

# Wenpin Hou, Ph.D.

**Date of Preparation:** July 27, 2024

## PERSONAL DATA

Name: Wenpin Hou  
Contact Information: Room 650, 722 West 168<sup>th</sup> Street, New York, NY 10032, USA

## ACADEMIC APPOINTMENTS / WORK EXPERIENCE

**Assistant Professor (*tenure-track*), Columbia University**, New York, NY, USA 7/2022-Present  
Department of Biostatistics, Mailman School of Public Health  
**Affiliated Member, Data Science Institute, Columbia University**, New York, NY, USA 1/2024-Present  
Center for Foundations of Data Science  
Center for Health Analytics

## EDUCATION

**Ph.D., Mathematics, The University of Hong Kong**, Hong Kong, China 9/2013-8/2017  
Mentor: Dr. Wai-Ki Ching  
Thesis: Mathematical modelling and optimization in biological networks and data  
Degree Awarded Date: 11/25/2017  
**B.Sc., Information and Computational Science, Sun Yat-sen University**, Guangzhou, China 9/2009-6/2013  
Advisor: Dr. Tianshou Zhou  
Degree Awarded Date: 6/19/2013

## TRAINING

### *Postdoctoral Fellow*

**Johns Hopkins University**, Department of Biostatistics, Baltimore, MD, USA 8/2019-06/2022  
Mentors: Drs. Stephanie C. Hicks and Hongkai Ji  
*K99 Phase* Mentors: Drs. Hongkai Ji, Stephanie C. Hicks, and Andrew P. Feinberg  
*K99 Phase* Advisors: Drs. Xiaobin Wang, Kasper Hansen, and Gregory Hager  
**Johns Hopkins University**, Department of Computer Science, Baltimore, MD, USA 8/2017-8/2019  
Mentors: Drs. Suchi Saria and Aravinda Chakravarti

### *Visiting Researcher*

**NYU Langone Health**, Center for Human Genetics and Genomics, New York, NY, USA 12/2018-12/2018  
**MD Anderson Cancer Center**, Department of Bioinformatics & Computational Biology, Houston, TX, USA 7/2017-8/2017  
**Kyoto University**, Bioinformatics Center, Kyoto, Japan 5/2016-8/2016  
**Kyoto University**, Bioinformatics Center, Kyoto, Japan 5/2015-8/2015  
**Soka University**, Bioinformatics Lab, Tokyo, Japan 6/2014-8/2014

## HONORS AND AWARDS

Maximizing Investigators Research Award (MIRA) for Early Stage Investigators, NIH/NIGMS 2023  
Emerging Leaders in Computational Oncology Award, Memorial Sloan Kettering Cancer Center 2021  
NIH Pathway to Independence Award (K99/R00), NIH/NHGRI 2021  
2021 Women in Statistics and Data Science Conference Award, American Statistical Association 2021  
First-place Winning Poster at the 13th Annual Symposium and Poster Session on Genomics and Bioinformatics 2019  
University Postgraduate Fellowships, Philip K H Wong Foundation, The University of Hong Kong 2013-2017  
Postgraduate Scholarship, The University of Hong Kong 2013-2017  
Excellent Teaching Award, Department of Mathematics, The University of Hong Kong 2016  
Doris Chen Postgraduate Travel Grants 2016

## ADMINISTRATIVE LEADERSHIP AND ACADEMIC SERVICE

### Academic Service

#### Co-found the Statistical Genetics and Genomics (SGG) Working Group

9/2022

- Form a group of 35 sign-up members and in charge of the mailing list
- Organize bi-weekly SGG seminars and invite six external speakers from UPenn, Duke, UMich, UNC Chapel Hill, NCI, Boston University, etc. from 9/2023 to 12/2024

#### Departmental Committees

- Member, PhD Admission Committee 10/2023-present
- Member, Application Qualifying Exams Committee 10/2023-present
- Member, Curriculum Committee 10/2023-present

#### Conference Award Committees

- The 12th International Chinese Statistical Association Conference ([ICSA2023](#))
- International Conference on Health Policy Statistics ([ICHPS 2023](#))

### Administrative Leadership

- Seminar speaker, PhD student recruitment visit day 2/2024
- Panelist, Doctoral Job Search: Academia workshop, Columbia Mailman School of Public Health, Virtual 10/2023
- Oral presenter and poster judge, Columbia Biostatistics Annual Research Symposium ([CBARS](#)) 9/2023

## PROFESSIONAL ORGANIZATIONS AND SOCIETIES

### Memberships

|  |                      |
|--|----------------------|
| Institute of Mathematical Statistics (IMS)             | 2023-2024            |
| International Chinese Statistical Association (ICSA)   | 2023-2024            |
| American Statistical Association (ASA)                 | 2021-2022, 2023-2024 |
| Eastern North American Region (ENAR)                   | 2019-2020            |
| International Society for Computational Biology (ISCB) | 2018-2019            |
| Society for Industrial and Applied Mathematics (SIAM)  | 2014-2018            |

### Journal Reviewer

Bioinformatics (5), Communications Biology, Genomics, Proteomics & Bioinformatics, Genome Biology (3), IEEE Transactions on Neural Networks and Learning Systems, NAR Genomics and Bioinformatics, Nature Communications (11), Nature Methods (3), Nature Portfolio, Neurocomputing, PLoS Computational Biology (4), Precision Nutrition

## GRANT SUPPORT *The \* indicates the grants cannot be accepted currently because of over-funded status*

### Present Support

#### R35GM150887 (R01-equivalent), NIH/NIGMS

9/2023-8/2028

Title: Methods for inferring and analyzing gene regulatory networks using single-cell multiomics and spatial genomics data

Role: Principal Investigator, 5.508 CM

Total Cost: \$ 2,031,164

#### K99/R00HG011468, NIH/NHGRI

3/2021-6/2025

Title: Computational methods for inferring single-cell DNA methylation and its spatial landscape

Role: Principal Investigator, 5.292 CM

Direct Cost: \$617,406

#### 1R01MH133561-01\*, NIH/NIMH

9/2023-6/2028

Title: Human brain multi-omics to decipher major depression pathophysiology

Role: Co-Investigator, 0.6 CM (PI: Boldrini, M.)

Total Cost: \$3,863,494

#### R01AG076949 Supplement\*, NIH

12/2023-11/2024

Title: Harmonization and joint analysis of human brain single-cell datasets from neurotypical aging controls and alzheimer's disease patients

Role: Co-Investigator, 3 CM (PI: Boldrini, M.)

Total Cost: \$250,000

**Pending Support****A2Pilot Award**, NIH/NIA

4/2025-4/2026

Title: Multi-modal Transformer for Alzheimer's Disease Outcome Simulation

Role: Co-Investigator, joint with Drs. Ying Wei and James M Noble

Total Cost: \$200,000 at maximum

Status: invited for the second round on 6/18/2024

**EDUCATIONAL CONTRIBUTIONS****Direct Teaching****Instructor**, Department of Biostatistics, Columbia University

## • P8131 Biostatistical Methods II

1/2024-5/2025

- Sole instructor for this mandatory course, providing three hours of instruction per week
- Curriculum includes Generalized Linear Models, Longitudinal Data Analysis, and Survival Analysis
- Taught 113 master's level students

**Guest Lecturer**, Department of Biostatistics, Columbia University

## • Graduate Student Research Seminar (GSRS), Columbia Biostatistics Department

10/2/2023

**Teaching Assistant and Lab Instructor**, Department of Mathematics, The University of Hong Kong

9/2013-2/2017

Certificate: Certificate of Teaching and Learning in Higher Education

Responsibility: give supplement lectures, programming lessons, and exercise class twice per week; design and grade assignments; provide instruction to individual or small groups of students to improve academic performance; advise students about their academic and career development

- MATH 1011 University Mathematics (1 semester)
- MATH 2601&3601 Numerical Analysis (2 semesters)
- MATH 1211&2211 Multivariable Calculus (3 semesters)

**Advising and Mentorship** (The † indicates that I am the primary mentor or practicum advisor.)**Postdoctoral Research Scientists**, Department of Biostatistics, Columbia University, New York, NY, USA

## • Won Eui Hong† (co-mentored by Dr. Ying Wei)

2/2024-Present

**PhD Students**, Department of Biostatistics, Columbia University, New York, NY, USA

## • Elly Kipkogei (Provost diversity fellow), mentor through SPRIS II course

9/2023-1/2024

**Master's Students**, Department of Biostatistics, Columbia University, New York, NY, USA

- Yifei Zhao†, (Y2022, Theory and Methods Track) 10/2023-Present
- Lehan Zou (Y2023, Theory and Methods Track) 9/2023-Present
- Aiying Huang (Y2023, Public Health Data Science Track) 9/2023-Present
- Jingyi Yao† (Y2022, Theory and Methods Track) 3/2023-Present
- Yiyi Wu (Y2023, Theory and Methods Track) 7/2023-8/2023
- Tianchuan Gao† (Y2021, Theory and Methods Track), current PhD student at Indiana University 9/2022-5/2023
- Wenhan Bao (Y2021, Theory and Methods Track), current PhD student at Florida University 8/2022-6/2023

**Community Education**

- Panelist, Harvard Medical School - Chinese Students and Scholars Association (HMS-CSSA) Career Development Series, Virtual 8/2022
- Panelistm Chan Zuckerberg Initiative (CZI) Faculty Search Bootcamp: Recent Jobseeker Panel, Virtual 8/2022

**PUBLICATIONS** *The \* indicates the corresponding author(s).***Methods for Single-cell Genomics and Epigenomics**

1. Hou, W.\*, and Ji, Z.\*, 2024. Assessing GPT-4 for cell type annotation in single-cell RNA-seq analysis. [Nature Methods](#), 2024 March 25. [IF: 48]. Software package: [GPTCelltype](#).

Note 1: Featured in 12 news outlets, such as [Columbia News Spotlight](#), [Columbia MSPH News](#), [Science Daily](#), [The Medical News](#), [Health Tech World](#), etc.

Note 2: This research output has an Altmetric Attention Score of 284. It ranked the top 1 when comparing to 75 others from the same source and published within six weeks.

2. **Hou, W.**, Ji, Z., Chen, Z., Wherry, E.J., Hicks, S.C. and Ji, H., 2023. A statistical framework for differential pseudotime analysis with multiple single-cell RNA-seq samples. [Nature Communications 14, 7286](#). Software package: [Lamian](#).
3. Dykema, A.G., Zhang, J., Cheung, L.S., Connor, S., Zhang, B., Zeng, Z., Cherry, C.M., Li, T., Caushi, J.X., Nishimoto, M., Munoz, A.J., Ji, Z., **Hou, W.**, Zhan, W., Singh, D., Zhang, T., Rashid, R., Mitchell-Flack, M., Bom, S., Tam, A., Ionta, N., Aye, T.H.K., Wang, Y., Sawosik, C.A., Tirado, L.E., Tomasovic, L.M., Spangler, J.B., Anagnostou, W., Yang, S., Spicer, J., Rayes, R., Taube, J., Brahmer, J.R., Forde, P.M., Yegnasubramanian, S.\*, Ji, H.\*, Pardoll, M.\*, and Smith K.N.\*, 2023. Lung tumor-infiltrating Treg have divergent transcriptional profiles and function linked to checkpoint blockade response. [Science Immunology, 8\(87\)](#). PMID: 37713507. PMCID: PMC10629528.
4. Wang, Y., Wang, W., Liu, D., **Hou, W.**, Zhou, T. and Ji, Z., 2023. GeneSegNet: A deep learning framework for cell segmentation by integrating gene expression and imaging. [Genome Biology 24, 235](#). Software package: [GeneSegNet](#).
5. **Hou, W.** and Ji, Z., 2022. Palo: Spatially-aware color palette optimization for single-cell and spatial data. [Bioinformatics, June 01, 2022](#). Software package: [Palo](#). PMID: 35642896.
6. **Hou, W.** and Ji, Z., 2022. Single-cell unbiased visualization with SCUBI. [Cell Reports Methods, 100135, 2022](#). Software package: [SCUBI](#). PMID: 35224531. PMCID: PMC8871596.
7. Caushi, J.X., Zhang, J., Ji, Z., Vaghasia, A., Zhang, B., Hsiue, E., Mog, B., **Hou, W.**, Justesen, S., Blosser, R., Tam, A., Anagnostou, V., Cottrell, T.R., Guo, H., Chan, H., Singh, D., Thapa, S., Dykema, A., Choudhury, C., Aparicio, L., Cheung, L., Lanis, M., Belcaid, Z., Asmar, M.E., Illei, P., Brock, M., Ha, J., Bush, E., Park, B., Bott, M., Naidoo, J., Marrone, K.A., Reuss, J.E., Velculescu, V.E., Chaff, J.E., Kinzler, K.W., Zhou, S., Vogelstein, B., Taube, J.M., Merghoub, T., Brahmer, J.R., Hellmann, M.D., Forde, P.M., Yegnasubramanian, S., Ji, H., Pardoll, D.M., Smith, K.N., 2021. Transcriptional programs of neoantigen-specific TIL in anti-PD-1-treated lung cancers. [Nature 596, 126–132](#). PMCID: PMC8338555.  
**Note 1:** Discussed in [Tumour antigen-induced T cell exhaustion – the archenemy of immune-hot malignancies](#) in [Nature Reviews Clinical Oncology 18, 749–750 \(2021\)](#).  
**Note 2:** I contributed to the pseudotime analysis and functional analysis (Figure 4g-h, Extended data Figure 12b-f).
8. **Hou, W.**, Ji, Z., Ji, H. and Hicks, S.C., 2020. A systematic evaluation of single-cell RNA-sequencing imputation methods. [Genome Biology 21, 218](#). PMID: 32854757. PMCID: PMC7450705.
9. Ji, Z., Zhou, W., **Hou, W.** and Ji, H., 2020. SCATE: single-cell ATAC-seq signal extraction and enhancement. [Genome Biology, 21,161](#). PMID: 32620137. PMCID: PMC7333383. Software packages: [SCATE](#). [SCATEData](#).

### Controllability in Boolean Networks

10. **Hou, W.**, Ruan, P., Ching, W.K. and Akutsu, T., 2019. On the number of driver nodes for controlling a Boolean network when the targets are restricted to attractors. [Journal of Theoretical Biology, 463, pp.1-11](#). PMID: 30543810.
11. **Hou, W.**, Tamura, T., Ching, W.K. and Akutsu, T., 2016. Finding and analyzing the minimum set of driver nodes in control of Boolean networks. [Advances in Complex Systems, 19\(03\), p.1650006](#). PMID: 30679639. PMCID: PMC6345816.

### Glycosylation Networks

12. **Hou, W.\***, Qiu, Y., Hashimoto, N., Ching, W.K. and Aoki-Kinoshita, K.F., 2016. A systematic framework to derive N-glycan biosynthesis process and the automated construction of glycosylation networks. [BMC Bioinformatics, 17\(7\), p.240](#). PMID: 27454116. PMCID: PMC4965717.

### Public Health for Low-income Minority

13. Xu, R., Hong, X., Ladd-Acosta, C., Buckley, J.P., Choi, G., Wang, G., **Hou, W.**, Wang, X., Liang, L. and Ji, H., 2023. Contrasting Association of Maternal Plasma Biomarkers of Smoking and 1-Carbon Micronutrients with Offspring DNA Methylation: Evidence of Aryl Hydrocarbon Receptor Repressor Gene–Smoking–Folate Interaction. [The Journal of Nutrition, 153\(8\), 2339-2351](#).
14. Huang, W., Igusa, T., Wang, G., Buckley, J.P., Hong, X., Bind, E., Steffens, A., Mukherjee, J., Haltmeier, D., Ji, Y., Xu, R., **Hou, W.**, Fan, Z., and Wang, X., 2022. In-utero co-exposure to toxic metals and micronutrients on childhood risk of overweight or obesity: new insight on micronutrients counteracting toxic metals. [International Journal of Obesity, 46, 1435–1445](#).
15. **Hou, W.\***, Zhang, M., Ji, Y., Hong, X., Wang, G., Xu, R., Liang, L., Saria, S. and Ji, H., 2022. A prospective birth cohort study of maternal prenatal ciga-rette smoking assessed by self-report and biomarkers on childhood risk of overweight or obesity. [Precision Nutrition, 1\(3\), e00017](#).
16. Xu, R., Hong, X., Zhang, B., Huang, W., **Hou, W.**, Wang, G., Wang, X., Igusa, T., Liang, L. and Ji, H., 2021. DNA methylation mediates the effect of maternal smoking on offspring birthweight: a birth cohort study of multi-ethnic US mother–newborn pairs. [Clinical Epigenetics, 13\(1\), pp.1-13](#). PMID: 33663600. PMCID: PMC7931602.
17. Ji, Y., Azuine, R.E., Zhang, Y., **Hou, W.**, Hong, X., Wang, G., Riley, A., Pearson, C., Zuckerman, B. and Wang, X., 2019. Association of cord plasma biomarkers of in utero acetaminophen exposure with risk of attention-deficit/hyperactivity

disorder and autism spectrum disorder in childhood. [JAMA psychiatry](#), 77(2), pp.180-189.. PMID: 31664451. PMCID: PMC6822099. (Featured in [NIH news](#), [Reuters health](#), [MedPage Today](#), [meaww](#), [LinksMedicus](#), [TechnologyNetworks](#))

## Machine Learning for Biomedical Data

18. Jiang, H., Qiu, Y., **Hou, W.**, Cheng, X., Yim, M.Y. and Ching, W.K., 2018. Drug side-effect profiles prediction: from empirical to structural risk minimization. [IEEE/ACM transactions on computational biology and bioinformatics](#), 17(2), pp.402-410. PMID: 29994681.
19. Jiang, H., Ching, W.K., Cheung, W.S., **Hou, W.** and Yin, H., 2017. Hadamard kernel SVM with applications for breast cancer outcome predictions. [BMC Systems Biology](#), 11(7), p.138. PMID: 29322919. PMCID: PMC5763304.
20. Jiang, H., Ching, W.K. and **Hou, W.**, 2016. On orthogonal feature extraction model with applications in medical prognosis. [Applied Mathematical Modelling](#), 40(19-20), pp.8766-8776.
21. Qiu, Y., Cheng, X., **Hou, W.** and Ching, W.K., On classification of biological data using outlier detection, [The 12th International Symposium on Operations Research and its Applications \(ISORA\)](#), pp.144-150, Luoyang, China, 2015.
22. Cheng, X., Ching, W.K., **Hou, W.** and Kinoshita, K., A multiple linear regression model for structure of *N*-linked oligosaccharides, [The 12th International Symposium on Operations Research and its Applications \(ISORA\)](#), pp.151-157, Luoyang, China, 2015.
23. Cheng, X., Qiu, Y., **Hou, W.** and Ching, W.K., A semi-tensor product approach for probabilistic Boolean networks, [IEEE Proceedings of the 8th International Conference on Systems Biology \(ISB\)](#), pp.88-93, Qingdao, China, 2014.

## Thesis

24. **Hou, W.** (2017) Mathematical modelling and optimization in biological networks and data. Ph.D. Thesis. The University of Hong Kong.

## Posters

25. CSHL Systems Immunology 2021, Virtual. "A computational framework for differential pseudotime analysis across conditions with multiple single-cell RNA-seq samples reveals T cell immune dynamics associated with COVID-19 disease severity." 4/2021
26. 13th Annual Symposium and Poster Session on Genomics and Bioinformatics, Johns Hopkins University, Baltimore, MD, USA. "A systematic evaluation of single-cell RNA-seq imputation methods." 10/2019 (awarded as *first-place winning poster*)
27. [11th annual RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges](#), New York University, New York, NY, USA. "Causal gene regulatory network construction using single-cell RNA-seq and single-cell ATAC-seq data." 12/2018
28. [Machine Learning Summer School](#), University of Cadiz, Cadiz, Spain. "On orthogonal feature extraction model with applications in cancer prediction." 5/2016

## PRESENTATIONS

### Invited Seminar Talks

1. University of Pennsylvania, Division of Biostatistics. Pennsylvania, USA. 4/29/2025 (scheduled)
2. Memorial Sloan-Kettering Cancer Center, Department of Epidemiology and Biostatistics. *"Expanding the Horizons of Genomics and Biomedical Analysis: GPT-4's Role in Automated Cell Type Annotation and Beyond"*. New York, USA. 6/26/2024
3. Statistical Genetics and Genomics Working Group at Columbia Biostatistics. *"Statistical Methods for Deciphering Cellular Trajectories in Single-cell and Spatial Transcriptomics Data"*. 9/20/2023.
4. Johns Hopkins University, Department of Biostatistics, Statistical Genetics Working Group. Baltimore, MD, USA. 12/9/2021
5. Johns Hopkins University, Department of Biostatistics. Baltimore, MD, USA. 3/2019
6. MD Anderson Cancer Center, Department of Bioinformatics and Computational Biology. Houston, TX, USA. 7/2017
7. Kyoto University, Bioinformatics Center. Kyoto, Japan. 3/2016
8. Kyoto University, Bioinformatics Center. Kyoto, Japan. 6/2015
9. Soka University, Department of Bioinformatics. Tokyo, Japan. 8/2014



## Invited Panel Discussion

1. Adapting to AI in Healthcare: an in-Person Workshop, Columbia University Irving Medical Center. *"Open AI in Basic & Translational Research — Opportunities in Health & Diseases"*. 4/29/2024

## Invited Job Talks

1. University of Michigan, Department of Computational Medicine and Bioinformatics. 3/8/2022
2. Duke University, Department of Biostatistics and Bioinformatics. 2/22/2022
3. Columbia University, Department of Biostatistics. 2/16/2022
4. Mount Sinai, Department of Genetics and Genomic Sciences. 2/10/2022
5. New York University, Department of Biostatistics. 2/7/2022
6. UNC Chapel Hill, Department of Mathematics. Chapel Hill, NC, USA. 2/3/2022
7. Weill Cornell Medicine, Department of Population Health Sciences. 2/1/2022
8. New York University, NYU Langone Institute for Systems Genetics. 1/18/2022
9. University of Pittsburgh, Department of Biological Sciences. 12/2021
10. University of Southern California, Division of Biostatistics at Keck School of Medicine. 10/2021
11. University of Southern California, Center for Craniofacial Molecular Biology. 9/2021

## Conference Talks

### Invited:

1. Annual Workshop in Computational Biology, University of Chicago and Toyota Technological Institute at Chicago. 9/10/2024 (scheduled)
2. Annual Synthetic Regeneration Symposium, Columbia University. New York, USA. *"Differential pseudotime analysis and spatio-temporal analysis in single-cell data"*. 7/14/2023
3. 2023 ICSA Applied Statistics Symposium. University of Michigan Ann Arbor, USA. *"Statistical Methods Development in Single-cell Genomics and Multi-omics Data"*. 6/14/2023
4. Columbia Stem Cell Initiative (CSCI) Retreat. Edith Macy Retreat Center, Briarcliff Manor, USA. *"Computational methods for spatial and temporal trajectory analysis in single-cell data"*. 5/4/2023
5. Emerging Leaders Symposium in Computational Oncology, Memorial Sloan Kettering Cancer Center, Virtual. *"Computational methods for analyzing gene expression and regulation dynamics at single-cell and spatial resolution"*. 10/14/2021

### Contributed:

1. ENAR 2024 Spring Meeting, Baltimore, USA. *"Decomposing spatial heterogeneity of cell trajectories with Paella"*. 3/10/2024
2. 2021 Joint Statistical Meetings (JSM), Virtual. *"Lamian: a statistical framework for differential pseudotime analysis in multiple single-cell RNA-seq samples"*. 8/2021
3. ENAR 2020 Spring Meeting, Virtual. *"A systematic evaluation of single-cell RNA-seq imputation methods"*. 3/2020
4. Biotechnology and Bioinformatics Symposium (BIOT) 2015, Provo, UT, USA. *"A systematic framework to derive N-glycan biosynthesis process and the automated construction of glycosylation networks"*. 12/2015