

# WENJING MA, PhD

*Last Updated October 31, 2025*

Postdoctoral Research Fellow, Department of Biostatistics, University of Michigan  
1415 Washington Heights, Ann Arbor, MI 48109-2029  
[mawenjing1993@gmail.com](mailto:mawenjing1993@gmail.com) | 917-496-1226 | <https://marvinquiet.github.io/>

## **Research Interests**

- Develop deep learning methods integrated with statistical modeling to analyze single-cell genomics data, including spatial transcriptomics, epigenomics, and multi-omics
- Investigate temporal dynamics of cellular processes using time-resolved single-cell data to reveal biological mechanisms such as spatial domain transitions, cell state changes, and gene regulatory network dynamics
- Apply developed methodologies to study dynamics in epigenetic disease progression, with a focus on neurodegenerative disorders and cancer

## **Education**

### **Emory University**

Ph.D., in Computer Science and Informatics (Biomedical Informatics Track)

Dissertation Title: *Cell type identification in single-cell genomics and its application*

Advisor: [Dr. Hao Wu](#)

Atlanta, GA

08/2019 - 05/2023

### **Beijing University of Posts and Telecommunications (BUPT)**

M.S. in Computer Science and Technology

Beijing, China

09/2014 - 06/2017

### **Beijing University of Posts and Telecommunications (BUPT)**

B.S. in Computer Science and Technology

Beijing, China

09/2010 - 06/2014

## **Working Experience**

### **University of Michigan**

Postdoctoral Research Fellow, Department of Biostatistics

Advisor: [Dr. Xiang Zhou](#)

Ann Arbor, MI

07/2023 - current

### **University of Virginia**

Visiting Scholar in Bioinformatics, Center for Public Health Genomics

Advisor: [Dr. Chongzhi Zang](#)

Charlottesville, VA

08/2018 - 06/2019

### **State Administration of Foreign Exchange Investment Center**

Database Administrator

Beijing, China

08/2017 - 05/2018

## **Publications (Reverse chronological order)**

Note: Authorship order by contribution; \* denotes equal-contribution;

### **Preprints**

1. **Wenjing Ma**, Siyu Hou, Lulu Shang, Jiaying Lu, Xiang Zhou. Optimal transport modeling uncovers spatial domain dynamics in spatiotemporal transcriptomics. *Under Revision at Nature Communications*, (2025). DOI [\[Python package\]](#) [\[Documentation\]](#)

2. Siyu Hou, **Wenjing Ma**, Xiang Zhou. FastCCC: A permutation-free framework for scalable, robust, and reference-based cell-cell communication analysis in single cell transcriptomics studies. *Nature Communications*, in press, (2025). [DOI](#)
3. Jie Xu\*, **Wenjing Ma**\*, Shaojun Yu\*, Yujing Li, Jidong Goo, Christina Michalski, Mengjun Zhang, Jianjun Wang, Yunhee Kang, Xiangxue Guo, Weibo Niu, Ying Zhou, Zhexing Wen, Peng Jin. A dynamic temporal regulatory role of human FMRP underlying altered developmental trajectories in fragile X syndrome-derived hippocampal organoids. *Under Revision at Nature Communications*, (2025).
4. Yulin Jin\*, Yiqu Cao\*, **Wenjing Ma**\*, Ronghua Li, Yujing Li, Yunhee Kang, Xiangxue Guo, Jing Huang, Michael Epstein, Natalia Rivera, Junghwa Lim, Emily Allen, Peng Jin. Integrative transcriptome-wide association reveals PRKCG-linked GABAergic dysfunction in Fragile X-associated Tremor/Ataxia Syndrome. *Under Revision at Nature Communications*, (2025).
5. Sumeet Sharma\*, **Wenjing Ma**\*, Kerry J. Ressler, Thea Anderson, Dan. C. Li, Peng Jin, Shannon L. Gourley, Zhaohui Qin. Dysregulation of prefrontal oligodendrocyte lineage cells across mouse models of adversity and human major depressive disorder. *bioRxiv*, (2022). [DOI](#)

#### Peer-Reviewed Journals

6. Xin Wei, **Wenjing Ma**, Zhijin Wu, Hao Wu. TORC: Target-oriented Reference Construction for supervised cell-type identification in scRNA-seq. *Genome Biology*, 2025; 26(1): 1-7. [DOI](#) (A conference version has been accepted by [IEEE BIBM 2024](#))
7. Hejie Cui, Jiaying Lu, Ran Xu, Shiyu Wang, **Wenjing Ma**, Yue Yu, Shaojun Yu, Xuan Kan, Chen Ling, Liang Zhao, Zhaohui S. Qin, Joyce Ho, Tianfan Fu, Jing Ma, Mengdi Huai, Fei Wang, Carl Yang. A review on knowledge graphs for healthcare: Resources, applications, and promises. *Journal of Biomedical Informatics*, 2025; 104861. [DOI](#). (A conference version has been accepted by [ICML 2023 Workshop on Interpretable Machine Learning in Healthcare](#))
8. Yulin Jin, Karen N Conneely, **Wenjing Ma**, Robert K. Naviaux, Teepu Siddique, Emily G. Allen, Sandra Gingrich, Robert M. Pascuzzi, Peng Jin. Whole-genome bisulfite sequencing of cell-free DNA unveils age-dependent and ALS-associated methylation alterations. *Cell & Bioscience*, 2025; 15(1): 26. [DOI](#)
9. Shilin Yu, Guanquan Meng, Wen Tang, **Wenjing Ma**, Rui Wang, Xiongwei Zhu, Xiaobo Sun, Hao Feng. cypress: an R/Bioconductor package for cell-type-specific differential expression analysis power assessment. *Bioinformatics*, 2024; 40(8): btae511. [DOI](#) [[R package](#)]
10. **Wenjing Ma**, Jiaying Lu, Hao Wu. Cellcano: supervised cell type identification for single cell ATAC-seq data. *Nature Communications*, 2023; 14(1): 1864. [DOI](#) [[Python package](#)] [[Documentation](#)]
11. Yulin Jin, Kenong Su, Ha Eun Kong, **Wenjing Ma**, Zhiqin Wang, Yujing Li, Ronghua Li, Emily Allen, Hao Wu, Peng Jin. Cell-type specific DNA methylome signatures reveal epigenetic mechanisms for neuronal diversity and neurodevelopment disorder. *Human Molecular Genetics*, 2023; 32(2): 218-230. [DOI](#)
12. **Wenjing Ma**, Sumeet Sharma, Peng Jin, Shannon L. Gourley, Zhaohui S. Qin. *LRcell*: detecting the source of differential expression at the sub-cell-type level from bulk RNA-seq data. *Briefings in Bioinformatics*, 2022; 23(3): bbac063. [DOI](#) [[R package](#)]
13. Shengen S. Hu, Lin Liu, Qi Li, **Wenjing Ma**, Michael J. Guertin, Clifford A. Meyer, Ke Deng, Tingting Zhang, Chongzhi Zhang. Intrinsic bias estimation for improved analysis of bulk and single-cell chromatin accessibility profiles using SELMA. *Nature Communications*, 2022; 13(1): 5533. [DOI](#), [[R package](#)]

14. **Wenjing Ma**, Kenong Su, Hao Wu. Evaluation of some aspects in supervised cell type identification for single-cell RNA-seq: classifier, feature selection, and reference construction. *Genome Biology*, 2021; 22: 1-23. [DOI](#) [[project link](#)]
15. **Wenjing Ma\***, Zhenjia Wang\*, Yifan Zhang, Neal E. Magee, Yayi Feng, Ruoyao Shi, Yang Chen, Chongzhi Zang. BARTweb: a web server for transcriptional regulator association analysis. *NAR Genomics and Bioinformatics*, 2021; 3(2): lqab022. [DOI](#) [[website](#)] [[RECOMB 2019 poster](#)]

### Book Chapters

16. Ronnie Y. Li, **Wenjing Ma**, Zhaohui S. Qin. Approaches to Marker Gene Identification from Single-Cell RNA-Sequencing Data. In *Handbook of Statistical Bioinformatics* (pp. 71-84). Springer, Berlin, Heidelberg, 2022; 71-84. [DOI](#)

### Peer-Reviewed Conferences

17. **Wenjing Ma**, Xiaoqing Yu, Jing Zhang, Jiaying Lu, Xiang Zhou, Xuefeng Wang. scPanKD: Distilling Pan-Cancer knowledge for enhanced T cell subtypes annotation in single-cell transcriptomics data. *IEEE BIBM 2025*, in press. [[project link](#)]
18. Shuyue Jiang, Wenjing Ma, Shaojun Yu, Chang Su, Runze Yan, Jiaying Lu. Integrating Epigenetic and Phenotypic Features for Biological Age Estimation in Cancer Patients via Multimodal Learning. *IEEE BIBM 2025*, in press.
19. Jiaying Lu, Shifan Zhao, **Wenjing Ma**, Hui Shao, Xiao Hu, Yuanzhe Xi, Carl Yang. Uncertainty-aware pre-trained foundation models for patient risk prediction via gaussian process. Companion Proceedings of the ACM Web Conference, 2024: 1162-1165. [DOI](#)
20. Jiaying Lu, Jiaming Shen, Bo Xiong, **Wenjing Ma**, Steffen Staab, Carl Yang. Hiprompt: Few-shot biomedical knowledge fusion via hierarchy-oriented prompting. Proceedings of the 46th International ACM SIGIR Conference on Research and Development in Information Retrieval, 2023; 2052-2056. [DOI](#)

### Teaching Experience

- [BIOS 555: High-throughput data analysis using R and Bioconductor](#) Emory University  
Teaching assistant and guest lecturer for Dr. Hao Wu (Course for *PhD students*) Fall 2022  
Lecture about advanced single-cell genomics sequencing technologies along with analysis techniques
- [OTM 100: Intro to Statistical Inference](#) Emory University  
Instructor (Course for *undergraduates*) Fall 2021  
Teach basic R coding and apply to perform statistical tests on real-world applications
- [CS 584: Biomedical Image Analysis](#) Emory University  
Teaching assistant for Dr. Imon Banerjee (Course for *PhD students*) Spring 2021
- [CS 253: Data Structures and Algorithms](#) Emory University  
Teaching assistant for Dr. Jinho Choi (Course for *undergraduates*) Fall 2020
- [CS 224: Foundations of Computer Science](#) Emory University  
Teaching assistant for Dr. Timothy Sun (Course for *undergraduates*) Spring 2020

## Mentoring Experience

- **Xin Wei**

Emory University

Summer 2022

Master in Biostatistics (Now *PhD student* at Brown University)

Co-mentored with Dr. Hao Wu.

Project: Identify reference datasets combination strategy for accurate cell type identification for single cell genomics data

Yielded a paper accepted by *IEEE BIBM 2024* and *Genome Biology*.

- **Rohan Dalal and Francis Wu**

High school students (Now *undergraduates* at Georgia Institute of Technology)

Summer 2022

Project: Evaluate how different deep neural network structures affect cell type prediction performance

Yielded a poster presentation.

## Fellowships, Awards and Honors

### Fellowships

- Women in Natural Sciences Fellowship

Emory University

2019 - 2023

### Awards

- Student Paper Award [[News](#)] [[Interview](#), Page 9] *American Statistical Association 2023*  
*ASA Section: Section on Statistics in Genomics and Genetics (SGG)*
- 1st place Young Scientist Excellence Award (YSEA) *MCBIOS 2023*  
*Category: Graduate Student*
- 1st place Poster Award *MCBIOS 2023*
- 3rd place Student Poster Presentation award (out of 47) [[News](#)] *Georgia Statistics Day 2022*
- Honorable Mention Poster *Georgia Statistics Day 2021*
- Best 5-minute presentation award *2nd Annual Workshop Emerging Data Science Methods for Complex Biomedical and Cyber Data 2021*

### Travel Grants

- 2023 Advances in Statistical and Computational Methods for Analysis of Biomedical, Genetic, and Omics Data (ABGOD) *Dallas, TX*
- 2022 Grad Cohort for Women *New Orleans, LA*

## Talks and Posters

### Talks

- 2025 Tools and Technology seminar series, University of Michigan [[video](#)] *Remote*  
SpaDOT: Optimal transport analysis of spatial genomics data reveals functional domain changes along time trajectories
- 2024 32nd International Biometric Conference *Atlanta, GA*  
SpaDOT: Optimal transport analysis of spatial genomics data reveals functional domain changes along time trajectories

**Invited session:** *New advances in statistical methods and applications for spatial transcriptomics and cellular heterogeneity* [[link](#)]

- 2023 Eastern North American Region Nashville, TN  
Cellcano: Supervised cell type identification for single cell ATAC-seq data  
**Contributed papers session:** *Machine learning - Methods and Applications*
- 2023 MCBIOS: Big data and artificial intelligence for genomics and therapeutics Dallas, TX  
Cellcano: Supervised cell type identification for single cell ATAC-seq data
- 2023 The Chinese University of Hong Kong, Shenzhen, School of Data Science forum Remote  
Supervised cell type identification for single-cell genomics and its applications
- 2022 Atlanta Workshop on Single-cell Omics (AWSOM) Atlanta, GA  
LRcell: detecting the source of differential expression at the sub-cell-type level from bulk RNA-seq data
- 2022 Computational Genomics Summer Institute (CGSI) Los Angeles, CA  
Supervised cell type identification for single-cell omics and its application
- 2021 Emerging Data Science Methods for Complex Biomedical and Cyber Data Remote  
Evaluation of some aspects in supervised cell type identification for single-cell RNA-seq

#### Posters

- 2022 Georgia Statistics Day Arthens, GA  
Cellcano: supervised cell type identification for single cell ATAC-seq data
- 2021 Georgia Statistics Day Atlanta, GA  
Evaluation of some aspects in supervised cell type identification for single-cell RNA-seq

#### **Professional Activities and Services**

- Invited reviewer for Journal of Applied Statistics.
- Invited reviewer for American Medical Informatics Association (AMIA) 2025.
- Invited reviewer for IEEE Transactions on Computational Biology and Bioinformatics.
- Invited reviewer for BMC Bioinformatics.
- Invited reviewer for Bioinformatics Advances.
- Invited reviewer for Bioinformatics.
- Invited Program Committee (PC) member for IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2024, IEEE BIBM 2023; Invited reviewer for IEEE BIBM 2022.
- Invited reviewer for International Journal of Computational Biology and Drug Design (IJCBD).
- Invited sub-reviewer for ISMB/ECCB 2023.
- Invited reviewer for Journal of Agricultural, Biological, and Environmental Statistics (JABE).

## **List of References**

### **Xiang Zhou**

Professor

Department of Statistics and Data Science

Yale University

Address: Kline Tower, Room 1135, 219 Prospect Street, New Haven, CT 06511

Email: [xiang.zhou.xz735@yale.edu](mailto:xiang.zhou.xz735@yale.edu)

Tel: (734) 764-5722

### **Hao Wu**

Distinguished Professor

Computer Science and Control Engineering

Shenzhen University of Advanced Technology

Address: No.1 Gongchang Road, Guangming District, Shenzhen, P.R.China

Email: [wuhao@suat-sz.edu.cn](mailto:wuhao@suat-sz.edu.cn)

### **Peng Jin**

Robert W. Woodruff Professor of Human Genetics

Chair, Department of Human Genetics, School of Medicine

Director, Emory Stephen T. Warren National Fragile X Research Center

Emory University

Address: 615 Michael Street, Suite 305E, Atlanta, GA 30322

Email: [peng.jin@emory.edu](mailto:peng.jin@emory.edu)

Tel: (404) 727-3729