

LAUREN SABO

(678) 780 - 1401 | laurensabo@gmail.com | linkedin.com/in/laurensabo | github.com/laurensabo

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)
<ul style="list-style-type: none">- <i>Concentrations</i>: Media & People <i>Major GPA</i>: 3.9- <i>Minor</i>: 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 Sequencing
Software (HiFi.asm, Flye, LJA), R/qtI2, 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* Jan. 2026 — Present

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 **Firestore** to deliver dynamic, real-time updates and ensure scalable performance for growing academic communities.

Undergraduate Research Assistant, *McGrath Lab* May 2022 — Dec. 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

“Development of a Low-Coverage QTL Mapping Pipeline to Identify a Male Sex Determiner in *Aulonocara* sp. “Yellow Head” Aug. 2025 — Present

- Engineered 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.”
- Applied probabilistic genotype inference with **Hidden Markov Models** to accurately impute offspring haplotypes, pinpointing candidate regions on LG10 that underlie male determination

“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

- Strengthened the *Metriaclima zebra* reference genome (UMD2a) by a custom long-read assembly pipeline, improving contiguity and coverage to support comparative genomic research across cichlid species.

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*)