

## EDUCATION

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**Stanford University Department of Genetics**, Stanford, California  
Ph.D Candidate in Ami Bhatt's lab. Expected graduation Fall 2021.

**Brown University**, Providence, Rhode Island.

Bachelor of Science in Computational Biology with Honors, May 2015 (Concentration GPA 3.8)

- Senior Biology Prize for Academic Excellence in Biological Sciences

## WORK EXPERIENCE

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**Dr. Ami Bhatt's Laboratory**, Stanford University Department of Genetics

April 2017 – Present: Ph.D Candidate

- Strain tracking in the microbiome: I'm interested in transmission of commensal and pathogenic microbes, and methods for studying transmission with metagenomic sequencing and genome assembly
- Reproducible computational biology and bioinformatics workflows with Snakemake/Nextflow, Conda and containerization, scaling pipelines adaptively on cloud compute architecture
- Developing high-molecular weight microbial DNA extraction methods, Nanopore metagenomic sequencing

**Imago Biosciences**, South San Francisco, CA

February 2021 - Present: Independent contractor. Developing pipelines for variant calling using GATK in exome sequencing data from patients with myeloproliferative neoplasms

**Institute for Disease Modeling**, Seattle, WA

November 2020 - May 2021: Independent contractor. Developed pipelines for variant calling using GATK in Guinea worm mitochondrial sequencing data. Linked variant data to geographic distribution of the parasite in Chad.

**Diamond Age Data Science**, Cambridge, MA

April - June 2017: Independent contractor working on RNA-Seq differential expression analysis.

**The Broad Institute of MIT and Harvard**, Cambridge, MA

July 2015 – July 2017: Associate Computational Biologist, Connectivity Map (CMap) group, Cancer Program

- With Dr. Uri-Ben David, Golub Lab: Profiled correlated genetic, transcription and drug response changes in supposedly identical cancer cell lines. Manuscript published in *Nature*.

**Dr. Nicola Neretti's Laboratory**, Brown University Department of Molecular and Cell Biology

January 2013 – May 2015: Undergraduate Researcher, Undergraduate Teaching and Research Award Fellow

- Developed a Hi-C data processing pipeline to investigate chromatin structure changes in replicative cellular senescence. Manuscript published in *Science Advances*.

**Freelance Writer, Corporate Writers LLC**. May 2013 – May 2015

- Wrote weekly biotechnology, computer systems and social media content for company websites.

**Teaching Assistant, Brown University Phage Hunters**. Fall 2012 – Spring 2015

I was a Phage Hunters TA for three years. I devoted countless hours to administering microbiology labs and leading motivated students in research projects. The experience has left me a better scientist, teacher and researcher.

## PUBLICATIONS

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**Siranosian, B.A.**, et al. Rare transmission of commensal and pathogenic bacteria in the gut microbiome of hospitalized adults. *Under review at Nature Medicine* (2021).

**Siranosian, B.A.**, Tamburini, F. B., Sherlock, G. & Bhatt, A. S. Acquisition, transmission and strain diversity of human gut-colonizing crAss-like phages. *Nature Communications* (2020).

Siranosian, J., ..., **Siranosian, B.**, ..., et al. Whole-blood dysregulation of actin-cytoskeleton pathway in adult spinal muscular atrophy patients. *Annals of Clinical and Translational Neurology* (2020).

Norona, J., ..., **Siranosian, B.**, ..., et al. Glucagon-like peptide 2 for intestinal stem cell and Paneth cell repair during graft-versus-host disease in mice and humans. *Blood* (2020).

Durrant, M. G., Li, M. M., **Siranosian, B. A.**, Montgomery, S. B. & Bhatt, A. S. A Bioinformatic Analysis of Integrative Mobile Genetic Elements Highlights Their Role in Bacterial Adaptation. *Cell Host & Microbe* (2019).

1.Kang, J. B.\*, **Siranosian, B.**,\* et al. Intestinal microbiota domination under extreme selective pressures characterized by metagenomic read cloud sequencing and assembly. *BMC Bioinformatics* (2019).

Ben-David, U., **Siranosian, B.**, et al. Genetic and transcriptional instability alters cancer cell line drug response. *Nature* (2018).

Hassan, M., ..., **Siranosian, B.**, ..., et al. Reflections on a journey: a retrospective of the ISCB Student Council symposium series. *BMC Bioinformatics* (2018).

Criscione, S.\*, Cecco, M.\*, **Siranosian, B.**, Zhang, Y., Kreiling, J.A., Sedivy, J.M., Neretti, N. Reorganization of chromosome architecture in replicative cellular senescence. *Science Advances* (2016).

**Siranosian, B.**, et al. Tetranucleotide usage highlights genomic heterogeneity among mycobacteriophages [version 2; referees: 2 approved]. *F1000Research* (2015).

Pope, W. H., ..., **Siranosian, B.**, ..., et al. Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. *eLife Sciences* (2015).

**Siranosian, B.**, et al. Tetranucleotide usage in mycobacteriophage genomes: alignment-free methods to cluster phage and infer evolutionary relationships. *BMC Bioinformatics*, (Suppl 2):A7 (2015).

**Siranosian, B.** and Neretti, N., A multi-scale Ensemble Model of Chromatin Conformation. Brown University Senior Honors Thesis in Computational Biology (2015).

## SELECTED PRESENTATIONS

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### 2021 Bay Area Microbial Pathogenesis Symposium

- “Transmission of Gut Microbiota in Hospitalized Hematopoietic Cell Transplantation Patients”

### 2018 Intelligent Systems for Molecular Biology, Chicago, IL

- Oral and poster presentation in EvolCompGen COSI: “Genetic and transcriptional instability alters cancer cell line drug response,” award for outstanding oral presentation in the Student Council Symposium.

## TECHNICAL AND LABORATORY SKILLS

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**Reproducible research:** I develop genomic data processing and analysis workflows with Snakemake and Nextflow and make them easy to use and reproducible with Conda environments, Singularity and Docker containers. View examples at my [personal Github](#) or the [Bhatt lab Github](#).

**Programming Languages:** Experienced in R, Snakemake, Python and Unix shell scripting. Skilled with the R plotly and shiny packages to create interactive web applications. Familiar with Java, HTML and CSS.

**Deep Learning for Biology:** In collaboration with Anshul Kundaje’s lab, I developed a deep learning framework to predict chromatin structure in single cells. [Details at my blog](#). In CS230: Deep Learning at Stanford, I built a convolutional neural network to classify phage genome sequences in metagenomic samples.

**Metagenomics and Bioinformatics:** Experienced with sequence alignment, metagenomic assembly, classification and binning, variant calling in human and bacterial sequencing data, differential expression analysis.

**Graphic Design:** Experienced in Adobe Illustrator for figure design and After Effects for scientific animation.

**Laboratory Skills:** Oxford Nanopore sequencing. Microbial DNA extraction, purification and library preparation. Bacteria and bacteriophage culturing, purification and analysis. 10X Genomics Chromium library preparation.

## **VOLUNTEERING, OUTREACH AND PERSONAL INTERESTS**

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**Mythos Biotechnology Fund:** Together with other Stanford students, we evaluate public biotechnology companies and invest \$150K AUM. I have been the Broker for the fund since 2020.

**Stanford Cycling Team:** I race road and mountain bikes for Stanford's club cycling team. I have been captain of the mountain bike team since 2019, and I organized a mountain bike race weekend in October 2019.

I have volunteered for the **International Society for Computational Biology Student Council** since 2014. I was the co-chair of the 2016 Student Council Symposium, a one-day international conference for students and early-career scientists in computational biology. My responsibilities included coordinating international volunteers, recruiting sponsorship from companies and administering day-of conference logistics. I have also managed the program and led review of research abstracts for 2017-2019 conferences.

**Computational Biology Department Undergraduate Group, co-president:** During my senior year at Brown, I organized outreach events, information sessions, study groups and research presentations for students interested in computational biology

**Sigma Xi:** Member, Brown University chapter