



Manuel Mangoni

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WORK EXPERIENCE

 **IRCCS CASA SOLLIEVO DELLA SOFFERENZA - MENDEL INSTITUTE** – ROMA, ITALY

BIOINFORMATICS RESEARCHER – 01/11/2022 – CURRENT

Deep Network Analysis on Genomic Data. Machine Learning Models (Network Based). Software development (Pyntacle). Time Series Analysis. Scientific Virtual Reality Experiences

Research interests

- Bioinformatics and Genomics
- Big data & Scientific programming
- Network Biology
- Blender and VR applied to Scientific Field
- GNN, Machine Learning
- Graph Embedding

EDUCATION AND TRAINING

01/11/2022 – CURRENT Rome, Italy

PHD STUDENT Sapienza, University of Rome

Medical Genetics and Human Biology - PNRR funded

Website <https://www.uniroma1.it/it/pagina-strutturale/home>

01/10/2020 – 15/07/2022 Verona, Italy

MASTER DEGREE IN MEDICAL BIOINFORMATICS Univeristy of Verona

Thesis: K-mer based method to detect effect of SNPs on Transcription Factors

Advisor: Rosalba Giugno

Co-Advisor: Luca Pinello - Associate Professor, MGH/Harvard Medical School/BROAD Institute, Boston

Score: 110/110

Graduation Date: 15 July 2022

Website <https://www.univr.it/it/> | **Field of study** Medical Bioinformatics

01/10/2017 – 17/07/2020 Roma, Italy

BACHELOR DEGREE IN BIOINFORMATICS Sapienza, University of Rome

Thesis: Disease Module Identification Algorithm

Thesis Subject: Modelling Simulation of Biomolecular Dynamical Systems

Advisor: Lorenzo Farina

Score: 110/110 cum Laude

Graduation Date: 17 July 2020

Website <https://www.uniroma1.it/it/pagina-strutturale/home>

LANGUAGE SKILLS

Mother tongue(s): **ITALIAN**

Other language(s):

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken production	Spoken interaction	
ENGLISH	C2	C1	C2	C2	C1

Levels: A1 and A2: Basic user; B1 and B2: Independent user; C1 and C2: Proficient user

● SKILLS

Microsoft Office | Microsoft Word | R Programming | Python advanced | Microsoft Excel | Microsoft Powerpoint | Social Media | Git & Githubs | SQL | Linux (Terminal Commands, Bash/Shell) | UNIX systems (Linux, macOS) | Genome Browser | Graph Theory | Data Analysis | Jupyter | Machine Learning | Blender | HTML | NCBI tools (Genbank, BLAST) | SnakeMake | SAMTOOLS | PyMol software for molecular visualization | deep learning | Microsoft Windows Systems | Statistical software and packages (Excel, STATA, SPSS, R)

● PUBLICATIONS

2025

[NetMD: Unsupervised Synchronization of Molecular Dynamics Trajectories via Graph Embedding and Time Warping](#)

Manuel Mangoni, Salvatore Daniele Bianco, Francesco Petrizzelli, Michele Pieroni, Pietro Hiram Guzzi, Viviana Caputo, Tommaso Biagini, Tommaso Mazza

doi: <https://doi.org/10.1101/2025.08.12.669871>

Link <https://www.biorxiv.org/content/10.1101/2025.08.12.669871v2.full>

2024

[Epigenetic and transcriptional control of adipocyte function by centenarian-associated SIRT6 N308K/A313S mutant](#)

Jan Frohlich, Niccolò Liorni, Manuel Mangoni, Gabriela Lochmanová, Pavlína Pírek, Nikola Kaštánková, Pille Pata, Jan Kucera, George N. Chaldakov, Anton B. Tonchev, Illar Pata, Vera Gorbunova, Eric Leire, Zbyněk Zdráhal, Tommaso Mazza & Manlio Vinciguerra

2024

[Deciphering Microbial Composition in Patients with Inflammatory Bowel Disease: Implications for Therapeutic Response to Biologic Agents](#)

Orazio Palmieri, Fabrizio Bossa, Stefano Castellana, Tiziana Latiano, Sonia Carparelli, Giuseppina Martino, Manuel Mangoni, Giuseppe Corritore, Marianna Nardella, Maria Guerra, Giuseppe Biscaglia, Francesco Perri, Tommaso Mazza, Anna Latiano

Microorganisms 2024, 12(7), 1260.

doi: [10.3390/microorganisms12071260](https://doi.org/10.3390/microorganisms12071260)

2024

[Exploring non-coding genetic variability in ACE2: Functional annotation and in vitro validation of regulatory variants.](#)

Giovannetti A, Lazzari S, Mangoni M, Traversa A, Mazza T, Parisi C, Caputo V.

PMID: 38570058

Gene. 2024 Jul 15;915:148422.

doi: [10.1016/j.gene.2024.148422](https://doi.org/10.1016/j.gene.2024.148422).

2023

[PanDelos-frags: A methodology for discovering pangenomic content of incomplete microbial assemblies](#)

Vincenzo Bonnici, Claudia Mengoni, Manuel Mangoni, Giuditta Franco, Rosalba Giugno

PMID: 37995844

doi: [10.1016/j.jbi.2023.104552](https://doi.org/10.1016/j.jbi.2023.104552)

2023

Investigating Mitochondrial Gene Expression Patterns in *Drosophila melanogaster* Using Network Analysis to Understand Aging Mechanisms

Manuel Mangoni, Francesco Petrizzelli, Niccolò Liorni, Salvatore Daniele Bianco, Tommaso Biagini, Alessandro Napoli, Marta Adinolfi, Pietro Hiram Guzzi, Antonio Novelli, Viviana Caputo, Tommaso Mazza
Appl. Sci. 2023, 13(12), 7342;
doi: 10.3390/app13127342

PROJECTS

01/11/2022 – CURRENT

Pyntacle/PyntacleMD

Software package and command line tool entirely written in Python (NetworkX and iGraph) that eases the analysis of graphs. It includes Pyntacle-MD, a computational framework which integrates the Pyntacle suite of algorithms with residue interaction network (RINs) generated from MD simulations.

Link <https://pyntacle.css-mendel.it/>

01/2024 – CURRENT

VRare - Terza Missione Sapienza

VRare - FROM VERY RARE TO VERY REAL: A journey to the discovery of neurodevelopmental diseases
Terza Missione, Sapienza

The initiative proposes an educational Virtual Reality pathway for secondary schools focused on rare genetic diseases. Created by teachers and doctoral students with the help of external researchers, it will offer immersive experiences in virtual environments to explore the molecular bases of diseases, manipulate DNA and molecules, conduct "in silico" experiments, and interact with patients and experts. The goal is to improve education, raise public awareness, and promote innovation in research.

The project, coordinated by Sapienza University with contributions from the CSS-Mendel Institute and the Bambino Gesù Pediatric Hospital, includes phases of information gathering, technological development, presentations in schools, and a final sharing event. The main beneficiaries are patients, families, students, and health professionals. Promotion will be carried out through a website, press releases, and social media.

05/2023 – 10/2023

GLUT1FY - Maker Faire Rome 2023

GLUT1FY: CONOSCERE E COMPRENDERE LE MALATTIE RARE ATTRAVERSO LE LENTI DELLA REALTÀ VIRTUALE

Enter GLUT1FY, our virtual reality environment, where you will encounter our research. Interact with our team in the virtual corner "Talk to the Experts", discover the disease through an engaging multimedia slideshow, and delve into the world of the GLUT1 protein at the molecular level, where you will witness firsthand the molecular dynamics behind its functioning and the consequences of genetic variants.

Liorni Niccolò, Petrizzelli Francesco, Napoli Alessandro, Biagini Tommaso, Bianco Salvatore Daniele, **Mangoni Manuel**, Adinolfi Marta, Giovannetti Agnese, Caputo Viviana, Mazza Tommaso.

PROFESSIONAL EXPERIENCES

04/2024 – 04/2024

HUGO 2024 - HUMAN GENOME MEETING 2024

Position: Author

Project: BEYOND MISSENSE: Expanding APOGEE's reach to tRNA variants in mitochondrial diseases

Supervisor: Tommaso Mazza

06/2023 – 06/2023

BITS 2023, Bari - Bioinformatics Italian Society

Position: Author

Project: Pyntacle-MD: Harnessing the Power of Parallel Computing for Large-Scale Network Analysis of Molecular Dynamics Simulations

Supervisor: Tommaso Mazza

06/2022 – 06/2022

BITS 2022, Verona - Bioinformatics Italian Society

Position: First Author

Project: Predicting genetic variants impact on transcription factor binding sites using k-mer-based motif models

Supervisor: Rosalba Giugno

06/2022 – 06/2022

BITS 2022, Verona - Bioinformatics Italian Society

Position: Speaker

Project: A systematic evaluation of computational tools for gene-oriented pangenome detection in fragmented genomes

Supervisor: Vincenzo Bonnici

● **PERSONAL DATA**

I hereby authorize the treatment of my personal data according to Italian Legislative Decree n. 196/2003 Regulation (EU) GDPR n.679/2016.
