Zhicheng Ji, Ph.D.

Department of Biostatistics and Bioinformatics
Duke University School of Medicine

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Education

2020 Ph.D. in Biostatistics, Johns Hopkins Bloomberg School of Public Health (*Mentor: Hongkai Ji, Ph.D.*)

2020 M.S.E. in Computer Science, Johns Hopkins Whiting School of Engineering (*Mentor: Suchi Saria, Ph.D.*)

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

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

The white numbers indicate first or senior author manuscripts. The * indicates equal contributions. The † indicates corresponding author. The underlines indicate mentees.

Research Articles

Articles in submission

1 **Ji Z**, Hou W, Ji H. RAISIN: Regression analysis in single-cell RNA-Seq with multiple samples. *In submission*.

Articles submitted and under review

2 Hou W, **Ji Z**†. Palo: Spatially-aware color palette optimization for single-cell and spatial data. *Minor Revision in Bioinformatics*. bioRxiv

3 Liu Y, Huang Z, Liu H, **Ji Z**, Arora A, Cai D, Liu Z, Simko E, Zhang Y, Periz G, Wang J. C9orf72 Hexanucleotide Repeat DNA Initiates Pathogenic Cascades Through Chromatin and Epigenome Regulator DAXX. *Under Review in Neuron*.

4 Zhang B, **Ji Z**, and Ji H. Tree-based Correlation Screen and Visualization for Exploring Phenotype-Cell Type Association in Multiple Sample Single-Cell RNA-Sequencing Experiments. *Under review in Genome Biology*. bioRxiv

5 Hou W, **Ji Z**, Chen Z, Wherry EJ, Hicks S, Ji H. A statistical framework for differential pseudotime analysis with multiple single-cell RNA-seq samples. *In revision in Nature Methods (Guided open access)*. bioRxiv

6 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. *Under review in Nucleic Acids Research*.

7 **Ji Z**†, Ma L†. Controlling taxa abundance improves metatranscriptomics differential analysis. *Submitted*. bioRxiv

8 Multimodal single cell data integration challenge: results and lessons learned. (Listed as a consortium coauthor). *Submitted*. bioRxiv

9 Zhang J, Wang X, **Ji Z**, Tian W. Large-scale prediction of key dynamic interacting proteins in multiple cancers. *Submitted*. bioRxiv

Peer-reviewed journal articles

10 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.

11 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.

12 Hou W, **Ji Z**†. Unbiased visualization of single-cell genomic data with SCUBI. *Cell Reports Methods*. 2022;2(1):100135. [Google Scholar citations: 1]

13 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.

14 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: 43]

Reviewed in Nature Reviews Clinical Oncology "Tumour antigen-induced T cell exhaustion – the archenemy of immune-hot malignancies"

15 **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.

16 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: 4]

17 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: 18]

18 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. [Google Scholar citations: 13]

19 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: 93]

20 **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: 15]

21 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.

22 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. [Google Scholar citations: 49]

Reviewed in Clinical Cancer Research "Elite Intratumoral T-cell Clonotypes (The 1%) Effect 'Trickle-Down Cytotoxicity'"

23 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: 14]

24 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: 39]

25 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. [Google Scholar citations: 246]

Reviewed in Immunity "Back to the future: effector fate during T cell exhaustion"

26 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: 19]

27 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: 9]

28 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: 27]

29 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. [Google Scholar citations: 8]

30 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: 11]

31 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: 126]

32 **Ji Z***, Zhou W*, Ji H. Single-cell regulome data analysis by SCRAT. *Bioinformatics*. 2017; 33(18):2930-2932. [Google Scholar citations: 36]

33 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: 21]

34 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: 16]

35 **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: 401]

Winner of ASA Section on Statistics in Genomics and Genetics Distinguished Student Paper Award

36 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: 48]

37 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: 68]

38 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: 2]

39 **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: 5]

Book Chapters

40 **Ji Z**, Ji H. Pseudotime Reconstruction Using TSCAN. *Methods in Molecular Biology*. 2019; 1935:115-124. [Google Scholar citations: 4]

41 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: 3]

Funding Support

Ongoing

The Duke Senescent Cell Evaluations in Normal Tissues (SCENT) Mapping Center (NIH U54AG075936)
Dates: 09/30/2021-08/31/2026. PI: Patty Lee. Total Amount: $12.7M
Role: Data Analysis Core Co-PI

Targeting Ferroptosis in Lethal RB1 Deficient Prostate Cancer (NIH R01CA269211)
Dates: 04/01/2022-03/31/2027. PI: Ming Chen. Total Amount: $2.5M
Role: Co-Investigator

Training Program in Bioinformatics at the Intersection of Cancer Immunology and Microbiome (NIH R25CA244070)
Dates: 07/01/2020-06/30/2025. PI: Kouros Owzar, Cliburn Chan, Joshua Granek. Total Amount: $1.5M
Role: Co-Investigator

Pending (as PI or co-PI)

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

Benchmarking deconvolution tools for spatial transcriptomics (Chan Zuckerberg Initiative)
PI: Zhicheng Ji.
Role: PI

Tensor methods for multi-sample multi-omics single-cell data (Chan Zuckerberg Initiative)
PI: Zhicheng Ji, Anru Zhang.
Role: PI

Interrogating the Molecular Basis of Alzheimer's Disease Susceptibility by Spatiotemporal Analysis (NIH)
PI: Simon Gregory, Shih-Hsiu Wang, Zhicheng Ji.
Role: Co-PI

Completed

Duke School of Medicine Whitehead Scholar Award
Date: 2021. PI: Zhicheng Ji. Total Amount: $250K.
Role: PI

Translating Duke Health Award
Date: 2021. PI: Zhicheng Ji. Total Amount: $50K.
Role: PI

Software

Palo: Spatially-aware color palette optimization [Github]

findPC: Automatic selection of number of principal components [Github]

SCUBI: Single-cell unbiased visualization [Github]

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

Editor

Guest editor of Biomedicines Special Issue: Single-Cell Genomics in Biomedicines

Guest editor of Frontiers in Genetics: Statistical Genetics and Methodology

Journal Review

Nature Methods; Nucleic Acids Research; Nature Communications; Genome Biology; Genomics, Proteomics & Bioinformatics; PLOS Computational Biology; Computational and Structural Biotechnology Journal; PLOS Genetics; Bioinformatics; Bioinformatics Advances; Frontiers in Oncology; NAR Genomics and Bioinformatics; BMC Medical Genomics; Cancers; Genes; Viruses; Biology; Life; Statistics in Biosciences; Biochemical Genetics; Frontiers in Molecular Biosciences; Frontiers in Immunology; Evolutionary Bioinformatics

Mentoring Experience

Postdoctoral Associate

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

Ph.D. 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

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

Ph.D. Thesis Committee

Qi Gao, Department of Biostatistics and Bioinformatics, Duke University

Arinze Okafor, Department of Cell Biology, Duke University

Visiting Ph.D. Student

Aybuge Altay, Max Planck Institute for Molecular Genetics

Master's Students

Tianbei Zhang, Department of Biostatistics and Bioinformatics, Duke University

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

Constantine Stavrianidis, Department of Biostatistics and Bioinformatics, Duke University

Dezhao Fu, Department of Biostatistics and Bioinformatics, Duke University

Caiwei Zhong, Department of Biostatistics and Bioinformatics, Duke University

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

Teaching Experience

Short Courses and Workshops

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

Guest Lecturer

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

Medical Research Council, UK Research and Innovation (UKRI)

Academic Services

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

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

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

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