BRIAN HIE

brianhie@mit.edu | github.com/brianhie | 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. (expected)   2017-Present

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 structure.

Stanford University, Palo Alto, CA

Shakeosphere Project, Digital Humanities   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

B. Hie, E. Zhong, B. Bryson, and B. Berger.
"Learning mutational semantics."
Conference on Neural Information Processing Systems (NeurIPS). To appear.   2020

B. Hie, B. Bryson, and B. Berger.
"Leveraging uncertainty in machine learning accelerates biological discovery and design."
Cell Systems. In press. *bioRxiv*, DOI: 10.1101/2020.08.11.247072.   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. Also appeared at RECOMB 2019.   2019

B. Hie, B. Bryson, and B. Berger.
"Efficient integration of heterogeneous single-cell transcriptomes using Scanorama."
Nature Biotechnology, 37:6.   2019

A.K. Tehranchi, **B. Hie**, M. Dacre, I.M. Kaplow, K.P. Pettie, P.A. Combs, and H.B. 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.K. Tehranchi, M. Myrthil, T. Martin, **B. Hie**, D. Golan, and H.B. Fraser.
"Pooled ChIP-seq links variation in transcription factor binding to complex disease risk."
Cell, 165:3.   2016

PREPRINTS

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

"Learning the language of viral evolution and escape."
bioRxiv, DOI: 10.1101/2020.07.08.193946.   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. Berger, and H. Cho.
"Realizing private and practical pharmacological collaboration."
US Patent App. 16/235,606.   2019

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)   2018-2021

AWARDS

RECOMB/National Science Foundation Travel Fellowship Award	2019
Hoefer 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