

# LAUREN SABO

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

## Education

<b>M.S. Bioinformatics</b> , Georgia Institute of Technology, Atlanta, GA	Jan. 2025 — May 2026 (expected)
<b>B.S. Computer Science</b> , Georgia Institute of Technology, Atlanta, GA	Aug. 2021 — Dec. 2025 (expected)
- Concentrations: Media & People   Major GPA: 3.9	
- Minor: Health & Medical Sciences	

## Skills

<b>Computing Languages &amp; Software</b>	<b>Bioinformatics</b>
Python, Java, React/ Node.js, Bash/ Shell, Git, HTML/ CSS, R, C++, C, Docker, Assembly Code, Swift	Software: BRAKER3, NCBI BLAST, Genome Assembly Software (HiFi.asm, Flye, LJA), R/qlt2, Genome Analysis Tool Kit (GATK), SAMtools, Bionano Solve
<b>Data Visualization &amp; Manipulation</b>	<i>Wet Lab:</i> Qubit Quantification, Nanodrop Quantification, DNA Isolation, Restriction Digest/PCR
D3, Tableau, plotly	

## Work Experience

<b>Graduate Research Assistant, McGrath Lab</b>	Aug. 2025 — Present
- Engineering a robust <b>QTL mapping</b> pipeline for ultra-low coverage (~0.1X) sequencing data, enabling reliable detection of sex-linked loci in <i>Aulonocara sp.</i> "Yellow Head."	
- Applying probabilistic genotype inference with <b>Hidden Markov Models</b> to accurately impute offspring haplotypes, pinpointing candidate regions on LG10 that underlie male determination	
<b>Co-founder &amp; Chief of Product Design, Quuri Co.</b>	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 <b>Firebase</b> to deliver dynamic, real-time updates and ensure scalable performance for growing academic communities.	
<b>Undergraduate Research Assistant, McGrath Lab</b>	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

<b>"Comprehensive Structural and Functional Genome Annotation of Lake Malawi Cichlids Using BRAKER3: Insights into Evolutionary Adaptation and Speciation."</b>	Jan. 2025 — May 2025
- In accordance with the President's Undergraduate Research Award (2025)	
- Advanced comparative genomics of five African cichlid species by integrating <b>PacBio HiFi</b> assemblies and <b>RNA-Seq data</b> in a <b>BRAKER3</b> -based annotation framework to detect lineage-specific adaptive genes.	
- Designed a <b>BLASTp</b> -centered annotation pipeline improving annotation completeness and accelerating downstream evolutionary analyses.	
<b>"Expanding the Lake Malawi cichlid genome using high quality long-read sequencing"</b>	Jan. 2024 — Dec. 2024
- Optimized the <i>Metriaclima zebra</i> 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 ( <b>Flye</b> , <b>HiFi.asm</b> , and <b>LJA</b> ) 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	
<b>Chattahoochee River Conditions App</b>	Jan. 2024 — Feb. 2024
- Built a real-time web application integrating <b>USGS Water Quality API data</b> to visualize river conditions, improving safety awareness and operational planning for the Georgia Tech Rowing Club.	

## Leadership

<b>Coxswain, Rower, &amp; Board Member, Georgia Tech Rowing</b>	Feb. 2022 — May 2025
- ACRA National Champion (2025) – Men's Lightweight 4+ (Coxswain)	