

Vivek Ramanan

Computational Biology Ph.D. Student
Brown University

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Education

2020 – Present	Ph.D. Computational Biology	Brown University
2024	M.S. Computational Biology	Brown University
2014 – 2018	B.A. Computer Science, B.A. Biology	Swarthmore College

Research

My primary research interest lies in the effects of the human microbiome, cancer, and infectious diseases on human health. With a computational lens, I particularly focus on understanding how bacterial (and other microbial) genomes play roles in affecting human health through metabolism and secondary effects. My previous and current research in cancer genomics and COVID-19 have also played critical roles in forming my research questions with the microbiome and understanding how pre-existing database bias can shape results. I hope to create new methods that utilize microbiome data and link them back to various human health conditions, both chronic and acute.

Publications

1. **Vivek Ramanan**, Indra Neil Sarkar. "Augmenting Bacterial Similarity Using a Graph-Based Genome Representation." *mSystems* 9(7). DOI: 10.1128/msystems.00497-24
Creating a novel distance measure to add to 16S rRNA using GenBank microbial genomes.
2. Rajita Menon, **Vivek Ramanan**, and Kirill Korolev. "Interactions between species introduce spurious associations in microbiome studies." *PLoS Computational Biology*. 16 December 2017. DOI:10.1371/journal.pcbi.1005939
Removing inter-microbial correlations that affect statistical analysis.
3. Russell Madison, Xiaojun Hu, **Vivek Ramanan**, Zhuxuan Xu, Richard Huang, Ethan Sokol, Garrett Frampton, Alexa Schrock, Siraj Ali, Shridhar Ganesan, and Subhajyoti De. "Clustered 8-Oxo-Guanine Mutations and Oncogenic Gene Fusions in Microsatellite-Unstable Colorectal Cancer". *JCO Precision Oncology*. 18 May 2022. DOI: 10.1200/PO.21.00477
Oncogenic fusion sequences of CRC associated with potential microbial DNA damage.
4. **Vivek Ramanan**, Shanti Mechery, and Indra Neil Sarkar. "Genbank as a source to monitor and analyze Host-Microbiome data." *Bioinformatics*. 8 July 2022. DOI: 10.1093/bioinformatics/btac487
Assessing non-traditional microbiome dataset and modeling host-microbiome evolution
5. **Vivek Ramanan**, Indra Neil Sarkar. "Characteristic Attribute Organization System (CAOS): Identifying Classification Rules Based on Phylogenetically Organized Sequences." In: DeSalle, R. (Eds) *DNA Barcoding: DNA Barcoding: Methods and Protocols* vol 2744. DOI:10.1007/978-1-0716-3581-0_21
Protocol detailing the methodology and use case scenarios for CAOS method

6. R. Huang, J. Haberberger, E. Sokol, A. Schrock, N. Danziger, R. Madison, S. Trabucco, D. Jin, D. Pavlick, **Vivek Ramanan**, K. Hole, K. McGregor, J. Venstrom, and J. Ross. "Clinicopathologic, genomic and protein expression characterization of 356 ROS1 fusion driven solid tumors cases". *International Journal of Cancer: Tumor Markers and Signatures*. 17 December 2020. DOI/10.1002/ijc.33447
Characterizing novel ROS1 fusions and gene alterations for ROS1 non small cell lung cancer

Research and Work Experience

Ph.D. Candidate in Computational Biology (4th year)

Brown University

2020 - Present

Advised by: Indra Neil Sarkar, PhD, MLIS

Committee Members: Tal Korem, Lorin Crawford, Shipra Vaishnav

- Utilizing **graph-based genome representation** to create a novel measure that utilizes functional orthologous genes shared between a pair of genomes, as an augmentation to 16S rRNA [{Github Repo}](#)
- Applying **reference free genome graphs** to measure strain-level variation between related bacteria, in context of food pathogens and early infant gut development
- Developed and published data monitoring framework on GenBank host-microbiome data, modeling co-evolution with hosts using microbiome composition data [{Github Repo}](#)
- Detailed Characteristic Attribution Organization System (CAOS) as a phylogenetic protocol [{Github Repo}](#)
- Analyzing paired genomic and demographic data from the State of Rhode Island, using phylogenetic modeling of SARS-CoV-2 variant data to predict and identify transmission and transmission type. Co-advised by *Dr. Katie Siddle* and *Dr. Elizabeth Chen* at Brown University]
- Exploring **genetic data privacy** from both technical and legal policy perspectives in the United States, in the context of increased direct-to-consumer testing and public health sequencing strategies. Advised by: *Dr. Suresh Venkatasubramanian* and *Dr. Sohini Ramachandran* with the Center for Tech Responsibility

Systems Biology Research Intern

Vedanta Biosciences

2024 May - August

Mentors: Rajita Menon, Jason Norman

- Developing **reference-free methods** for analyzing fecal microbiota transplants, engraftment, and success rates in *intestinal bowel disease*, *ulcerative colitis*, and *C. difficile*
- Applied sourmash, SimkaMin, and spaceGraphCats in proof-of-concept studies in comparison to reference-based tools, sourmashGather and Kraken2/Bracken
- Working with **NextFlow** and **AWS** services for programming pipelines and working with metagenomic data for developing live biotherapeutic products in the microbiome space

Clinical Bioinformatics Analyst

Foundation Medicine, Inc.

2018 Aug - 2020 Aug

Mentors: Siraj Ali, Russell Madison, Nikita Agarwal, Kyle Fedorchak

Analyst II: 2019 - 2020

- Led team of 8 analysts to create company-wide knowledge base, with integrated data from internal cancer genetics data alongside external databases of NCBI PubMed, clinicaltrials.gov, and PFAM kinase domains
- Collaborated on numerous research projects: [1] gene fusions of MSI-H colorectal cancer using **self-developed sequences tool with single base pair resolution** (published); [2] pan-tumor ROS1 alterations (published); [3] correlation patterns across company test types
- Supported team internship program with ongoing research project support and presentations

Analyst I: 2018 - 2019

- Curated 22,000+ genomic profiles of somatic variants based on next-generation sequencing data of cancer patient samples, providing targeted clinical therapies for patients
- Developed company-wide tool to analyze **mutational signatures of genomic profiles**, used for clinical case analysis and misdiagnosis identification
- Increased scalability of standard workflow tasks and data queries using SQL
- Created machine learning metric to predict patient response to immunotherapy at FMI Hackathon
- Presented at 6 internal tumor boards on unique cancer cases and trained 16 new members of team on variant curation

Summer Data Analyst Intern

NuMedii, Inc.

2017 June-Aug

- Designed literature mining pipeline on 700,000+ PubMed articles
- Implemented Ensemble Biclustering Classification (EBC) algorithm using NLP techniques
- Examined drug-gene-disease co-occurrences within sentences and compared to Drug Bank and NCBI gene databases to find candidate drug/targets for treatment

Bioinformatics REU Student (BRITE: Bioinformatics Research and Interdisciplinary Training Experience)

Boston University

2016 June-Aug

Mentors: Rajita Menon, Kirill Korolev

- Tested new method of removing statistical interactions between data points on largest Crohn's Disease microbiome dataset (700+ samples)
- Simulated data based on sample distribution of original dataset to test mathematical model, based on maximum entropy principles (published)
- Awarded "Best Poster Session" at Mt. Sinai Undergraduate Research Symposium 2016

Research Assistant

Swarthmore College

2016 Jan - May

Mentor: Brad Davidson

- Quantified enhancer co-motifs of FoxF heart cell migration gene in 6 tunicate genomes to find translational differences of proteins

Summer Research Assistant

Stanford University

2015 June-Aug

Mentors: Russell Fernald, Sebastian Alvarado

- Optimized western blot workflow for DNMT3A, a methylating protein in *A. burtoni*
- Presented research at Sigma Xi (Swarthmore) and HB-REX program (Stanford)

Awards, Talks, and Conferences

2023	Poster Presentation at ISMB 2023: "Data Scaling for Bacterial 16S Pairwise Similarity using a Novel Measure Based on Gene Order"
2022	NIH T32 Predoctoral Trainee in Biological Data Science (2022 - 2023)
2022	(Selected) Rhode Island Microbiome Symposium: January 14 th , 2022 "A novel approach for monitoring host-microbiome data in GenBank"
2021	NSF Graduate Fellowship: Honorable Mention
2018-2020	Foundation Medicine Tumor Board Presenter (6 presentations)
2016	Mt. Sinai Research Symposium for Undergraduates (Best Poster)

Teaching and Leadership

2021 - 2023	Industry Lead of MIT Microbiome Club <ul style="list-style-type: none">○ 2022 Fall: Organized industry seminar series○ 2022 Spring: Co-organized microbiome industry mentorship program, consisting of 17 mentors and 21 student mentees
2022	Teaching Assistant , Brown University BIOL 1250 Host-Microbiome Interactions
2016 - 2018	Tutor and Grader, Swarthmore College CPSC 021 Introduction to Computer Science
2017-2018	Swarthmore Journal of Science, Swarthmore College Copy Editor and Contributor <i>"What's bugging you? A Glance at the Human Microbiome and Behavior"</i>

Skills

Data Analysis, Machine Learning, Pipeline Creation, Network and Graph Analysis, Next-Generation Sequencing Data, Metagenomic Sequencing Data, Python, Julia, R, Adobe Illustrator