

# 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.