

# BRIAN HIE

brianhie@stanford.edu | [github.com/brianhie](https://github.com/brianhie) | [brianhie.com](https://brianhie.com)

**Interests:** Machine learning, computational biology, protein engineering and evolution, systems biology.

## CURRENT POSITIONS

- Stanford University School of Medicine**, Palo Alto, CA  
*Stanford Science Fellow* 2021-Present
- ♦ Machine learning at the host-pathogen interface.
- Meta Platforms, Inc.**, Menlo Park, CA 2022-Present  
*Visiting Researcher, Meta AI*
- ♦ Machine learning for protein biology.

## 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

- 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.
  - ♦ Insightful and 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  
*Software Engineer, Cloud Infrastructure* 2016-2017
- ♦ Robust performance monitoring of globally distributed core application infrastructure.
- Stanford University**, Palo Alto, CA  
*Undergraduate Researcher, Biology* 2013-2016
- ♦ Statistics and machine learning for computational genomics.

**Stanford University**, Palo Alto, CA

***Undergraduate Researcher, Digital Humanities, Stanford Humanities Center*** 2016

- ♦ Graph-theoretic analysis of the social network of early modern authors and publishers.

**Microsoft Corporation**, Redmond, WA

***Software Engineering Intern, Azure Compute and Microsoft Research*** 2015

- ♦ Distributed scheduling algorithms and their impact on data center utilization and availability.

**Synaptics, Inc.**, San Jose, CA

***Systems Architecture/Algorithms Intern*** 2014

- ♦ Algorithm design and implementation for embedded touchscreen firmware.

## PUBLICATIONS

\*Equal contribution. †Corresponding author.

### Journal articles

**B. Hie**<sup>†</sup>, K.K. Yang, and P.S. Kim<sup>†</sup>.

*"Evolutionary velocity with protein language models predicts evolutionary dynamics of diverse proteins."*

*Cell Systems*, 13:4 (featured article). 2022

M.C. Maher, I. Bartha, S. Weaver, J. di Iulio, E. Ferri, L. Soriaga, F.A. Lempp, **B. Hie**, B. Bryson, B. Berger, D.L. Robertson, G. Snell, D. Corti, H.W. Virgin, S.L. 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.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 article). 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

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

## Preprints

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."*  
*bioRxiv*, DOI: 10.1101/2022.07.20.500902v2. 2022

**B. Hie**<sup>†</sup>, D. Xu, V. Shanker, T. Bruun, P. Weidenbacher, S. Tang, and P.S. Kim<sup>†</sup>.

*"Efficient evolution of human antibodies from general protein language models and sequence information alone."*  
*bioRxiv*, DOI: 10.1101/2022.04.10.487811. 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

## PATENTS

**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

## SOFTWARE

**Scanorama**, Primary Developer

<https://github.com/brianhie/scanorama>, 82k+ PyPI downloads

**Geosketch**, Primary Developer

<https://github.com/brianhie/geosketch>, 56+ PyPI downloads

**Evolocity**, Primary Developer

<https://github.com/brianhie/evolocity>, 8k+ PyPI downloads

**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*, *Nautilus*, *Quanta Magazine*, *Swiss Radio*, *Wall Street Journal*, and *Wired*

### 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 Nexus*, *Research in Computational Molecular Biology (RECOMB)*, and *Science Translational Medicine*

## AWARDS AND FELLOWSHIPS

STAT Wunderkids	2022
Stanford Science Fellows Program	2021-Present
Department of Defense (DoD) National Defense Science and Engineering Graduate (NDSEG) Fellowship	2019-2021
RECOMB/National Science Foundation Travel Fellowship Award	2019
Hofer 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