Zhicheng Ji

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Duke University	Homepage: https://zji90.github.io/

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

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

Journal Articles and Articles under Review

1. Anil Dangi, Naveen Natesh, Irma Husain, **Zhicheng Ji**, Laura Barisoni, Jean Kwun, Xiling Shen, Edward B. Thorp, Xunrong Luo. Single-cell transcriptomics of mouse kidney transplants reveals a potentially novel myeloid cell pathway for transplant rejection. JCI Insight. Under revision.

2. Xitiz Chamling, Alyssa Kallman, Weixiang Fang, Cynthia Berlinicke, Joseph L. Mertz, Prajwal Devkota, Itzy E. Morales Pantoja, Matthew D. Smith, **Zhicheng Ji**, Calvin Chang, Aniruddha Kaushik, Liben Chen, Katie Whartenby, Peter A. Calabresi, Hai-Quan Mao, Hongkai Ji, Tza-Huei Wang, and Donald J. Zack. Single-Cell Transcriptomic Analysis Reveals Molecular Diversity and Developmental Heterogeneity of PDGFRα expressing Human Oligodendrocyte Lineage Cells. Nature Communications. Under revision.

3. Hou W, **Ji Z**, Ji H, Hicks S. A Systematic Evaluation of Single-cell RNA-sequencing Imputation Methods. Genome Biology. 2020; 21(1):218.

4. **Ji Z**, Zhou W, Hou W, Ji H. Single-cell ATAC-seq signal extraction and enhancement with SCATE. Genome Biology. 2020; 21(1):161.

5. 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.

6. 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.

7. 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.

8. 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.

9. 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.

   Featured in ACIR and ScienceDaily

10. 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.

11. 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.

12. 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.

13. 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.

14. 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)

15. **Ji Z***, Zhou W*, Ji H. Single-cell regulome data analysis by SCRAT. Bioinformatics. 2017; 33(18):2930-2932.

16. 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.

17. 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.

18. **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

   250+ Citations on Google Scholar

19. 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.

20. 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.

21. 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.

22. **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

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

24. 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]

Teaching

Guest lecturer, Statistics in Genomics. 2018, 2019, 2020

Lead teaching assistant and lab instructor, Statistical Methods in Public Health. 2016-2019

Teaching assistant, Statistical Methods in Public Health. 2014, 2015

Editorial Activities

Journal Referee

PLOS Computational Biology

Bioinformatics

NAR Genomics and Bioinformatics

Statistics in Biosciences

Presentations

Contributed Talks

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