

# BRIAN HIE

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## EDUCATION

**Massachusetts Institute of Technology**, Cambridge, MA

*Electrical Engineering and Computer Science, Ph.D. candidate* 2019-Present

*Electrical Engineering and Computer Science, M.S.* 2017-2019

- ♦ GPA: 4.9/5.0; Areas of concentration: Machine learning, algorithms, computational biology

**Stanford University**, Palo Alto, CA

*Computer Science, B.S. with Honors and Distinction* 2012-2016

*Minor in English Literature*

- ♦ GPA: 3.9/4.0; Areas of concentration: Machine learning, computational biology, distributed systems

## RESEARCH AND WORK EXPERIENCE

**Massachusetts Institute of Technology**, Cambridge, MA

*Computer Science and Artificial Intelligence Laboratory (CSAIL)* 2017-Present

- ♦ Applying novel algorithmic techniques that scale to large, high-dimensional data sets to derive better biological insight from single cell experiments (<https://github.com/brianhie/scanorama> and <https://github.com/brianhie/geosketch>).
- ♦ Achieved privacy-preserving and scalable neural network training on large, cryptographically hidden data sets, applied to drug-target interaction prediction (<https://github.com/brianhie/secure-dti>).

**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 assignments/exams, leading discussion sections, and holding office hours.

**X Development, LLC.**, Mountain View, CA

*Artificial Intelligence/Machine Learning Resident* 2019

- ♦ Machine learning for early-pipeline moonshots within Alphabet/Google.

**Illumina, Inc.**, San Diego, CA

*Machine Learning Intern* 2018

- ♦ Early stage, experimental project requiring analysis of large genomic data sets via novel unsupervised and semi-supervised statistical machine learning methods.

**Salesforce.com, Inc.**, San Francisco, CA

*Software Engineer, Cloud Infrastructure* 2016-2017

- ♦ Developed algorithms and a distributed pipeline that scaled to petabytes of system log and metric data to generate accurate key performance indicators visible to top company leadership.

**Stanford University**, Palo Alto, CA

**Hunter Fraser Laboratory, Biology**

2013-2016

- ♦ Applied machine learning methods to predict associations between transcription factor binding and gene expression.
- ♦ Used statistical methods to explore the relationship between genotype and the formation and function of circular RNAs.

**Stanford University**, Palo Alto, CA

**Shakeosphere Project, Digital Humanities**

2016

- ♦ Applied graph-theoretic algorithms to understand the evolution of social networks of early modern English authors, printers, publishers, and booksellers.

**Microsoft Corporation**, Redmond, WA

**Software Engineering Intern, Azure Compute and Microsoft Research**

2015

- ♦ Investigated different distributed scheduling algorithms and their impact on utilization and availability on a simulated Azure data center.

**Synaptics, Inc.**, San Jose, CA

**Systems Architecture/Algorithms Intern**

2014

- ♦ Developed and implemented an algorithm for optimal touchscreen finger tracking by solving the minimum weight bipartite matching problem.

## PUBLICATIONS

**B. Hie**, H. Cho, B. Bryson, and B. Berger.

*"Coexpression uncovers a unified single-cell transcriptomic landscape."*

*bioRxiv* (Preprint).

2019

**B. Hie\***, H. Cho\*, B. DeMeo, B. Bryson, and B. Berger. (\*Equal contribution.)

*"Geometric sketching of single-cell data preserves transcriptional structure."*

*Cell Systems*, 8:6.

2019

**B. Hie**, B. Bryson, and B. Berger.

*"Efficient integration of heterogeneous single-cell transcriptomes using Scanorama."*

*Nature Biotechnology*, 37:685-691.

2019

A.K. Tehranchi, **B. Hie**, M. Dacre, I.M. Kaplow, K.P. Pettie, P.A. Combs, and H.B. 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.K. Tehranchi, M. Myrthil, T. Martin, **B. Hie**, D. Golan, and H.B. Fraser.  
*"Pooled ChIP-seq links variation in transcription factor binding to complex disease risk."*  
*Cell*, 165:3. 2016

## PATENTS

**B. Hie**, B. Berger, and H. Cho.  
*"Realizing private and practical pharmacological collaboration."*  
US Patent App. 16/235,606. 2019

## AWARDS

National Defense Science and Engineering Graduate (NDSEG) Fellow	2019-Present
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