

Roger Casals-Franch

Computational Biologist · PhD Candidate in Bioinformatics

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PhD defence expected July 2027

RESEARCH INTERESTS

Computational biologist developing mechanistic and predictive models of immune-cell state transitions from single-cell and multimodal data. My research integrates transcriptomic, epigenomic, metabolic and T-cell receptor repertoire data to investigate how T and NKT cells respond to vaccination, chronic infection, cancer and immunotherapy. I focus on gene regulatory network inference, trajectory analysis and perturbation modelling, and I am increasingly exploring deep-learning and biological foundation-model approaches for large perturbational datasets. My long-term goal is to combine mechanistic systems biology with modern AI to generate interpretable hypotheses about immune control, dysfunction and therapeutic response.

RESEARCH EXPERIENCE

Bioinformatics Research Support – HIV Vaccination

May 2025 – present

IrsiCaixa AIDS Research Institute, Badalona – group of Prof. Christian Brander

- Analyse single-cell transcriptomic and epigenomic data from BCN03, a therapeutic HIV vaccine trial, to characterise vaccine-induced changes in gene regulation.
- Integrate T- and NKT-cell state annotation with TCR repertoire analysis to compare clonotype usage and immune-response patterns between people with HIV and healthy controls.

PhD Candidate in Bioinformatics

Sept 2023 – present

Universitat de Vic – Universitat Central de Catalunya (UVic-UCC)

- Develop mechanistic and predictive methods for GRN inference from single-cell multi-omic data, focused on cell-state transitions and responses to perturbation.
- Developing Boolyne, a Boolean GRN framework designed to reproduce observed cell states and transitions and support interpretable in silico perturbation analysis.
- Applied trajectory inference and regulatory network analysis to characterise T-cell reprogramming during PD-1 blockade, resolving distinct cytotoxic, exhausted, helper and regulatory programs.
- Co-authored the GRETA benchmark of multimodal single-cell GRN inference methods with the Saez-Rodriguez group, Heidelberg.

Bioinformatics Support and HPC Administrator

Sept 2023 – present

Institute for Research and Innovation in Life Sciences and Health in Central Catalonia (IRIS-CC), UVic-UCC

- Provide bioinformatics analysis, workflow development and technical support to multidisciplinary life-science and health research groups.
- Administer a Linux/Slurm HPC environment, including user support, fair-share resource allocation and reproducible computing practices. [Research workflows](#).

Visiting Researcher – Metabolic Modelling

May – June 2025

Biomedical Center, University of Iceland, Reykjavík

- Gene expression-informed prediction of metabolism.

Visiting Researcher – Regulatory Network Inference

May – July 2024

Saez-Rodriguez group, University of Heidelberg

- Benchmarked GRN inference from multimodal single-cell data; co-authored the GRETA preprint (Publication 2).

MSc Research Project

May – July 2023

Vall d'Hebron Institute of Oncology (VHIO), Barcelona

- Benchmarked single-cell RNA-seq trajectory inference methods in cancer biology.

PUBLICATIONS

Accepted

1. **Casals-Franch R**, Villà-Freixa J, Nonell L, López García de Lomana A. Transcriptional reprogramming of tumor-infiltrating T cells during PD-1 blockade revealed through gene regulatory network and trajectory inference in squamous cell carcinoma. **Accepted, Springer Protocols** (2026). Preprint: *bioRxiv* (2025), [doi:10.1101/2025.10.15.682506](https://doi.org/10.1101/2025.10.15.682506)

Under review

2. Badia-i-Mompel P, **Casals-Franch R**, Wessels L, Müller-Dott S, Trimbou R, Yang Y, Ramirez Flores RO, Saez-Rodriguez J. Comparison and evaluation of methods to infer gene regulatory networks from multimodal single-cell data. Under revision at *Nature Methods*. Preprint: *bioRxiv* (2024), [doi:10.1101/2024.12.20.629764](https://doi.org/10.1101/2024.12.20.629764)
3. **Casals-Franch R**, Nonell L, Villà-Freixa J, López García de Lomana A. Integrating trajectory inference and gene regulatory network analysis to resolve transcriptional programs of T cell state transitions in the tumor microenvironment. Under revision at *PLOS ONE*. Protocol preprint: *bioRxiv* (2026), [doi:10.64898/2026.05.12.724558](https://doi.org/10.64898/2026.05.12.724558)

SOFTWARE

Boolyne – Boolean GRN framework for mechanistic modelling of cell-state transitions and interpretable in silico perturbation analysis. *In development*.

TECHNICAL SKILLS

Programming and analysis: Python, R, Bash, Git; pandas, NumPy, scikit-learn and scientific visualisation.

Single-cell and multi-omics: scRNA-seq analysis, cell-state annotation, trajectory inference, GRN inference, epigenomic integration, TCR repertoire analysis and perturbation modelling; Scanpy/scverse, Monocle3, decoupler, SCENIC/SCENIC+, CellOracle and Pando.

Machine learning: PyTorch, supervised and unsupervised learning, variational autoencoders, representation learning and deep learning for perturbational data.

Reproducible computing and HPC: Linux, Slurm, GPU computing, Snakemake, Docker and Apptainer/Singularity.

AWARDS AND DISTINCTIONS

- Open Problems – Single-Cell Perturbations: ranked in the top 10% globally for predicting gene-expression responses to unseen perturbations using variational autoencoders.
- Audience Award, Catalan final, "Present Your Thesis in 4 Minutes" (FCRI), 2026.
- Winner, 9th UVic-UCC "Present Your Thesis in 4 Minutes" competition, 2026.
- Selected for the VHIO Computational Oncology Master's Thesis Award, 2024.

FUNDING

- Investigo predoctoral research contract, 2023 – present.
- Erasmus+ mobility grant for a research stay in Iceland, 2025.
- Erasmus+ mobility grant for a research stay in Germany, 2024.
- Travel grant, scverse conference, Stanford University, 2025.

SELECTED TALKS AND POSTERS

- **Poster** – On the prediction of observed cell states from inferred gene regulatory networks. 25th European Conference on Computational Biology (ECCB), Geneva, September 2026.
- **Talk and poster** – Mechanistic inference of cell state transitions via Boolean GRNs from single-cell data. JBI Conference, Madrid, October 2025; scverse conference, Stanford University, November 2025.
- **Poster** – Trajectory inference on T cell response upon immunotherapy in non-melanoma skin cancer. 1st Congress of the Spanish Society of Bioinformatics and Computational Biology (SEBiBC), València, October 2024.
- **Flash talk and poster** – Trajectory inference methods comparison in cancer immunotherapy. VHIO Computational Oncology Master's Thesis Award, Barcelona, February 2024.
- Five additional presentations at UVic-UCC and Catalan interuniversity PhD workshops, 2024–2025.

EDUCATION

PhD in Bioinformatics

2023 – expected 2027

Universitat de Vic – Universitat Central de Catalunya (UVic-UCC)

Supervisors: Jordi Villà-Freixa and Adrián López García de Lomana.

MSc in Bioinformatics and Biostatistics

2022 – 2023

Universitat Oberta de Catalunya (UOC) / Universitat de Barcelona (UB)

Average grade: 8.58/10; honours in Statistical Inference. Thesis: scRNA-seq trajectory inference methods for T-cell dynamics in the tumour microenvironment.

BSc in Biotechnology

2018 – 2022

Universitat Autònoma de Barcelona (UAB)

Bachelor's research project grade: 9/10; honours in Plant Physiology.

TEACHING AND MENTORING

Instructor, UVic-UCC:

- Bioinformatics II – BSc Biotechnology, 3rd year, 3 ECTS (2026).
- Mathematics – BSc Business Administration, 1st year, 6 ECTS (2026).
- Integrated Project I – BSc Biomedicine, 1st year, 3 ECTS (2025, 2026).
- Tools and workflows in HPC environments – internal research staff workshop (2025).

Mentoring: currently co-supervising one BSc thesis on single-cell transcriptomics; previously supervised four undergraduate students in data analysis and research methodology.

LANGUAGES

Catalan and Spanish (native) • English (fluent) • French (intermediate) • German (basic).

EARLIER EXPERIENCE

R&D and quality technician roles in food biotechnology (Embotits Monells, 2022–2023; Casa Tarradellas, 2021) and a university internship in fermentation, cloning and strain screening for 3-HP production (Chemical Engineering Department, UAB, 2021–2022).