Zhicheng Ji

Department of Biostatistics and Bioinformatics

School of Medicine

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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. Kimberly E Stephens, Weiqiang Zhou, Zachary Renfro, **Zhicheng Ji**, Hongkai Ji, Yun Guan, Sean D Taverna. Dynamics of global gene expression and chromatin accessibility of the peripheral nervous system in animal models of persistent pain. Submitted.

5. Jifeng Zhang, Xiao Wang, **Zhicheng Ji**, Weidong Tian. Large-scale prediction of key dynamic interacting proteins in multiple cancers. Submitted. bioRxiv

6. Justina Caushi, Jiajia Zhang, **Zhicheng Ji***, Ajay Vaghasia*, Boyang Zhang , Emily Hsiue , Brian Mog , Wenpin Hou , Sune Justesen , Lee Blosser , Ada Tam , Valsamo Anagnostou , Tricia Cottrell , Haidan Guo , Hok Yee Chan , Dipika Singh , Sampriti Thapa , Arbor Dykema , Begum Choudhury , Luis Aparicio , Laurene Cheung , Mara Lanis , Zineb Belcaid , Margueritta El Asmar , Peter Illei , Rulin Wang , Jennifer Meyers , Kornel Schuebel , Anuj Gupta , Alyza Skaist , Sarah Wheelan , Jarushka Naidoo , Kristen Marrone , Malcolm Brock , Jinny Ha , Errol Bush , Bernard Park , Matthew Bott , David Jones , Joshua Reuss , Victor Velculescu , Jamie Chaft , Kenneth Kinzler , Shibin Zhou , Bert Vogelstein , Janis Taube , Matthew Hellmann , Julie Brahmer , Taha Merghoub , Patrick Forde , Srinivasan Yegnasubramanian , Hongkai Ji , Drew Pardoll, Kellie Smith. Distinct transcriptional programs characterize neoantigen-specific T cells in lung cancers treated with neoadjuvant PD-1 blockade. Nature. Accepted.

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, Chaft 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***, Ngiow 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

SCATE: Single-cell ATAC-seq signal extraction and enhancement [Github]

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

BIRD: Big data regression for predicting DNase I hypersensitivity [Github]

SCRAT: Single-cell regulome analysis tool [Github] [GUI]

STIP: State transition inference prediction [Github]

GSCA: Gene set context analysis [Bioconductor] [Github] [GUI]

DynaMO: Dynamic motif occupancy analysis [Github]

RMRCE: Regularized maximum rank correlation estimator [Github]

Editorial Activities

Journal Referee

Nature Methods
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. *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

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 Student

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 (rotating student)

PhD Thesis Committee

Qi Gao, Department of Biostatistics and Bioinformatics, Duke University

Students Working on Projects

Haotian Zhuang, Department of Biostatistics and Bioinformatics, Duke University

Brian Du, Department of Computer Science, Duke University

Guest Lecturer

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

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

Funding Support

Pending

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: Principal Investigator

Translating Duke Health award (PI: Ji)

Amount: $50,000

Date: 2020

Role: Principal Investigator