

Education

University of Washington, Seattle

Ph.D. candidate in Genome Sciences (entering class of 2014)

University of Washington, Seattle

B.S. in Bioengineering with College Honors (2012)

3.79 Departmental GPA; 3.69 Overall GPA

Research Experience

Shendure Lab of University of Washington Department of Genome Sciences

9/2014 – Present

Ph.D. Candidate

- Computational and molecular biology methods development for:
 - Scalable genetic screens of protein-coding and regulatory regions using single-cell assays as readouts.
 - Large-scale atlases of chromatin accessibility in mammalian tissues using single-cell ATAC-seq and integration with existing single-cell RNA-seq atlases.
- Contributed to methods for prediction of cell types contributing to cell-free DNA in blood plasma samples from cancer patients using changes in inferred nucleosome positioning.
- Co-developer of an interactive data visualization tool to explore spatiotemporal measurement of gene expression in developing *C. Elegans* embryos ([EPICViz](#)).

Brotman-Baty Institute Advanced Technology Lab

10/2018 – 12/2018

Consultant

- Software development for combinatorial indexing single-cell RNA-seq (sci-RNA-seq) pipeline.

10X Genomics

9/2016 – 1/2017

Consultant

- Continued software development of single-cell VDJ visualization tool described below.

10X Genomics

6/2016 – 9/2016

Computational Biology Intern

- R&D to enable co-measurement of paired expression profiles and VDJ sequences in single-cells.
- Developed interactive visualization tools using React/D3.js to explore complex single-cell VDJ datasets.
- Software development for cellranger, a distributed pipeline for single-cell RNA-seq and VDJ analysis.
- R&D support for V2 single-cell RNA-seq protocol.
- Co-developed and deployed secondary analysis toolkit for 10X single-cell RNA-seq datasets in R.

MacArthur Lab of Massachusetts General Hospital/Broad Institute of MIT and Harvard

9/2013 – 9/2014

Research Assistant

- Called and analyzed multi-nucleotide polymorphisms derived from ~65K exome sequencing samples that change variant interpretation compared to individual variants.
- Developed methods for automating detection of misannotated protein coding exons in GENCODE using metrics for evolutionary conservation, constraint in a large reference panel, and tissue expression levels.
- Developed python API to extract/refine data from Leiden Open Variation Databases.

Tekscan, Inc.

9/2012 – 1/2014

Applications Engineer

- Conducted research on new applications of force and pressure sensors.
 - Implemented algorithms to estimate shoe-size from noisy pressure sensor data.
 - Signal processing and data analysis for IMU position/angle tracking of human gait.
- Developed automated test fixtures and data-analysis scripts with MATLAB and LabVIEW.
- Provided engineering support and/or training to customers and all internal departments.

Undergraduate Research Assistant

- Online Modeling of the *In Vivo* Mechanical Properties of Soft Tissue for Robotic Surgery
 - Designed, built, and programmed electromechanical device to quantify in vivo tissue dynamics.
 - Developed Unscented Kalman Filter/signal processing using MATLAB/C++.
- Co-developed hardware and microcontroller code for haptic-enabled glove.
- Developed hardware and microcontroller code to detect peg-contact in FLS block-transfer task.

Professor Joan Sanders Lab

8/2009 – 1/2010

Undergraduate Research Assistant

- Collected/analyzed data to calibrate tri-axis piezoelectric force sensor for amputee gait analysis.
- Designed and built Plexiglas housing for patient-mounted electronics.

Publications

* co-first authorship

- José L. McFaline-Figueroa, **Andrew J. Hill**, Xiaojie Qiu, Dana Jackson, Jay Shendure, Cole Trapnell. A multiplex single-cell genetic screen identifies regulatory barriers in the continuum of the epithelial-to-mesenchymal transition. **Under review.**
- Qingbo Wang, Emma Pierce-Hoffman, Beryl B. Cummings, Konrad J. Karczewski, Jessica Alföldi, Laurent C. Francioli, Laura D. Gauthier, **Andrew J. Hill**, Anne H. O'Donnell-Luria, Genome Aggregation Database (gnomAD) Production Team, Genome Aggregation Database (gnomAD) Consortium, Daniel G. MacArthur. Landscape of multi-nucleotide variants in 125,748 human exomes and 15,708 genomes. **March 2019. bioRxiv.**
- Junyue Cao*, Malte Spielmann*, Xiaojie Qiu, Daniel M. Ibrahim, Xingfan Huang, **Andrew J. Hill**, Fan Zhang, Stefan Mundlos, Lena Christiansen, Frank J. Steemers, Cole Trapnell, Jay Shendure. The dynamic transcriptional landscape of mammalian organogenesis at single cell resolution. **February 2019. Nature** 566,496–502.
- Molly Gasperini, **Andrew J. Hill**, José L. McFaline Figueroa, Beth Martin, Cole Trapnell, Nadav Ahituv, Jay Shendure. A genome-wide framework for mapping gene regulation via cellular genetic screens. **January 2019. Cell** 176, 1-14.
- Junyue Cao, Darren A. Cusanovich, Vijay Ramani, Hannah Pliner, **Andrew Hill**, Delasa Aghamirzaie, Riza Daza, Jose McFaline, Jonathan S. Packer, Lena Christiansen, Frank J. Steemers, Cole Trapnell, Jay Shendure. Joint profiling of chromatin accessibility and transcription in ~15,000 single cells by combinatorial indexing. **August 2018. Science** 10.1126/science.aau0730.
- Darren A. Cusanovich*, **Andrew J. Hill***, Delasa Aghamirzaie, Riza M. Daza, Hannah A. Pliner, Joel B. Berletch, Galina N. Filippova, Lena Christiansen, William S. DeWitt, Choli Lee, Samuel G. Regalado, David F. Read, Frank J. Steemers, Christine M. Disteche, Cole Trapnell, Jay Shendure. A first generation atlas of in vivo mammalian chromatin accessibility at single cell resolution. **August 2018. Cell** 174, 1309–1324.
- **Andrew J Hill***, José L McFaline-Figueroa*, Lea M Starita, Molly J Gasperini, Kenneth A Matreyek, Jonathan Packer, Dana Jackson, Jay Shendure, Cole Trapnell. On the design of CRISPR-based single-cell molecular screens. **February 2018. Nature Methods** 15, 271–274.
- Xiaojie Qiu, **Andrew Hill**, Jonathan Packer, Dejun Lin, Yian Ma, Cole Trapnell. Single-cell mRNA quantification and differential analysis with Census. **January 2017. Nature Methods** 14, 309–315.
- Exome Aggregation Consortium, Monkol Lek, Konrad J Karczewski, Eric V Minikel, Kaitlin E Samocha, Eric Banks, Timothy Fennell, Anne H O'Donnell Luria, James S Ware, **Andrew J Hill**, Beryl B Cummings, Taru Tukiainen, Daniel P Birnbaum, Jack A Kosmicki, Laramie Duncan, Karol Estrada, Fengmei Zhao, James Zou, **[54 additional**

authors], Mark J Daly, Daniel G MacArthur. Combined analysis of protein-coding genetic variation in 60,706 humans. **August 2016. Nature** 536,285–291.

- Matthew W Snyder*, Martin Kircher*, **Andrew J Hill**, Riza Daza, and Jay Shendure. Cell-free DNA Comprises an *In Vivo* Nucleosome Footprint that Informs Its Tissues-Of-Origin. **January 2016. Cell**, 164(1-2), 57–68.
- Xinxian Deng*, Wenxiu Ma*, Vijay Ramani, **Andrew Hill**, Fan Yang, Ferhat Ay, Joel B. Berletch, Carl Anthony Blau, Jay Shendure, Zhijun Duan, William S. Noble, and Christine M. Disteche. Bipartite structure of the inactive mouse X chromosome. **August 2015. Genome Biology**, 16:152.

Selected Awards and Honors

- National Science Foundation Graduate Research Fellowship (5 year fellowship, 3 years funding)
- Mary Gates Research Scholarship
- USA Gymnastics Men’s Program Scholarship
- 4-time USA Gymnastics Junior Olympic National Championships Competitor
- Friends of Gymnastics Scholarship

Invited Talks

- *High-throughput molecular profiling of single cells with combinatorial indexing*. 2018 GECCO Investigator Meeting.
- *Expanding the scope of genetic screens with single-cell genomics*. Advanced Genomic Technology Development Grantee Meeting. May 2017.
- *Phased annotation of protein-coding variants across 60,706 human exomes*. 65th Annual Meeting of The American Society of Human Genetics. October 2015.
- *Pseudotemporal ordering of cells undergoing immune stimulation and perturbations to cell-cell signaling*. Genome Training Grant Symposium invited trainee speaker. July, 2015.
- *Calibration and Synchronized Data Acquisition for High-Speed Applications*. Tekscan North American Distributor Meeting. Boston, MA. April, 2013.
- *Online Modeling of the In Vivo Mechanical Properties of Soft Tissue for Robotic Surgery*. University of Washington Mary Gates Undergraduate Research Symposium. May 2012.

Selected Coursework

Data Visualization (CSE 512)	Applied Biostatistics I/II (BIOSTAT 514/517)	Linear algebra/Diff. Equations
Embedded Microcomputer Systems (EE 472)	Digital Signal Processing	Computational Molecular Biology

Independent Coursework

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| – Machine Learning | Coursera (Stanford) |
| – Algorithms Design and Analysis – Part 1 | Coursera (Stanford) |
| – Circuits and Electronics | MIT Open Courseware |
| – Manual Machining and Layout (Mill and Lathe) | Artisan’s Asylum |

Other Skills

- **Computing:** Python, R, bash, parallel computing with SGE/LSF, various workflow management tools, Java, MATLAB
- **Web Development:** HTML, CSS, JavaScript, D3.js, React.js

Coaching and Teaching Experience

Genome Science 466: Cancer Genetics <i>Teaching Assistant</i>	Winter 2018
Genome Sciences 361: Fundamentals of Genetics and Genomics <i>Teaching Assistant</i>	Autumn 2016
iD Tech Camps <i>Summer Camp Instructor: Programming in Java and Adventures in Robotics</i>	Summer 2012
UW Bioengineering Department Circuitry Workshops <i>Volunteer Instructor</i>	Winter 2012
UW Bioengineering Outreach Program <i>Ultrasound Education Module Co-Developer and Instructor</i>	12/2011 – 6/2012
United States Gymnastics Training Camps <i>Counselor and Coach</i>	Summers 2005 – 2010

Leadership Experience and Activities

Dana-Farber Cancer Institute, Brigham and Women's Hospital <i>Volunteer – Kraft Family Blood Donor Center</i>	9/2012 – 4/2013
UW Biomedical Engineering Society <i>Vice President and Webmaster</i>	6/2011 – 6/2012
UW Honors Department <i>Peer Mentor</i>	9/2008 – 9/2009
Washington Men's Gymnastics Team <i>Team Member</i>	8/2008 – 10/2009

Study Abroad

– Creative Travel Writing and Sustainability in Ecuador	Summer 2010
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