Ferran Cardoso Rodriguez

Curriculum Vitae

Computational biologist experienced in analysing sc-*omic* and other high-dimensional and graph-structured biodata. With a strong biology and bioinformatics (R/Python) foundation, I have presented collaborative research on characterising CRC dynamics, deployed data analysis pipelines, and developed 1) ML classifier models, 2) KG-based approaches to study cell communications, 3) and visualisation tools.

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CURRENT POSITION

SEPT. 2019 – PRESENT

UCL CI, PhD in Computational Biology
Single-Cell Omic Analysis

Analysed single-cell *omic* profiles of CRC organoids and their TME using established and novel computational approaches in both local and remote environments.

Developed and **Deployed** tools in package repositories, as web-tools or Docker containers.

Visualised results using bespoke and automated interactive report generation.

Disseminated outputs via oral presentations, scientific posters, and scientific research articles.

Collaborated with peers in subjects ranging from drug screening (Ramos Zapatero & Tong *et al.* 23) to CAR T-cell engineering (Michelozzi *et al.* 23).

Community work via public engagement events and BSc. student teaching support.

Current Position Highlights

CRC Stem Cell Polarisation — Main Research Project
Characterised **dynamics** regulating stromal and oncogenic **stem cell** polarisation in the context of **colorectal cancer**. Leveraged **remote compute** as well as state-of-the-art **scRNA-seq** analysis workflows including **compositional** and **cell-cell communication** analyses, and **VAE**-based **label transfer** and **integration** with patient cohorts. Outputs in the form of articles, public data share and code repositories, and guided by illustrated **Jupyter** notebooks.
Publication: Cardoso Rodriguez & Qin et al. 2023 📄
Project repository ⌗

VRland — Method Development
Valley-Ridge score to generate data-driven **Waddington**-like **landscapes** of cellular **plasticity** and **differentiation** from **scRNA-seq** data. In active development to become a cloud-hosted interactive web-app.
Publication: Cardoso Rodriguez & Qin et al. 2023 📄
Project repository ⌗

CyGNAL — Analysis Pipeline
Pipeline for the **analysis** and interactive **visualisation** of **mass cytometry** data via PTM signalling and cell-state **classification** via ensemble **ML** methods.
Publication: Sufi & Qin et al. 2021 📄
Project repository ⌗

PAST EXPERIENCE

AUG. – OCT. 2022

Yale University, Visiting Researcher
KGs for Cell Communication

Awarded with the UCL-Yale PhD exchange bursary.
Explored novel methods to characterise inter- and intra-cellular communications using signalling knowledge graphs, including embedding of directed gene networks, and *omic* profile projection.
Assembled and **Embedded** custom signalling KGs leveraging remote GPU compute.
Developed a Python package to compute hierarchy scores on directed graphs.
Disseminated outputs on international conferences.
Collaborated on-site with Smita Krishnaswamy's lab at Yale University.
Blog on conference paper 🌐

JAN. – SEPT. 2019

Imperial College London, Bioinformatics
MSc Computational Projects

Masters degree at Imperial College London uniquely characterised by **three** distinct computational **projects** and reports.

MSc Project 3 — JUN. – SEPT. 2019
Genomic Annotation Pipeline
Developed AnnoRE, a **pipeline** for **API-based** querying of databases and downstream **annotation** of **genetic variants** and metabolomics high-throughput data to study **complex trait** diseases.
Project repository ⌗

MSc Project 2 — APR. – JUN. 2019
scRNAseq data analysis
Analysis of droplet-based **scRNA-seq** datasets to characterise **cardiac** stem populations and **development**.
Web report 🌐

MSc Project 1 — JAN. – APR. 2019
Flux-Balance app development
Group project developing MetEOr, a Flask-based **web-app** for visualising and performing **Flux Balance Analysis** on whole-organism **metabolic models**. **Back-end** developer responsible for the FBA logic and codebase.
Project repository ⌗

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SELECTED OUTPUTS

PUBLICATION	**Cardoso Rodriguez & Qin *et al.*, 2023**
	A SINGLE-CELL PERTURBATION LANDSCAPE OF COLONIC STEM CELL POLARISATION
	DOI: BioRxiv (accepted at Cell)
PACKAGE	○ **FerranC96/pyKrack**
	COMPUTING KRACKHARDT HIERARCHY SCORE ON DIRECTED GRAPHS
	PyPI: pykrack
PIPELINE	○ **TAPE-Lab/CyGNAL**
	CYTOF SIGNALLING ANALYSIS (CYGNAL) PIPELINE
	*DOI: Zenodo	Nat. Protocols*
TOOL	○ **FerranC96/VRland**
	VALLEY-RIDGE SCORE FOR SINGLE-CELL WADDINGTON-LIKE LANDSCAPES
	DOI: BioRxiv

EDUCATION

2019 – 2023	**PhD Computational Biology**
	UNIVERSITY COLLEGE LONDON
	PhD programme at Dr. Chris Tape's lab (UCL Cancer Institute).
	Viva passed w/o corrections
2022	**UCL-Yale PhD Exchange**
	Collaborative exchange at Prof. Smita Krishnaswamy's lab (YSM/SEAS Yale University)
2018 – 2019	**MSc Bioinformatics and Theoretical Systems Biology**
	IMPERIAL COLLEGE LONDON
	Multi-project programme. Merit
2014 – 2018	**BSc Biotechnology**
	UNIVERSITAT DE BARCELONA
	Molecular Biotechnology specialisation.
	1st Class (8.7/10)
2018	**Erasmus Exchange**
	BSc. thesis in immune infiltrate of craniopharyngiomas (QMUL).
	1st Class (9.5/10)
2017	**IBEC Visiting Student**
	Contribution to Núria Montserrat's group (i)Pluripotency for organ regeneration.
2012 – 2014	**Sciences Baccalaureate**
	IES JOAN MIRÓ, CORNELLÀ DE LL.
	1st Class (12.8/14)

SKILLS

COMMUNITY	**Collaboration** both within and outside research group.
	Volunteering at public and patient engagement events.
	Teaching tutorials for BSc students and ESL teaching experience.
	Public speaking at international conferences and events.
	FAIR and **FOSS** advocate.
TECHNICAL	**Languages**: Proficiency in Python and R. LaTeX, Markdown, web technologies.
	Reporting: Publication-grade figures, interactive visualisations, web-apps.
	Workflows: Remote computing (CPU and GPU-accelerated) in HPC, nextflow pipelines, containerisation.
ANALYSIS	**Pipelines**: BCL to FASTQ, custom transcriptome references, sequence alignment.
	sc-*omic* data: Dim. reduction, clustering, dif. expression, compositional analysis, cell-cell communications, cellular dynamics, data integration.
	ML applications: Knowledge-graph embedding, graph signal processing, classification models, PyTorch.
DEV.	**Team Projects**: Version control and collaboration through git, kanban-based tools.
	Build and deployment: Multi-language tools, interactive reports, PyPI and conda packaging, nbdev for notebook-centric development, container deployment.