CHRISTIAN AYALA-ORTIZ

I have experience working with NGS data and have performe a wide array of analysis using bioinformatics. Currently working with metabolomics data and looking for ways to integrate it with other multiomics. Actively developing myself to become a bioinformatician/data scientist by improving my programming skills. I am motivated to pursue a career as a computational biologist applying multiomics approaches to better understand biological systems.
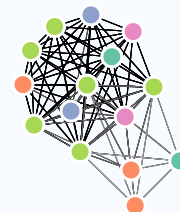
🎓 EDUCATION

PhD. Student, Environmental Science (minor Ecosystem Genomics)

University of Arizona 📍 Tucson, AZ

current | 2021

- Focused on the development of software pipelines for the analysis and visualization of metabolomics data
- Using multiomics data to understand how changes in resource availability affect soil ecosystems
- Major Advisor: Dr. Malak Tfaily

M.S., Entomology and Plant Pathology

Oklahoma State University 📍 Stillwater, OK

2019 | 2017

- Thesis title: Comparative genomics of six species of Deltocephalinae leafhoppers to discover vector competence-related genes
- Major Advisor: Dr. Astri Wayadande

B.S., Engineering in Biotechnology

University of the Armed Forces 📍 Sangolqui, Ecuador

2016 | 2009

- Thesis title: Molecular characterization of Globisporangium sp. populations obtained from New York City ornamental greenhouses during 2014 using SSR microsatellites.

💻 RESEARCH EXPERIENCE

Graduate Research Assistant

Tfaily Laboratory 📍 University of Arizona

current | 2021

- Testing the use of retention time prediction using ML algorithms for improving metabolomics annotation
- Developing a Shiny app for the analysis of untargeted metabolomics data
- Developed MetaboDirect, a data analysis pipeline for direct injection FT-ICR MS data

View this CV online with links at _https://github.com/Coayala/cv/raw/main/outputs/_

CONTACT

✉ cayalaortiz@arizona.edu

🐦 cayalaortiz

🐙 github.com/Coayala

in linkedin.com/in/christian-ayala-2141a38b/

LANGUAGE SKILLS

R

Bash

Python

2020 | 2019

Research Scientist
Hagen Laboratory   📍 Oklahoma State University

· Differential gene expression analysis of two species of burying beetles (Nicrophorus spp.).
· Native RNA-seq and cDNA sequencing using Oxford Nanopore Technologies' MinION.
· Analysis of RNA modifications in the transcriptome of the Apis mellifera using native RNA-seq

2019 | 2017

Graduate Research Assistant
Wayadande Laboratory   📍 Oklahoma State University

· Assembly and annotation of leafhopper genomes and transcriptomes
· Silencing of genes using interference RNA (RNAi)

2015 | 2015

Intern
Garzon Laboratory   📍 Oklahoma State University

· Molecular characterization of Globisporangium spp. obtained from ornamental greenhouses of New York using SSRs.

TRAINEESHIPS AND FELLOWSHIPS

current | 2021

National Science Foundation Traineeship
BRIDGES NRT   📍 University of Arizona

· The BRIDGES NSF Research Traineeship is a competitive program in Ecosystem Genomics for students in participating graduate programs.

2021 | 2021

Roots for Resilience Program Fellow
Data Science Institute   📍 University of Arizona

· Program trains selected graduate students in the use of open science and computational infrastructure

POSTER AND ORAL PRESENTATIONS

2022

MetaboTandem And MetaboDirect: Software Pipelines for the Analysis of High Throughput Metabolomics Data for Complex Environmental Samples
AGU Fall Meeting   📍 Chicago, IL

2021

Stable isotope labelling to trace litter degradation pathways: A view into the carbon cycling processes occurring in a peat bog
AGU Fall Meeting   📍 New Orleans, LA

2020

Comparative analysis of the Deltocephaline leafhopper transcriptomes for the elucidation of vector competence genes
The Plant & Animal Genome Conference XXVIII   📍 San Diego, CA

2019 ● Exploring the Deltocephaline leafhopper transcriptomes, a comparative analysis for the elucidation of vector competence genes.
Entomology 2019 (ESA Annual meeting) 📍 St. Louis, MO

2019 ● Selection of an internal reference gene for functional genomics or gene expression analysis in Dalbulus maidis (Hemiptera: Cicadellidae)
67th Annual Meeting of the ESA SW Branch 📍 Tulsa, OK

· Third place - Graduate poster competition

2018 ● Looking for vector competence genes: Transcriptome comparison of vector and non-vector Deltocephaline leafhoppers
11th Annual Arthropod Genomics Symposium (AGS) 📍 Urbana, IL

📖 PUBLICATIONS

· **Ayala-Ortiz, C.**, Graf-Grachet, N., Freire-Zapata, V., Fudyma, J., Hildebrand, G., AminiTabrizi, R., Howard-Varona, C., Corilo, Y. E., Hess, N., Duhaime, M., Sullivan, M., & Tfaily, M. (2023). MetaboDirect: An Analytical Pipeline for the processing of FTICR-MS-based Metabolomics Data. BioRxiv, 2022.2006.2010.495699. https://doi.org/10.1101/2022.06.10.495699 (Accepted in Microbiome) - Leewis, M.-C., Lawrence, C. R., Schulz, M. S., Tfaily, M. M., **Ayala-Ortiz, C. O.**, Flores, G. E., Mackelprang, R., & McFarland, J. W. (2022). The influence of soil development on the depth distribution and structure of soil microbial communities. Soil Biology and Biochemistry, 174, 108808. https://doi.org/https://doi.org/10.1016/j.soilbio.2022.108808 - **Ayala-Ortiz, C. O.**, Farriester, J. W., Pratt, C. J., Goldkamp, A. K., Matts, J., Hoback, W. W., Gustafson, J. E., & Hagen, D. E. (2021). Effect of food source availability in the salivary gland transcriptome of the unique burying beetle *Nicrophorus pustulatus* (Coleoptera: Silphidae). PLOS ONE, 16(9), e0255660. https://doi.org/10.1371/journal.pone.0255660

COMMUNITY INVOLVEMENT

current
|
2019 ● Data Carpentries Instructor

2022 ● Helper
ResBazaar 📍 University of Arizona