
BIOGRAPHICAL SKETCH

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NAME: Rosalba Giugno

COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Professor In Medical Bioinformatics in University of Verona, Computer Science, (Tenure Track), Research group leader

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Catania, Italy	MSc.	03/1998	Computer Science
University of Catania, Italy	Ph.D.	01/2003	Computer Science and Bioinformatics
University of Catania, Italy	Post doc	01/2006	Bioinformatics
University of Catania, Italy	Assistant Professor	05/2016	Computer Science and Bioinformatics

A.Positions and Honors

Positions and employment

2023 -	Professor, University of Verona, Italy
2016- 2023	Associate Professor, University of Verona, Italy
2006-2016	Assistant Professor, University of Catania, Italy
2003-2006	Postdoc, University of Catania, Italy
1998- 2003	PhD in Computer Science, University of Catania, Italy

Coordinator roles: Director of the International Master Degree in Medical Bioinformatics, Univ. Verona, Italy.
Coordinators of several European Social Fund projects.

Director roles: Director of the Italian National Laboratory of Bioinformatics, coordinating 35 Italian academic groups of Bioinformatics researchers
President of the Center for BioMedical Computing (CBMC), University of Verona
Director of the Internal PhD School in Imaging genetics, Verona, Italy
co-Director of the J. T. Schwartz International School for Scientific Research on Computational Life Science, July, Lipari, Italy

Awards

Several grants from Bioinformatics Societies and Society of Mathematics for best activity research for dissemination activities (2010-2019). Winner of Memory Usage and Time Usage Contest on Graph Matching Algorithms for Pattern Search in Biological Databases, ICPR (2014). Best Paper Award, Annual Int. Conf. on Computational Systems Bioinformatics (2012).

B. Publications and Statement linked to Research

Number of citations: 6837
H-index: 41

For my PhD program, I spent three years of research at the University of Maryland, at the New York University, and at the Cornell University. Since I moved in Verona in 2016, I'm the PI of the InfOmics laboratory at University of Verona and I lead a research group of 3 post-docs, 6 PhD students. The strategic rationale of the lab is to bring together all of investigative strategies developed over the last twenty years in Bioinformatics and related computer science research community, going by the algorithms, models, up to the formal systems, to form the bulk required to address critical issues in medical applications. I have supervised 8 PhD thesis to completion, primary supervisor for ongoing 3 PhD students and 2 postdocs, secondary supervisor for additional 2 PhD students.

I have established strong academic and scientific collaborations with Harvard Medical School for the design of efficient tools for the search of Off-targets in CRISPR/Cas. Our research focuses on the development of innovative computational methods to investigate gene regulation by integrating genetic and epigenetic variation, with particular emphasis on non-coding genomic regions and chromatin structure. A key objective of my work is to model individual-specific genetic variability and to study its impact on transcription factor binding and genome editing outcomes. I have developed variant-aware approaches for the identification of CRISPR off-target effects and for the analysis of transcription factor binding affinity changes at the population level, leveraging advanced data representations such as genome graphs. These research activities have resulted in publications in international peer-reviewed journals, presentations at international conferences, and the release of open-source software tools that are publicly available and broadly adopted by the research community.

The algorithms and methods developed are available online and released under academic licenses. They are available here https://infomics.github.io/InfOmics/index.html.

List of Selected publication in last 3 years

1 Viesi, E., Perricone, U., Aloy, P., Giugno, R.
APBIO: bioactive profiling of air pollutants through inferred bioactivity signatures and prediction of novel target interactions(2025) Journal of Cheminformatics, 17 (1), art. no. 13 DOI: 10.1186/s13321-025-00961-1

2 Tognon, M., Kumbara, A., Betti, A., Ruggeri, L., Giugno, R.
Benchmarking transcription factor binding site prediction models: a comparative analysis on synthetic and biological data (2025) Briefings in Bioinformatics, 26 (4), art. no. bbaf363DOI: 10.1093/bib/bbaf363

3 Micale, G., Di Maria, A., Grasso, R., Bonnici, V., Ferro, A., Shasha, D., Giugno, R., Pulvirenti, A.
MultiGraphMatch: A Subgraph Matching Algorithm for Multigraphs(2025) ACM Transactions on Knowledge Discovery from Data, 19 (5), art. no. 97 DOI: 10.1145/3728361

4 Fraccaroli, L., Busato, F., Giugno, R., Bombieri, N.
An efficient solution for GPUs to the ST-connectivity problem on dynamic graphs (2025) Pattern Recognition Letters, 191, pp. 110 – 116 DOI: 10.1016/j.patrec.2025.02.034

5 Aparo, A., Avesani, S., Parmigiani, L., Napoli, S., Bertoni, F., Bonnici, V., Cascione, L., Giugno, R.
EasyCircR: Detection and reconstruction of circular RNAs post-transcriptional regulatory interaction networks (2025) Computers in Biology and Medicine, 188, art. no. 109846 DOI: 10.1016/j.compbiomed.2025.109846

6 Bonnici, V., Grasso, R., Micale, G., Maria, A.D., Shasha, D., Pulvirenti, A., Giugno, R.
ArcMatch: high-performance subgraph matching for labeled graphs by exploiting edge domains (2024) Data Mining and Knowledge Discovery, 38 (6), pp. 3868 – 3921 DOI: 10.1007/s10618-024-01061-8

7 Aparo, A., Bonnici, V., Avesani, S., Cascione, L., Giugno, R.
DiGAS: Differential gene allele spectrum as a descriptor in genetic studies (2024) Computers in Biology and Medicine, 179, art. no. 108924 DOI: 10.1016/j.compbiomed.2024.108924

8 Caligola, S., Giacobazzi, L., Canè, S., Vella, A., Adamo, A., Ugel, S., Giugno, R., Bronte, V.
GateMeClass: Gate Mining and Classification of cytometry data (2024) Bioinformatics, 40 (5), art. no. btae322 DOI: 10.1093/bioinformatics/btae322

9 Di Camillo, B., Giugno, R.
From translational bioinformatics computational methodologies to personalized medicine (2024) Journal of Biomedical Informatics, 151, art. no. 104619 DOI: 10.1016/j.jbi.2024.104619

10 Cruciani, F., Aparo, A., Brusini, L., Combi, C., Storti, S.F., Giugno, R., Menegaz, G., Boscolo Galazzo, I.
Identifying the joint signature of brain atrophy and gene variant scores in Alzheimer's Disease (2024) Journal of Biomedical Informatics, 149, art. no. 104569 DOI: 10.1016/j.jbi.2023.104569

11 Bonnici, V., Mengoni, C., Mangoni, M., Franco, G., Giugno, R.
PanDelos-frags: A methodology for discovering pangenomic content of incomplete microbial assemblies (2023) Journal of Biomedical Informatics, 148, art. no. 104552 DOI: 10.1016/j.jbi.2023.104552

12 Heer, M., Giudice, L., Mengoni, C., Giugno, R., Rico, D.
Esearch3D: Propagating gene expression in chromatin networks to illuminate active enhancers (2023) Nucleic Acids Research, 51 (10), pp. E55 - E55 DOI: 10.1093/nar/gkad229

13 Tognon, M., Giugno, R., Pinello, L.
A survey on algorithms to characterize transcription factor binding sites (2023) Briefings in Bioinformatics, 24 (3), art. no. bbad156 DOI: 10.1093/bib/bbad156

14 Viesi, E., Sardina, D.S., Perricone, U., Giugno, R.
APDB: a database on air pollutant characterization and similarity prediction (2023) Database : the journal of biological databases and curation, 2023, art. no. baad046 DOI: 10.1093/database/baad046

15 Chi-Shing Cho, W.C., Pérez-Tur, J., Giugno, R., Pirooznia, M., Boris-Lawrie, K., Greenbaum, D., Rastegar, M., Henrique, R., Xu, P., Rocha, J.B.T.D., Rogina, B. Editorial: 10 years of Frontiers in genetics: past discoveries, current challenges and future perspectives (2023) Frontiers in Genetics, 14, art. no. 1192071 DOI: 10.3389/fgene.2023.1192071

14 Cancellieri, S., Zeng, J., Lin, L.Y., Tognon, M., Nguyen, M.A., Lin, J., Bombieri, N., Maitland, S.A., Ciuculescu, M.-F., Katta, V., Tsai, S.Q., Armant, M., Wolfe, S.A., Giugno, R., Bauer, D.E., Pinello, L. Human genetic diversity alters off-target outcomes of therapeutic gene editing (2023) Nature Genetics, 55 (1), pp. 34 – 43 DOI: 10.1038/s41588-022-01257-y

15 Di Camillo, B., Giugno, R.
From translational bioinformatics computational methodologies to personalized medicine (2022) Journal of Biomedical Informatics, 133, art. no. 104170 DOI: 10.1016/j.jbi.2022.104170

16 Bonnici, V., Giugno, R.
PANPROVA: Pangenomic prokaryotic evolution of full assemblies (2022) Bioinformatics, 38 (9), pp. 2631 – 2632 DOI: 10.1093/bioinformatics/btac158

17 Avesani, S., Viesi, E., Alessandri, L., Motterle, G., Bonnici, V., Beccuti, M., Calogero, R., Giugno, R.
Stardust: improving spatial transcriptomics data analysis through space-aware modularity optimization-based clustering (2022) GigaScience, 11, art. no. giac075 DOI: 10.1093/gigascience/giac075

C. Research Support (since 2016)

YEAR	FUNDING SOURCE
2025	**MDR-RA (HORIZON)** HORIZON-HLTH-2024-DISEASE-03-14- Defining Clinical and Molecular Phenotypes of Multi-Drug Resistance in difficult to treat Rheumatoid Arthritis (MDR-RA) (www.mdr-ra.eu/) 101155807 Role: WP leader
2020	**ERANET COFUND (H2020),** The EU Joint Programme - Neurodegenerative Disease Research, ADAIR - From air pollution to brain

	pollution - novel biomarkers to unravel the link of air pollution and Alzheimer's disease. Role:Unit PI
2020	**TUBE (H2020)** Transport derived Ultrafines and the Brain Effects. Role:Unit PI
2020	**Private research foundation** EDIPO: A computational solution for bringing neuroimaging genetic into translational research, Role: Bioinformatics PI
2018	**European Social Fund - Regional Operative Program 2014/2020**, INFO-BACT-MAR: Development of a computational platform for the traceability of microorganisms in agro-food processes using patented HPME markers. Role: PI
2017	**Academy of Italian project and Private entity** University of Verona and Private entity NeoDataGroup PREDYCOS:Personalized REsponsive Dynamic COmplex System. Role: PI
2017	**Academy of Italian project and Private entity** Project with Provite entity VEyes ONLUS Scientific responsibility 2017 vEyes Wear: open hardware and software wearable platform. Role:PI
2017	**Academy of Italian project and Private entity** Project with University Hospital Meyer Firenze Developing a computational platform for analysis of genomes subjected to chromothripsis phenomena. Role:PI
2016	**European Social Fund - Regional Operative Program 2014/2020** InfoGenAgriFood: Bioinformatics platform integrated in the genomics of food production. Role:PI

D. Contributions to Science

Professional activities

Editor for Nature Elsevier Information Systems, Frontiers in Genetics, and Frontiers in Bioinformatics.
Reviewer for Bioinformatics, Nucleic Acids Research, Database, BMC Bioinformatics, BMC Genomics, Journal Of Bioinformatics and Computational Biology, Nature Biotechnology, Information System, IEEE Transactions on Knowledge and Data Engineering, IEEE Transactions on Pattern Analysis and Machine Intelligence, Proceeding of the ACM Symposium on Principles of Database Systems(PODS), IEEE/ACM Transactions on Computational Biology and Bioinformatics.
Invited speaker at several research centers such as the Memorial Sloan-Kettering Cancer Center in New York, the New York University, the Wyeth Research Lab in Boston, Bioinformatics Unit center and Instituttе of Oncology research in Bellinzona.
President of the Master degree in Medical Bioinformatics, University of Verona. Main contact person for the quality assurance of the Master Degree in Medical Bioifnormatics. Scientific Committee of international conferences and schools. Member of the Doctoral program of Computer Science at University of Verona (2019 to present).

Research translation

miR-Synth: a computational resource for the design of multi-site multi-target Nov. 2014 synthetic mirnas. CM Croce. International patent Ohio State University, code: sdf313081. ROBERTINO

Additional information for Contribution to science

1. I started her activity dealing with the problem of searching in graph databases and in large networks for the representation and analysis of molecules, proteins, and protein interaction networks. The first significant contribution in this field dates back to 2002, when she, during the Doctorate years, published an efficient system for research in graph databases. The contribution has been internationally recognized as the reference point for the mining research of the graph and for the use of graph search algorithms in the field of bioinformatics. I have continued her research in this field by proposing systems based on suffix tree as a

data structure for indexing, low support mining algorithms for reducing the number of indexed structures, efficient algorithms for both exact and approximate graph matching, parallel algorithms for searching in biological networks, efficient algorithms for network alignment, and empiric and analytic methods for searching motifs. I have developed an algorithm for the search in a single graph (e.g., biological network and protein) which resulted the faster and more accurate among the algorithms in the literature (ICPR2014 Contest on Graph Matching Algorithms for Pattern Search in Biological Databases"). The algorithm, in collaboration with Jure Leskovec from Stanford University, has been added to the SNAP library.

2. I have developed tools and algorithms for the simulation of the dynamics of biological systems. I studied the emerging properties through qualitative modeling of the intracellular signalling network controlling integrin activation mediating leukocyte recruitment from the blood into the tissues. I have developed semi-qualitative modelling and efficient simulation of the purine metabolism to reproduce the metabolomics data obtained from naive lymphocytes and autoreactive T cells implicated in the induction of experimental autoimmune disorders. I have applied my modeling and simulation framework for the robustness and sensitivity analysis of the Colitis-associated Colon Cancer network and for the analysis of the drug combinations that target the mitochondria in leukemia.

3. I have addressed the problem of classification of profiles through association, machine learning and clustering rules in the analysis of multi omics data. She is an expert of data integration, data quality and reproducibility of results. In the field of RNA analysis, she has implemented methods for the construction, prediction, and analysis of networks of interactions between ncRNA, circulating miRNAs, mRNAs, diseases, and drugs. She developed efficient sequential and parallel algorithms for searching off- target sites of Cas RNA-guided endonucleases. She highlighted the fundamental role of algorithms for network analysis to understand more complex and little investigated regulatory mechanisms such as prediction of off- targets of drugs and drug combinations or prediction of the effects of RNA editing, which acting at the post transcriptional level can affect the expression and function of proteins and miRNAs. She developed the design of synthetic miRNAs able to target multiple genes with multiple interaction sites. She analyzes miRNA, non coding, and mRNA expressions for the detection of markers for several pathologies, such as, prostate cancer, thyroid cancer, lymphoma cancer, and neuroinflammatory diseases.

E. Personal Statement

My research aims to analyse biomedical data efficiently, in particular I develop new methods to mining biological networks, integrate heterogeneous data, analyse omics, and to classify patients. I use theory coming from machine learning, data science, mathematics and graph theory.

The success of my work is demonstrated by the educational responsibilities assigned to me, the coordinator roles of several national bioinformaticians groups, the founding I have obtained since I have been associate professor at University of Verona, the growing number of research papers also in collaboration with international centers, and the number of finished PhD degrees under my supervision. I have demonstrated the ability for research translation through obtaining one patent for a novel miRNA targeting design.

I authorize the treatment of my personal data.

Verona, Marc 18th 2026 Rosalba Giugno