

BRIAN HIE

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Interests: Machine learning, computational biology, protein engineering and evolution, systems biology.

CURRENT POSITIONS

Stanford University School of Medicine, Palo Alto, CA

Stanford Science Fellow 2021-Present

- ♦ Machine learning at the host-pathogen interface.

Meta Platforms, Inc., Menlo Park, CA

Visiting Researcher, Meta AI 2022-Present

- ♦ Machine learning for protein biology.

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

- ♦ Areas of concentration: Computational biology, machine learning, statistics.

Stanford University, Palo Alto, CA

Computer Science, Bachelor of Science with Honors and Distinction 2012-2016

English Literature, Academic Minor

- ♦ 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.
- ♦ 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.

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.

"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

- 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."
International Conference on Machine Learning (ICML). 2022
- 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

- Z. Lin*, H. Akin*, R. Rao*, **B. Hie***, Z. Zhu, W. Lu, A. dos Santos Costa, M. Fazel-Zarandi, T. Sercu, S. Candido, and A. Rives.
"Language models of protein sequences at the scale of evolution enable accurate structure prediction."
bioRxiv, DOI: 10.1101/2022.07.20.500902. 2022
- 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. 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>, 73k+ PyPI downloads

Geosketch, Primary Developer

<https://github.com/brianhie/geosketch>, 49k+ PyPI downloads

Evolocity, Primary Developer

<https://github.com/brianhie/evolocity>, 7k+ 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

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*, *Wall Street Journal*, 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