

# Zhicheng Ji

Department of Biostatistics  
Bloomberg School of Public Health  
Johns Hopkins University

Office Phone: (410) 614-5135  
Email: zji4@jhu.edu  
Homepage: <http://www.zji90.com>

## Education

Ph.D in Biostatistics, Johns Hopkins University, 2020 (expected).

M.S.E in Computer Science, Johns Hopkins University, 2018 (expected).

ScM in Biostatistics, Johns Hopkins University, 2015.

B.S. in Statistics, Fudan University, 2013.

## Professional Experience

Research Assistant, Department of Biostatistics, Johns Hopkins University. 2013-present. Advisor: Hongkai Ji

Research Assistant, Institute of Biostatistics, Fudan University. 2011-2013. Advisor: Weidong Tian

Research Assistant, CAS-MPG Partner Institute Key Laboratory for Computational Biology, Chinese Academy of Sciences. 2012-2013. Advisor: Jing-Dong Jackie Han

## Honors and Awards

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

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

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.

## Publications

### Peer-reviewed Journal Articles

1. Fang Han, Hongkai Ji, **Zhicheng Ji** and Honglang Wang. (2017) A Provable Smoothing Approach for High Dimensional Generalized Regression with an Application in Genomics. *Electronic Journal of Statistics*. 11(2):4347-4403.
2. 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.
3. 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.
4. **Zhicheng Ji\***, Weiqiang Zhou\* and Hongkai Ji. (2017) Single-cell regulome data analysis by SCRAT. *Bioinformatics*. 33(18):2930-2932.

---

\* Equal contributions

5. 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
6. 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 essential for the maintenance and survival of chondrogenic progenitor cells in the limb bud. *Development*. 143(24):4608-4619.
7. 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.
8. **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  
90+ Citations on Google Scholar
9. 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.
10. JingJing Zuo, Yuejun Tang and **Zhicheng Ji**. (2016) Government Intervention, Marketization Reform and Corporate R&D Innovation. *R&D Management*. 2016(6).
11. 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. Pongratic, 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.
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. **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.

## Preprints

1. Weiqiang Zhou, **Zhicheng Ji**, Hongkai Ji. Global Prediction of Chromatin Accessibility Using RNA-seq from Small Number of Cells. *bioRxiv*, doi:10.1101/035816.

## Software

Gene Set Context Analysis (GSCA) [Bioconductor] [Github] [GUI]  
 Tools for Single-Cell ANalysis (TSCAN) [Bioconductor] [Github] [GUI]  
 Single-Cell Regulome Analysis Tool (SCRAT) [Github] [GUI]  
 Regularized Maximum Rank Correlation Estimator (RMRCE) [Github]  
 Reproducible Interactive Data Exploration Tool (ixplore) [GUI]  
 Extendable Search Engine for Gene Expression Omnibus (GEOsearch) [Bioconductor] [Github] [GUI]

## Teaching

Guest Lecturer, Statistics in Genomics. 2018.

Lead Teaching Assistant and Lab Instructor, Statistical Methods in Public Health. 2016-2018

Teaching Assistant, Statistical Methods in Public Health. 2014-2015

## Editorial Activities

### *Journal Referee*

Bioinformatics

Statistics in Biosciences

## Professional Activities

### *Presentations*

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*

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*