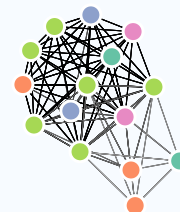


CHRISTIAN AYALA-ORTIZ

I have experience working with NGS data and have performed 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

current
|
2021

- **PhD. Student, Environmental Science (minor Ecosystem Genomics)**
University of Arizona 📍 Tucson, AZ
 - 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

2019
|
2017

- **M.S., Entomology and Plant Pathology**
Oklahoma State University 📍 Stillwater, OK
 - Thesis title: Comparative genomics of six species of Deltocephalinae leafhoppers to discover vector competence-related genes
 - Major Advisor: Dr. Astri Wayadande

2016
|
2009

- **B.S., Engineering in Biotechnology**
University of the Armed Forces 📍 Sangolquí, Ecuador
 - Thesis title: Molecular characterization of Globisporangium sp. populations obtained from New York City ornamental greenhouses during 2014 using SSR microsatellites.

RESEARCH EXPERIENCE

current
|
2021

- **Graduate Research Assistant**
Tfaily Laboratory 📍 University of Arizona
 - 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 at <https://coayala.github.io/cv/>

CONTACT

✉ cayalaortiz@arizona.edu
🐦 [cayalaortiz](https://twitter.com/cayalaortiz)
🐙 github.com/Coayala
🌐 [linkedin.com/in/christian-ayala-2141a38b/](https://www.linkedin.com/in/christian-ayala-2141a38b/)

LANGUAGE SKILLS



Made with the R package
[pagedown](#).

The source code is available on
github.com/Coayala/cv.

Last updated on 2023-02-17.

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., AminTabrizi, 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/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