

# BRIAN HIE

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**Interests:** Machine learning, statistics, computational biology, systems biology, host-pathogen interactions.

## CURRENT POSITION

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

*Postdoctoral Fellow, Peter Kim Laboratory, Biochemistry*

2021-Present

- ♦ Machine learning at the host-pathogen interface.

## 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*

- ♦ GPA: 4.9/5.0; Areas of concentration: Computational biology, machine learning, statistics.

**Stanford University**, Palo Alto, CA

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

2012-2016

*Minor in English Literature*

- ♦ GPA: 3.9/4.0; 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.
- ♦ Bayesian 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, Hunter Fraser Laboratory, Biology*

2013-2016

- ♦ Statistics and machine learning for computational genomics, including fundamental problems involving transcription factor binding, chromatin accessibility, and circular RNA function.

**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

### Journal articles

R. Singh\*, **B. Hie\***, A. Narayan, and B. Berger. (\*Equal contribution.)

*"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. 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. (\*Equal contribution.)

*"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. (\*Equal contribution.)

*"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**, K.K. Yang, P.S. Kim.  
*"Evolutionary velocity with protein language models."*  
*bioRxiv*, DOI:10.1101/2021.06.07.447389. 2021

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

**B. Hie**, H. Cho, B. Bryson, and B. Berger.  
*"Coexpression enables multi-study cellular trajectories of development and disease."*  
*bioRxiv*, DOI: 10.1101/719088. 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. 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

**B. Hie**, 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>, 45k+ PyPI downloads

**Geosketch**, Primary Developer

<https://github.com/brianhie/geosketch>, 25k+ PyPI downloads

**Evolocity**, Primary Developer

<https://github.com/brianhie/evolocity>, 1k+ PyPI downloads

## 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

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*, *IEEE Spectrum*, *Inverse*, *NSF The Discovery Files*, *Nautilus*, *Quanta*, *Swiss Radio*, and *Wired*

### Peer Review

Contributed reviews to *Bioinformatics*, *Cell*, *Cell Systems*, *GigaScience*, *Intelligent Systems for Molecular Biology (ISMB)*, *Nature*, *Nature Biotechnology*, *Nature Methods*, *PLoS Computational Biology*, *Research in Computational Molecular Biology (RECOMB)*, and *Science Translational Medicine*

### Program Committees

NeurIPS 2020 Workshop on Machine Learning in Structural Biology

## GRANTS AND FELLOWSHIPS

Stanford Science Fellows Program 2021-2024

Department of Defense (DoD) National Defense Science and Engineering Graduate (NDSEG) Fellowship 2019-2022

## AWARDS

RECOMB/National Science Foundation Travel Fellowship Award 2019

Hofer Prize for Writing in the Major, Nominated, *Stanford University* 2016

Tau Beta Pi Engineering Honors Society 2015-Present

Lunsford Award for Oral Presentation, Nominated, *Stanford University* 2014

Boothe Prize for Excellence in Writing, Honorable Mention, *Stanford University* 2013

President's Award for Academic Achievement, *Stanford University* 2013

National Merit Scholarship Finalist 2012