Lincoln J. Harris

Curriculum Vitae

499 Illinois St
San Francisco, CA 94158
✉ lincoln.harris@czbiohub.org
⊕ lincoln-harris

Last Updated: November 15, 2019

Aspiring computational biologist with strong interests in big data, disease evolution and genomics, teaching, and open source code/science

Education

2017 **B.A., Biology**, *Swarthmore College*, Swarthmore, PA.

Experience

2017– **Chan Zuckerberg Biohub**, *Spyros Darmanis Laboratory*, San Francisco, CA, Research
Present Associate II.

Investigated large biological datasets with a variety of tools including Docker, Python (`pandas, SciPy, Matplotlib, scikit-learn`), AWS, and workflow management systems such as Reflow. Worked as part of a collaborative team in a fast-paced, cutting-edge scientific environment.

Projects:
- Built a software tool for fast and memory-efficient summarizing of vcf (variant calling format) file entries following a sequencing experiment (`https://github.com/czbiohub/cerebra`)
- Identified mutations in single-cell RNA-seq patient samples as part of a larger effort to better characterize changes in the lung tumor microenvironment across disease progression. In collaboration with the Bivona lab of UCSF, manuscript submitted to *Cell*
- Investigated the gene expression and alternate splicing dynamics of neuroendocrine cells in the developing lung, in collaboration with the Christin Kuo lab of Stanford

2016–2017 **Brad Davidson Laboratory**, *Swarthmore College Biology Department*, Swarthmore, PA, Computational Biology Research Assistant.

Assembled the genome and embryonic transcriptome of *Corella Inflata* (sea squirt). Helped construct an improved phylogenetic tree for the *Tunicate* subphylum, in collaboration with the Joe Ryan Lab of the University of Florida Whitney Marine Station

Research Training

2015–2016 **Nick Kaplinsky Laboratory**, *Swarthmore College*, Swarthmore, PA.

Developed web-based pipelines for differential gene expression tests in RNA-seq samples

2013–2014 **Evan Vosburgh Laboratory**, *Cancer Institute of New Jersey*, New Brunswick, NJ.

Investigated the effects of several cancer drugs on expression of key oncogenes, in cell culture.

Honors and Awards

2019 NSF Graduate Research Fellowship Program – *Applicant*

2016 – Sigma Xi National Science Honors Society
Present

Publications

Articles

[1] Maynard A, McCoach C, Rotow J*, **Harris L***, Darmanis S, Blakely C, Bivona T, et al. Heterogeneity and targeted therapy-induced adaptations in lung cancer revealed by single-cell RNA-seq. *submitted to Cell*, 2019.
*These authors contributed equally to this work.

[2] DeBiasse M, Colgan W, **Harris L**, Ryan J, and Davidson B. The genome of Corella inflata and phylogeny of Tunicata. *submitted to Molecular Biology and Evolution*, 2019.

[3] **Harris L**, Vanheusden R, and Darmanis S. Cerebra: a tool for high-throughput variant call processing. *manuscript in preparation*, 2019.

[4] **The Tabula Muris Consortium**. The murine transcriptome reveals global aging nodes with organ-specific phase and amplitude. *bioRxiv*, 2019.

Conference Posters

[1] **Harris L**, Maynard A, McCoach C, Rotow J, , Darmanis S, Blakely C, Bivona T, et al. Single-cell characterization of the tumor microenvironment in advanced stage Lung Adenocarcinoma. In *Chan Zuckerberg Biohub Inter-lab Confab*, San Francisco, CA, October 2018.

[2] **Harris L**, Schug J, Kaplinsky N, and Davidson B. Towards an assembled genome and transcriptome of *Corella Inflata*. In *Sigma Xi National Honor Society Student Research Showcase*, Swarthmore, PA, October 2016.

[3] **Harris L**, Vanheusden R, and Darmanis S. Cerebra: a new tool for high-throughput variant call processing. In *Algorithms and models for Single-cell genomics*, Irvine, CA, June 2019.

Talks

* indicates invited talk

2019 **New methods for high-throughput variant call processing**, *Beyond the Cell Atlas Conference*, Berkeley, CA*.

2018 **Single-cell characterization of cancer hallmarks in advanced stage Lung Adenocarcinoma**, *Chan Zuckerberg Biohub Internal Seminar Series*, San Francisco, CA.

2017 **The genome and embryonic transcriptome of *Corella Inflata***, *Undergraduate Biology Department Research Symposium*, Swarthmore College, Swarthmore, PA.

Software

cerebra Performs high-throughput summarizing of vcf entries following a sequencing experiment.
`https://github.com/czbiohub/cerebra` (16 stars on GitHub)

motifScan Scans an enhancer region for putative transcription factor binding sites.
`https://github.com/lincoln-harris/motifScan`

Teaching, Leadership and Interests

2016–2017 **Instructor**, *Cupcakes and Coding*, Chan Zuckerberg Biohub, San Francisco, CA.
Volunteer instructor at weekly beginner-friendly coding sessions

2016–2017 **Co-host**, *Tactical Chunder*, WSRN Radio Station, Swarthmore, PA.
Co-hosted a popular weekly radio program for two semesters

2016–2017 **Volunteer Instructor**, *Youth Swim Lessons*, Swarthmore, PA.
Taught bi-weekly swim lessons for children ages 5-12

2016 **Student teacher**, *Swarthmore Rutledge Elementary School*, Swarthmore, PA.
Taught science lessons for 5th grade students at a local elementary school

2013–2017 **Member**, *Swarthmore College Swim Team*, Swarthmore, PA.
Four-year varsity team member of a Division III swim program

2012–2013 **Captain**, *South Brunswick High School Swim Team*, South Brunswick, NJ.
Lead varsity team to a dual-meet record of 6-4

Mentees

2019 **Rohan Vanheusden**, *Nueva High School*, San Mateo, CA, High School Student.