# Sara Geraghty (Camilli)

scamilli@princeton.edu ♦ 732-614-3295 ♦ https://orcid.org/0000-0002-6476-0207

#### **EDUCATION**

Princeton University, Princeton NJ

**Ph.D.** in Quantitative and Computational Biology (QCB)

Expected May 2024

M.A. in Quantitative and Computational Biology (QCB)

April 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

**B.S.** in Biology & Computer Science, summa cum laude, ΦβK

May 2019

**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 (New Orleans), 2022
- University of Richmond Scholar, 2015-2019
  - o Full-tuition, merit-based scholarship with associated grant funding opportunities, dedicated advisors, and other benefits
- Barry Goldwater Scholar Honorable Mention, 2018
- University of Richmond Clarence Denoon Award, 2018
  - o Awarded to a rising senior for excellence in the natural sciences

# RESEARCH EXPERIENCE

# A Machine Learning Framework for Uncovering the Transcriptional Impact of Somatic Mutations in Cancer: Novel Implications for Cancer Metabolism

Princeton University, Princeton, NJ

Graduate Researcher

Sept. 2019 - Present

- 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
- Incorporating global and local genetic ancestry phenotypes to uncover how the effects of somatic mutations are
  modulated by germline variants, in an effort to create more equitable machine learning models that are
  effective for patients across diverse ancestries

# Harnessing Single Cell RNA-Sequencing to Uncover Functional Somatic Mutation-Gene Transcription Relationships in Distinct Cancer Cell Populations

Princeton University, Princeton, NJ

July 2022 - Present

Graduate Researcher and Undergraduate Mentor

- Developed a pipeline to identify somatic mutations and copy number changes in individual cancer cells from Smart-Seq2 single cell RNA-sequencing data
- Implementing a suite of machine learning approaches to relate somatic mutations to cell-type specific transcriptional outcomes in cancer

### Ephydatia Sponge Genome Annotation

Bates College, Lewiston, ME

Research Assistant

May 2019 - July 2019

- 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 – July 2019

Undergraduate Researcher

- Studied 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

July 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 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. Forthcoming in *Frontiers in Ecology and Evolution*. (2023). 10.3389/fevo.2023.1221012
- 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). 10.1093/gbe/evab252
- 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). 10.7717/peerj.10654
- 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). 10.1038/s41467-020-17397-w

# 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 Metabolic Dysregulation Across 22 Cancer Types. In prep for *Cell Systems*, expected submission Nov. 2023.

- 2. **Geraghty S**, Zhang Z, Singh M. Ancestry-derived germline variants modulate the transcriptional effects of driver gene mutations in triple negative breast cancers. In prep for *Genome Medicine*, expected submission May 2024.
- 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 for *Cell Systems*, expected submission May 2024.
- 4. **Geraghty S,** Singh M. Perturbed physical networks in cancer: The importance of disrupted protein-nucleic acid binding. In prep for *Nature Reviews Genetics*, expected submission Jan. 2023.

#### **POSTERS & PRESENTATIONS**

- 1. **Geraghty S**, Singh M. Interpreting cancer genomes: A machine learning framework for discovering the functional impact of somatic alterations.
  - Talk presented at the Ludwig Science Meeting, Princeton Branch (2021)
  - Poster presented at the NIH NHGRI Research Training & Career Development Meeting (2021), CRA-WP Grad Cohort Meeting (2022), Cold Spring Harbor Laboratory 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).
- 3. Gentile G, Dwaah H, **Camilli S**, Hall C, Delbeau M, Elmaleh S, Riesgo A, Soriono O, Hill M, Hill A. Development of a model system to study sponge:algal symbiosis. Poster presented at Society for Integrative and Comparative Biology (2018).

# TEACHING EXPERIENCE

# Genomics (COS/QCB 311)

Teaching Assistant Spring 2023

 Developed course goals and materials and designed and taught lectures for a new, undergraduate-targeted genomics course

# Introduction to Genomics and Computational Molecular Biology (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**

# **Laboratory Skills**

- <u>General Lab Skills</u>: 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
- <u>Spectroscopy & Microscopy</u>: UV spectroscopy; IR spectroscopy; Mass spectroscopy; H NMR and C NMR spectroscopy; Compound light microscopy, fluorescent microscopy, confocal microscopy
- <u>Molecular Biology</u>: 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
- <u>Cell Culture</u>: Bacterial culturing and inoculation; Mammalian and plant cell culture (seeding, splitting, changing media, screening, isolation, counting, harvesting, transfection)
- <u>Model Organisms</u>: C. elegans; Freshwater sponge (E. fluviatilis, E. muelleri)

**Programming Languages:** Python, R, Java, C++, Swift

**Computing Skills:** Design, analysis, and implementation of advanced computer algorithms, including machine learning and network algorithms; design and implementation of discrete and continuous stochastic models; computer architecture and organization concepts, such as processor data path design, assembly languages, and memory systems

**Computational Biology Skills:** Sequence similarity and alignment analysis, phylogenic inference, gene recognition, gene expression analysis, structure prediction, population and comparative genomics, single-cell sequencing multiomic analysis, gene set enrichment analysis, epigenomic data analysis

### ACADEMIC AND COMMUNITY SERVICES

# Graduate Peer Coaching Program, McGraw Center for Teaching and Learning

Graduate Peer Coach 2021-Present

- Trained in effective coaching strategies and methodology, with a focus on issues common to the graduate student experience (i.e. thesis writing, relationships with advisors, work productivity)
- Design and facilitate programming for the McGraw Center, including founding "Imposters Anonymous", a support group for graduate students experiencing imposter stress, and various workshops and panels
- Developing a Learning Mentorship course, annual 'Centering Mentoring' summit, and Mentorship Transcript Program for graduate students in collaboration with Dr. Laura Murray

# 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* (insights.princeton.edu, @pu\_insights), an online publication that highlights groundbreaking Princeton research through short, accessible reviews
- Write accessible reviews of recent work and lead a team of over 40 writers, including managing deadlines and editing articles prior to publication

### **Princeton ReMatch+**

Undergraduate Research Mentor

Summer 2022

- Attended weekly professional development sessions in best practices for mentorship
- Connected with Princeton undergraduates interested in scientific research
- Mentoring a Princeton undergraduate student (Suhani Balachandran) on a machine learning summer project, now senior thesis project

# **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

# PROFESSIONAL MEMBERSHIPS

- Association for Computing Machinery (ACM) Student Member
- American Association for the Advancement of Science (AAAS) Student Member

# **REFERENCES**

Mona Singh, PhD

Wang Family Professor in Computer Science

Computer Science Department & Lewis-Sigler Institute for Integrative Genomics, Princeton University mona@cs.princeton.edu

Yuri Pritykin, PhD

**Assistant Professor** 

Computer Science Department & Lewis-Sigler Institute for Integrative Genomics, Princeton University pritykin@cs.princeton.edu

April Hill, PhD

Wagener Family Professor of Equity and Inclusion in STEM Biology Department, Bates College ahill5@bates.edu

Laura Murray, PhD Assistant Director, Learning Programs McGraw Center for Teaching and Learning, Princeton University lcmurray@princeton.edu