Jose Miguel Serradell Noguera

POSTDOCTORAL RESEARCHER 🌐 BARCELONA, SPAIN ✉ josemiguel.serradell@gmail.com

DETAILS

Barcelona

Spain

+34 667877887

josemiguel.serradell@gmail.com

LINKS

www.linkedin.com/in/jose-miguel-serradell-noguera-

SKILLS

Genomics & Big Data

Machine Learning

Analytical & problem-solving skills

Critical thinking

Excellent communication skills

Team Player

LANGUAGES

Spanish

Catalan

English

👤 PROFILE

Highly motivated PhD with demonstrated research expertise in population genetics and evolution. Formal background in Genetics, specifically in Population Genetics and Molecular Anthropology, Experience in demographic modelling with fastSimcoal and application of Deep Learning, Metaheuristic techniques as well as the use of Approximate Bayesian Computation. Additional experience in GWAS methodologies and genomic data tools like PLINK, BCFTools, etc.

Computer skills: Unix/Linux/Windows; R, Java, Python, etc.

🖥 EMPLOYMENT HISTORY

Postdoctoral Researcher at CIC-BioGune, Bilbao

MARCH 2024 – JUNE 2024

As part of Marigorta's Lab, I've been working on the Meta-Marax (MM) haplotype-GWAS project, producing the Polygenic Risk Scores for the probabilities obtained by MM. I've been also working on deciphering the demographic history of Southeast Asian populations with interest in the effect of Early Modern Human and Denisova Introgression to current day human populations in Asia applying ABC-DL & GP4GP.

PhD Student at IBE – UPF, Barcelona

APRIL 2020 – DECEMBER 2023

I applied Approximate Bayesian Computations (ABC) techniques with deep learning to develop a model to explain the demographic history of North Africa using whole genome data. We also develop a new software to construct demographic models based on meta-heuristics - Genetic Programming for Population Genetics (GP4PG)

Internship at CNAG – UB, Barcelona

DECEMBER 2017 – SEPTEMBER 2018

As part of my master's degree, I worked as an intern at UB-CNAG. My job consisted in the study of CAD as an evolutionary trait. Using mostly R, but also PLINK and other statistical software, I was trying to find if there is any change in the risk of CAD between ancient Homo sapiens and contemporary humans.

Internship at CREAF, Bellaterra

JUNE 2016 - SEPTEMBER 2016

As part of my bachelor's degree, I worked as an intern at CREAF. My job was to generate and edit a database of quantitative traits of Leontodon taraxacoides and perform statistical analysis with R to find evolutionary consequences driven by climate pressures.

🎓 EDUCATION

PhD in Biomedicine, Universitat Pompeu I Fabra, Barcelona

SEPTEMBER 2020-JUNE 2024

Title: Demographic Inference in complex populations: the North African case

Grade: Excellent *Cum Laude*

Master's in Biological Anthropology, Universitat de Barcelona & Universitat Autónoma de Barcelona, Barcelona

SEPTEMBER 2017- JUNE 2018

Bachelor's in Genetic, Universitat Autónoma de Barcelona, Bellaterra

SEPTEMBER 2013-JUNE 2017

COURSES

Linear Regression with Numpy and Python, Coursera

MAY 2023

Introduction to Nextflow, Universitat Pompeu I Fabra

MARCH 2023

Técnicas de Machine Learning basadas en árboles para Investigación científica con R, Museo Nacional de Ciencias Naturales

OCTOBER 2022 – NOVEMBER 2022

Data Science Math Skills, Duke University - Coursera

SEPTEMBER 2022 – OCTOBER 2022

IBE PhD Course, Institut Biologia Evolutiva

JULY 2022

Java Programming I & II, MOOC – University of Helsinki

JUNE 2021

SCIENTIFIC PUBLICATIONS

Serradell, J. M., Lorenzo-Salazar, J. M., Flores, C., Lao, O. & Comas, D. (2024). Modelling the demographic history of human North African genomes points to soft split divergence between populations. Genome Biology, 25:201. https://doi.org/10.1186/s13059-024-03341-4

Lucas-Sánchez, M., Serradell, J. M., & Comas, D. (2021). Population history of North Africa based on modern and ancient genomes. Human Molecular Genetics, 30(R1), R17–R23. https://doi.org/10.1093/hmg/ddaa261

CONFERENCES

Talk at *IV IBE PhD Symposium*, Barcelona

1ST JUNE 2023

Title: Establishing a demographic model for North Africa populations using genome wide data

Talk at *X Jornada de Bioinformàtica I Genòmica*, Valencia

15TH & 16TH DECEMBER 2022

Title: North Africa demographic history through an ABC-DL

REFERENCES

Dr. Oscar Lao Grueso from IBE-CSIC

oscar.lao@ibe.upf-csic.es

Dr. David Comas Martinez from IBE-UPF

david.comas@upf.edu