

LUIS FELIPE ARIAS GIRALDO

PhD in Plant Protection | Data Science & Bioinformatics

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PROFESSIONAL EXPERIENCE

Instituto Valenciano de Investigaciones Agrarias - IVIA

Postdoctoral Fellow

Sep 2025 – Present

Valencia, Spain

- Project: High-Throughput Sequencing and Bioinformatics Service (SESARBI-IVIA).

Institute for Sustainable Agriculture - CSIC

Research assistant

May 2019 – Ago 2025

Córdoba, Spain

- Involved in several projects: **KODA-IPEC**, **P18-RT-4184**, **BeXYL**, **XF-ACTORS**, **POnTE**, and **SoilMan**.
- Activities: data analysis, ecological modeling, bioinformatics support, and server administration of a local Linux-based HPC cluster.

Institute for Integrative Systems Biology (I2SysBio UV-CSIC)

Graduate Intern

Oct 2017 – Apr 2019

Valencia, Spain

- Project: Implementation and testing of bioinformatic tools for NGS data analysis.
- Activities: data analysis, software testing, and bioinformatics support.

SmVaK-Aqualia Microbiology Laboratory

Undergraduate Summer Intern

Jul 2017 – Oct 2017

Ostrava, Czech Republic

- Project: Monitoring and analysis of water quality in compliance with EU environmental regulations.
- Activities: microbiological analysis (culture-based methods, microscopy), PCR, and qPCR.

EDUCATION

Ph.D. in Agronomy, Food, Forestry and Rural Development Engineering

University of Córdoba, Spain

Nov 2019 – Oct 2025

Thesis: "Epidemiological and microbial ecology approaches for the *Verticillium* wilt control in the olive tree".

Grade: *Cum Laude*

M.Sc. in Bioinformatics

University of Valencia, Spain

Sep 2017 – Apr 2019

Thesis: "Meta-transcriptomic dynamics approach to *Verticillium* wilt of the olive tree".

B.Sc. in Biochemistry

University of Córdoba, Spain

Sep 2013 – Jun 2017

Thesis: "RNA-seq analysis time course of *Olea europaea* in roots and leaves infected by *Verticillium dahliae*" with honor.

PROFESSIONAL SKILLS

Languages

Spanish (native), English (fluent)

Statistics

Univariate and multivariate analyses; machine learning

Programming

Proficient in R and Bash; intermediate in Python

Data Management

Basic knowledge of MySQL and MongoDB

Workflow Tools

Nextflow, Snakemake, Conda, Docker

General computer skills

Broad Linux & Microsoft Windows; GIS data processing; large-scale data handling; excellent command of Microsoft Office; LaTeX

FELLOWSHIPS & GRANTS

EMBO Scientific Exchange Grant (8,370 €)

Mar 2024 – Jun 2024

Research stay at AIT Austrian Institute of Technology, Bioresources Unit (Tulln an der Donau, Austria).

Project: *Deciphering beneficial plant-microbiome networks for managing vascular diseases in olive trees.*

Supervisors: Dr. Stéphane Compant & Dr. Livio Antonielli

Erasmus + Mobility Grant (3,200 €)

Mar 2023 – Jun 2023

Research stay at the Biodiversity Institute, Dept. of Ecology and Evolutionary Biology, University of Kansas (KS, USA).

Project: *Biodiversity and dynamics of Verticillium wilt in olive trees and geographical patterns of risk.*

Supervisors: Prof. Dr. A. Town Peterson & Dr. Marlon E. Cobos


OPEN SOURCE SOFTWARE

enmpa

R package

Ecological niche modeling using presence/absence data.


Role: Creator and maintainer.

 github.com/Luisagi/enmpa**kuenm2**



R package

Detailed development and evaluation of ecological niche models.

Role: Contributor and co-maintainer.

 github.com/marloncobos/kuenm2

MOST RELEVANT PUBLICATIONS

Full list of publications available on : 0000-0003-4861-8064 or Google Scholar : Luis F. Arias-Giraldo

- **Arias-Giraldo, L. F.**, Cobos, M. E., Peterson, A. T., Landa, B. B., & Navas-Cortés, J. A. (2025). *Modeling the ecological niche of Verticillium dahliae in southern Spain: Current patterns and projected shifts under climate change.* Plant Disease. In Press.
- **Arias-Giraldo, L. F.**, Cobos, M. E., Peterson, A. T., Landa, B. B., & Navas-Cortés, J. A. (2025). *Unraveling the ecological niche signals of Verticillium dahliae: Insights from Mediterranean landscapes.* Plant Disease. doi.org/10.1094/PDIS-02-24-0443-RE
- **Arias-Giraldo, L. F.**, & Cobos, M. E. (2024). *enmpa: An R package for ecological niche modeling using presence-absence data and generalized linear models.* Biodiversity Informatics, 18. doi.org/10.17161/BI.V18I.21742
- Velasco-Amo, M. P., **Arias-Giraldo, L. F.**, & Landa, B. B. (2024). *Complete genome assemblies of several Xylella fastidiosa subspecies multiplex strains reveals high phage content and novel plasmids.* Phytopathologia Mediterranea, 63(1). doi.org/10.36253/phyto-14931
- Fondevilla, S., **Arias-Giraldo, L. F.**, García-León, F. J., & Landa, B. B. (2023). *Molecular Characterization of Peronospora variabilis Isolates Infecting Chenopodium quinoa and Chenopodium album in Spain.* Plant Disease, 107(4). doi.org/10.1094/PDIS-05-22-1198-SC
- Velasco-Amo, M. P., **Arias-Giraldo, L. F.**, Román-Écija, M., ..., & Landa, B. B. (2023). *Complete Circularized Genome Resources of Seven Strains of Xylella fastidiosa subsp. fastidiosa Using Hybrid Assembly Reveals Unknown Plasmids.* Phytopathology, 113(6). doi.org/10.1094/PHYTO-10-22-0396-A
- O'Leary, M. L., **Arias-Giraldo, L. F.**, Burbank, L. P., de La Fuente, L., & Landa, B. B. (2022). *Complete Genome Resources for Xylella fastidiosa Strains AlmaEM3 and BB08-1 Reveal Prophage-Associated Structural Variation Among Blueberry-Infecting Strains.* Phytopathology, 112(3). doi.org/10.1094/PHYTO-08-21-0317-A
- **Arias-Giraldo, L. F.**, Guzmán, G., Montes-Borrego, M., Gramaje, D., Gómez, J. A., & Landa, B. B. (2021). *Going beyond soil conservation with the use of cover crops in Mediterranean sloping olive orchards.* Agronomy, 11(7). doi.org/10.3390/agronomy11071387
- Landa, B. B., **Arias-Giraldo, L. F.**, Henricot, B., Montes-Borrego, M., Shuttleworth, L. A., & Pérez-Sierra, A. M. (2021). *Diversity of Phytophthora species detected in disturbed and undisturbed British soils using high-throughput sequencing targeting ITS rRNA and COI mtDNA regions.* Forests, 12(2). doi.org/10.3390/f12020229
- **Arias-Giraldo, L. F.**, Giampetruzzi, A., Metsis, M., ..., & Landa, B. B. (2020). *Complete circularized genome data of two Spanish strains of Xylella fastidiosa (IVIA5235 and IVIA5901) using hybrid assembly approaches.* Phytopathology, 110(5). doi.org/10.1094/PHYTO-01-20-0012-A
- Martí, J. M., **Arias-Giraldo, L. F.**, Díaz-Villanueva, W., Arnau, V., Rodríguez-Franco, A., & Peña-Garay, C. (2020). *Metatranscriptomic dynamics after Verticillium dahliae infection and root damage in Olea europaea.* BMC Plant Biology, 20(1). doi.org/10.1186/s12870-019-2185-0

CONFERENCE PRESENTATIONS

Talks

- **The 17th Congress of the Mediterranean Phytopathological Union (MPU)** — Bari, Italy, 6–10 Jul 2025
Machine learning-based prediction of olive tree health against Verticillium wilt using rhizosphere microbiome profiles.
- **AGRO HUB II Andalucía PhD Meeting** — Granada, Spain, 11–12 Mar 2025
Epidemiological and microbial ecology approaches for Verticillium wilt control in olive crop.
- **XX Spanish Conference of Phytopathology (SEF)** — Córdoba, Spain, 16–19 Sep 2024
Analysis of the rhizosphere-associated microbiome as an indicator of the phytosanitary status of olive groves affected by Verticillium wilt in Andalusia.
- **XX Spanish Conference of Phytopathology (SEF)** — Valencia, Spain, 24–26 Oct 2022
Modeling of the environmental factors that determine the incidence and potential distribution of olive vascular pathogens in Andalusia.
- **The 16th Congress of the Mediterranean Phytopathological Union (MPU)** — Limassol, Cyprus, 4–8 Apr 2022
Modelling potential climatic suitability for olive vascular diseases in Southern Spain.
Award: Best Oral Presentation (3rd Prize)
- **II Congress of Young Researchers in Agroalimentary Sciences** — Almería, Spain, 17 Oct 2019
Use of Next-Generation Sequencing approaches to determine the complete genome of two Spanish strains of Xylella fastidiosa.

Posters

- **III European Conference on Xylella fastidiosa (EFSA) & XF-ACTORS Final** — Online, 26–30 Apr 2021
Detection of recombination events in Xylella fastidiosa genomes of different Spanish strains.
- **XIV Symposium on Bioinformatics (BSC and INB/ELIXIR-ES)** — Granada, Spain, 14–16 Nov 2018
Analysis of the temporal evolution of infection by pathogenic fungi in plants: A new metagenomic approach to Verticillium wilt of olive tree.

PROFESSIONAL REFERENCES

- ◇ Available upon request.