

# Gustaf Ahdriz

gahdriz@g.harvard.edu · +1 914-506-0204

[Google Scholar](#), [GitHub](#)

## Education

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### Graduate School of Arts and Sciences, Harvard University

Ph.D., Computer Science.

Sept. 2022 – Present

Advisors: Prof. Boaz Barak and Jonathan Frankle

### School of Engineering and Applied Sciences, Columbia University

M.Sc., Computer Science. GPA: 4.08

Sept. 2020 – May 2021

Advisor: Prof. Mohammed AlQuraishi

### Columbia College, Columbia University

B.A. (*summa cum laude*), Computer Science & History. GPA: 4.07

Sept. 2016 – May 2020

Advisors: Profs. Kathleen McKeown and Matthew Connelly

## Work Experience

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### AIML @ Apple

Ph.D. Intern

April 2024 – September 2024

Worked on uncertainty quantification, especially for language models. Produced a preprint (“Provable Uncertainty Decomposition via Higher-Order Calibration”).

### AlQuraishi Lab @ Columbia University

Researcher

May 2021 – Aug. 2022

Continued work on OpenFold as a predoctoral researcher.

### Apple

Software Engineering Intern

Summer 2020

Designed, developed, and tested a new macOS application for the Screen Time device management team.

## Publications and Preprints

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- [1] **G. Ahdriz**, A. Gollakota, P. Gopalan, C. Peale, U. Wieder. Provable Uncertainty Decomposition via Higher-Order Calibration. *Under review*, 2024.
- [2] \*G. Tanzer, \***G. Ahdriz**, L. Melas-Kyriazi. Modeling Real-Time Interactive Conversations as Timed Diarized Transcripts. *arXiv*, 2024.
- [3] \***G. Ahdriz**, \*T. Qin, N. Vyas, B. Barak, B.L. Edelman. Distinguishing the Knowable from the Unknowable with Language Models. *ICML 2024*, 2024.
- [4] **G. Ahdriz**, N. Bouatta, S. Kadyan, L. Jarosch, D. Berenberg, I. Fisk, A. M. Watkins, R. Bonneau, M. AlQuraishi. OpenProteinSet: Training data for structural biology at scale. *NeurIPS 2023 (Datasets and Benchmarks track)*, 2023.
- [5] S. Song, B. Krufft, M. Zhang, C. Li, S. Chen, C. Zhang, M. Tanaka, X. Wu, M. AlQuraishi, **G. Ahdriz**, C. Floristean, R. Stevens, V. Vishwanath, A. Ramanathan, S. Foreman, K. Hippe, P. Balaprakash, Y. He. DeepSpeed4Science Initiative: Enabling Large-Scale Scientific Discovery through Sophisticated AI System Technologies. *4th AI for Science Workshop at NeurIPS 2023*, 2023.

- [6] \*L. Bailey, \***G. Ahdrizt**, \*A. Kleiman, S. Swaroop, F. Doshi-Velez, W. Pan. Soft prompting might be a bug, not a feature. *Workshop on Challenges in Deployable Generative AI at ICML 2023*, 2023.
- [7] \***G. Ahdrizt**, \*N. Bouatta, S. Kadyan, Q. Xia, W. Gerecke, T. J. O’Donnell, D. Berenberg, I. Fisk, N. Zanichelli, B. Zhang, A. Nowaczynski, B. Wang, M. M. Stepniewska-Dziubinska, S. Zhang, A. Ojewole, M. Efe Guney, S. Biderman, A. M. Watkins, S. Ra, P. Ribalta Lorenzo, L. Nivon, B. Weitzner, Y. A. Ban, S. Chen, M. Zhang, C. Li, S. L. Song, Y. He, P. K. Sorger, E. Mostaque, Z. Zhang, R. Bonneau, M. AlQuraishi. OpenFold: Retraining AlphaFold2 yields new insights into its learning mechanisms and capacity for generalization. *Nature Methods* 21:1514-1524, 2024.
- [8] R. Chowdhury, N. Bouatta, S. Biswas, C. Floristean, A. Kharkar, K. Roy, C. Rochereau, **G. Ahdrizt**, J. Zhang, G. M. Church, P. K. Sorger, M. AlQuraishi. Single-sequence protein structure prediction using a language model and deep learning. *Nature Biotechnology* 40:1617–1623, 2022.

## Invited Talks

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### **SBGrid Consortium**

April 2023

*OpenFold: Retraining AlphaFold2 yields new insights into its learning mechanisms and capacity for generalization*

### **OpenBioML**

Jan. 2023

*OpenFold: Retraining AlphaFold2 yields new insights into its learning mechanisms and capacity for generalization*

### **Mosaic NLP Workshop**

Oct. 2022

*OpenFold*

### **NSF ICICLE AI Institute**

Sept. 2022

*OpenFold: Technical Overview*

## Open-Source Software and Datasets

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### **OpenFold**

Aug. 2021 – Present

Wrote and currently maintain the first trainable open-source reproduction of AlphaFold2. Includes original AlphaFold2 parameters under an open license. Work featured at NVIDIA GTC and by AWS, TechCrunch, and Weights and Biases.

### **OpenProteinSet**

June 2022

Produced the largest public database of protein alignment data, including multiple sequence alignments and template hits for more than 4 million diverse protein sequences. Can be used to train or finetune machine learning models for protein-related tasks at the scale of AlphaFold2.

## Academic Awards and Fellowships

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### **Kempner Institute Graduate Fellowship**

Sept. 2023

Five-year fellowship awarded by Harvard’s Kempner Institute to “pursue research central to the Kempner’s core mission of understanding the basis of intelligence in natural and artificial systems.”

**Ashford Fellowship**

Sept. 2022

Five-year fellowship awarded to Harvard GSAS students “highly likely to make a substantial impact in their chosen field of study, as well as in society.”

**Andrew P. Kosoresow Memorial Award**

May 2020

Awarded to teacher’s assistants in the Columbia SEAS Computer Science Department “for outstanding contributions to teaching in the Department of Computer Science and exemplary service to the Department and its mission.”

**Dean Hawkes Memorial Prize**

April 2019

Awarded to the Columbia College junior “judged to be the most deserving on the basis of work in the humanities.”

## Teaching

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**Harvard CS229br: Foundations of Deep Learning**

Spring 2023

Teaching Fellow

Professor: Boaz Barak

**Columbia COMS3157: Advanced Programming**

Spring 2019 – Spring 2021

Head Teaching Assistant (S20 – S21), Teaching Assistant (S19 – F19)

Professor: Jae Woo Lee

## Reviewing

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ICLR

2025

ICLR, ICML, NeurIPS

2024

ICML, NeurIPS (top reviewer), Current Opinion in Structural Biology

2023