LAUREN SABO

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Education

M.S. Bioinformatics, Georgia Institute of Technology, Atlanta, GA — Jan. 2026 — May 2027 (expected)

B.S. Computer Science, Georgia Institute of Technology, Atlanta, GA — Aug. 2021 — Dec. 2025 (expected)

- *Concentrations:* Media & People | *Major GPA:* 3.9
- *Minor:* Health & Medical Sciences

Skills

Computing Languages & Software

Python, Java, React/ Node.js, Bash/ Shell, Git, HTML/ CSS, R, C++, C, Docker, Assembly Code, Swift

Data Visualization & Manipulation

D3, Tableau, plotly

Bioinformatics

Software: BRAKER3, NCBI BLAST, Genome Assembly Software (HiFi.asm, Flye, LJA), R/qtl2, Genome Analysis Tool Kit (GATK), SAMtools, Bionano Solve

Wet Lab: Qubit Quantification, Nanodrop Quantification, DNA Isolation, Restriction Digest/PCR

Work Experience

Graduate Research Assistant, *McGrath Lab* — Aug. 2025 — Present

- Engineering a robust **QTL mapping** pipeline for ultra-low coverage (~0.1X) sequencing data, enabling reliable detection of sex-linked loci in *Aulonocara sp.* "Yellow Head."
- Applying probabilistic genotype inference with **Hidden Markov Models** to accurately impute offspring haplotypes, pinpointing candidate regions on LG10 that underlie male determination

Co-founder & Chief of Product Design, *Quuri Co.* — May 2024 — Present

- Led the end-to-end product design process for a research networking platform, transforming user discovery data into an intuitive interface that improved engagement and information accessibility.
- Engineered full-stack functionality with **Firebase** to deliver dynamic, real-time updates and ensure scalable performance for growing academic communities.

Undergraduate Research Assistant, *McGrath Lab* — May 2022 — Aug. 2025

- Accelerated genome assembly and scaffolding workflows for African cichlid species by developing optimized Python pipelines tailored for long-read sequencing data (PacBio HiFi).
- Improved genomic data accuracy and assembly depth through rigorous quality control, read filtering, and alignment, strengthening downstream comparative and evolutionary analyses.

Projects

"Comprehensive Structural and Functional Genome Annotation of Lake Malawi Cichlids Using BRAKER3: Insights into Evolutionary Adaptation and Speciation." — Jan. 2025 — May 2025

- In accordance with the President's Undergraduate Research Award (2025)
- Advanced comparative genomics of five African cichlid species by integrating **PacBio HiFi** assemblies and **RNA-Seq data** in a **BRAKER3**-based annotation framework to detect lineage-specific adaptive genes.
- Designed a **BLASTp**-centered annotation pipeline improving annotation completeness and accelerating downstream evolutionary analyses.

"Expanding the Lake Malawi cichlid genome using high quality long-read sequencing" — Jan. 2024 — Dec. 2024

- Optimized the *Metriaclima zebra* reference genome using a custom PacBio pipeline, improving contiguity and coverage to enable more accurate comparative genomic analyses across Lake Malawi cichlids.
- Benchmarked long-read assemblers **(Flye, HiFi.asm, and LJA)** using reference-free quality metrics to determine optimal strategies for resolving repetitive and heterozygous genomic regions.
- Integrated PacBio HiFi sequencing with Bionano optical mapping to validate large-scale structural integrity

Chattahoochee River Conditions App — Jan. 2024 — Feb. 2024

- Built a real-time web application integrating **USGS Water Quality API data** to visualize river conditions, improving safety awareness and operational planning for the Georgia Tech Rowing Club.

Leadership

Coxswain, Rower, & Board Member, *Georgia Tech Rowing* — Feb. 2022 — May 2025

- **ACRA National Champion (2025)** – Men's Lightweight 4+ *(Coxswain)*