Matteo Manfredi

ABOUT ME

I am a research fellow at the Bologna Biocomputing Group working in the field of Bioinformatics. I have worked on applying different computational methods, primarily based on Machine Learning, to the study of protein features. In particular, to the prediction of i) protein solvent accessibility, ii) protein-protein interaction sites, and iii) the relation between single residue variations and diseases in humans. I also take great interest in the application of embedding techniques derived from Protein Language Models.
All the predictors that I developed are part of the ELIXIR ecosystem of tools for the annotation of proteins and protein variants.

EDUCATION AND TRAINING

PhD in Biotechnological, Biocomputational, Pharmaceutical and Pharmacological Sciences

University of Bologna [31/10/2019 – 31/01/2023]

Address: Bologna (Italy)

Level in EQF: EQF level 8

SSD: BIO10
Admitted to the final exam, scheduled on June 23rd 2023

ELIXIR-GOBLET Train-the-Trainer

ELIXIR EU [08/03/2022 – 11/03/2022]

Address: Virtual

Website: https://elixir-europe.org/platforms/training/train-the-trainer

Field(s) of study: Education: *Teacher training without subject specialisation*

- Principles of learning and how they apply to training;
- Training techniques for enhancing learner engagement and participation,
- Design of engaging sessions, materials and courses;
- Assessment and feedback in training.

Master Degree in Bioinformatics

University of Bologna [23/10/2017 – 24/09/2019]

Address: Bologna (Italy)

Final grade: 110 L /110 – **Level in EQF:** EQF level 7

Thesis: Prediction of residue solvent accessibility from protein sequence with deep-learning approaches

- Algorithms and Data Structures specifically useful for computational biology
- Structural Bioinformatics
- Proteomics
- Genomics
- Phylogenetics

The master is international, so it was held in English.

Bachelor degree in Computational Science

University of Parma [20/09/2014 – 25/10/2017]

Address: Parma (Italy)

Final grade: 110 L /110 – **Level in EQF:** EQF level 6

Thesis: "DOMINI 3-D E FILTRAGGIO PER CSP SU PROTEINE"

- Theory of computational science

- Programming experience with multiple languages, mainly C, C++, Java and Python
- Knowledge of important Algorithms and Data Structures
- Development of complex projects, both alone and with a team

INTERNATIONAL EXPERIENCES

PhD Mobility Abroad - Munich, Germany

[01/10/2022 – 01/12/2022]

During my PhD, I spent a period of three months working at the laboratory of prof. Burkhard Rost, under the supervision of Tobias Olenyi, at the Technische Universität München (TUM), Munich.

My project there focused on the prediction of structural domain boundaries using protein embeddings.

This experience allowed me to better understand how ProtT5, a Protein Language Model they developed, was trained and how to employ it efficiently for downstream predictive tasks.

Erasmus+ - Leeds, UK

[13/09/2016 – 13/07/2017]

During my Bachelor Degree I spent my third year studying at the University of Leeds (UK) as part of the Erasmus+ program

PUBLICATIONS

ISPRED-SEQ: Deep neural networks and embeddings for predicting interaction sites in protein sequences

[2022]

Matteo Manfredi, Castrense Savojardo, Pier Luigi Martelli, Rita Casadio,

bioRxiv 2022.10.24.513521; doi: https://doi.org/10.1101/2022.10.24.513521

Submitted to Journal of Molecular Biology

E-SNPs&GO: Embedding of protein sequence and function improves the annotation of human pathogenic variants

[2022]

Matteo Manfredi, Castrense Savojardo, Pier Luigi Martelli, Rita Casadio,

Bioinformatics, Volume 38, Issue 23, 1 December 2022, Pages 5168–5174; https://doi.org/10.1093/bioinformatics/btac678

IF2021: 6.931

DeepREx-WS: A web server for characterising protein–solvent interaction starting from sequence

[2021]

Matteo Manfredi, Castrense Savojardo, Pier Luigi Martelli, Rita Casadio

Computational and Structural Biotechnology Journal, Volume 19, 2021, Pages 5791-5799, ISSN 2001-0370; https://doi.org/10.1016/j.csbj.2021.10.016.

IF2021: 6.155; Citations: 1 (Scopus, Dec 2022)

Solvent Accessibility of Residues Undergoing Pathogenic Variations in Humans: From Protein Structures to Protein Sequences

[2021]

Castrense Savojardo, Matteo Manfredi, Pier Luigi Martelli, Rita Casadio

Front. Mol. Biosci., 07 January 2021 Sec. Structural Biology; https://doi.org/10.3389/fmolb.2020.626363

IF2021: 6.113; Citations: 23 (Scopus, Dec 2022)

AVAILABLE TOOLS

ISPRED-SEQ

A deep learning-based method for the prediction of Interaction Sites starting from protein sequence

Link: https://ispredws.biocomp.unibo.it/sequence/

E-SNPs&GO

A machine learning-based method for the pathogenicity of human variations

Link: https://esnpsandgo.biocomp.unibo.it/

DeepREx-WS

A deep learning-based method for the prediction of Residue solvent Exposure starting from protein sequence

Link: http://deeprex.biocomp.unibo.it/

CONFERENCES AND SEMINARS

ECCB2022 - 21st European Conference on Computational Biology

[Sitges, Barcelona, 12/09/2022 – 21/09/2022]

Presented a poster with the title "**E-SNPs&GO: Embedding of protein sequence and function improves the prediction of human pathogenic variants"**

Link: https://eccb2022.org/

BITS 2022 - 18th Annual Meeting of the Bioinformatics Italian Society

[Verona, 27/06/2022 – 29/06/2022]

Presented a poster with the title "**E-SNPs&GO: Embedding of protein sequence and function improves the prediction of human pathogenic variants"**

Link: https://bioinformatics.it/bits2022

ISMB 2021 - 29th Conference on Intelligent Systems for Molecular Biology

[Virtual, 22/07/2021 – 29/07/2021]

Took part to the corresponding Hackathon, working on the project **2D Topology/Sequence Map Templates** and presenting a final report.

Link: https://www.iscb.org/ismbeccb2021

BioHackathon Europe 2020

[Virtual, 08/11/2020 – 12/11/2020]

Worked on the project **ELIXIR Service Bundle for Epidemic Response** and presented daily reports

Link: https://2020.biohackathon-europe.org/

ISMB 2020 - 28th Conference on Intelligent Systems for Molecular Biology

[Virtual, 12/07/2020 – 15/07/2020]
Link: https://www.iscb.org/ismb2020

Bologna Winter School 2019 - Data Science for Bioinformatics

[Bologna, 17/02/2019 – 21/02/2019]
Link: http://www.biocomp.unibo.it/~school2019/

Bologna Winter School 2018 - Big Data and Bioinformatics

[Bologna, 11/02/2018 – 15/02/2018]
Link: http://www.biocomp.unibo.it/~school2018/

ORGANIZATION ACTIVITIES

Bologna Winter School 2022 - Structural Bioinformatics in the era of AlphaFold2

[08/02/2022 – 24/02/2022]

Virtual

Part of the organization committee

Bologna Winter School 2021 - Bioinformatics for Discovery in Structural and Functional Biology

[08/02/2021 – 18/02/2021]

Virtual

Part of the organization committee

Bologna Winter School 2020 - What can we learn from protein structure?

[16/02/2020 – 20/02/2020]

Bologna

Part of the organization committee

TEACHING EXPERIENCES

Tutor for 2 YEARS INTERNATIONAL MASTER IN BIOINFORMATICS - COMPUTATIONAL METHODS FOR BIOINFORMATICS 2022/2023

[01/11/2022 – 31/01/2023]

In charge of exercise sessions with the students, co-teaching the second module of the course and assisting with the exam sessions

Total of 40 hours

Tutor for 2 YEARS INTERNATIONAL MASTER IN BIOINFORMATICS - LABORATORY OF BIOINFORMATICS 2 2022/2023

[01/09/2022 – 31/10/2022]

In charge of assisting the lecturer and helping the students with the laboratory activities of the course

Total of 20 hours

Tutor for 2 YEARS INTERNATIONAL MASTER IN BIOINFORMATICS - COMPUTATIONAL METHODS FOR BIOINFORMATICS 2021/2022

[01/11/2021 – 31/01/2022]

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[01/11/2020 – 31/01/2021]

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Total of 40 hours

PERSONAL SKILLS

Job-related Skills

Proficient programmer:

- Expert user of Python
- Knowledge of multiple other languages, most notably C++, Java, and Javascript.
- Ability to quickly learn how to use any new language.
- Ability to create and curate databases using MySQL and PostgreSQL
- Expert user of a Linux Shell

Experienced in developing Machine Learning-based tools:

- Extended knowledge of different architectures, including Random Forests, Support Vector Machines, Convolutional Networks, Recurrent Networks, and Attention-based Networks
- Proficiency in using python libraries dedicated to machine learning applications, including scikit-learn, Keras, TensorFlow and PyTorch
- Experience in training procedures, model optimization and fair evaluation
- Ability to deploy a web server to make the developed tools available to the scientific community

Experienced in applying computational methods to biological problems:

- Expert in the field of protein structural bioinformatics
- Expert in the handling of Big Data
- Ability to quickly parse data formats common in biological databases
- Experience in the curation of high-quality datasets
- Efficient consideration of the most relevant biological features to extract for the problem at hand
- Knowledge of statistical analysis for assessing the quality of the results

Good lecturer

- Experience in teaching theoretical and practical lectures for courses of a Master's Degree
- Experience with live-coding techniques for teaching programming skills

LANGUAGE SKILLS

Mother tongue(s): **Italian**

Other language(s):

English

LISTENING C1 **READING** C2 **WRITING** C2

SPOKEN PRODUCTION C1 **SPOKEN INTERACTION** C1