

Benjamin D. Harris

Summary Statement

I am a computational biologist interested in genetics, transcriptomics, and development. My goal is to join a dynamic team solving challenging problems in biology. I have led projects studying the functional landscape of neurons (Harris et al 2021) and the developmental trajectory of hematopoiesis (in preparation). I made significant contributions to a collaboration studying maize meristem development (Xu et al 2021) and published software central to all of the above projects (Fisher et al 2021). I specialize in applying traditional statistical and machine learning methods in a robust meta-analytic framework. I use parallel, distributed, and GPU computing to process and analyze large scale genomics data.

Education

- 2017–2021 **PhD**, *Cold Spring Harbor Laboratory (CSHL)*, Cold Spring Harbor, NY, Biological Sciences.
- 2013–2017 **Bachelors of Arts**, *Colgate University*, Hamilton, NY, *Computer Science, Biology*. Biology Honors, Computer Science Honors, Cum Laude, Upsilon Pi Epsilon (CS honors society), Beta Beta Beta (Biology honors society), Christopher Oberheim Memorial Award (Biology research award)

Research Experience

- 2018–Present **PhD Thesis Research**, *Gillis Lab*, CSHL.
My research focuses on applying meta-analytic statistical methods to large-scale single-cell RNA-sequencing datasets in order to generate a robust representation of the functional space that defines cell types.
- 2016–2017 **Summer Intern**, *Atwal Lab*, CSHL.
I analyzed RNA-sequencing data from the Genome Tissue Expression (GTEx) database and The Cancer Genome Atlas (TCGA) to classify cancer-testis antigens that could be used as cancer vaccines.
- 2015 **Summer Intern**, *Sobie Lab*, Icahn School of Medicine.
I modeled parameters for ion channels involved in drug-induced cardiac arrhythmia using a Hodgkin-Huxley model and CUDA GPU computing.
- 2012–2014 **Summer Intern**, *Simonds Lab*, National Institute of Diabetes, Digestive Diseases and Kidneys.
I studied the role of G protein coupled receptors in neuroendocrine signaling in mice and drosophila using CRISPR and behavioral assays

Relevant Skills

I have been programming for 10 years. The past six of those have been primarily focused on bioinformatics and computational biology. For the past four years, I have been programming in Python, Bash and R daily, and consider myself an expert in all 3. I have at least 8 months of regular work in each of the remaining languages. *All skills with expert knowledge are in italics* and ordered by level of expertise.

Programming Languages, *Python, Bash, R, C, C++, Java, Matlab.*

Bioinformatics Software, *Scanpy, Seurat, Monocle, STAR, DESeq2, SRA-toolkit, Samtools* (this is a non-exhaustive list).

Other Software, *Seaborn + Matplotlib, Numpy/Scipy/Pandas, Conda, UGE/SGE, GNU parallel, tidyverse, Sklearn, Git, tidyverse, Linux, Snakemake, Shiny, CUDA.*

5A Aberdeen Drive
Huntington, NY 11743
United States
✉ bdharris17 at gmail.com

Major Publications

Harris, Benjamin D., Megan Crow, Stephan Fischer, and Jesse Gillis. Single-cell co-expression analysis reveals that transcriptional modules are shared across cell types in the brain. *Cell Systems*, 2021

Harris, Benjamin D. and Jesse Gillis. A Meta-Analytic Atlas of Mouse Hematopoietic Development. *In Preparation*, 2021

Stephan Fischer, Megan Crow, **Harris, Benjamin D.**, and Jesse Gillis. Scaling up reproducible research for single cell transcriptomics using MetaNeighbor. *Nature Protocols (In press)*, 2021

Xiaosa Xu, Megan Crow, Brian R. Rice, Forrest Li, **Harris, Benjamin** ..., Jesse Gillis, and David Jackson. Single-cell RNA sequencing of developing maize ears facilitates functional analysis and trait candidate gene discovery. *Developmental Cell*, 56(4):557–568.e6, 2021

Presentations

2020 **Multiscale Co-Expression in the Brain**, *Oral Presentation*, Intelligent Systems for Molecular Biology Network Biology COSI.

2020 **Multiscale Co-Expression in the Brain**, *Poster*, Biology of Genomes.

2019 **Methods and Statistics for Differential Co-expression in scRNAseq**, *Poster*, Single Cell Analysis.

Outreach and Service

2021 **Research Mentor**, *CSHL Undergraduate Research Program*.

2019, 2021 **Lecturer**, *CSHL Undergraduate Research Program Programming Bootcamp*.

2020-Present **Co-organizer**, *Programming Skills Seminar Series*, CSHL Quantitative Biology Department.

2019-Present **Graduate Student Representative**, *Cold Spring Harbor Laboratory Sustainability Committee*.

2019 **Graduate School Programming Bootcamp**, *CSHL*, 2 Lectures Taught.

Other Publications

Toby P. Aicher, Dániel L. Barabási, **Harris, Benjamin D.**, Ajay Nadig, and Kaitlin L. Williams. Ten simple rules for getting the most out of a summer laboratory internship. *PLOS Computational Biology*, 2017

Mritunjay Pandey, Jian-Hua Zhang, Santosh K. Mishra, Poorni R. Adikaram, Mark A. **Harris, Benjamin**, ..., and William F. Simonds. A central role for R7bp in the regulation of itch sensation. *PAIN*, 2017

Jian-Hua Zhang, Mritunjay Pandey, John F. Kahler, Anna Loshakov, **Harris, Benjamin**, Pradeep K. Dagur, Yin-Yuan Mo, and William F. Simonds. Improving the specificity and efficacy of CRISPR/CAS9 and gRNA through target specific DNA reporter. *Journal of Biotechnology*, 189(Science 337 2012):1–8, 2014