Luiz Felipe Piochi

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______ EDUCATION _____

UNIVERSITY OF LORRAINE - IAEM | PhD in Computer Science

2024 - ongoing

Thesis: "Learning host-pathogen surface interactome to design novel therapeutics."

UNIVERSITY OF COIMBRA - DCV | MSc in Cell and Molecular Biology

2020 - 2023

· GPA: 3.9; Extensive coursework in Bioinformatics, Statistics; Top 3% of the University

EXPERIENCE _____

INRIA - CAPSID

PhD Student

Nancy, France

September 2024 – ongoing

- · Working with advanced deep learning for protein design and drug development
- Developing a deep learning model for the prediction of protein-ligand interactions

ERBEL.EUSGenomics Data Scientist

Bilbao, Spain

June 2024 – Sep 2024

- · Contributed to an EU-level and a national-level project for the study of beekeeping and metagenomics
- Built two automated metagenomics pipelines for NGS data processing, speeding up the in-house workflow more than 70%
- Processed and analyzed over 1TB of metagenomics sequencing data

BIOCANT - DATA-DRIVEN MOLECULAR DESIGN LAB Bioinformatics Researcher

Cantanhede, Portugal Nov 2021 – Dec 2023

- Developed and published a deep learning tool for drug-resistance prediction in a high impact bioinformatics journal
- Processed and analyzed multi-omics data from over 10 public datasets and hundreds of cell lines
- Established a pipeline for the virtual screening of over 300 compounds against proteins of interest in neurodevelopment

CNC-UC - MITOLAB Undergraduate Researcher Coimbra, Portugal Oct 2019 – July 2020

- · Implemented multiple metabolic assays and characterized the dynamics and patterns of different cancer cell lines
- Developed a brief in-house Python pipeline for the analysis and visualization of different data types, contributing to a 30% reduction in time spent on repetitive tasks by different project members
- · Compiled and published project a in review format on a high impact ageing journal

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Programming Python, R, Bash, SQL, JavaScript, Snake- Languages Portuguese (native), English (fluent), Spanish make (C2), French (A0), German (A1)

Frameworks numpy, pandas, torch, tensorflow

GORGON PROJECTS ________

Python [Numpy, Pandas], R [Phyloseq, gaplot2], Snakemake

- Developed a modular and scalable metagenomics pipeline for rapid processing and analysis of large-scale NovaSeq datasets
- Streamlined complex processes from raw data preprocessing to detailed reporting, yielding quick insights
- Designed for reproducibility across different computational environments and efficient handling of varying dataset sizes

DELFOS 2023

- Python [Numpy, Pandas, TensorFlow], R [Tidyverse, Seurat]
- Developed an AI model learning from drug chemistry and multi-omics data, including single-cell data, to predict how cells will respond to different compounds
- Outperformed state-of-the-art algorithms at the time, achieving high regression metrics across several validation steps
- · Published on Oxford University Press Bioinformatics