

# LAUREN SABO

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## Education

- M.S. Bioinformatics**, Georgia Institute of Technology, Atlanta, GA Jan. 2025 — May 2026 (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/qlt2, 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 *Metriaclicma 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*)