

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

Stanford Science Fellow

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

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.K. Pond, and A. Telenti.
"Predicting the mutational drivers of future SARS-CoV-2 variants of concern."
medRxiv, DOI: 10.1101/2021.06.21.21259286. 2021

B. Hie and K.K. Yang.
"Adaptive machine learning for protein engineering."
arXiv, [q-bio.QM] 2106.05466. 2021

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>, 48k+ PyPI downloads

Geosketch, Primary Developer

<https://github.com/brianhie/geosketch>, 29k+ PyPI downloads

Evolocity, Primary Developer

<https://github.com/brianhie/evolocity>, 2k+ 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*, *Nucleic Acids Research*, *PLOS Computational Biology*, *PLOS ONE*, *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

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, <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