Gianfranco Michele Maria Politano

CURRICULUM VITAE

SURNAME AND NAME	Politano Gianfranco Michele Maria
Nationality	Italian

Italian National Scientific Qualifications awarded for Full Professor positions (*"Abilitazioni Scientifiche Nazionali di I fascia"*)

Academic Recruitment Field (*"Settore Concorsuale"*)
09/H1 - I Fascia (Bando 2012 (DD n. 589/2021)) valid until 15/Jun/2034

Academic Position

Qualification/Title	**Associate Professor**
University	**Politecnico di Torino**
Department	**Department of Control and Computer Engineering (DAUIN)**
Academic Recruitment Field (if the candidate holds a position in an Italian University, she/he should insert the *"Settore Concorsuale")*	**09/H1 SISTEMI DI ELABORAZIONE DELLE INFORMAZIONI**
Academic Discipline (formally named *"Settore Scientifico Disciplinare",* only for candidates who hold a position in an Italian University)	**ING-INF/05**

Working experience (please use the following table in order to briefly describe the working positions covered by the candidate)

Dates (from .. to..)	2007-2010
Name and address of the Employer (Public or/and private institution/body)	Politecnico di Torino
Position held (for positions in Universities, the candidate should indicate the Faculty/College/School and the Department; in case of Italian Universities the candidate is also requested to indicate the "Settore Scientifico Disciplinare")	Dottorando (ing-inf/05 presso DAUIN)
Main activities/responsibilities	Reasearch / Teaching

Dates (from .. to..)	2011-2017
Name and address of the Employer (Public or/and private institution/ body)	Politecnico di Torino
Position held (for positions in Universities, the candidate should indicate the Faculty/College/School and the Department; in case of Italian Universities the candidate is also requested to indicate the "Settore Scientifico Disciplinare")	Post Doc (ing-inf/05 presso DAUIN)

Main activities/responsibilities	Reasearch / Teaching

Dates (from .. to..)	2017-2019
Name and address of the Employer (Public or/and private institution/ body)	Politecnico di Torino
Position held (for positions in Universities, the candidate should indicate the Faculty/College/School and the Department; in case of Italian Universities the candidate is also requested to indicate the "Settore Scientifico Disciplinare")	RTD tipo A (ing-inf/05 presso DAUIN)
Main activities/responsibilities	Reasearch / Teaching

Dates (from .. to..)	2019-2022
Name and address of the Employer (Public or/and private institution/ body)	Politecnico di Torino
Position held (for positions in Universities, the candidate should indicate the Faculty/College/School and the Department; in case of Italian Universities the candidate is also requested to indicate the "Settore Scientifico Disciplinare")	RTD tipo B (ing-inf/05 presso DAUIN)
Main activities/responsibilities	Reasearch / Teaching

Dates (from .. to..)	2019-to date
Name and address of the Employer (Public or/and private institution/ body)	Politecnico di Torino
Position held (for positions in Universities, the candidate should indicate the Faculty/College/School and the Department; in case of Italian Universities the candidate is also requested to indicate the "Settore Scientifico Disciplinare")	Professore Associato
Main activities/responsibilities	Reasearch / Teaching

Education and Training (please use the following table to describe Degrees awarded, by only indicating the information concerning Bachelor's Degree, Master of Science's Degree or/and PhD)

Date	29/01/2007
Institution which issued the degree	Politecnico di Torino
Type of Degree awarded (only Bachelor's Degree, Master of Science's Degree, PhD)	**Master degree in Computer Engineering**

Date	11 April 2011
Institution which issued the degree	Politecnico di Torino
Type of Degree awarded (only Bachelor's Degree, Master of Science's Degree, PhD)	**Ph.D. degree in Computer Engineering**

EVALUATION FIELDS

1. **Scientific Activity**

The **three most important outcomes/results** of the research activity of the candidate accompanied by the tangible and verifiable evidence that the presented results:

Notice: Reported Quartiles data refer to the publication year

	Quartile		Citations		WOS IF	Scop. SJR	Impact
Title	**SJR**	**WOS**	**SCH**	**SJR**			
1) Statistical Reliability…	Q1 (CS)	Q1 (CS)	46	34	*2,663*	*0,679*	*FP7 Project*
2) CyTRANSFINDER…	Q1 (CS)	Q2 (Comp.Bio)	14	11	*3,169*	*1,567*	*Best paper/Int. recognition*
3) Modelling antibiotic resistance…	Q1 (CS)	Q2 (Comp.Bio)	11	5	*2,048*	*0,972*	*Patents*

1. (2012) "*Statistical Reliability Estimation of Microprocessor-Based Systems*" Savino A.; Di Carlo S.; Politano G.; Benso A.; Di Natale G.; Bosio A., **IEEE Transactions on Computers**, IEEE Computer Society, Vol. 61, 2012, pp. 1521-1534, DOI: 10.1109/TC.2011.188
Quartile: SCOPUS: Q1 (Computer Science) – WOS: Q2 (Computer Science), Citation: SCOPUS: 34, Scholar: 46, IF: 2,663, SJR:0,679
Discussion: this paper presents results related to my first research activity, before to move to the Bioinformatics field, I in fact started working on fault tolerance systems. This new methodology is designed to assess the reliability of a microprocessor system by taking into account both the hardware level and the software level using a probabilistic model. This solution allows to avoid massive fault simulation experiments that still represent the bottleneck in most computer systems' reliability assessments. The main fallback of this work was the stimulus for the formation of a European network that led to the European project FP7 CLERECO (Ga. 611404) coordinated by one of my group advisors. Although this work has been a team effort, my primary contribution in this paper is the development of the first design of the probabilistic framework, and the assessment and preliminary managing of conditional loop unrolling problem resorting to Bayesian approaches.

2. (2016) "*CyTRANSFINDER: A Cytoscape 3.3 plugin for three-component (TF, gene, miRNA) signal transduction pathway construction*" Politano, Gianfranco Michele Maria; Orso, Francesca; Raimo, Monica; Benso, Alfredo; Savino, Alessandro; Taverna, Daniela; Di Carlo, Stefano, **BMC Bioinformatics**, BioMed Central Ltd., Vol. 17, 2016, pp. 1-17, DOI: 10.1186/s12859-016-0964-2
Quartile: SCOPUS: Q1 (Computer Science) – WOS: Q1 (Computational Biology), Citation: SCOPUS: 11, Scholar: 14, IF: 3,169, SJR:1,567
Discussion: this product is the result of a collaboration with researchers of the University of Turin (prof. Taverna and dott. Orso). It is a milestone in my research activity for two main reasons: the first is that the paper presents a methodology that allowed to use Computer Science to obtain a biologically significant result (the preliminary results of this work won the Best Paper Award at the Bioinformatics 2014 conference). The second reason is that it demonstrates the effectiveness of a top-down engineering approach to address a problem typically approached using bottom-up methodologies. The methodological difference between engineering and traditional Life Sciences is one of the biggest challenges for a Systems Biologist. This paper gave my group more credibility in the scientific community and showed our "biological" counterpart that a computational approach not only is able to show biologically useful results, but it is also able to save time and money by directing the lab experiments towards more plausible hypotheses. The methodology developed in this work allowed my group to initiate other fruitful collaborations with different Italian Life Science researchers. Although this work has been a team effort, my main contribution was the design of pathways template, the overall optimization logic and the complete development of the tool.

3. (2018) "*Modelling antibiotic resistance in the microbiota using Multi-level Petri Nets*" Bardini, Roberta; Di Carlo, Stefano; Politano, Gianfranco; Benso, Alfredo, **BMC Systems Biology**, BioMed Central, Vol. 12, 2018, pp. 1-21, DOI: 10.1186/s12918-018-0627-1
Quartile: SCOPUS: Q1 (Computer Science) – WOS: Q2 (Computational Biology) , Citation: SCOPUS: 5, Scholar: 11, IF: 2,048 SJR:0,972

Discussion: this product a very gratifying result of my research activities on systems biology. The important novelty of this work is the introduction of a particular class of Petri-Nets (the Nets-Within-Nets) as a new formalism to model biological systems. This work is the precursor of several activities that focused on the integration of a modelling language that we developed (BiSDL), a modelling formalism (Nets-Within-Nets), and a simulator engine, to create an unprecedented flexible and efficient environment to model and simulate very complex biological systems. The main fallback of this activity is the filing of three patents, two of which (one international and one national) have already been granted. Although this work has been a team effort, my main contribution was in the definition of the biological design of microbiota to better model the behaviour against antibiotics. I also took part in the overall design of the language model.

✦ List of the submitted publications (with a maximum number of 17) in addition to those listed at point 1.1. For each publication and/or set of publications, the candidate is required to briefly describe his/her contribution, their scientific/technical significance and individual importance, the overall impact of the results in the international scientific community.

(2022) **The integration of clinical data in the assessment of multiple sclerosis-A review, Computer Methods and Programs in Biomedicine**, Ostellino, Sofia; Benso, Alfredo; Politano, Gianfranco, Elsevier, DOI:10.1016/j.cmpb.2022.106900

    Quartile: Q1 (Computer Science)
    Citations: SCOPUS: 1 SCHOLAR: 3
    SJR: 1,118 IF: n/a

This paper is the result of a the work of my first PhD student as her full tutor. It presents a reasoned review of automated and partially-automated methods for the assessment of multiple sclerosis. This is extremely important given the current Ai advancements and attempts to approach MS diagnosis / stadiation by investigating correlations between cognitive impairment and clinical data that refer to multiple etherogeneous domains. I overall supervised and took part in the entire work from the preliminary conceptualisation of the paper up to its final design. I also coordinated and tutored my PhD Student

(2021) "**Nets-within-nets for modeling emergent patterns in ontogenetic processes**", Bardini, R.; Benso, A.; Politano, G.; Di Carlo, S.; Computational and Structural Biotechnology Journal, DOI: https://doi.org/10.1016/j.csbj.2021.10.008

    Quartile: Q1 (Computer Science)
    Citations: SCOPUS: 0 SCHOLAR: 2
    SJR: 1,538 IF: n/a

This paper proposes a solid formalisation on how to use the Nets-Within-Nets formalism in modelling biological systems. It combines Petri Nets' simplicity with the capability to represent and simulate the interplay between different layers of regulation connected by non-trivial and context-dependent hierarchical relations. The paper shows how this approach can be used to simulate a real biological system and how the obtained simulations are representative of the actual real life system behaviour. This paper summarise the main results of three years of research done with Roberta Bardini during her PhD.

(2020) "**IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis**" Politano, G.; Benso, A., PLoS Computational Biology, Public Library of Science, Vol. 16, 2020, DOI: 10.1371/journal.pcbi.1008238

    Quartile: Q1 (Computer Science)
    Citations: SCOPUS: 4 SCHOLAR: 2
    SJR: 2,628 IF: n/a

This paper presents a computational study of the COVID regulatory network done using the biological network analysis tools developed by me and my colleagues. It was written during the first lockdown of the COVID pandemic and it presented possible insights into both the mechanisms that the virus uses to function into the human host, and possible drug target proteins. Both authors contributed equally to the work that led to this paper.

(2019) "'**One DB to rule them all' - the RING: a Regulatory INteraction Graph combining TFs, genes/proteins, SNPs, diseases and drugs**" Politano, Gianfranco; Di Carlo Stefano; Benso, Alfredo, Database: the journal of biological databases and curation, Oxford University Press, Vol. 2019, 2019, pp. 1-14, DOI: 10.1093/database/baz108

    Quartile: Q1 (Computer Science)
    Citations: SCOPUS: 4 SCHOLAR: 7
    SJR: 2,248 IF: n/a

The database presented in this paper is a complete framework for biological data integration. The integration has been performed starting from automated scraping pipelines that gathered raw data from all the major curated public biological repositories available at the time of publication. The data has then been organised in a relational database and integrated following a curated set of ontologies that allowed standardisation of naming and information (a major issue in biological data integration). Finally, the relational database has been translated into an advanced data model based on a graph representation. This model allows to perform large-scale aggregated network analysis tasks. The database is freely available online (https://precious.polito.it/theringdb/) through a web interface that provides both access to the raw data and to advanced analysis algorithms. I developed the overall design, the backend, I managed all the data sources and their internal representation. My contribution in this paper is in the definition and implementation of the graph layer, the design and implementation of the databases and of several of the network analysis algorithms. All authors contributed equally in writing the paper.

(2019) "**Beyond Homology Transfer: Deep Learning for Automated Annotation of Proteins**" Nauman, Mohammad; Ur Rehman, Hafeez; Politano, Gianfranco; Benso, Alfredo, Journal of Grid Computing, Springer, Vol. 17, 2019, pp. 225-237, DOI: 10.1007/s10723-018-9450

    Quartile: Q1 (Computer Science)
    Citations: SCOPUS: 26 SCHOLAR: 30
    SJR: 0,64 IF: n/a

This paper proposes a Deep Learning approach to hypothesise the function of a protein starting from its structure. This is a known and very complex problem in biological research since researchers know the existence of thousands of proteins whose functionality is still unknown. This algorithm, developed in collaboration with one the former PhD students of our group, now a professor in Pakistan, is a significant contribution to this topic because it showed how a Deep Learning architecture is able to generate insightful knowledge from already available data, as recognised by several citing papers. My main contribution in this paper was the formalisation of the biological problem in computational terms so that it could be solved using a Deep Learning approach.

(2019) "**Extracellular nicotinate phosphoribosyltransferase binds Toll like receptor 4 and mediates inflammation**", Managò, Antonella; Audrito, Valentina; Mazzola, Francesca; Sorci, Leonardo; Gaudino, Federica; Gizzi, Katiuscia; Vitale, Nicoletta; Incarnato, Danny; Minazzato, Gabriele; Ianniello, Alice; Varriale, Antonio; D'Auria, Sabato; Mengozzi, Giulio; Politano, Gianfranco; Oliviero, Salvatore; Raffaelli, Nadia; Deaglio, Silvia, NATURE COMMUNICATIONS, ISSN:2041-1723, DOI:10.1038/s41467-019-12055-2

    Quartile: Q1 (Biology)
    Citations: SCOPUS: 40 SCHOLAR: 46
    SJR: 5,569 IF: n/a

This paper, published on Nature Communications, is one of my first work with a large group of solely life-science scientists, it took about three years to complete the collection of data and apply all the corrections required to the experimental design to be accepted by the prestigious journal. I learned a lot about high profile publications process. The paper identified a novel bio marker useful in early sepsis prognosis, which is currently often hard to identify in useful time especially for patients who present other comorbidities. My main contributions were participation to the design of the validation setup, the data analysis, and the statistical supervision.

(2018) **DNA Pool Analysis-based Forgery-Detection of Dairy Products**, Rossi, Francesco; Modesto, Paola; Biolatti, Cristina; Benso, Alfredo; Di Carlo, Stefano; Politano, Gianfranco; Acutis, Pierluigi; International Journal of Electrical and Computer Engineering (IJECE), Institute of Advanced Engineering and Science (IAES), DOI:10.11591/ijece.v8i6

    Quartile: Q2 (Computer Science)
    Citations: SCOPUS: 0 SCHOLAR: 1
    SJR: 0,3 IF: 0,43

This work is the result of a collaboration with the Istituto Zooprofilattico Sperimentale del Piemonte Liguria e Valle d'Aosta. It presents a modelling approach to better evaluate a traceability index between dairy products and their producer. This is extremely important since food integrity and food safety fields have received much attention in recent years due to the dramatic increase in number of food frauds. My main contribution has been in guiding and supervising the work of our PhD student Francesco Rossi, and this result was also part of the tasks of the project, HEART VDA, I was coordinating (5.4 and 5.6, sub-project: "Dairy products and by-products").

(2017) "**Multi-level and hybrid modelling approaches for systems biology**" Bardini, Roberta; Politano, Gianfranco Michele Maria; Benso, Alfredo; Di Carlo, Stefano, Computational and Structural Biotechnology Journal, Elsevier, Vol. 15, 2017, pp. 396-402, DOI: 10.1016/j.csbj.2017.07.005

    Quartile: Q1 (Computer Science)
    Citations: SCOPUS: 38 SCHOLAR: 50
    SJR: 1,284 IF: 3,16
    This paper discusses the main problems in modelling and simulating biological systems and suggests the most promising computer-based scenarios to correctly address them. The paper focuses mainly on a particular class of models usually referred to as multi-level and hybrid models. Based on this definition, we define models which are both multi-level and hybrid as representations supporting different formalisms and organised in levels encompassing multiple systems scales. All authors contributed equally to this paper.

(2017) "**Estimation of sickness absenteeism among Italian healthcare workers during seasonal influenza epidemics**", Gianino, Maria Michela; Politano, Gianfranco Michele Maria; Scarmozzino, Antonio; Charrier, Lorena; Testa, Marco; et al., PLOS ONE, ISSN:1932-6203, DOI:10.1371/journal.pone.0182510Das

    Quartile: Q1 (Biology)
    Citations: SCOPUS: 40 SCHOLAR: 52
    SJR: 1,201 IF: 2,806
    This paper is the first work of a very prolific collaboration with Prof. Gianino of the Department of Hygiene and public health of Università degli Studi di Torino. This collaboration leaded me to a new sub field of interdisciplinary collaboration with life science world. In particular, the field of biostatistics copes with statistics applied to life science applications and deals with their problems (i.e., real data, noise, [1] presence of outliers, unbalancing in population, etc.). Data often require a lot of processing and evaluation to properly remove any source of error/noise, moreover, given their peculiar shape, often specific methods for statistical analysis should be chosen or custom ones defined. This paper addresses the problem of vaccination against flu, to prevent absenteeism in hospital personnel. At the time of writing only two other papers on this topic were available related to European countries. The analysis has been performed on the entire "Città della Salute" population. My main contributions were participation to the definition of the problem and the design of the entire setup, I also personally took care of the data processing, the definition of the statistical model, and the development of the whole computational pipeline.

(2016) **Common integration sites of published datasets identified using a graph-based framework**, Vasciaveo, Alessandro; Velevska, Ivana; Politano, Gianfranco; Savino, Alessandro; Schmidt, Manfred; Fronza, Raffaele; Computational and Structural Biotechnology Journal, Elsevier, DOI:10.1016/j.csbj.2015.11.004

    Quartile: Q1 (Computer Science)
    Citations: SCOPUS: 1 SCHOLAR: 2
    SJR: 1,284 IF: 3,16
    This work is the result of an international collaboration we had with the National Center for Tumor Diseases in Heidelberg, Germany. It presents the application of a model we developed to better understand where viruses attack the DNA of their host. This is extremely important in therapeutic approaches that use viruses to target the patient DNA in order to repair or counteract the effect of pathological mutations. My main contribution was in the initial definition of the graph to be used to model integration sites..

(2015) **Cross-layer reliability evaluation, moving from the hardware architecture to the system level: A CLERECO EU project overview**, Vallero, Alessandro; Tselonis, Sotiris; Foutris, Nikos; Kaliorakis, Manolis; Kooli, Maha; Savino, Alessandro; Politano, Gianfranco; Bosio, Alberto; Di Natale, Giorgio; Gizopoulos, Dimitris; Microprocessors and Microsystems, Elsevier, DOI:10.1016/j.micpro.2015.06.003

This work is the result of an international collaboration with the European network developed in the European project FP7 CLERECO (Ga. 611404) coordinated by one of my group advisors. This work has been a team effort. My primary contribution in this paper is the development of the first design of the probabilistic framework to handle conditional loop unrolling patterns in the simulation of hardware cascade of circuits and take active part to the design of the first probabilistic model whose final expression is summarized in this paper.

(2014) **Alice in" Bio-Land": Engineering Challenges in the World of Life Sciences**, Benso, Alfredo; Di Carlo, Stefano; Politano, Gianfranco; Savino, Alessandro; Bucci, Enrico; IT Professional, IEEE, DOI:10.1109/MITP.2014.45

This article discusses the role of systems and computational biology as a fundamental methodological "middle-ground" between the two distant worlds of engineering and life sciences. At the time of writing the paper the discussion presented in the paper was very novel and relevant since multidisciplinary sciences in the field of computer engineering and life sciences were starting consolidating. We co-writed this paper with a biologist, this allowed all of us to try to find a middle ground to help to better identify and highlight the most common set of problems that arises in multidisciplinary collaboration like Bioinformatics. All authors contributed equally to this paper.

(2014) "**Using Boolean Networks to Model Post-transcriptional Regulation in Gene Regulatory Networks**" Politano G.; Benso A.; Di Carlo S.; Savino A.; Ur Rehman H.; Vasciaveo A., Journal of Computational Science, Elsevier, Vol. 5, 2014, pp. 332-344, DOI: 10.1016/j.jocs.2013.10.005

This paper proposes and enhanced model to represent regulatory networks. Traditionally, metabolic and signalling pathways are represented by small networks of genes. Unfortunately, genes are not the only actors involved in gene regulation. In this work we show how to use Boolean-networks to model microRNA/gene interactions in order to obtain more reliable and biologically realistic networks. My main contribution was the main idea, the overall design and its implementation. I also designed the regulatory circuits to assess the overall capabilities of the Boolean model.

(2014) "**ReNE: A Cytoscape Plugin for Regulatory Network Enhancement**", Politano G.; Benso A.; Savino A.; Di Carlo S., PLOS ONE, ISSN:1932-6203, DOI:10.1371/journal.pone.0115585

This paper proposes a model to represent regulatory networks interactions that take place among regulatory and post-regulatory biological entities. Traditionally, those regulations are represented by small networks of genes. Unfortunately, when transcriptional and post transcriptional regulators are added to a gene network the complexity explodes, resulting in a humanly un-manageable graph. This paper addresses this problem by providing a fully automated software capable of efficiently build up complex regulatory network by allowing users to filter regulations of interest. My main contribution was the main idea, the overall design and its implementation. I also designed the biological experimental setup to validate the overall capabilities of the tool.
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(2013) "**A systematic analysis of a mi-RNA inter-pathway regulatory motif**", Di Carlo S.; Politano G.; Savino A.; Benso A., JOURNAL OF CLINICAL BIOINFORMATICS, ISSN:2043-9113, DOI:10.1186/2043-9113-3-20

Quartile: Q1 (Health Informatics)

Citations: SCOPUS: 11 SCHOLAR: 16

SJR: 0,907 IF: n/a

This work is one of my first attempts to deal with the inner complexity of miRNA regulaations induced on gene expression. This preliminary work also leads to the further development of both the ReNE and CyTransFinder tools. In this work we designed a biological hypothesis about the role of micrornas as protectors against cross regulatory fluctuations, among multiple concurrent signalling pathways. This hypothesis lead to the design of an in-silico regulatory model that has been tested pathways wide, to identify hallmarks of pathway-to-pathway mirna induced protection. A non-parametric statistical model on top of the computations allowed us to identify the most promising candidate protective loops that may take place between pathways. My main contribution was taking part to the draft of the preliminary idea, the overall design and implementation of the network analysis with the inclusion of microRNA. I also designed the study case required to demonstrate in the paper the biological validity of the novel regulatory pattern we identified

(2011) "**Building Gene Expression Profile Classifiers with a Simple and Efficient Rejection Option in R**" Benso A.; Di Carlo S.; Politano G.; Savino A.; Ur Rehman H., BMC Bioinformatics, BioMed Central, Vol. 12, 2011, pp. 1-15, DOI: 10.1186/1471-2105-12-S13-S3

Quartile: Q1 (Computer Science)

Citations: SCOPUS: 6 SCHOLAR: 8

SJR: 1,467 IF: 2,448

Following the work presented in the paper "A cDNA Microarray Gene Expression Data Classifier for Clinical Diagnostics Based on Graph Theory" (here presented as product), we expanded and improved our classifier for gene expression data. In this work we introduce a rejection option that allows to improve the classification engine sensitivity and specificity. My main contribution was the identification of the problem and the design of the rejection rule and the implementation of the tool.

(2010) "**A cDNA Microarray Gene Expression Data Classifier for Clinical Diagnostics Based on Graph Theory**" Benso A.; Di Carlo S.; Politano G, IEEE/ACM Transactions on Computational Biology and Bioinformatics, IEEE Computer Society, Vol. 8, 2011, pp. 577-591, DOI: 10.1109/TCBB.2010.90

Quartile: Q2 (Mathematics)

Citations: SCOPUS: 18 SCHOLAR: 28

SJR: 0,648 IF: 1,995

This is the first relevant paper I published in a peer-reviewed Life Science journal. It is mainly based on my PhD work. The paper is innovative because it presents a new machine learning algorithm to classify gene expression data. For my group this was also a milestone in understanding the scientific community that we were going to have to collaborate with. Thanks to this initial work I understood how, to work in the Life Science world, a proper training was necessary. My main contribution was the development and the assessment of the whole graph model and the selection of experimental (cDNA microarray) data to design meaningful experiments to assess the overall validity of the algorithm.

✦ Complete list of all the significant publications of the candidate, including those listed at points 1.1 and 1.2 (to be attached to the end of the Curriculum).
    ✦ See appendix A

Indicators related to overall scientific production – In accordance with art. 4 of the notice of competition

Journal Articles		Citations		H Index		DB
Total	Last 10 yrs	Total	Last 15 yrs	Total	Last 15 yrs	
98	81	1472	1472	17	17	SCHOLAR
74	62	960	960	14	14	SCOPUS

2. Coordination of research groups and projects and research development in the "third mission"

✦ Coordination and management of the research groups, possibly with international relationships and collaborations, with explicit mention of the number and of the type of PhD and Post-Doc students of whom the candidate has been the academic supervisor;

Research groups: From 2020 I am the vice-leader of the *Systems Biology (SysBio) group* at the Department of Control and Computer Engineering (DAUIN) of Politecnico di Torino. The group is composed of 2 full professors, 1 associate professor, one RTD-A researcher, and several PhD students. Since 2015 I also managed and supervised activities in Systems Biology e Bio-Statistics area in the group.

PhD and Post Docs: 1 Academic Supervisor - 4 Collaboration in tutorship:

- Academic Supervisor - XXXVI cycle: Ostellino Sofia (currently in her PhD) – Titolo: "ADVANCED COMPUTATIONAL METHODS FOR BIOMEDICAL DATA INTEGRATION AND ANALYSIS"

- Collaboration in tutorship - XXVI cycle: UrRehman Hafeez (now Associate Professor and Head of Department at the National University of Computer and Emerging Sciences, Pakistan) – Titolo: "INTEGRATION AND ANALYSIS OF HETEROGENEOUS BIOLOGICAL DATA"

- Collaboration in tutorship - XXIX cycle: Vasciaveo Alessandro (now post-doc at Columbia University, USA) – Titolo: "COMPUTATIONAL MODELS AND ALGORITHMS TO SOLVE LARGE-SCALE PROBLEMS IN NETWORK BIOLOGY"

- Collaboration in tutorship - XXX cycle: Rossi Francesco – Titolo: "INTEGRATION OF IMAGING AND SYSTEMS BIOLOGY APPROACHES FOR ADVANCED CAD (COMPUTER AIDED DETECTION) METHODOLOGIES"

- Collaboration in tutorship - XXXI cycle: Bardini Roberta (now post-doc at Politecnico di Torino) – Titolo: "MODELLING OF STRUCTURE/FUNCTION RELATIONS IN COMPLEX BIOLOGICAL SYSTEMS"

International relationships: I had several international relationships, in both research and volunteer work for international organisations. As far as scientific collaborations I'd like to mention the following:

- *Prof. Lars Ronn Olsenn* (Denmark Technical University, Copenhagen, Denmark) - ongoing projects on i) the design of an innovative algorithm and tool to support the design of spectrometry experiments and ii) large scale bibliometric analysis

- *Prof. Hafeez Ur Rehman* (National University of Computer & Emerging Sciences, Hayatabad, Pakistan) several ongoing projects on Artificial Intelligence applied in the field of Life Sciences

- *Prashanth N Suravajhala* (Birla Institute of Scientific Research, India)

- *Prof. Gagik Karhamian* (L.A. Orbeli Institute of Physiology, Yerevan, Armenia): collaboration on data analysis of electrophysiological devices for stress evaluation on biological entities

✦ Scientific responsibility (Principal investigator) of Italian and International research projects, awarded through a peer-review process;

- 2016-2019 - **Responsibilty** - tasks 5.2 and 5.6, sub-project: "Innovation in Agrifood VDA", project: HEART VDA (Health and agrifood tech VDA)" founded by Regione Valle d'Aosta, 2016
- 2016-2019 - **Responsibilty** - tasks 5.4 and 5.6, sub-project: "Dairy products and by-products", project: HEART VDA (Health and agrifood tech VDA)" founded by Regione Valle d'Aosta, 2016
- 02/2020 - 10/2020 - **Unit Responsibilty** . Research Project 2020 IZS PLV Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta - DIDEs -POLITANO - RID20POL01 - Founded by Ministeri-Ricerca - Budget Eur10,000 (Duration 8 months)
- 26-01-2023 to date - **Unit Responsibilty** - Partner. Spoke 6 del progetto PNRR - PE14 - RESTART - Services and systems for extreme environments and domain-specific scenarios - Budget 232.314,24 Eur. - Start Jan.2023, duration 3 years.

✦ Scientific responsibility of Italian and International research projects, ruled through partnership agreements with companies and/or public/private bodies which are leaders in their own sector;

- 08/2021-09/2021 -**PI-Responsibilty** . Preliminary feasibility study to support R&D activities to improve diagnosis capabilities and ultrasonic stadiation in colon-rectal cancer - Founded by eResult srl - Budget Eur. 25000 (Duration 1 month)
- 2015-2020 - **Responsibilty** - Statistical assessment in regional workgroup "Infezioni correlate all'assistenza" (Direzione SANITA') for data analisi and reporting on "Sorveglianza Delle Infezioni del Sito Chirurgico in Piemonte" coordinator: prof. Carla Zotti

✦ Outcomes obtained in the application and in the enhancement of research by technology transfer activity, in particular:

- **International Patent for Industrial Invention (Brevetto per Invenzione Industriale) N. 102019000009969 – Class G16B**
  Bardini Roberta, Di Carlo Stefano, Benso Alfredo, Politano Gianfranco
  "*Metodo di simulazione via computer dell'ontogenesi di un sistema biologico e, opzionalmente, di generazione di un protocollo di coltura*"
  The invention consists of a computational method for modelling biological systems intended for culture processes. The models that follow the proposed method allow to generate the culture protocols to guide the system towards specific objectives.

- **Italian patent N. 102020000016987**
  Bardini Roberta, Di Carlo Stefano, Benso Alfredo, Politano Gianfranco
  "Metodo computerizzato per generare protocolli di coltura per bio-manufacturing".
  The patent describes a computer-based method for the generation of culture protocols for bio-manufacturing of biological artifacts.

- **Publication Number WO/2020/261154 - International Application No. PCT/IB2020/055990 - Status: published - 30.12.2020**
  Bardini Roberta, Di Carlo Stefano, Benso Alfredo, Gianfranco Politano
  "Computer Implemented Method for Generating a Culture Protocol for Bio-Manufacturing".
  The claims of the patent describe a computer-based system able to simulate the ontogenesis of a biological system that could be exploited for the generation of culture protocols.

✦ Outcomes obtained in the application and in the enhancement of research by Public Engagement activity, in particular:

- The paper [1] resulted in an interview by Nature being one of the largest multi-regional assessment available about burden related to covid. Interview is available at https://www.nature.com/articles/d41586-022-01341-7 (Article in PDF also available in titles attached)

     [1] *2021 Gianino, Maria Michela; Savatteri, A; Politano, G; Nurchis, Mario Cesare; Pascucci, Domenico; Damiani, Gianfranco; Burden of COVID-19: disability-adjusted life years (DALYs) across 16 European countries, Eur Rev Med Pharmacol Sci, Verduci Editore*

- Since 2011, **25+ journal papers** have been published as **Open Access (Open Science) products**

- 2013-2016 - Member of Scientific Committee of Museo Regionale di Scienze Naturali di Torino

- 2009 – Invited Speaker to the round table at conference "Development, Energy, Environment". Sponsored by: Confindustria del Canavese

3. National and international reputation and professional activity for the scientific community

   ✦ Participation in the Editorial Board of Journals with international reputation (in the role of Associate Editor or equivalent), participation in the Editorial Board of book series, encyclopedias and essays of recognized prestige;

   - From 2018 - Member of Editorial Board di IEEE/CS ITProfessional (ITPRO)
   - 2014-2016 - Member of Editorial Board del Journal of Bioinformatics Research Studies
   - 2019 - Guest editor of the Special Issue on Best Practices in Modeling and Simulation of Biological Systems, Journal of Computational Science, Elsevier
   - 2021-2022 - Guest editor of the Special Issue on Computational Techniques to Annotate Macro-Molecules for Personalized Medicine on Frontiers.

   ✦ Offices in the Governing bodies of national and international scientific societies;

   - from 2023 - Vice Chair of IEEE/Computer Society Technical Committee on Computational Life Sciences (TCCLS)
   - from 2022 – Senior Member IEEE
   - from 2014 - OC member: Webchair for IEEE/Computer Society Test Technology Technical Council (IEEE-TTTC)
   - 2018-2022 – Member of Operations Committee: Webmaster per IEEE/Computer Society ITProfessional
   - from 2018 - Member of Operations Committee: Webchair per l'IEEE/Computer Society European Test Technology Technical Council (IEEE-eTTTC)
   - 2015-2022 - Member of Operations Committee: Members Outreach Chair di IEEE/Computer Society Technical Committee on Computational Life Sciences (TCCLS)
   - 2015-2017 - Member of Operations Committee - IEEE/Computer Society Digital Library Operations Committee (DLOC)

   ✦ Prizes and awards awarded to the candidate for his/her scientific activity and project activity in the Academic Recruitment Fields ("Settori Concorsuali"), where this is appropriate;

- 2022 – Senior Member IEEE
- 2022 - Paper featured in an interview by Nature being one of the largest multi-regional assessment available about burden related to covid. Interview is available at https://www.nature.com/articles/d41586-022-01341-7 (Article in PDF also available in titles attached)
- 2014 - Best Paper Award at International Conference on Bioinformatics Models, Methods and Algorithms. BIOINFORMATICS-2014. (A Computational Study to Identify TP53 and SREBF2 as Regulation Mediators of miR-214 in Melanoma Progression)
- 2012 - Best Paper Award at the IEEE International Conference on Automation, Quality and Testing, Robotics (Using Gnome Wide Data For Protein Function Prediction By Exploiting Gene Ontology Relationships)
- 2011 - Featured Paper and Video on ComputingNow website homepage. What's New in December 2011. (Statistical reliability estimation of microprocessor-based systems)
- 2010 - Best Paper Award at the IEEE International Conference on Automation, Quality and Testing, Robotics (GPU Acceleration for Statistical Gene Classification)

✦ Participation in international conferences, as a distinguished invited speaker; participation in the scientific committees of International Conferences;

- 2019 to date - Member of the **Program Committee** of the symposium "Smart & Connected Health" @ COMPSAC
- 2016 to date - Member of the **Program Committee** of BIOINFORMATICS / BIOSTEC
- 2019 - **Program Chair** of International Rural and Elderly Health Informatics Conference (IREHI)
- 2018 - **Program Chair** of Workshop on Challenges and Opportunities in Large-Scale Network Analysis in Systems Biology (co-hosted by BIBM)
- 2018 - Member of the **Organising Committee** of International Rural and Elderly Health Informatics Conference (IREHI)
- 2017 - Member of the **Program Committee** of "New Trends in Information Technology" (NTIT)
- 2016 - **Session Chair** - Session 16 of IEEE International Conference on Bioinformatics and Biomedicine (BIBM)
- 2014 – Member of the **Organizing Committee** of IEEE International Workshop in Energy Systems Reliability and Resiliency (ESR2 2014)
- 2014 - Member of the **Program Committee** of "Pattern Recognition in Bioinformatics" (PRIB 2014)
- 2013 - Member of the **Technical Committee** IAPR TC-20 (Technical Committee on Pattern Recognition for Bioinformatics)
- 2012 - Member of the **Program Committee** of "Pattern Recognition in Bioinformatics" (PRIB 2013)
- 2012 - Member of the **Program Committee** of "Computational Intelligence Methods for Bioinformatics and Biostatistics" (CIBB 2013)
- 2009 - Member of the **Program Committee** of "IEEE Congress on Evolutionary Computation" (CEC 2009). Trondheim, (Norway)
- 2009 – **Invited Speaker** at conference "Development, Energy, Environment". Sponsored by: Confindustria del Canavese

4. Teaching activity

✦ Formal responsibility of Bachelor's (Laurea) and Master of Science's (Laurea Magistrale) degree courses in Italian and/or foreign universities.

@POLITO

- 2021 to date - Bioinformatics, Master Degree in Computer Science Engineering (english) (Politecnico di Torino). (60 ore)
- 2018 to date - Informatica, Bachelor Degree in Computer Science Engineering (Politecnico di Torino). (60 ore)

@UNITO
- 2012 to date - Controlli automatici - Corso di Laurea Interfacoltà in Scienze Strategiche (Università degli Studi di Torino) (42 ore)
- 2018 2020 - Informatica - Corso di laurea magistrale in scienze infermieristiche ed ostetriche (Università degli Studi di Torino) (30 ore)
- 2014 2015 - Seminar on Sistemi di Elaborazione - Corso di laurea magistrale in scienze infermieristiche ed ostetriche (Università degli Studi di Torino)(20 ore)

@Turin Tashkent Polytechnic University, Uzbekistan
- 2013 2014 - Operating Systems (co-responsibility with Prof.Serra TTPU, Tashkent (UZ) (60 ore)
- 2013 2014 – Computer Architecture (co-responsibility with Prof.Serra TTPU, Tashkent (UZ) (20 ore)
- 2012 2013 - Operating Systems TTPU, Tashkent (UZ) (80 ore)

@PhD/Master
- 2019 2020 - Biological Network Analysis for precision medicine -Scuola di Dottorato dell'Università del Salento
- 2019 2021 - Elaborazione delle Informazioni - Master in Infermieristica di Sanità Pubblica (Università degli Studi di Torino – CoREP)

✦ Thesis work with a highly qualifying profile in scientific and professionalizing terms for the student or for inclusion in highly qualified business and organizational contexts, or for inclusion in projects of high scientific value at an international level.

@POLITO

- 2021 to date - Bioinformatics, Master Degree in Computer Science Engineering (english) (Politecnico di Torino). (60 ore)
- 2022 DE STEFANO CARMINE Deep Learning approaches for prediction of Hepatocellular Carcinoma Recurrence post Liver Transplantation
- 2021 DE GIOVANNI CARMEN - Analisi dello sguardo e dell'EEG per la diagnosi precoce delle malattie dello spettro autistico
- 2021 GALAZZO ROSARIO - Analisi dello sguardo e dell'EEG per la diagnosi precoce delle malattie dello spettro autistico
- 2021 MONALDI IGOR - Deep Learning per analisi di dati di riabilitazione propriocettiva e posturale
- 2019 ISOLA MARGHERITA - Analisi di reti di co-espressione genica coinvolte nell'autismo
- 2019 LETIZIA ANNALISA - Analisi di reti di co-espressione genica coinvolte nell'autismo

@UNITO
- Advisor of more than 30 thesis (MS degrees) mostly with research topics in the field of military operations

✦ Student evaluations

@UNITO

- 2013 2014 – Acknowledge letter about didactical quality of President of Corso di Laurea Magistrale In Scienze Infermieristiche e ostetriche.

@POLITO

- 2022 2023 - Informatica - 3.44
- 2021 2022 - Bionformatics - 3.55
- 2020 2021 - Informatica - 3.62
- 2020 2021 - Algorithms and Programming - 2.91
- 2019 2020 - Informatica - 3.40
- 2019 2020 - Algorithms and Programming - 3.42
- 2018 2019 - Algorithms and Programming - 3.41
- 2017 2018 - Informatica - 3.04
- 2017 2018 - Ipermedia e sviluppo web - 3.25
- 2016 2017 - Informatica - 3.53
- 2016 2017 - Ipermedia e sviluppo web - 3.40
- 2015 2016 - Informatica - 3.53
- 2015 2016 - Ipermedia e sviluppo web - 2.57
- 2014 2015 - Informatica - 3.17
- 2014 2015 - Ipermedia e sviluppo web - 2.94
- 2013 2014 - Informatica - 2.94
- 2013 2014 - Informatica - 2.70
- 2012 2013 - Informatica - 3.21
- 2012 2013 - Informatica - 3.33
- 2011 2012 - Informatica - 3.27
- 2011 2012 - Informatica - 3.25

5. **Institutional offices and roles in Italian and foreign Universities and/or public and private institutions**

   ✦ Management roles in Universities, as part of Faculty duties;

   - 2019 2021 - Member of the exam commission "Informatica - C"
   - 2020 2021 - Responsible for online exams "Informatica - C"
   - 2021 2022 – Responsible for online exams "Informatica - Python"
   - 2020 2023 - "Docente di riferimento" for Corso di Laurea in INGEGNERIA DEL CINEMA E DEI MEZZI DI COMUNICAZIONE
   - 2020 - Department Responsible - Study Commission for agreement and development of Huawei ICT Academy Huawei
   - From 2020 - Responsible of Master Degree, Computer Science sector, in the Stage commission of Collegio di Ingegneria Informatica, del Cinema e Meccatronica

   ✦ Offices in the Governing bodies, Board of Governors, Scientific Advisory Boards of public and private institutions.

   - 2013-2016 - Member of Scientific Committee of Museo Regionale di Scienze Naturali di Torino

Appendix A: Full publication List
Elenco Pubblicazioni prof. Gianfranco Michele Maria Politano

Publication Summary (from 2008 to 2023)

Article - *The integration of clinical data in the assessment of Multiple Sclerosis - a review* Ostellino, Sofia; Benso, Alfredo; Politano, GIANFRANCO MICHELE MARIA. - In: COMPUTER METHODS AND PROGRAMS IN BIOMEDICINE. - ISSN 0169-2607. - ELETTRONICO. - 221:(2022), p. 106900. [10.1016/j.cmpb.2022.106900]	2022
Chapter - *"Engineering Minds for Biologists"* Benso, Alfredo; Di Carlo, Stefano; Politano, Gianfranco, 2021, pp. 79-90, DOI: 10.1007/978-981-15-9544-8_9	2021
Article - *"Nets-within-nets for modeling emergent patterns in ontogenetic processes"* Bardini, Roberta; Benso, Alfredo; Politano, Gianfranco; Di Carlo, Stefano, Computational and Structural Biotechnology Journal, Elsevier, 2021, pp. 1-40, quartile: Q1, DOI: 10.1016/j.csbj.2021.10.008	2021
Article - *"IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis"* Politano, G.; Benso, A., PLoS Computational Biology, Public Library Of Science, Vol. 16, 2020, quartile: Q1, cit.scopus: 3, cit.scholar: 2, DOI: 10.1371/journal.pcbi.1008238	2020
Article - *"‘One DB to rule them all’ - the RING: a Regulatory INteraction Graph combining TFs, genes/proteins, SNPs, diseases and drugs"* POLITANO, GIANFRANCO MICHELE MARIA; DI CARLO, STEFANO; BENSO, ALFREDO, Database : the journal of biological databases and curation, Oxford University Press, Vol. 2019, 2019, pp. 1-14, quartile: Q1, cit.scopus: 4, DOI: 10.1093/database/baz108	2019
Article - *"Extracellular nicotinate phosphoribosyltransferase binds Toll like receptor 4 and mediates inflammation"* Managò, Antonella; Audrito, Valentina; Mazzola, Francesca; Sorci, Leonardo; Gaudino, Federica; Gizzi, Katiuscia; Vitale, Nicoletta; Incarnato, Danny; Minazzato, Gabriele; Ianniello, Alice; Varriale, Antonio; D’Auria, Sabato; Mengozzi, Giulio; Politano, Gianfranco; Oliviero, Salvatore; Raffaelli, Nadia; Deaglio, Silvia, Nature Communications, Nature Publishing Group, Vol. 10, 2019, quartile: Q1, cit.scopus: 31, cit.scholar: 34, DOI: 10.1038/s41467-019-12055-2	2019
Article - *"Beyond Homology Transfer: Deep Learning for Automated Annotation of Proteins"* Nauman, Mohammad; Ur Rehman, Hafeez; Politano, Gianfranco; Benso, Alfredo, Journal of Grid Computing, Springer, Vol. 17, 2019, pp. 225-237, quartile: Q1, cit.scopus: 23, cit.scholar: 26, DOI: 10.1007/s10723-018-9450-6	2019
Chapter - *"Computational Tools for Applying Multi-level Models to Synthetic Biology"* Bardini, R.; Politano, G.; Benso, A.; Di Carlo, S., 2018, pp. 95-112, cit.scopus: 1, cit.scholar: 2, DOI: 10.1007/978-981-10-8693-9_7	2018
Article - *"Modeling antibiotic resistance in the microbiota using Multi-level Petri Nets"* Bardini, Roberta; DI CARLO, Stefano; Politano, GIANFRANCO MICHELE MARIA; Benso, Alfredo, BMC Systems Biology, BioMed Central, Vol. 12, 2018, pp. 1-21, quartile: Q1, cit.scopus: 3, cit.scholar: 7, DOI: 10.1186/s12918-018-0627-1	2018
Article - *"DNA Pool Analysis-based Forgery-Detection of Dairy Products"* Rossi, F.; Modesto, P.; Biolatti, C.; Benso, A.; Di Carlo, S.; Politano, G.; Acutis, P. L., International Journal of Electrical and Computer Engineering, IAES, Vol. 8, 2018, pp. 3913-3922, quartile: Q2, cit.scholar: 1, DOI: 10.11591/ijece.v8i6	2018
Article - *"Multi-level and hybrid modelling approaches for systems biology"* Bardini, Roberta; Politano, Gianfranco Michele Maria; Benso, Alfredo; Di Carlo, Stefano, Computational and Structural Biotechnology Journal, Elsevier, Vol. 15, 2017, pp. 396-402, quartile: Q1, cit.scopus: 33, cit.scholar: 46, DOI: 10.1016/j.csbj.2017.07.005	2017
Article - *"In-silico cardiac aging regulatory model including microRNA post-transcriptional regulation"* Politano, Gianfranco; Logrand, Federica; Brancaccio, Mara; Di Carlo, Stefano, Methods, Academic Press Inc., Vol. 124, 2017, pp. 57-68, quartile: Q1, cit.scopus: 3, cit.scholar: 4, DOI: 10.1016/j.ymeth.2017.06.002	2017
Article - *"Common integration sites of published datasets identified using a graph-based framework"* Vasciaveo, Alessandro; Velevska, Ivana; Politano, Gianfranco; Savino, Alessandro; Schmidt, Manfred; Fronza, Raffaele, Computational and Structural Biotechnology Journal, Elsevier, Vol. 14, 2016, pp. 87-90, quartile: Q1, cit.scopus: 1, cit.scholar: 2, DOI: 10.1016/j.csbj.2015.11.004	2016
Article - *"CyTRANSFINDER: A Cytoscape 3.3 plugin for three-component (TF, gene, miRNA) signal transduction pathway construction"* Politano, Gianfranco Michele Maria; Orso, Francesca; Raimo, Monica; Benso, Alfredo; Savino, Alessandro; Taverna, Daniela; Di Carlo, Stefano, BMC Bioinformatics, BioMed Central Ltd., Vol. 17, 2016, pp. 1-17, quartile: Q1, cit.scopus: 9, cit.scholar: 13, DOI: 10.1186/s12859-016-0964-2	2016
Proceeding - *"Cross-layer system reliability assessment framework for hardware faults"* Vallero, A.; Savino, A.; Politano, G.; Di Carlo, S.; Chatzidimitriou, A.; Tselonis, S.; Kaliorakis, M.; Gizopoulos, D.; Riera, M.; Canal, R.; Gonzalez, A.; Kooli, M.; Bosio, A.; Di Natale, G.Proceedings Of The International Test Conference 2016, 2016, pp. 1-10, cit.scopus: 7, cit.scholar: 29, DOI: 10.1109/TEST.2016.7805863	2016
Chapter - *"A computational pipeline to identify new potential regulatory motifs in melanoma progression"* Politano, Gianfranco; Benso, Alfredo; Di Carlo, Stefano; Orso, Francesca; Savino, Alessandro; Taverna, Daniela, Communications in Computer and Information Science, Springer International Publishing, Vol. 511, 2015, pp. 181-194, cit.scholar: 1, DOI: 10.1007/978-3-319-26129-4_12	2015

PAPER	YEAR
Article - *"Alice in "Bio-land": engineering challenges in the world of Life-Sciences"* Benso A.; Di Carlo S.; Politano G.; Savino A.; Bucci E., IT Professional, IEEE Computer Society, Vol. 16, 2014, pp. 38-47, quartile: Q2, cit.scopus: 1, DOI: 10.1109/MITP.2014.45	2014
Article - *"A systematic analysis of a mi-RNA inter-pathway regulatory motif"* Di Carlo S.; Politano G.; Savino A.; Benso A., Journal of Clinical Bioinformatics, BIOMED CENTRAL LTD, Vol. 3, 2013, pp. 1-14, quartile: Q1, cit.scopus: 11, cit.scholar: 16, DOI: 10.1186/2043-9113-3-20	2013
Article - *"Statistical Reliability Estimation of Microprocessor-Based Systems"* Savino A.; Di Carlo S.; Politano G.; Benso A.; Di Natale G.; Bosio A., IEEE Transactions on Computers, IEEE Computer Society, Vol. 61, 2012, pp. 1521-1534, quartile: Q1, cit.scopus: 34, cit.scholar: 45, DOI: 10.1109/TC.2011.188	2012
Article - *"A cDNA Microarray Gene Expression Data Classifier for Clinical Diagnostics Based on Graph Theory"* Benso A.; Di Carlo S.; Politano G, IEEE/ACM Transactions on Computational Biology and Bioinformatics, IEEE Computer Society, Vol. 8, 2011, pp. 577-591, quartile: Q2, cit.scopus: 18, cit.scholar: 27, DOI: 10.1109/TCBB.2010.90	2011
Article - *"Building Gene Expression Profile Classifiers with a Simple and Efficient Rejection Option in R"* Benso A.; Di Carlo S.; Politano G.; Savino A.; Ur Rehman H., BMC Bioinformatics, BioMed Central, Vol. 12, 2011, pp. 1-15, quartile: Q1, cit.scopus: 6, cit.scholar: 7, DOI: 10.1186/1471-2105-12-S13-S3	2011
PAPER	**YEAR**
Article - *Determinants of COVID-19 vaccination worldwide: a retrospective observational study* Peano, Alberto, Gianfranco Politano, and Maria M. Gianino. In Population Medicine 5 no. Supplement (2023): A1766. doi:10.18332/popmed/165077	2023
Article - *Impact of the Timing of Integrated Home Palliative Care Enrolment on Emergency Department Visits* Scacchi, Alessandro; Savatteri, Armando; Politano, Gianfranco; Conti, Alessio; Dalmasso, Marco; Campagna, Sara; Gianino, Maria Michela. - In: INTERNATIONAL JOURNAL OF HEALTH POLICY AND MANAGEMENT. - ISSN 2322-5939. - 11:12(2022), pp. 2964-2971. [10.34172/ijhpm.2022.5783]	2022
Article - *Impact of COVID-19 on emergency department visits among palliative home care recipients: a retrospective population-based cohort study in the Piedmont region, Italy* Scacchi, Alessandro; Conti, Alessio; Politano, Gianfranco; Dalmasso, Marco; Ostellino, Sofia; Gianino, Maria Michela. - In: PALLIATIVE CARE AND SOCIAL PRACTICE. - ISSN 2632-3524. - 16:(2022), pp. 1-12. [10.1177/26323524221136880]	2022
Article - *Impact of COVID-19 on emergency department use among home care recipients* Peano, A; Minutiello, E; Politano, G; Dalmasso, M; Gianino, Mm. - In: EUROPEAN JOURNAL OF PUBLIC HEALTH. - ISSN 1101-1262. - 32:Supplement_3(2022). [10.1093/eurpub/ckac129.253]	2022
Article - *Trajectories and determinants of emergency department use among nursing home residents: a time series analysis (2012-2019)* Giacomini, Gianmarco; Minutiello, Ettore; Politano, Gianfranco; Dalmasso, Marco; Albanesi, Beatrice; Campagna, Sara; Gianino, Maria Michela. - In: BMC GERIATRICS. - ISSN 1471-2318. - 22:1(2022), p. 418. [10.1186/s12877-022-03078-4]	2022
Article - *Screening and Identification of Putative Long Non-Coding RNA in Childhood Obesity: Evaluation of Their Transcriptional Levels* Cabiati, Manuela; Fontanini, Martina; Giacomarra, Manuel; Politano, GIANFRANCO MICHELE MARIA; Randazzo, Emioli; Peroni, Diego; Federico, Giovanni; Del Ry, Silvia. - In: BIOMEDICINES. - ISSN 2227-9059. - 10:3(2022), p. 529. [10.3390/biomedicines10030529]	2022
Proceeding - *A Deep Learning Framework for the Prediction of Conversion to Alzheimer Disease* Ostellino, Sofia; Benso, Alfredo; Politano, GIANFRANCO MICHELE MARIA. - ELETTRONICO. - 13346:(2022), pp. 395-403. (Intervento presentato al convegno IWBBIO - 9th International Work-Conference on Bioinformatics and Biomedical Engineering tenutosi a Spain) [10.1007/978-3-031-07704-3_32].	2022
Proceeding - *LE CARATTERISTICHE DEGLI ACCESSI AI DIPARTIMENTI DI EMERGENZA DEGLI OSPITI DELLE RESIDENZE SANITARIE ASSISTENZIALI: UNO STUDIO RETROSPETTIVO OSSERVAZIONALE DAL 2015 AL 2019* Albanesi, Beatrice; Alessio, Conti; Politano, GIANFRANCO MICHELE MARIA; Dimonte, Valerio; Gianino Maria Michela, ; Sara, Campagna. - (2022), pp. 26-27. (Intervento presentato al convegno 67° Congresso SIGG - LA LONGEVITÀ DECLINATA AL FEMMINILE tenutosi a Roma nel 30 Novembre - 3 Dicembre 2022).	2022
Article - *Spectracular: minimizing spectral overlap in multicolor flow cytometry experiments*, Mike Bogetofte Barnkob, Alfredo Benso, Gianfranco Politano, Lars Rønn Olsen, bioRxiv preprint doi: Spectracular: minimizing spectral overlap in multicolor flow cytometry experiments, Mike Bogetofte Barnkob, Alfredo Benso, Gianfranco Politano, Lars Rønn Olsen, bioRxiv preprint doi: https://doi.org/10.1101/2021.03.17.435861	2021
Article - *Emergency-department accesses in home care paediatric patients: Occurrence and risks of use in a six-year retrospective investigation in Northern Italy* Campagna, S.; Borraccino, A.; Politano, G.; Dalmasso, M.; Ravaglia, A.; Dimonte, V.; Gianino, M. M.. - In: PLOS ONE. - ISSN 1932-6203. - 16:12(2021), p. e0262085. [10.1371/journal.pone.0262085]	2021
Article - *Evaluation of the Strategies to Control COVID-19 Pandemic in Four European Countries* Gianino, Maria Michela; Nurchis, Mario Cesare; Politano, Gianfranco; Rousset, Stefano; Damiani, Gianfranco. - In: FRONTIERS IN PUBLIC HEALTH. - ISSN 2296-2565. - ELETTRONICO. - 9:(2021). [10.3389/fpubh.2021.700811]	2021
Article - *"miRNAs Potentially Involved in Post Lung Transplant-Obliterative Bronchiolitis: The Role of miR-21-5p"* Bozzini, S.; Pandolfi, L.; Rossi, E.; Inghilleri, S.; Zorzetto, M.; Ferrario, G.; Di Carlo, S.; Politano, G.; De Silvestri, A.; Frangipane, V.; Porzio, M.; Kessler, R.; Calabrese, F.; Meloni, F.; Morbini, P., Cells, MDPI, Vol. 10, 2021, pp. 1-13, quartile: Q1, DOI: 10.3390/cells10030688	2021
Article - *"Burden of COVID-19: Disability-Adjusted Life Years (DALYs) across 16 European countries"* Gianino, M. M.; Savatteri, A.; Politano, G.; Nurchis, M. C.; Pascucci, D.; Damiani, G., European Review for Medical and Pharmacological Sciences, Verduci Editore S.r.l., Vol. 205, 2021, pp. 5529-5541, quartile: Q2, cit.scopus: 10, cit.scholar: 13, DOI: 10.26355/eurrev_202109_26665	2021

Article - *"Determinants Associated With the Risk of Emergency Department Visits Among Patients Receiving Integrated Home Care Services: A 6-Year Retrospective Observational Study in a Large Italian Region"* Campagna, Sara; Borraccino, Alberto; Politano, Gianfranco; Benso, Alfredo; Dalmasso, Marco; Dimonte, Valerio; Gianino, Maria Michela, International Journal of Health Policy and Management, Kerman University Of Medical Sciences, 2020, quartile: Q1, cit.scopus: 1, DOI: 10.34172/ijhpm.2020.79	2020
Article - *"Severe and moderate seasonal influenza epidemics among Italian healthcare workers: A comparison of the excess of absenteeism"* Gianino, M. M.; Kakaa, O.; Politano, G.; Scarmozzino, A.; Benso, A.; Zotti, C. M., Influenza and other Respiratory Viruses, Blackwell Publishing Ltd, Vol. 0, 2020, pp. 1-10, quartile: Q1, cit.scopus: 3, cit.scholar: 4, DOI: 10.1111/irv.12777	2020
Article - *"Determinants of aggression against all health care workers in a large-sized university hospital"* Viottini, E.; Politano, G.; Fornero, G.; Pavanelli, P. L.; Borelli, P.; Bonaudo, M.; Gianino, M. M., BMC Health Services Research, BioMed Central Ltd., Vol. 20, 2020, quartile: Q1, cit.scopus: 12, cit.scholar: 28, DOI: 10.1186/s12913-020-05084-x	2020
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