Roham Razaghi

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Executive Summary

- Collaborative bioinformatician/computational biologist and molecular biologist with 5+ years of experience in utilizing statistical methods to analyze genomic, epigenomic, and transcriptomic datasets
- Adept in library preparation and data analysis for both next-generation sequencing (Illumina) and third-generation sequencing (Nanopore, PacBio) platforms. Vast experience in calling methylation, base modification, and tandem repeats using long-read sequencing
- Experienced in working with large datasets and applying exploratory analysis, statistical models (linear regression, time series modelling), multivariate analysis (dimensionality reduction, clustering, classification), probability sampling methods (random, stratified, cluster), and optimization (gradient descent)
- Expert in using python and R libraries for data interpretation and visualization. Basic familiarity with SQL (sqlite) and Apache Spark (pyspark) to analyze large datasets efficiently
- Experienced in leadership and teamwork: initiated and led collaborations and met deadlines within academia and with industry including an international consortium of six laboratories. Working with two companies (New England BioLabs, Immagina Biotechnology) to develop new products for next/third-generation sequencing
- Excellent written and oral communicator: invited speaker at an international conference, three poster presentations, taught computational biology courses to PhD students, published seven manuscripts in high-impact journals (one as a co-first author), two preprints (currently under review at journals), and two manuscripts currently in preparation

Education

Johns Hopkins School of Medicine — Baltimore, MD
Ph.D. Biomedical Engineering — *June 2017 – May 2022 (expected)*

University of California, San Diego — La Jolla, CA
B.S. Bioengineering — *September 2014 – May 2017*

Fresno City College — Fresno, CA
Engineering — *September 2012 – June 2014*

Technical Skills

Computational: Python, R, Bash, Linux, Nanopore sequencing, PacBio Sequencing, Single-Cell RNA-seq, ATAC-seq, ChIP-seq, CUT&RUN, Bisulfite sequencing, Jupyter, Google Colab, Snakemake, SQL (sqlite3), AWS (S3, EC2, Spark, Elastic MapReduce), Statistical Methodologies, Data Visualization, HTML/CSS, Adobe Illustrator, ImageJ
Molecular Biology: Third/Next Generation Sequencing Sample Preparation, HMW DNA extraction, Viral Transduction/Transfection, DNA/RNA Exogenous Labeling, Cloning, Protein Expression, PCR

Experience

Graduate Student Researcher — June 2017 – Present
Johns Hopkins School of Medicine — *Baltimore, MD*

Nanopore Sequencing for Measurement of Endogenous and Exogenous Modifications in Nucleic Acids

Thesis Advisor, PI: Winston Timp

- Developed modbamtools (https://rrazaghi.github.io/modbamtools/), software suite for the visualization, manipulation, and comparison of nucleic acid modifications encoded in modified base bam files
- Developed computational methods to investigate allele-specific alternative splicing, polyadenylation, and modifications using long-read direct-RNA sequencing data
- Efficiently lead and participate in collaborations within JHU and outside, including international consortia
- Developed computational methods to study RNA structure using third generation sequencing platforms
- Developing tools to explore genomic and transcriptomic data including single-cell and long-read data. Expert in haplotype phasing of long-read data based on variants and methylation
- Utilizing extensive suite of wet lab and computational techniques to develop an assay for simultaneous profiling of methylation, chromatin accessibility, and lamina associated domains using third-generation sequencing

Bioinformatics, Data Scientist June 2021 – August 2021
Gilead Sciences *Foster City, CA*
Biomarker Department Intern

- Collaborated with clinical bioinformaticians, biomarker scientists, and data scientists to conduct multi-omics analyses of biomarker data collected from clinical studies to help uncover modes of action of Gilead's cure therapeutics in HBV patients
- Developed an analysis pipeline to analyze single-cell RNA sequencing data from multiple clinical trial cohorts
- Implemented a workflow to detect and visualize viral integrations from targeted long read Pacbio sequencing data

Senior Design Engineer and Undergraduate Researcher Nov 2015 – May 2017
University of California, San Diego *La Jolla, CA*
Neural Interaction Laboratory

Advisor, PI: Todd Coleman

- Developed a light-controllable genetic switch through the binding interaction of hybrid molecules in order to promote controlled and precise gene, protein, and hormone production endogenously

Teaching and Leadership

JHU BME Equity, Diversity, and Inclusion Committee | *Co-Founder and Co-Chair* June 2020 – June 2021
We are a group of Ph.D. students in the biomedical engineering department at Johns Hopkins University working to make our department and communities more equitable, diverse, and inclusive (EDI). I co-founded this group in 2020 after the murder of George Floyd and the subsequent discussions centered around race, equity, diversity, and inclusion. We are working with faculty and staff in the BME department to advocate for Ph.D. students and EDI issues

- BME EDI launched the BME PhD Mentorship Program, a program to pair first-year students with upper-year students, who can be a resource for navigating the BME PhD experience
- Successfully advocated for and placed student representatives on both faculty and admission committee meetings
- Developed an online mini-course series including guidelines to courses online that are aligned with each track in the biomedical engineering department
- Launched REU/Internship Application Assistance Program to expand our efforts to help URM and first-generation students reach graduate school
- Implemented mental health and wellness education resources for students

Teaching Jan 2019 – May 2020
The best way to convey material is to first give students a grasp of the basic fundamentals underlying more advanced processes. To that end, I have taught different foundational lab classes, both benchwork and computational labs. Having the students perform experiments or work problems, either coding or in wet labs, gives students new insights. When paired to the didactic coursework already present in our curriculum this gives the students a stronger foundation to move forward in their careers.

Methods in Nucleic Acid Sequencing (Head TA and Instructor):

Sequencing technology is a rapidly progressing field that requires experience in both wet (molecular biology) and dry (computational analysis) techniques. This laboratory course consists of three experimental modules that will provide students with valuable hands-on experience in DNA sequencing and analysis. Students learn basic sequencing library preparation, perform sequencing experiments and analyze the resulting data. Experiments include human targeted sequencing, metagenomic sequencing and genome assembly.

- Designed genomics, metagenomics, and transcriptomics experiments
- Taught DNA/RNA extraction methods, NGS library preparation, Nanopore sequencing
- Deployed a local GALAXY server to host and analyze the generated sequencing data
- Developed lectures and held coding sessions

Computational Biology and Bioinformatics (TA and Instructor):

BCMB core course, taught November-January. This course challenges students to explore publicly available tools and resources that they can use in their own research, and to understand the basic molecular biology and computational concepts that the tools are built on.

- Designed lectures and held office hours
- Created problem sets (Unix, Bash, genomic data manipulation, BLAST, sequence alignment, etc)

Computational Biology Bootcamp (Head TA and Instructor):

This intensive one week class is meant to immerse students in computation, and to provide them with the foundational tools to be able to apply modern computational techniques and appropriate statistics to their data. Students learn how to work in a command line shell and different "notebook" style computing environments including Jupyter and Rmarkdown. Throughout the course, students apply these skills to different practical analysis problems for exploratory data analysis, visualization, and interpretation. The presented problems run the gamut from biophysics to cellular and systems biology to genomics.

- Designed and created the course content using Jupyter Notebooks
- Taught Python, Unix, Bash scripting, data visualization, and exploratory analysis
- Deployed the course on Microsoft Azure (JupyterHub)
- Held frequent coding sessions and office hours

Publications

* co-first author

Peer Reviewed

W. Stephenson, **R. Razaghi**, S. Busan, K. M. Weeks, W. Timp, and P. Smibert, "Direct detection of RNA modifications and structure using single molecule nanopore sequencing," *Cell genomics*, vol. 2, no. 2, p. 100 097, 2022.

A. Gershman, M. E. Sauria, P. W. Hook, S. J. Hoyt, **R. Razaghi**, S. Koren, N. Altemose, G. V. Caldas, M. R. Vollger, G. A. Logsdon, A. Rhie, E. E. Eichler, M. C. Schatz, R. J. O'Neill, A. M. Phillippy, K. H. Miga, and W. Timp, "Epigenetic patterns in a complete human genome," *Science*, 2022. DOI: 10.1126/science.abj5089.

A. Gershman, T. G. Romer, Y. Fan, **R. Razaghi**, W. A. Smith, and W. Timp, "De novo genome assembly of the tobacco hornworm moth (manduca sexta)," *G3*, vol. 11, no. 1, pp. 1–9, 2021.

A. J. Kandathil, A. L. Cox, K. Page, D. Mohr, **R. Razaghi**, K. G. Ghanem, S. A. Tuddenham, Y.-H. Hsieh, J. L. Evans, K. E. Coller, *et al.*, "Plasma virome and the risk of blood-borne infection in persons with substance use disorder," *Nature communications*, vol. 12, no. 1, pp. 1–7, 2021.

I. Lee, **R. Razaghi**, T. Gilpatrick, M. Molnar, A. Gershman, N. Sadowski, F. J. Sedlazeck, K. D. Hansen, J. T. Simpson, and W. Timp, "Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing," *Nature Methods*, pp. 1–9, 2020.

S. Kovaka, A. V. Zimin, G. M. Pertea, **R. Razaghi**, S. L. Salzberg, and M. Pertea, "Transcriptome assembly from long-read RNA-seq alignments with StringTie2," *Genome biology*, vol. 20, no. 1, pp. 1–13, 2019.

R. E. Workman*, A. D. Tang*, P. S. Tang*, M. Jain*, J. R. Tyson*, **R. Razaghi***, P. C. Zuzarte, T. Gilpatrick, A. Payne, J. Quick, *et al.*, "Nanopore native RNA sequencing of a human poly (A) transcriptome," *Nature methods*, vol. 16, no. 12, pp. 1297–1305, 2019.

Preprints

D. M. Tiek, **R. Razaghi**, L. Jin, N. Sadowski, C. Alamillo-Ferrer, J. R. Hogg, B. R. Haddad, D. H. Drewry, C. I. Wells, J. E. Pickett, *et al.*, "Targeting destabilized DNA G-quadruplexes and aberrant splicing in drug-resistant glioblastoma," *bioRxiv*, p. 661 660, 2019.

Conference Talks and Posters

Posters

R. Razaghi and W. Timp, "Measurement of DNA methylation and nuclear organization with nanopore sequencing," *Advances in Genome Biology and Technology (AGBT)*, 2020.

R. Razaghi, T. Gilpatrick, N. Sadowski, P. Tang, R. Workman, J. Simpson, and W. Timp, "Signal analysis of nanopore RNA sequencing to interrogate poly (a) tails and post-transcriptional modifications," *Biophysical Journal*, vol. 116, no. 3, 356a, 2019.

R. Razaghi, T. Gilpatrick, N. Sadowski, P. Tang, R. Workman, J. Simpson, and W. Timp, "Signal analysis of nanopore RNA sequencing to interrogate poly (a) tails and post-transcriptional modifications," *NHGRI Advanced Genomic Technology Development Meeting*, 2019.

Talks

R. Razaghi, P. Hook, M. Jain, K. Hansen, and W. Timp, "Shedding light on the long-range interaction of the human epigenome using ultra-long nanopore sequencing," Talk, Oxford Nanopore Technologies London Calling, London, UK, May 21, 2021.

R. Razaghi and W. Timp, "Measurement of dna methylation and nuclear organization with nanopore sequencing," Talk, Genetics Virtual Week, US, Apr. 21, 2021.

R. Razaghi and W. Timp, "Measurement of DNA methylation and lamina-associated domains with nanopore sequencing," Talk, 4th International Conference on Epigenetics and Bioengineering (EpiBio), 2020.

R. Razaghi and W. Timp, "Signal analysis of nanopore RNA sequencing to interrogate poly(A) tails and post-transcriptional modifications," Talk, ABRF 2019 Annual Meeting, 2019.