

Zhicheng Ji

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Education

2020 Ph.D. in Biostatistics, Johns Hopkins Bloomberg School of Public Health
2020 M.S.E. in Computer Science, Johns Hopkins Whiting School of Engineering
2013 B.S. in Statistics, Fudan University

Professional Experience

08/2020-present Assistant Professor
Department of Biostatistics and Bioinformatics, Duke University School of Medicine

Honors and Awards

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
2012 First-class Scholarship, Fudan University

Publications

[Google Scholar](#)

* indicates equal contributions † indicates corresponding authors

Journal Articles and Articles under Review

1. Wenpin Hou, Zhicheng Ji, Zeyu Chen, E. John Wherry, Stephanie C. Hicks, Hongkai Ji. A statistical framework for differential pseudotime analysis with multiple single-cell RNA-seq samples. Submitted. [bioRxiv](#)
2. Rachel K. Lex, Weiqiang Zhou, **Zhicheng Ji**, Kristin N. Falkenstein, Kaleigh E. Schuler, Kathryn E. Windsor, Joseph D. Kim, Hongkai Ji, Steven A. Vokes. GLI transcriptional repression is inert prior to Hedgehog pathway activation. Submitted. [bioRxiv](#)
3. Wenpin Hou, **Zhicheng Ji**[†]. Single-cell Unbiased Visualization with SCUBI. Under Review. [SSRN](#)

4. Jifeng Zhang, Xiao Wang, **Zhicheng Ji**, Weidong Tian. Large-scale prediction of key dynamic interacting proteins in multiple cancers. Submitted. [bioRxiv](#)
5. 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. *J Neuroinflammation*. 2021 Aug 26;18(1):185. doi: 10.1186/s12974-021-02228-6.
6. 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, Chافت 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 Aug;596(7870):126-132.
7. **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.
8. 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.
9. 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.
10. 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):e14132.
11. Hou W, **Ji Z**, Ji H, Hicks S. A Systematic Evaluation of Single-cell RNA-sequencing Imputation Methods. *Genome Biology*. 2020; 21(1):218.
12. **Ji Z**, Zhou W, Hou W, Ji H. Single-cell ATAC-seq signal extraction and enhancement with SCATE. *Genome Biology*. 2020; 21(1):161.
13. 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.
14. Zhang J*, **Ji Z***, Caushi JX*, El Asmar M*, Anagnostou V, Cottrell TR, Chan HY, Suri P, Guo H, Merghoub T, Chافت 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.
15. 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.
16. 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.
17. Chen Z*, **Ji Z***, Ngio 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.
150+ citations on Google Scholar
18. 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.

19. 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.
20. 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.
21. 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(2):4347-4403.
22. Seyednasrollah F, et al. A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. *JCO Clinical Cancer Informatics*. 2017; doi: 10.1200/CCI.17.00018. (Listed as consortium coauthor)
23. 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. *Lancet Oncology*. 2017; 18(1):132-142. (Listed as consortium coauthor)
24. **Ji Z***, Zhou W*, Ji H. Single-cell regulome data analysis by SCRAT. *Bioinformatics*. 2017; 33(18):2930-2932.
25. 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.
26. 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.
27. **Ji Z**, Ji H. TSCAN: Pseudo-time reconstruction and evaluation in single-cell RNA-seq analysis. *Nucleic Acids Research*. 2016; 44(13):e117.
Winner of ASA Section on Statistics in Genomics and Genetics Distinguished Student Paper Award
300+ citations on Google Scholar
28. 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.
29. 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.
30. 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.
31. **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.

Book Chapters

32. **Ji Z**, Ji H. Pseudotime Reconstruction Using TSCAN. *Methods in Molecular Biology*. 2019; 1935:115-124.
33. 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.

Software

SCUBI: Single-cell Unbiased Visualization [\[Github\]](#)

SCATE: Single-cell ATAC-seq signal extraction and enhancement [\[Github\]](#)

TSCAN: Pseudo-time reconstruction in single-cell RNA-seq analysis [\[Bioconductor\]](#) [\[Github\]](#) [\[GUI\]](#)

SCRAT: Single-cell regulome analysis tool [\[Github\]](#) [\[GUI\]](#)

STIP: State transition inference prediction [\[Github\]](#)

GSCA: Gene set context analysis [\[Bioconductor\]](#) [\[Github\]](#) [\[GUI\]](#)

RMRCE: Regularized maximum rank correlation estimator [\[Github\]](#)

Editorial Activities

Journal Referee

Nature Methods
Nucleic Acids Research
Nature Communications
Genome Biology
PLOS Computational Biology
Computational and Structural Biotechnology Journal
Bioinformatics
NAR Genomics and Bioinformatics
BMC Medical Genomics
Cancers
Viruses
Biology
Life
Statistics in Biosciences

Professional Activities

Academic Services

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

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

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

American Statistical Association (ASA) (2016-2017)

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

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

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

Teaching

PhD Students

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

Changxin Wan, Computational Biology and Bioinformatics Program, Duke University

PhD Thesis Committee

Qi Gao, Department of Biostatistics and Bioinformatics, Duke University

Arinze Okafor, Department of Cell Biology, Duke University

Master's Students

Haotian Zhuang, Department of Biostatistics and Bioinformatics, Duke University

Huimin Wang, Department of Biostatistics and Bioinformatics, Duke University

Undergraduate Students

Brian Du, Computer Science major, Duke University

Wei Wang, Applied Mathematics major, The College of William & Mary

Guest Lecturer

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

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

Funding Support

Pending

High-resolution Spatial Maps of Gene Expression and Gene Regulatory Programs (PI: Ji)

Dates: 9/1/2022 - 8/31/2027

Role: PI

Targeting Ferroptosis in Lethal RB1 Deficient Prostate Cancer (PI: Chen)

Dates: 4/1/2022 - 3/31/2027

Role: Co Investigator

The role of epithelial derived cytokines and group 2 innate lymphoid cells in chronic allograft dysfunction after human lung transplantation (PI: Todd)

Dates: 7/1/2021 - 6/30/2026

Role: Biostatistician Investigator

Interrogating the Molecular Basis of Alzheimer's Disease Susceptibility by Spatiotemporal Analysis (PI: Gregory/Wang/Ji)

Dates: 9/1/2021 - 8/31/2023

Role: Co-PI

The Duke Senescent Cell Evaluations in Normal Tissues (SCENT) Mapping Center Data Analysis Core (PI: Lee, Core PI: Cliburn/Ji)

Dates: 12/1/2021 - 11/30/2026

Role: Core Co-PI

Completed

Whitehead Scholar award (PI: Ji)

Amount: \$250,000

Date: 2020

Role: PI

Translating Duke Health award (PI: Ji)

Amount: \$50,000

Date: 2020

Role: PI