ALVARO REGANO

COMPUTATIONAL BIOLOGIST

+34 676 371 361

HARD SKILLS

- Data Analysis
- Statistical Modeling
- Bioinformatics
- Multiomics
- Immunology & Angiogenesis
- scRNASeq & bulk RNASeq
- Next Generation Sequencing (NGS)
- Illumina, Nanopore Sequencing
- High Performance Computing (HPC)
- Docker, Nextflow
- Linux systems (UNIX)
- Scientific writing
- Adobe Suite: Illustrator, inDesign
- MS Office: Excel, Word, PowerPoint

PROGRAMMING

R: Seurat, SingleR, ggplot2, dplyr, Bioconductor, tidyverse, RMarkdown

Python: scanpy, numpy, pandas, matplotlib, scikit-learn, Biopython

Julia, JavaScript, SQL, HTML, CSS, LaTex

SOFT SKILLS

- Insightful
- Autonomy
- Communicator
- Focused

PROFILE

Dedicated Computational Biologist with bench work experience finishing his PhD in Computational & Molecular Biology. My main expertise lay in single cell multiomic (transcriptomic, epigenomic) data acquisition, processing, analysis and visualization.

WORK EXPERIENCE

June 2020 - Present

Research Scientist *Molecular Genetics of Angiogenesis, 3N,CNIC*

- In charge of scRNASeq experimental design, following computational analysis and visualization of over 10 datasets for 5 different projects, some in tandem with scATACseq data.
- Developed bioinformatic pipeline tools and bioassays for iFlpscLineage, a new scLT technology coupled with transcriptomics.
- Managed the Github repository of the research group
- Fostered collaborations with the Theoretical Systems Biology group at DKFZ and Single Cell Genomics unit at CNAG

March 2018 - June 2018

Research Intern *Dpt of Biochemistry and Immunology, TCD*

- Computational analysis of bulk RNASeq data
- FACS, RT-PCR bioassays for validating in silico findings

September 2016 - June 2017

Undergraduate Research Intern *Dpt of Pharmacy, TCD*

- Sinthesized and *in vitro* tested various types of Nanoparticles
- Platelet Isolation, Cell Culture, Zymography, RNA isolation, qPCR

February 2019 - November 2019

Web Developer *Cuidado Mayor*

- Conceptualization and website design with Wordpress, HTML & CSS

February 2019 - December 2019

ESC Volunteer *APS Tavola Rotonda*

January 2018 - June 2018

Invigilator & Demonstrator *Trinity College Dublin*

EDUCATION

PhD Computational & Molecular Biology 2020 - Present

Universidad Autónoma de Madrid (UAM) Pending defense only!

Thesis: Single cell transcriptomical analysis of endothelial to hematopoietic transition

Python programming & algorithms for AI 2024 - Present

Escuela de Organización Industrial (EOI) partnered with Samsung

Web App Dev and Amazon Web Services. 2018-2019

Generation Spain, a McKinsey Social Initiative

MSc. Immunology 2017 - 2018

Trinity College Dublin (TCD). Grade: 74% (Pass with Distinction)

Thesis: The function of γδ T cells and a novel T cell subtype in autoimmune disease

BSc Biochemistry 2013 - 2017

Universidad Complutense de Madrid (UCM). Grade: 8,25

Thesis: Cellular interactions and safety testing of chitosan coated ferrite nanoparticles

LANGUAGES

Spanish	Native	
English	C2	CPE
Italian	B2	CILS
German	B2	TELC

STAYS ABROAD

EMBO PhD. DKFZ, Heidelberg, Germany (March-May 2023)

ESC Volunteer. Anticoli Corrado, Rome, Italy. (2019)

ERASMUS & MSc Student. Trinity College Dublin, Ireland. (2016-2018)

High School Student. Wilton, Connecticut (CT), USA. (2010-2011)

PUBLICATIONS

- Fernández-Chacón, M., Mühleder, S., Regano, A. et al. Incongruence between transcriptional and vascular pathophysiological cell states. Nature Cardiovascular Research 2, 530–549 (2023). https://doi.org/10.1038/s44161-023-00272-4
- Garcia-Gonzalez I, Rocha SF, Hamidi A, Garcia-Ortega L, Regano A, et al. Sanchez-Muñoz MS, Lytvyn M, Garcia-Cabero A, Roig-Soucase S, Schoofs H, Castro M, Sabata H, Potente M, Graupera M, Makinen T, Benedito R. iSuRe-HadCre is an essential tool for effective conditional genetics. Nucleic Acids Res. 2024 Jul 22;52(13):e56. doi: 10.1093/nar/gkae472. PMID: 38850155; PMCID: PMC11260470.
- Garcia-Gonzalez, I., Gambera, S., Regano, A., et al. (2023). iFlpMosaics: A method for the ratiometric induction and high-throughput comparative analysis of mutant and wildtype cells. bioRxiv.