

Marco Anteghini, PhD

Contact

Work Address

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Links

LinkedIn
GitHub
NVO Bioinformatika - Bioinform
Google Scholar

Languages

Italian: mother tongue

English C1

German A2

Experienced and dynamic bioinformatician with a solid track record in handling complex projects in both academic and corporate settings. I excel in team environments, contributing my expertise to help achieve common goals, and I am equally adept at managing and executing projects independently. My adaptability and broad skill set are demonstrated by my contributions to various research areas related to bioinformatics and education.

Education

2019-2023	PhD in Bioinformatics Thesis: Revealing function, interactions, and localization of peroxisomal proteins using Deep Learning-based approaches	Wageningen University and Research
2017-2019	M.Sc. in Bioinformatics Thesis: Building MSMs and HMMs from MD data of the A- β 40	University of Bologna
2013-2017	B.Sc. in Biological sciences Thesis: Dietary indications for triathletes	University of Ferrara

Research and Development experience

May 2024-ongoing	BioFold - Università di Bologna <i>Bioinformatician</i> Developing advanced bioinformatics pipelines for the analysis of nutrigenomic and microbiota data. My role involves designing and implementing robust and efficient workflows to process and interpret complex biological datasets, contributing to innovative research in personalized nutrition and gut microbiome health. This work entails close collaboration with interdisciplinary teams to translate data-driven insights into actionable health and dietary recommendations.	Bologna, Italy
Oct 2023-ongoing	NGB Genetics <i>Bioinformatician</i> Developing pipelines for the analysis and integration of biomolecular data related to rare neurodegenerative diseases, aiming to uncover novel mechanisms and improve risk detection.	Bologna, Italy
Oct 2023-Apr 2024	LifeGlimmer GmbH <i>Bioinformatician and Operational Manager</i> Leading bioinformatics research in Decision Support Systems and AI, driving innovations in data analysis and predictive modeling. Assisting in the coordination of European projects, managing cross-functional teams, and overseeing project logistics and compliance. Contributing to research initiatives and grant proposals and optimizing operational processes.	Berlin, Germany
Dec 2022-Sep 2023	Zuse Institut Berlin <i>Data Scientist and Data Engineer at the Medical Bioinformatics group</i> The position was funded by the project 'Data and AI-supported early warning system to stabilize the German economy' (DAKI). The main tasks centered around the creation of a platform for data sharing, visualization, and analysis that enables researchers to execute AI workflows. The data are mainly biomedical.	Berlin, Germany
Oct 2019-Sep 2023	LifeGlimmer GmbH <i>PhD Student and Employee in association with the System and Synthetic Biology Group, Wageningen University, The Netherlands.</i> This project was part of an Innovative Training Network funded by the Marie Skłodowska-Curie Actions. The main research topic of my PhD was to explore the flexibility and applicability of deep learning-based protein sequence embedding in performing various prediction tasks.	Berlin, Germany

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Interests

Professional

Co-founder of "Bioinform", an NGO that organise training schools in bioinformatics and AI.

Personal

Sport (Triathlon and Hiking)

Music (guitar player and singer)

Most relevant publications

PortPred: exploiting deep learning embeddings of amino acid sequences for the identification of transporter proteins and their substrates

Marco Anteghini, Vitor AP Martins dos Santos, Edoardo Saccenti.

Insights Into the Peroxisomal Protein Inventory of Zebrafish

Maki Kamoshita, Rechal Kumar, Marco Anteghini, Markus Kunze, Markus Islinger, Vitor Martins dos Santos and Michael Schrader.

Easy sematification of bioassays

Marco Anteghini, Jennider D'Souza, Vitor Martins dos Santos, Soeren Auer.

SciBERT-based Semantification of Bioassays in the Open Research Knowledge Graph

Marco Anteghini, Jennider D'Souza, Vitor Martins dos Santos, Soeren Auer.

In-Pero: Exploiting deep learning embeddings of protein sequences to predict the localisation of peroxisomal proteins

Marco Anteghini, Vitor Martins dos Santos, Edoardo Saccenti

Thermodynamics and kinetics of the amyloid- β peptide revealed by Markov state models based on MD data in agreement with experiment

Arghadwip Paul, Suman Samantray, Marco Anteghini, Birgit Strodel