BRIAN HIE

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CURRENT POSITIONS

Stanford University, Palo Alto, CA

Principal Investigator, Laboratory of Evolutionary Design

Assistant Professor of Chemical Engineering

The Dieter Schwarz Foundation SDS Faculty Fellow, Stanford Data Science 2024-Present

Faculty Fellow, Sarafan ChEM-H

Affiliate, Institute for Human Centered Artificial Intelligence (HAI)

Member, Stanford Bio-X

- Learning from evolution to enable next-generation biological discovery.
- Accelerating evolution via programmable generative models.
- Forecasting and responding to evolution to enable safe biological AI.

Arc Institute, Palo Alto, CA

Innovation Investigator 2024-Present

- Genomic sequence modeling for biological prediction and design.

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

Stanford University School of Medicine, Palo Alto, CA

Stanford Science Fellow 2021-2023

- Machine learning at the host-pathogen interface.

Meta Platforms, Inc., Menlo Park, CA

Visiting Researcher, Meta AI FAIR 2022-2023

- Machine learning for protein biology.

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.
- 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, 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. †Co-corresponding author.

Journal articles

L.S. Mille-Fragoso*, C. Driscoll*, J. Wang*, H. Dai*, T. Widatalla*, J. Zhang*, X. Zhang, B. Rao, L. Feng, **B. Hie**†, and X. Gao†.
"Efficient generation of epitope-targeted antibodies with Germinal."
Nature Biotechnology, DOI: 10.1038/s41587-026-03187-0. 2026

G. Brixi*, M. Durrant*, J. Ku*, M. Naghipourfar*, M. Poli*, G. Sun*, G. Brockman, D. Chang, A. Fanton, G. Gonzalez, S. King, D. Li, A. Merchant, E. Nguyen, C. Ricci-Tam, D. Romero, J. Schmok, A. Taghibakshi, A. Vorontsov, B. Yang, *et al.*, D. Burke, H. Goodarzi, P. Hsu†, and **B. Hie**†.
"Genome modeling and design across all domains of life with Evo 2."
Nature, 652, 1349-1361. 2026

V. Tran, M. Nemeth, L. Bartie, S. Chandrasekaran, A. Fanton, H. Moon, **B. Hie**, S. Konermann, and P. Hsu
"Rapid directed evolution guided by protein language models and epistatic interactions."
Science, 392, eaea1820. 2026

A. Merchant, S. King, E. Nguyen, and **B. Hie**.
"Semantic design of functional de novo genes from a genomic language model."
Nature, 649:749-758. 2025

M. Filsinger Interrante, S. Tang, S. Kim, V. Shanker, **B. Hie**, T. Bruun, W. Wu, J. Pak, D. Fernandez, and P. Kim.
"Utilizing machine learning to improve neutralization potency of an HIV-1 antibody targeting the gp41 N-heptad repeat."
ACS Chemical Biology, 20:7. 2025

E. Nguyen*, M. Poli*, M. Durrant*, B. Kang*, D. Katrekar*, D. Li*, L. Bartie, A. Thomas, S. King, G. Brixi, J. Sullivan, M. Ng, A. Lewis, A. Lou, S. Ermon, S. Baccus, T. Hernandez-Boussard, C. Ré, P. Hsu†, and **B. Hie**†.
"Sequence modeling and design from molecular to genome scale with Evo."
Science, 386:6723 (cover article, featured with a Perspective by Theodoris). 2024

V. Shanker, T. Bruun, **B. Hie**†, and P. Kim†.
"Unsupervised evolution of protein and antibody complexes with a structure-informed language model."
Science, 385:6704. 2024

B. Hie†, S. Kim, T. Rando, B. Bryson†, and B. Berger†.
"Scanorama: integrating large and diverse single-cell transcriptomic datasets."
Nature Protocols, 19:2283-2297. 2024

S. Hendrix, Y. Mreyoud, M. McNelan, A. Smirnov, S. Chavez, **B. Hie**, M. Chamberland, T. Bradstreet, A. Webber, D. Kreamalmeyer, R. Taneja, B. Bryson, B. Edelson, and C. Stallings.
"BHLHE40 regulates myeloid cell polarization through IL-10-dependent and -independent mechanisms."
Journal of Immunology, 212:11. 2024

A. Winnifrith, C. Outeiral†, and **B. Hie**†.
"Generative artificial intelligence for de novo protein design."
Current Opinion in Structural Biology, 86: June 2024. 2024

B. Hie†, D. Xu, V. Shanker, T. Bruun, P. Weidenbacher, S. Tang, W. Wu., and J. Pak, and P. Kim†.
"Efficient evolution of human antibodies from general protein language models and sequence information alone."
Nature Biotechnology, 42:275-283 (featured with a News and Views by Outeiral and Deane). 2023

Z. Lin*, H. Akin*, R. Rao*, **B. Hie***, Z. Zhu, W. Lu, N. Smetanin, R. Verkuil, O. Kabeli, Y. Shmueli, A. dos Santos Costa, M. Fazel-Zarandi, T. Sercu, S. Candido, and A. Rives.
"Evolutionary-scale prediction of atomic level protein structure with a language model."
Science, 379:6637. 2023

B. Hie†, K. Yang, and P. Kim†.

"Evolutionary velocity with protein language models predicts evolutionary dynamics of diverse proteins."
Cell Systems, 13:4 (featured with a Preview by Sandhu et al.). 2022

M. Maher, I. Bartha, S. Weaver, J. di Iulio, E. Ferri, L. Soriaga, F. Lempp, **B. Hie**, B. Bryson, B. Berger, D. Robertson, G. Snell, D. Corti, H. Virgin, S. 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. 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 with a Perspective by Kim and Przytycka). 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

T. Widatalla*, R. Shuai*, **B. Hie**†, and P. Huang†.
"Sidechain conditioning and modeling for full-atom protein sequence design with FAMPNN."
International Conference on Machine Learning (ICML). 2025

M. Poli, A. Thomas, E. Nguyen, S. Massaroli, P. Ponnusamy, B. Deiseroth, K. Kersting, T. Suzuki, **B. Hie**, S. Ermon, C. Ré, and C. Zhang.
"Mechanistic design and scaling of hybrid architectures."
International Conference on Machine Learning (ICML). 2024

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

Book chapters

K. Johnston*, C. Fannjiang*, B. Wittmann*, **B. Hie***, K. Yang*, and Z. Wu*.
"Machine learning for protein engineering."
Machine Learning in Molecular Sciences, Challenges and Advances in Computational Chemistry and Physics. Springer Nature. 2023

Preprints

A. Merchant*, D. Guo*, B. Viggiano*, L. Brennan-Almaraz, E. Hur, T. Mai, P. Yin, S. King, E. Ashley, and **B. Hie**.
"A high-level programming language for generative biology with Proto."
bioRxiv, DOI: 10.64898/2026.06.22.733870. 2026

S. King, C. Driscoll, D. Li, D. Guo, A. Merchant, G. Brixi, M. Wilkinson, and **B. Hie**.
"Generative design of novel bacteriophages with a genome language model."
bioRxiv, DOI: 10.1101/2025.09.12.675911. 2025

L.S. Mille-Fragoso, J. Wang, C. Driscoll, H. Dai, T. Widatalla, X. Zhang, **B. Hie**†, and X. Gao†.
"Efficient generation of epitope-targeted de novo *antibodies with Germinal."*
bioRxiv, DOI: 10.1101/2025.09.19.677421. 2025

J. Ku, E. Nguyen, D. Romero, G. Brixi, B. Yang, A. Vorontsov, A. Taghibakhshi, A. Lu, D. Burke, G. Brockman, S. Massaroli, C. Ré, P. Hsu, **B. Hie**, S. Ermon, and M. Poli.
"Systems and algorithms for convolutional multi-hybrid language models at scale."

arXiv, DOI: 10.48550/arXiv.2503.01868. 2025

B. Hie*, S. Candido*, Z. Lin, O. Kabeli, R. Rao, N. Smetanin, T. Sercu, and A. Rives.
"A high-level programming language for generative protein design."
bioRxiv, DOI: 10.1101/2022.12.21.521526. 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

SOFTWARE

Evo 2, Primary Developer
https://github.com/arcinstitute/evo2

Evo, Primary Developer
https://github.com/evo-design/evo

Proto, Primary Developer
https://github.com/evo-design/proto-language
https://github.com/evo-design/proto-tools

Scanorama, Primary Developer
https://github.com/brianhie/scanorama

Geosketch, Primary Developer
https://github.com/brianhie/geosketch

Evolocity, Primary Developer
https://github.com/brianhie/evolocity

esm, Contributor
https://github.com/facebookresearch/esm

scverse, Contributor
https://github.com/scverse

TEACHING

Stanford University, Palo Alto, CA

Instructor, Data Science for Computational Molecular Biology (DATASCI 194B/294B) 2025-2026

Machine learning and its applications to biology. Topics include protein language modeling, protein structure prediction, molecular representation learning, Bayesian optimization, single-cell genomics, and genomic language modeling.

Instructor, Data Science and Machine Learning Approaches in Chemical and Materials Engineering (CHEMENG 177/277, MATSCI 166/176) 2025-2026

Applications of data science and machine learning approaches to modern problems in chemical, materials, and biological engineering.

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
- Stanford University, Undergraduate thesis research 2024-Present
- Stanford University, ADVANCE Undergraduate Institute 2025-Present
- University of Toronto, iGEM competition team 2021
- Massachusetts Institute of Technology, Masters of Engineering thesis research 2020-2021

Advisory Boards

- Board of Reviewing Editors, *Science* magazine

Public Engagement and Science Communication

Press interviews for *Asahi Shimbun, Freethink, Hunan Television, Ideas Roadshow, IEEE Spectrum, Inverse, Al Jazeera, Korean Broadcasting System (KBS), MIT Technology Review, Nature News, Nautilus, New York Times, Nikkei, National Public Radio (NPR), NSF The Discovery Files, Quanta Magazine, Science News*, *The Sunday Times*, *Swiss Radio, Tagesspiegel, Wall Street Journal, Washington Post, WebMD/Medscape*, and *Wired*

Policy and Ethics

- Congressional Leadership Accelerator for Biotechnology. *Biotechnology and Artificial Intelligence.* 2026
- National Academies of Sciences, Engineering, and Medicine. *The Age of AI in the Life Sciences: Benefits and Biosecurity Considerations* 2025
- National Institutes of Health. *Toward an Ethical Framework for Artificial Intelligence in Biomedical and Behavioral Research* 2024

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 Communications, Nature Genetics, Nature Methods, NeurIPS Workshop on Machine Learning in Structural Biology (MLSB), Nucleic Acids Research, PLOS Computational Biology, PLOS ONE, PNAS, PNAS Nexus, Research in Computational Molecular Biology (RECOMB), Science,* and *Science Translational Medicine*

PATENTS

B. Hie, V. Shanker, and P.S. Kim.

"Antibody compositions and optimization methods."

US Patent App. 18/854,205. 2023

A. Thugabere Jagadeesh and **B. Hie**.

"Hyperspectral scanning to determine skin health."

US Patent No. 11,532,400. 2022

B. Hie, B. Berger, and H. Cho.
"Realizing private and practical pharmacological collaboration using a neural network architecture configured for reduced computation overhead."
US Patent No. 11,450,439. 2022

B. Hie, B. Bryson, and B. Berger.
"Escape profiling for therapeutic and vaccine development."
US Patent No. 11,011,253. 2021

AWARDS AND FELLOWSHIPS

Schmidt Sciences AI2050 Early Career Fellow 2025-Present
Innovation Investigator, Arc Institute 2024-Present
STAT Wunderkinds 2022
Stanford Science Fellows Program 2021-2023
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, *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