

BRIAN HIE

brianhie@stanford.edu | github.com/brianhie | brianhie.com

Interests: Machine learning, algorithms, computational biology, protein engineering, systems biology.

CURRENT POSITIONS

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

EDUCATION

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

PROFESSIONAL EXPERIENCE

Massachusetts Institute of Technology , Cambridge, MA <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.	
Google LLC , Mountain View, CA <i>Artificial Intelligence/Machine Learning Resident, X – The Moonshot Factory</i>	2019
♦ Machine learning for early-pipeline moonshots.	
Illumina, Inc. , San Diego, CA <i>Machine Learning Intern, Bioinformatics</i>	2018
♦ Statistical signal processing for genomics-based health monitoring.	
Salesforce.com, Inc. , San Francisco, CA <i>Software Engineer, Cloud Infrastructure</i>	2016-2017
♦ Robust performance monitoring of globally distributed core application infrastructure.	
Stanford University , Palo Alto, CA <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[†], K.K. Yang, and P.S. Kim[†].

"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[†]**, D. Xu, V. Shanker, T. Bruun, P. Weidenbacher, S. Tang, and P.S. Kim[†].
"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. 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>, 63k+ 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 and undergraduate honors 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