Jingtao Wang

Email: jingtao.wang@mail.mcgill.ca
GitHub: https://github.com/JingtaoWang22

RESEARCH INTEREST

My research focuses on developing AI methods, such as deep generative models, to analyze complex biological data, particularly single-cell omics, with the goal of uncovering insights that bridge gaps in our understanding of cellular processes. By advancing computational approaches to address challenges in omics data analysis, I aim to drive discoveries that enhance our understanding of disease mechanisms and inform advancements in diagnostics and therapeutics.

EDUCATION

Degree Programs:

McGill University, Montreal, Canada   **GPA: 4.00/4.00**
Doctor of Philosophy, Experimental Medicine, September 2021 - Present
Supervisors: Dr. Jun Ding and Dr. Gregory Fonseca
Selected Coursework: Reinforcement Learning   Molecular Meths in Medical Research

Carnegie Mellon University, Pittsburgh, USA   **GPA: 3.93/4.33**
Master of Science, Automated Science, August 2019 - June 2021
Selected Coursework: Fundamentals of Bioinformatics   Applied Cell and Molecular Biology
                       Machine Learning for Scientists   Automated Laboratory Methods I&II

Harbin Institute of Technology, Harbin, China   **Major GPA: 85.10/100**
Bachelor of Engineering, Computer Science and Technology, September 2014 - June 2018
Selected Coursework: Operation Research and Optimization   The Design and Analysis of Algorithms
                       Data Structures and Algorithms   Design and Practice of Software I&II

Visiting Studies:

Columbia University, New York, NY, USA   **GPA: 3.67/4.33**
Harbin Institute of Technology visiting student program, August-December 2016
Selected Coursework: Computer Science Theory, Statistical Machine Learning

National University of Singapore, Singapore   **GPA: A+**
Harbin Institute of Technology visiting student program, July-August 2016
Selected Coursework: Biometrics in Depth

TOP CONFERENCE PRESENTATIONS

- *Research in Computational Molecular Biology (RECOMB)* — **Oral Presentation**
  "scCross: A Deep Generative Model for Unifying Single-Cell Multi-Omics with Seamless Integration, Cross-Modal Generation, and In Silico Exploration", Seoul, April 26-29 2025

- *Research in Computational Molecular Biology (RECOMB)* — **Poster Presentation**
  "RAMEN Efficiently Unveils Clinical Variable Networks for Complex Diseases Using Absorbing Random Walks and Genetic Algorithms", Seoul, April 26-29 2025

- *Intelligent Systems in Molecular Biology (ISMB)* — **Oral Presentation**
  "Enabling Affordable Single-Cell Data in Large Cohort Studies via Deep Generative Neural Networks and Active Learning", Montreal, July 20-24 2024

GRANTS & FUNDING

Digital Research Alliance of Canada – Resources for Research Groups (RRG) Grant
Project: Decoding Cellular Dynamics in Complex Diseases with Deep Generative AI for In-Silico Therapeutics
Role: Co-contributor **PI:** Dr. Jun Ding | **Awarded Resources:** 200 core-years (CPU), 64 RGU-years (GPU), 200 TB storage **Total Value:** ~$111,460 CAD | **Status:** Awarded, Active (July 2025 – April 2026)

PUBLICATIONS

Published Work (†: Co-first authors)

Wang, Jingtao , Gregory J. Fonseca, and Jun Ding. *"scSemiProfiler: Advancing large-scale single-cell studies through*

semi-profiling with deep generative models and active learning." Nature communications 15.1 (2024): 5989.
- **Highlighted by the editors as a Top 50 paper in the field**
- **Featured in *Nature*: Technology Feature [Link](#)**

Xiong, Yiwei†, **Jingtao Wang**†, Xiaoxiao Shang, Tingting Chen, Douglas D. Fraser, Gregory Fonseca, Simon Rousseau, and Jun Ding. *"Efficient and scalable construction of clinical variable networks for complex diseases with RAMEN." Cell Reports Methods,* Accepted, 2025.

Song, Qi, **Jingtao Wang**, and Ziv Bar-Joseph. *"scSTEM: clustering pseudotime ordered single-cell data." Genome Biology* 23.1 (2022): 150.

Hasanaj, Euxhen, **Jingtao Wang**, Arjun Sarathi, Jun Ding, and Ziv Bar-Joseph. *"Interactive single-cell data analysis using Cellar." Nature communications* 13.1 (2022): 1998.

Pang, Steph A., Manuel Flores Molina, Pamela Thébault, Yuming Zheng, Hsiang Chou, Christophe Goncalves, **Jingtao Wang.**, et al. *"Molecular predictors and mechanisms of immune checkpoint inhibitor-induced myocarditis: A case-control study with translational correlates." Journal of Clinical Oncology* 42, no. 16_suppl (2024): 12031-12031.

Manuscripts Under Revision

Wagner, D.E., Alsafadi, H.N., Mitash, N., ... **Wang, J.**, Sembrat, J., Hilgendorff, A., Ding, J**.**, Günther, A., Chambers, R., et al. *"Inhibition of epithelial cell YAP-TEAD/LOX signaling attenuates pulmonary fibrosis." Nature Communications*, Under revision, 2025.

Preprints

Pumeng, Shi†, **Jingtao Wang**†, Hijazin Michel†, and Jun Ding. *"DTPSP: A Deep Learning Framework for Optimized Time Point Selection in Time-Series Single-Cell Studies." bioRxiv* (2024): 2024-12.

Tai, Huilin †, Qian Li †, **Jingtao Wang** †, Jiahui Tan, Ryann Lang, Basil J. Petrof, and Jun Ding. *"CellSexID: Sex-Based Computational Tracking of Cellular Origins in Chimeric Models." bioRxiv* (2024): 2024-12.
(Under revision at *Cell Reports Methods*)

Papers to be Submitted

Wang, Jingtao†, Pumeng Shi†, Nicole Heimbach, David Eidelman, and Jun Ding. *"Universally Enhancing Deep Learning Models by Injecting Human Knowledge Through Task-Driven Reverse Probing."*
Wang, Jingtao, Sinian Zhang, and Jun Ding. *"Transforming Deep Learning with Genetic Algorithms: A Comprehensive Framework for Enhancing Structure Learning, Optimization, and Backpropagation Surrogates."*

HONORS

2025 RI-MUHC Studentship and Fellowship Competition, Ph.D.
Top 50 Best Papers in *Nature Communications* Editors' Highlights (Biotechnology and Methods Category), 2024
MEAKINS-CHRISTIE LABORATORIES 2022-2023 COLLABORATIVE RESEARCH AWARD
MEAKINS-CHRISTIE LABORATORIES 2021-2022 COLLABORATIVE RESEARCH AWARD
Harbin Institute of Technology Second-class Scholarship, 2017

OTHER PRESENTATION & TEACHING

Meakins Genomics Workshop **Teaching Assistant**, *Aug 2022 and Aug 2024*
RI-MUHC Respiratory Research Day **Oral Presentation**, *Apr 2024*
RI-MUHC Respiratory Research Day **Poster Presentation**, *Jun 2023*

RESEARCH CONTRIBUTIONS & COLLABORATIONS

Nature Communications Paper Review (*Jan 2025*)
PLOS Computational Biology Paper Review (*Jan 2025*)
Nature Communications Paper Review (Sep 2024)
SickKids Myocarditis Single-Cell Data Analysis (*Mar 2024*)
Biobanque québécoise de la COVID-19 (*BQC-19*) Patient Data Analyses (*Oct 2021*)

OTHER RESEARCH EXPERIENCES

Capstone Project, Carnegie Mellon University (*Sep 2020 – Dec 2020*)
    Automated HeLa cell line staining, imaging, and passage using robotic labware. Conducted comparative analysis of manual versus robotic performance in these operations.

Deep Learning Researcher, SenseTime, Hangzhou, China (*Aug 2018 – Aug 2019*)

Developed a transformer-based deep learning model for compound-protein interaction prediction, achieving state-of-the-art performance on benchmark datasets at the time. Implementation: https://github.com/JingtaoWang22/CPI_prediction. Project details: https://arxiv.org/abs/2009.00805