

Education

University of Cambridge. Cambridge, UK - PhD in Biological Science. 2017-2020.

University of Cambridge. Cambridge, UK - MPhil in Biological Science. 2016-2017.

Tecnológico de Monterrey. State of Mexico, Mexico - BSc in Biotechnology. 2011-2015.
First class degree with distinction.

RWTH Aachen. Aachen, Germany - Mathematical Simulation Summer Program. 2014.
Excellent performance award.

University of Auckland. Auckland, New Zealand - Study Abroad program. 2013.

Experience

Wellcome Sanger Institute - PhD research (2017-2020)

Supervisor: Dr Gosia Trynka

This project assessed the impact of GWAS variants for immune diseases in T cell function. It comprised 3 areas:

1. Integration of epigenetic data from CD4+ T cells with GWAS variants for immune-mediated diseases. This revealed that T cell activation might be altered in disease.
2. Integration of RNA-seq, scRNA-seq, and proteomics data from CD4+ T cells. This revealed that CD4+ T cells are formed of a continuum of cell states.
3. T cell activation eQTL map. We mapped single-cell eQTLs across 100 individuals and 4 time points during CD4+ T cell activation and integrated these results with GWAS signals.

I performed cell isolation, cell culture, flow cytometry, library preparation, sequencing data analysis (RNA-seq and scRNA-seq), proteomics data analysis, and method development.

Oxbridge Academic Programs - Teaching Position (2018)

I designed and delivered a 5-week long course on Data Science. I used R and covered topics such as analysis of multivariate data, statistical testing, dimensionality reduction, linear models, and principles of machine learning.

Wellcome Sanger Institute - MPhil research (2016-2017)

Supervisor: Dr Gosia Trynka

This project investigated how CD4+ T cells and macrophages respond to cytokines.

I isolated, cultured, differentiated, and stimulated primary immune cells from peripheral blood. I also performed RNA-seq data analysis.

Lymphopoiesis Lab, XXI Century Medical Centre, Mexico City - Research internship

Supervisor: Dr Rosana Pelayo

In this 4-month internship I studied how niches in the bone marrow are modified during acute lymphoblastic leukaemia.

I performed cell culture and flow cytometry to investigate how hypoxia impacts the phenotype of lymphoblasts in 3D cultures.

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| Awards | <p>2019 - Reviewer's choice poster award at ASHG meeting. Houston, TX, USA.</p> <p>2016-2017 - Twice receiver of the Gates Cambridge Scholarship. Cambridge, UK.</p> <p>2015 - Mexican representative at Novartis International BioCamp. Basel, Switzerland.</p> <p>2014 - Silver medal at the iGEM competition. Boston, MA, USA.</p> |
| Conferences | <p>Posters</p> <p>2019 - American Society of Human Genetics (ASHG) Meeting. Houston, TX USA. <i>Single-cell transcriptomics identifies an effectorness gradient of CD4+ T cells.</i></p> <p>2019 - Gordon Research Conference (GRC) in Human Genetics and Genomics. Waterville Valley, NH, USA. <i>Single-cell transcriptomics identifies an effector gradient of CD4+ T cells.</i></p> <p>2018 - Computational Models in Immunology Meeting. Paris, France. <i>Multi-omic characterisation of the response of CD4+ T cells to cytokines.</i></p> <p>Talks</p> <p>2019 - Illuminating the Druggable Genome Symposium. Wellcome Genome Campus, Hinxton, UK. <i>Mapping immune disease causal cell types for effective target identification.</i></p> <p>2019 - Gordon Research Seminar (GRS) in Human Genetics and Genomics. Waterville Valley, NH, USA. <i>Single-cell transcriptomics identifies an effector gradient of CD4+ T cells.</i></p> |
| Programming skills | R, Python, Bash, HTML, version control (Git) |
| Laboratory skills | Cell isolation, cell culture, flow cytometry, RNA-seq, scRNA-seq, ChIP-seq, ATAC-seq. |
| Publications | <p>Cano-Gamez E, Soskic B, Roumeliotis, TI, <i>et al.</i> (2019). Single-cell transcriptomics identifies an effectorness gradient shaping the response of CD4+ T cells to cytokines. <i>BioRxiv</i>. doi: https://doi.org/10.1101/753731</p> <p>Soskic B, Cano-Gamez E, Smyth DJ, <i>et al.</i> (2019). Chromatin activity at GWAS loci identifies T cell states driving complex immune diseases. <i>Nature Genetics</i>. 51, 1486–1493. https://doi.org/10.1038/s41588-019-0493-9</p> <p>Cano-Gamez E, Trynka G. (2020). From GWAS to function: using functional genomics to identify the mechanisms underlying complex diseases. <i>Frontiers in Genetics</i> [in review].</p> <p>Bossini-Castillo L, Glinos DA, Kunowska N, <i>et al.</i> (2019). Immune disease variants modulate gene expression in regulatory CD4+ T cells and inform drug targets. <i>BioRxiv</i>. https://doi.org/10.1101/654632</p> |
| Languages | English (C1), French (B2), Italian (B2), German (A2/B1), Spanish (native speaker). |
| Additional experience | Secretary of Cambridge University Mexican Society, Volunteer at STEM Ambassadors Program, Editor for the Gates Cambridge magazine, Social Secretary for Gates Cambridge Student Council. |