

PERSONAL INFORMATION

Rosalba Giugno



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🌐 <http://www.di.univr.it/?ent=persona&id=35790> <https://infomics.github.io/InfOmics/>

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WORK EXPERIENCE

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|--------------|--|
| 2017–Present | Expert Reviewer for the European Commission H2020 FET OPEN RIA Call |
| 2017–Present | Member of the PhD teaching board in Computer Science University of Verona
Verona (Italy) |
| 2016–Present | Referent for Practical Students Commission Master Degree in Medical
Bioinformatics University of Verona
Verona (Italy) |
| 2016–Present | President of the International Master Degree in Medical Bioinformatics, University
of Verona
Verona (Italy) |

- 2016–Present Research group leader of Bioinformatics lab, InfOmics, University of Verona,
<https://infomics.github.io/InfOmics/index.html> , Verona (Italy)
- 2016–Present President of the Quality Assurance Commission of Master Degree in Medical
Bioinformatics University of Verona
Verona (Italy)
- 2012–Present Member of the spin-off HTLab (Healthcare Technology Lab) and vEyes (virtual
Eyes)-ONLUS
www.veyes.it, www.htlab.it, Milo (Italy)
- 2016–Present Firefighting Team member and First Aid Department of Computer Science,
University of Verona.
- 2023–Present Full Professor Computer Science, Section of Medical Bioinformatics, University of
Verona,
Verona (Italy)
- 2016–2023 Associate Professor Computer Science, Section of Medical Bioinformatics,
University of Verona,
Verona (Italy)
- 2015–2016 Visiting research, Department of Computer Science, University of Verona
Verona (Italy)
- Aug 2012–Jun 2013 Maternity leave University of Catania
Catania (Italy)
- Aug 2010–Feb 2011 Maternity leave University of Catania
Catania (Italy)
- 2012–2016 Member of teaching board of the PhD program in Molecular Medicine, University
of Catania.
Catania (Italy)
- 2010–2012 Member of teaching board of the PhD program in Biotechnology University of
Catania.
Catania (Italy)
- 2009–2010 Member of teaching board of the PhD program in Pathology and Clinical
Hematology, Experimental and Computational, University of Catania.
Catania (Italy)
- 2006–2016 Assistant Professor, Department of Clinical and Molecular Biomedicine, Department of
Computer Science, University of Catania, Catania (Italy)

2003–2006

Postdoc, Department of Computer Science, University of Catania, Catania (Italy)

Research topic: Probabilistic Database. Indexing of large databases of complex objects with particular regard to graph databases and their applications in bioinformatics.

1998–1999

Research Grant, Department of Computer Science, University of Catania

Research Topic: Consistency Check in Probabilistic Databases.

EDUCATION AND TRAINING

Mar 1998

MSc. Computer Science

University of Catania, Catania (Italy)

Rating: 110/110 cum laude, Thesis Topic: Correction and control of programs according to M. Blum's theory. Theory and Applications. Tutor: Prof. Alfredo Ferro (University of Catania) and Prof. Ronitt Rubinfeld (Cornell University)

Jan 2003

Ph.D. Computer Science and Bioinformatics

University of Catania, Catania (Italy)

PhD work obtained in collaboration with the database and data mining groups of New York University and Maryland University. Thesis: Searching Algorithms and Data Structures for Combinatorial, Temporal and Probabilistic Databases. Tutor: Prof. Alfredo Ferro (University of Catania), Prof. Dennis Shasha (New York University), and Prof. VS Subrahmanian (University of Maryland).

PERSONAL SKILLS

Mother tongue(s)

Italian

Foreign language(s)

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken interaction	Spoken production	
English	C2	C2	C2	C2	C2

Levels: A1 and A2: Basic user - B1 and B2: Independent user - C1 and C2: Proficient user
Common European Framework of Reference for Languages

Communication skills

Excellent communication skills gained through my experience as professor and researcher

Organisational / managerial skills

- Leadership (currently responsible for a team of 15 people)
- 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 International 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

ADDITIONAL INFORMATION

Short Introduction

Rosalba Giugno is Associate Professor in Computer Science at the Department of Computer Science, University of Verona since May 2016.

She received the bachelor degree in Computer Science at the University of Catania in 1998. Her thesis was on the probabilistic programming checking following the Manuel Blum theory with Prof.

Ronitt Rubinfeld at the Cornell University (NY). She received the PhD in Computer Science from the University of Catania in the 2003. For her PhD program, she spent three years of research abroad, at the University of Maryland, working with Prof. VS Subrahmanian, and at the New York University working with Prof. Dennis Shasha.

Her research is focused on algorithms for graphs and biological networks, integration and analysis of biomolecular data, modeling of biological systems, modelling of remote telemedicine systems, medical genetics imaging analysis. She is author of 130 scientific publications, 54 in international journals such as 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. In 2014, she received the Award for the design and implementation of the most efficient algorithm for searching in graphs in Bioinformatics from the IARP-ICPR society.

She has been 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. She participated in several national and European projects, also with industrial partners.

She is the president of the Master degree in Medical Bioinformatics, University of Verona. She teaches at the Master Degree in Medical Bioinformatics the course titled programming laboratory for bioinformatics. She is the main contact person for the quality assurance of the Master Degree in Medical Bioinformatics. Since she moved in Verona, she leads a research group of 2 post-docs, 4 PhD students, and 16 undergraduate master thesis students.

She was tutor of 2 masters students in Computer Science at the New York University.

She is in the Scientific Committee of international conferences and schools. She is co-chair of the Jacob T. Schwartz International School for Scientific Research in Bioinformatics and Computational Biology (with the Nobel Laureate M. Levitt) and the Jacob T. Schwartz International School for Scientific Research in Social Complex Systems. She is co-director of the Imaging Genetics PhD School at University of Verona. She is referee for several international conferences and journals such as Bioinformatics and IEEE TCBB, and review editor of Frontiers in Bioengineering and Biotechnology. She was Guest editor for Information Systems, BMC Bioinformatics, and Briefings in Bioinformatics.

Since 2017, she is the director of the Italian CINI Inter-University laboratory of Bioinformatics named Infolife involving 35 Italian Universities.

Since she is in Verona (A 2017), she is head and founder of InfOmics Lab at Department of Computer Science in Verona, <https://infomics.github.io/InfOmics/>. The lab is leading several founded projects involving the design of an integrated platform for the genomics of agrifood production, the design of a open hardware and software wearable platform, and the study of personalized responsive dynamic complex systems, computational platform for the traceability of microorganisms, design of high-performance decision support system to diagnose of uncharacterized and rare diseases. She has a patent on the design of synthetic miRNAs. She is a faculty member in the PhD program in Computer Science at the University of Verona. She also established new academic and scientific collaborations with Harvard Medical School for the design of an efficient tool for the search of Off-targets in CRISPR/Cas,

the Institute of Oncology Research of Switzerland for the design of efficient methods for the analysis high-throughput genomics data in Lymphoma,

the University of Eastern Finland for modeling neuroinflammation diseases, the Immunology and Hematology sections of University of Verona, the Meyer children hospital of Florence, the Graduate School of Public Health and Healthy Policy of New York to develop efficient algorithm and data structure in R/Bioconductor for accurate algorithms reproducibility, data quality control, and scalable data analysis. She actively maintains the collaborations with the Bioinformatics and Computer Science groups of University of Catania, New York University, and the Donnelly Centre at the University of Toronto for the design of network analysis algorithms distributed also in Cytoscape platform.

Research Interests Rosalba Giugno's research activity is focused on the fields of Bioinformatics, Computational Biology and Systems Biology.

She 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.

She has 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. She has 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.

She has developed tools and algorithms for the simulation of the dynamics of biological systems. She studied the emerging properties through qualitative modeling of the intracellular signalling network controlling integrin activation mediating leukocyte recruitment from the blood into the tissues. She has 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. RG has applied her 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.

She has addressed the problem of classification of profiles through association and clustering rules in the analysis of gene expression data. 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.

Through a combined method of experimental biology and computational biology (with the application of the above mentioned techniques and statistical methods) and after establishing close collaborations with physicians and biologists, she has tackled the problem of protein backtranslation with application to gene design that has allowed the identification of a human TBPL2 gene with high homology to TBP and in vitro and in silico cloning of SOD2 of *Xenopus laevis*.

She has worked for the characterization and analysis (i) of the apoptotic machinery (machinery composed of about 300 genes with anti or pre-apoptotic functions, which regulate the life cycle of the cell from birth to death), (ii) the effects of proton flows on cell death, and (iii) involvement of the NC2 β protein in Neuroblastoma.

The algorithms and methods developed are available online and released under academic licenses. They are requested and cited frequently in articles in international journals and conferences. Rosalba Giugno (orcid.org/0000-0001-9843-7638) has 2669 citations reported in Google scholar, h-index 24, including 1828 since 2012. In Scopus she has 1781 citations from 99 articles, h-index 20.

Commissions

RTDb examining committee, Field of Computer Science, 01/B1, Department of Bioscience and Biotechnology, University of Milan (2019).

RTDb examining committee, Field of Computer Science, 01/B1, Department of Computer Science, University of Verona (2019).

President of the examining committee and of the relative secretary of the public competition for qualifications and examinations for the employment with full-time and permanent employment contract of 1 unit of Researcher Technical Staff, VI professional level at the Institute of Biomedical Technologies - Bari related to the Department of Biomedical Sciences of the National Research Council (2017).

Representative for the Bioinformatics and Medical Informatics area in the evaluation committee, for the co-financing of research grants for the FUR 2016 II Call (2017).

PhD Committee in Computer Science Department of Computer Science, University of Turin (2017).

President of the PhD Committee in Computer Science at the DAUIN Department of Automation and Computer Science of the Polytechnic of Turin (2017).

Scientific Collaborations

Rosalba Giugno mainly collaborates on the issues concerning the development of algorithms for the research in graphs and the analysis of biological networks, the modeling of biological systems, the analysis of sequencing data and the characterization of altered genomes with: Prof. Dennis Shasha, New York University, Prof. Gary Bader, University of Toronto, Prof. Roded Sharan, Tel-Aviv University, Prof. Luca Pinello, Harvard Medical School, Prof. Carlo Laudanna, University of Verona, Prof. Gabriela Constantin, University of Verona, PhD. Francesco Bertoni and Ivo Kwee, Institute of Oncology Research, Switzerland, Prof. Soren Brunak, University of Copenhagen, Prof. Alfredo Ferro, University of Catania.

On issues concerning the development of algorithms for computational analysis of post-transcriptional gene regulation mechanisms with particular emphasis on ncRNAs (prediction of editing and target events, integration of relationships and functions), Rosalba Giugno mainly collaborates with: Prof. Carlo Maria Croce, OHIO State University, Prof. Vincenzo Bronte, University of Verona, Prof. Mauro Krampera, University of Verona, Prof. Tarja Malm, University of Eastern Finland, vEyes (virtual Eyes) - ONLUS <http://www.veyes.it/>.

The design of probabilistic algorithms for graph search and the development of probabilistic databases is conducted in collaboration with: Prof. VS Subrahmanian, University of Maryland Prof. Thomas Lukasiewicz, Oxford University.

The design of efficient, scalable, reproducible algorithms and data structure in R/Bioconductor Prof. Levi Waldron, raduate School of Public Health and Healthy Policy of New York and Prof. Davide Risso, Padova University.

Activities of Chair, Organizer and Direction of Research Schools

Chair and co-Director of the Internal PhD School in Imaging genetics. Verona, Italy November, 2019

Chair and Organizer MS-Based untarget proteomics and metabolomics: cancer metabolism, therapeutic targets and biomarkers international conference joint with the Advanced School in Bioinformatics tools for mass spectrometry-based omic data: from pathways reconstruction to multi-omic data integration. Verona, Italy July 2019

Chair and Organizer of the Special Session Is Imaging genetics the frontier for precision medicine? at the IEEE International Symposium on Biomedical Imaging (ISBI), Venice, Italy. April, 2019

Chair and Organizer of the International Workshop on Data and Text Mining Biomedical Informatics (DTMBio 2018) at the 27th ACM International Conference on Information and Knowledge Management (CIKM), Lingotto, Turin, Italy. October 22-26, 2018

Chair and co-Director of the J. T. Schwartz International School for Scientific Research on Computational Life Science. 2009 -2019

Chair and Organizer of the Section on Biocuration and Integration of Biomedical Databases CIBB 2016: Computational Intelligence methods for Bioinformatics and Biostatistics, University of Stirling, Scotland UK. September 2016

Organizer of the 26th International Workshop on Combinatorial Algorithms IWOCOA 2015, Verona. October 2015

Chair and Organizer of the Seventh International Conference on Fun With Algorithms, Lipari. July 2014

Organizer of the NGS and non-coding RNA data analysis, Bari. April 2013

Chair and Organizer of the Bioinformatics Italian Society Annual Meeting, Catania. May 2012

Chair and co-Director of the J. T. Schwartz International School for Scientific Research on Computational Complex System. 2012 -Present

Organizer of the SISAP 2011, International Workshop on Similarity Search and Applications, Lipari. July, 2011

Chair and Organizer of the NETTAB 2009 Network Tools And Applications In Biology. Catania, June 2009

Participation in editorial Committees of Journals

Editor of Information System for the area of Bioinformatics Systems. since 2019

Editor of Frontiers in Bioinformatics. since 2020

Editor of Frontiers in Computational Genomics, Frontiers in Genetics. since 2020

Editor for Frontiers in Bioinformatics and Computational Biology in Frontiers in Genetics IF=3,789 (since 2016)Topic: New Trends on Genome and Transcriptome Characterizations.

Guest Editor for BMC Bioinformatics, Special Issue on Methods, tools for Personalized Medicine in the Big Data Era. 2018

Guest Editor for BMC Bioinformatics 2013. Special Issue on The ninth annual meeting of the Italian Society of Bioinformatics.

Guest Editor for Information Systems, Special edition on Advances in Similarity Search. 2013

Editor for EMBnet.journal. Bioinformatics in Action, Special edition on Ninth Annual Meeting of the Bioinformatics Italian Society. 2012

Guest Editor for Briefings in Bioinformatics Special edition on Network Tools and Applications in Biology. 2011

Editor for Datasets Papers in Biology. 2011

Technical Program Committee
Member for International
Conferences

The 35th ACM Symposium On Applied Computing, SAC2020

The 8th International Conference on Complex Networks and Their Applications. Complex Networks 2019

IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology. CIBCB 2019

The Sixth International Workshop on Computational Network Biology: Modeling, Analysis, and Control CNB-MAC 2019

The International Conference on Similarity Search and Applications SISAP 2018

International Joint Conference on Knowledge Discovery, Knowledge Engineering and Knowledge Management. KDIR 2013-2019

International Symposium "From Data to Models and Back DataMod 2017

International Workshop Methods, tools & platforms for Personalized Medicine in the Big Data Era NETTAB2017

IAPR-TC15 Workshop on Graph-based Representations in Pattern Recognition. GbR17 2017

European Conference on Evolutionary Computation, Machine Learning and Data Mining in Computational Biology. EVOBIO 2005-2018

International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics. CIBB 2013, 2016

ACM International Conference on Genetic and Evolutionary Computation Conference 2015

International Conference on Similarity Search and Applications. SISAP 2013-2015

International Conference on Pattern Recognition. ICPR 2010-2018

International Workshop on Graph Data Management: Techniques and Applications. GDM 2010-2014

IAPR conference on Pattern Recognition in Bioinformatics. PRIB 2010-2014

Workshop focused on Semantic, Social, and Mobile Applications for Bioinformatics and Biomedical Laboratories. NETTAB 2009,2013

Bioinformatics Italian Society Annual Meeting. BITS 2012-2013

International Workshop on Data Mining in Bioinformatics. BIODDD 2010-2011

Conference on Database and Expert Systems Applications. DEXA 2010-2011

International Workshop on Graph Database. IWGD 2010

IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology. CIBCB 2004

International Workshop on Algorithmic Aspects of Wireless Sensor Networks. AlgoSensors 2004

Scientific Review Activity

Nature Scientific Reports, Bioinformatics, BMC Bioinformatics, Briefing in Bioinformatics, Nucleic Acids Research, Frontiers, PLOS ONE, Natural Computing, GENE, Data Mining and Knowledge Discovery, IEEE-ACM Transaction on Computational Biology and Bioinformatics, Information System, Journal of Discrete Algorithms, ACM Transactions on Database Systems, IEEE Transaction on Pattern Analysis and Machine Intelligence, IEEE Transactions on Knowledge and Data Engineering, Journal of Data Semantics, Uncertainty Fuzziness and KnowledgeBased Systems

Grants, Awards, and Selected Talks

RECOMB 2020

The Italian Society of Biophysics and Molecular Biology Annual meeting. Invited Talk: Tools and Methodologies for Genome Editing and Patients Classification. 2019

IOR| Institute of Oncology Research, Institute for Research in Biomedicine (IRB) Invited talk: Network querying, data integration and annotation in System Biology. 2019

Next Generation Sequencing Conference 2018 (NGS 2018), Hosted by the International Society for Computational Biology (ISCB) and the Centre for Genomic Regulation (CRG), Barcellona, Spain Talk: Network-based smoothing of somatic mutations improves patient classification from sparse genetic data. 2018

Next Generation Sequencing Conference 2018 (NGS 2018), Hosted by the International Society for Computational Biology (ISCB) and the Centre for Genomic Regulation (CRG), Barcellona, Spain Talk: Identification and validation of novel and annotated LncRNAs in canine B-cell lymphoma by RNA-Seq. 2018

Workshop on DataMod Approaches to Systems Analysis (WDA 2018) Pisa, Italy, Invited talk: Network Analysis in System Biology. 2018

INDAM-GNCS Grant for research work presentation at Next Generation Sequencing Conference 2018 (NGS 2018)

Patent for miR-Synth: a computational resource for the design of multi-site multi-target synthetic mimas. A Lagan'a, M Acunzo, G Romano, A Pulvirenti, D Veneziano, L Cascione, R Giugno, P Gasparini, D Shasha, A Ferro, and CM Croce. International patent Ohio State University, code: sdf313081. 2014

Cooperint Grant from the University of Verona for joint research and teaching activities of the Department of Computer Science and University of Eastern Finland. 2018

Bioinformatics Italian Society Invited talk: High Performance Graph Traversal and Analysis. 2017

INDAM-GNCS Grant for the project: High performing computational models for biomedical information extraction and integration. 2017

INDAM-GNCS Grant for the project: Integrating national and international spontaneous adverse drug reaction knowledge bases for pattern discovery in pharmacovigilance. 2016

INDAM-GNCS Grant for the participation of ISMB/ECCB 2015. 2015

Winner of Memory Usage Contest on Graph Matching Algorithms for Pattern Search in Biological Databases, ICPR. 2014

Winner of Time Usage Contest on Graph Matching Algorithms for Pattern Search in Biological Databases, ICPR. 2014

INDAM-GNCS Grant for the project: Analysis of biological networks for the identification of critical factors of thyroid cancer. 2014

INDAM-GNCS Sponsorship for the participation of BITS. 2013

Best Paper Award at CSB 2009 Stanford University. The 8th Annual International Conference on Computational Systems Bioinformatics. 2009

J. T. Schwartz International School for Scientific Research on Bioinformatics and Computational Biology, Pharmacogenomics Invited talk: Network Analysis in Systems Pharmacology. 2012

University of Verona Invited talk: Algorithms in Life Science. 2011

J. T. Schwartz International School for Scientific Research on Computational Social Sciences , Computational Models of Political and Social Events. Invited talk: Data Mining using Weka. 2009

J. T. Schwartz International School for Scientific Research on Biological Networks: Evolution, Interaction and Computation Algorithms. Invited talk: Fast Heuristics for Matching and Comparison of Biological Networks. 2008

Memorial Sloan-Kettering Cancer Center New York Invited talk: Search in Indexing in Graphs and Biological Networks. 2008

J. T. Schwartz International School for Scientific Research on Bioinformatics and Computational Biology , Advanced Computational Proteomics: Structure, Imaging and Control. Invited talk: Network Analysis Systems for Biomedical Applications. 2007

Gloria Coluzzi Lab, New York University Invited talk: NetMatch for Querying Biological Network. 2007

Bud Mishra Bioinformatics Lab, New York University Invited talk: GraphGrep and NetMatch, Querying Biological Networks and Molecular Databases. 2007

Wyeth Research Lab, Catania Invited talk: Querying and Indexing Biological Networks and Molecular Databases. 2007

ITALIA-ISRALE FIRB meeting, Pisa Invited talk: On graph Searching. 2007

Bud Mishra Bioinformatics Lab, New York University Invited talk: Issues on Searching Structured Data. 2006

Wyeth Research Lab, Boston, Invited talk: Indexing Molecular Databases. 2006

Conference on Biotechnology, Cooperation Group in Biotechnology, Mario Teti Foundation Invited talk: Research activity of the Bioinformatics Group of the University of Catania. 2005

Conference for the research project PRIN-2003, Lipari Invited talks: Approximate Algorithms for Metric Spaces Stratification, Structural and Functional Genomics of the Apoptotic Machinery. 2004

Conference of the MURST co-funded research project: Models for the treatment of partial knowledge in decision-making, Lipari Invited talks: Approximate Search in the Database of Structured Images, An Overview on Temporal Probabilistic Object Bases. 2000

Conference for the MURST co-funded research project: Models for the treatment of partial knowledge in the decision-making process, Perugia Invited talks: A General Probabilistic Database, Approximated Search in the Database of Structured Images. 1999

IRST, Bruno Kessler Foundation, Trento Invited talk: Correction and Control of Programs According to the Theory of M. Blum, Theory and Applications. 1998

Scholarship for the development of the degree thesis in Foreign University Awarded for competition to deserving students. 1997

Scholarship for the development of the degree thesis in Foreign University Awarded for competition to deserving students. 1996

Participation in International Research Institutions

New York University. Prof. Dennis Shasha. Research topic: Motif search and unlabeled search in structured data. 2014, 1M ; Combinatorial algorithms in genomics and pharmacogenomics. 2012, 1M; RNA analysis. 2011, 3M; Graph Algorithm. 1999,2003-2008, 1M; PHD thesis work. 2000, 28M

University of Maryland. Prof.VS Subrahmanian. Research topic: Design and development of a probabilistic model for the approximate search of substructures in large graphs (order of thousands of nodes) with applications from bioinformatics to social sciences (F1-status as Faculty Member). 2009, 1M; PHD thesis work. 2000, 6M

Cornell University. Prof. Ronitt Rubinfeld. Research topic: Undergraduate Thesis work (F1-status) 1996-1997,1M

Teaching and Research Qualification

Full Professor Qualification (Abilitazione Scientifica Nazionale per il Settore Concorsuale) 09/H1 - Engineering Computer Technology -Information processing systems 2017.

Associate Professor Qualification (Abilitazione Scientifica Nazionale per il Settore Concorsuale) 09/H1 Engineering Computer Technology -Information processing systems 2015; 01/B1 - Computer Science 2014.

Secondary Schools Professor Qualification A047 Mathematics 2001; A042 Computer Science 2001. Winner of Teaching Position on both classes.

Scientific Participation in International and National Research Projects

The following projects have been eligible for funding based on competitive calls for peer review.

Project PRIN Coordination and Research. Probabilistic and fuzzy methodologies for uncertain reasoning in databases and knowledge bases supporting decision-making processes, 24 M. 1999

Project INTERLINK INT01AB7BE Coordination and Research. Internationalization Project, Catania-New York Convention between the University for the Doctorate in Computer Science (Triennial Computer Science) with New York University and Columbia University. 36M. 2001-2003

Project FIRB ITALIA-ISRAEL n. RBIN04BYZ7-003 Coordination and Research. Algorithms for the discovery and retrieval pattern in discrete structures with applications in Bioinformatics, 36M. 2003

Project PRIN Coordination and Research. Area 09 Catania Unit, Industrial and Information Engineering, Randomization and Indexing Techniques for Clustering and Efficient Approximate Queries on Large Data Bases with Applications to Biology, 24M. 2003

Project POR Sicilia 3.14 Coordination and Research. Realization of a satellite tracking system on mobile means for the optimization of the distribution logistics function, decree n. 1752 of 18.11.2004, 12M. 2004

Project Law 297 (GURI 17/11/2004) Coordination and Research. Data Cleaning Techniques and Data Mining via Clustering and their applications to Business Intelligence, 24M. 2004

Project Programs for Incentives of the Internationalization. Process of the University System International Inter-University Collaborations (D.M. 5 August 2004 No. 262 - Art. 23) Coordination and Research. From Benchwork to Bedside: Molecular and Bioinformatic Analysis of Pathological Phenotypes. Programming 2004-2006 Prot. II04C9775H, 36M. 2004

Project POR 3.14 (GURS n. 15 8/4/2005) Coordination and Research. Research and Development suite of programs for biological analysis, named: BIOWARE, 18M. 2005

Project Law 297 Coordination and Research. QUALIA Training Project (2005-2006) Training of researchers and research technicians for the "QUALIA" project. Head of ACSE SPA Carate-Catania. 6M, 2005

Project PON Sviluppo Imprenditoriale locale P.I.A. Coordinamento e Ricerca. BALANCE SCORECARD Size 2, Integrated Package of Facilities. 24M. 2006

Research Agreement between the INFRACOM Society and the University of Catania (PON Project, 2008-2010) Coordination and Research, 2008 Poker: Pattern Oriented Datawarehouse, Markup Languages, Automated Knowledge Discovery and Constructive Recommendation Systems as Enabling Technologies for Custom Marketing of Intangible Products. 24M.

Project with private entity DM20919 Wyeth Coordination and Research. Data Mining techniques for the analysis of gene expression profiles and functional enrichment on the pathway "(PON Project, Convention stipulated April 27, 2009). 36M. 2009

Project PO. ERDF 2007-2013 - Sicily - Intervention Line 4.1.1.2. Coordination and Research. BIOWINE Multidisciplinary approach to improving the quality of wine production (DDG No. 5761/3 of

13/12/2011), 18M. 2011

PON01 SIGMA Coordination and Research. Integrated sensor system in the cloud for advanced multi-risk management (Directorial Decree No. 678 / Rec. Of October 15, 2012), 36M. 2012

PON04A2A - PRISMA Ricerca Flat cloud Interoperable for SMARt-government (D.D. No. 32 84 / Ric of 02/03/2012, D.D. No. 255 / Ric of 30/05/2012, D.D. No. 370 / Ric of 06/26/2012), 32M. 2012

PON0101078 Tutor in training and research Identification of biomarkers and development of diagnostic and therapeutic methods in the field of oncology and vascular biology, 12M. 2013

Project with National Scientific Computing Group (GNCS) Scientific Coordinator. Analysis of biological networks for identifying critical factors of thyroid cancer. 12M. 2014

Project FIR 2014, Physical Sciences and Engineering Research Analysis and Decoding of Neuronal Apoptosis - Algorithms and BioCAD Methods for Neuroinformatics. 24M. 2015

Project with National Scientific Computing Group (GNCS) Search. Integrating national and international spontaneous adverse drug reaction knowledge bases for pattern discovery in pharmacovigilance, 12M. 2016

European Social Fund - Regional Operative Program 2014/2020 Research and coordination InfoGenAgriFood: Bioinformatics platform integrated in the genomics of food production, 24M, One research position open (12 M). 2016

Project with GNCS Responsibility for scientific and coordination National Group for Scientific Computation. Title: High performing computational models for biomedical information extraction and integration, 12M. 2017

Project with University Hospital Meyer Firenze Research and coordination. Developing a computational platform for analysis of genomes subjected to chromothripsis phenomena. 24M, One research position open (12M). 2017-2018

Project with Private entity NeoDataGroup Scientific responsibility and coordination. <http://www.neodatagroup.com/en/> Title: PREDYCOS: Personalized REsponsive Dynamic COMplex System. 24 M, Two research open positions (12 M each). 2017-2019

Project with Private entity VEyes ONLUS Scientific responsibility vEyes Wear: open hardware and software wearable platform. 12 M, One research open position (6M). 2017-2019

Project Programs for Incentives of the Internationalization. Grants for collaboration with CUNY School of Public Health in New York City. 2019

European Social Fund - Regional Operative Program 2014/2020 Research and coordination, 24M, NFO-BACT-MAR: Development of a computational platform for the traceability of microorganisms in agro-food processes using patented HPME markers. One research position open (12 M). 2018-2019

Project with Private entity Neurovisual Science Technology srl Title: High-Performance Decision Support System to Diagnose Uncharacterized Eye Diseases. (24M) Two research open positions (12 M each). 2019-2021

ULTIMI PROGETTI DA INSERIRE

Business Consultancy Through Convention Agreement with The University

Consultant for the MICROBION SRL Technical-scientific assistance contract for the execution of experimental bioinformatics research in the field of genomics and metagenomics of micro-organisms of agro-industrial interest to support the development of new services and new products. since 2017

Consultant for the Pio Foundation Istituto De Ferrari Brignole Sale in Voltage Pre-Cancer Prognosis and Prostatic Carcinoma in the Early Phase and for the Biological and Genetic-Molecular Characterization of the Cancerogenesis Phase and Clinical Significance of the New Markers, 24M. 2012

Consultant for the Ragusa Information Technology. Technical and scientific collaboration for the realization of a "Data Mining System for Agri-Food Companies", 6M. 2005

Convention for training and orientation apprentices Stipulated between the University of Catania (Faculty of Sciences MM.F.N.) and the company I.M.P.R.E.S.A. of Catania, 36M. 2003

Consultant for the CORE company in Bologna Development of an Algorithm for the consolidation of the Census Sections for the optimization of the workloads of the detectors, 2M. 2001

Activities Of Academic Tutor

4 post-docs at University of Verona since 2016; 4 PhD students at University of Verona since 2016; 25 undergraduate master thesis students at University of Verona since 2016; 4 PhD students at University of Catania; 60 undergraduate master thesis students at University of Catania; 2 masters students at the school of computer science at New York University.

Teaching Activity

University of Verona, Computer Science Department Master Degree in Medical Bioinformatics (teaching in English)

- Programming laboratory for bioinformatics (12 CFU) AA 2017-2018; AA 2018-2019; AA 2019-2020
- Programming laboratory for bioinformatics (11 CFU) AA 2016-2017

University of Verona, Computer Science Department Bioinformatic course

- Riconoscimento e recupero dell'informazione per bioinformatica (1 CFU) AA 2016-2017

University of Catania Computer Science Degree

- Analisi e gestione dei dati (9CFU) AA 2013-2014
- Bioinformatica, Analisi di reti biologiche (3 CFU) AA 2013-2014, 2010-2011, 2009-2010
- Basi di Dati (9 CFU) AA 2011-2012, 2010-2011, 2009-2010, 2008-2009,
- Programmazione 2 (9 CFU) AA 2007-2008, 2006-2007, 2005-2006,
- Data Analysis and Management (6 CFU) AA 2007-2008
- Algoritmi per la Bioinformatica (3 CFU) AA 2007-2008

University of Catania Medical schools courses

- L'informatica per capire la genetica delle malattie (4 CFU); Corso di Specializzazione Biochimica AA 2013-2014
- BioInformatica (4 CFU), 2013-2014 Corso di Specializzazione in Nefrologia AA 2013-2014

University of Catania Computer Science degree

- Basi di Dati I (6 CFU) AA 2007-2008, 2006-2007, 2005-2006,
- Basi di Dati II (6 CFU) AA 2006-2007,
- Laboratorio di Informatica AA 2004-2005,

University of Catania Degree in Political Science

- Informatica I (6 CFU) AA 2007-2008, 2006-2007, 2005-2006, 2004-2005, 2003-2004
- Informatica II (6 CFU) AA 2007-2008, 2006-2007, 2005-2006, 2004-2005, 2003-2004

- Docenza corsi ECDL AA 2007-2008, 2006-2007, 2005-2006, 2004-2005, 2003-2004

University of Catania Degree in Psychological Sciences and Techniques

- Laboratorio di Rappresentazione della Conoscenza e Data Mining (3 CFU) AA 2005-2006, 2004-2005, 2003-2004

University of Catania Degree in Cultural Heritage and in Administration Sciences

- Informatica Avanzata (3 CFU) AA 2004-2005,
- Informatica II (3 CFU) AA 2003-2005

University of Catania Master in Disaster Evaluation in the Agrarian Scope

- Informatica di Base AA 2004-2005, 2003-2004

University of Catania Master in E-Business.

- Introduzione ai Database Relazionali AA 2003-2004, 2002-2003
- Data Mining AA 2003-2004, 2002-2003

University of Catania Master in Computational Biology

- Algoritmi e Tecniche Informatiche per la Gestione di Database Biologici AA 2002-2003

Publications

Journals

2020

Bonnici V, Maresi E, Giugno R,

Challenges in gene-oriented approaches for pangenome content discovery.

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DOI: 10.1093/bib/bbaa198. Online ahead of print.

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Cancellieri S, Cancer CM, Bombieri N, Giugno R*, Pinello L*,

Crispritz: rapid, high-throughput, and variant-aware in silico off-target site identification for crispr genome editing

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DOI: 10.1093/comnet/cnz008

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