

# Ferran Cardoso Rodriguez

## Curriculum Vitae

### SELECTED OUTPUTS

PUBLICATION	<b>Cardoso Rodriguez &amp; Qin et al., 2023</b> A SINGLE-CELL PERTURBATION LANDSCAPE OF COLONIC STEM CELL POLARISATION DOI: <a href="#">BioRxiv</a>
PACKAGE	<b>FerranC96/pyKrack</b> COMPUTING KRACKHARDT HIERARCHY SCORE ON DIRECTED GRAPHS PyPI: <a href="#">pykrack</a>
PIPELINE	<b>TAPE-Lab/CyGNAL</b> CYTOF SIGNALLING ANALYSIS (CYGNAL) PIPELINE DOI: <a href="#">Zenodo</a>

### RELEVANT EXPERIENCE

SEPT. 2019 – PRESENT

UCL, PhD Thesis

#### *Single-Cell Omic Analysis* –(Misc.)

Using novel computational approaches to study **CRC organoids** and the **TME** through single-cell *omics*.

**UCL-Yale Collab** –(Python)

Collaboration

Orchestrated an on-site **collaboration** between UCL and **Yale** aiming to characterise cellular **communications** using **graph-based** approaches. Blog entry [📝](#)

**VRland** –(Python)

Method Development

Valley-Ridge score to generate data-driven **Waddington**-like **landscapes** of cellular **plasticity** and **differentiation** from **scRNA-seq** data. Project repository [🔗](#)

Publication: Cardoso Rodriguez & Qin et al. 2023 [📄](#)

**CyGNAL** –(Python/R)

Analysis Pipeline

**Pipeline** for the **analysis** and interactive **visualisation** of **mass cytometry** data via PTM signalling and cell-state classification via ensemble MLS. Project repository [🔗](#)

Publication: Sufi Qin et al. 2021 [📄](#)

#### *MSc Computational Projects*

Imperial, MSc Project 3

Jun. – Sept. 2019

**AnnoRE pipeline** –(Python/R)

**Pipeline** for downstream annotation of **genetic variants** and metabolomics high-throughput data to study **complex trait** diseases. Project repository [🔗](#)

Imperial, MSc Project 2

Apr. – Jun. 2019

**scRNAseq data analysis** –(R)

Analysis of **scRNA-seq** datasets to characterise **cardiac** development. Web report [📄](#)

Imperial, MSc Project 1

Jan. – Apr. 2019

**FBA Flask app back-end** –(Python)

Group project developing MetEO, an **online tool** for visualising and performing **Flux Balance Analysis** on whole-organism **metabolic models**. Project repository [🔗](#)

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### EDUCATION

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

### SKILLS

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