

Haoran Hu

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QUALIFICATION SUMMARY

- Proficient in statistical programming with R and Python; familiar with SAS and STATA
- Experienced in effectively collaborating with non-statisticians in the medical field
- Strong background in statistical machine learning and statistical modeling in single-cell multi-omics data
- Theoretical foundation and practical experience in longitudinal data analysis, survival analysis, and clinical trial design

EDUCATION

University of Pittsburgh, School of Public Health, Pittsburgh, PA Sep 2021 – present
Ph.D. student in Biostatistics

- **Advisor:** Prof. Wei Chen, PhD
- **Research interest:** Statistical machine learning, Statistical modeling, Multi-omics data analysis
- **Cross-registered courses at Carnegie Mellon University:** Introduction to Machine Learning (CMU-10601), Advanced Deep Learning (CMU-10707)

Columbia University, Mailman School of Public Health, New York, NY Sep 2018 – May 2020
Master of Science in Biostatistics;

- **GPA:** 4.00/4.00
- **Selected courses taken:** Introduction to Randomized Clinical Trial (BIOST-8140), Clinical Trial Methodology (BIOST-8142), Statistical Methods for Causal Inference (BIOST-8122)

South China University of Technology (SCUT), Guangzhou, China Sep 2014 – Jun 2018
Bachelor of Science in Mathematics and Applied Mathematics;

- **GPA:** 3.78/4.00, Top 4 among 50 students

WORK EXPERIENCE

University of Pittsburgh Medical Center (UPMC) Division of Pulmonary, Pittsburgh, PA Sep 2022 – present

Graduate Student Researcher

Supervisor: Prof. Sally E. Wenzel

- Coordinated single-cell data collection from 8 severe asthma patients and 5 healthy controls
- Conducted statistical analyses on gene expression across disease statuses and authored comprehensive reports to support data-driven insights
- Delivered monthly presentations to interdisciplinary teams, contributing to research strategy

UPMC Division of Gastroenterology, Pittsburgh, PA Jan 2022 – present

Graduate Student Researcher

Supervisor: Prof. Richard H. Duerr

- Established statistical analysis pipelines for cutting-edge single-cell multi-omics data, such as DOGMA-seq data and RNA isoform data from long-read sequencing
- Investigated factors promoting or inhibiting CD4 T-cell activation in Crohn's disease patients

UPMC Children's Hospital of Pittsburgh, Pittsburgh, PA

Sep 2021 – present

Graduate Student Researcher

Supervisor: Prof. Wei Chen

- Developed novel statistical methods for analyzing single-cell multi-omics data

Columbia University, Department of Biostatistics, New York, NY

Aug 2019 – Apr 2020

Research Assistant

Supervisor: Prof. Zhezhen Jin

- Investigated the relationship of education level and Apoe4 gene status with the rate of decline in cognitive level

PEER-REVIEWED PAPERS

^: co-first author

Methodology

- **Hu H**, Wang X, Feng S, Xu Z, Liu J, O'Hare E, Chen Y, Yue M, Zeng L, Ding Y, Huang H, Duerr R, Chen W. A unified model-based framework for doublet or multiplet detection in single-cell multiomics data. *Nature Communications* 15, 5562 (2024).
<https://doi.org/10.1038/s41467-024-49448-x>
Selected as a featured article in "Biotechnology and methods" section
<https://www.nature.com/collections/idhhgedgig>
- Chen Y, Wu X, Ni K, **Hu H**, Yue M, Chen W, Huang H. Robust and Accurate Doublet Detection of Single-Cell Sequencing Data via Maximizing Area Under Precision-Recall Curve. bioRxiv; **doi:** <https://doi.org/10.1101/2023.10.30.564840>
- Wang X, Xu Z, **Hu H**, Zhou X, Zhang Y, Lafyatis R, Chen K, Huang H, Ding Y, Duerr R, Chen W. SECANT: a biology-guided semi-supervised method for clustering, classification, and annotation of single-cell multi-omics. *PNAS Nexus*. 2022 Sep; 1(4): pgab165
- Rong Z[^], **Hu H**[^], Duan J, Liu T, Feng S, Zhao C, Duerr, R, Zhou X, Chen W. scDitu: a cluster-free method for identifying isoform-level differential transcript usage in sparse single-cell long-read sequencing data. Under review at *RECOMB* conference
- Yue M, Cai M, Zhao C, Tao S, Liu J, **Hu H**, Chen Y, Celedon J, Wang J, Huang H, Chen W. Multi-Omics intermediate Fusion Enable Digital White Blood Cells Count Prediction. Submitted to *Genome Medicine*
- Yuan R, Rong Z, **Hu H**, Liu T, Tao S, Chen W. Harmony-Based Data Integration for Distributed Single-Cell Multi-Omics Data. Submitted to *Nature Communications*

Collaborative work

- Xu Z, Tao S, Feng S, Wang T, **Hu H**, O'Hare E, Chen W, Duerr R. Dissecting PGE2-Driven inhibition of T Cell Activation Using Single-Cell Multi-Omic and Inflammatory Bowel Disease Genetic Association Analysis. *Nature Genetics (In revision)*, 2024

BOOK CHAPTER

- Wang X, **Hu H**, Chen W. Model-based Clustering of Single-cell Data. Book Chapter In: Handbook of Statistical Bioinformatics (2nd Edition) 2022 (pp. 85-108). Chapman & Hall/CRC.

PRESENTATIONS

- (Contributed talk) "A unified model-based framework for doublet or multiplet detection in single-cell multiomics data", Joint Statistical Meetings, Portland, OR, August 2024
- (Contributed talk) "COMPOSITE: A Novel Compound Poisson Model for Enhanced Multiplet Detection in Single-Cell Multiomics Data", Biostatistics Research Day, University of Pittsburgh, Pittsburgh, PA, February 2024
- (Contributed talk) Exploration: Can SECANT clustering uncertainty benefit downstream trajectory inference? Biostatistics Research Day, University of Pittsburgh, Pittsburgh, PA, February 2022

HONORS AND AWARDS

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| ▪ University of Pittsburgh Biostatistics Research Day Honorable Mentions | 2022 |
| ▪ Outstanding graduate award of school of mathematics (SCUT) | 2018 |
| ▪ "Hongping Changqing" Science and Technology Innovation Award | 2018 |
| ▪ Merit Student in South China University of Technology | 2015-2017 |
| ▪ "Meritorious Winner" in the COMAP's Mathematical Contest in Modeling (MCM) | 2016 |
| ▪ Macao alumni scholarship (SCUT) | 2016 |
| ▪ Excellent leader of the student organizations (SCUT) | 2015 |

PROGRAMMING SKILLS

R, Python, MATLAB - Frequently used in research projects

Stata, SAS, SQL, Mathematica, C++, C# - Frequently applied in coursework

SERVICES

- Organizer, University of Pittsburgh Biostatistics Journal Club, Spring 2024
- Teaching Assistant, University of Pittsburgh Next Generation Sequencing Workshops, Fall 2023
- Teaching Assistant, University of Pittsburgh Next Generation Sequencing Workshops, Spring 2023

PROFESSIONAL AFFILIATIONS

- Member of American Statistical Association (ASA)
- Member of Eastern North American Region International Biometric Society (ENAR)
- Member of International Chinese Statistical Association (ICSA)