



ALVARO REGANO
COMPUTATIONAL BIOLOGIST



HARD SKILLS

- Data Analysis
- Statistical Modeling
- Machine Learning
- Bioinformatics
- Multiomics
- 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
- Communication
- Focused
- Resourceful

PROFILE

Dedicated Computational Biologist with bench work experience. My main expertise lays in single cell multiomic data acquisition, processing, analysis and visualization. Passionate about leveraging technology to improve our understanding of living systems.

WORK EXPERIENCE

February 2025 - Present

Postdoc Bioinformatics *Genomics and Epigenomics of Pediatric Brain Tumors, 4-1G1, PMC*

- Work on cerebellum organoid validation via transcriptomic data analysis (snRNAseq, Flex scRNAseq).
- Study the tumor microenvironment (TME) in various rare pediatric brain cancer tumors (Medulloblastoma and Ependymoma).

June 2020 - November 2024

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

- In charge of scRNASeq experimental design, following computational analysis employing supervised and unsupervised ML methods and visualization of over 10 datasets for 5 projects.
- Developed bioinformatic pipeline tools and bioassays for iFlpscLineage, a new scLT technology coupled with transcriptomics.
- 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*

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

February 2019 - November 2019

Web Developer *Cuidado Mayor*

EDUCATION

PhD Computational & Molecular Biology 2020 - 2024

Universidad Autónoma de Madrid (UAM)

Thesis: Single cell transcriptomical analysis of endothelial to hematopoietic transition

Course Artificial Intelligence in Python 2024 - 2025

Escuela de Organización Industrial partnered with Samsung (400h)

Web App Dev and Amazon Web Services. 2018-2019

Generation Spain, a McKinsey Social Initiative (400h)

MSc. Immunology 2017 - 2018

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

Thesis: The function of $\gamma\delta$ 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

Postdoc. Princess Maxima Center,
Utrecht, Netherlands (2025 – Present)

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. 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. (2024). iFlpMosaics: A method for the ratiometric induction and high-throughput comparative analysis of mutant and wildtype cells. *Nature Methods* (*in Review*).