

# Alba Refoyo-Martínez

Driven by curiosity and a strong sense of organization, I develop reproducible pipelines, create containerised environments, and apply advanced modelling to tackle challenges in omics and health data. With 6+ years of bioinformatics expertise, I focus on meaningful insights through efficiency, reproducibility, and FAIR principles. I'm seeking an inspiring role where I can contribute meaningfully while continuing to grow, innovate, and challenge myself.

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[github.com/albarema](https://github.com/albarema)

## SKILLS

- Bioinformatics workflows & pipeline development
- Data analysis & visualization
- Data management
- Omics data integration
- Collaboration in cross-disciplinary groups
- Cloud computing & containerization

## EXPERTISE

- Python & R
- Docker & Conda
- Snakemake & Nextflow
- nf-core
- Git & GitHub
- Shiny

## PERSONAL QUALITIES

- Motivated by challenges
- Proactive learner
- Highly organized
- Analytical
- Independent
- Decision-making
- Positive

## LANGUAGES

- English: proficiency
- Spanish: native
- Danish: beginner

## VOLUNTEERING

- Conference chair, Evolutionary and Population Genetics in Denmark – EPIC 2023
- Conference organizer, Evolutionary and Population Genetics in Denmark – EPIC 2022
- Member, Globe PhD Committee

## EXPERIENCE

### University of Copenhagen

#### Data scientist

Section for Health Data Science and AI, Public Health

Feb 2024 - Present

- Developed and deployed containerised training modules on Danish HPC systems for omics data
- Designed toolkits for efficient research data management (RDM)
- Optimised workflows for large-scale omics pipelines
- Delivered workshops on containerisation, HPC, scalable and reproducible workflows, and data science practices
- Maintained version-controlled GitHub repositories and managed project documentation using Quarto

#### Postdoctoral researcher

Section for Molecular Ecology and Evolution, Globe Institute

Nov 2022 – Jan 2024

- Developed and optimised computational pipelines for processing omics data
- Implemented novel computational tools tailored to specific research inquiries
- Conducted genetic modelling in collaboration with Variant Bio to explore genetic variation and disease mechanisms.

#### PhD student

Lundbeck Foundation Geogenetics Centre, Globe Institute

Oct 2019 - Oct 2022

Department of Integrative Biology at University of California, Berkeley

Sep 2022 - Oct 2022

- Developed computational pipelines for genomic data analysis
- Utilised whole-genome sequence data to predict genetic disease risk
- Performed data visualization of complex time-series genomic data

#### Graduate researcher

Apr 2018 - Sep 2019

- Developed R-based software to identify genetic selection signatures in next-generation sequencing (NGS) data

## EDUCATION

#### Doctor in Philosophy (DPhil), Bioinformatics

Change of research environment

**University of Copenhagen** 2019-2022

*University of California, Berkeley* Sep. 2022

#### Master of Science (MSc) in Bioinformatics

Elective student

**University of Copenhagen** 2017-2019

*Copenhagen Business School*

#### Bachelor of Science (BSc) in Health Biology

Erasmus program

**Universidad de Alcalá** 2013-2017

*Vrije Universiteit Brussel* 2016-2017

## SCIENCE COMMUNICATION

I have contributed to numerous high-impact publications and developed my communication skills by presenting at global conferences. Check [My Google Scholar](#) to see the list of publications.