

# BRIAN HIE

brianhie@stanford.edu | github.com/brianhie | brianhie.com

## CURRENT POSITIONS

**Stanford University**, Palo Alto, CA

*Assistant Professor of Chemical Engineering and Data Science*

*David T. Morgenthauer II Faculty Fellow, School of Engineering*

2024-Present

**Arc Institute**, Palo Alto, CA

*Innovation Investigator*

2024-Present

- ♦ Aligning biological machine learning with human good.

## EDUCATION

**Massachusetts Institute of Technology**, Cambridge, MA

*Electrical Engineering and Computer Science, Doctor of Philosophy*

2017-2021

*Electrical Engineering and Computer Science, Master of Science*

- ♦ Areas of concentration: Computational biology, machine learning, statistics.

**Stanford University**, Palo Alto, CA

*Computer Science, Bachelor of Science with Honors and Distinction*

2012-2016

*English Literature, Academic Minor*

- ♦ Areas of concentration: Computational biology, computer systems, machine learning.

## PROFESSIONAL EXPERIENCE

**Stanford University School of Medicine**, Palo Alto, CA

*Stanford Science Fellow*

2021-2023

- ♦ Machine learning at the host-pathogen interface.

**Meta Platforms, Inc.**, Menlo Park, CA

*Visiting Researcher, Meta AI FAIR*

2022-2023

- ♦ Machine learning for protein biology.

**Massachusetts Institute of Technology**, Cambridge, MA

*Graduate Researcher, Computer Science and Artificial Intelligence Laboratory*

2017-2021

- ♦ Neural language modeling of viral evolution.
- ♦ Machine learning for biological discovery and design under uncertainty.
- ♦ Efficient geometric algorithms for single-cell biology.
- ♦ Cryptographically secure neural network training.

**Google LLC**, Mountain View, CA

*Artificial Intelligence/Machine Learning Resident, X – The Moonshot Factory*

2019

- ♦ Machine learning for early-pipeline moonshots.

**Illumina, Inc.**, San Diego, CA

*Machine Learning Intern, Bioinformatics*

2018

- ♦ Statistical signal processing for genomics-based health monitoring.

**Salesforce.com, Inc.**, San Francisco, CA

<b>Software Engineer, Cloud Infrastructure</b>	2016-2017
♦ Robust performance monitoring of globally distributed core application infrastructure.	
<b>Stanford University</b> , Palo Alto, CA	
<b>Undergraduate Researcher, Biology</b>	2013-2016
♦ Statistics and machine learning for computational genomics.	
<b>Stanford University</b> , Palo Alto, CA	
<b>Undergraduate Researcher, Digital Humanities, Stanford Humanities Center</b>	2016
♦ Graph-theoretic analysis of the social network of early modern authors and publishers.	
<b>Microsoft Corporation</b> , Redmond, WA	
<b>Software Engineering Intern, Azure Compute and Microsoft Research</b>	2015
♦ Distributed scheduling algorithms and their impact on data center utilization and availability.	
<b>Synaptics, Inc.</b> , San Jose, CA	
<b>Systems Architecture/Algorithms Intern</b>	2014
♦ Algorithm design and implementation for embedded touchscreen firmware.	

## PUBLICATIONS

\*Equal contribution. †Co-corresponding author.

### Journal articles

- S. Hendrix, Y. Mreyoud, M. McNelan, A. Smirnov, S. Chavez, **B. Hie**, M. Chamberland, T. Bradstreet, A. Webber, D. Kreamalmeyer, R. Taneja, B. Bryson, B. Edelson, and C. Stallings.  
*"BHLHE40 regulates myeloid cell polarization through IL-10-dependent and -independent mechanisms."*  
*Journal of Immunology*, ji2200819. 2024
- A. Winniffrith, C. Outeiral<sup>†</sup>, and **B. Hie**<sup>†</sup>.  
*"Generative artificial intelligence for de novo protein design."*  
*Current Opinion in Structural Biology*, 86: June 2024. 2024
- B. Hie**<sup>†</sup>, D. Xu, V. Shanker, T. Bruun, P. Weidenbacher, S. Tang, W. Wu., and J. Pak, and P. Kim<sup>†</sup>.  
*"Efficient evolution of human antibodies from general protein language models and sequence information alone."*  
*Nature Biotechnology*, DOI: 10.1038/s41587-023-01763-2 (featured with a News and Views by Outeiral and Deane). 2023
- Z. Lin\*, H. Akin\*, R. Rao\*, **B. Hie**\*, Z. Zhu, W. Lu, N. Smetanin, R. Verkuil, O. Kabeli, Y. Shmueli, A. dos Santos Costa, M. Fazel-Zarandi, T. Sercu, S. Candido, and A. Rives.  
*"Evolutionary-scale prediction of atomic level protein structure with a language model."*  
*Science*, 379:6637. 2023
- B. Hie**<sup>†</sup>, K. Yang, and P. Kim<sup>†</sup>.  
*"Evolutionary velocity with protein language models predicts evolutionary dynamics of diverse proteins."*

*Cell Systems*, 13:4 (featured with a Preview by Sandhu et al.). 2022

M. Maher, I. Bartha, S. Weaver, J. di Iulio, E. Ferri, L. Soriaga, F. Lempp, **B. Hie**, B. Bryson, B. Berger, D. Robertson, G. Snell, D. Corti, H. Virgin, S. Kosakovsky Pond, and A. Telenti.  
*"Predicting the mutational drivers of future SARS-CoV-2 variants of concern."*  
*Science Translational Medicine*, 14:633. 2022

**B. Hie** and K. Yang.  
*"Adaptive machine learning for protein engineering."*  
*Current Opinion in Structural Biology*, 72: February 2022. 2022

R. Singh\*, **B. Hie\***, A. Narayan, and B. Berger.  
*"Schema: Metric learning enables interpretable synthesis of heterogeneous single-cell modalities."*  
*Genome Biology*, 22:131. 2021

**B. Hie**, E. Zhong, B. Berger, and B. Bryson.  
*"Learning the language of viral evolution and escape."*  
*Science*, 371:6526 (featured with a Perspective by Kim and Przytycka). 2021

**B. Hie**, B. Bryson, and B. Berger.  
*"Leveraging uncertainty in machine learning accelerates biological discovery and design."*  
*Cell Systems*, 11:5. 2020

**B. Hie\***, J. Peters\*, S. Nyquist\*, A. Shalek, B. Berger, and B. Bryson.  
*"Computational methods for single-cell RNA sequencing."*  
*Annual Review of Biomedical Data Science*, 3:1. 2020

**B. Hie\***, H. Cho\*, B. DeMeo, B. Bryson, and B. Berger.  
*"Geometric sketching compactly summarizes the single-cell transcriptomic landscape."*  
*Cell Systems*, 8:6 (cover article). 2019

**B. Hie**, B. Bryson, and B. Berger.  
*"Efficient integration of heterogeneous single-cell transcriptomes using Scanorama."*  
*Nature Biotechnology*, 37:6. 2019

A. Tehranchi, **B. Hie**, M. Dacre, I. Kaplow, K. Pettie, P. Combs, and H. Fraser.  
*"Fine-mapping cis-regulatory variants in diverse human populations."*  
*eLife*, 8:e39595. 2019

**B. Hie\***, H. Cho\*, and B. Berger.  
*"Realizing private and practical pharmacological collaboration."*  
*Science*, 362:6417. 2018

A. Tehranchi, M. Myrthil, T. Martin, **B. Hie**, D. Golan, and H. Fraser.  
*"Pooled ChIP-seq links variation in transcription factor binding to complex disease risk."*  
*Cell*, 165:3. 2016

## Conference papers

- M. Poli, A. Thomas, E. Nguyen, S. Massaroli, P. Ponnusamy, B. Deiseroth, K. Kersting, T. Suzuki, **B. Hie**, S. Ermon, C. Ré, and C. Zhang.  
*"Mechanistic design and scaling of hybrid architectures."*  
*International Conference on Machine Learning (ICML).* 2024
- C. Hsu, R. Verkuil, J. Liu, Z. Lin, **B. Hie**, T. Sercu, A. Lerer, and A. Rives.  
*"Learning inverse folding from millions of predicted structures."*  
*International Conference on Machine Learning (ICML).* 2022
- B. Hie**, E. Zhong, B. Bryson, and B. Berger.  
*"Learning mutational semantics."*  
*Neural Information Processing Systems (NeurIPS).* 2020
- B. Hie**, H. Cho, B. DeMeo, B. Bryson, and B. Berger.  
*"Geometric sketching of single-cell data preserves transcriptional structure."*  
*Research in Computational Molecular Biology (RECOMB).* 2019

## Book chapters

- K. Johnston\*, C. Fannjiang\*, B. Wittmann\*, **B. Hie\***, K. Yang\*, and Z. Wu\*.  
*"Machine learning for protein engineering."*  
*Machine Learning in Molecular Sciences, Challenges and Advances in Computational Chemistry and Physics.* Springer Nature. 2023

## Preprints

- E. Nguyen, M. Poli, M. Durrant, A. Thomas, B. Kang, J. Sullivan, M. Ng, A. Lewis, A. Patel, A. Lou, S. Ermon, S. Baccus, T. Hernandez-Boussard, C. Ré, P. Hsu<sup>†</sup>, and **B. Hie<sup>†</sup>**.  
*"Sequence modeling and design from molecular to genome scale with Evo."*  
*bioRxiv*, DOI: 10.1101/2024.02.27.582234. 2024
- V. Shanker, T. Bruun, **B. Hie<sup>†</sup>**, and P. Kim<sup>†</sup>.  
*"Inverse folding of protein complexes with a structure-informed language model enables unsupervised antibody evolution."*  
*bioRxiv*, DOI: 10.1101/2023.12.19.572475. 2023
- B. Hie\***, S. Candido\*, Z. Lin, O. Kabeli, R. Rao, N. Smetanin, T. Sercu, and A. Rives.  
*"A high-level programming language for generative protein design."*  
*bioRxiv*, DOI: 10.1101/2022.12.21.521526. 2022
- C. Itoh, C. Gunnarson, G. Babunovic, A. Nibasumba, Ngomu A., M. Wadsworth III, T. Hughes II, S. Solomon, **B. Hie**, B. Berger, A. Shalek, S. Fortune, and B. Bryson.  
*"GM-CSF differentiation of human monocytes stabilizes macrophage state via oxidative signaling."*  
*bioRxiv*, DOI: 10.1101/2020.09.29.318352. 2020

## SOFTWARE

**Evo**, Primary Developer

<https://github.com/evo-design/evo>

**Scanorama**, Primary Developer

<https://github.com/brianhie/scanorama>

**Geosketch**, Primary Developer

<https://github.com/brianhie/geosketch>

**Evolocity**, Primary Developer

<https://github.com/brianhie/evolocity>

**esm**, Contributor

<https://github.com/facebookresearch/esm>

**scverse**, Contributor

<https://github.com/scverse>

## TEACHING

**Massachusetts Institute of Technology**, Cambridge, MA

**Teaching Assistant, Algorithms for Inference (6.438)** 2019

Graduate-level course on statistical inference with probabilistic graphical models. Responsible for preparing exams/assignments, leading discussion sections, and holding office hours.

## ACADEMIC SERVICE

### Mentorship

Stanford University, Doctoral thesis research 2021-Present

University of Toronto, iGEM competition team 2021

Massachusetts Institute of Technology, Masters of Engineering thesis research 2020-2021

### Public Engagement and Science Communication

Press interviews for *Al Jazeera*, *Freethink*, *Ideas Roadshow*, *IEEE Spectrum*, *Inverse*, *MIT Technology Review*, *NSF The Discovery Files*, *Nature News*, *Nautilus*, *Quanta Magazine*, *Swiss Radio*, *Wall Street Journal*, *WebMD/Medscape*, and *Wired*

### Policy and Ethics

National Institutes of Health, *Toward an Ethical Framework for Artificial Intelligence in Biomedical and Behavioral Research*, workshop participant 2024

### Peer Review

Contributed reviews to *Bioinformatics*, *BMC Bioinformatics*, *Cell*, *Cell Systems*, *Frontiers in Genetics*, *GigaScience*, *Intelligent Systems for Molecular Biology (ISMB)*, *Journal of Molecular Biology*, *Nature*, *Nature Biotechnology*, *Nature Communications*, *Nature Methods*, *NeurIPS Workshop on Machine Learning in Structural Biology (MLSB)*, *Nucleic Acids Research*, *PLOS Computational Biology*, *PLOS ONE*, *PNAS*, *PNAS Nexus*, *Research in Computational Molecular Biology (RECOMB)*, and *Science Translational Medicine*

## PATENTS AND PATENT APPLICATIONS

**B. Hie**, V. Shanker, and P.S. Kim.

"Antibody compositions and optimization methods."

US Patent App. PCT/US23/17977. 2023

A. Thugabere Jagadeesh and <b>B. Hie</b> . <i>"Hyperspectral scanning to determine skin health."</i> US Patent No. 11,532,400.	2022
<b>B. Hie</b> , B. Berger, and H. Cho. <i>"Realizing private and practical pharmacological collaboration using a neural network architecture configured for reduced computation overhead."</i> US Patent No. 11,450,439.	2022
<b>B. Hie</b> , B. Bryson, and B. Berger. <i>"Escape profiling for therapeutic and vaccine development."</i> US Patent No. 11,011,253.	2021
H. Ma, <b>B. Hie</b> , and B. Ni. <i>"Quality control in electronic nose sensing."</i> US Patent App. 16/738,586.	2020
H. Ma, <b>B. Hie</b> , and B. Ni. <i>"Analyte classification using electronic noses."</i> US Patent App. 16/737,648.	2020

## AWARDS AND FELLOWSHIPS

STAT Wunderkinds	2022
Stanford Science Fellows Program	2021-2023
Department of Defense (DoD) National Defense Science and Engineering Graduate (NDSEG) Fellowship	2019-2021
RECOMB/National Science Foundation Travel Fellowship Award	2019
Hoefer Prize for Writing in the Major, Nominated, <i>Stanford University</i>	2016
Tau Beta Pi Engineering Honors Society	2015-Present
Lunsford Award for Oral Presentation, Nominated, <i>Stanford University</i>	2014
Boothe Prize for Excellence in Writing, Honorable Mention, <i>Stanford University</i>	2013
President's Award for Academic Achievement, <i>Stanford University</i>	2013
National Merit Scholarship Finalist	2012