Sara Geraghty (Camilli)

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EDUCATION

Princeton University, Princeton NJ
Ph.D. in Quantitative and Computational Biology (QCB) Expected Jul. 2024
M.A. in Quantitative and Computational Biology (QCB) Apr. 2021

- **Thesis Committee Members:** Drs. Mona Singh (Advisor), Olga Troyanskaya, Yuri Pritykin
- **Dissertation Title:** Interpreting Cancer Genomes: Machine Learning Approaches to Uncover the Functional Impacts of Somatic Mutations

University of Richmond (UR), Richmond, VA May 2019
B.S in Biology & Computer Science, *summa cum laude,* ΦβK

Study Abroad: Maastricht University, University College Maastricht, The Netherlands Sept. – Dec. 2017

AWARDS, FELLOWSHIPS, AND GRANTS

- National Science Foundation (NSF) Graduate Research Fellowship Recipient, 2021-Present
- Schmidt Science Scholars Fellowship Program, Princeton Nominee, 2023
- Princeton Teaching Transcript Program Certificate Recipient, 2023
- CRA-WP Grad Cohort Scholarship Recipient, April 2022 (New Orleans), 2022
- University of Richmond Scholar (Full-tuition, merit-based scholarship), 2015-2019
- Barry Goldwater Scholar Honorable Mention, 2018
- University of Richmond Clarence Denoon Award (for Excellence in the Natural Sciences), 2018

RESEARCH EXPERIENCE

An ML Framework for Uncovering the Transcriptional Impact of Somatic Mutations in Cancer

Princeton University, Princeton, NJ Sept. 2019 - Present
Graduate Researcher

- Created an integrative machine learning framework that identifies novel relationships between somatic alterations in key cancer driver genes and downstream transcriptional outcomes
- Identified patient-specific drivers of molecular phenotypes in cancer cells using this framework
- Applying this framework to metabolic pathways, in collaboration with Dr. Joshua Rabinowitz's group and the Princeton Ludwig Branch, to identify novel metabolic vulnerabilities in cancer

Discovery of Novel Germline Variant Interactions with Driver Gene Somatic Mutations in Cancer

Princeton University, Princeton, NJ Jan. 2023 – Present
Graduate Researcher

- Created statistical models of global and local genetic ancestry phenotypes to uncover how the effects of somatic mutations are modulated by ancestry-relevant germline variants
- Discovered links between these key germline variants and patient survival and drug response, offering new insights into how to effectively treat cancer patients from diverse ethnic backgrounds presenting common somatic mutations

Harnessing Single Cell Long-Read RNA-Sequencing to Uncover Functional Somatic Mutation-Gene Transcription Links in Distinct Cancer Cell Populations

Princeton University, Princeton, NJ Jul. 2022 – Present
Graduate Researcher and Undergraduate Mentor

- Developed a pipeline to call somatic mutations in individual cancer cells from long-read single cell RNA-sequencing data
- Created a ML model to relate mutations to cell-type specific transcriptional outcomes in cancer

Ephydatia Sponge Genome Annotation

Bates College, Lewiston, ME May 2019 – Jul. 2019

Research Assistant

- Collaborated with Drs. April Hill, Sally Leys, and Ana Riesgo and other researchers to annotate the *Epydatia muelleri* sponge genome
- Researched genetic pathways of interest in *Ephydatia* and explored the evolution of these pathways in early *Porifera* through *Homo sapiens*
- Investigated gene pathways involved in *Ephydatia's* symbiotic relationships with algae

Genetics & Dynamics of Sponge:Algal Symbiosis

Univ. of Richmond, Richmond, VA Aug. 2016 – Jul. 2019

Undergraduate Researcher

- Study the genetic pathways involved in the evolution of animal symbioses using freshwater sponges (*E. fluviatilis* & *E. muelleri)*, their algal symbionts, and a variety of experimental, computational, and microscopy techniques
- Applied a population-based approach to understanding sponge:algal symbioses via an agent-based model, which explores the relationship between sponge host and algal symbiont under varying symbiotic and environmental conditions

Bioinformatics Analysis of *Ephydatia* Sponge

Natural History Museum, London, England Jul. 2018

Undergraduate Researcher

- Analyzed Illumina sequencing data from freshwater sponge mRNA samples by trimming the reads, assembling and mapping reads to a reference genome, quantifying the reads, and performing differential expression analysis

PUBLICATIONS

1. Hill M, Lawson B, Cain JW, Rahman N**,** Toolsiass S**,** Wang T**, Geraghty S**, Raymundo E, Hill A. Sustained Beneficial Infections: Priority Effects, Competition, and Specialization Drive Patterns of Association in Intracellular Mutualisms. *Frontiers in Ecology and Evolution* **11,** 1221012 (2023).
2. **Geraghty S**, Koutsouveli V, Hall C, Chang L, Sacristan-Soriano O, Hill M, Riesgo A, Hill A. Establishment of host:algal endosymbioses: Genetic response to symbiont versus prey in a sponge host. *Genome Biology and Evolution* **13**(11), evab252 (2021).
3. Hall C, **Camilli S**, Dwaah H, Kornegay B, Lacy C, Hill, MS, Hill AL. Freshwater sponge hosts and their green algae symbionts: a tractable model to understand intracellular symbiosis**.** *PeerJ* **9**, e10654 (2021).
4. Kenny NJ, Francis WR, Rivera-Vicéns RE, Juravel K, de Mendoza A, Díez-Vives C, Lister R, Bezares-Calderon L, Grombacher L, Roller M, Barlow, LD, **Camilli S**, Ryan JF, Wörheide G, Hill AL, Riesgo A, Leys SP. Tracing animal genomic evolution with the chromosomal-level assembly of the freshwater sponge *Ephydatia muelleri***.** *Nat Commun* **11**, 3676 (2020).

MANUSCRIPTS IN PREPARATION

1. **Geraghty S,** Boyer J, Fazek-Zarandi M, Arzouni N, McBride M, Parsons LR, Rabinowitz J, Singh M**.** Integrative Computational Framework, *Dyscovr*, Links Mutated Driver Genes to Transcriptional Dysregulation Across 19 Cancer Types (2023). In prep for *Cell Systems.*
2. **Geraghty S**, Zhang Z, Singh M. Ancestry-derived germline variants modulate the transcriptional effects of driver gene mutations. In prep for *Bioinformatics.*
3. **Geraghty S,** Balachandran S, Singh M. Harnessing single cell RNA-sequencing data to uncover functional coding mutation-transcription relationships in distinct cancer cell populations. In prep.
4. **Geraghty S,** Singh M. Perturbed physical networks in cancer: The importance of disrupted protein-nucleic acid binding. In prep.

POSTERS & PRESENTATIONS

1. **Geraghty S**, Singh M**.** Interpreting cancer genomes: A machine learning framework for discovering the functional impact of somatic alterations.
    a. Talk presented at the Ludwig Science Meeting, Princeton Branch (2021), accepted at NCI Spring Schools on Algorithmic Cancer Biology (2024).
    b. Poster presented at the NIH NHGRI Research Training & Career Development Meeting (2021), CRA-WP Grad Cohort Meeting (2022), Cold Spring Harber Genome Informatics Meeting (2023).
2. Hall C, **Geraghty S**, Dwaah H, Kornegay B, Lacy C, Hill, MS, Hill AL. The freshwater sponge, *Ephydatia muelleri*, and its chlorophyte symbiont: a model to understand intracellular symbiosis. Talk presented at Society for Integrative and Comparative Biology (2021).

TEACHING EXPERIENCE

- **Genomics** *(COS/QCB 311, Teaching Assistant)* Spring 2023
    - Developed course goals and materials and designed and taught lectures for this undergraduate-focused course
- **Introduction to Genomics & Computational Molecular Biol.** *(COS/QCB 551, Teaching Assistant)* Fall 2022
    - Implemented and instructed a graduate-level course concerning statistical and computational approaches to deciphering genomes
- **SciComm Bootcamp: Building Science Advocacy Skills, from Social Media to Capitol Hill** *(Co-Leader and Facilitator)* Winter 2022
    - Designed, advertised, and co-led a Wintersession course for Princeton undergraduates focused on building skills in science communication and advocacy
- **Crash Course in Genomics** *(Princeton SPLASH, Leader and Facilitator)* Spring 2023
    - Designed and taught an introduction to the field of genomics at 2023 Princeton SPLASH, an event designed to create educational opportunities for high school students

TECHNICAL SKILLS

Programming Languages: Python, R, Java, C++, Swift, LaTeX
Software: Microsoft Office Suite, Adobe Illustrator
Operating Systems: Windows, UNIX, Linux, Mac

Computational Biology Skills

- Familiarity with NGS platforms and hands-on experience with all steps for analyzing NGS data
- Develop and optimize analysis workflows to analyze 10x and long-read sequencing data, including bulk/single cell RNA-seq, whole-exome sequencing, DNA methylation, ChIP- and ATAC-seq, CRISPR and RNAi perturbation screens, metabolomic profiling
- Build predictive statistical and machine learning models that integrate multiple data types, including linear and nonlinear ML models as well as deep learning models
- Analyze publicly available cancer datasets (CCLE, DepMap, TCGA, ICGC) and other public bioinformatics resources (ENCODE, GTEx, gnomAD)
- Implement SNV- and CNA-calling pipelines and run variant effect prediction software
- GSEA and pathway enrichment analysis, gene-gene and protein-protein network analysis, survival analysis, GWAS, phylogenetic analysis
- Deep understanding of biostatistics and data analysis tools and packages in Python/ R (e.g. scikit-learn, numpy) and data visualization (e.g. ggplot2)
- Proper documentation of code, workflows, and analyses, HPC computing, version control using Git

Laboratory Skills

- *General Lab Skills:* Measuring concentration and purity of proteins, DNA & RNA (spectroscopy and Nanodrop technology)*;* Use of data collection and imaging software
- *Chromatography & Purification:* Column and radial chromatography; Recrystallization; TLC
- *Spectroscopy & Microscopy:* UV spectroscopy; IR spectroscopy; Mass spectroscopy; H NMR and C NMR spectroscopy; Compound light microscopy, fluorescent microscopy, confocal microscopy
- *Molecular Biology:* Molecular cloning; Bacterial transformation; DNA fingerprinting; DNA microarray; Restriction enzyme digestion; siRNA transfection; ELISA testing; Gel electrophoresis; Southern/ Western blots; Gram staining; PCR, rtPCR, & qPCR; Ames Assay; Cell Migration Assay
- *Cell Culture*: Bacterial culturing and inoculation; Mammalian and plant cell culture (seeding, splitting, changing media, screening, isolation, counting, harvesting, transfection)
- *Model Organisms*: *C. elegans*; Freshwater sponge (*E. fluviatilis, E. muelleri*)

Lab Management:

- Prepare and submit compelling grant funding applications
- Provide research and professional mentorship to lab constituents
- Lead multidisciplinary, global teams and small-group discussions regarding experimental design, data analysis and interpretation of results

Communication: Communicate and deliver presentations to cross-functional and non-technical teams

ACADEMIC AND COMMUNITY SERVICES

Graduate Peer Coaching Program, McGraw Center for Teaching and Learning

Graduate Peer Coach 2021-Present

- Secured >$3K in grant funding for a Mentorship Summit
- Founded a popular workshop that has run semi-annually for over two years
- Developing a Learning Mentorship course and Mentorship Transcript Program for graduate students
- Trained in effective coaching strategies and methodology

Princeton's Quantitative and Computational Biology (QCB) Program

Colloquium Organizer and Graduate Interviewer 2020-Present

- Interview prospective graduate students and provide recommendations to administrators and faculty
- Co-organized the annual QCB Spring Colloquium series

Princeton Insights

Co-founder, Editor & Secretary 2019-Present

- Co-founded *Princeton Insights*, an online publication that highlights groundbreaking Princeton research through short, accessible reviews
- Co-manage a team of over 40 writers and editors

Princeton ReMatch+

Undergraduate Research Mentor Summer 2022

- Mentor a Princeton undergraduate student (Suhani Balachandran) on a ML senior thesis project
- Completed a summer course in best practices for mentorship

Strive for College

UStrive Mentor 2020-Present

- Mentor high school girls from underserved backgrounds in the process of navigating college applications, admissions, school selection, financial aid, and other areas of need

Biotechnology High School

Advisory Board Member 2021-Present

- Advise representatives of Biotechnology H.S. on the skills and coursework that would be most useful to their student body, particularly students interested in academic research careers