Michael Murphy

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Education

Massachusetts Institute of Technology	**Cambridge, MA**
Doctor of Philosophy (Ph.D.), Computational and Systems Biology	*Sep 2017 – Present*

Advisors: Profs. Ernest Fraenkel (Bioengineering) and Stefanie Jegelka (CSAIL)

University of Toronto	**Toronto, ON**
Bachelor of Applied Science (B.A.Sc., High Hons.), Engineering Science	*Sep 2012 – Apr 2017*

Major in Electrical and Computer Engineering (GPA 3.9/4.0)

Research Experience

Graduate Researcher	**Cambridge, MA**
Massachusetts Institute of Technology	*Sep 2018 – Present*

My PhD research primarily involves developing deep learning methods to extract biological signals from noisy, large-scale imaging, mass spectrometry, and single-cell omics datasets. My work in the Fraenkel lab has also entailed supporting medical and biological collaborations with applied bioinformatics analyses.

Data Science Intern	**Cambridge, MA**
Enveda Biosciences	*Jun 2022 – Aug 2022*

As a research intern at a Series B-stage biotech startup, I led a project with ex-Amazon Science, HuggingFace, and UC Davis researchers to develop a graph neural network for predicting mass spectra of small molecules. My work discovered a previously-unknown property of small molecule mass spectrometry data, which led to a novel representation that resolved a tradeoff suffered by previous methods and delivered state-of-the-art performance.

Software Applications Research Developer	**Toronto, ON**
AB Sciex	*May 2015 – Sep 2016*

As a research intern at a major global scientific instrument manufacturer, I developed signal processing algorithms for large-scale raw datasets generated by "Scanning SWATH", a prototype instrument control methodology for mass spectrometry. My work established initial viability of the approach and was awarded a patent, leading to subsequent commercialization.

Undergraduate Researcher	**Toronto, ON**
University of Toronto	*May 2013 – Apr 2015*

As a research assistant in Prof. Greg J. Evans' laboratory, the Southern Ontario Center for Atmospheric Aerosol Research, I performed data analysis and developed software for clustering and visualization of chemical measurements of atmospheric particulates.

Patents

G. Ivosev, N. Bloomfield, **M. Murphy**, S. Tate. Systems and Methods for Identifying Precursor and Product Ion Pairs in Scanning SWATH Data, U.S. Patent 10651019B2.

Publications and Posters

M. Murphy, S. Jegelka, E. Fraenkel, T. Kind, D. Healey, T. Butler. Efficiently predicting high resolution mass spectra with graph neural networks. *International Conference on Machine Learning (ICML)* 2023.

M. Murphy, S. Jegelka, E. Fraenkel. Self-supervised learning of cell type specificity from immunohisto-chemical images, *International Conference on Intelligent Systems in Molecular Biology (ISMB)* 2022.

M. Murphy, K. Yang, S. Jegelka, E. Fraenkel. Learning representations from mass spectra for peptide property prediction, *ICML Workshop on Computational Biology* (2022).

A. Ali, S. Davidson, E. Fraenkel, ..., **M. Murphy**, J. Sweedler, C. Zhu. Single-cell metabolism: current and future trends, *Metabolomics* (2022).

S. Sarkar, **M. Murphy**, E. Dammer, L. Olsen, S. Rangaraju, E. Fraenkel, M. Feany. Comparative proteomic analysis highlights metabolic dysfunction in α-synucleinopathy, *npj Parkinsons Disease* (2020).

E. Evans, C. Duvallet, N. Chu, M. Oberst, **M. Murphy**, I. Rockafellow, D, Sontag, E. Alm. Predicting human health from biofluid-based metabolomics using machine learning, *Scientific Reports* (2020).

M. Murphy, G. Ivosev, N. Bloomfield, Y. Kang, S. Tate. Using scanning SWATH windows to improve both quantitative and qualitative data over conventional SWATH and IDA methodologies, *Conference of the American Society of Mass Spectrometry* (2016).

R. Healy, G. Evans, **M. Murphy**, et al. Single-particle speciation of alkylamines in ambient aerosol at five European sites, *Analytical and Bioanalytical Chemistry* (2015).

R. Healy, N. Riemer, J. Wenger, **M. Murphy**, et al. Single particle diversity and mixing state measurements, *Journal of Atmospheric Chemistry and Physics* (2014).

R. Healy, G. Evans, **M. Murphy**, et al. Predicting hygroscopic growth using single particle chemical composition estimates, *Journal of Geophysical Research: Atmospheres* (2014).

Peer reviewer for: *Nature Methods*; *IEEE Transactions on Medical Imaging*; *eBioMedicine*.

Teaching Experience

Department of Biological Engineering	**Cambridge, MA**
Massachusetts Institute of Technology	*Feb 2021 – May 2021*

Tutored 20.401: Machine Learning for Molecular Engineering. Led coding clinics for graduate students.

Department of Biology	**Cambridge, MA**
Massachusetts Institute of Technology	*Feb 2019 – May 2019*

Tutored 7.09: Quantitative and Computational Biology. Led recitations, wrote and graded problem sets.

Awards

Alexander Graham Bell Canadian Graduate Scholarship	*June 2020 – June 2023*
IBBME Director's Summer Research Opportunity	*May 2017*
University of Toronto Dean's Honour List	*Sep 2012 – Apr 2017*
University of Toronto Excellence Award	*May 2014*
Center for Global Change Science Internship	*May 2014*
University of Toronto Scholars' Entrance Award	*May 2012*

Coursework and Technical Skills

Machine Learning: Machine Learning, Algorithms for Inference, Bayesian Modelling and Inference, Optimization Methods, Inference and Information, Random Processes, Probability and Statistics. Applied data analysis and visualization.

Engineering: Systems Software, Computer Organization, Databases, Algorithms and Data Structures, Linear Systems and Control, Signal Analysis and Communication.

Programming: Python (PyTorch, NumPy, pandas, scikit-learn, scikit-image, RDKit, Scanpy). Some experience in Linux shell scripting, SLURM, AWS, SQL, C.

Biology: Systems Biology, Advanced Computational Biology, Biochemistry, Molecular Biology. Practical bioinformatics (single-cell omics, image omics, mass spectrometry) and bioimage analysis.