Curro Campuzano Jiménez

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WHO AM I

I am a PhD student at the Svardal lab (Antwerp University). I am currently working on developing tools to study speciation from genomic data. Before, I worked in the evolutionary ecology of thyme and in meta-transcriptomics to study the microbial diversity of the ice sheet. I have experience in high-performance computing for data analysis and scripting in R, Julia, and Python. I am very interested in reproducible research, Bayesian statistics, and scientific computing.

EXPERIENCE

PhD student at Svardal lab   September 2024 — Present
University of Antwerp   *Antwerp, Belgium*

I aim to understand the population dynamics of invasions and how they can affect the process of speciation. I am interested in simulation-based methods, machine learning, and ancestral recombination graphs. Currently, I am working on inferring very recent demographic processes from genomic data.

Student programmer   September 2022 — July 2024
Environmental Sciences Department, Aarhus University *Roskilde, Denmark* I focused on enhancing the reproducibility and efficiency of the bioinformatics pipelines of the sequencing center. Specifically, I worked on automating and containerizing pipelines on large-TotalRNA meta-transcriptomics, long-reads amplicon sequencing, and whole-genome sequencing and genome mining. Additionally, I co-authored several articles, including one that was awarded the best article at the 2023 FEMS Microbiology Ecology award.

MSc thesis   January 2023 — July 2024
Bioinformatics Research Center, Aarhus University *Aarhus, Denmark* I was supervised by Thomas Bataillon and Genis Garcia Erill. I worked on a set of methods named genomic offsets that aim to predict population vulnerability due to climate change. I evaluated their limitations using simulated data and expanded the quantitative genetics theory behind them. We are currently finalizing a manuscript, and I also published an open-source Julia package to perform genomic offset analysis(GenomicOffsets.jl).

Internship   February 2023 — July 2023
Bioinformatics Research Center, Aarhus University *Aarhus, Denmark* Supervised by Thomas Bataillon, I worked in obtaining a chromosome-level assembly of Mediterranean thyme using PacBio HiFi. I improved the highly fragmented de novo assembly by scaffolding utilizing the genome of a closely related species(slides available for more information).

Internship   February 2022 — July 2022
Andalusian Research Institute in Data Science and Computational Intelligence *Granada, Spain* Supervised by Coral del Val, I worked in developing tools that use hidden Markov models' profiles to analyze homologous sequences. I improved the annotation of a cancer therapeutic target (Fascin protein), and I trained a Random Forest classifier based on the amino acid sequence. Using LIME and Shapley Values, I also found that my model paid particular attention to the presence of specific motifs in the binding sites (without prior information about them).

Student programmer   February 2022 — July 2022
Physical Chemistry Department, University of Granada

Granada, Spain I worked with Irene Luque and Coral del Val in studying protein coevolution using a technique known as Statistical Coupling Analysis. I found two putative groups of coevolving residues that are potentially responsible for the allosterism of the Fascin protein.

EDUCATION

Aarhus University   Aarhus, Denmark
Master of Science in Bioinformatics   *2022 — 2024*
- Highest grade in the courses Evolutionary Thinking, Data Science in Bioinformatics, Statistical and Machine Learning, Algorithms in Bioinformatics, and in my MSc thesis.
- PhD course: Next Generation Sequencing Data Analysis.

University of Granada   Granada, Spain

Degree in Biotechnology   *2018 — 2022*

- Research initiation grant.
- I graduated with honors in my bachelor's thesis in Bioinformatics.