

Curro Campuzano Jiménez

Brussels, Belgium | curro.campuzanojimenez@uantwerpen.be | github.com/currocam | currocam.github.io

PROFILE

I am a PhD student at the Svoldal 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 Svoldal 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 allostery 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

Degree in Biotechnology

Granada, Spain

2018 — 2022

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