

## Education

### University of Washington, Seattle

Ph.D. in Genome Sciences (2019)

### University of Washington, Seattle

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

## Research Experience

### Infinimmune

*Scientist (Computational Biology)*

12/2023 - Present

### Tune Therapeutics

*Senior Computational Biologist*

05/2022 – 08/2023

- Led planning, library design, and/or analysis for numerous types of pooled screens
  - o Scanning tiles of genes in search of new effectors for use in epigenetic editing systems
  - o Pooled screening of potential DNA binding protein designs
  - o CRISPRa and CRISPRi screens in non-trivial systems such as primary T-cells and iPSCs, both in the context of bulk screens and single-cell RNA-seq readouts and multiple delivery modalities
- Developed general pipeline (rust/python) for processing, QC, and differential count testing in the context of pooled screens. Developed R package for easy querying and visualization of screening data. Mentored junior employee throughout development of a Shiny app for browsing of screen results.
- Led planning, pipeline development, and analysis for projects using single-cell assays such as single-cell RNA-seq and Gene Expression Flex as well as bulk RNA-seq, ATAC-seq, methyl-seq, CHIP-seq, Cut&Run, and SELEX.
- Second computational biologist at company and have helped to expand our team, provide technical guidance, and integrate our group into project teams throughout the company.

### 10x Genomics

*Senior Computational Biologist*

10/2021 – 04/2022

*Computational Biologist II*

08/2019 – 10/2021

- Led a team of three as computational biology lead for Gene Expression Flex (formerly Fixed RNA Profiling) product, a high throughput probe-based assay for *in situ* single-cell gene expression and antibody measurements.
  - o Iterated on and finalized designs for whole transcriptome panel of RNA-templated ligation probes, led software development for customer facing software product, and led pipeline development and bespoke analyses internally to enable rapid and robust iteration.
  - o Substantial contributions to ideas around novel uses of RNA-templated ligation, workflow optimizations, alternate schemes for sample multiplexing, and product configurations.
- Led RNA-templated ligation probe design for Spatial Gene Expression for FFPE product and contributed to early work on equivalent designs for Xenium In Situ platform.
- Team member for targeted gene expression product, primarily contributing to hybrid capture bait design and a custom panel design tool offered on 10x Cloud.
- Computational biology lead for early stages of Chromium X and low/high throughput kit development, primarily modeling of various product configurations.

**Shendure Lab of University of Washington Department of Genome Sciences**

09/2014 – 08/2019

**Graduate Student**

- 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**

6/2016 – 01/2016

**Computational Biology Intern → Consultant**

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 gene expression and VDJ analysis.
- R&D support for V2 Chromium single-cell gene expression assay.
- Co-developed and deployed secondary analysis toolkit for 10X single-cell gene expression datasets in R.

**MacArthur Lab of MGH/Broad Institute of MIT and Harvard**

09/2013 – 09/2014

**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.**

09/2012 – 01/2014

**Applications Engineer**

- Conducted research on new applications of force and pressure sensors.
  - Implemented algorithms to estimate foot 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.

**UW Biorobotics Lab (Professors Blake Hannaford and Howard Chizeck)**

01/2010 – 06/2012

**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**

08/2009 – 01/2010

**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, Sanjay Srivatsan, **Andrew J. Hill**, Molly Gasperini, Dana L. Jackson, Lauren Saunders, Silvia Domcke, Samuel G. Regalado, Paul Lazarchuck, Sarai Alvarez, Raymond J. Monnat Jr, Jay Shendure, Cole Trapnell. Multiplex single-cell chemical genomics reveals the kinase dependence of the response to targeted therapy. **March 2023. bioRxiv.**
- Amanda Janesick, Robert Shelansky, Andrew D. Gottscho, Florian Wagner, Morgane Rouault, Ghezel Beliakoff, Michelli Faria de Oliveira, Andrew Kohlway, Jawad Abousoud, Carolyn A. Morrison, Tingsheng Yu Drennon, Seayar H. Mohabbat, Stephen R. Williams, **10x Development Teams**, and Sarah E.B. Taylor. High resolution mapping of the breast cancer tumor microenvironment using integrated single cell, spatial, and in situ analysis of FFPE tissue. **November 2022. bioRxiv.**
- Silvia Domcke\*, **Andrew J. Hill\***, Riza M. Daza\*, Junyue Cao, Diana R. O'Day, Hannah A. Pliner, Kimberly A. Aldinger, Dmitry Pokholok, Fan Zhang, Jennifer H. Milbank, Michael A. Zager, Ian A. Glass, Frank J. Steemers, Dan Doherty, Cole Trapnell, Darren A. Cusanovich, Jay Shendure. A human Cell Atlas of Fetal Chromatin Accessibility. **November 2020. Science** 370, eaba7612.
- 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. **September 2019. Nature Genetics** 51, 1389–1398.
- 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** 361, 1380-1385.
- 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 Presentations

- [Poster] *High sensitivity single cell RNA profiling of fixed cells via in situ RNA-templated ligation*. 2022 Advances in Genome Biology and Technology (ABGT) meeting.
- *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*. 65<sup>th</sup> 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 Skills

- **Computing:** Python, R, rust, bash, fish, parallel computing with SGE/LSF, various workflow languages. Git/github for source control, code review, and testing. Experience using AWS services such as EC2, S3, FSX Lustre, and batch. Statistics and probability, simulations. Some experience with TensorFlow, sklearn, and other tools for machine learning. Past experience with Java, MATLAB, and LabVIEW.
- **Molecular Biology:** experience in wet and dry lab with NGS assays, single-cell genomic technologies, spatial transcriptomics technologies, cloning of single constructs and libraries, CRISPR screens, various delivery modalities such as lentivirus, tissue culture, etc.

- **Web Development:** Some past experience with HTML, CSS, JavaScript, D3, React Statistics and probability, simulations. Some experience with TensorFlow, sklearn, and other tools for machine learning. Past experience with Java, MATLAB, and LabVIEW.

## Selected Coursework (University of Washington)

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    |

## Coaching and Teaching Experience

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|---|---------------------|
| <b>Genome Science 466: Cancer Genetics</b>                                    | Winter 2018         |
| <i>Teaching Assistant</i>   |                     |
| <b>Genome Sciences 361: Fundamentals of Genetics and Genomics</b>             | Autumn 2016         |
| <i>Teaching Assistant</i>   |                     |
| <b>iD Tech Camps</b>  | Summer 2012         |
| <i>Summer Camp Instructor: Programming in Java and Adventures in Robotics</i> |                     |
| <b>UW Bioengineering Department Circuitry Workshops</b>                       | Winter 2012         |
| <i>Volunteer Instructor</i>   |                     |
| <b>UW Bioengineering Outreach Program</b>                                     | 12/2011 – 06/2012   |
| <i>Ultrasound Education Module Co-Developer and Instructor</i>                |                     |
| <b>United States Gymnastics Training Camps</b>                                | Summers 2005 – 2010 |
| <i>Counselor and Coach</i>  |                     |

## Leadership Experience and Activities

**Dana-Farber Cancer Institute, Brigham and Women's Hospital**  
*Volunteer – Kraft Family Blood Donor Center*

09/2012 – 04/2013

**UW Biomedical Engineering**  
*Society Vice President and*

06/2011 – 06/2012

**UW Honors Department**  
*Peer Mentor*

09/2008 – 09/2009

**Washington Men's Gymnastics Team**  
*Team Member*

08/2008 – 10/2009

## Study Abroad

- Creative Travel Writing and Sustainability in Ecuador

Summer 2010