

# BRIAN HIE

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

## CURRENT POSITIONS

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

## EDUCATION

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|---|-----------|
| <b>Massachusetts Institute of Technology</b> , Cambridge, MA<br><i>Electrical Engineering and Computer Science, Doctor of Philosophy</i><br><i>Electrical Engineering and Computer Science, Master of Science</i> | 2017-2021 |
| ♦ Areas of concentration: Computational biology, machine learning, statistics.  |           |
| <b>Stanford University</b> , Palo Alto, CA<br><i>Computer Science, Bachelor of Science with Honors and Distinction</i><br><i>Minor in English Literature</i>  | 2012-2016 |
| ♦ Areas of concentration: Computational biology, computer systems, machine learning.  |           |

## PROFESSIONAL EXPERIENCE

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|---|-----------|
| <b>Massachusetts Institute of Technology</b> , Cambridge, MA<br><i>Graduate Researcher, Computer Science and Artificial Intelligence Laboratory</i> | 2017-2021 |
| ♦ Neural language modeling of viral evolution.  |           |
| ♦ Bayesian machine learning for biological discovery and design under uncertainty.  |           |
| ♦ Insightful and efficient geometric algorithms for single-cell biology.  |           |
| ♦ Cryptographically secure neural network training.   |           |
| <b>Google LLC</b> , Mountain View, CA<br><i>Artificial Intelligence/Machine Learning Resident, X – The Moonshot Factory</i>                         | 2019      |
| ♦ Machine learning for early-pipeline moonshots.  |           |
| <b>Illumina, Inc.</b> , San Diego, CA<br><i>Machine Learning Intern, Bioinformatics</i>   | 2018      |
| ♦ Statistical signal processing for genomics-based health monitoring.   |           |
| <b>Salesforce.com, Inc.</b> , San Francisco, CA<br><i>Software Engineer, Cloud Infrastructure</i>   | 2016-2017 |
| ♦ Robust performance monitoring of globally distributed core application infrastructure.  |           |
| <b>Stanford University</b> , Palo Alto, CA<br><i>Undergraduate Researcher, Hunter Fraser Laboratory, Biology</i>                                    | 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. (\*Equal contribution.)

*"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

- 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

- 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. Hsu, R. Verkuil, J. Liu, Z. Lin, **B. Hie**, T. Sercu, A. Lerer, and A. Rives.  
*"Learning inverse folding from millions of predicted structures."*  
*bioRxiv*, DOI: 10.1101/2022.04.10.487779. 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. Bryson, and B. Berger.  
*"Escape profiling for therapeutic and vaccine development."*

US Patent No. 11,011,253.	2021
H. Ma, <b>B. Hie</b> , and B. Ni. "Quality control in electronic nose sensing."	
US Patent App. 16/738,586.	2020
H. Ma, <b>B. Hie</b> , and B. Ni. "Analyte classification using electronic noses."	
US Patent App. 16/737,648.	2020
<b>B. Hie</b> , B. Berger, and H. Cho. "Realizing private and practical pharmacological collaboration."	
US Patent App. 16/235,606.	2019

## SOFTWARE

**Scanorama**, Primary Developer  
<https://github.com/brianhie/scanorama>, 64k+ PyPI downloads

**Geosketch**, Primary Developer  
<https://github.com/brianhie/geosketch>, 42k+ PyPI downloads

**Evolocity**, Primary Developer  
<https://github.com/brianhie/evolocity>, 6k+ 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*, *Swiss Radio*, 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 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

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
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