Benjamin Siranosian, PhD

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EDUCATION

Stanford University Department of Genetics, Stanford, California
Ph.D in Genetics, October 2021. Thesis: Transmission of the Human Microbiome: From Infants to Infections

Brown University, Providence, Rhode Island.
Bachelor of Science in Computational Biology with Honors, May 2015

WORK EXPERIENCE - FULL TIME

Formic Labs, South San Francisco, CA
September 2022 - present: Head of Bioinformatics

Cellular Longevity Inc. dba Loyal, San Francisco, CA
October 2021 - September 2022: Head of Bioinformatics
  - Developed genomics pipelines with Nextflow and AWS Batch to process thousands of canine samples.
  - Led a team of four to develop backend algorithms for the upcoming X-Thousand Dogs consumer product.
  - Promoted from Senior Scientist to Head of Bioinformatics after three months.

Dr. Ami Bhatt's Laboratory, Stanford University Department of Genetics
April 2017 – October 2021: Ph.D Candidate
  - My PhD research focused on discovering fundamental principles of community assembly in the human microbiome. How do we acquire and transmit bacteria and phages? What rules govern which species persist?
  - I characterized the first examples of bacteria transmitted between the microbiome of adults, and of phages transmitted from the microbiome of a mother to her infant. This required using advanced metagenomic techniques, developing methods for tracking individual strains, and processing data at cloud scale.
  - Meanwhile, I developed software for reproducible computational biology and bioinformatics research. These Snakemake and Nextflow pipelines continue to be used by my lab and researchers worldwide.

The Broad Institute of MIT and Harvard, Cambridge, MA
July 2015 – July 2017: Associate Computational Biologist, Connectivity Map (CMap) group, Cancer Program
  - Profiled correlated genetic, transcription and drug response changes in supposedly identical cancer cell lines with Dr. Uri-Ben David, Golub Lab. Second author on the publication 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 Hi-C data processing pipeline. Investigated chromatin structure changes in replicative cellular senescence. Manuscript published in *Science Advances*.

WORK EXPERIENCE - CONTRACT

Wild Biotech, Rehovot, Israel.
February 2022 - Present: Developed pipelines for metagenomic data processing, genome assembly, and annotation.

Imago Biosciences, South San Francisco, CA
February 2021 - Present: Developed pipelines for exome variant calling in myeloproliferative neoplasm patients.

Institute for Disease Modeling, Seattle, WA
November 2020 - May 2021: Developed pipelines for variant calling using GATK in Guinea worm mitochondrial sequencing data. Linked variant data to geographic distribution of the parasite in Chad.

Corporate Writers LLC, Boston, MA
May 2013 – May 2015: Freelance Writer. Wrote weekly biotechnology content for company websites.

PUBLICATIONS

Severyn, Christopher J., **Siranosian, B. A.,** et al. "Microbiota Dynamics in a Randomized Trial of Gut Decontamination during Allogeneic Hematopoietic Cell Transplantation." *JCI Insight* (2022).

Siranosian, B. A., et al.. "Rare Transmission of Commensal and Pathogenic Bacteria in the Gut Microbiome of Hospitalized Adults." *Nature Communications* (2022).

Yan, J., …, **Siranosian, B**., …, et al. A compilation of fecal microbiome shotgun metagenomics from hematopoietic cell transplantation patients. Sci Data 9, 219 (2022).

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

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

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

Mythos Biotechnology Fund: Together with other Stanford students, we evaluate public biotechnology companies and invest $150K AUM. I was the Broker for the fund in 2020 and 2021.

Stanford Cycling Team: I race road and mountain bikes for Stanford's club cycling team. I was captain of the mountain bike team in 2019 and 2020, and I organized a mountain bike race weekend in October 2019.

International Society for Computational Biology Student Council: I volunteered for the ISCB-SC since from 2014-2020. 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