

**Date of birth:** 12/07/1994 | **Nationality:** Italian | **Gender** Male | (+39) 00000000000 | [giovanni.madeo3@unibo.it](mailto:giovanni.madeo3@unibo.it) |

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About me: I am a PhD student currently enrolled in the second year of Biotechnological, Biocomputational, Pharmaceutical and Pharmacological Sciences at the University of Bologna, supervised by Prof. Pier Luigi Martelli, Associate Professor and Director of Second Cycle Degree of Bioinformatics. My scholarship is provided by the region Emilia-Romagna, in the context of the training projects for the "Human Resources for a Digital Economy: Big Data". Therefore, my research goal is the development of innovative methods for the "Omics" Big Data analysis. I have a background in the field of Biological Sciences and Biotechnology, acquired during my bachelor's degree, combined with an in-depth knowledge of computational biology methods provided by the Master's Degree in Bioinformatics.

● **EDUCATION AND TRAINING**

2018 – CURRENT  
**PHD IN BIOTECHNOLOGICAL, BIOCOMPUTATIONAL, PHARMACEUTICAL AND PHARMACOLOGICAL SCIENCES** – University of Bologna

**Scholarship:** provided by the training projects of the region Emilia-Romagna, in the context of the theme "Human Resources for a Digital Economy: Big Data"  
**Tutor:** Prof. Pier Luigi Martelli, Associate Professor and Director of Second Cycle Degree of Bioinformatics  
**Workplace:** Biocomputing Group (Via San Giacomo, 9/2 Bologna (BO), Italy)  
**Project:** Development of Innovative Methods for "Omics" Big Data Analysis  
In the context of my research project, I am currently working on a Deep Learning-based method for outer membrane proteins detection and topology prediction in Gram-negative bacteria.

2016 – 2018 – Bologna, Italy  
**MASTER'S DEGREE IN BIOINFORMATICS** – University of Bologna

- Computational Biology
- Genomics and Proteomics
- Programming for Bioinformatics
- Algorithm and Data Structures
- Phylogenetics

110/110 cum laude | Improving Transmembrane Beta-Barrels Topology Prediction with Deep Learning

2013 – 2016  
**BACHELOR'S DEGREE IN BIOLOGICAL SCIENCES AND TECHNOLOGIES** – University of Calabria

- Molecular Biology
- Biochemistry
- Genetics
- Biostatistics
- Physiology
- Laboratory Techniques

110/110 | L'Epigenetica del Disturbo Bipolare

● **LANGUAGE SKILLS**

**Mother tongue(s):** ITALIAN

**Other language(s):**

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken production	Spoken interaction	
<b>ENGLISH</b>	B2	B2	B2	B2	B2

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

## ● CONFERENCES AND SEMINARS

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13/07/2020 – 16/07/2020 – Virtual

**ISMB 2020 - 28th conference on Intelligent Systems for Molecular Biology**

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17/02/2020 – 21/02/2020 – Bologna

**21th Bologna Winter School: "What We Can Learn From Protein Structures?"**

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24/06/2019 – 28/06/2019 – Bologna

**Summer School: "Chemical And Genomics Based Strategies In The Discovery Of Novel Drug Targets"**

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18/02/2019 – 22/02/2019 – Bologna

**20th Bologna Winter School: "Data Science for Bioinformatics"**

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12/02/2018 – 17/02/2018 – Bologna

**19th Bologna Winter School: "Big Data and Bioinformatics"**

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04/09/2017 – 08/09/2017 – CRO, Aviano (PN)

**Special Course on NGS Data Analysis**

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13/02/2017 – 17/02/2017 – Bologna

**18th Bologna Winter School: "Revisiting Bioinformatics Foundations"**

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## ● INTERNATIONAL EXPERIENCES

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01/2016 – 06/2016

**Erasmus+**

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During the third year of my Bachelor's Degree, I spent six months studying at the University of Cardiff (UK) as part of the Erasmus+ project, where I successfully passed three exams, namely:

- Plant Development and Physiology
- Genomics, Proteomics and Bioinformatics
- Genetic Models of Disease

## ● SKILLS

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### **Job-related Skills**

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- I have a good knowledge of Python and R programming languages.
- I am familiar with all major databases and resources available for structural and functional annotation and able to extract and integrate information from them.
- I can perform sequence and structural alignments, homology modeling and building of Hidden Markov Models from multiple sequence alignments.
- I am able to develop methods based on Deep Learning (Long Short-Term Memory, Convolutional Neural Network) or other Machine Learning approaches (Support Vector Machine), as well as statistical models (Hidden Markov Model, Conditional Random Field).