Vivek Ramanan

Computational Biology Ph.D. Student
Brown University

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Education

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

Research

My research focuses on applying computational methods to microbiology problems, particularly those related to the human microbiome. My projects include: [1] using transfer learning to model environmentally varied datasets of microbiome data from infant guts across multiple time points; [2] linking statewide health record data with genomic data on food-borne pathogens; [3] determining synteny or location dynamics of genes associated with human health from microbial genomes.

Publications

1. **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
2. Russell Madison, Xiaoju Hu, **Vivek Ramanan,** Zhuxuan Xu, Richard Huang, Ethan Sokol, Garrett Frampton, Alexa Schrock, Siraj Ali, Shridar 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.
3. 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.
4. 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

Research and Work Experience

Ph.D. Candidate in Computational Biology (3rd year)

Brown University   2020 - Present
Advised by: Indra Neil Sarkar, PhD, MLIS
Committee Members: Tal Korem, Lorin Crawford, Shipra Vaishnava

- Developed and published data monitoring pipeline on GenBank host-microbiome data, modeling co-evolution with host using microbiome composition data {*https://github.com/bcbi/genbank_holobiome*}
- Analyzed impact of COVID-19 on rural cancer patient populations
- Using synteny (or gene order and location) to analyze horizontal gene transfer and functional gene groups in bacteria
- Applying transfer learning techniques and multi-source domain adaptation to longitudinal microbiome datasets, analyzing environmental factors of infant gut development
- Linking food-borne pathogen data to clinical electronic health record information across the State of Rhode Island to analyze long-term health trends

Clinical Bioinformatics Analyst

Foundation Medicine, Inc. 2018-2020
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

Analyst I: 2018 - 2019
- Curated 20,000+ genomic profiles of somatic variants based on next-gen 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 original distribution to apply mathematical model (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 and Talks

2022	**NIH T32 Predoctoral Trainee in Biological Data Science**
2022	(*Selected*) **Rhode Island Microbiome Symposium**: January 14th, 2022 "A novel approach for monitoring host-microbiome data in GenBank"
2021	**NSF Graduate Fellowship: Honorable Mention**

Teaching and Leadership

2021 - Present	**Industry Lead of MIT Microbiome Club**
	o 2022 Fall: Organizing industry seminar series
	o 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 Copy Editor and Contributor *"What's bugging you? A Glance at the Human Microbiome and Behavior"*

Skills

Data Analysis, Pipeline Creation, Next-Generation Sequencing Data
Programming Languages: Python, Julia, R, Linux/Unix, Entrez
Tools: IGV, COSMIC, Tableau, Adobe Illustrator