

# BRIAN HIE

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## CURRENT POSITIONS

**Stanford University**, Palo Alto, CA

*Assistant Professor of Chemical Engineering*

*The Dieter Schwarz Foundation SDS Faculty Fellow, Stanford Data Science*

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

E. Nguyen*, M. Poli*, M. Durrant*, B. Kang*, D. Katrekar*, D. Li*, L. Bartie, A. Thomas, S. King, G. Brixi, J. Sullivan, M. Ng, A. Lewis, A. Lou, S. Ermon, S. Baccus, T. Hernandez-Boussard, C. Ré, P. Hsu <sup>†</sup> , and <b>B. Hie</b> <sup>†</sup> . <i>"Sequence modeling and design from molecular to genome scale with Evo."</i> <i>Science</i> , 386:6723 (cover article, featured with a Perspective by Theodoris).	2024
V. Shanker, T. Bruun, <b>B. Hie</b> <sup>†</sup> , and P. Kim <sup>†</sup> . <i>"Unsupervised evolution of protein and antibody complexes with a structure-informed language model."</i> <i>Science</i> , 385:6704.	2024
<b>B. Hie</b> <sup>†</sup> , S. Kim, T. Rando, B. Bryson <sup>†</sup> , and B. Berger <sup>†</sup> . <i>"Scanorama: integrating large and diverse single-cell transcriptomic datasets."</i> <i>Nature Protocols</i> , DOI: 10.1038/s41596-024-00991-3.	2024
S. Hendrix, Y. Mreyoud, M. McNelan, A. Smirnov, S. Chavez, <b>B. Hie</b> , M. Chamberland, T. Bradstreet, A. Webber, D. Kreamalmeyer, R. Taneja, B. Bryson, B. Edelson, and C. Stallings. <i>"BHLHE40 regulates myeloid cell polarization through IL-10-dependent and -independent mechanisms."</i> <i>Journal of Immunology</i> , 212:11.	2024
A. Winniffrith, C. Outeiral <sup>†</sup> , and <b>B. Hie</b> <sup>†</sup> . <i>"Generative artificial intelligence for de novo protein design."</i> <i>Current Opinion in Structural Biology</i> , 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*, 42:275-283 (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

G. Brixi\*, M. Durrant\*, J. Ku\*, M. Poli\*, G. Brockman, D. Chang, G. Gonzalez, S. King, D. Li, A. Merchant, M. Naghipourfar, E. Nguyen, C. Ricci-Tam, D. Romero, G. Sun, A. Taghibakshi, A. Vorontsov, B. Yang, *et al.*, D. Burke, H. Goodarzi, P. Hsu<sup>†</sup>, **B. Hie<sup>†</sup>**.  
*"Genome modeling and design across all domains of life with Evo 2."*  
*bioRxiv*, DOI: 10.1101/2025.02.18.638918. 2025

R. Shuai\*, T. Widatalla\*, P. Huang<sup>†</sup>, **B. Hie<sup>†</sup>**.  
*"Sidechain conditioning and modeling for full-atom protein sequence design with FAMPNN."*

*bioRxiv*, DOI: 10.1101/2025.02.13.637498. 2025

J. Ku, E. Nguyen, D. Romero, G. Brix, B. Yang, A. Vorontsov, A. Taghibakhshi, A. Lu, D. Burke, G. Brockman, S. Massaroli, C. Ré, P. Hsu, **B. Hie**, S. Ermon, M. Poli.  
*"Systems and algorithms for convolutional multi-hybrid language models at scale."*  
*arXiv*, DOI: 10.48550/arXiv.2503.01868. 2025

A. Merchant, S. King, E. Nguyen, **B. Hie**.  
*"Semantic mining of functional de novo genes from a genomic language model."*  
*bioRxiv*, DOI: 10.1101/2024.12.17.628962. 2024

**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. Hie**.

*"Hyperspectral scanning to determine skin health."*

US Patent No. 11,532,400. 2022

**B. Hie**, B. Berger, and H. Cho.

*"Realizing private and practical pharmacological collaboration using a neural network architecture configured for reduced computation overhead."*

US Patent No. 11,450,439. 2022

**B. Hie**, B. Bryson, and B. Berger.

*"Escape profiling for therapeutic and vaccine development."*

US Patent No. 11,011,253. 2021

H. Ma, **B. Hie**, and B. Ni.

*"Quality control in electronic nose sensing."*

US Patent App. 16/738,586. 2020

H. Ma, **B. Hie**, and B. Ni.

*"Analyte classification using electronic noses."*

US Patent App. 16/737,648. 2020

## AWARDS AND FELLOWSHIPS

Innovation Investigator, Arc Institute 2024-Present

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