

Roberto Sánchez Navarro

Bioinformatician - Biotechnologist



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About me

Bioinformatician looking for real-world challenges. I'm curious about the data, so I often take the extra step until it makes sense. Then, I like presenting it in a way that tells a story.

I'm continuously under training, learning new technologies every week, and when I pick one up, I enjoy passing that knowledge along to my peers.

Soft skills

Attentive to detail
Focused on quality
Good communicator
Highly motivated

Areas of specialization

Data Science
Data Analysis
Bioinformatics
Big Data

Interests

Running
Cycling
Hiking

EXPERIENCE

2022-2023

PhD Candidate

AALBORG UNIVERSITY · Denmark

Development of a python application for the detection and analysis of exopolysaccharide gene clusters in bacterial metagenomes. This entailed:

- Retrieving all exopolysaccharide clusters from the published literature and extracting all existing genetic knowledge about them.
- Development of a Snakemake pipeline that uses DIAMOND, hmmer, biopython, and visualization tools, among others, to mine public genome databases to collect sequence data to train models.
- Exploratory analysis of these sequences using the phylogenetic python suite ete3 to redefine the classification of these clusters.
- Using all this knowledge to develop de novo HMMs to be used in the new application.



2021-2022

Research Assistant

AALBORG UNIVERSITY · Denmark

Genome mining of metagenome-assembled genomes from wastewater treatment plants looking for biosynthetic gene clusters.



EDUCATION

2023-2024

Big Data Analysis

MSc. · University of Murcia



2019-2021

Biotechnology

MSc. · Aalborg University



2015-2019

Biotechnology

BSc. · University of Murcia



2017-2018

Exchange Year

ISEP · University of Tennessee



PROGRAMMING

R

4 years



python

3 years



bash

3 years



LaTeX

4 years



SQL

1 year



TECHNICAL SKILLS

NGS
Genomics
Phylogenetics
Data Wrangling
Visualization
Big Data
Machine Learning
Development
Other

Nanopore · Illumina · Assembly
biopython · metagenomics · transcriptomics
gtdb-tk · ete3 · treeio · iTOL
pandas · dplyr · tidyr · purrr
matplotlib · plotly · ggplot2 · ggiraph · Shiny
Hadoop · slurm · Spark · Snakemake
caret · Keras · scikit-learn · TensorFlow
conda/mamba · Docker · Git
regex · API integration (Requests & http)

LANGUAGES

English

C1 (Advanced) + full professional proficiency

Spanish

Mother tongue

French

B1 Certificate

Danish

Beginner

PUBLICATIONS

Sánchez-Navarro et. al, 2022

Long-Read Metagenome-Assembled Genomes Improve Identification of Novel Complete Biosynthetic Gene Clusters in a Complex Microbial Activated Sludge Ecosystem. *mSystems*. 10.1128/msystems.00632-22