

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** Nancy, France
PhD Student 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.EUS** Bilbao, Spain
Genomics Data Scientist 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** Cantanhede, Portugal
Bioinformatics Researcher 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** Coimbra, Portugal
Undergraduate Researcher 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

SKILLS

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

Frameworks numpy, pandas, torch, tensorflow

PROJECTS

- GORGON** 2024
• Python [Numpy, Pandas], R [Phyloseq, ggplot2], 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
- DELFO** 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