

Zhicheng Ji, Ph.D.

Department of Biostatistics and Bioinformatics
Duke University School of Medicine

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Education

2015-2020 Ph.D. in Biostatistics, Johns Hopkins Bloomberg School of Public Health (*Mentor: Hongkai Ji, Ph.D.*)
2018-2020 M.S.E. in Computer Science, Johns Hopkins Whiting School of Engineering (*Mentor: Suchi Saria, Ph.D.*)
2009-2013 B.S. in Statistics, Fudan University

Professional Experience

08/2020-present Tenure-track Assistant Professor
Department of Biostatistics and Bioinformatics, Duke University School of Medicine
08/2020-present Co-Director, Statistical and Computational Immunology
Duke Center for Human Systems Immunology
04/2021-present Affiliated Faculty
Computational Biology and Bioinformatics Program, Duke University

Honors and Awards

2024 Maximizing Investigators' Research Award, National Institute of General Medical Sciences
2021 Whitehead Scholar, Duke University
2018 Margaret Merrell Award, Department of Biostatistics, Johns Hopkins University
2018 June B. Culley Award, Department of Biostatistics, Johns Hopkins University
2017 Runner-up, ENCODE-DREAM *in vivo* Transcription Factor Binding Site Prediction Challenge
2016 ASA Section on Statistics in Genomics and Genetics Distinguished Student Paper Award
2015 Top Performers, Prostate Cancer DREAM Challenge
2014 Kocherlakota Award, Department of Biostatistics, Johns Hopkins University

Publications

[Google Scholar](#)

The white numbers displayed in black boxes represent first-author or senior-author manuscripts. The * represents equal contributions. The † represents corresponding author. The underlines represent mentees. The bolded names indicate **lab members**.

Selected publications

1 **Zhuang H**, Shang X, Hou W[†], **Ji Z**[†]. Identifying cell-type-specific spatially variable genes with ctSVG. *Genome Biology*. Accepted. [Preprint](#).

- 2 **Qu Y, Ji B**, Dong R, Gu L, Chan C, Xie J, Glass C, Wang X, Nixon A, **Ji Z[†]**. Single-cell and spatial detection of senescent cells using DeepScience. *Cell Genomics*. 2025. [Google Scholar citations: 11]
-Highlighted in Cancer Cell “Senescence in cancer”
- 3 **Ma H, Zhang X, Qu Y**, Zhang AR, **Ji Z[†]**. Vispro improves imaging analysis for Visium spatial transcriptomics. *Genome Biology*. 2025;26(1):173. [Google Scholar citations: 1]
- 4 Hou W[†], **Ji Z[†]**. Comparing large language models and human programmers for generating programming code. *Advanced Science*. 2025;12(8):e2412279. [Google Scholar citations: 55]
- 5 Hou W[†], **Ji Z[†]**. Assessing GPT-4 for cell type annotation in single-cell RNA-seq analysis. *Nature Methods*. 2024;21(8):1462-1465. [Google Scholar citations: 192]
-Featured in Nature Methods “Embedding AI in biology” and “Toward learning a foundational representation of cells and genes”
-Essential Science Indicators (ESI) highly cited paper: top 1% cited in the field of Biology & Biochemistry
- 6 **Wang Y***, Wang W*, Liu D*, Hou W, Zhou T[†], **Ji Z[†]**. GeneSegNet: a deep learning framework for cell segmentation by integrating gene expression and imaging. *Genome Biology*. 2023;24(1):235. [Google Scholar citations: 37]
- 7 Caushi JX, Zhang J, **Ji Z**, Vaghasia A, Zhang B, Hsiue EH, Mog BJ, Hou W, Justesen S, Blosser R, Tam A, Anagnostou V, Cottrell TR, Guo H, Chan HY, Singh D, Thapa S, Dykema AG, Burman P, Choudhury B, Aparicio L, Cheung LS, Lanis M, Belcaid Z, El Asmar M, Illei PB, Wang R, Meyers J, Schuebel K, Gupta A, Skaist A, Wheelan S, Naidoo J, Marrone KA, Brock M, Ha J, Bush EL, Park BJ, Bott M, Jones DR, Reuss JE, Velculescu VE, Chaft JE, Kinzler KW, Zhou S, Vogelstein B, Taube JM, Hellmann MD, Brahmer JR, Merghoub T, Forde PM, Yegnasubramanian S, Ji H, Pardoll DM, Smith KN. Transcriptional programs of neoantigen-specific TIL in anti-PD-1-treated lung cancers. *Nature*. 2021;596(7870):126-132. [Google Scholar citations: 499]
-Featured in Nature Reviews Clinical Oncology “Tumour antigen-induced T cell exhaustion – the archenemy of immune-hot malignancies”
-Essential Science Indicators (ESI) highly cited paper: top 1% cited in the field of Clinical Medicine
- 8 Chen Z*, **Ji Z***, Ngiew SF, Manne S, Cai Z, Huang AC, Johnson J, Staupe RP, Bengsch B, Xu C, Yu S, Kurachi M, Herati RS, Vella LA, Baxter AE, Wu JE, Khan O, Beltra JC, Giles JR, Stelekati E, McLane LM, Lau CW, Yang X, Berger SL, Vahedi G, Ji H, Wherry EJ. TCF-1-Centered Transcriptional Network Drives an Effector versus Exhausted CD8 T Cell-Fate Decision. *Immunity*. 2019; 51(5):840-855.e5. [Google Scholar citations: 708]
-Featured in Immunity “Back to the future: effector fate during T cell exhaustion”
-Essential Science Indicators (ESI) highly cited paper: top 1% cited in the field of Immunology
- 9 **Ji Z**, Ji H. TSCAN: Pseudo-time reconstruction and evaluation in single-cell RNA-seq analysis. *Nucleic Acids Research*. 2016; 44(13):e117. [Google Scholar citations: 697]
-Winner of ASA Section on Statistics in Genomics and Genetics Distinguished Student Paper Award
-Highlighted in Nature Reviews Genetics “Challenges in unsupervised clustering of single-cell RNA-seq data”
-Essential Science Indicators (ESI) highly cited paper: top 1% cited in the field of Biology & Biochemistry

Other publications

- 10 Qi G, Lila E, **Ji Z**, Shojai A, Battle A, Sun W. Transcriptome-wide association studies at cell-state level using single-cell eQTL data. *Cell Genomics*
- 11 Shang X, Liao X, **Ji Z**, Hou W. Benchmarking large language models for genomic knowledge with GeneTuring. *Briefings in Bioinformatics*. 2025;26(5):bbaf492. [Google Scholar citations: 51]
- 12 **Wan C, Ji Z[†]**. Smmit: A pipeline for integrating multiple single-cell multi-omics samples. *Computational and Structural Biotechnology Journal*. 2025;27:3785-3791.
- 13 Li S, Agudelo Garcia PA, Aliferis C, Becich MJ, Calyeca J, Cosgrove BD, Elisseeff J, Farzad N, Fertig EJ, Glass C, Gu L, Hu Q, **Ji Z**, Königshoff M, LeBrasseur NK, Li D, Ma A, Ma Q, Menon V, Mitchell JT, Mora AL, Nagaraj S, Nelson AC, Niedernhofer LJ, Rojas M, Taha HB, Wang J, Wang S, Wu PH, Xie J, Xu M, Yu M, Zhang X, Zhao Y, Adams PD, Aguayo-Mazzucato C, Baker DJ, Benz C, Bernlohr DA, Bueno M, Chen J, Childs BG, Chuang JH, Chung D, Dileepan M, Ding L, Dong M, Duncan F, Enniful A, Flynn WF, Franco AC, Furman D, Garovic V, Halene S, Herman AB, Hertz AV, Iwasaki K, Jeon H, Kang JW, Karmakar S, Kirkland JL, Korstanje R, Kummerfeld E, Lee JH, Liu Y, Lu Y, Lugo-Martinez

- J, Martini H, Melov S, Musi N, Passos JF, Peters ST, Rahman I, Ramasamy R, Rindone AN, Robbins PD, Robson P, Rodriguez-Lopez J, Rosas L, Rosenthal N, Schafer MJ, Schilling B, Schmidt EL, Schneider K, Sengupta K, Shu J, So PTC, Sun L, Tchkonja T, Teneche MG, Vanegas N, Wang J, Xie J, Yin S, Zhang K, Zhu Q, Fan R; SenNet Consortium. Advancing biological understanding of cellular senescence with computational multiomics. *Nature Genetics*. 2025.
- 14 Dai Q*, **Wan C***, Xu Y, Fei K, Olivere LA, Shafique H, Sadeghmousavi S, Johnson C, Garrett B, Akers L, Peters D, Otto J, Kontos CD, **Ji Z**, Diao Y, Southerland KW. Vascular adhesion molecule 1+ fibro-adipogenic progenitors mark fatty infiltration in chronic limb-threatening ischemia. *JVS-Vascular Science*. 2025.
 - 15 Kanu EN, Fletcher AA, Bao J, Agritelley ES, Button J, Eckhoff AM, Comatas K, Wang T, Hwang BJ, Lidsky ME, Zani S, Blazer DG, Allen PJ, **Ji Z**, Lowery FJ, Krishna S, Klemen ND, Nussbaum DP, Crosby EJ. A platform for multisite immune profiling of premetastatic pancreatic cancer at single-cell resolution. *Cancer Immunology, Immunotherapy*. 2025;74(9):291.
 - 16 **Wan C**, **Qu Y**, **Ye Z**, **Zhang T**, **Ma H**, Chen M, Hou W, **Ji Z**[†]. Comparative analysis of gene regulation in single cells using Compass. *Cell Reports Methods*. 2025;5(5):101035. [Google Scholar citations: 1]
 - 17 Hou W[†], Liu Q, **Ma H**, **Qu Y**, **Ji Z**[†]. Assessing large multimodal models for one-shot learning and interpretability in biomedical image classification. *Advanced Intelligent Systems*. 2025. [Google Scholar citations: 15]
 - 18 Jackson C, Cherry C, Bom S, Dykema AG, Wang R, Thompson E, Zhang M, Li R, **Ji Z**, Hou W, Zhan W, Zhang H, Choi J, Vaghasia A, Hansen L, Wang W, Bergsneider B, Jones KM, Rodriguez F, Weingart J, Lucas CH, Powell J, Elisseeff J, Yegnasubramanian S, Lim M, Bettgowda C, Ji H, Pardoll D. Distinct myeloid-derived suppressor cell populations in human glioblastoma. *Science*. 2025;387(6731):eabm5214. [Google Scholar citations: 44]
-Essential Science Indicators (ESI) highly cited paper: top 1% cited in the field of Clinical Medicine
 - 19 Rosner S, Connor S, Sanber K, Zahurak M, Zhang T, Gurumurthy I, Zeng Z, Presson B, Singh D, Rayes R, Sivapalan L, Pereira G, **Ji Z**, Thummalapalli R, Reuss JE, Broderick SR, Jones DR, Deutsch JS, Cottrell TR, Chaft J, Spicer J, Taube J, Anagnostou V, Brahmer JR, Pardoll DM, Ji H, Forde PM, Marrone KA, Smith KN. Divergent clinical and immunologic outcomes based on STK11 co-mutation status in resectable KRAS-mutant lung cancers following neoadjuvant immune checkpoint blockade. *Clinical Cancer Research*. 2025;31(2):339-351. [Google Scholar citations: 5]
 - 20 **Wang Y***, Zhao J*, Xu H*, Han C, Tao Z, Zhou D, Geng T, Liu D[†], **Ji Z**[†]. A systematic evaluation of computational methods for cell segmentation. *Briefings in Bioinformatics*. 2024;25(5):bbae407. [Google Scholar citations: 16]
 - 21 Mahmood K*, **Wang H***, **Ji Z**, Giovacchini CX, Wahidi MM, Dorry M, Shofer SL, Clarke JM, Antonia SJ, Shaz BH, Steadman K, Weinhold KJ, Yi J. Differences in microenvironment of lung cancer and pleural effusions by single-cell RNA sequencing. *Lung Cancer*. 2024;193:107847.
 - 22 Glass M, **Ji Z**, Davis R, Pavlisko E, DiBernardo L, Carney J, Fishbein G, Luthringer D, Miller D, Mitchell R, Larsen B, Butt Y, Bois M, Maleszewski J, Halushka M, Seidman M, Lin CY, Buja M, Stone J, Dov D, Carin L, Glass C. A Machine Learning Algorithm Improves the Diagnostic Accuracy of the Histologic Component of Antibody Mediated Rejection (AMR-H) in Cardiac Transplant Endomyocardial Biopsies. *Cardiovascular Pathology*. 2024;72:107646.
 - 23 Gao Q, **Ji Z**, Wang L, Owzar K, Li Q, Chan C, Xie J. SifiNet: A robust and accurate method to identify feature gene sets and annotate cells. *Nucleic Acids Research*. 2024;52(9):e46. [Google Scholar citations: 4]
 - 24 **Liu M**, **Ji Z**, Jain V, Smith VL, Hocke E, Patel AP, McLendon RE, Ashley DM, Gregory SG, López GY. Spatial transcriptomics reveals segregation of tumor cell states in glioblastoma and marked immunosuppression within the perinecrotic niche. *Acta Neuropathologica Communications*. 2024;12(1):64. [Google Scholar citations: 26]
 - 25 Stephens KE, Moore C, Vinson DA, White BE, Renfro Z, Zhou W, **Ji Z**, Ji H, Zhu H, Guan Y, Taverna SD. Identification of Regulatory Elements in Primary Sensory Neurons Involved in Trauma-Induced Neuropathic Pain. *Molecular Neurobiology*. 2024;61(3):1845-1859.
 - 26 Hou W, **Ji Z**, Chen Z, Wherry EJ, Hicks SC, Ji H. A statistical framework for differential pseudotime analysis with multiple single-cell RNA-seq samples. *Nature Communications*. 2023;14(1):7286. [Google Scholar citations: 76]

- 27 Dykema AG, Zhang J, Cheung LS, Connor S, Zhang B, Zeng Z, Cherry CM, Li T, Caushi JX, Nishimoto M, Munoz AJ, **Ji Z**, Hou W, Zhan W, Singh D, Zhang T, Rashid R, Mitchell-Flack M, Bom S, Tam A, Ionta N, Aye THK, Wang Y, Sawosik CA, Tirado LE, Tomasovic LM, VanDyke D, Spangler JB, Anagnostou V, Yang S, Spicer J, Rayes R, Taube J, Brahmer JR, Forde PM, Yegnasubramanian S, Ji H, Pardoll DM, Smith KN. Lung tumor-infiltrating Treg have divergent transcriptional profiles and function linked to checkpoint blockade response. *Science Immunology*. 2023;8(87):eadg1487. [Google Scholar citations: 52]
- 28 Loh ZN, Wang ME, **Wan C**, Asara JM, **Ji Z**, Chen M. Nuclear PTEN Regulates Thymidylate Biosynthesis in Human Prostate Cancer Cell Lines. *Metabolites*. 2023;13(8):939. [Google Scholar citations: 3]
- 29 Gurkar AU, Gerencser AA, Mora AL, Nelson AC, Zhang AR, Lagnado AB, Enniful A, Benz C, Furman D, Beaulieu D, Jurk D, Thompson EL, Wu F, Rodriguez F, Barthel G, Chen H, Phatnani H, Heckenbach I, Chuang JH, Horrell J, Petrescu J, Alder JK, Lee JH, Niedernhofer LJ, Kumar M, Königshoff M, Bueno M, Sokka M, Scheibye-Knudsen M, Neretti N, Eickelberg O, Adams PD, Hu Q, Zhu Q, Porritt RA, Dong R, Peters S, Victorelli S, Pengo T, Khaliullin T, Suryadevara V, Fu X, Bar-Joseph Z, **Ji Z**, Passos JF. Spatial mapping of cellular senescence: emerging challenges and opportunities. *Nature Aging*. 2023;3(7):776-790. [Google Scholar citations: 101]
-Essential Science Indicators (ESI) highly cited paper: top 1% cited in the field of Neuroscience & Behavior
- 30 Khatri A, Todd JL, Kelly FL, Nagler A, **Ji Z**, Jain V, Gregory SG, Weinhold KJ, Palmer SM. JAK-STAT activation contributes to cytotoxic T cell-mediated basal cell death in human chronic lung allograft dysfunction. *JCI Insight*. 2023;8(6):e167082. [Google Scholar citations: 21]
- 31 **Ji Z**[†], Ma L[†]. Controlling taxa abundance improves metatranscriptomics differential analysis. *BMC Microbiology*. 2023;23(1):60. [Google Scholar citations: 4]
- 32 Liu Y, Huang Z, Liu H, **Ji Z**, Arora A, Cai D, Wang H, Liu M, Simko EAJ, Zhang Y, Periz G, Liu Z, Wang J. DNA-initiated epigenetic cascades driven by C9orf72 hexanucleotide repeat. *Neuron*. 2023;111(8):1205-1221.e9. [Google Scholar citations: 22]
-Featured in Neuron "The DAXX tax: C9orf72 DNA repeat expansions drive gain- and loss-of-function pathology in c9FTD/ALS"
- 33 Fang Y, **Ji Z**^{*}, Zhou W^{*}, Abante J^{*}, Koldobskiy M, Ji H, Feinberg A. DNA methylation entropy is associated with DNA sequence features and developmental epigenetic divergence. *Nucleic Acids Research*. 2023;51(5):2046-2065. [Google Scholar citations: 12]
- 34 NIH SenNet Consortium to map senescent cells throughout the human lifespan to understand physiological health. (Listed as a consortium coauthor) *Nature Aging*. 2022;2(12):1090-1100. [Google Scholar citations: 111]
- 35 Zhang J, Wang X, **Ji Z**, Tian W. Large-scale prediction of key dynamic interacting proteins in multiple cancers. *International Journal of Biological Macromolecules*. 2022;220:1124-1132. [Google Scholar citations: 3]
- 36 Hou W, **Ji Z**[†]. Palo: Spatially-aware color palette optimization for single-cell and spatial data. *Bioinformatics*. 2022;38(14):3654-3656. [Google Scholar citations: 7]
- 37 **Zhuang H**, **Wang H**, **Ji Z**[†]. findPC: An R package to automatically select number of principal components in single-cell analysis. *Bioinformatics*. 2022;38(10):2949-2951. [Google Scholar citations: 36]
- 38 Lex RK, Zhou W, **Ji Z**, Falkenstein KN, Schuler KE, Windsor KE, Kim JD, Ji H, Vokes SA. GLI transcriptional repression is inert prior to Hedgehog pathway activation. *Nature Communications*. 2022;13(1):808. [Google Scholar citations: 34]
- 39 Hou W, **Ji Z**[†]. Unbiased visualization of single-cell genomic data with SCUBI. *Cell Reports Methods*. 2022;2(1):100135. [Google Scholar citations: 10]
- 40 Stephens KE, Zhou W, Renfro Z, **Ji Z**, Ji H, Guan Y, Taverna SD. Global gene expression and chromatin accessibility of the peripheral nervous system in animal models of persistent pain. *Journal of Neuroinflammation*. 2021;18(1):185. [Google Scholar citations: 14]
- 41 **Ji Z**, Ji H. Discussion of "Exponential-family Embedding with Application to Cell Developmental Trajectories for Single-cell RNA-seq Data". *Journal of the American Statistical Association*. 2021;116(534):471-474. [Google Scholar citations: 2]

- 42 Zhang J, Miao G, Hu S, Sun Q, Ding H, **Ji Z**, Guo P, Yan S, Wang C, Kan X, Nie L. Quantification and evolution of mitochondrial genome rearrangement in Amphibians. *BMC Ecology and Evolution*. 2021;21(1):19. [Google Scholar citations: 19]
- 43 Chamling X, Kallman A, Fang W, Berlinicke CA, Mertz JL, Devkota P, Pantoja IEM, Smith MD, **Ji Z**, Chang C, Kaushik A, Chen L, Whartenby KA, Calabresi PA, Mao HQ, Ji H, Wang TH, Zack DJ. Single-cell transcriptomic reveals molecular diversity and developmental heterogeneity of human stem cell-derived oligodendrocyte lineage cells. *Nature Communications*. 2021;12(1):652. [Google Scholar citations: 101]
- 44 Dangi A, Natesh NR, Husain I, **Ji Z**, Barisoni L, Kwun J, Shen X, Thorp EB, Luo X. Single-cell transcriptomics of mouse kidney transplants reveals a myeloid cell pathway for transplant rejection. *JCI Insight*. 2020; 5(20):e141321. [Google Scholar citations: 53]
- 45 Hou W, **Ji Z**, Ji H, Hicks S. A Systematic Evaluation of Single-cell RNA-sequencing Imputation Methods. *Genome Biology*. 2020; 21(1):218. [Google Scholar citations: 344]
- 46 **Ji Z**, Zhou W, Hou W, Ji H. Single-cell ATAC-seq signal extraction and enhancement with SCATE. *Genome Biology*. 2020; 21(1):161. [Google Scholar citations: 51]
- 47 Zhang J, Yan S, Jiang C, **Ji Z**, Wang C, Tian W. Network Properties of Cancer Prognostic Gene Signatures in the Human Protein Interactome. *Genes (Basel)*. 2020; 11(3):247. [Google Scholar citations: 3]
- 48 Zhang J*, **Ji Z***, Caushi JX*, El Asmar M*, Anagnostou V, Cottrell TR, Chan HY, Suri P, Guo H, Merghoub T, Chaff JE, Reuss JE, Tam AJ, Blosser RL, Abu-Akeel M, Sidhom JW, Zhao N, Ha JS, Jones DR, Marrone KA, Naidoo J, Gabrielson E, Taube JM, Velculescu VE, Brahmer JR, Housseau F, Hellmann MD, Forde PM, Pardoll DM, Ji H, Smith KN. Compartmental Analysis of T-cell Clonal Dynamics as a Function of Pathologic Response to Neoadjuvant PD-1 Blockade in Resectable Non-Small Cell Lung Cancer. *Clinical Cancer Research*. 2020; 26(6):1327-1337. [Google Scholar citations: 151]
-Featured in Clinical Cancer Research "Elite Intratumoral T-cell Clonotypes (The 1%) Effect 'Trickle-Down Cytotoxicity'"
- 49 Lex RK*, **Ji Z***, Falkenstein KN*, Zhou W, Henry JL, Ji H, Vokes SA. GLI transcriptional repression regulates tissue-specific enhancer activity in response to Hedgehog signaling. *Elife*. 2020; 9:e50670. [Google Scholar citations: 42]
- 50 Stephens KE, Zhou W, **Ji Z**, Chen Z, He S, Ji H, Guan Y, Taverna SD. Sex differences in gene regulation in the dorsal root ganglion after nerve injury. *BMC Genomics*. 2019; 20(1):147. [Google Scholar citations: 89]
- 51 Zhou W, **Ji Z**, Fang W, Ji H. Global prediction of chromatin accessibility using small-cell-number and single-cell RNA-seq. *Nucleic Acids Research*. 2019; 47(19):e121. [Google Scholar citations: 36]
- 52 Kuang Z, **Ji Z**, Boeke JD, Ji H. Dynamic motif occupancy (DynaMO) analysis identifies transcription factors and their binding sites driving dynamic biological processes. *Nucleic Acids Research*. 2018; 46(1):e2. [Google Scholar citations: 10]
- 53 Zhou W, Sherwood B, **Ji Z**, Xue Y, Du F, Bai J, Ying M, Ji H. Genome-wide prediction of DNase I hypersensitivity using gene expression. *Nature Communications*. 2017; 8(1):1038. [Google Scholar citations: 46]
- 54 Han F, Ji H, **Ji Z**, Wang H. A provable smoothing approach for high dimensional generalized regression with applications in genomics. *Electronic Journal of Statistics*. 2017; 11:4347-4403. [Google Scholar citations: 15]
- 55 Seyednasrollah F, et al. A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. (Listed as a consortium coauthor). *JCO Clinical Cancer Informatics*. 2017;1:1-15. [Google Scholar citations: 19]
- 56 Guinney J, et al. Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. (Listed as a consortium coauthor). *Lancet Oncology*. 2017; 18(1):132-142. [Google Scholar citations: 171]
- 57 **Ji Z***, Zhou W*, Ji H. Single-cell regulome data analysis by SCRAT. *Bioinformatics*. 2017; 33(18):2930-2932. [Google Scholar citations: 55]

- 58 Li Q, Lex RK, Chung H, Giovanetti SM, **Ji Z**, Ji H, Person MD, Kim J, Vokes SA. The Pluripotency Factor NANOG Binds to GLI Proteins and Represses Hedgehog-mediated Transcription. *Journal of Biological Chemistry*. 2016; 291(13):7171-82. [Google Scholar citations: 34]
- 59 Norrie JL, Li Q, Co S, Huang BL, Ding D, Uy JC, **Ji Z**, Mackem S, Bedford MT, Galli A, Ji H, Vokes SA. PRMT5 is essential for the maintenance of chondrogenic progenitor cells in the limb bud. *Development*. 2016; 143(24):4608-4619. [Google Scholar citations: 33]
- 60 Hong X, Ladd-Acosta C, Hao K, Sherwood B, Ji H, Keet CA, Kumar R, Caruso D, Liu X, Wang G, Chen Z, Ji Y, Mao G, Walker SO, Bartell TR, **Ji Z**, Sun Y, Tsai HJ, Pongracic JA, Weeks DE, Wang X. Epigenome-wide association study links site-specific DNA methylation changes with cow's milk allergy. *Journal of Allergy and Clinical Immunology*. 2016; 138(3):908-911.e9. [Google Scholar citations: 73]
- 61 Wang G, Hu FB, Mistry KB, Zhang C, Ren F, Huo Y, Paige D, Bartell T, Hong X, Caruso D, **Ji Z**, Chen Z, Ji Y, Pearson C, Ji H, Zuckerman B, Cheng TL, Wang X. Association Between Maternal Prepregnancy Body Mass Index and Plasma Folate Concentrations With Child Metabolic Health. *JAMA Pediatrics*. 2016; 170(8):e160845. [Google Scholar citations: 104]
- 62 Deng D, Du Y, **Ji Z**, Rao K, Wu Z, Zhu Y, Coley RY. Predicting survival time for metastatic castration resistant prostate cancer: An iterative imputation approach. *F1000Research*. 2016; 5:2672. [Google Scholar citations: 3]
- 63** **Ji Z**, Vokes SA, Dang CV, Ji H. Turning publicly available gene expression data into discoveries using gene set context analysis. *Nucleic Acids Research*. 2016; 44(1):e8. [Google Scholar citations: 22]

Conference proceedings

- 64 Multimodal single cell data integration challenge: results and lessons learned. (Listed as a consortium coauthor). *Proceedings of the NeurIPS 2021 Competitions and Demonstrations Track, Proceedings of Machine Learning Research*. 2022;176:162-176. [Google Scholar citations: 101]

Book Chapters

- 65** **Ji Z**, Ji H. Pseudotime Reconstruction Using TSCAN. *Methods in Molecular Biology*. 2019; 1935:115-124. [Google Scholar citations: 16]
- 66 Zhang J, **Ji Z**, Smith KN. Analysis of TCR β CDR3 sequencing data for tracking anti-tumor immunity. *Methods in Enzymology*. 2019; 629:443-464. [Google Scholar citations: 9]

Editorial

- 67 Hou L, **Ji Z**, Wang J, Xie J. Editorial: Statistical and computational methods for single-cell sequencing analysis. *Frontiers in Genetics*. 2023;14:1235174.

Funding Support

The white numbers displayed in black boxes represent grants for which I serve as the PI or core lead.

Current

- 1** Title: Computational methods for in situ spatial transcriptomics
 Project Number: R35-GM154865
 PD/PI: Zhicheng Ji
 Source of Support: National Institutes of Health (NIH) / National Institute of General Medical Sciences (NIGMS)
 Project Start and End Date: 8/1/2024 - 6/30/2029
 Role: PI

Total Award Amount: \$1,963,069

Effort: 39%

- 2** Title: The Duke Senescent Cell Evaluations in Normal Tissues (SCENT) Mapping Center
Project Number: U54-AG075936
PD/PI: Andrew B. Nixon
Source of Support: National Institutes of Health (NIH) / National Institute on Aging (NIA)
Project Start and End Date: 9/30/2021 - 8/31/2026
Role: Data Analysis Core Co-Lead
Total Award Amount: \$12,705,171
Effort: 10%
- 3** Title: Center of Excellence for Systems Modeling of Infection and Immunity across Biological Scales
Project Number: U54-AI191253
PD/PI: Cliburn Chan
Source of Support: National Institutes of Health (NIH) / National Institute of Allergy and Infectious Diseases (NIAID)
Project Start and End Date: 6/13/2025 - 5/31/2030
Role: Model and Data Sharing Core Co-Lead
Total Award Amount: \$24,693,218
Effort: 10%
- 4** Title: NSF Engineering Research Center for Precision Microbiome Engineering (PreMiEr)
Project Number: EEC-2133504
PD/PI: Claudia Gunsch
Source of Support: National Science Foundation (NSF)
Project Start and End Date: 9/1/2022 - 8/31/2027
Role: Co-I
Total Award Amount: \$26,000,000
Effort: 5%
- 5** Title: Training Program in Bioinformatics at the Intersection of Cancer Immunology and Microbiome
Project Number: R25-CA244070
PD/PI: Kouros Owzar
Source of Support: National Institutes of Health (NIH) / National Cancer Institute (NCI)
Project Start and End Date: 7/1/2020 - 6/30/2025
Role: Training Faculty
Total Award Amount: \$1,222,432
Effort: 5%
- 6** Title: A Window-of-Opportunity Trial Using Neoadjuvant Hepatic Artery Chemotherapy for Patients With Localized Pancreas Cancer
Project Number: 23-14
PD/PI: Peter J. Allen
Source of Support: Marc Lustgarten Pancreatic Cancer Foundation
Project Start and End Date: 12/1/2023 - 8/31/2026
Role: Co-I
Total Award Amount: \$1,368,231
Effort: 5%

- 7 Title: Targeting Ferroptosis in Lethal RB1 Deficient Prostate Cancer
Project Number: R01-CA269211
PD/PI: Ming Chen
Source of Support: National Institutes of Health (NIH) / National Cancer Institute (NCI)
Project Start and End Date: 4/1/2022 - 3/31/2027
Role: Co-I
Total Award Amount: \$2,071,290
Effort: 4.25%
- 8 Title: Perinatal Per- and Polyfluoroalkyl Substances (PFAS) exposure and Immunotoxicity in early life
Project Number: R01-ES035037
PD/PI: Liping Feng
Source of Support: National Institutes of Health (NIH) / National Institute of Environmental Health Sciences (NIEHS)
Project Start and End Date: 4/20/2023 - 1/31/2028
Role: Investigator
Total Award Amount: \$2,476,848
Effort: 4%

Past

- 9 Title: Whitehead Scholar Award
PD/PI: Zhicheng Ji
Source of Support: Duke University School of Medicine
Project Start and End Date: 2021 -
Role: PI
Total Award Amount: \$250,000
- 10 Title: Translating Duke Health Award
PD/PI: Zhicheng Ji
Source of Support: Duke University School of Medicine
Project Start and End Date: 2021 -
Role: PI
Total Award Amount: \$50,000
- 11 Title: Single-cell omics approaches to investigate TMD
Project Number: UH2-DE032202
PD/PI: Shad Smith
Source of Support: National Institutes of Health (NIH) / National Institute of Dental and Craniofacial Research (NIDCR)
Project Start and End Date: 9/9/2022 - 8/31/2024
Role: Statistician
Total Award Amount: \$402,487

- 12 Title: Neuro-immune modulation of pain in health and disease
 Project Number: R01-DE031053
 PD/PI: Chris Donnelly
 Source of Support: National Institutes of Health (NIH) / National Institute of Dental and Craniofacial Research (NIDCR)
 Project Start and End Date: 9/1/2022-8/31/2027
 Role: Co-I
 Total Award Amount: \$3,311,196
- 13 Title: Statistical modeling of cross-sample variation and learning of latent structures in microbiome sequencing data
 Project Number: R01-GM135440
 PD/PI: Li Ma
 Source of Support: National Institutes of Health (NIH) / National Institute of General Medical Sciences (NIGMS)
 Project Start and End Date: 9/15/2020-8/31/2025
 Role: Investigator
 Total Award Amount: \$1,717,909
- 14 Title: Neural Architecture of the Murine and Human Temporomandibular Joint
 Project Number: UC2-AR082197
 PD/PI: Christopher R. Donnelly
 Source of Support: National Institutes of Health (NIH) / National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS)
 Project Start and End Date: 9/23/2022 - 8/31/2025
 Role: Co-I
 Total Award Amount: \$5,734,560

Editorial Activities

Editor

Guest editor, [Statistical Genetics and Methodology](#), [Frontiers in Genetics](#)

Review Editor, [Cancer Immunity and Immunotherapy](#), [Frontiers in Immunology](#)

Review Editor, [Integrative Genetics and Genomics](#), [Frontiers in Systems Biology](#)

Reviewer for Journals (selected)

Science; Nature Biotechnology; Nature Methods; Nature Aging; Nature Computational Science; Cell Discovery; Cell Genomics; Nature Communications; Nucleic Acids Research; Nature Protocols; Genome Biology; Genome Medicine; Advanced Science; npj Digital Medicine; Cell Reports; Genome Research; Briefings in Bioinformatics; Genomics, Proteomics & Bioinformatics; GigaScience; Communications Biology; Clinical and Translational Medicine; PLOS Computational Biology; PLOS Genetics; Computational and Structural Biotechnology Journal; Bioinformatics; Annals of Applied Statistics

Mentoring Experience

Bold indicates that I am the thesis or graduation project advisor.

Current Trainees

Postdoctoral Associate

Huifang Ma, Department of Biostatistics and Bioinformatics, Duke University (co-advise with Dr. Anru Zhang)

Ph.D. Students

Huimin Wang, Department of Biostatistics and Bioinformatics, Duke University (co-advise with Dr. Simon Gregory)

-Precision Genomics Collaboratory-OBGE Graduate Student Pilot Research Grant Award

Haotian Zhuang, Department of Biostatistics and Bioinformatics, Duke University

Xingyuan Zhang, Program of Computational Biology and Bioinformatics, Duke University

Master's Students

Jingyun Liu, Department of Biostatistics and Bioinformatics, Duke University

Beijie Ji, Department of Biostatistics and Bioinformatics, Duke University

Changyue (William) Zhao, Department of Biostatistics and Bioinformatics, Duke University

Alumni

Postdoctoral Associate

Yuxing Wang, Department of Biostatistics and Bioinformatics, Duke University

-After graduation: Machine Learning Engineer, Nvidia

Ph.D. Students

Changxin Wan, Program of Computational Biology and Bioinformatics, Duke University

-Precision Genomics Collaboratory-OBGE Graduate Student Pilot Research Grant Award

-After graduation: Bioinformatics Research Scientist, St. Jude Children's Research Hospital

Mengyi (Miko) Liu, Computational Biology and Bioinformatics Program, Duke University (co-advise with Dr. Simon Gregory)

-Paul and Lauren Ghaffari Graduate Fellowship

-After graduation: Senior Bioinformatics Engineer, Novogene

Yuxing Wang, Department of Computer Engineering, Rochester Institute of Technology (visiting student)

Constantine Stavrianidis, Program of Computational Biology and Bioinformatics, Duke University (rotation student)

Tzu-Chieh (Jackie) Liao, Department of Immunology, Duke University (rotation student)

Aybuga Altay, Max Planck Institute for Molecular Genetics (visiting student)

Master's Students

Anthony Qu, Department of Biostatistics and Bioinformatics, Duke University

-Outstanding Master's Project Award

-After graduation: PhD student, Graduate Group in Genomics and Computational Biology, University of Pennsylvania

Yuan Wang, Department of Biostatistics and Bioinformatics, Duke University (co-advise with Dr. Yarui Diao)

Hao Wang, Department of Statistical Science, Duke University

-After graduation: PhD student, Department of Biostatistics, University of Pittsburgh

Constantine Stavrianidis, M.S. Department of Biostatistics and Bioinformatics, Duke University

-After graduation: PhD student, Program of Computational Biology and Bioinformatics, Duke University

Caiwei Zhong, M.S. Department of Biostatistics and Bioinformatics, Duke University

-After graduation: statistician, Dana-Farber Cancer Institute

Huimin Wang, M.S. in Biostatistics and Bioinformatics, Duke University

-After graduation: PhD student, Department of Biostatistics and Bioinformatics, Duke University

-Outstanding Master's Project Award

Haotian Zhuang, M.S. in Biostatistics and Bioinformatics, Duke University

-After graduation: PhD student, Department of Biostatistics and Bioinformatics, Duke University

-Degree Marshall Award

-Overall Academic Achievement Award

Tianbei Zhang, Department of Biostatistics and Bioinformatics, Duke University

-After graduation: PhD student, Department of Biomedical Engineering, Johns Hopkins University

Xiaotan Sun, Department of Biostatistics and Bioinformatics, Duke University (co-advise with Dr. Anru Zhang)

-After graduation: research data scientist, Cleveland Clinic

Zhiyou Ye, Department of Biomedical Engineering, Duke University

Dezhao Fu, Department of Biostatistics and Bioinformatics, Duke University

-After graduation: PhD student, Program in Health Data Science, The George Washington University

Undergraduate Students

Brian Du, B.S. in Computer Science, Duke University

-After graduation: MD student, Baylor College of Medicine

Wei Wang, B.S. in Applied Mathematics, The College of William & Mary (Visiting student)

-After graduation: PhD student, Department of Biostatistics, University of Minnesota

Ph.D. Thesis Committee

Carol Wang, Department of Statistical Science, Duke University

Qi Gao, Department of Biostatistics and Bioinformatics, Duke University

Arinze Okafor, Department of Cell Biology, Duke University

Hongbin Liu, Department of Electrical and Computer Engineering, Duke University

Tzu-Chieh (Jackie) Liao, Department of Immunology, Duke University

Zihan Yan, Department of Cell and Molecular Biology, Duke University

Ph.D. Preliminary Exam Committee

Giwon Cho, Department of Biomedical Engineering, Duke University

Teaching Experience

Courses

BIOSTAT 824. Case Studies in Biomedical Data Science. 2025, Department of Biostatistics and Bioinformatics, Duke University

-Designed the entire course content, covering topics such as single-cell and spatial genomics, large language models, and deep learning.

-Course website: <https://canvas.duke.edu/courses/53123>.

-Received the highest score (5/5) across all categories in student evaluations during the inaugural offering.

Short Courses and Workshops

Microbiome Immunology Cancer Bioinformatics Short Course. 2022-2025, Department of Biostatistics and Bioinformatics, Duke University

Practical Genomics Workshop: From Biology to Biostatistics. 2021, Johns Hopkins Center for Computational Genomics.

Guest Lecturer

MATH 590: Advanced Special Topics in Mathematics. 2023, Duke University

BIOSTAT 900: Current Problems in Biostatistics. 2020, Duke University

140.688: Statistics for Genomics. 2018-2020, Johns Hopkins University

Teaching Assistant

140.621: Statistical Methods in Public Health. 2014-2015 & 2016-2019, Johns Hopkins University

Professional Activities

Grant Review

Ad hoc reviewer, NIH, Small Business: Computational, Modeling, and Biodata Management (MCST (14)) study section

Ad hoc reviewer, NIH, Computational Approaches for Data Curation, Biomedical Informatics and Data Science (ZRG1 BBOT-K (87)) study section

Ad hoc reviewer, NIH, Molecular Neurogenetics (MNG) standing study section

Mail reviewer, NIH, Director's Early Independence Awards (DP5).

Mail reviewer, Medical Research Council, UK Research and Innovation (UKRI)

Academic Services

Co-chair, Imaging Mapping Working Group, NIH Common Fund's Cellular Senescence Network (SenNet)

Co-organizer, Duke single cell initiative research in progress seminar series

Organizer, Immunology Data Science Challenge for Master's students, Department of Biostatistics and Bioinformatics, Duke University

Screeners, Duke University School of Medicine MD admissions

Reviewer, Duke University School of Medicine Virtual Research Week Poster Session

Reviewer, ASA Section on Statistics in Genomics and Genetics Student Paper Competition

Professional Memberships

American Statistical Association (ASA) (2016-present)

Eastern North American Region (ENAR) (2017-present)

International Society for Computational Biology (ISCB) (2018-2019)

International Chinese Statistical Association (ICSA) (2016-2017)

American Society of Human Genetics (ASHG) (2015-2016)

International Genetic Epidemiology Society (IGES) (2015-2016)

Presentations

Invited Talks

Applications of Commercial LLMs in Genomic Research. Joint Statistical Meetings. Aug, 2025

TCRfoundation: a multimodal foundation model for single-cell immune profiling. Center for Human Systems Immunology Virtual Symposium. Duke University. June, 2025

EpiFoundation: A Foundation Model for Single-Cell ATAC-seq via Peak-to-Gene Alignment. STATGEN 2025: Conference on Statistics in Genomics and Genetics. May, 2025

Single-cell and spatial detection of senescent cells using DeepScience. SenNet Consortium Spring 2025 Meeting. Apr, 2025

Expanding the Horizons of Genomics and Biomedical Analysis: GPT-4's Role in Automated Cell Type Annotation and Beyond. ICIBM. Oct, 2024

Computational methods for decoding cellular senescence. Department Colloquium, Department of Computational Mathematics, Science and Engineering, Michigan State University. Aug, 2024

GeneSegNet: a deep learning framework for cell segmentation by integrating gene expression and imaging. MCBIOS 2024. March, 2024

Democratizing genomic data science with large language models. Statistical Genetics and Genomics Seminar, Department of Biostatistics, Columbia University. November, 2023

Decomposing spatial heterogeneity of cell trajectories for spatial transcriptomics data. ICSA Applied Statistics Symposium, June, 2023

Applications of ChatGPT and GPT models to genomic research. Duke Center for Human Systems Immunology Retreat, June, 2023

Analyzing and Comparing Multiple Spatial Gene Expression Samples with POLYspace. Joint Statistical Meeting, August, 2022

Statistical Methods for Decoding Gene Regulation in Single Cells. Statistical Genetics Seminar, The University of North Carolina at Chapel Hill, March, 2022

Integrative analysis of multi-study single-cell RNA-sequencing datasets identifies conserved immune landscape of COVID-19 patients. Inaugural Duke Center for Human Systems Immunology Virtual Symposium, August, 2021

Integrative analysis of multi-study single-cell RNA-sequencing datasets identifies conserved immune landscape of COVID-19 patients. Single-cell and Spatial Colloquium, Duke University, March, 2021

Computational Methods for Decoding Gene Regulation in Single Cells. Computational Biology and Bioinformatics Seminar, Duke University, February, 2021

Single-cell RNA-seq, power to analyze at a single cell level and broader view of statistical approach to employ in single cell analysis. Duke Transplant Infectious Diseases Research Symposium, November, 2020

Contributed Talks

Assessing GPT-4 for cell type annotation in single-cell RNA-seq analysis. ENAR, March, 2024

Single-cell Unbiased Visualization with SCUBI. Joint Statistical Meeting, August, 2021

Reconstruction of conserved immune landscape in COVID-19 patients via multi-study integrative analysis of single-cell RNA-sequencing data. Cold Spring Harbor meeting on Systems Immunology, April, 2021

Single-cell ATAC-seq signal extraction and enhancement with SCATE. ENAR, March, 2020

Reproducible interactive data visualization and exploration with iXplore. ENAR, March, 2017

Reproducible interactive data visualization and exploration with iXplore. The 10th International Chinese Statistical Association International Conference, December, 2016

TSCAN: Pseudo-time reconstruction and evaluation in single-cell RNA-seq analysis. Joint Statistical Meeting, August, 2016

Posters

Single-cell ATAC-seq signal extraction and enhancement with SCATE. RECOMB/ISCB Conference on Regulatory & Systems Genomics, December, 2018

Turning publicly available gene expression data into discoveries using gene set context analysis. The American Society of Human Genetics Annual Meeting, October, 2015

Turning publicly available gene expression data into discoveries using gene set context analysis. International Genetic Epidemiology Society Annual Meeting, October, 2015