

JEFERYD YEPES-GARCÍA

Bioinformatician and Data Scientist

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SUMMARY

Bioinformatics researcher and PhD candidate specializing in metagenomics, microbial ecology, and reproducible computational workflows. My work is focused on lignocellulosic biomass degradation and sustainable agriculture, integrating advanced genomic analyses to address environmental challenges and promote circular bio-economy solutions.

EDUCATION

Doctor of Philosophy - *PhDc*, Bioinformatics

Université de Fribourg - Universität Freiburg  In progress

Master of Sciences in Engineering - *MSc*

University of Antioquia  12/2020

Specialist in Lab. Management (ISO/IEC 17025)

Servicio Nacional de Aprendizaje (SENA)  12/2020

Biotechnologist

I.U Colegio Mayor de Antioquia  06/2015

EXPERIENCE

Bioinformatician

SIB Swiss Institute of Bioinformatics  09/2022  Fribourg


Laboratory Analyst


Iluma Alliance  01 - 08/2022  Medellin

PUBLICATIONS

2Pipe starts with a question: matching you with the correct pipeline for MAG reconstruction


mSystems


 01/2026

 DOI: <https://doi.org/10.1128/msystems.00844-25>

Genome-Resolved Metagenomics of Rice Straw Degradation Experiments in Colombian Fields

Scientific Data

 11/2025

 DOI: <https://doi.org/10.1038/s41597-025-06113-2>




LANGUAGES


Spanish Native 

English Proficient 


French Intermediate 


COURSES


 Statistics and Machine Learning for Life Sciences

 Multiomics Data Analysis and Integration

AWARDS

 SIB Remarkable Output 2024

 The Best poster in Bioinformatics (LS² Annual Meeting 2025)

 Swiss Excellence Scholarship holder (FCS)

TOOLS



VOLUNTEERING



Student Representative
FGLM



Nextflow Ambassador



Student Representative
CUSO StarOmics

Referees:

Dr. Laurent Falquet, Group Leader

University of Fribourg and Swiss Institute of Bioinformatics

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Prof. Pedro Romero, Group Leader

Department of Oncology, University of Lausanne

Email: pedro.romero@unil.ch

Full list of publications:

Yepes-García, J. & Falquet, L. (2026). 2Pipe: It Starts with a Question. Matching You with the Correct Pipeline for MAG Reconstruction. *mSystems*, 0:e00844-25. <https://doi.org/10.1128/msystems.00844-25>

Yepes-García, J. & Falquet, L. (2025). TaxoFlow: The Tutorial. An Educational Nextflow Pipeline for Metagenomics Taxonomic Profiling. *Preprints*. <https://doi.org/10.20944/preprints202512.1989.v1>

Yepes-García, J., Novoa-Montenegro, N., Otero-Jiménez, V. et al. (2025). Genome-Resolved Metagenomics of Rice Straw Degradation Experiments in Colombian Fields. *Scientific Data*, 12(1823). <https://doi.org/10.1038/s41597-025-06113-2>

Yepes-García, J. & Falquet, L. (2024). Metagenome quality metrics and taxonomical annotation visualization through the integration of MAGFlow and BlgMAG. *F1000Research*, 13:640. <https://doi.org/10.12688/f1000research.152290.2>

Falquet, L., Yepes-García, J., Gonzalez, I. M., & Hernandez, E. B. (2024). Report on the Swiss-Colombian workshop 2024: “Metagenomics data analysis of mixed microbial communities.” *EMBnet.journal*, 30(0). <https://doi.org/10.14806/ej.30.0.1063>

Yepes-García, J., Caicedo-Montoya, C., Pinilla, L., Toro, L. F., & Ríos-Esteva, R. (2020). Morphological differentiation of *Streptomyces clavuligerus* exposed to diverse environmental conditions and its relationship with clavulanic acid biosynthesis. *Processes*, 8(9). <https://doi.org/10.3390/pr8091038>

Caicedo-Montoya, C., Pinilla, L., Toro, L. F., Yepes-García, J., & Ríos-Esteva, R. (2019). Comparative analysis of strategies for de novo transcriptome assembly in prokaryotes: *Streptomyces clavuligerus* as a case study. *High-Throughput*, 8(4). <https://doi.org/10.3390/ht8040020>