Noah Austin Legall

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# **Research Interests**

Bioinformatics, Pangenomics, Bacterial Evolution, Microbial Community Dynamics

# **Education**

Aug. 2018 – Mar. 2023

Ph.D. Graduate Research Assistant

*University of Georgia, Institute of Bioinformatics*

GPA: 3.83

May 2014 - May 2018

B.Sc. Quantitative Biology

*University of North Carolina at Chapel Hill*

GPA: 3.2

# **Work Experience**

January 2023 Intelligence Community Postdoctoral Fellowship

*University of South Florida – Tampa, Florida*

*Project:* Merging multi-omics and bacterial genomics to predict antagonistic microbiome interactions

June 2022 – September 2022 Bioinformatics Intern

*Illumina, Inc. – San Diego, California*

*Project:* Investigation of Infinium BeadChip efficiency as Males Age (aka Old Man Syndrome).

Skills Learned: **Snowflake, Statistical Inference, Machine Learning, Genome Wide Association Studies**

June 2018 – Mar 2023 Graduate Research Assistant

*Institute of Bioinformatics, University of Georgia, Georgia*

*Project*: Genomic factors leading to host range in *Mycobacterium bovis*

Skills Learned: **Bioconda, HPC computing, Github, NGS Big Data, Nextflow**

Fall 2014 – Spring 2018 Undergraduate Researcher

*School of Medicine Biochemistry and Biophysics, University North Carolina - Chapel Hill, North Carolina*

*Project:* Bioinformatics analysis of non-coding circRNA intronic regions.

Skills Learned: **Perl**, **Python**, **R**.

# **Publications**

**Legall N** and Salvador LCM (2022) Selective sweep sites and SNP dense regions differentiate *Mycobacterium bovis* isolates across scales. *Front. Microbiol*. 13:787856. doi: 10.3389/fmicb.2022.787856

Duan, N., Bai, Y., Sun, H., Wang, N., Ma, Y., Li, M., **Legall, N.**, … Chen, X. (2017). Genome re-sequencing reveals the history of apple and supports a two-stage model for fruit enlargement. *Nature Communications*, *8*(1), 249. <https://doi.org/10.1038/s41467-017-00336-7>. Contributions included SNP identification and phylogenetic comparison of the *Ma1* gene locus of domesticated apple genome.

# **Contributed presentations**

December 2021 **Legall N**., Salvador L. *Mbovpan: a Mycobacterium bovis whole-genome sequencing pangenomic framework*. CRWAD (Conference of Research Workers in Animal Diseases). Oral.

October 2020 **Legall, N.**, *Pangenome analysis of Mycobacterium bovis isolates to unravel geographic and host specific genomic clustering*. Steeve Giguere Science of Veterinary Medicine Conference. Oral.

# **Fellowships**

*May 2022 Intelligence Community Postdoctoral Fellowship*

Grant to lead a project for integrating different omics with microbiome data

*May 2020 Interdisciplinary Disease Ecology Across Scales (IDEAS) Fellowship*

Training young scientists to use leading-edge conceptual and methodological approaches to solve pressing infectious disease problems.

# **Awards**

*June 2022 Illumina Bioinformatics Internship*

Was offered a competitive internship opportunity from Illumina, a sequencing platform company utilizing bioinformatics to solve issues in human health.

*October 2020 Steeve Giguere Science of Veterinary Medicine Oral Presentation Winner*

Gave an oral presentation of current research in establishing genomic signatures in *Mycobacterium bovis* through pangenomics and multivariate data analysis.

# **Leadership and Diversity**

*July 2020 – July 2021*

Acting as the first African American President of the Bioinformatic Graduate Student Association (BIGSA)

*February 2019*

Visit to Clark Atlanta University, a Historically Black University, to encourage students to apply to bioinformatic grad program.