

Beatriz De Moraes Caldas Lopes Manso

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Bioinformatics scientist with a PhD in Bioinformatics and hands-on experience in transcriptomic analysis, machine learning for genomic data, and reproducible computational pipelines. Skilled in translating complex genomic and transcriptomic data into robust, reproducible software using Python, R, Snakemake, and modern machine learning frameworks. Background spans academic research, open-source software development, and teaching leadership, with a focus on applying computational methods to real-world biomedical and clinical problems.

Technical Skills

- Programming & Tools: Python, R, C++, Bash, Git, Snakemake, Linux, Cloud Computing, HPC
- Machine Learning: Deep Learning (CNNs, ANNs), Scikit-learn, Keras, TensorFlow
- Genomics & Bioinformatics: RNA-seq, Microarray, Differential Expression, Variant Annotation, limma, Bioconductor
- Other: Web Development, Project Management, Technical Writing

Research Interests

- Genomic data integration & transcriptomic analysis
- Deep learning for gene expression prediction (ANNs, CNNs)
- Rare diseases and cancer genomics
- Variant annotation & interpretation pipelines

Education

PhD in Bioinformatics

University of West London, UK | Sep 2022 – May 2026

Focus: Deep learning approaches for classifying brain tissue from microarray gene expression data, with cross-validated model selection and benchmarking against classical machine learning methods.

Methods: Differential gene expression analysis, CNN/ANN development in C++ and Python, repeated stratified cross-validation, non-parametric statistical testing

MSc in Bioinformatics – Distinction

University of West London, UK | Feb 2021 – Aug 2022

BSc in Biomedical Sciences

CESPU, Porto, Portugal | Sep 2016 – Aug 2020

Erasmus Program

Universitat de Valencia, Spain | Jan 2019 – Jul 2019

Teaching Experience

Course Leader, MSc Bioinformatics & Module Leader, BSc Modules

University of West London | Sep 2025 – Present

- Lead curriculum design, delivery, and quality assurance for the MSc Bioinformatics programme
- Serve as module leader for two BSc modules, overseeing content design, delivery, and assessment
- Manage teaching staff and coordinate timetabling, liaising with programme leadership on course development
- Continue mentoring and supervising MSc and BSc students on computational biology coursework and projects

Teaching Assistant – MSc Bioinformatics

University of West London | Sep 2022 – Aug 2025

- Delivered lectures and practical sessions for modules including Bioinformatics and Genome Analysis and Functional Genomics
- Designed and delivered practical lab materials and exercises, guiding students through hands-on computational biology work

- Marked assessments and provided feedback to MSc and BSc students, fostering strong engagement and understanding

Professional Experience

Bioinformatics Software Developer – Internship

OakVar (Remote) | Jan 2023 – Aug 2023

- Built Snakemake wrappers for OakVar's variant annotation platform, enabling streamlined, reproducible genomic workflows for clinical variant interpretation
- Collaborated with bioinformatics developers to improve reproducibility, scalability, and modularity of workflows
- Contributed to open-source development and documentation

Web Content Manager

Noveris, LDA, Porto | Oct 2018 – Nov 2021

- Led optimization of company website through performance analytics, content strategy, and branding
- Managed internal and external projects, coordinating cross-functional teams
- Analyzed site analytics to drive continuous UX and performance improvements
- Oversaw full project lifecycle: content creation, brand development, and marketing delivery
- Partnered with IT to implement cybersecurity practices and strengthen project lifecycle management

PhD Research Overview

PhD Thesis Project

- Developed convolutional and artificial neural network models from first principles in C++ for classifying brain tissue from microarray gene expression data
- Performed differential expression analysis on public microarray datasets (GEO / CuMiDa) to select candidate gene features for classification
- Integrated machine learning pipelines with standard bioinformatics tooling for reproducible, version-controlled analysis
- Applied repeated stratified cross-validation, Friedman testing and Bonferroni-corrected post-hoc comparisons to evaluate model performance

Academic Presentations

- Internal PhD Seminars, University of West London: Presented on gene expression classification and CNN-based modelling
- Manuscript in preparation

Additional Information

- Eligible to work in the UK
- Fluent in English and Portuguese