

# Zhicheng Ji

Department of Biostatistics  
Bloomberg School of Public Health  
Johns Hopkins University

Mobile Phone: (410) 736-0905  
Email: zji4@jhu.edu  
Homepage: <http://www.zji90.com>

## Education

Ph.D. in Biostatistics, Johns Hopkins Bloomberg School of Public Health, 2020 (expected)

*Thesis Advisor: Hongkai Ji, Ph.D.*

M.S.E. in Computer Science, Johns Hopkins Whiting School of Engineering, 2020 (expected)

Sc.M. in Biostatistics, Johns Hopkins Bloomberg School of Public Health, 2015 (transferred to Ph.D. program)

B.S. in Statistics, Fudan University, 2013

## Honors and Awards

Margaret Merrell Award, Department of Biostatistics, Johns Hopkins University, 2018

Recognizes outstanding research by a doctoral student; Unique recipient

June B. Culley Award, Department of Biostatistics, Johns Hopkins University, 2018

Honors outstanding achievement by a doctoral student on schoolwide examination paper; Unique recipient

Runner-up, ENCODE-DREAM in vivo Transcription Factor Binding Site Prediction Challenge, 2017

Team leader; 4th place out of 50 teams

ASA Section on Statistics in Genomics and Genetics Distinguished Student Paper Award, 2016

Top Performers, Prostate Cancer DREAM Challenge, 2015

Kocherlakota Award, Department of Biostatistics, Johns Hopkins University, 2014

Honors outstanding achievement by a master's student on the first-year comprehensive examination; Unique recipient

First-class Scholarship, Fudan University, 2012

## Publications

[Google Scholar](#)

\* indicates equal contributions

### Journal Articles and Articles under Review

#### Methods for analyzing single-cell genomic data

1. **Zhicheng Ji** and Hongkai Ji. (2016) TSCAN: Pseudo-time reconstruction and evaluation in single-cell RNA-seq analysis. *Nucleic Acids Research*. 44(13): e117  
Winner of ASA Section on Statistics in Genomics and Genetics Distinguished Student Paper Award  
200+ Citations on Google Scholar; 14000+ downloads on Bioconductor
2. **Zhicheng Ji\***, Weiqiang Zhou\* and Hongkai Ji. (2017) Single-cell regulome data analysis by SCRAT. *Bioinformatics*. 33(18):2930-2932

3. Weiqiang Zhou, **Zhicheng Ji**, Weixiang Fang and Hongkai Ji. (2019) Global prediction of chromatin accessibility using small-cell-number and single-cell RNA-seq. *Nucleic Acids Research*, 47(19):e121.
4. Zeyu Chen\*, **Zhicheng Ji**\*, Shin Foong Ngiow, Sasikanth Manne, Zhangying Cai, Alexander C. Huang, John Johnson, Ryan P. Staupe, Bertram Bengsch, Caiyue Xu, Sixiang Yu, Makoto Kurachi, Ramin S. Herati, Laura A. Vella, Jennifer E. Wu, Omar Khan, Erietta Stelekati, Laura M. Mclan, Chi Wai Lau, Xiaolu Yang, Shelley L. Berger, Golnaz Vahedi, Hongkai Ji and E. John Wherry. (2019) TCF-1-Centered Transcriptional Network Drives an Effector versus Exhausted CD8 T Cell-Fate Decision. *Immunity*, 51(5): 840-855.e5  
Featured in [ACIR](#) and [ScienceDaily](#)
5. **Zhicheng Ji**, Weiqiang Zhou and Hongkai Ji. Single-cell ATAC-seq signal extraction and enhancement with SCATE. *Genome Biology*, First round revision [bioRxiv](#)
6. Wenpin Hou, **Zhicheng Ji**, Hongkai Ji and Stephanie Hicks. A Systematic Evaluation of Single-cell RNA-sequencing Imputation Methods. [bioRxiv](#)

#### Methods for analyzing large-scale multi-modal genomic data

7. **Zhicheng Ji**, Steven A. Vokes, Chi V. Dang and Hongkai Ji. (2015) Turning publicly available gene expression data into discoveries using gene set context analysis. *Nucleic Acids Research*, 44(1): e8  
10000+ downloads on Bioconductor
8. Weiqiang Zhou, Ben Sherwood, **Zhicheng Ji**, Yingchao Xue, Fang Du, Jiawei Bai, Mingyao Ying, and Hongkai Ji. (2017) Genome-wide prediction of DNase I hypersensitivity using gene expression. *Nature Communications*. 8(1):1038
9. Zheng Kuang, **Zhicheng Ji**, Jef D. Boeke and Hongkai Ji. (2017) Dynamic motif occupancy (DynaMO) analysis identifies transcription factors and their binding sites driving dynamic biological processes. *Nucleic Acids Research*. 46(1): e2

#### Methods for high-dimensional statistics

10. Fang Han, Hongkai Ji, **Zhicheng Ji** and Honglang Wang. (2017) A provable smoothing approach for high dimensional generalized regression with applications in genomics. *Electronic Journal of Statistics*. 11(2):4347-4403

#### Applications of methods to biology

##### *Cancer immunology*

11. Jiajia Zhang\*, **Zhicheng Ji**\*, Justina Caushi\*, Margueritta El Asmar\*, Valsamo Anagnostou, Tricia Cottrell, Hok Yee Chan, Perna Suri, Haidan Guo, Taha Merghoub, Jamie Chaff, Joshua Reuss, Ada Tam, Richard Blosser, Mohsen Abu-Akeel, John-William Sidhom, Ni Zhao, Jinny Ha, David Jones, Kristen Marrone, Jarushka Naidoo, Edward Gabrielson, Janis Taube, Victor Velculescu, Julie Brahmer, Franck Housseau, Matthew Hellmann, Patrick Forde, Drew Pardoll, Hongkai Ji, and Kellie Smith. Compartmental analysis of T cell clonal dynamics as a function of pathologic response to neoadjuvant PD-1 blockade in resectable NSCLC. *Clinical Cancer Research*, In press

##### *Developmental biology and gene regulation*

12. Qiang Li, Rachel K. Lex, HaeWon Chung, Simone M. Giovanetti, **Zhicheng Ji**, Hongkai Ji, Maria D. Person, Jonghwan Kim and Steven A. Vokes. (2016) The pluripotency factor NANOG binds to GLI proteins and represses Hedgehog-mediated transcription. *Journal of Biological Chemistry*, 291(13):7171-82
13. Jacqueline L. Norrie, Qiang Li, Swanie Co, Bau-Lin Huang, Susan Mackem, Ding Ding, **Zhicheng Ji**, Mark T. Bedford, Antonella Galli, Hongkai Ji and Steven A. Vokes. (2016) PRMT5 is necessary to form distinct cartilage identities in the knee and long bone. *Development*. 143(24):4608-4619
14. Kimberly E. Stephens, Weiqiang Zhou, **Zhicheng Ji**, Zhiyong Chen, Shaoqiu He, Hongkai Ji, Yun Guan and Sean D. Taverna. (2019) Sex differences in gene regulation in the dorsal root ganglion after nerve injury. *BMC Genomics*. 20:147

15. Rachel K. Lex\*, **Zhicheng Ji\***, Kristin N. Falkenstein\*, Weiqiang Zhou, Joanna L. Henry, Hongkai Ji and Steven A. Vokes. (2020) GLI transcriptional repression regulates tissue-specific enhancer activity in response to Hedgehog signaling. *eLife*, 9:e50670

#### Public health and epidemiology research

16. Xiumei Hong, Christine Ladd-Acosta, Ke Hao, Ben Sherwood, Hongkai Ji, Corinne A. Keet, Rajesh Kumar, Deanna Caruso, Xin Liu, Guoying Wang, Zhu Chen, Yuelong Ji, Guanyun Mao, Sheila Ohlsson Walker, Tami R. Bartell, **Zhicheng Ji**, Yifei Sun, Hui-Ju Tsai, Jacqueline A. Pongracic, Daniel E. Weeks and Xiaobin Wang. (2016) Epigenome-wide association study links site-specific DNA methylation changes with cow's milk allergy. *The Journal of Allergy and Clinical Immunology*, 138(3):908-911.e9
17. Guoying Wang, Frank B. Hu, Kamila B. Mistry, Cuilin Zhang, Fazheng Ren, Yong Huo, David Paige, Tami Bartell, Xiumei Hong, Deanna Caruso, **Zhicheng Ji**, Zhu Chen, Yuelong Ji, Colleen Pearson, Hongkai Ji, Barry Zuckerman, Tina L. Cheng and Xiaobin Wang. (2016) Association between maternal prepregnancy body mass index and plasma folate concentrations with child metabolic health. *JAMA Pediatrics*. 170(8): e160845
18. Detian Deng, Yu Du, **Zhicheng Ji**, Karthik Rao, Zhenke Wu, Yuxin Zhu and Yates Coley. (2016) Predicting survival time for metastatic castration resistant prostate cancer: An iterative imputation approach. *F1000research*. 5:2672
19. Justin Guinney et al. (2017) 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. *The Lancet Oncology*. 18(1):132-142 (Listed as consortium coauthor)

#### Book Chapters

20. **Zhicheng Ji** and Hongkai Ji. (2019) Pseudotime reconstruction using TSCAN. *Computational Methods for Single-Cell Data Analysis*, 115-124. Springer
21. Jiajia Zhang, **Zhicheng Ji** and Kellie Smith. (2019) Analysis of TCR  $\beta$  CDR3 sequencing data for tracking anti-tumor immunity. *Methods in Enzymology*. Elsevier.

#### Articles in Preparation

22. **Zhicheng Ji**, Wenpin Hou and Hongkai Ji. RAISIN: Regression analysis for single-cell RNA-seq data with multiple samples
23. Wenpin Hou, Dongwon Lee, **Zhicheng Ji**, Suchi Saria and Aravinda Chakravarti. The empirical relationship between chromatin accessibility and gene expression in humans
24. Jiajia Zhang\*, **Zhicheng Ji\***, Justina X. Caushi\*, Margueritta El Asmar\*, Valsamo Anagnostou, Tricia R. Cottrell, Hok Yee Chan, Prerna Suri, Haidan Guo, Taha Merghoub, Jamie E. Chaff, Joshua Reuss, Kristen A. Marrone, Jarushka Naidoo, Janis M. Taube, Julie R. Brahmer, Victor E. Velculescu, Ni Zhao, Matthew D. Hellmann, Patrick M. Forde, Drew M. Pardoll, Srinivasan Yegnasubramanian, Hongkai Ji and Kellie N. Smith. Peripheral T cell repertoire evolution in resectable NSCLC patients treated with neoadjuvant PD-1 blockade
25. Justina X. Caushi\*, **Zhicheng Ji\***, Jiajia Zhang\*, Margueritta El Asmar\*, Valsamo Anagnostou, Tricia R. Cottrell, Hok Yee Chan, Haidan Guo, Taha Merghoub, Wolchok JD, Jarushka Naidoo, Kristen A. Marrone, Jamie E. Chaff, Hellmann MD, Gabrielson E, Janis M. Taube, Julie R. Brahmer, Victor E. Velculescu, Ni Zhao, Danilova L, Cope L, Patrick M. Forde, Drew M. Pardoll, Hongkai Ji, Srinivasan Yegnasubramanian and Kellie N. Smith. Transcriptional profiling of neoantigen specific T cells in resectable NSCLC treated with neoadjuvant anti-PD-1
26. Varenka Rodriguez DiBlasi\*, **Zhicheng Ji\***, Weiqiang Zhou\*, Hongkai Ji and Andrew P. Feinberg. Changes in the epigenetic landscape and chromatin structure variability in metastatic pancreatic cancer
27. Michael Koldobskiy, **Zhicheng Ji**, Weiqiang Zhou, Hongkai Ji and Andrew P. Feinberg. Epigenetic stochasticity during embryonic stem cell pluripotency transitions
28. **Zhicheng Ji** and Hongkai Ji. GEOsearch: Extendable search engine for gene expression omnibus

29. **Zhicheng Ji** and Hongkai Ji. Reproducible interactive data visualization and exploration with iXplore
30. **Zhicheng Ji** and Hongkai Ji. Single-cell RNA-seq gene expression pattern analysis with SEPA
31. **Zhicheng Ji** and Hongkai Ji. Analyzing single-cell immune profiling and gene expression data with SIMEX

## Software

### Methods for analyzing single-cell genomic data

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 [\[Github\]](#)

iXplore: Reproducible interactive data exploration tool [\[GUI\]](#)

SEPA: Single-cell gene expression pattern analysis [\[Bioconductor\]](#) [\[Github\]](#) [\[GUI\]](#)

SIMEX: Single-cell immune profiling and gene expression [\[GUI\]](#)

### Methods for analyzing large-scale multi-modal genomic data

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

BIRD: Big data regression for predicting DNase I hypersensitivity [\[Github\]](#)

DynaMO: Dynamic motif occupancy analysis [\[Github\]](#)

GEOsearch: Extendable search engine for gene expression omnibus [\[Bioconductor\]](#) [\[Github\]](#) [\[GUI\]](#)

### Methods for high-dimensional statistics

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

### Software designed for teaching

Statistics toolbox [\[Apple App Store\]](#)

Graderanalytics [\[GUI\]](#)

## Teaching

Guest lecturer, Statistics in Genomics. 2018, 2019

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

Bioinformatics

Statistics in Biosciences

## Presentations

### Contributed Talks

Reproducible interactive data visualization and exploration with iXplore. *ENAR, Washington DC, USA, March, 2017*

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

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

### Posters

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

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

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

## Reference

Hongkai Ji, Ph.D.

Professor & Director of the Graduate Program

Department of Biostatistics

Johns Hopkins Bloomberg School of Public Health

615 North Wolfe Street, Room E3638

Baltimore, MD 21205, USA

Phone: (410) 955-3517

Fax: (410) 955-0958

Email: [hji@jhu.edu](mailto:hji@jhu.edu)

Drew M. Pardoll, M.D., Ph.D.

Abeloff Professor of Oncology

Director, Bloomberg~Kimmel Institute for Cancer Immunotherapy

Director, Cancer Immunology Program

The Sidney Kimmel Comprehensive Cancer Center

Johns Hopkins University School of Medicine

CRB1 Room 444

1650 Orleans Street

Baltimore, MD 21287

Phone: 410-955-7866

Fax: 410-614-0549

Email: [dpardoll@jhmi.edu](mailto:dpardoll@jhmi.edu)

Steven A. Vokes, Ph.D.

Associate Professor  
Department of Molecular Biosciences  
Institute for Cellular & Molecular Biology  
The University of Texas at Austin  
Phone: (512) 232-8359  
Fax: (512) 232-3432  
Email: svokes@austin.utexas.edu

Fang Han, Ph.D.  
Assistant Professor  
Department of Statistics  
University of Washington  
B-308, Padelford Hall  
University of Washington  
Seattle, WA 98195  
Email: fanghan@uw.edu

Stephanie C. Hicks, Ph.D.  
Assistant Professor  
Department of Biostatistics  
Johns Hopkins Bloomberg School of Public Health  
615 North Wolfe Street  
Baltimore, MD 21205-2179 USA  
Phone: (410) 614-7838  
Email: shicks19@jhu.edu

Marie Diener-West, Ph.D.  
Chair, Master of Public Health Program  
Abbey-Merrell Professor of Biostatistics  
Johns Hopkins Bloomberg School of Public Health  
615 North Wolfe Street W1015  
Baltimore, MD 21205-2179  
Phone: (410) 502-6894  
Email: mdiener@jhu.edu