Gabriel A. A. Silva

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Summary

Computational biologist and PhD candidate with extensive experience in high-throughput omics analysis, reproducible workflow development, and scalable computational research in Linux and HPC environments. Strong foundation in molecular biology, theoretical and applied statistics, and interdisciplinary collaboration. Committed to reproducible science, data visualization, and supporting team-based research initiatives.

Technical Skills

Programming & Scripting: Python, R, Bash, Linux CLI, LaTeX

Reproducible & Scalable Research: Nextflow, Git, GitHub, Conda, Singularity

Omics Data Analysis: Genomics, transcriptomics, metagenomics, genome assembly, variant calling, taxonomic profiling, functional annotation

Computational Infrastructure: High Performance Computing (SLURM/PBS), workflow scaling, job scheduling

Statistics & Data Visualization: Theoretical and applied statistics, ggplot2, reproducible reporting, multi-layer omics visualization

Research Experience

Doctoral Researcher 2023 – Present
Auburn University *Auburn, AL*

- Develop computational workflows for genomic and metagenomic analyses of plant–pathogen systems.
- Implement reproducible pipelines for long- and short-read sequencing using HPC environments.
- Process Nanopore sequencing data from raw signal to genome assembly and downstream analyses.
- Integrate population genomics and metagenomics to investigate host–pathogen interactions.
- Produce statistical analyses, reproducible reports, and publication-ready figures.
- Collaborate closely with interdisciplinary teams, translating biological questions into structured computational analyses.

Bioinformatics Intern 2022
Brazilian Agricultural Research Corporation (Embrapa) *Brazil*

- Analyzed metagenomic and RNA-seq datasets from plant, animal, and microbial systems.
- Developed and deployed Nextflow pipelines to standardize laboratory workflows.
- Performed functional annotation and taxonomic profiling of microbial communities.
- Contributed to viral pathogen genomics and agricultural disease research.

Undergraduate Thesis: Benchmarking of Metagenome Classification Methods 2022
Bahia State University *Brazil*

- Designed reproducible HPC pipelines in Bash and Python to benchmark metagenomic classifiers.
- Evaluated classification accuracy, runtime, and performance across tools.
- Performed statistical analyses and visualizations in R and Krona.

Research Intern 2019 – 2021
Federal University of the São Francisco Valley *Brazil*

- Conducted genome assembly and comparative genomics of bacterial pathogens.
- Performed pan-genome analyses and microbial community profiling.
- Supported metagenomic studies investigating livestock microbiomes.

Publications (Selected order)

Silva, G. A. A., et al. (2024). Detectability of runs of homozygosity is influenced by analysis parameters and population-specific demographic history. *PLOS Computational Biology*, 20(10), e1012566. DOI: 10.1371/journal.pcbi.1012566

Silva, G. A. A., et al. (2026). Quantitative comparison of fungal genome assembly strategies using short and long reads from simulated and empirical sequencing data. *Submitted*.

Maia, J. C. D. S., **Silva, G. A. A.**, et al. (2023). Genomic characterization of *Aeromonas veronii* provides insights into taxonomic assignment and reveals widespread virulence and resistance genes throughout the world. *Antibiotics*, 12(6), 1039. DOI: 10.3390/antibiotics12061039

Silva, G. A. A., et al. (2026). Biology, detection, and management of *Lecanosticta acicola*: Emerging challenges for the management of brown spot needle blight in pine forests. *Forest Pathology*. DOI: 10.1111/efp.70061

Miranda Paez, A., Sattler, R., Lamka, G. F., **Silva, G. A. A.**, et al. (2026). Persistent genetic connectivity in the Mulchatna caribou herd after prolonged population decline with predictions of future population divergence. *PeerJ*, 14, e20912 DOI: 10.7717/peerj.20912.

Folorunso, T., Lamka, G., Paez, A., **Silva, G. A. A.**, et al. (2026). Ecological and evolutionary insights into fungal pathogens and their management across plant and animal kingdoms. *Accepted*.

Mwema, T., Lamka, G., Paez, A., **Silva, G. A. A.**, et al. (2025). Comparative genomic signatures of species introductions across diverse taxa. *In revision*.

Folorunso, T. R., **Silva, G.**, et al. (2025). Optimized protocol for culturing and extracting DNA from fungal isolates associated with brown spot needle blight in pine trees. *PLOS ONE*, 20(11), e0337218. DOI: 10.1371/journal.pone.0337218

Dinas, S. S. E., **Silva, G. A. A.**, et al. (2025). Development and evaluation of alternative culture media for the multiplication of *Bacillus amyloliquefaciens* and *Chromobacterium subtsugae*. In *Estudos Multidisciplinares em Microbiologia: Teoria e Prática*. DOI: 10.37885/2503189751 [1]

Silva, G. A. A., et al. (2020). Use of in silico and in vivo tools for the analysis of the genotoxic potential of ultra-processed foods. In *Scientific Initiation and its Multiple Applications*. [1]

[1] Original publication not in English

Conference Presentations

Silva, G. A. A., et al. (2025). *Lecanosticta acicola*'s genome features and its significance in BSNB. *4th Annual Brown Spot Needle Blight Assessment Workshop*, Auburn, AL, USA. (Oral)

Silva, G. A. A., et al. (2025). Comparative assessment of fungal genome assembly pipelines using Nanopore and Illumina sequencing. *Evolution 2025*, Athens, GA, USA. (Poster)

Silva, G. A. A., et al. (2025). Integrative bioinformatic and molecular approaches to elucidate the genomics of *Lecanosticta acicola* and its impacts on Brown Spot Needle Blight. *3rd Annual Brown Spot Needle Blight Assessment Workshop*, Auburn, AL, USA. (Oral)

Silva, G. A. A., et al. (2021). Combining taxonomic tools for metagenome analysis. *XXIII Northeast Genetics Meeting*. (Poster)[1]

Silva, G. A. A., et al. (2018). Toxnet platform as complementary tool in the evaluation of toxicity from industrialized food. *7th Brazilian Biotechnology Congress & 2nd Biotechnology Ibero-American Congress*, Brasília, Brazil. (Poster)[1]

Silva, G. A. A., et al. (2018). Use of the Toxnet platform as a tool for in silico toxicity evaluation of routine reagents in research laboratories. *V Bahia Congress of Sanitary and Environmental Engineering*, Brazil. (Oral)[1]

Tinel, J. L. S., Silva, R. F., **Silva, G. A. A.**, Sousa, A. O. (2018). Evaluation of the genotoxic and mutagenic potential of industrialized sauces. *XXII Northeast Genetics Meeting*, Brazil. (Poster)[1]

Silva, R. F., Tinel, J. L. S., **Silva, G. A. A.**, Sousa, A. O. (2018). Cytotoxic, genotoxic and mutagenic effects of powdered soft drinks. *XXII Northeast Genetics Meeting*, Brazil. (Poster)[1]

Guimarães, M. L., **Silva, G. A. A.**, et al. (2017). Isolation and selection of wastewater-degrading bacteria associated with *Eichhornia crassipes*. *II Interdisciplinary Symposium of the São Francisco Valley*, Brazil. (Oral)[1]

[1] Original work not in English

Teaching Experience

Teaching Assistant — Introduction to Computational Biology Fall 2023
Auburn University *Auburn, AL*

- Delivered lectures and live coding demonstrations for biological data analysis.
- Communicated computational concepts to students with diverse backgrounds.
- Assisted students with R, scripting, and computational workflows.
- Developed structured instructional materials to support programming and data analysis training.

Education

Auburn University Auburn, AL
Ph.D. Wildlife Sciences, GPA: 4.0 *2023 – 2026 (Expected)*
Computational Biology Graduate Certificate

Bahia State University Brazil
B.S. Bioprocesses & Biotechnology Engineering, GPA: 3.7 *2017 – 2022*

Awards

Best Undergraduate Project Presentation (2019)

Outstanding Student Award (2017)

References

Dr. Janna Willoughby Auburn, AL, USA
Assistant Professor, Auburn University *jwilloughby@auburn.edu*

Dr. Avril Harder Huntsville, AL, USA
Computational Biologist, HudsonAlpha Institute for Biotechnology *aharder@hudsonalpha.org*

Dr. Priscila Grynberg Brasília, DF, Brazil
Researcher, Brazilian Agricultural Research Corporation (Embrapa) *priscila.grynberg@embrapa.br*