Kamal Maher

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Computational scientist with a PhD from MIT, specializing in graph theory, signal processing, and large-scale biological data. My research develops mathematically grounded representations of tissues, with a focus on single-cell spatial transcriptomics.

Currently seeking to apply this expertise to problems at the interface of machine learning and computational biology.

EDUCATION

MIT
PhD in Computational Biology
Advisor: Xiao Wang
2020 - 2025

CORNELL UNIVERSITY
BS in Neuroscience
2014 - 2018

COURSEWORK

COMPUTATION
Machine Learning
Real Analysis
Linear Algebra
Multivariable Calculus
Probability and Statistics
Data Science
Data Structures

BIOLOGY
Computational Biology
Systems Biology
Molecular Biology
Neurobiology
Biochemistry

SKILLS

THEORY
Unsupervised learning
Signal processing
Spectral graph theory
Experimental design

COMPUTATION
Python (numpy, pandas, scipy)
Machine learning (PyTorch, scikit-learn)
Single-cell (scanpy, squidpy)
Packaging (flit, .toml)
HPC (UGE, SLURM)

EXPERIENCE

BROAD INSTITUTE/MIT | Graduate Researcher
Xiao Wang Lab
May 2021 - Present
- Derived a unified theoretical framework for representing multicellular regions and intercellular interactions in tissues
- Leveraged this framework for unsupervised anatomical annotation of a large-scale spatial atlas of the entire mouse brain

GENENTECH | Summer Intern
Aviv Regev Lab
June 2024 - September 2024
- Cell-cell interaction identification using graph signal processing
- Accelerated feature identification from a months long process to an hours long process

MIT | Research Assistant
Steven Flavell Lab
May 2018 - May 2020
- Optogenetics, image processing, and quantitative modeling to characterize neuronal activity in *C. elegans*.

CORNELL UNIVERSITY | Undergraduate Researcher
Jesse Goldberg Lab
May 2015 - May 2018
- Electrophysiology and fluorescent imaging to map neural circuitry in zebra finches and mice.

PUBLICATIONS

[1] K. Maher and X. Wang. Harmonic representations of regions and interactions in spatial transcriptomics. *bioRxiv*, 2024.

[2] K. Maher, M. Wu, Y. Zhou, J. Huang, Q. Zhang, and X. Wang. Mitigating autocorrelation during spatially resolved transcriptomics data analysis. *bioRxiv*, 2023.

[3] H. Shi, Y. He, Y. Zhou, J. Huang, K. Maher, B. Wang, Z. Tang, S. Luo, P. Tan, M. Wu, Z. Lin, J. Ren, Y. Thapa, X. Tang, K. Y. Chan, B. E. Deverman, H. Shen, A. Liu, J. Liu, and X. Wang. Spatial atlas of the mouse central nervous system at molecular resolution. *Nature*, 622(7983):552–561, 2023.