Daramola Oluwasegun Isaac

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OBJECTIVE

A computational biologist eager to leverage my skills in computational genomics and bioinformatics research to contribute to innovative solutions in biomedical sciences.

EDUCATION

Bachelors' of Medical Laboratory Science (B.MLS) | May 2018 – July 2023

College of Medicine, University of Ibadan | Nigeria

- Related coursework: Advanced Biochemistry, Genetics, Molecular Biology, Enzymology, Medical Physics, Computational Biology, Virology, Microbiology, Advanced Cell Genomics, Bioinformatics.
- Activities: Sci-comm Committee member, National Science Policy Network (2023-Current); SEAPHAGES Team Leader, Ibadan Bacteriophage Research Team (2020-2023)

TECHNICAL SKILLS

- **Programming Languages**: R, Python, Bash, Groovy.
- **Technologies:** Workflow systems (Nextflow, WDL, Cromwell), Docker, Git, Streamlit.
- **Operating System**: Windows, Unix/Linux
- **Computational Genomics**: Cell Segmentation using Celltool, Genome analysis, BLAST packages, protein structure dynamics, phylogenetics, CLI and GUI biological tools.
- **Proteomics analysis**: Mass spectrometry-based proteomics analysis and visualization using Perseus
- **Molecular analysis**: DNA/RNA Extraction, Primer design, PCR Amplification, Gel electrophoresis
- **Wet Lab**: Phage isolation, Viral tissue culture passaging and isolation, Environmental sample processing.

RESEARCH EXPERIENCE

Undergraduate Thesis Project | Department of Virology, College of Medicine | November 2022 – August 2023

- Studied the prevalence of Epstein-Barr Virus (EBV) in patients with Sickle-cell disease (SCD)
- Performed DNA extraction on serum samples for genomic analysis. Optimized PCR protocols and conducted electrophoretic gel analysis.

Research Student | HHMI - SEA-PHAGES Program, University of Ibadan | 2019 – 2023

- Completed the genome annotation of five novel sequenced bacteriophages: Dothraki, Sedona, Phishy, Popper, Gretchen, Bianmat, and Salvador; published annotation on NCBI Genome Database.

Remote Research Intern | Reniere Laboratory, University of Washington, Seattle | March 2021 – August 2022

- Quantified and compared the dimensions of ΔspxA1 filaments with wildtype listeria monocytogenes using the cell segmentation software Celltool. Designed primers, deletion and over-expressed variants of different genes to observe respective effects on morphology using Benchling.
- Analyzed whole-cell proteomics data for gene expression folds across mutant and wildtype listeria monocytogenes to identify significant genes with probable functions contributing to observed morphological differences.
- Analyzed raw mass spectrometry-based label-free proteomics quantifications using the computational platform Perseus.

Research Candidate | AltREU for Undergrad on Computational Modeling, Teuscher Lab, Portland State University | June – August 2021

- Designed a linear regression model to predict Azithromycin dispensation in the United Kingdom using Time series forecast modeling in R.

Remote Research Intern | Horswill Laboratory | University of Colorado, Anschutz | September – December 2020

- Identified anti-infective regions in Staphylococcus warneri using computational genomics tools.

Remote Intern | National Summer Undergraduate Research Project | University of Arizona | July – August 2020

- Conducted a review on Staphylococcal Cassette Chromosome *mec* (SCCmec) in Methicillin-Resistant Staphylococcus aureus (MRSA)
- Conducted a comparative genomic and phylogenetic analysis on the different SCC*mec* types of MRSA, juxtaposing genomic features between already-defined and novel SCC*mec types.*

AWARDS

1st Place, AI for Life Sciences Hackathon 2023, Austria | *December 2023*

For *developing a cutting-edge AI-powered dashboard (gaia) that leverages Artificial Intelligence models, advanced geographic visualization and analysis to provide accurate predictions and develop a deeper understanding of the role of the soil microbiome to improving soil health.*

Finalist, Vivli AMR Surveillance Open Data Re-use Data Challenge 2023, United Kingdom | September 2023

For *designing a two-tiered interactive dashboard application (PATHFINDER) capable of presenting evolving patterns of microbial resistance to antimicrobial agents while serving as a decision-support tool that assists healthcare providers in making evidence-based conclusions regarding genomic susceptibility status and antibiotic selection.*

1st Runner-up, African Biohackathon Competition 2022, South Africa | September 2022

For *designing a web tool (ADEPT-AI) for the Prediction of Adverse Drug Reactions for Rheumatoid Arthritis using a machine-learning model.*

RESEARCH PUBLICATIONS

Agboeze T, **Daramola O**, Akomolafe A et al. (2024). A predictive algorithm for the analysis of AMR trends and healthcare decision support [awaiting peer review]. *Wellcome Open Res* 2024, 9:274 https://doi.org/10.12688/wellcomeopenres.21289.1

Daramola, O.I., Jimenez, N.R. (2023). A database to identify the human gut virome. *Nature Microbiology* **8**, 5. https://doi.org/10.1038/s41564-022-01280-z

Cesinger, M. R., **Daramola, O. I.**, Kwiatkowski, L. M., & Reniere, M. L. (2022). The Transcriptional Regulator SpxA1 Influences the Morphology and Virulence of *Listeria monocytogenes*. *Infection and immunity*, e0021122. https://doi.org/10.1128/iai.00211-22

Daramola, O.I. (2021). Modeling the Effect of the COVID-19 Pandemic on Azithromycin Prescription in General Practices Across the UK. *altREU Projects*. https://pdxscholar.library.pdx.edu/altreu_projects/8.