

LOGAN BLAINE

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SUMMARY

Ph.D. candidate in Biomedical Informatics at Harvard Medical School using machine learning and statistics to infer causal biological mechanisms from large-scale single-cell perturbation experiments

SKILLS

- Designing and training large-scale machine learning models with PyTorch and Lightning
- Implementing probabilistic models for single-cell and perturbational data using Pyro and scvi-tools
- Understanding theory and implementation details behind state-of-the-art ML / AI approaches and architectures, e.g. language models (attention), diffusion, flow matching, graph neural networks, VAEs
- Implementing reproducible workflows for single-cell and multiomic data analysis in Python and R
- Contributing to open-source software with good software development practices (git, GitHub)
- Creating web-based dashboard applications for scientific data using Streamlit and Shiny
- Building cross-platform bioinformatics pipelines using Nextflow and Snakemake
- Basic biology and chemistry laboratory techniques

EDUCATION

Harvard Medical School

Boston, MA

Ph.D. student in Bioinformatics and Integrative Genomics

Sep. 2020–Dec. 2026 (Expected)

DISSERTATION ADVISOR: Luca Pinello

Princeton University

Princeton, NJ

A.B. in Molecular Biology, *magna cum laude*

2014–2018

SENIOR THESIS: "The relationship between epistasis and clustering of amino acid substitutions under simulated purifying selection"

CERTIFICATES: Applications of Computing, Quantitative and Computational Biology

RESEARCH

Harvard Medical School

Cambridge, MA

Graduate Student Researcher

2022 – Present

ADVISOR: Luca Pinello

- Developed PerTurbo: a scalable Bayesian analysis framework for large-scale Perturb-seq screens
 - GPU-accelerated implementation of probabilistic model using PyTorch, Pyro, Lightning
- Co-led construction of a Nextflow pipeline for analyzing single-cell CRISPR screen data within the IGVF consortium CRISPR Focus Group
- Refined computational strategies for single-cell lineage tracing analysis using mitochondrial mutations

Harvard University

Cambridge, MA

Rotation Student

Summer 2021

ADVISOR: Jason Buenrostro

- Piloted use of mitochondrial mutations for lineage tracing in SHARE-seq single-cell multiomic data from cultured hematopoietic stem cells

Harvard Medical School

Boston, MA

Rotation Student

Spring 2020

ADVISOR: Shamil Sunyaev

- Improved methods for prioritizing *de novo* coding variants from the Undiagnosed Diseases Network (UDN) cohort by integrating a new mutation rate model with existing variant annotations.

Dana-Farber Cancer Institute

Boston, MA

Associate Computational Biologist

2018–2020

ADVISOR: David Pellman CO-ADVISOR: Cheng-Zhong Zhang

- Created in-house Snakemake pipelines for calling copy number variants, structural variants, and single nucleotide variants from single cell whole genome sequencing data
- Formulated a statistical approach (hidden Markov model) to accurately detect haplotype-specific loss of heterozygosity in single cells with chromothripsis
- Wrote an efficient variant caller to sensitively identify single-stranded mutations from raw reads from "bottleneck" duplex sequencing experiments

Princeton University

Princeton, NJ

Undergraduate Research Assistant

2016–2018

ADVISOR: Peter Andolfatto

- Implemented a simulation framework based on the FoldX software package to perform *in silico* simulations of protein evolution under physicochemical constraint

Princeton University

Princeton, NJ

Summer Undergraduate Research Assistant

Summer 2015

ADVISOR: Martin Semmelhack

- Synthesized a solvatochromic fluorophore probe covalently linked to the autoinducing peptide AI-2 from *Staphylococcus aureus* to study bacterial quorum sensing

TEACHING

Teaching Fellow, Harvard Medical School, Biomedical Web Apps with R/Python Shiny (BMI 709) Spring 2026

Teaching Fellow, Harvard Medical School, Foundations of Biomedical Informatics I (BMI 701) Fall 2023

Teaching Fellow, Harvard Medical School, Concepts in Genome Analysis (BMIF 201) Fall 2021

Undergraduate Teaching Assistant, Princeton University, Organic Chemistry II with Biological Emphasis (CHM304B) Spring 2016 – 2017

Undergraduate Teaching Assistant, Princeton University, Organic Chemistry I (CHM303) Fall 2015 – 2017

PUBLICATIONS & MANUSCRIPTS

Blaine L.,* Liu J,* Ryu J, Ferreira L, Jankowiak M, Heinig M, Pinello L. A scalable Bayesian analysis method for large single cell CRISPR screens. *In preparation*. 2026.

Ferreira DaSilva, L.*, **Blaine, L.***, Jiang, E., Barrera, A., Nzima, M., Whaling, I., Barry, T., Che, E., Kyle, A., Becerra, B., Rai, R., Gschwind, A., Pushkarev, O., Geraghty, S., Raghavan, S., Cowart, T., Vinh, Q., Park, C., Boeshaghi, S., Yi, S. S., Sherwood, R., Hitz, B., Bauer, D., Gersbach, C., Hon, G., Engreitz, J., Katsevich, E., Pinello, L. A unified end-to-end pipeline for reproducibility analysis of consortium -scale single-cell CRISPR screen datasets. *In preparation*. 2026.

Papathanasiou S, Markoulaki S, **Blaine L.**, Leibowitz ML, Zhang C-Z, Jaenisch R, et al. Whole chromosome loss and genomic instability in mouse embryos after CRISPR-Cas9 genome editing. *Nat Commun*. 2021; 12: 5855.

Leibowitz ML, Papathanasiou S, Doerfler PA, **Blaine L.**, Sun L, Yao Y, et al. Chromothripsis as an on-target consequence of CRISPR-Cas9 genome editing. *Nat Genet*. 2021; 53: 895–905.

Umbreit NT, Zhang C-Z, Lynch LD, **Blaine L.**, Cheng AM, Tourdot R, et al. Mechanisms generating cancer genome complexity from a single cell division error. *Science*. 2020; 368.

PRESENTATIONS

Arc Institute scverse Satellite Workshop – Workshop Presentation	November 2025
scverse Conference 2025 – Abstract Talk	November 2025
American Society of Human Genetics (ASHG) Annual Meeting – Platform Talk	October 2025
STATGEN 2024 Conference, Pittsburgh, PA – Platform Talk	May 2024
Cell Circuits and Epigenomics Seminar, Broad Insitute, Cambridge, MA – Presenter	May 2024

HONORS AND AWARDS

Ruth L. Kirschstein Predoctoral Individual National Research Service Award (F31),	2024–2026
Sigma Xi Scientific Research Honor Society Nominee, Princeton University	2018
Summer Undergraduate Research Fellow in Chemistry (SURF-C), Princeton University	2015

EXTRACURRICULARS

Harvard Biotech Club Crossover Program	Fall–Winter 2025
Harvard GSAS Business Club Mini-MBA Program	Summer 2025
Bioinformatics and Integrative Genomics (BIG) Student Committee, Founding Member	2021–2022
Princeton University Cycling Club, President	2016–2017