James P. Roney

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Education

Harvard University   **Cambridge, MA**
A.B. Computer Science and A.M. Statistics   *May 2022*
Summa Cum Laude with Highest Thesis Honors

Experience

DE Shaw Research   **New York, NY**
Research Engineer   *August 2022-Present*

○ Working on problems at the intersection of machine learning and drug discovery

Sergey Ovchinnikov Lab   **Cambridge, MA**
Undergraduate Researcher   *September 2021–November 2022*

○ Investigated the internal workings of AlphaFold
○ 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
○ 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

○ Hoopes Prize for an outstanding senior thesis
○ Elected to Phi Beta Kappa, Alpha Iota of Massachusetts
○ Detur Book Prize for freshman year academic performance
○ 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*.