

# Zhicheng Ji, Ph.D.

Department of Biostatistics and Bioinformatics  
Duke University School of Medicine

Email: [zhicheng.ji@duke.edu](mailto:zhicheng.ji@duke.edu)  
Homepage: <https://zji90.github.io/>

## 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
- 08/2020-present Co-Director, Statistical and Computational Immunology  
Duke Center for Human Systems Immunology
- 04/2021-present Affiliated faculty  
Computational Biology and Bioinformatics Program, Duke University

## 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 for me or my mentees. The \* indicates equal contributions. The † indicates corresponding author. The underlines indicate mentees.

## Research Articles

*Articles submitted and in revision*

- 1 Wenguan Wang\*, Yuxing Wang\*, Dongfang Liu\*, Wenpin Hou, Tianfei Zhou†, **Zhicheng Ji**†. GeneSegNet: A deep learning framework for cell segmentation by integrating gene expression and imaging. *Submitted.* [bioRxiv](#)

- 2 Kamran Mahmood\*, Huimin Wang\*, **Zhicheng Ji**, Coral X Giovacchini, Momen M Wahidi, Michael Dorry, Scott L Shofer, Jeffrey M Clarke, Scott J Antonia, Beth H Shaz, Katelyn Steadman, Kent Weinhold, John Yi. Comparison of Immune Microenvironment of Lung Cancer and Matched Pleural Effusions using Single-cell RNA Sequencing. *Submitted*.
- 3 Hou W<sup>†</sup>, **Ji Z<sup>†</sup>**. Decomposing spatial heterogeneity of cell trajectories with Paella. *Submitted*. [bioRxiv](#)
- 4 Stephens K, Moore C, Vinson D, White B, Renfro Z, Zhou W, **Ji Z**, Ji H, Zhu H, Guan Y, Taverna S. Identification of regulatory elements in primary sensory neurons involved in neuropathic pain. *Submitted*. [bioRxiv](#)
- 5 Khatri A, Todd J, Kelly F, Nagler A, **Ji Z**, Jain V, Gregory S, Weinhold K, Palmer S. JAK-STAT activation contributes to recruitment of cytotoxic T cells and basal cell death in human chronic lung allograft dysfunction. *Submitted*.
- 6 Multimodal single cell data integration challenge: results and lessons learned. (Listed as a consortium coauthor). *Submitted*. [bioRxiv](#)
- 7 Dykema A, Zhang J, Zhang B, Cheung L, Cherry C, Li T, Caushi J, Nishimoto M, Connor S, **Ji Z**, Munoz A, Hou W, Zhan W, Singh D, Rashid R, Mitchell-Flack M, Bom S, Tam A, Ionta N, Wang Y, Sawosik C, Tirado L, Tomasovic L, VanDyke D, Spangler J, Anagnostou V, Yang S, Spicer J, Rayes R, Taube J, Brahmer J, Forde P, Yegnasubramanian S, Ji H, Pardoll D, Smith K. Lung tumor-infiltrating Treg subsets have divergent transcriptional profiles and function linked to checkpoint blockade response. *Submitted*. [bioRxiv](#)
- 8 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. *Submitted*. [bioRxiv](#)
- 9 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](#)
- 10 **Ji Z<sup>†</sup>**, Ma L<sup>†</sup>. Controlling taxa abundance improves metatranscriptomics differential analysis. *In revision in BMC Microbiology*. [bioRxiv](#)

#### Peer-reviewed journal articles

- 11 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. *Nucleic Acids Research*. Accepted.
- 12 Liu Y, Huang Z, Liu H, **Ji Z**, Arora A, Cai D, Liu Z, Simko E, Zhang Y, Periz G, Wang J. DNA-dependent Pathogenic Cascades Initiated by C9orf72 Hexanucleotide Repeat. *Neuron*. Accepted.
- 13 NIH SenNet Consortium to map senescent cells throughout the human lifespan to understand physiological health. (Listed as a consortium coauthor) *Nature Aging*. 2022;2:1090-1100.
- 14 Zhang J, Wang X, **Ji Z**, Tian W. Large-scale prediction of key dynamic interacting proteins in multiple cancers. *International Journal of Biological Macromolecules*. 2022;220:1124-1132.
- 15 Hou W, **Ji Z<sup>†</sup>**. Palo: Spatially-aware color palette optimization for single-cell and spatial data. *Bioinformatics*. 2022;38(14):3654-3656.
- 16 Zhuang H, Wang H, **Ji Z<sup>†</sup>**. findPC: An R package to automatically select number of principal components in single-cell analysis. *Bioinformatics*. 2022;38(10):2949-2951. [Google Scholar citations: 2]
- 17 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. [Google Scholar citations: 8]
- 18 Hou W, **Ji Z<sup>†</sup>**. Unbiased visualization of single-cell genomic data with SCUBI. *Cell Reports Methods*. 2022;2(1):100135. [Google Scholar citations: 3]
- 19 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. [Google Scholar citations: 3]

- 20 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, Chaff 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: 122]  
Reviewed in Nature Reviews Clinical Oncology "Tumour antigen-induced T cell exhaustion – the archenemy of immune-hot malignancies"
- 21 **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.
- 22 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: 6]
- 23 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: 30]
- 24 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: 20]
- 25 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: 161]
- 26 **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: 24]
- 27 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.
- 28 Zhang J\*, **Ji Z\***, Caushi JX\*, El Asmar M\*, Anagnostou V, Cottrell TR, Chan HY, Suri P, Guo H, Merghoub T, Chaff 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: 74]  
Reviewed in Clinical Cancer Research "Elite Intratumoral T-cell Clonotypes (The 1%) Effect 'Trickle-Down Cytotoxicity'"
- 29 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: 22]
- 30 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: 54]
- 31 Chen Z\*, **Ji Z\***, Ngio 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: 308]  
Reviewed in Immunity "Back to the future: effector fate during T cell exhaustion"
- 32 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: 22]
- 33 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]

- 34 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: 29]
- 35 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]
- 36 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: 14]
- 37 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: 142]
- 38 Ji Z\***, Zhou W\*, Ji H. Single-cell regulome data analysis by SCRAT. *Bioinformatics*. 2017; 33(18):2930-2932. [Google Scholar citations: 40]  
Winner of ASA Section on Statistics in Genomics and Genetics Distinguished Student Paper Award
- 39 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: 25]
- 40 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: 19]
- 41 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: 472]
- 42 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: 53]
- 43 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: 81]
- 44 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]
- 45 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: 8]

## Book Chapters

- 46 Ji Z**, Ji H. Pseudotime Reconstruction Using TSCAN. *Methods in Molecular Biology*. 2019; 1935:115-124. [Google Scholar citations: 6]
- 47 Zhang J, **Ji Z**, Smith KN. Analysis of TCR  $\beta$  CDR3 sequencing data for tracking anti-tumor immunity. *Methods in Enzymology*. 2019; 629:443-464. [Google Scholar citations: 4]

## Funding Support

### Pending

Integrative analysis methods for spatial transcriptomics and single-cell multi-omics data

Role: PI

## Ongoing

The Duke Senescent Cell Evaluations in Normal Tissues (SCENT) Mapping Center (NIH U54AG075936)

Dates: 09/30/2021-08/31/2026. PI: Patty Lee.

Role: Data Analysis Core Co-Lead

Neuro-immune modulation of pain in health and disease (NIH 1R01DE031053-01A1)

Dates: 09/01/2022 - 08/31/2027. PI: Christopher R. Donnelly.

Role: Co-Investigator

Sexually dimorphic pain signaling mechanisms (NIH 1R01DE032227-01)

Dates: 09/13/2022 - 07/31/2026. PI: Christopher R. Donnelly.

Role: Co-Investigator

Single-cell omics approaches to investigate TMD (NIH 1UH2DE032202-01)

Dates: 09/09/2022 - 08/31/2023. PI: Shad Smith.

Role: Co-Investigator

Neural Architecture of the Murine and Human Temporomandibular Joint (NIH 1UC2AR082197-01)

Dates: 09/23/2022 - 08/31/2025. PI: Christopher R. Donnelly.

Role: Co-Investigator

Targeting Ferroptosis in Lethal RB1 Deficient Prostate Cancer (NIH R01CA269211)

Dates: 04/01/2022-03/31/2027. PI: Ming Chen.

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.

Role: Co-Investigator

NSF Engineering Research Center for Precision Microbiome Engineering (PreMiEr) (NSF EEC-2133504-01)

Dates: 09/01/2022 - 08/31/2027. PI: Claudia Gunsch.

Role: Co-Investigator

## 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

GeneSegNet: A deep learning framework for cell segmentation by integrating gene expression and imaging [\[Github\]](#)

Paella: Decomposing spatial heterogeneity of cell trajectories [\[Github\]](#)

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, [Statistical Genetics and Methodology](#), *Frontiers in Genetics*

Review Editor, [Cancer Immunity and Immunotherapy](#), *Frontiers in Immunology*

Review Editor, [Integrative Genetics and Genomics](#), *Frontiers in Systems Biology*

### Journal Review

Nature Biotechnology; Nature Methods; Nucleic Acids Research; Nature Communications; Genome Biology; Genome Medicine; Genomics, Proteomics & Bioinformatics; GigaScience; 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; Frontiers in Oncology; Evolutionary Bioinformatics; Transplantation

## Mentoring Experience

**Bold** indicates I am the thesis or graduation project advisor

### Current students

#### 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)

-Paul and Lauren Ghaffari Graduate Fellowship

**Changxin Wan**, Computational Biology and Bioinformatics Program, Duke University

Haotian Zhuang, Department of Biostatistics and Bioinformatics, Duke University

Huimin Wang, Department of Biostatistics and Bioinformatics, Duke University

Yuxing Wang, Department of Computer Engineering, Rochester Institute of Technology (visiting student)

#### Master's Students

**Constantine Stavrianidis**, Department of Biostatistics and Bioinformatics, Duke University

**Caiwei Zhong**, Department of Biostatistics and Bioinformatics, Duke University

Dezhao Fu, Department of Biostatistics and Bioinformatics, Duke University

Anthony Qu, Department of Biostatistics and Bioinformatics, Duke University

#### **Alumni**

##### Ph.D. Students

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

Aybuga Altay, Max Planck Institute for Molecular Genetics (visiting student)

##### Master's Students

**Huimin Wang**, M.S. in Biostatistics and Bioinformatics, Duke University

- Currently PhD student, Department of Biostatistics and Bioinformatics, Duke University
- Outstanding Master's Project Award

Haotian Zhuang, M.S. in Biostatistics and Bioinformatics, Duke University

- Currently PhD student, Department of Biostatistics and Bioinformatics, Duke University
- Degree Marshall Award
- Overall Academic Achievement Award

Tianbei Zhang, Department of Biostatistics and Bioinformatics, Duke University

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

##### Undergraduate Students

**Brian Du**, B.S. in Computer Science, Duke University

- Currently MD student, Baylor College of Medicine

Wei Wang, B.S. in Applied Mathematics, The College of William & Mary (Visiting student)

- Currently PhD student, Department of Biostatistics, University of Minnesota

#### **Ph.D. Thesis Committee**

Qi Gao, Department of Biostatistics and Bioinformatics, Duke University

Arinze Okafor, Department of Cell Biology, Duke University

#### **Ph.D. Preliminary Exam Committee**

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

Zihan Yan, Department of Cell and Molecular Biology, Duke University

## Teaching Experience

### Short Courses and Workshops

Microbiome Immunology Cancer Bioinformatics Short Course. 2022, Department of Biostatistics and Bioinformatics, Duke University

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)

Co-organizer, Duke single cell initiative research in progress seminar series

Organizer, Immunology Data Science Challenge for Master's students, Department of Biostatistics and Bioinformatics, Duke University

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**

Analyzing and Comparing Multiple Spatial Gene Expression Samples with POLYspace. Joint Statistical Meeting, August, 2022

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