Amir **Shanehsazzadeh**

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Education

Harvard University — *Cambridge, MA*

A.B. (Bachelor's) Candidate in Mathematics, S.M. (Master's) Candidate in Statistics, GPA: 3.878/4.0 — *May 2022*

- **Relevant Coursework:** Math 55A: Honors Abstract and Linear Algebra, Stat 210: Probability I, CS 182: Artificial Intelligence, Math 55B: Honors Real and Complex Analysis, CS 229R: Information Theory, CS 229BR: Biology and Complexity, CS 229CR: High-dimensional Probability, Stat 212: Probability II, CS 281: Advanced Machine Learning, Stat 211: Inference I, Stat 244: Linear and Generalized Linear Models, Math 212A: Advanced Real Analysis, 213A: Advanced Complex Analysis, Stat 213 Inference II, Physics 160: Quantum Information, Math 274y: Spectral Theory and Quantum Spin Systems, CS 229R: Coding Theory, Math 99R: Classical Mechanics and Symplectic Geometry, Math 231: Algebraic Topology, Math 221: Algebra, Stat 230: Multivariate Statistical Analysis, Physics 181: Statistical Mechanics, Physics 91r: Reading Course in Quantum Information, CS 238: Optimized Democracy, CS 231: Quantum Computing and Complexity, Physics 231: Computational Neuroscience, CS 282R: Advancements in Probabilistic ML, Programming Models for ML, Causality
- **Teaching:** Teaching Assistant for Math 114: Measure Theory and Functional Analysis (Fall 2019 and Fall 2020), Math 154: Probability Theory (Spring 2020 and Spring 2022), CS 182: Artificial Intelligence (Fall 2020 and Fall 2021), Math 112: Real Analysis (Spring 2021)
- **Awards:** Derek Bok Certificate of Distinction in Teaching, John Harvard Scholar
- **Organizations:** Treasurer of Harvard College Iranian Association (HCIA), Member of Harvard Computer Society (HCS)

Experience

AI Scientist — *New Yory, NY*

Absci — *Jun 2022 - Present*

- Modeling and designing antibodies using state-of-the-art machine-learning techniques with the goal of *de novo* design
- Changing the world, one protein at a time

Machine Learning Associate Scientist — *Cambridge, MA*

Dyno Therapeutics — *Dec 2019 - May 2020, Aug 2020 - Jun 2022*

- Built machine learning models for sequence prediction and design pipeline of Adeno-Associated Virus (AAV) for gene therapy
- Helped automate viral library design process by accelerating machine learning related steps
- Explored applications of state-of-the-art deep learning models for *de novo* protein design and representation

Research Intern — *Mountain View, CA; Cambridge, MA*

Google Brain — *May 2020 - August 2020*

- Worked with the Sequin (computational biology, protein and DNA sequence design) team on applying Transformer (BERT) models to biological sequence design, specifically protein family prediction
- Project explored the use of contextual lenses from NLP for developing fixed-length vector representations of proteins
- First-authored two accepted workshop papers (see Projects) and open sourced project

Computational Sciences Research Intern — *New York, NY*

D. E. Shaw Research (DESRES) — *May 2019 - Aug 2019*

- Applied techniques from deep learning and natural language processing to problems in protein structure
- Built DESSEQUENCE, a tool for autonomously measuring the performance of molecular dynamics (MD) simulations using an underlying neural network model, and performed validation on MD trajectories from the Anton supercomputer
- Trained and validated a seq2seq translation model between sequences of amino acid residues (peptides) and sequences of binary labels which represent the resolution (a measure of order) of each residue in the PDB

Computational Biology and Data Science Researcher — *Philadelphia, PA*

Dunbrack Lab - Fox Chase Cancer Center — *Aug 2017 - Aug 2018*

- Developed DIHNOSIR, a clustering algorithm that combines numerous iterations of DBSCAN with a graph-theoretic approach
- Clustered protein structural conformations in the form of Ramachandran plots for use in structure prediction, design, and validation
- First author of paper on DIHNOSIR (currently in publishing/preprinting process), source code for DIHNOSIR on personal GitHub

Projects

Senior Thesis on Geometric Deep Learning

Awarded High Honors by the Mathematics Department at Harvard University

Fixed-Length Protein Embeddings using Contextual Lenses

Accepted at MLCB (Machine Learning in Computational Biology) 2020

Is Transfer Learning Necessary for Protein Landscape Prediction?

Accepted at MLSB (Machine Learning for Structural Biology) 2020