

Wenpin Hou, Ph.D.

Date of Preparation: November 1, 2024

PERSONAL DATA

Name: Wenpin Hou
 Contact Information: Room 650, 722 West 168th 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. Aravinda Chakravarti and Suchi Saria

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

Institutional 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, Research Advisory Committee 9/2024-present
- Member, PhD Admission Committee 10/2023-present
- Member, Application Qualifying Exams Committee 10/2023-present
- Member, Curriculum Committee 10/2023-present

Summer Programs

- Mentor, SIBDS program 6/2024

Miscellaneous

- 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

External Service

NIH Grant Reviewer

Genomics, Computational Biology and Technology Study Section (GCAT) 10/2024

Journal Reviewer

Bioinformatics (5), Biometrics, Communications Biology, Genomics, Proteomics & Bioinformatics, Genome Biology (3), IEEE Transactions on Neural Networks and Learning Systems, NAR Genomics and Bioinformatics, Nature Communications (13), Nature Genetics, Nature Methods (4), Nature Portfolio, Neurocomputing, PLoS Computational Biology (4), Precision Nutrition

Conference Award Committees

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

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

Present Support

R35GM150887 (R01-equivalent), NIH/NIGMS, PI, 5.508 CM 9/2023-8/2028

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

Total Cost: \$ 2,031,164

K99/R00HG011468, NIH/NHGRI, PI, 5.292 CM 3/2021-6/2025

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

Total Cost: \$1,030,861

1R01MH133561-01*, NIH/NIMH, co-I(PI: Boldrini, M.), 0.6 CM 9/2023-6/2028

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

Total Cost: \$3,863,494

R01AG076949 Supplement*, NIH, co-I(PI: Boldrini, M.), 3 CM 12/2023-11/2024

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

Total Cost: \$250,000

EDUCATIONAL CONTRIBUTIONS

Direct Teaching

Instructor, Department of Biostatistics, Columbia University

- P8131 Biostatistical Methods II Spring 2024, 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 100+ master's level students

Guest Lecturer, Department of Biostatistics, Columbia University

- Graduate Student Research Seminar Fall 2023, 2024

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

- Xu Liao‡, Ph.D., incoming, offer accepted 12/2024-
- Qi Liu, Ph.D. (co-mentored by Dr. Ying Wei) 10/2024-Present
- Won Eui Hong‡, Ph.D. (co-mentored by Dr. Ying Wei) 2/2024-Present

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

- Chhiring Y. Lama (Y2024) 9/2024 - Present
- Elly Kipkogei (Y2023, Provost diversity fellow), mentor through SPRIS II course 9/2023-1/2024

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

- Xinyi Shang‡, (Y2023, Theory and Methods Track) 5/2023-Present
- Yifei Zhao‡, (Y2022, Theory and Methods Track), current computer engineer at DISH 10/2023-Present
- Lehan Zou‡ (Y2023, Theory and Methods Track) 9/2023-Present
- Aiyang Huang‡ (Y2023, Public Health Data Science Track) 9/2023-Present
- Jingyi Yao‡ (Y2022, Theory and Methods Track), current PhD student at Boston University 3/2023-5/2024
- Yiyang 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

Undergraduate Students

- Mathew Eichner, Pomona College, mentor through SIBDS program 6/2024-present
- Alexandra Duta, University of Illinois Urbana-Champaign, mentor through SIBDS program 6/2024-7/2024

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 and senior author(s).*

In Preprint

1. **Hou, W.***, and Ji, Z.*, 2024. GPT-4V exhibits human-like performance in biomedical image classification. [bioRxiv, 2024 January 1](#). In Journal Review.
2. **Hou, W.*** and Ji, Z.*, 2023. GeneTuring tests GPT models in genomics. [bioRxiv, pp.2023-03](#). In Journal Review.
3. Jackson, C., Cherry, C., Bom, S., Dykema, A., Thompson, E., Zheng, M., Ji, Z., **Hou, W.**, Li, R., Zhang, H. and Choi, J.,

Rodriguez, F., Weingart, J., Yegnasubramanian, S., Lim, M., Bettegowda, C., Powell, J., Eliesseff, J., Ji, H., and Pardoll, D. 2023. Distinct myeloid derived suppressor cell populations promote tumor aggression in glioblastoma. [bioRxiv, 2023 Jan 1](#). In Journal Review.

4. **Hou, W.*** and Ji, Z.*, 2022. Decomposing spatial heterogeneity of cell trajectories with Paella. [bioRxiv, pp.2022-09](#). Software package: [Paella](#). In Revision.

Published and Accepted:

Methods for Single-cell Genomics and Epigenomics

1. Montagne, J.M. Mitchell, J.T., Tandurella, J.A., Christenson, E.S., Danilova, L.V., Deshpande, A., Melanie L., Sidiropoulos, D.N., Davis-Marcisak, E., Bergman, D.R., Zhu, Q., Wang, H., Kagohara, L.T., Engle, L.L., Green, B.F., Favorov, A.V., Ho, W.J., Lim, S.J., Zhang, R., Li, P., Gai, J., Mo, G., Mitchell, S., Wang, R., Vaghasia, A., **Hou, W.**, Xu, Y., Zimmerman, J.W., Elisseff, J.H., Yegnasubramanian, S., Anders, R.A., Jaffee, E.M., Zheng, L. and Fertig, E.J. 2024. CD137 agonism enhances anti-PD1 induced activation of clonally expanded CD8+ T cells in a neoadjuvant pancreatic cancer clinical trial. Accepted for publication in *iScience*.
2. **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: As of May/June 2024, this highly cited paper received enough citations to place it in the **top 1%** of the academic field of Biology & Biochemistry based on a highly cited threshold for the field and publication year. **Note 2:** Featured in 12 news outlets, such as [Columbia News Spotlight](#), [Columbia MSPH News](#), [Science Daily](#), [The Medical News](#), [Health Tech World](#), etc. **Note 3:** Reviewed in Nature Methods "Embedding AI in biology" and "Toward learning a foundational representation of cells and genes".
3. **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](#).
4. 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.
5. 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](#).
6. **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.
7. **Hou, W.** and Ji, Z., 2022. Single-cell unbiased visualization with SCUBI. [Cell Reports Methods, 100135, 2022](#). Software package: [SCUBI](#). PMID: 35224531. PMCID: PMC8871596.
8. 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., Chaft, 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).
9. **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.
10. 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

11. **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.
12. **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

13. **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

14. 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.
15. 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.
16. **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.
17. 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.
18. Ji, Y., Aзуine, 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

19. 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.
20. 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.
21. 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.
22. 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.
23. 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.
24. 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

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

Posters

26. 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
27. 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*)
28. [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
29. [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, Department of Biostatistics, Epidemiology and Informatics. Pennsylvania, USA. 4/29/2025 (scheduled)
2. Boston University, Statistical Genetics & Genomics at Department of Biostatistics. Virtual. 12/6/2024 (scheduled)
3. 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
4. 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.
5. Johns Hopkins University, Department of Biostatistics, Statistical Genetics Working Group. Baltimore, MD, USA. 12/9/2021
6. Johns Hopkins University, Department of Biostatistics. Baltimore, MD, USA. 3/2019
7. MD Anderson Cancer Center, Department of Bioinformatics and Computational Biology. Houston, TX, USA. 7/2017
8. Kyoto University, Bioinformatics Center. Kyoto, Japan. 3/2016
9. Kyoto University, Bioinformatics Center. Kyoto, Japan. 6/2015
10. 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. ENAR 2025 Spring Meeting invited session, Orleans, LA, 3/23-26/2025 (scheduled)
2. International Conference on Intelligent Biology and Medicine (ICIBM 2024), Houston Medical Center. 10/10-12/2024 (scheduled)
3. Annual Workshop in Computational Biology, University of Chicago and Toyota Technological Institute at Chicago. 9/10/2024
4. Annual Synthetic Regeneration Symposium, Columbia University. New York, USA. *"Differential pseudotime analysis and spatio-temporal analysis in single-cell data"*. 7/14/2023
5. 2023 ICASA Applied Statistics Symposium. University of Michigan Ann Arbor, USA. *"Statistical Methods Development in Single-cell Genomics and Multi-omics Data"*. 6/14/2023
6. 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
7. 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