

CURRICULUM VITAE BY PhD STUDENT BARBARA PUCCIO

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Work Positions

February 2023-present: Enrolment in the Professional Register of Engineers of Catanzaro, Italy.

November 2022-present: PhD student in "Biomarkers of chronic and complex diseases" -
Curriculum: Digital Medicine - University "Magna Graecia" of Catanzaro, Italy;

January 2022-February 2023: Research Collaborator - Validated Question Answering - VQA
Project (Horizon 2020 - PON 2014-2020 FESR).

Education

2021: Qualifying examination for Profession of Engineer, University of Calabria, Rende, Italy;

2021: Master's Degree in Biomedical Engineering - "Network Embedding per l'analisi di
Protein Contact Network: Applicazione al Complesso ACE2-SPIKE di SARS-CoV-2"-
University "Magna Graecia" of Catanzaro, Italy;

2020: 24 CFUs for Italian Teaching Certification (Exam taken: Antropologia Modulo 1-6
CFUs, Metodologia e tecnologie didattiche Modulo 1-6 CFUs, Metodologia Generale Modulo

1-6 CFUS, Psicologia Modulo 1-6 CFUs)

2019: Bachelor's Degree in Computer and Biomedical Engineering, University "Magna Graecia" of Catanzaro, Italy.

Summary of Research Activity

During my work experience as a research assistant, my activity focused on the study of protein structures using an emerging paradigm called the protein contact network, through which the 3D structure of a protein can be represented through a non-weighted graph. In particular, within the VQA project, the result of which was the development of the implementation of a semi-automatic system for annotating characteristics, answering questions and enriching data, my contribution was related to protein annotation. The research therefore focused on the analysis of the Spike protein of the Sars Cov 2 virus and its variants of interest. Now, a first line of research is projected on the study of RNA-sequencing data. A pipeline that allows to obtain the counting matrix of the gene expression data, starting from the Fastq files has been outlined. It was tested on Fastq files generated from RNA samples sequenced from mouse cardiac cells (myocytes). In this regard, I completed a course, which allowed me to discover the conceptual bases of working with RNA-seq data, notably differential gene expression analysis, and learn how to analyze this kind of data in R.

In this moment, my research is also focusing on two new activities:

- Exploring the use of pseudo time for building AI models of trajectories of disease
- Investigating the use of generative models for building longitudinal synthetic data

Attended courses

1. Analysis of RNA-seq data (online 31 Oct - 5 Dec 2022) - Mondego Science
2. Bioinformatics and Deep learning for biodata analysis - 24th BOLOGNA WINTER SCHOOL (Online - 14 - 27 Feb 2023)
3. Lipari School on Computational Life Sciences - Single-Cell Analysis with application in Biology and Medicine (Lipari - July 23 -July 29 2023)

List of Publications of the year (2022)

1. Springer Nature

Structural analysis of SARS-CoV-2 Spike Protein variants through Graph Embedding, P.H. Guzzi, U. Lomoio, B. Puccio, P. Veltri - Springer Nature - Network Modeling Analysis in Health Informatics and Bioinformatics <https://doi.org/10.1007/s13721-022-00397-9>

2. Preprints

A Network Embedding Approach for Annotating Protein Structures

B. Puccio, L. Di Paola, U. Lomoio, P. Veltri, P.H. Guzzi, 10.20944/preprints202204.0027.v1

List of Publications of the year (2023)

1. Scientific reports

Computational Analysis of the Sequence-Structure Relation in SARS-CoV-2 Spike Protein using Protein Contact Networks, P.H. Guzzi, L. Di Paola, B. Puccio, U. Lomoio, A. Giuliani, P. Veltri, *Sci Rep* 13, 2837 (2023) <https://doi.org/10.1038/s41598-023-30052-w>.

2. PlosOne

SARS-CoV-2 protein structure and sequence mutations: Evolutionary analysis and effects on virus variants, U. Lomoio, B. Puccio, G. Tradigo, P.H. Guzzi, P. Veltri *PLOS ONE* 18(7): e0283400, <https://doi.org/10.1371/journal.pone.0283400>

List of Conference Communications of the year(2022)

1. **Complex Network 2022 - The 11th International Conference on Complex Networks and their Applications- 8-10 November 2022, Palermo, Italy** <https://2022.complexnetworks.org/>
Poster presentation
Structural analysis of SARS-CoV-2 Spike Protein variants through Graph Embedding, P.H. Guzzi, U. Lomoio, B. Puccio, P. Veltri.
2. **2022 IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 6-9 December 2022, Las Vegas, NV, USA & Changsha China**
<https://ieeebim.org/BIBM2022/>
CBPBI. Workshop - Conference Paper
On the use of the analysis for EEG functional connectivity networks in epilepsy - B. Puccio, P. Vizza, P. Veltri.

List of Conference Communications of the year(2023)

1. **GNB 2023- VIII National Congress Of Bioengineering- 21-23 June 2023, Padova, Italy**
<http://gnb2023.it/index.html>
Short paper presentation
Validating biomedical and clinical data via an annotations based framework: experiences within the PON VOA project - B. Puccio, U. Lomoio, R. Giancotti, M. Cannistrà, S. Flesca, F. Scala, G. Tradigo, P.H. Guzzi, P. Veltri, P. Vizza.
2. **BITS 2023 - 19th Annual Meeting of the Bioinformatics Italian Society**
June 21-23, 2023, Bari, Italy
<http://www.bitsonline.org/2023/06/21/2023-06-21-23-2023>
Paper presentation
A pipeline proposal for RNA-seq data analysis - B.Puccio, P.H. Guzzi, P. Veltri

Additional Information

In compliance with the Italian Legislative Decree no. 196 dated 30/06/2003, I hereby authorize the recipient of this document to use and process my personal details for the purpose of recruiting and selecting staff and I confirm to be informed of my rights in accordance to art. 7 of the above mentioned decree.

ATANZARO
25-09-2023

