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

10X Genomics 9/2016 – 1/2017

Consultant

Software development for single-cell VDJ product.

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.

Shendure Lab of University of Washington Department of Genome Sciences *Ph.D. Candidate*

9/2014 – Present

- 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).

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.

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

8/2009 – 1/2010

- 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
 - Molly Gasperini, Andrew J. Hill, José L. McFaline Figueroa, Beth Martin, Cole Trapnell, Nadav Ahituv, Jay Shendure. crisprQTL mapping as a genome-wide association framework for cellular genetic screens. Biorxiv 2018. http://dx.doi.org/10.1101/314344
 - 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

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

Skills

- Computing: Python, R, bash, Java, MATLAB, parallel computing with SGE/LSF, LabVIEW
- Web Development: HTML, CSS, JavaScript, D3.js, React.js
- Operating Systems: Mac OSX, Linux, Windows
- Embedded Systems: ARM and Arduino embedded system programming
- Machining: CNC mill, lathe, band-saw, drill-press, various hand tools

Coaching and Teaching Experience

Genome Science 466: Cancer Genetics Winter 2018

Teaching Assistant

Genome Sciences 361: Fundamentals of Genetics and Genomics

Autumn 2016

Teaching Assistant

Summer 2012

iD Tech Camps
Summer Camp Instructor: Programming in Java and Adventures in Robotics

UW Bioengineering Department Circuitry Workshops Winter 2012

Volunteer Instructor

UW Bioengineering Outreach Program 12/2011 – 6/2012

Ultrasound Education Module Co-Developer and Instructor

United States Gymnastics Training CampsSummers 2005 – 2010

Counselor and Coach

Leadership Experience and Activities

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

Study Abroad

Creative Travel Writing and Sustainability in Ecuador
 Summer 2010