of Population & Quantitative Health Sciences, Case Western Reserve University School of Medicine.
- STAT 395: **Senior Project in Statistics**. [3 credits] (2022). Department of Mathematics, Applied Mathematics, and Statistics, Case Western Reserve University College of Arts and Sciences.

Guest Lecturer

- PQHS 401: Research Seminar for MS program in Biostatistics. (Spring 2024 – current). *High-throughput Bioinformatics Data Analysis.* Department of Population & Quantitative Health Sciences, Case Western Reserve University School of Medicine.
- PQHS 452: Statistical Methods in Human Genetics. (Spring 2021 – current). *Multiple Testing and Statistical Power.* Department of Population & Quantitative Health Sciences, Case Western Reserve University School of Medicine.
- PQHS 457: Current Issues in Genetic Epidemiology: Design and Analysis of Sequencing Studies. (Spring 2020 – current). *Epigenetics and Its Statistical Methods.* Department of Population & Quantitative Health Sciences, Case Western Reserve University School of Medicine.

Group Discussion Facilitator

- (2024 – 2025) IBMS 500: **On Being a Professional Scientist**, Case Western Reserve University School of Medicine.

Short Courses and Tutorials

- (2023 Spring ENAR Meeting) ENAR Tutorials: **Cell-type-aware Differential Analysis for Bulk Transcriptome Data**. International Biometric Society (IBS) – ENAR.

Teaching Associate

- BIOS 731: **Advanced Statistical Computing**. (2018). Department of Biostatistics and Bioinformatics, Emory University Rollins School of Public Health.
- BIOS 738: **Bayesian and Empirical Bayesian Methods**. (2017). Department of Biostatistics and Bioinformatics, Emory University Rollins School of Public Health.
- BIOS 555: **High-throughput data analysis using R and Bioconductor**. (2016). Department of Biostatistics and Bioinformatics, Emory University Rollins School of Public Health.

Teaching Assistant

- BIOS 550: **Sampling Applications**. (2016). Department of Biostatistics and Bioinformatics, Emory University Rollins School of Public Health.
- BIOS 500: **Statistical Methods I**. (2015). Department of Biostatistics and Bioinformatics, Emory University Rollins School of Public Health.

Mentoring

Doctoral trainees

- Yixiang Hong (2025 -), Ph.D. student in Biostatistics and Data Science
- Daoyu Duan (2020 - 2025), Ph.D. student in Epidemiology and Biostatistics
- Guanqun Leslie Meng (2020 - 2025), Ph.D. student in Epidemiology and Biostatistics

Dissertation committee

- Sein Lee (2026 -), Ph.D. student in Biostatistics and Data Science
- Jooyeon Lee (2026 -), Ph.D. student in Biostatistics and Data Science
- Yuchen Zhang (2026 -), Ph.D. student in Biostatistics and Data Science
- Naishu Kui (2026 -), Ph.D. student in Biostatistics and Data Science
- Yutong Pan (2025 -), Ph.D. student in Biostatistics and Data Science
- Wanheng Zhang (2025 - 2026), Ph.D. student in Biostatistics and Data Science
- Kehe Zhang (2025 -), Ph.D. student in Biostatistics and Data Science
- Yanning Wu (2024 - 2026), Ph.D. student in Epidemiology and Biostatistics
- Aditi Singh (2023 - 2025), Ph.D. student in Wayne State University
- Noah Lorincz-Comi (2021 - 2024), Ph.D. student in Epidemiology and Biostatistics

- Xueyi Zhang (2021 - 2024), Ph.D. student in Epidemiology and Biostatistics
- Michael Osterman (2020 - 2023), Ph.D. student in Epidemiology and Biostatistics
- Bowen Jin (2021 - 2023), Ph.D. student in Systems Biology and Bioinformatics
- Zuxi (Terry) Cui (2020 - 2024), Ph.D. candidate in Epidemiology and Biostatistics
- Ju Zhang (2019 - 2021), Ph.D. candidate in Epidemiology and Biostatistics

Academic advisee

- Janeth Alexandra Sandoval (2026 -), MS student in Biostatistics and Data Science
- Divya Saravanan (2026 -), MS student in Biostatistics and Data Science
- Aranxa Anahilea Valencia (2026 -), MS student in Biostatistics and Data Science
- Bo Yang (2026 -), Ph.D. student in Biostatistics and Data Science
- Zixi Wang (2026 -), Ph.D. student in Biostatistics and Data Science
- Yiying Wu (2025 -), Ph.D. student in Biostatistics and Data Science
- Shuyi Guo (2025 -), Ph.D. student in Biostatistics and Data Science
- Yukun Yang (2025 -), Ph.D. student in Biostatistics and Data Science

Rotation graduate students

- Lingzhu Shen (2024), Ph.D. student in Biomedical and Health Informatics
- Chenyu Liu (2023 - 2024), Ph.D. student in Epidemiology and Biostatistics
- Katrina Prantzalos (2020 - 2021), Ph.D. student in Biomedical and Health Informatics
- Dipak Prasad Upadhyaya (2020 - 2021), Ph.D. student in Biomedical and Health Informatics
- Jing Zhang (2019 - 2020), Ph.D. candidate in Epidemiology and Biostatistics
- Shiying Liu (2019 - 2020), Ph.D. candidate in Epidemiology and Biostatistics

Master's capstone

- Project Committee for Nicolas Kaplan (2019 - 2021), MPH candidate

Visiting students

- Aditi Singh (2022), Graduate Student, Wayne State University, Center for Molecular Medicine and Genetics.

Undergraduate students and high school students

- Dounia Ouzidane (2024-2025), CWRU, undergraduate research assistant.
- Sijia He (2021-2022), CWRU, undergraduate capstone.
- Julia Zhu (2021), Hathaway Brown School, summer research project.

Service Activities

Grant review

- National Institutes of Health (NIH) Special Emphasis Panel/Scientific Review Group for Biodata Management, Modeling, and Genomic Sciences ZRG1 BCTB-L (83) S, Member. November, 2026.
- National Science Foundation (NSF) Directorate for Biological Sciences (BIO) Innovation Panel, Member. September, 2026.
- National Medical Research Council (NMRC)'s Population Health Research Grant (PHRG), Singapore. September 2026.
- John S. Dunn Foundation Collaborative Research Award, Reviewer. April, 2026.
- National Institutes of Health (NIH) ZRG1 HSS-S (90) Special Emphasize Panel, Member. January, 2026.
- Department of Defense (DoD) Congressionally Directed Medical Research Programs (CDMRP), Biostatistician Specialist Reviewer. November 2025.
- National Medical Research Council (NMRC)'s Population Health Research Grant (PHRG), Singapore. September 2025.
- National Science Foundation (NSF), Small Business Innovation Research/Small Business Technology Transfer (SBIR/STTR). Panel Reviewer. 2024
- National Science Foundation (NSF), Graduate Research Fellowship Program (GRFP). Panel Reviewer. 2024.
- Department of Defense (DoD) Congressionally Directed Medical Research Programs (CDMRP), Biostatistician Specialist Reviewer. 2022-current.
- National Institutes of Health (NIH) Genomics, Computational Biology and Technology (GCAT) Study Section, Early Career Reviewer. 2023.
- Sector Innovation Program at Genome British Columbia (GENOME BC), Vancouver, BC, Canada. May 2020.

Committee service
At UTHealth:

- 2026 - current, Member, Student Scholarship Committee
- 2025 - current, Member, Departmental Admission Committee
- 2025 - current, Member, Departmental Qualify Exam Committee
- 2025 - current, Member, External PhD Dissertation Supervisor Review Committee

At Case Western Reserve University:

- 2023 - 2025, Member, PQHS departmental Committee on Appointments Promotions and Tenure (dCAPT)
- 2023 - 2025, Member, CWRU School of Medicine (SOM) Curriculum Committee
- 2022 - 2024, Chair, PQHS departmental seminar series committee
- 2021- 2025, Member, Biomedical & Health Informatics (BHI) admission and curriculum committee
- 2019 - 2021, Member, Biostatistics Faculty Search Committee
- 2020, Member, Epidemiology and Biostatistics Ph.D. Admission Committee

- 2020, Member, PQHS Student Activity Committee
- 2019, Member, Emory Biostatistics Department Website Committee

Conference program

- Organizer and Chair: 2027 ENAR Invited Session "Statistical Learning for Next-Generation Functional Genomics." Boston, MA. March 2027.
- Organizer: 2026 ICSA Applied Statistics Symposium, Invited Session "Statistical Advances in Integrative Genomics and Spatial Transcriptomics." Arlington, VA. June 2026.
- Organizer and Chair: STATGEN 2024, Topic-contributed Session "Dissecting and testing heterogeneous transcriptome and chromatin signals." STATGEN 2024: Conference on Statistics in Genomics and Genetics, Pittsburgh, PA. May 2024.
- Program Committee: IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM). 2022 & 2023.
- Organizer: JSM, Topic-contributed Session "Methodological Advances in Cell Type Deconvolution and Discrimination." JSM 2023, Toronto, Ontario, Canada. August 2023.
- Chair: "WNAR 2023 session – Speed Talk 1". WNAR 2023, Anchorage, AK. June 2023.
- Organizer and Chair: ICSA Applied Statistics Symposium, Invited Session "Statistical Methods Development in Single-cell Genomics and Multi-omics Data." ICSA Applied Statistics Symposium, Ann Arbor, MI. June 2023.
- Award Committee: ENAR conference poster award committee. 2023
- Chair: "ENAR session – Contributed Papers: Genomics". ENAR 2022, Houston, TX. March 2022.
- Organizer and Chair: Invited Session "Statistical method advancement for analyzing omics data". ICSA 2020 Applied Statistics Symposium, Houston, TX. December 2020.

Editorial Activities

Editorial board member

- Scientific Reports (2026 -)
- International Journal of Computational Biology and Drug Design (2020 - 2023)

Journal Reviewer

- Aging, American Journal of Tropical Medicine and Hygiene, Annals of Applied Statistics, Bioinformatics, Bioinformatics Advances, Biomedicine and Pharmacotherapy, Biometrics, Briefings in Bioinformatics, BMC Bioinformatics, BMC Genomics, BMC Supplements, Cell Reports Methods, Cell Systems, Cell Genomics, Cell & Bioscience, Communication Biology, Genes & Diseases, Genetic Epidemiology, Genome Biology, Journal of Applied Statistics, Journal of Alzheimer's Disease, Meta Gene, Nature Communications, Nucleic Acids Research, NAR Genomics and Bioinformatics, Nature Communications, PeerJ, PLOS Computational Biology, PLOS Genetics, PLOS ONE, RECOMB, Statistical Analysis and Data Mining, Scientific Reports, Statistical Methods in Medical Research, Statistics in Biosciences.

Professional Membership

American Statistical Association (ASA)
The International Biometric Society — Eastern North American Region (ENAR)
International Chinese Statistical Association (ICSA)
International Society for Computational Biology (ISCB)
American Society of Human Genetics (ASHG)