BRIAN HIE

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CURRENT POSITIONS

Stanford University, Palo Alto, CA

Assistant Professor of Chemical Engineering and Data Science

David T. Morgenthaler II Faculty Fellow, School of Engineering 2024-Present

Arc Institute, Palo Alto, CA

Innovation Investigator 2024-Present

- Aligning biological machine learning with human good.

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

A. Winnifrith, C. Outeiral[†], and **B. Hie**[†].
"Generative artificial intelligence for de novo protein design."
Current Opinion in Structural Biology, 86: June 2024. 2023

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, DOI: 10.1038/s41587-023-01763-2 (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

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

M. Poli, A. Thomas, E. Nguyen, P. Ponnusamy, B. Deiseroth, K. Kersting, T. Suzuki, **B. Hie**,
S. Ermon, C. Ré, C. Zhang, and S. Massaroli.
"Mechanistic design and scaling of hybrid architectures."
arXiv, DOI: 10.48550/arXiv.2403.17844.   2024

E. Nguyen, M. Poli, M. Durrant, A. Thomas, B. Kang, J. Sullivan, M. Ng, A. Lewis, A. Patel,
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."
bioRxiv, DOI: 10.1101/2024.02.27.582234.   2024

V. Shanker, T. Bruun, **B. Hie**[†], and P. Kim[†].
"Inverse folding of protein complexes with a structure-informed language model enables
unsupervised antibody evolution."
bioRxiv, DOI: 10.1101/2023.12.19.572475.   2023

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

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

scverse, Contributor

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, Nature News, Nautilus, Quanta Magazine, Swiss Radio, Wall Street Journal, WebMD/Medscape*, and *Wired*

Policy and Ethics

National Institutes of Health, *Toward an Ethical Framework for Artificial Intelligence in Biomedical and Behavioral Research*, workshop participant   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 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)*, and *Science Translational Medicine*

PATENTS AND PATENT APPLICATIONS

B. Hie, V. Shanker, and P.S. Kim.
"Antibody compositions and optimization methods."
US Patent App. PCT/US23/17977.   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

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

AWARDS AND FELLOWSHIPS

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