

# BRIAN HIE

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

**Interests:** Machine learning, statistics, computational biology, immunology, host-pathogen interactions, drug discovery, systems biology, genomics, geometric algorithms.

## EDUCATION

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

*Electrical Engineering and Computer Science, Ph.D.* 2017-2021 (Expected)

*Electrical Engineering and Computer Science, M.S.*

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

**Stanford University**, Palo Alto, CA

*Computer Science, B.S. with Honors and Distinction* 2012-2016

*Minor in English Literature*

- ♦ GPA: 3.9/4.0; Areas of concentration: Computational biology, distributed systems, machine learning.

## PROFESSIONAL EXPERIENCE

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

*Computer Science and Artificial Intelligence Laboratory (CSAIL)* 2017-Present

- ♦ Neural language modeling of viral evolution (<https://github.com/brianhie/viral-mutation>).
- ♦ Bayesian machine learning for biological discovery and design under uncertainty (<https://github.com/brianhie/uncertainty>).
- ♦ Insightful and efficient geometric algorithms for single-cell biology (<https://github.com/brianhie/scanorama> and <https://github.com/brianhie/geosketch>).
- ♦ Cryptographically secure neural network training (<https://github.com/brianhie/secure-dti>).

**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

*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

*Shakeosphere Digital Humanities Project, 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

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

*"Learning the language of viral evolution and escape."*

*Science*, in press. 2020

**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

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

*"Metric learning enables synthesis of heterogeneous single-cell modalities."*

*bioRxiv*, DOI: 10.1101/834549. 2020

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.

*"Language modeling for viral escape prediction."*

US Patent App. 63/049,676. 2020

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>, 31k+ PyPI downloads

**Geosketch**, Primary Developer

<https://github.com/brianhie/geosketch>, 13k+ 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

### Peer Review

*Bioinformatics, Cell, Cell Systems, GigaScience, Nature Biotechnology, PLoS Computational Biology*

### Program Committee Member

NeurIPS 2020 Workshop on Machine Learning in Structural Biology

## GRANTS AND FELLOWSHIPS

### Department of Defense (DoD) National Defense Science and Engineering Graduate (NDSEG) Fellowship Program

Total Funding: \$158,400 (direct costs) 2019-2022

## AWARDS

|   |              |
|---|--------------|
| 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         |