Giorgia Del Missier

📞 +44 7923892819
✉ delmissiergiorgia@gmail.com
in /giorgia-del-missier
⌗ /gioodm

🥧 Experience

Imperial College London (Ledesma-Amaro Synthetic Biology group) — London, UK
Computational biologist (contract researcher) — Sep. 2023 – Present
Computational biologist (internship) — Nov. 2022 – Jun. 2023

I am currently working at the intersection of structural biology and bioengineering, leveraging computational tools to identify and enhance protein targets in industrially relevant organisms, especially yeast.

During my research at the Ledesma-Amaro group I designed and developed a novel pipeline to perform protein functional annotation using AlphaFold-predicted structural models. Tasks included:

> algorithm design, and Python and Unix scripting, optimising code for speed and efficiency through parallel programming techniques

> use of state-of-the-art structural and sequence alignment tools to enable a comprehensive analysis at a whole-proteome level

> use of REST APIs for web scraping to extract valuable data from bioinformatics databases

> use of network analysis, statistical testing and enrichment techniques for protein function inference

> design of an intuitive web application using Python DASH for user-friendly visualisation of results

> design and execution of benchmark analyses to assess pipeline performance

> application of the developed pipeline for Genome-scale Metabolic models curation and phylogenetic cross-organism comparison

> communication of findings through presentations and reports, ensuring accessibility and clarity for all team members

> drafting manuscript for scientific publication (in progress)

> participation in the selection, evaluation, and interview process of new candidates for internships and collaborations

> supervising and mentoring of students for computational projects, providing guidance and support to enhance their research skills and project outcomes

Maastricht Center for Systems Biology — Maastricht, NL
Lab technician (internship) — Jun. 2021 – Sep. 2021

My goal was to functionally validate proteins associated with mitochondrial dynamics mechanisms, as predicted through computational models. Lab activities included:

> PCR and quantitative PCR assays

> construction of esiRNAs

> molecular cloning and Gibson assembly techniques

> write and present weekly reports on experimental procedures and findings to the rest of the team

> manage lab resources and supplies to optimise inventory levels

IRCSS Institute of Neurological Sciences   Bologna, IT
Bioinformatician (internship)   Nov. 2020 – Apr. 2021

I worked in the Neurogenetics lab, which focuses on identification of the molecular basis and pathogenic mechanisms of mitochondrial neurological diseases. My activities included:

> examination of Whole-Exome Sequencing data for a cohort of 64 patients with hereditary optic neuropathies

> design and implementation of Python, R and Unix scripts for fast and streamlined analysis of Next Generation Sequencing data

> evaluation and use of phenotype-driven tools for variant prioritisation, with the aim of identifying new genetic markers of disease

> use of software tools in conjunction with relevant databases for genomics data exploration and variant analysis

> preparation of regular reports to communicate findings to a multidisciplinary team

🖥 Skills

Programming languages   Python (advanced), R (advanced), Unix (advanced) and MATLAB (intermediate); experience with Linux, MacOS, Windows and HPC platforms

Developer tools   version control with Git and GitHub; web development with HTML/CSS markup and Python DASH; experience with REST APIs for data retrieval and integration; Neo4j graph database management system and Cypher query language

Scientific expertise   Machine Learning (supervised and unsupervised learning, model building and optimisation, feature selection, regression and classification tasks - R, Python scikit-learn); Data cleaning (Pandas, NumPy, SciPy) and visualisation (Matplotlib, Plotly, Seaborn); Mechanistic Modeling (ODEs, PDEs, agent-based, constraint-based); Omics data analysis (BLAST, SAM and BAMtools, bcftools, plink, BioConductor, IGV, R limma, Cytoscape); Structural biology (AlphaFold, ChimeraX); Linear and Non-Linear Dynamical systems

Productivity softwares   LaTeX, Microsoft Office tools (Word, Excel, PowerPoint)

🎓 Education

Maastricht University   Maastricht, NL
MSc Systems Biology   Sep. 2021 – Jul. 2023

> Final grade: GPA: 8.5/10, *cum laude*
> Dissertation title: "WASP: A new Pipeline for Functional Annotation of Proteins using AlphaFold Structural Models"
> Modules included: Systems Biology, Modelling Biosystems, Dynamic Game Theory, Dynamical Systems and Non-Linear Dynamics, Network Biology, Machine Learning and Multivariate Statistics

Alma Mater Studiorum - University of Bologna   Bologna, IT
BSc Genomics   Sep. 2017 – Mar. 2021

> Final grade: 110/110, *with honours*
> Dissertation title: "Phenotype-driven Variant Prioritisation Tools: Analysis of Whole Exome Sequencing in Patients with Hereditary Optic Neuropathy"
> Modules included: Bioinformatics, Programming, Statistics and Data Science, Molecular Biology and Genetics, Epigenomics, Metagenomics, Metabolomics, Proteomics and Structural Biology