# James P. Roney

# **Education**

Massachusetts Institute of Technology

Ph.D. Computational and Systems Biology

**Harvard University** 

A.B. Computer Science and A.M. Statistics Summa Cum Laude with Highest Thesis Honors Cambridge, MA

September 2024-Present

Cambridge, MA

September 2018-May 2022

# **Experience**

**DE Shaw Research** 

New York, NY

Research Engineer August 2022–September 2024

Worked on problems at the intersection of machine learning and drug discovery

**Sergey Ovchinnikov Lab** *Undergraduate Researcher*  Cambridge, MA

September 2021-November 2022

Investigated the internal workings of AlphaFold

o First author on paper published in Physical Review Letters

DE Shaw Research New York, NY

Machine Learning Intern

May – August 2021, May – August 2020

- Designed and built a 3D-Equivariant generative model for small molecules
- o Created a novel 3D-Equivariant transformer architecture for end-to-end protein structure prediction
- Developed a deep learning model to predict protein structures using attention mappings from self-supervised machine learning

Franziska Michor Lab Cambridge, MA

Undergraduate Researcher

December 2018–February 2020

- Created novel statistical methods for Bayesian estimation of arbitrary branching process models
- First author on paper published in *Bioinformatics*

Harvard University Cambridge, MA

Teaching Fellow January 2020 – January 2021

- Teaching assistant for CS 121: Introduction to Theoretical CS at Harvard (Fall 2020)
- Teaching assistant for Stat 111: Statistical Inference at Harvard (Spring 2020)
- Held sections and office hours, prepared materials for students, graded student work

# **Honors and Awards**

- Hertz Fellowship (\$250,000 fellowship to support my graduate studies at MIT)
- Hoopes Prize (\$5,000 award for an outstanding senior thesis at Harvard)
- Elected to Phi Beta Kappa, Alpha lota of Massachusetts
- Harvard Certificate of Distinction in Teaching

# **Publications**

- 1. Roney J, and Ovchinnikov S (2022). State-of-the-Art estimation of protein model accuracy using AlphaFold. *Physical Review Letters*.
- 2. Roney J, Appel T, Pinisetti P, Mickens J (2021). Identifying valuable pointers in heap data. *Workshop on Offensive Technologies*.
- 3. Roney J, Ferlic J, Michor F, McDonald TO (2020). ESTIpop: A computational tool to simulate and estimate parameters for continuous-time Markov branching processes. *Bioinformatics*.