

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 and 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.

🏠 N16 – London (UK)
☎ +44 07597532973
✉ ferran.cardoso.19@ucl.ac.uk
fcardoso96@outlook.com
🌐 <https://github.com/FerranC96>
🌐 ORCID: 0000-0002-1376-1242

RELEVANT EXPERIENCE

SEPT. 2019 – PRESENT

UCL Cancer Institute, 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.

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 🌐

AUG. – OCT. 2022

Yale University, Visiting Researcher

KGs for Cell Communication

Awarded with the UCL-Yale PhD **exchange** bursary, I orchestrated a **collaboration** with Smita Krishnaswamy's lab.

During my stay in **Yale** I explored novel methods to characterise inter- and intra-**cellular communications** using signalling **knowledge graphs**, including gene **embedding** approaches of **directed gene networks**, and projecting *omic* profiles of cells as **signals** on the gene graphs.

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 MetEO, 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 <i>DOI: BioRxiv (in revision at Cell)</i>
PACKAGE	 FerranC96/pyKrack COMPUTING KRACKHARDT HIERARCHY SCORE ON DIRECTED GRAPHS <i>PyPI: pykrack</i>
PIPELINE	 TAPE-Lab/CyGNAL CYTOF SIGNALLING ANALYSIS (CYGNAL) PIPELINE <i>DOI: Zenodo Nat. Protocols</i>
TOOL	 FerranC96/VRland VALLEY-RIDGE SCORE FOR SINGLE-CELL WADDINGTON-LIKE LANDSCAPES <i>DOI: BioRxiv</i>

EDUCATION

2019 – 2023(EST)	PhD Computational Biology UNIVERSITY COLLEGE LONDON <i>PhD programme at Dr. Chris Tape's lab (UCL Cancer Institute).</i>
2022	UCL-Yale PhD Exchange <i>Collaborative exchange at Prof. Smita Krishnaswamy's lab (YSM/SEAS Yale University).</i>
2018 – 2019	MSc Bioinformatics and Theoretical Systems Biology IMPERIAL COLLEGE LONDON <i>Multi-project programme.</i>
2014 – 2018	BSc Biotechnology UNIVERSITAT DE BARCELONA <i>Erasmus at WHRI (QMUL).</i>

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.