

# Sara Carioscia

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## Education

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### Johns Hopkins University

PhD in Cell, Molecular, Developmental Biology & Biophysics

Aug 2019 - Present

Baltimore, MD

### Georgetown University

BS in Biology and Classical Studies

Aug 2013 - May 2017

Washington, DC

## Work Experience

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### Computational Biology Researcher

Johns Hopkins University

Aug 2019 - Present

Baltimore, MD

- Conducting heritability and genome-wide association studies focused on fertility phenotypes, including chromosomal abnormalities
- Developed new computational and statistical methods for determining chromosomal karyotype in data from IVF embryos
- Created [R package](#) to effectively utilize sparse haploid DNA sequencing data (0.01x), enabling improved analysis at reduced experimental cost
- Collaborated with academic and industry scientists to leverage real-world data from clinics and fertility centers

### Course Instructor

Johns Hopkins University, Department of Biology

Aug 2020 - Dec 2023

Baltimore, MD

- Designed and taught [course](#) in simulation and visualization for 10 undergrads, using SLiM and R
- Developed and delivered [course](#) in modeling biological populations to 12 undergrads using Python and Jupyter Notebooks
- Teaching Assistant for grad-level computational biology courses (Python, Bash) and undergrad courses in Developmental Genetics

### Computational Biology Associate, Translational Research

Tempus Labs

Summer 2023

Chicago, IL

- Developed an R package to conduct integration tests for company datasets and analysis processes, improving the reliability of the pipeline
- Created a Shiny app for visualizing pipeline status, used by the team to monitor data and pipeline quality
- Launched extension in Quarto markdown language to ensure consistent styling and features across client-facing scientific reports
- Established unit tests for team software packages and utilities
- Contributed to team computational pipelines for analysis of DNA, RNA, and exome sequencing data

### Technology Fellow

Johns Hopkins University

June 2021 - June 2023

Baltimore, MD

- Created a computational [module](#) for CRISPR reagent design, successfully integrating it into the curriculum of an undergraduate biology course
- Developed [Python resource](#) for genome analysis and comparison, used by Hopkins researchers as well as community members

### Science Policy Fellow

Institute for Defense Analyses, Science and Technology Policy Institute

July 2017- Aug 2019

Washington, DC

- Responded to short- and long-term analysis questions from Federal entities including the White House Office of Science and Technology Policy
- Conducted evaluations of internal and external programs across Federal agencies (NIH, NASA, Department of Energy)
- Authored reports for government clients regarding topics including dual use research of concern (DURC) and genomic database regulations

## Computational Skills

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### Programming and computation

- R, Python, Bash, Java, C++, Git/GitHub, snakemake, HTML/CSS, SQL
- Slurm/high performance computing, cloud computing (Google), Docker, Kubernetes,  $\LaTeX$ , RMarkdown, Quarto

### Software development

- **trreports** R package to execute integration tests of team markdown reports, run on a kubernetes cronjob and displayed via Shiny app (proprietary, Tempus Labs)
- **rhapsodi** [R package](#) for analysis of low-coverage single-cell haploid DNA sequencing data. Package performs haplotype phasing, genotype imputation, and discovery of meiotic recombination events.

## Grants & Awards

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2021	<b>Graduate Research Fellowship</b> National Science Foundation	\$138,000
2021	<b>Victor G. Corces Teaching Award</b> Johns Hopkins Department of Biology	\$400
2021	<b>Instructional Enhancement Grant</b> Johns Hopkins Center for Teaching Excellence & Innovation	\$5,500
2018	<b>Young Professionals Scholarship</b> Secure World Foundation	\$1,500