

# LOGAN BLAINE

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## EDUCATION

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**Harvard Medical School** Boston, MA  
Ph.D. student in Bioinformatics and Integrative Genomics 2020–2026 (Expected)

DISSERTATION ADVISOR: Luca Pinello

RESEARCH INTERESTS: Single cell genomics, functional genomics, Bayesian inference, deep learning

**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

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**Harvard Medical School** Cambridge, MA  
Graduate Student Researcher 2022 – Present  
ADVISOR: Luca Pinello

- Designing statistical methods and deep learning models for the analysis of optical pooled screens
- Developing software to identify differentiation trajectories from single cell ATAC-seq data by using mitochondrial variants as a source of lineage information

**Harvard University** Cambridge, MA  
Rotation Student Summer 2021  
ADVISOR: Jason Buenrostro

- Demonstrated feasibility of mitochondrial lineage tracing in SHARE-seq (single cell RNA-seq + ATAC-seq) data from cultured hematopoietic stem cells

**Harvard Medical School** Boston, MA  
Rotation Student Spring 2020  
ADVISOR: Shamil Sunyaev

- Re-analyzed *de novo* coding variants from the Undiagnosed Diseases Network (UDN) cohort using an in-house mutational model to test for genes with higher than expected mutation load

**Dana-Farber Cancer Institute** Boston, MA  
Associate Computational Biologist 2018–2020  
ADVISOR: David Pellman CO-ADVISOR: Cheng-Zhong Zhang

- Improved in-house pipelines for calling copy number variants, structural variants, and single nucleotide variants from single cell whole genome sequencing data
- Designed a Hidden Markov Model to detect haplotype-specific loss of heterozygosity in single cells with chromothripsis
- Wrote a variant caller to sensitively identify single-stranded mutations from "bottleneck" duplex sequencing experiments

**Princeton University** Princeton, NJ  
Undergraduate Research Assistant 2016–2018  
ADVISOR: Peter Andolfatto

- Devised a simulation framework using FoldX to perform *in silico* simulations of protein evolution under physicochemical constraint
- Formulated statistical tests to determine if epistasis is responsible for spatially autocorrelated amino acid substitutions

## Princeton University

Summer Undergraduate Research Assistant

ADVISOR: Martin Semmelhack

Princeton, NJ

Summer 2015

- Performed organic synthesis of a solvatochromic fluorophore probe covalently linked to the autoinducing peptide AI-2 from *Staphylococcus aureus*

## PROJECTS

### Bayesian Modeling and Inference (MIT 6.435)

Winter 2021

TITLE: "Estimating Player Skills in Real-World Communities using Variational Inference"

- Designed a Bayesian hierarchical Bradley-Terry model, inspired by epidemiology, to accurately model chess player strengths when average strength is very different between weakly-connected regions
- Implemented model using Pyro and estimated parameters using stochastic variational inference
- Evaluated predictions on simulated and real data and saw improved accuracy over Microsoft TrueSkill

## TEACHING

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

Papathanasiou S, Markoulaki S, **Blaine LJ**, 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 LJ**, 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 LJ**, Cheng AM, Tourdot R, et al. Mechanisms generating cancer genome complexity from a single cell division error. *Science.* 2020; 368.

## HONORS AND AWARDS

Sigma Xi Scientific Research Honor Society Nominee, Princeton University

2018

Summer Undergraduate Research Fellow in Chemistry (SURF-C), Princeton University

2015

## CAMPUS INVOLVEMENT AND LEADERSHIP

Bioinformatics and Integrative Genomics (BIG) Student Committee, Founding Member

Summer 2022–

Princeton University Sport Club Executive Council, Vice President

2016–2017

Princeton University Cycling Club, President

2016–2017

## SKILLS

PROGRAMMING AND SCRIPTING LANGUAGES: Python, R, C, C++, MATLAB, Java, Perl, HTML/JavaScript, bash

LABORATORY TECHNIQUES: Mammalian cell culture, *E. coli* and *S. cerevisiae* screens, protein & DNA gels, PCR

LANGUAGES: Upper Intermediate proficiency in Spanish (CEFR Level B2)