Maria Lui

Researcher at IRCCS
Neurolesi Bonino Pulejo

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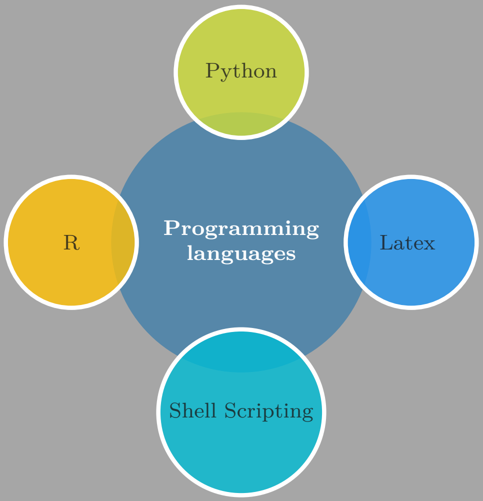
Social Network

- Overleaf Link
- Researchgate Link
- Github Project Page Link

Languages

Italian	● ● ● ● ●
English	● ● ● ● ○



About Me

An ambitious and passionate researcher keen on learning new things every day. Enthusiastic about undertaking any tasks aimed at furthering the research in the bioinformatics and neuroscience fields. Aiming to use both my problem solving and teamwork skills and develop them to the next level .
I firmly believe that "The noblest pleasure is the joy of understanding."

Education

Study

2021 – Now **PHD fellow in Translational Molecular Medicine and Surgery** Università degli studi di Messina

Focus: Apply new strategies to improve anticancer potential of natural substances with a translational approach.

2018 – 2020 **Master studies Bioinformatics (LM/6)** Alma Mater Studiorum,Università di Bologna

Focus: Store and analyze of High throughput biological data in the field of applied genomics, phylogenetics, proteomics and next generation sequencing.
During the master I acquired the technical skills needed to manage, generate and handling biological data; together with their analysis. The study program I attended aims indeed to apply computational technologies to biology, biotechnology and medicine, in order to support the analysis and description of highly complex biological systems and rapidly menage large quantities of data, or developing new pipelines for very heterogeneous data types.

Master Theses
My master thesis, "Effects of social contacts on epidemics spreading: A network science approach", involved the construction of epidemiological prediction model, entirely written in house using python programming language. This Network-based Compartmental Model, can possibly help monitoring short and long term impacts of communicable disease. Specifically it mainly analyzes the spreading of the newly discovered SARS-CoV-2 including simulations on different hypothesized lockdown polices.

2014 – 2017 **Bachelor studies Biotechnology** Università degli studi di Messina
Focus: theoretical and practical knowledge about the medical, veterinary, pharmaceutical and agro-food fields. During my bachelor studies I've achieved an in-depth knowledge of the biochemical and genetic aspects of prokaryotic and eukaryotic cells and cell culture techniques. Moreover I had the opportunity to in depth study pharmacologically active compounds and their mechanism of action.

Bachelor Theses
My bachelor thesis, "Computational pathway analysis and personalized medicine", propose the use of pathway mining algorithm to infer the effect of any gene disregulation caused by selected drug on the pathways of interest, in the HER2-positive breast cancer.

2009 – 2014 **High School Diploma** Liceo scientifico Archimede
Scientific High School- maxisperimentale Brocca

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Computational skills

- Machine learning
- High throughput data analysis
- Homology Modeling
- Text Mining
- Biological Databases
- Pathway Analysis
- Cloud computing
- Sequence Alignment

Wet lab skills

- Eukaryotic and bacterial cell culture
- PCR
- Gel Electrophoresis
- Western Blot
- ELISA
- RNA and DNA extraction
- Retrotranscription
- Site-specific genomic targeting with CRISPR/Cas9
- DNA, RNA and Protein Quantification

Working Experience

2023-Now **Researcher** IRCCS Center Neurolesi Bonino Pulejo, Messina

Focus: Experimental Neuroscience through computational Biology, Machine Learning, and the integration of multi-omics data (transcriptomics, proteomics, and genomics) for rehabilitation applications. My work aims to improve the lives of individuals with neurological conditions through data-driven solutions. My research encompasses modeling neural systems, applying machine learning for diagnostics and personalized treatment, and leveraging multi-omics data to understand molecular aspects of neurological disorders. I collaborate across diverse disciplines and envision a future that includes advanced technologies, expanded datasets, and the translation of research into clinical practice.

2020-2021 **Bioinformatician** IcareX, Milano

Focus: Transcriptomic data collection from the publicly available datasets, together with their analysis and processing.
Python programming language was used to programmatically access the Geo database and parse the data, the input for the Machine learning classifier. Then, oafter data collection, it is possible to infer the response to a specific treatment, making predictions with a Machine Learning model. The ultimate aim of the working experience at IcareX consists on the Biomarkers identification for the treatment of rheumatic diseases.

2020 **Master Internship** Alma Mater Studiorum, Università di Bologna

I had the opportunity to acquire new coding skills such as the usage of specific python libraries as Networx. Moreover developed to an higher level my knowledge of Graph theory together with compartimental models and their usage in the epidemiologic field.

2017 **Bachelor Curricular Internship** Università degli studi di Messina

Thanks to which I further improved my confidence with different techniques such as western blot, real time PCR, RNA or DNA extraction from tissue or cells culture and its quantification.
I also got the chance to extensively utilize both animal and bacterial cells in culture, together with the implementation of heat shock transformation with bacteria and the use of Crispr/cas9 system with specific plasmids.

Certifications

2022 **Bioinformaics workshop-Multi Omics box**

by Decode Life Bioinformatics training institute.
Improving core Bioinformatics skills for cutting edge research.

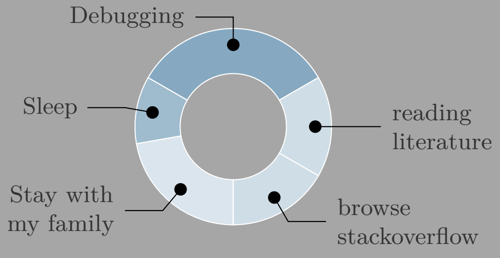
2021 **An Introduction to Practical Deep Learning**

by Intel and offered through Coursera.
Acquisition of skills that aim to harness the enormous amounts of data that we are surrounded by with artificial neural networks, allowing for the development of self-driving cars, speech interfaces, genomic sequence analysis and algorithmic trading.

2021 **Design and Interpretation of Clinical Trials**

by Johns Hopkins University and offered through Coursera.
Acquisition of the basic principles for design of randomized clinical trials and how they should be reported. Study of the terminology used in clinical trials and the several common designs used for clinical trials, such as parallel and cross-over designs.

A day of my life



Alignment tools:

BLAST · ClustalW · MUSCLE · LALIGN · T-Coffee · BWA · Exonerate · Cactus · Bowtie

Database mining

DrugBank	●●●●
OMIM	●●●○
CIVIC	●●●●
RCSV PDB	●●●●
Chembl	●●●○
UniProt	●●●●
CATH	●●●○
Pfam	●●●○
SCOP	●●●○

Most Proud of

Perseverance
I had in achieving my goals

My great improvements
in coding skills.

Mutual esteem and cooperation
gained with my colleagues

2021	**Hands-On Keras for Machine Learning Engineers** Acquisition of advanced techniques for developing state-of-the-art deep learning models and building large models for image and text data. Knowledge about Keras deep learning library usage together the development and evaluation of neural network models.
06/06/2018	**B2 English certification**

Publications & Posters

Lui, M., Giosa, D., Romeo, O., & Bitto, A. (2022). **Computational Pathways Analysis and Personalized Medicine in HER2- Positive Breast Cancer**. Current Pharmacogenomics and Personalized Medicine. DOI: 10.2174/1875692119666

D Giosa, L Giuffrè, MR Felice, G Rigano, M Lui, R Aiese Cigliano, L M Lopes Bezerra, O Romeo. **Whole-transcriptome analysis of Sporothrix brasiliensis grown in mold- and yeast-inducing conditions**. Med Mycol. 2022 Sep; doi: 10.1093/mmy/myac072.P421

A Bonomo, G Rigano, M Lui, L Giuffrè, R Aiese Cigliano, O Romeo, D Giosa. **Sporothrix genome database update and whole phylogenomic analysis**. Bioinformatics and Computational Biology Conference (BBCC), 2022. https://doi.org/10.7490/f1000research.1119311.1

Maria Lui, Gabriele Rigano, Andrea Bonomo, Letterio Giuffrè, Orazio Romeo, D Giosa. **Bioinformatics analysis of six Candida parapsilosis genome assemblies obtained using whole-genome optical maps and Illumina short-read data**. Bioinformatics and Computational biology Conference (BBCC), 2022. https://doi.org/10.7490/f1000research.1119306.1

Computational skills

- Cloud computing:
  Access to shared pools of configurable system resources and higher-level services that can be rapidly provisioned.
- BLAST, Needle, ClustalW, MUSCLE:
  Pairwise sequence alignment and Multiple sequence alignment to compute degrees of similarity between two or more sequences.
- HMMer:
  Biosequence analysis using profile hidden Markov Models
- Biological Database mining:
  DrugBank, CIVIC,Ensembl, RCSB PDB,UniProt, CATH, OMIM, Pfam, SCOP, Chembl
- R, Python and Bash programming languages
- Machine Learning python libraries:
  pytorch, numpy, pandas, SciKit-Learn, scipy, seaborn, matplotlib
- Latex and beamer class: Overleaf usage to write papers or presentation
- GitHub:
  for software development and version control.
- Usage of principal operative systems:
  MacOS, Windows, Linux
- Rasmol, Swiss-Model, Chimera:
  visualization of protein structure.