# Zhicheng Ji, Ph.D.

Department of Biostatistics and Bioinformatics

Duke University School of Medicine

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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

## Publications

[Google Scholar](#)

The white numbers displayed in black boxes represent first-author or senior-author manuscripts attributed to either me or my mentees. The * represents equal contributions. The $^\dagger$ represents corresponding author. The underlines represent mentees.

**Research Articles**

*Preprints*

1. Zhuang H, **Ji Z**$^\dagger$. PreTSA: computationally efficient modeling of temporal and spatial gene expression patterns. bioRxiv

2. Hou W$^\dagger$, **Ji Z**$^\dagger$. A systematic evaluation of large language models for generating programming code. arXiv

3. Wang Y, Zhao J, Xu H, Han C, Tao Z, Zhao D, Zhou D, Tong G, Liu D[†], **Ji Z**[†]. A systematic evaluation of computation methods for cell segmentation. bioRxiv

4. Hou W[†], **Ji Z**[†]. GPT-4V exhibits human-like performance in biomedical image classification. bioRxiv

5. Qu Y, **Ji Z**[†]. A tissue ubiquitous gene set for cellular senescence. bioRxiv

6. Wang H, **Ji Z**[†]. T-cell receptor sequences correlate with and predict gene expression levels in T cells. bioRxiv

7. Jackson C, Cherry C, Bom S, Dykema A, Thompson E, Zheng M, **Ji Z**, Hou W, Li R, Zhang H, Choi J, Rodriguez F, Weingart J, Yegnasubramanian S, Lim M, Bettegowda C, Powell J, Eliesseff J, Ji H, Pardoll D. Distinct Myeloid Derived Suppressor Cell Populations Promote Tumor Aggression in Glioblastoma. bioRxiv

8. Wan C, **Ji Z**[†]. Integrating multiple single-cell multi-omics samples with Smmit. bioRxiv

9. Hou W[†], **Ji Z**[†]. GeneTuring tests GPT models in genomics. bioRxiv

10. Hou W[†], **Ji Z**[†]. Decomposing spatial heterogeneity of cell trajectories with Paella. bioRxiv

11. 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. bioRxiv

*Peer-reviewed journal articles*

12. Mahmood K*, Wang H*, **Ji Z**, Giovacchini CX, Wahidi MM, Dorry M, Shofer SL, Clarke JM, Antonia SJ, Shaz BH, Steadman K, Weinhold KJ, Yi J. Differences in microenvironment of lung cancer and pleural effusions by single-cell RNA sequencing. *Lung Cancer*. 2024;193:107847.

13. Glass M, **Ji Z**, Davis R, Pavlisko E, DiBernardo L, Carney J, Fishbein G, Luthringer D, Miller D, Mitchell R, Larsen B, Butt Y, Bois M, Maleszewski J, Halushka M, Seidman M, Lin CY, Buja M, Stone J, Dov D, Carin L, Glass C. A Machine Learning Algorithm Improves the Diagnostic Accuracy of the Histologic Component of Antibody Mediated Rejection (AMR-H) in Cardiac Transplant Endomyocardial Biopsies. *Cardiovascular Pathology*. 2024;72:107646.

14. Gao Q, **Ji Z**, Wang L, Owzar K, Li Q, Chan C, Xie J. SifiNet: A robust and accurate method to identify feature gene sets and annotate cells. *Nucleic Acids Research*. 2024;52(9):e46. [Google Scholar citations: 1]

15. Liu M, **Ji Z**, Jain V, Smith VL, Hocke E, Patel AP, McLendon RE, Ashley DM, Gregory SG, López GY. Spatial transcriptomics reveals segregation of tumor cell states in glioblastoma and marked immunosuppression within the perinecrotic niche. *Acta Neuropathologica Communications*. 2024;12(1):64.

16. Hou W[†], **Ji Z**[†]. Assessing GPT-4 for cell type annotation in single-cell RNA-seq analysis. *Nature Methods*. 2024. [Google Scholar citations: 19]

17. Stephens KE, Moore C, Vinson DA, White BE, Renfro Z, Zhou W, **Ji Z**, Ji H, Zhu H, Guan Y, Taverna SD. Identification of Regulatory Elements in Primary Sensory Neurons Involved in Trauma-Induced Neuropathic Pain. *Molecular Neurobiology*. 2024;61(3):1845-1859.

18. Hou W, **Ji Z**, Chen Z, Wherry EJ, Hicks SC, Ji H. A statistical framework for differential pseudotime analysis with multiple single-cell RNA-seq samples. *Nature Communications*. 2023;14(1):7286. [Google Scholar citations: 23]

19. Wang Y*, Wang W*, Liu D*, Hou W, Zhou T[†], **Ji Z**[†]. GeneSegNet: a deep learning framework for cell segmentation by integrating gene expression and imaging. *Genome Biology*. 2023;24(1):235. [Google Scholar citations: 17]

20. Dykema AG, Zhang J, Cheung LS, Connor S, Zhang B, Zeng Z, Cherry CM, Li T, Caushi JX, Nishimoto M, Munoz AJ, **Ji Z**, Hou W, Zhan W, Singh D, Zhang T, Rashid R, Mitchell-Flack M, Bom S, Tam A, Ionta N, Aye THK, Wang Y, Sawosik CA, Tirado LE, Tomasovic LM, VanDyke D, Spangler JB, Anagnostou V, Yang S, Spicer J, Rayes R, Taube J, Brahmer JR, Forde PM, Yegnasubramanian S, Ji H, Pardoll DM, Smith KN. Lung tumor-infiltrating Treg have divergent transcriptional profiles and function linked to checkpoint blockade response. *Science Immunology*. 2023;8(87):eadg1487. [Google Scholar citations: 13]

21 Loh ZN, Wang ME, Wan C, Asara JM, **Ji Z**, Chen M. Nuclear PTEN Regulates Thymidylate Biosynthesis in Human Prostate Cancer Cell Lines. *Metabolites*. 2023;13(8):939.

22 Gurkar AU, Gerencser AA, Mora AL, Nelson AC, Zhang AR, Lagnado AB, Enninful A, Benz C, Furman D, Beaulieu D, Jurk D, Thompson EL, Wu F, Rodriguez F, Barthel G, Chen H, Phatnani H, Heckenbach I, Chuang JH, Horrell J, Petrescu J, Alder JK, Lee JH, Niedernhofer LJ, Kumar M, Königshoff M, Bueno M, Sokka M, Scheibye-Knudsen M, Neretti N, Eickelberg O, Adams PD, Hu Q, Zhu Q, Porritt RA, Dong R, Peters S, Victorelli S, Pengo T, Khaliullin T, Suryadevara V, Fu X, Bar-Joseph Z, **Ji Z**, Passos JF. Spatial mapping of cellular senescence: emerging challenges and opportunities. *Nature Aging*. 2023;3(7):776-790. [Google Scholar citations: 30]

23 Khatri A, Todd JL, Kelly FL, Nagler A, **Ji Z**, Jain V, Gregory SG, Weinhold KJ, Palmer SM. JAK-STAT activation contributes to cytotoxic T cell-mediated basal cell death in human chronic lung allograft dysfunction. *JCI Insight*. 2023;8(6):e167082. [Google Scholar citations: 6]

24 **Ji Z**†, Ma L†. Controlling taxa abundance improves metatranscriptomics differential analysis. *BMC Microbiology*. 2023;23(1):60.

25 Liu Y, Huang Z, Liu H, **Ji Z**, Arora A, Cai D, Wang H, Liu M, Simko EAJ, Zhang Y, Periz G, Liu Z, Wang J. DNA-initiated epigenetic cascades driven by C9orf72 hexanucleotide repeat. *Neuron*. 2023;111(8):1205-1221.e9. [Google Scholar citations: 9]
  -Reviewed in Neuron "The DAXX tax: C9orf72 DNA repeat expansions drive gain- and loss-of-function pathology in c9FTD/ALS"

26 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*. 2023;51(5):2046-2065. [Google Scholar citations: 4]

27 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. [Google Scholar citations: 41]

28 Multimodal single cell data integration challenge: results and lessons learned. (Listed as a consortium coauthor). *Proceedings of the NeurIPS 2021 Competitions and Demonstrations Track, Proceedings of Machine Learning Research*. 2022;176:162-176. [Google Scholar citations: 50]

29 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. [Google Scholar citations: 1]

30 Hou W, **Ji Z**†. Palo: Spatially-aware color palette optimization for single-cell and spatial data. *Bioinformatics*. 2022;38(14):3654-3656. [Google Scholar citations: 4]

31 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. [Google Scholar citations: 15]

32 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: 21]

33 Hou W, **Ji Z**†. Unbiased visualization of single-cell genomic data with SCUBI. *Cell Reports Methods*. 2022;2(1):100135. [Google Scholar citations: 9]

34 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: 10]

35 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: 308]
  -Reviewed in Nature Reviews Clinical Oncology "Tumour antigen-induced T cell exhaustion – the archenemy of immune-hot malignancies"
  -Essential Science Indicators (ESI) highly cited paper

36 **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. [Google Scholar citations: 2]

37 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: 10]

38 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: 59]

39 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: 36]

40 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: 264]

41 **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: 36]

42 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. [Google Scholar citations: 2]

43 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: 110]

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

44 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: 34]

45 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: 75]

46 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: 522]

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

   -Essential Science Indicators (ESI) highly cited paper

47 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: 31]

48 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]

49 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: 37]

50 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: 13]

51 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: $19$]

52 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: $160$]

53 **Ji Z\***, Zhou W\*, Ji H. Single-cell regulome data analysis by SCRAT. *Bioinformatics*. 2017; 33(18):2930-2932. [Google Scholar citations: $47$]

54 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: $31$]

55 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: $26$]

56 **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: $611$]

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

  -Highlighted in Nature Reviews Genetics "Challenges in unsupervised clustering of single-cell RNA-seq data"

57 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: $63$]

58 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: $97$]

59 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: $3$]

60 **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: $15$]

**Book Chapters**

61 **Ji Z**, Ji H. Pseudotime Reconstruction Using TSCAN. *Methods in Molecular Biology*. 2019; 1935:115-124. [Google Scholar citations: $8$]

62 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: $7$]

**Editorial**

63 Hou L, **Ji Z**, Wang J, Xie J. Editorial: Statistical and computational methods for single-cell sequencing analysis. *Frontiers in Genetics*. 2023;14:1235174.

# Funding Support

**Ongoing**

1. U54-AG075936, NIH/The NIH Common Fund

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

   Dates: 09/30/2021 - 08/31/2026

   PI: Patty Lee

   Role: Data Analysis Core Co-Lead

2. PC ID-1074759, Marc Lustgarten Pancreatic Cancer Foundation

   A Window-of-Opportunity Trial Using Neoadjuvant Hepatic Artery Chemotherapy for Patients With Localized Pancreas Cancer

   Dates: 9/1/2023 - 8/31/2027

   PI: Peter Allen

   Role: Co-Investigator

3. R01-ES035037, NIH/NIEHS

   Perinatal Per- and Polyfluoroalkyl Substances (PFAS) exposure and Immunotoxicity in early life

   Dates: 4/20/2023 - 1/31/2028

   PI: Liping Feng

   Role: Co-Investigator

4. R01-DE031053, NIH/NIDCR

   Neuro-immune modulation of pain in health and disease

   Dates: 09/01/2022 - 08/31/2027

   PI: Christopher R. Donnelly

   Role: Co-Investigator

5. R01-DE032227, NIH/NIDCR

   Sexually dimorphic pain signaling mechanisms

   Dates: 09/13/2022 - 07/31/2026

   PI: Christopher R. Donnelly

   Role: Co-Investigator

6. UH2-DE032202, NIH/NIDCR

   Single-cell omics approaches to investigate TMD

   Dates: 09/09/2022 - 08/31/2023

   PI: Shad Smith

   Role: Co-Investigator

7. UC2-AR082197, NIH/NIAMS

   Neural Architecture of the Murine and Human Temporomandibular Joint

   Dates: 09/23/2022 - 08/31/2025

   PI: Christopher R. Donnelly

   Role: Co-Investigator

8. R01-CA269211, NIH/NCI
   Targeting Ferroptosis in Lethal RB1 Deficient Prostate Cancer
   Dates: 04/01/2022 - 03/31/2027
   PI: Ming Chen
   Role: Co-Investigator

9. R25-CA244070, NIH/NCI
   Training Program in Bioinformatics at the Intersection of Cancer Immunology and Microbiome
   Dates: 07/01/2020 - 06/30/2025
   PI: Kouros Owzar, Cliburn Chan, Joshua Granek
   Role: Co-Investigator

10. EEC-2133504-01, NSF/EEC
    NSF Engineering Research Center for Precision Microbiome Engineering (PreMiEr)
    Dates: 09/01/2022 - 08/31/2027
    PI: Claudia Gunsch
    Role: Co-Investigator

11. R01-GM135440, NIH/NIGMS
    Statistical modeling of cross-sample variation and learning of latent structures in microbiome sequencing data
    Dates: 09/15/2020 - 08/31/2025
    PI: Li Ma
    Role: Co-Investigator

12. Whitehead Scholar Award, Duke School of Medicine
    Dates: 2021 - present
    PI: Zhicheng Ji
    Total Amount: $250K
    Role: PI

13. Translating Duke Health Award, Duke School of Medicine
    Dates: 2021 - present
    PI: Zhicheng Ji
    Total Amount: $50K
    Role: PI

**Pending**

R35-GM154865, NIH/NIGMS
Computational methods for in situ spatial transcriptomics
Role: PI
Impact score: 18

# Software

PreTSA: computationally efficient modeling of temporal and spatial gene expression patterns [Github]

GPTCelltype: cell type annotation with GPT-4 in single-cell RNA-seq analysis [Github]

Smmit: Integrating multiple single-cell multi-omics samples [Github]

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

### Reviewer for Journals (selected)

Nature Biotechnology; Nature Methods; Cell Discovery; Nucleic Acids Research; Nature Communications; Genome Biology; Genome Medicine; npj Digital Medicine; Genome Research; Briefings in Bioinformatics; Genomics, Proteomics & Bioinformatics; GigaScience; PLOS Computational Biology; PLOS Genetics; Computational and Structural Biotechnology Journal; Bioinformatics

# Mentoring Experience

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

**Current Students**

<u>Postdoctoral Associate</u>

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

<u>Ph.D. Students</u>

**Mengyi (Miko) Liu**, Computational Biology and Bioinformatics Program, Duke University (co-advise with Dr. Simon Gregory)
  -Paul and Lauren Ghaffari Graduate Fellowship

**Changxin Wan**, Program of Computational Biology and Bioinformatics, Duke University
  -Precision Genomics Collaboratory-OBGE Graduate Student Pilot Research Grant Award

**Huimin Wang**, Department of Biostatistics and Bioinformatics, Duke University
  -Precision Genomics Collaboratory-OBGE Graduate Student Pilot Research Grant Award

**Haotian Zhuang**, Department of Biostatistics and Bioinformatics, Duke University

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

<u>Master's Students</u>

**Anthony Qu**, Department of Biostatistics and Bioinformatics, Duke University
-Outstanding Master's Project Award

**Yuan Wang**, Department of Biostatistics and Bioinformatics, Duke University (co-advise with Dr. Yarui Diao)

Hao Wang, Department of Statistical Science, Duke University

Xi Liang, Department of Biostatistics and Bioinformatics, Duke University

Zhiyou Ye, Department of Biomedical Engineering, Duke University

**Alumni**

<u>Ph.D. Students</u>

Constantine Stavrianidis, Program of Computational Biology and Bioinformatics, Duke University (rotation student)

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

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

<u>Master's Students</u>

**Constantine Stavrianidis**, M.S. Department of Biostatistics and Bioinformatics, Duke University
  -Currently PhD student, Program of Computational Biology and Bioinformatics, Duke University

**Caiwei Zhong**, M.S. Department of Biostatistics and Bioinformatics, Duke University
  -Currently statistician, Dana-Farber Cancer Institute

**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
-Currently data analyst, Bloomberg Kimmel Institute for Cancer Immunotherapy, Johns Hopkins University School of Medicine

Xiaotan Sun, Department of Biostatistics and Bioinformatics, Duke University (co-advise with Dr. Anru Zhang)
-Currently research data scientist, Cleveland Clinic

Dezhao Fu, Department of Biostatistics and Bioinformatics, Duke University

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

Hongbin Liu, Department of Electrical and Computer Engineering, 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**

MATH 590: Advanced Special Topics in Mathematics. 2023, Duke University

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**

Ad hoc reviewer, NIH Molecular Neurogenetics (MNG) study section

Ad hoc reviewer, 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

Screener, Duke University School of Medicine MD admissions

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**

GeneSegNet: a deep learning framework for cell segmentation by integrating gene expression and imaging. MCBIOS 2024. March, 2024

Democratizing genomic data science with large language models. Statistical Genetics and Genomics Seminar, Department of Biostatistics, Columbia University. November, 2023

Decomposing spatial heterogeneity of cell trajectories for spatial transcriptomics data. ICSA Applied Statistics Symposium, June, 2023

Applications of ChatGPT and GPT models to genomic research. Duke Center for Human Systems Immunology Retreat, June, 2023

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**

Assessing GPT-4 for cell type annotation in single-cell RNA-seq analysis. ENAR, March, 2024

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