

Zhen Miao

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EDUCATION

Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA

2019-Present

Ph.D. in Genomics & Computational Biology

- *Advisor:* Dr. Junhyong Kim
- *Thesis:* Statistical modeling of single cell multiomics data

Wharton School, University of Pennsylvania, Philadelphia, PA, USA

2019-Present

Dual M.A. in Statistics

- *Courses:* Applied Regression & Analysis of Variance, Probability, Advanced Statistical Inference I & II, Bayesian Statistics, Stochastic Process, Nonparametric Statistics, Big Data in Genomics, Categorical Data Analysis & Survival Analysis
- *Advisor:* Dr. Nancy Zhang
- *Thesis:* Statistical modeling with spatial transcriptomics at single cell or sub-cellular resolution

Nankai University, Tianjin, China

2015-2019

B.S. in Biological Sciences with a minor in Applied Mathematics

- *Program:* Being selected to Poling Program, a research-training program for elite students
- *Ranking:* 1/27 in Poling Program
- *Honors:* Merit Student Title for all years, National Scholarship, and Outstanding Graduate title

RESEARCH INTERESTS

- Multi-omics data integration for analyzing tissue dynamics & complex disease traits
- Computational methods in single cell & spatial biology data
- Nephron development and renal diseases

SELECTED PUBLICATIONS

* indicates co-first authorship

First or co-first author:

1. **Miao Z**, Wang J, Park K, Kuang D, and Kim J. Model-based compound hypothesis testing for snATAC-seq data with PACS. *bioRxiv* (2023)
2. **Miao Z** and Kim J. Uniform quantification of single nucleus ATAC-seq data with Paired-Insertion Counting (PIC) and model-based insertion rate estimator. *Nature Methods* (In Press).
3. **Miao Z**, Humphreys BD, McMahon AP, Kim J. Multiomics integration in the age of million single cell data. *Nature Reviews Nephrology* (2021)
4. **Miao Z***, Balzer MS*, Ma Z*, et al., Single cell resolution regulatory landscape of the mouse kidney highlights cellular differentiation programs and renal disease targets. *Nature Communications* (2021)

Contributing author:

5. Liu H, Doke T, ..., **Miao Z**, et al., Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease. *Nature Genetics* (2022)
6. Govek KW*, Troisi EC*, **Miao Z**, et al., Single-Cell Transcriptomic Analysis of mIHC Images via Antigen Mapping. *Science Advances* (2021)
7. Zhao Q, Wang J, **Miao Z**, Zhang N, Hennessy S, Small D. S, & Rader D. J. "The role of lipoprotein subfractions in coronary artery disease: A Mendelian randomization study." *eLife* (2021)
8. Sheng X*, Guan Y*, Ma Z, Wu J, Liu H, Qiu C, Vitale S, **Miao Z**, et al., Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. *Nature genetics* (2021)

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9. Nguyen A*, Wang K*, Hu G*, Wang X, Miao Z, et al., APOE and TREM2 regulate amyloid-responsive microglia in Alzheimer's disease. *Acta Neuropathologica* (2020)
10. Zhong L, Yao L, Tower RJ, Wei Y, Miao Z, et al., Single cell transcriptomics identifies a unique adipose lineage cell population that regulates bone marrow environment. *eLife* (2020)
11. Gao J, Miao Z, Zhang Z, Wei H, and Kurgan L. "Prediction of Ion Channels and Their Types from Protein Sequences: Comprehensive Review and Comparative Assessment." *Current Drug Targets* (2018)
12. Tan T, Zhang X, Miao Z, Yu Y, Du S, Hou X, and Cai J. "A single point mutation in *hmgA* leads to melanin accumulation in *Bacillus thuringiensis* BMB181." *Enzyme and Microbial Technology* (2018)

CONFERENCES PRESENTATIONS

Platform Presentations:

- NIH Junior Atlas Builder 2023 meeting (3 min lightning talk)
 - Title: Atlas-scale integrative analysis of snATAC-seq data with PACS
- ReBuilding A Kidney (RBK) 2021 semi-annual meeting (25 min platform presentation)
 - Title: Probabilistic modeling of single cell epigenomics data
- Penn IRM Stem Cell Club 2021 (25 min platform presentation)
 - Title: Charting kidney development through single cell multiomics study
- The American Society of Nephrology (ASN) 2020 annual meeting (8 min platform presentation)
 - Title: Single-cell resolution regulatory landscape of the kidney highlights cellular differentiation programs and renal disease targets
- The 69th American Society of Human Genomics (ASHG) 2019 annual meeting (15 min platform presentation)
 - Title: Characterizing cellular communication in human central nervous system by single-cell RNA-seq
- MidAtlantic Bioinformatics 2019 Conference (5 min lightning talk)
 - Title: Charting cellular communication network in Alzheimer's Disease

Chalk Talks:

- GCB program 2022 and 2023 chalk talks (25 min platform presentation)

Poster Presentations:

- The 72nd American Society of Human Genomics (ASHG) annual meeting (2022)
- The American Society of Nephrology (ASN) annual meeting (kidney week, 2022)
- The 70th American Society of Human Genomics (ASHG) annual meeting (2020)
- Mid-Atlantic Bioinformatics Conference (2020)
- Fox Chase Epigenetics Symposium (2019)

AWARDS

- Blavatnik Family Fellowship in Biomedical Research, awarded to six students across Penn Medicine Ph.D. candidates (2022-2023) [[link](#)]
- Charles J. Epstein Trainee Awards, awarded to the top 10% of the presenters in Human Genetics Research for the 69th ASHG annual meeting (2019) [[link](#)]
- ACGA Trainee Awards, awarded to the top 3 predoctoral students' platform presentations (2019)
- UPenn BGS Travel Grant, awarded to selected students who present in scientific conferences (2019,2022)
- Outstanding Graduate of Nankai University, awarded to selected students with top academic performance (2019)
- National Scholarship, awarded to the top 0.2% of students for academic excellence (2017, 2019)
- Poling Scholarship, awarded to top 10 students in the Poling Program for achievement in Biological Sciences (2018)
- The Fifth Life Sciences Students' Experimental Skills Competition in Tianjin, the First Prize (2017)
- Biochemistry Experimental Skills Competition in Nankai University, the First Prize (2017)

RESEARCH EXPERIENCE

Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA

July 2019-Present

Ph.D. candidate in Dr. Junhyong Kim's Lab, Department of Biology and Department of Computer Sciences

Project 1: Statistical modeling of single nucleus ATAC-sequencing (snATAC-seq) data

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- Constructed a statistical framework for snATAC-seq data that adjust for the coverage disparities present in each cell and the problems with excessive zero
- Applied the statistical framework for real data application in cell label prediction, doublet identification, and differentially accessible region identification
- First-authored a paper that is on *bioRxiv*

Project 2: Reviewing existing computational models for single cell multiomics integration

- Summarized the existing approaches into two major categories: integration for matched data and for unmatched data, and discussed four high-level ideas of data integration and their pros and cons
- Reviewed the challenges and future directions for the field of single cell multiomics
- First-authored a peer-reviewed paper that published in *Nature Reviews Nephrology*

Rotation student in Dr. Pablo Camara's Lab, Department of Genetics

- Contributed to the development of STvEA, a computational tool for integrating spatial proteomics data with CITE-seq data (single cell transcriptome and epitopes)
- Evaluated the performance of STvEA under scenarios with down-sampled cells or protein penal, and implemented a LASSO-based feature selection algorithm for STvEA
- Co-authored a peer-reviewed paper that published in *Science Advances*

Rotation student in Dr. Katalin Susztak's Lab, Department of Genetics

- Analyzed kidney snATAC-seq data in adult and P0 murine kidney, conducted manual cell type annotation and cell-type specific open chromatin peak calling
- Identified transcription factors (TFs) that are specific to major kidney cell types
- Investigated the open chromatin dynamics during kidney cell differentiation from nephron progenitors to proximal or distal tubules, and revealed potential genes that are involved to the process
- First-authored a peer-reviewed paper that published in *Nature Communications*

Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA

July 2018-June 2019

Research Intern in Dr. Mingyao Li's Lab, Department of Biostatistics, Epidemiology & Informatics

- Built a ligand-receptor interaction network between microglial sub-clusters, based on single-nuclei RNA sequencing data from 16 human brains with or without Alzheimer's disease (AD)
- Analyzed expression patterns of GWAS identified genes in microglial sub-clusters, indicating a disease-related dysfunctional sub-cluster
- Investigated the relationship between APOE, TREM2 (the top two risk genes for AD), and the complement pathway in each microglial sub-cluster
- Studied the pseudo-time dynamics of transcription factors in microglial sub-clusters, and investigated TFs that trigger the change of microglial states

School of Mathematical Sciences, Nankai University, Tianjin, China

October 2017-July 2018

Undergraduate Researcher in Dr. Jianzhao Gao's Lab, Department of Informatics and Data Science

- Mapped m6A modification data onto GRCh38 genome, encoded features based on flanking sequence, nearby 3-mer nucleotide frequency, and solvent accessibility computed *in silico*
- Conducted feature selection, trained Support Vector Machine (SVM) by selected features, and optimized SVM parameters by 5-fold cross-validation to build an m6A modification predictor

TEACHING EXPERIENCE

Graduate teaching assistant, University of Pennsylvania, Philadelphia, PA

2021 Fall

GCB-534 Statistics for genomics and biomedical informatics

Advising committee for GCB students, University of Pennsylvania, Philadelphia, PA

2021-2023

Role: offer advice on courses for first-year Ph.D. students tailored by their background and research interest, offer advice and guidance on candidacy exam for second-year Ph.D. students

Student Supervisory

Research Assistants: Ziyuan Ma, Keryu Park

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SKILLS

- *Programming*: Proficient in Python, R, C++, Shell Scripting
- *Statistical Modeling*: categorical data analysis (GLM), Bayesian modeling (EM algorithm, MCMC), time-series data analysis, survival analysis, non-parametric statistics
- *Bioinformatics packages*: Proficient in Seurat, SnapATAC, ArchR, edgeR, limma, STAR, GenomicRanges

INTERNSHIP & SUMMER SCHOOL

Computational Biology group, 23andMe, Sunnyvale, CA, USA

June-Aug 2022

Graduate Student Intern, Supervisor: Robert Tunney, Ph.D.

- Engineered codes to enable parallel computing and more efficient data handling for identifying tissue-of-action (TACTICAL), so that the speed is ~200X faster
- Extended the TACTICAL framework to apply to single cell ATAC-seq data for fine-grained detection of disease-associated cell types

Institute for Interdisciplinary Information Sciences, Tsinghua University, Beijing, China

June 2018

Computer Science and Technology Summer School Participant

- Attended lectures on bioinformatics and learned interdisciplinary knowledge on science
- Initiated a project on *The Prediction of Novel Drug-Target Interaction* based on diverse drug-related information, and gave an oral presentation on the methods

Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences, Shenzhen, China

July 2017

Synthetic Biology Summer School Participant

- Attended lectures and seminars on *the Current Development of Synthetic Biology & Synthetic Genomics*
- Wrote a proposal on *Genetically Modified Microbes in Heavy Metal Control* with 5 other participants, and gave an oral presentation, ranked 1st among 10 groups