Dr. Olabiyi **Obayomi**

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Summary: I am a passionate bioinformatician skilled in omics data analysis particularly metagenomics, transcriptomics, microbial genomics, programming languages, and microbiology with the desire to develop and apply computational techniques to advance and accelerate biological research. I have over 5 years of experience working in bioinformatics both as a Ph.D. student and a Postdoctoral Researcher. I have developed complex computational pipelines (https://github.com/olabiyi/) and provided insights on various next-generation sequencing datasets including but not restricted to metagenomics, transcriptomics, population genetics, and genome assembly.

Education

Ben Gurion University of the Negev, Jacob Blaustein Institute for Desert Research   *Israel*
Ph.D. Environmental Microbiology   2019
<u>Cumulative GPA:</u> 96.5
<u>Core Modules:</u> Microbial Pathogens, microbial communities, next-generation sequencing, microbial ecology
<u>Skills and Learning:</u>

- Characterized and tracked the source of microbiomes (bacteria and protists) including pathogens in soil, water and crop samples using both culture- dependent and independent approaches including amplicon (16S and 18S) sequencing
- Analyzed and processed data with various bioinformatics tools, including QIIME, SourceTracker, R Bioconductor packages
- Developed a tool for detection, statistical analysis, and visualization of pathogens in environmental samples using amplicon sequences https://github.com/olabiyi/16s_pathogen_analysis
- Wrote scripts in Bash, R and Python that used high performance clusters to decrease execution time on tasks
- Wrote and contributed to four manuscripts for publication

Technical Skills

- ***Pipeline development***: Snakemake, Nextflow and Make
- ***Biostatistics and machine learning***: multivariate statistics, hypothesis testing, regression, normalization, correlation, constrained analysis, correction for multiple hypothesis testing, ggplot2 and machine learning techniques
- ***Bioinformatics analysis***: metagenomics (amplicon and shotgun), transcriptomics (model and non-model organisms), metatranscriptomics, population genetics, genomics, variant calling, phylogenetics, gene functions and pathways enrichment analysis
- ***Bioinformatics tools***: QIIME (1 and 2), PICRUST 2, Bioconductor, MEGA 7, MetaPhlan2, trinity, trinonate, cdhit, bwa, Stacks, Diamond, GATK4, bcftools, mauve, Humann2, megahit, samtools etc.
- ***Computer programming***: R, Python, and Bash
- ***Network analysis***: R
- ***High performance computing***: SGE and SLURM
- ***Report generation***: R markdown, R shiny, Jupyter, Jupyter notebook
- ***Biological data repositories***: NCBI, KEGG, MetaCyc etc
- ***Version control***: Git and GITHUB
- ***Containerization***: Docker, Singularity and Conda
- ***Operating systems***: Linux, Windows

- ***Cloud computing***: AWS EC2 and S3
- ***Microbiology:*** Culture dependent and independent techniques for microbiomes

Personal Skills

- Poised communication, presentation, analytical, organizational, and problem-solving skills
- Excellent interpersonal skills, a team player
- Ability to handle multiple tasks concurrently and in a timely fashion
- Hardworking, result oriented, able to work under pressure with minimum or no supervision
- Proactive, dynamic, curious, and a quick learner

Professional Experience

Texas A&M AgriLife Research, Texas A&M University, Stephenville, Texas   June 2021 - present
Postdoctoral Researcher in Bioinformatics
- Actively involved in several metagenomics, transcriptomics, and population genetics projects by assisting PI-s across Texas A&M University system for bioinformatics analysis
- Characterized the microbiome of several environmental samples including water, soil, feces and skin samples of salamander, biochar, Texas beaches, cows, and crops
- Performed RNA-seq and pathway analysis for model plants (Arachis ipaensis) and humans
- Performed RNA-Seq and pathway analysis for non-model plants (Arachis dardanii, little blue stem and Indian grass)
- Compared the transcriptome profiles between plants. Between Arachis ipaensis and Arachis dardanii and between little bluestem and Indian grass.
- Developed a pipeline for the analysis of amplicon (16S, 18S, ITS) sequencing dataset using QIIME2 and PICRUSt - https://github.com/olabiyi/snakemake-workflow-qiime2
- Assembled and annotated the genomes of bacteria (E. coli) and virus (fowl pox virus)
- Analyzed RAD-Seq dataset of little blue stem grasses across Texas to understand the genetic basis for their diversity
- Assembled and assigned taxonomy to near full-length 16S rRNA sequences of peanut endophytes
- Mined NCBI database for sequences to be used for primer design in a Texas sea turtles study
- Participating in project conceptualization and grant writing
- Teaching graduate students how to perform statistics using R
- Submitting raw sequences to NCBI
- Writing manuscripts for publication.

Ben Gurion University of the Negev, Bioinformatics Core facility, Beersheba   Nov 2019 – June 2021
Postdoctoral Researcher in Bioinformatics
- Applied omics tools for the development of pipelines to analyze Illumina and Oxford nanopore sequencing data to gain biological insights
- Developed a pipeline for RNA-Seq analysis of non-model organisms using NeatSeq_Flow to automate database creation, QC, mapping, assembly, annotation, statistical, clustering and enrichment analysis - https://neatseq-flow modules.readthedocs.io/en/latest/Workflow_docs/RNA_seq_non_model.html
- Characterized the microbiome of Wolffia globosa and identified potential cobalamin synthesizing bacteria using 16S amplicon sequences and shotgun metagenomics.
- Characterized the functional and taxonomic diversity of the microbiome of biofilters receiving sand and granular activated carbon treatments using shotgun metagenomics.

- Performed RNA-Seq and pathway analysis for non-model crustaceans (Hippolyte inermis and Cherax quadricarinatus)
- Performed comparative genomics between Z and W chromosomes of Macrobrachium rosenbergii in to identify sex linked genes
- Developed a pipeline for host associated shotgun metagenomics using snakemake - https://github.com/olabiyi/shotgun-metagomics-pipeline
- Developed a pipeline for metatranscriptomics using both read based and assembly approaches - https://github.com/olabiyi/snakemake-workflow-metatranscriptomics
- Drafted custom scripts in R, Bash, Python and Perl for omics data analysis
- Presented and delivered my analyses results to customers on our bioinformatics core facility computer servers. This involved database management using SQL, MySQL and PHP, scripting with HTML and CSS and HTML report generation using RMarkdown
- Contributed to manuscripts for publication.

Ben Gurion University of the Negev, Zuckerberg Inst. For Water Research, Sde Boker   May 2019 – October 2019
Post-doctoral Researcher in Bioinformatics
- Characterized the microbiomes of soil, water and crop samples that were sequenced with Illumina and Oxford Nanopore platforms
- Analyzed and processed data with various bioinformatics tools, including QIIME, SourceTracker, R, and others
- Assisted and mentored fellow students (Masters and PhD) with analyzing their bioinformatics-related data
- Developed a bioinformatics pipeline for the analysis of amplicon sequences generated by Oxford Nanopore
- Developed scripts for detecting pathogens using amplicon sequences
- Wrote and contributed to manuscripts for publication

Publications

https://scholar.google.com/citations?user=zppxGbkAAAAJ

Publications under preparation
- Valerio Zupo; Maria Costantini; Eliahu David Aflalo; Tom Levy; Vered Chalifa-Caspi; **Olabiyi Obayomi**; Mirko Mutalipassi; Nadia Ruocco; Francesca Glaviano; Emanuele Somma; Thomas Viel; Paola Nieri; Amir Sagi. (2023). Ferroptosis precedes apoptosis to facilitate specific cell—death signaling by fatty acids. Submitted to Cell.

- LeviRam I., A. Gross, A. Lintern, **O. Obayomi**., O. Gillor, M. Herzberg, D. McCarthy (2023). Engineering Biofilter microbiome towards Sustainable Stormwater Bioremediation. Submitted to Science of the Total Environment.

- Tiffany Lujana, **Olabiyi Obayomi**, Faith Cox, Kristin Sefcika, Nathan F. Bendik, Dee Ann Chamberlain, Jesse M. Meika, Jeff Brady, and Dustin Edwards. Spatiotemporal Variation in Microbiota Community Structure in Wild and Captive Barton Springs Salamanders (Eurycea sosorum) and Austin Blind Salamanders (Eurycea waterlooensis) (2023). Under preparation.

Publications acknowledged for my Bioinformatics Contributions

- Shai A. Shaked, Shai Abehsera, Tome Levey, Vered Chalifa-Capsi, Amir Sagi. (2020). From sporadic single genes to a broader transcriptomic approach: Insights into the formation of the biominineralized exoskeleton in decapod crustaceans. Journal of Structural Biology. 212:107612. https://doi.org/10.1016/j.jsb.2020.107612. (*Transcriptomics*)

- Yang Yang, Anne Bogler, Zeev Ronen, Gideon Oron, Moshe Herzberg, and Roy Bernstein (2020). Initial Deposition and Pioneering Colonization on Polymeric Membranes of Anaerobes Isolated from an Anaerobic Membrane Bioreactor (AnMBR). 55:5832-5842. https://doi.org/10.1021/acs.est.9b06763. (*16S Amplicon sequencing*).

- Vered Chalifa-Caspi (2021). RNA-Seq in Nonmodel Organisms. In: Noam Shomron (ed.), Deep Sequencing Data Analysis, Methods in Molecular Biology, vol. 2243: 143-167, Springer Science Business Media, LLC, part of Springer Nature. https://doi.org/10.1007/978-1-0716-1103-6_8. (*Non-model RNA-Seq pipeline*)

- Talia Gabay, Guy Rotem, Osnat Gillor, Yaron Ziv (2022). Understanding changes in biocrust communities following phosphate mining in the Negev Desert. Environmental Research. 207: 112200. https://doi.org/10.1016/j.envres.2021.112200. (*16S Amplicon sequencing*).

Professional Development

- **Next generation sequencing analysis training for clinical pathogen genomics by the American society for microbiology (ASM)**   2023
  3-month long workshop and seminars on next generation sequencing infrastructure, techniques, and analysis for pathogen genomics.

- **Biological data science workshop, online via zoom by Drexel University**   2022
  Five-day workshop on bash, cloud computing, containerization, NCBI, Biopython, machine learning and deep learning.

- **Texas A&M University workshops** online via zoom   2021-
  Annual short train workshops on high performance computing, containerization, python, Fortran, etc

- **Linux bootcamp: Command-line, AWK and SED; Vi editor and Grep** on udemy.com   2019
  10 hours of learning to program with Linux and Linux tools

- ***Advanced R*** on udemy.com   *2019*
  4.5 hours of training on advanced topics in R such as environments, creating packages, parallelization etc.

- **Data Analysis with Python and Pandas** on stoneriverelearning.com   2019

- **4ᵗʰ Haifa Winter Workshop in Bioinformatics**: statistics and data visualization for omics studies   2018
  University of Haifa, Israel
  Five-day workshop on statistical analysis and visualization of various omics studies

- **Next Generation Sequencing Workshop**   2018
  Tel Hai college, Israel
  Five-day workshop on analysis of NGS dataset: phylogenetics analysis, variant calling, RNA-seq etc.

- **Data Analysis of Metagenomic Samples using QIIME**   2017
  Ben Gurion University of the Negev, Beersheba, Israel
  One-day workshop on the analysis of metagenomics samples using QIIME