Curriculum Vitae et Studiorum of **Vincenzo Bonnici**

Personal information

Telephone	+39 0521 906909
Email	vincenzo.bonnici@unipr.it
URL	https://personale.unipr.it/it/ugovdocenti/person/230820
ORCID	orcid.org/0000-0002-1637-7545
Affiliation	Department of Mathematical, Physical and Computer Sciences, University of Parma, Italy
Work Address	Parco Area delle Scienze, 53/A, 43124, Parma, Italy

Italian National Scientific Qualification as Associate Professor, sector 01/B1, valid from 29/04/2021 to 29/04/2033.
Italian National Scientific Qualification as Associate Professor, sector 09/H1, valid from 14/07/2025 to 14/07/2037.

Current position

since 2025	President of the Unified Study Course Council of the Degree Course in Computer Science and the Master's Degree Course in Computer Science, Department of Mathematical, Physical and Computer Sciences, University of Parma.
since 2024	Associate Professor of Computer Science at the Department of Mathematical, Physical and Computer Sciences, University of Parma, Italy.
since 2021	Teacher in charge of the courses “Algorithms for artificial intelligence” and “Laboratory of Artificial Intelligence” at the master’s degree in Computer Science, and of the course “Software Engineering” at the bachelor’s degree in Computer Science, University of Parma, Italy.
since 2020	Member of the PhD board in Computer Science, Department of Computer Science, University of Verona.
since 2024	Deputy director of the CINI (Consorzio Interuniversitario Nazionale per l’Informatica) national laboratory InfoLife.

Education

2017	Internship at Fondazione per la Ricerca e la Cura dei Linfomi nel Ticino, Istituto Oncologico della Svizzera Italiana, 6500 Bellinzona (CH).
2012 – 2015	Ph.D. in Computer Science, Department of Computer Science, University of Verona, Italy. Thesis title: “Informational and Relational Analysis of Biological Data”. Advisor Prof. V. Manca. Co-Advisor Dr. R. Giugno.
2013 – 2014	Visiting Researcher Scholar at Institute for Genomics and Bioinformatics (IGB), University of California, Irvine. Advisor Prof. P. Baldi.
2008 – 2011	Master’s degree at the Department of Mathematics and Computer Science, University of Catania, Italy. Score 110/110. Thesis title: “MultiGraphGrep e RI: due algoritmi per la ricerca efficiente in database di grafi e tra due grafi”. Advisor Dr. R. Giugno.

2004 – 2008 Bachelor's degree in computer science, Department of Mathematics and Computer science, University of Catania, Italy. Score: 110/110. Thesis title: "Tecniche di refactoring ad aspetti applicate al codice C del GLOBUS Toolkit".
Advisor Prof. Ing. E. Tramontana.

Research statement

Research topics: Bioinformatics, Computational Biology, Algorithms and data structures, graph theory, parallel computing.

Research goals: My research activities aim at studying biological systems by means of computational methodologies and tools. The structure of the cellular "source code", coded as DNA strings, and the way in which it reacts to external stimuli by means of complex intra- and inter-cellular networks, come with analogies in the artificial word that are a source of inspiration of mine for developing new informational technology.

Short description: I started my research activities during my master's degree when I started to study the problem of searching substructures within biomedical graphs. Throughout the years, I continued my studies in these fields by extending them to the creation, integration and analysis of biological networks. I have published several scientific publications in prestigious journals, such as Bioinformatics, BMC and IEEE/ACM regarding such a field and I have been awarded in international events such as ICPR contests. The searching algorithms, to which I contributed to develop, are currently at the state of the art. I extend such techniques for the graph-based representation of source code. [R34,R30,R23,R20,R18,R12,R10,R7,R3,R2,R1,A23,A17,A15,A14,A13,A12,A10,A3,A2,A1]

During my Ph.D. program, I have extended my research interests to Computational genomics by studying innovative methods for the analysis of genomic sequences. The methods are based on information theory and on the alignment-free and reference-free concepts. I have contributed to a research line regarding informational genomics by developing new algorithms and computational frameworks for the entropic analysis of genomes. These studies have been published in journals such as Nature Scientific Reports. In this field, I have included the study of phylogenetics and phylogenomics, and, more recently, the searching of pangenomic contents by means of sequence homology, and the design of machine-learning models for classification and prediction by means of genomic features. [B1,R32,R31,R28,R25,R23,R22,R19,R17,R16,R11,R9,R8,C3,A31,A28,A26,A25,A22,A20,A18,A12,A7]

After my Ph.D. period, I have extended my interests regarding the biological networks to the creation and integration of "Big Data" by means of NoSQL technologies. The novelty of these techniques allowed me to study the relational aspects of non-coding RNAs and drugs. I also work on the analysis of NGS data, both genomic and transcriptomic data, for detecting structural variants in order to develop diagnosis methods in the context of precise and personalized medicine. [A32,R33,R29,R27,R24,R15,R13,R6,R5,R4,C2,C1,A27,A24,A19,A16,A11,A9,A8,A6,A5,A4]

A cross-cutting theme of my scientific interest is the development of innovative parallel solutions on top of several types of architectures, from SMP to GPGPUs. [R14,R10,R2,A15,A14,A10]

Research assignments

2021 - 2024 Temporary assistant Professor with tenure track at the Department of Mathematical, Physical and Computer Sciences, University of Parma, Italy.

2019 - 2021 Temporary Assistant Professor of Computer Science at the Department of Computer Science, University of Verona, Italy.

2018 - 2019 Associate researcher at the Department of Computer Science, University of Verona. Research project: “Design and implementation of methods for the analysis of complex systems”

2017 - 2018 Associate researcher at the Department of Computer Science, University of Verona. Research project: “computational analysis of genomic diseases.”.

2016 - 2017 Associate researcher at the Department of Computer Science, University of Verona. Research project: “InfoGenAgriFood: an integrated bioinformatic platform for genomic in the agrifood field”.
Regional European Funds FSE project number 1695-2-2121-2015.

2016 Associate researcher at the Department of Computer Science, University of Verona. Research project: “Studio e progettazione dei sistemi di mapping e di analisi dei dati delle CDN (Content Delivery Network)”

2015 Associate researcher at the Department of Computer Science, University of Verona. Research project: “Infogenomics: computational analysis of genomes and biological networks”.

Research projects

This section reports the list of projects which involved research of development activities.

2025 Substitute Principal Investigator. Bando di Ateneo 2024 per la Ricerca, Università di Parma. Title: “Text Analysis and SDG-based Assessment of Corporate Sustainability Reports”.

2024 Principal Investigator. Bando di Ateneo 2024 per la Ricerca, Università di Parma. Titolo: “Recurrence-distance distributions as genomic features for machine-learning approaches in bioinformatics”. 11200 euro.

2024 Unit head, bando a cascata PNRR, spoke “NATIONAL BIODIVERSITY FUTURE CENTER (NBFC)”. CUP B83C22002930006 CODICE IDENTIFICATIVO CN00000033. Project title “Una tassonomia Biomolecolare, delle Biofonti e delle Bioattività per liberare il potenziale della Biodiversità attraverso una piattaforma basata sul Web”. 280/780.000 euro.

2023 Principal investigator. Bando di Ateneo 2023 per la Ricerca, Università di Parma. Title:” Recurrence-distance distributions as genomic features for machine-learning approaches in bioinformatics”. Positively evaluated by the commission.

2023 Component of HORIZON-IA project. Title “MISHELL: Microbial innovations to extend food shelf life and reduce food loss and waste”. HORIZON-CL6-2023-FARM2FORK-01. Positively evaluated by the European commission.

2023 Component of PRIN: PROGETTI DI RICERCA DI RILEVANTE INTERESSE NAZIONALE – Bando 2022 PNRR. Title: “CARING (Ct-scan Automated Reasoning INterpretation Guidance) for xAI (explainable Artificial Intelligence)”. Prot. P2022XYCWM. Positively evaluated by the Italian ministry.

2023 Component of “SUS-MIRRI.IT - Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy”. Funded by National Recovery and Resilience Plan (PNRR), granted by the European Commission’s NextGenerationEU programme. Code N° IR0000005. 16,949,360 euro.

2023 GNCS (Gruppo Nazionale per il Calcolo Scientifico) INdAM (Istituto Nazionale di Alta Matematica “Francesco Severi”). “ARICSxAI: Automated Reasoning Interpretation of Ct-Scans and xAI”. CUP_E53C22001930001

2022 GNCS (Gruppo Nazionale per il Calcolo Scientifico) INdAM (Istituto Nazionale di Alta Matematica “Francesco Severi”). “InSANE: Investigating Sparse Algorithms in the post von Neumann Era”.

2022 Principal Investigator. Bando di Ateneo 2021 per la Ricerca, University of Parma. Title: “BIOCHAIN-AI: a platform for securely sharing and analysing microbiological data”. Project number MUR_DM737_B_MAFI_BONNICI.

2020 GNCS (Gruppo Nazionale per il Calcolo Scientifico) INdAM (Istituto Nazionale di Alta Matematica “Francesco Severi”) project: “Automated Reasoning about Time in Medical and Business Applications”.

2018 Principal investigator. GNCS (Gruppo Nazionale per il Calcolo Scientifico) Giovani Ricercatori 2018/2019 project: “Sistemi eterogenei per misure di connettività inter- e intra-cromosomica”. Istituto Nazionale di Alta Matematica Francesco Severi.

2018 FSE (Fondo Sociale Europeo) of Regione del Veneto project: “INFO-BACT-MAR: Sviluppo di una piattaforma computazionale per la tracciabilità di microrganismi nei processi agro-alimentari utilizzando marcatori brevettati HPME”.

2017 JOINT PROJECTS 2016 n. JPVR16FNCL: “PREDYCOS: Una piattaforma reattiva per un sistema complesso che sia personalizzato e dinamico”.

2017 Project in collaboration with Azienda Ospedaliera Universitaria Meyer of Firenze: “Developing a computational platform for analysis of genomes subjected to chromothripsis phenomena”.

2017 GNCS (Gruppo Nazionale per il Calcolo Scientifico) project: “High performing computational models for biomedical information extraction and integration”.

2016 GNCS (Gruppo Nazionale per il Calcolo Scientifico) project: “Integrating national and international spontaneous adverse drug reaction knowledge bases for pattern discovery in pharmacovigilance”.

2015 GNCS (Gruppo Nazionale per il Calcolo Scientifico) project:“Analisi di reti biologiche per identicare fattori critici del cancro alla tiroide”.

Awards

2018 Travel grant for WEPA2018. 2nd International Workshop on Enumeration Problems and Applications. 5th-8th November 2018, Pisa (Italy). Offered by National Institute of Informatics of Japan.

2016 Best poster award by IEEE Technical Committee on Computational Life Science Society at the research school J.T. Schwartz International School for Scientific Research. Lipari, Italy.

2014 Winner of the first international contest “Graph Matching Algorithms for Pattern Search in Biological Datasets” for “Time Usage” with the algorithm “RI”.
ICPR (International Conference on Pattern Recognition), Stockholm (Sweden).

2014	Winner of the first international contest “Graph Matching Algorithms for Pattern Search in Biological Datasets” for “Memory Usage” with the algorithm “RI-DS”. ICPR (International Conference on Pattern Recognition), Stockholm (Sweden).
2012	Winner of the Cooperint scholarship for international mobility offered by the University of Verona, scientific area “Engineering & Technology: Computer Science and Information Systems”. Destination: University of California, Irvine, USA.
2012	Travel grant offered by COST, European Cooperation in Science and Technology, to attend the course “Next generation sequencing data analysis with Chipster”. CSC-IT center for Science LTD. Espoo (Finland).

Scientific collaborations

List of scientific collaborations related to current or past activities.

Prof. Rosalba Giugno. University of Verona, Italy	Graph theory, data science and their application in bioinformatics.
Prof. Giuditta Franco University fo Verona	Bioinformatics
Prof. Nicola Bombieri University of Verona	Parallel computing, graph algorithms
Prof. Alfredo Pulvirenti, University of Catania, Italy	Graph theory, data mining and their application in bioinformatics.
Prof. Alfredo Ferro, University of Catania, Italy	Graph theory, data mining and their application in bioinformatics.
Prof. Dennis Shasha, New York University, USA	Graph theory, algorithms and data structures, parallel computing.
Prof. Soren Brunak, University of Copenhagen, Denmark	MicroRNA and heterogenous networks in biological systems.
Bioinformatics group, ITB, CNR Bari, Italy.	Non-coding RNA, their classification and interaction at the physical and system cellular level.
Prof. Tarja Malm, University of Eastern Finland, Finland	Differential analysis and functional enrichment of non-coding RNAs related to neurological diseases.
Bioinformatics Core Unit, Institute of Oncology Research, Switzerland	Graph theory applied for studying biological systems. Development of parallel methodologies for graph analysis. Characterization of non-coding RNAs in cancer.
Prof. Levi Waldron, CUNY Institute, USA	Development of new methodologies for analysing biomedical data by means of clustering analysis.
Prof. Marco Beccuti, University of Turin, Italy	Algorithms and data structures for graph analysis.
Prof. Luca Pinello, GH/Harvard Medical School/BROAD Institute, USA	Development of new tools for the analysis of genomic data by means of graph-based representations.

Speaker

2025	CIBB 2025. 20th conference on Computational Intelligence methods for Bioinformatics and Biostatistics. September 10-12, 2025, Milano, Italy.
2024	BBCC 2024. 19th edition of the annual conference "BBCC2024 Bioinformatics and Computational Biology". Naples, Italy, November 27-29, 2024.
2024	CIBB 2024. 19th conference on Computational Intelligence methods for Bioinformatics and Biostatistics. September 4 - 6 in Benevento, Italy
2024	BITS 2024. 20th Annual Meeting of the Bioinformatics Italian Society. June 12-14, 2024, Trento, Italy
2023	LOD 2023. 9th International Conference on machine Learning, Optimization & Data science. Sept 22-26, Lake District England, UK.
2023	IDEAS 2023. The 27th international database engineered applications symposium. Heraklion, Crete, Greece. May 5-7, 2023.
2023	UCNC 2023: 20th International Conference on Unconventional Computation and Natural Computation. March 13 - 17, 2023. University of North Florida, Jacksonville, Florida, USA.
2021	LOD 2021: The 7th International Online & Onsite Conference on Machine Learning, Optimization, and Data Science. Grasmere, Lake District, England – UK.
2021	ISIT 2021 - IEEE International Symposium on Information Theory 12-20 July 2021, online.
2021	BITS – Annual meeting of the Bioinformatics Italian Society 2021. 1-2 July 2021, online.
2021	IARIA – BIOTECHNO 2021 - The Thirteenth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies. May 30, 2021 to June 03, 2021 - Valencia, Spain, and online.
2020	WEPA 2020 - Fourth International Workshop on Enumeration Problems and Applications. Online.
2019	Il Fondo Sociale Europeo nella ricerca scientifica: nuovo bando, premiazioni dei progetti 2018 e buone pratiche. 6th November 2019, Univeristy of Padova, Padova, Padova, Italy.
2019	16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology. 9th-11th July 2019, Certosa di Pontignano, Siena, Italy.
2019	PDP2019. 27th Euromicro International Conference on Parallel, Distributed and Network-based Processing. 13th-15th February 2019, Pavia, Italy.
2018	Challenges and Opportunities in Large Scale Network Analysis in Systems Biology (COLNASB'18). IEEE BIBM co-located workshop. 3th December 2018, Madrid, Spain.
2018	WEPA2018. 2nd International Workshop on Enumeration Problems and Applications. 5th-8th November 2018, Pisa (Italy)
2018	Laboratory Workshop del CINI (Centro Interuniversitario Nazionale per l'Informatica) InfoLife. Politecnico di Milano. 25th September 2018, Milano, Italy.
2018	15th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics. Caparica, Portugal. 6th-8th September 2018.

2018 1st Informal Workshop on DataMod Approaches to Systems Analysis (WDA 2018). 1st-2nd March 2018. Pisa, Italy.

2017 Laboratory Workshop del CINI (Centro Interuniversitario Nazionale per l'Informatica) InfoLife. Abstract: "Multi Omics Integration for Personalized Health". The European Center for Living Technology, University Ca' Foscari of Venezia. 21-23 September 2017, Venezia, Italy.

2017 Giornata di presentazione del Fondo sociale europeo 2016-2017 dedicato a "La ricerca a sostegno della trasformazione aziendale" University of Verona. 24th January 2017, Verona, Italy.

2017 Reproducibility, standards and SOP in bioinformatics. Combined CHARME – EMBnet and NETTAB 2017 Workshop. 16th-18th October 2017, Roma, Italy.

2016 Focus tematico per le Ricerche Innovative Job&Orienta – Agroalimentare e Turismo. Verona Fiere. 28th-30th November 2016, Verona, Italy.

2014 22nd International Conference on Pattern Recognition (ICPR2014) - Contest on Graph Matching Algorithms for Pattern Search in Biological Databases. 24th-28th August 2014, Stockholm, Norway.

2010 5th IAPR International Conference on Pattern Recognition in Bioinformatic. Lecture Notes in Bioinformatics. 22-24 September 2010, Nijmegen, the Netherlands.

Invited talks

2025 Keynote speaker. BIOINFORMATIHA 12. Dodicesima Edizione della Giornata Toscana di Bioinformatica e Systems Biology, 15-16 settembre 2025.

2019 Invited speaker. Cross-cutting computational approaches for the multi-omics scene. Università della Svizzera Italiana, Lugano, Switzerland, 22th September 2019.

Member in organizations

ACM: Association for Computing Machinery
GRIN: GRuppo di INformatica
IEEE Computer Society Technical Committee on Computational Life Sciences (TCCLS)
IEEE Computer Society
BITS (Bioinformatics Italian Society)
GNCS (Gruppo Nazionale per il Calcolo Scientifico) – IndAM
InfoLife Laboratory – CINI (Consorzio Interuniversitario Nazionale per l'Informatica)
Digital Health National Laboratory – CINI (Consorzio Interuniversitario Nazionale per l'Informatica)
InfOmics laboratoy, University of Verona
AHEAD LAB. Computer Science Lab @ UniPR. University of Parma
Synbionics. University of Parma

Organization of scientific conferences and workshops

2025/2026 Program committee. DATA 2026. 15th international conference on data science, technology and applications. 16 – 18 July, 2026. Porto, Portugal.

2025/2026 Technical Program Committee. BIOTECHNO 2026. The Eighteenth International Conference on Advances in Databases, Knowledge, and Data Applications. March 8 - 12, 2026 in Valencia, Spain.

2025/2026 Technical Program Committee. DBKDA 2026. The Eighteenth International Conference on Advances in Databases, Knowledge, and Data Applications. March 8 - 12, 2026 in Valencia, Spain.

2025/2026 Program Committee. BIOINFORMATICS 2026. 17th international conference on bioinformatics models, methods and algorithms. 2-4. March 2026, Marabella, Spain.

2025 Coordinator. Single-Cell RNA-seq data analysis tutorial. CIBB 2025. 20th conference on Computational Intelligence methods for Bioinformatics and Biostatistics. September 9, 2025, Milano, Italy.

2025 Program Committee. CIBB 2025. 20th conference on Computational Intelligence methods for Bioinformatics and Biostatistics. September 10 - 12, 2025, Milano, Italy.

2025 Program Committee and Session chair. Annual meeting of the Bioinformatics Italian Society (BITS) 2025. Napoli, 10-13 July, 2025.

2025 Organizer and Webinar speaker. First International Biohackathon of BITS. In conjunction with the annual meeting of the Bioinformatics Italian Society (BITS) 2025. Napoli, 9 July, 2025.

2025 Technical Program Committee. FAIEMA 2025. 3rd International Conference on Frontiers of Artificial Intelligence, Ethics, and Multidisciplinary Applications. September 18-19, 2025, Stavanger, Norway.

2025 Program committee. DATA 2025. 14th international conference on data science, technology and applications. 10-12 June, 2025. Bilbao, Spain.

2025 Program committee. LOD2025. The 11th International Conference on Machine Learning, Optimization and Data Science. September 21 – 24, 2025. Grosseto, Italy.

2025 Program committee. IEEE INTERNATIONAL CONFERENCE ON DIGITAL HEALTH ICDH 2025. Part of the 2025 IEEE World Congress on SERVICES. July 7-12, Helsinki, Finland.

2025 Program Committee. ECAI 2025. 28TH EUROPEAN CONFERENCE ON ARTIFICIAL INTELLIGENCE, 25-30 October 2025, Bologna, Italy.

2025 Technical Program Committee. DATA ANALYTICS 2025. The Fourteenth International Conference on Data Analytics. September 18 – October 2, 2025 in Lisbon, Portugal

2024/2025 Technical Program Committee. DBKDA 2025. The Seventeenth International Conference on Advances in Databases, Knowledge, and Data Applications. March 9 - 13, 2025 in Lisbon, Portugal.

2024/2025 Technical Program Committee. BIOTECHNO 2025. The Seventeenth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies. March 9 - 13, 2025 in Lisbon, Portugal.

2024/2025 Program Committee. BIOINFORMATICS 2025. 16th international conference on bioinformatics models, methods and algorithms. 20-22 Feb. 2025. Porto. Portugal.

2024 Program Committee and Session Chair. BBCC 2024. 19th edition of the annual conference "BBCC2024 Bioinformatics and Computational Biology". Naples, Italy, November 27-29, 2024.
Session organizer. “Round table with the session speakers and representatives of the youngBITS, young-infolife, and RGS-Italy ISCB groups”

2024 Scientific Committee, Local Organizer. Young Minds at Work: Blending Biochemistry and Bioinformatics, workshop. 10-12 December 2024, online.

2024 Program Committee. Annual meeting of the Italian Bioinformatics Society (BITS 2024). June 12-14, 2024, Trento, Italy

2024 Scientific Committee. YOUNG BITS, RSG-Italy & CINI Young-InfoLife Symposium, in junction with the Annual meeting of the Italian Bioinformatics Society (BITS 2024). June 12-14, 2024, Trento, Italy.

2024 Program Committee. 2nd International Workshop on challenges and opportunities in Network Medicine and Multi-Omics bioinformatics' approaches for studying human complex diseases. BIBM 2024. IEEE International Conference on Bioinformatics & Biomedicine. December 3-6, 2024, Lisbon, Portugal.

2024 Technical Program Committee. DATA ANALYTICS 2024. The thirteenth International Conference on Data Analytics. 29 sep.- 3 oct, 2024, Venice, Italy.

2024 Program Committee. CIBB 2024. 19th conference on Computational Intelligence methods for Bioinformatics and Biostatistics. September 4 - 6 in Benevento, Italy

2024 Program Committee. 10th International Conference on machine Learning, Optimization & Data science - LOD 2024. Sept 22-25, Grosseto, Italy.

2023/2024 Program Committee. ECAI 2024. 27TH EUROPEAN CONFERENCE ON ARTIFICIAL INTELLIGENCE, 19-24 October 2024, Santiago de Compostela, Spain.

2023/2024 Technical Program Committee. DBKDA 2024. The Sixteenth International Conference on Advances in Databases, Knowledge, and Data Applications. March 10, 2024 to March 14, 2024 - Athens, Greece.

2023/2024 Technical Program Committee. BIOTECHNO 2024. The Sixteenth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies. March 10, 2024 to March 14, 2024 - Athens, Greece.

2023 Program Committee. The 21st IEEE International Conference on Pervasive Intelligence and Computing (PiCom 2023). 14-17 Nov, 2023 - Hybrid Conference - Abu Dhabi, UAE.

2023 Organization committee e Chair: MODIMO – Workshop "Multi-Omics Data Integration for Modelling Biological Systems (second edition)", in conjunction with CIKM2023, 21-25- Ottobre 2023, University of Birmingham and Eastside Rooms, UK

2023 Scientific Committee. YOUNG BITS, RSG-Italy & CINI Young-InfoLife Symposium, in junction with the Annual meeting of the Italian Bioinformatics Society (BITS). 22-23 June 2023, Bari, Italy.

2023 Program Committee. ECAI 2023. 26th European Conference on Artificial Intelligence. 30.09 - 5.10, 2023, Kraków, Poland.

2023 Program Committee. IEEE SERVICES 2023. IEEE World Congress on Services. Chicago, Illinois, USA. July 2-8, 2023.

2023 Program Committee. Workshop on challenges and opportunities in Network Medicine and Multi-Omics bioinformatics. 2023 IEEE International Conference on Bioinformatics and Biomedicine (BIBM). 5-8 Dec, 2023. Istanbul, Turkey.

2023 Session Chair. IDEAS 2023. The 27th international database engineered applications symposium. Heraklion, Crete, Greece. May 5-7, 2023.

2023 Program Committee: CIBB 2023, 18th conference on computational intelligent methods for bioinformatics and biostatistics. September 6-8 2023, Padova, Italy.

2023 Program Committee: IEEE ICDH 2023. IEEE International Conference on Digital Health. Chicago, Illinois, USA. July 2-8, 2023.

2023 Special session chair e organizer. An Italian snapshot on present and future informatics research in bioinformatics. CIBB 2023: 18TH conference on computational intelligent methods for bioinformatics and biostatistics. September 6-8 2023, Padova, Italy.

2023 Special session organizer. Modelling and simulation methods for computational biology and systems medicine. CIBB 2023: 18TH conference on computational intelligent methods for bioinformatics and biostatistics. September 6-8 2023, Padova, Italy.

2023 Program Committee: 9th International Conference on machine Learning, Optimization & Data science - LOD 2023. Sept 22-26, Lake District England, UK.

2022 Conference Chair. 18th Annual meeting of the Bioinformatics Italian Society (BITS). 27-29 June 2022, Verona, Italy.

2022 Program Committee: 8th International Conference on machine Learning, Optimization & Data science - LOD 2022. Castelnuovo Berardenga (Siena), Italy, September 19-22, 2022.

2022 Technical Program Committee: The Fourteenth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies (BIOTECHNO 2022) May 22-26, 2022, Venice, Italy.

2021 Organization committee – Special session “Modeling and simulation methods for computational biology and systems medicine” at CIBB 2021 (the 17th international conference on Computational Intelligence Methods for Bioinformatics and Biostatistics). 15-17 November 2021, online.

2021 Organization committee and Chair: MODIMO – Workshop on “Multi-Omics Data Integration for Modelling Biological Systems”, in conjunction with CIKM2021, 1-5 November 2021, online.

2021 Organization committee and Chair: AIRDEGEN – Workshop on “Linking air pollution and neurodegenerative disorders: data, methods, and biological validation”, in conjunction with BIBM 2021, 9 - 12 December 2021 - Houston, TX, USA.

2021 Technical Program Committee: The Thirteenth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies (BIOTECHNO 2021) May 30-June 03, 2021, Valencia, Spain

2021 Program Committee: The 7th International Online & Onsite Conference on Machine Learning, Optimization, and Data Science. June 29-July 2, 2021. Grasmere, Lake District, England, UK

2019-2020 Organizing committee and Chair: Meeting Annuale della Società Italiana di Bioinformatica (BITS). 2020, Verona, Italy.

2019 Organizing committee and Chair: Ph.D. school in Imaging genetics. 2th-6th December 2019, Verona, Italy.

2019 Organizing committee: International proteomics & metabolomics conference and advanced school. 1st-2nd July 2019, Verona, Italy.

2018 Program committee: WORKSHOP on Challenges and Opportunities in Large Scale Network Analysis in Systems Biology (COLNASB’18). IEEE BIBM co-located workshop. 3th December 2018, Madrid, Spain.

Editorial activities

2022-	Academic Editor for the journal “PLOS One”, ISSN 1932-6203, PLOS
2021-	Editorial board member for the journal “Healthcare analytics”, ISSN 2772-4425, ELSEVIER.
2022	Guest Editor for the special issue “Deep Learning and Computer Vision for Object Recognition”, Applied Sciences (ISSN: 2076-3417) ,MDPI.
2022-	Topic Editor for Frontiers in Bioinformatics, Integrative Bioinformatics
2022 -	Topic Editor for Frontiers in Genetics, Computational Genomics
2022 -	Associate Editor for the journal Frontiers in Medical Engineering, section Computational Medicine
2022	Associate Editor for BMC Supplements, Springer Nature
2020-2022	Editorial board member for the journal “Computational Biology and Bioinformatics (CBB)”, ISSN print 2330-8256, ISSN online 2330-8281, Science Publishing Group.
2021-2022	Lead guest editor for the special issue “Computational Intelligence in Bioinformatics and Computational Biology” , Applied Sciences (ISSN 2076-3417) di MDPI.
2022	Review Editor for the journal Frontiers in Medical Engineering, section Computational Medicine
2020–	Reviewer Editor for the journal Frontiers in Bioinformatics, section Network Bioinformatics
2019-	Reviewer Editor for the journal Frontiers in Genetics, section Computational Genomics
2019 - 2021	Lead Guest Editor for the special issue “Information Theoretical Methods in Biological System”, Entropy (ISSN 1099-4300), MDPI.
2018 – 2019	Lead Guest Editor for the special issue “Energy-Aware Smart Systems in Healthcare”, Energies (ISSN 1996-1073), MDPI.
2018 - 2019	Lead Guest Editor for the special issue “Smart Systems for Healthcare”, Future Internet (ISSN 1999-5903), MDPI.
2017-2019	Reviewer Editor for the journal Frontiers in Applied Mathematics and Statistics, section Optimization.

Scientific reviewer

Journals	Access, IEEE Algorithmica, Springer Artificial Intelligence in Medicine, Elsevier Bioinformatics, Oxford Academic BMC Bioinformatics, Springer Nature Briefings in Bioinformatics, Oxford University Press Cancers, MDPI Clinical Pharmacology and Therapeutics, Wiley-Blackwell

Computational and Structural Biotechnology Journal, Elsevier
CPT: Pharmacometrics & Systems Pharmacology, Wiley-Blackwell
DATABASE, Oxford University Press
Data Mining and Knowledge Discovery, Springer
Discrete Applied Mathematics, Elsevier
Evolutionary Bioinformatics, SAGE
Expert Systems With Applications, Elsevier
Frontiers in Artificial Intelligence, section Machine Learning and Artificial Intelligence
Frontiers in Applied Mathematics and Statistics, section Optimization
Frontiers in Bioengineering and Biotechnology, section Bioinformatics and Computational Biology
Frontiers in Cell and Developmental Biology
Frontiers in Genetics, section Bioinformatics and Computational Biology
Frontiers in Plant Science, section Bioinformatics and Computational Biology
Future Internet, MDPI
Genomics, Elsevier
Genomics, Proteomics & Bioinformatics, Oxford Academic
Information Systems, Elsevier
International Journal of Data Science and Analytics, Springer
Journal of Biomedical and Health Informatics, IEEE/EMB
Journal of Computational Science, Elsevier
Journal of Statistical Computation and Simulation, Taylor & Francis
Journal of Theoretical Biology, Elsevier
Knowledge and Information Systems, Springer
Life Sciences, Elsevier
Pattern Recognition, Elsevier
PLOS ONE, Public Library of Science
Soft Computing, Springer
The journal of supercomputing, Springer Nature
Transactions on Computational Biology and Bioinformatics, IEEE/ACM
Transactions on Computational Social Systems, IEEE
Transactions on Knowledge Discovery from Data, ACM
Wiley Interdisciplinary Reviews: Systems Biology and Medicine

Conferences

IEEE ICDM 2024 - 24th IEEE International Conference on Data Mining
9-12 December 2024, Abu Dhabi, UAE

ECAI-2023 26th European Conference on Artificial Intelligence ECAI 2023
30.09 - 4.10, 2023, Kraków, Poland.

LOD2022. The 8th International Conference on Machine Learning, Optimization, and Data Science. September 18 – 22, 2022 – Certosa di Pontignano, Siena – Tuscany, Italy

CIBB2021 · International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics. 15-17 November 2021. Online.

ESA (European Symposium on Algorithms) 2021. September 6-8, 2021, Lisbon, Portugal.

LOD2020. The Sixth International Conference on Machine Learning, Optimization, and Data Science – July 19-23, 2020 – Certosa di Pontignano, Siena – Tuscany, Italy

Collegial bodies

2025 – 2028 President of the Unified Study Course Council of the Degree Course in Computer Science and the Master's Degree Course in Computer Science, Department of Mathematical, Physical and Computer Sciences, University of Parma.

2024 - Deputy Director of the “InfoLife” national laboratory in CINI

2024 -	Research Delegate of the Department of Mathematical, Physical and Computer Sciences, University of Parma.
2024 -	Member of the departmental commission for third mission of the Department of Mathematical, Physical and Computer Sciences, University of Parma.
2024 -	Member of the Technical and Scientifical Committee for scientific calculus and high performance computing of the University of Parma.
2022 - 2024	Member of the Joint Commission for Teachers and Students for the bachelor's degree in Computer Science, Department of Mathematical, Physical and Computer Sciences, University of Parma.
2022 - 2023	Member of the Didactic Council of the degree in Mathematics, Department of Mathematical, Physical and Computer Sciences, University of Parma.
2021 -	Member of the Department Council, Department of Mathematical, Physical and Computer Sciences, University of Parma.
2021 -	Member of the Didactic Council of bachelor's and Master's degree in Computer Science, Department of Mathematical, Physical and Computer Sciences, University of Parma.
2020 -	Member of the PhD board in Computer Science, Department of Computer Science, University of Verona.
2020 - 2021	Member of the Computer Science Department Council - Department of Computer Science, University of Verona.
2015 - 2021	Member of the Didactic Council, Department of Computer Science, University of Verona.

Teaching activities

2024 -	Teacher in charge of the course "Software engineering" at the Bachelor's degree in Computer Science, Department of Mathematical, Physical and Computer Sciences, University of Parma.
2024	Teacher in charge of the course "Non-relational Database Management Systems", Master's course "Social Data Science", Università degli Studi di Milano-Bicocca.
2024	Teacher in charge of the course "Basic Social Network Analysis", Master's course "Social Data Science", Università degli Studi di Milano-Bicocca.
2023	Teacher in charge of the Ph.D. course "A practical interdisciplinary PhD course on exploratory data analysis", Department of Computer Science, University of Verona.
2023	Teacher in charge of the Ph.D. course "Informational Genomics: information content of genomes and its divergence from randomness", Department of Computer Science, University of Verona.
2022 -	Teacher in charge of the course Laboratory of artificial intelligence at the master's degree in computer science, Department of Mathematical, Physical and Computer Sciences, University of Parma.
2021 -	Teacher in charge of the course Algorithms for artificial intelligence at the master's degree in computer science, Department of Mathematical, Physical and Computer Sciences, University of Parma.

2021 - 2024	Teacher in charge of the course Algorithms and data structures at the Bachelor's degree in computer science, Department of Mathematical, Physical and Computer Sciences, University of Parma.
2021	Teacher in charge of the Ph.D. course "A practical interdisciplinary PhD course on exploratory data analysis", Department of Computer Science, University of Verona.
2021	Teacher in charge of the Ph.D. course "Informational Genomics: information content of genomes and its divergence from randomness", Department of Computer Science, University of Verona.
2020 - 2021	Teacher in charge of the course Discrete Biological Models, Bachelor's degree in Bioinformatics, Department of Computer Science, University of Verona.
2020	Teacher in charge of the Ph.D. course "Informational Genomics: information content of genomes and its divergence from randomness", Department of Computer Science, University of Verona.
2019 – 2020	Teacher in charge of the course Discrete Biological Models, Bachelor's degree in Bioinformatics, Department of Computer Science, University of Verona.
2018 – 2019	Teacher in charge of the course Discrete Biological Models, Bachelor's degree in Bioinformatics, Department of Computer Science, University of Verona.
2018 - 2019	Remissive winner: teacher for the course Programming language C, Bachelor's degree in Mathematics Department of Computer Science, University of Verona.
2017- 2018	Teacher for the course Programming Laboratory I, Bachelor's degree in Computer Science, Department of Computer Science, University of Verona.
2016 - 2017	Teacher for the course Programming Laboratory I, Bachelor's degree in Computer Science, Department of Computer Science, University of Verona.
2015 - 2016	Teacher for the course Programming Laboratory I, Bachelor's degree in Computer Science, Department of Computer Science, University of Verona.
2014 - 2015	Teacher for the course Programming Laboratory I, Bachelor's degree in Computer Science, Department of Computer Science, University of Verona.

Teaching assistant

2019	Hands-on: multi-omics data integration by systems biology (Cytoscape). Advanced school "Bioinformatics tools for mass spectrometry-based omic data: from pathways reconstruction to multi-omic data integration". 2nd July 2019, Verona, Italy.
2019 - 2020	Teaching assistant and student project assistant, course of Programming laboratory for bioinformatics, master's degree in Medical Bioinformatics, Department of Computer Science, University of Verona.
2019 - 2020	Teaching assistant and student project assistant, course of Natural Computing, master's degree in in Bioinformatics and Medical Biotechnologies, Department of Computer Science, University of Verona.
2018 - 2019	Teaching assistant and student project assistant for the course Programming laboratory for bioinformatics, master's degree in Medical Bioinformatics, Department of Computer Science, University of Verona.

2018 - 2019	Teaching assistant and student project assistant, course di Natural Computing, master degree in in Bioinformatics and Medical Biotechnologies, Department of Computer Science, University of Verona.
2018	Teacher for a set of lessons: “Introduzione alla bioinformatica e informatica biomedicale”. CdL in Ingegneria Informatica, Facoltà di Ingegneria e Architettura, Università degli Studi di Enna Kore.
2017 - 2018	Teaching assistant and student project assistant for the course Programming laboratory for bioinformatics, Master’s degree in Medical Bioinformatics, Department of Computer Science, University of Verona.
2017 - 2018	Teaching assistant and student project assistant for the course Natural Computing, Master’s degree in Bioinformatics and Medical Biotechnologies, Department of Computer Science, University of Verona.
2016 - 2017	Teaching assistant and student project assistant for the course Programming laboratory for bioinformatics, Master degree Bioinformatics and Medical Biotechnologies, Department of Computer Science, University of Verona.
2015 - 2016	Teaching assistant and student project assistant for the course Natural computing, master’s degree in Bioinformatics and medical Biotechnologies, Department of Biotechnologies, University of Verona.
2014 - 2015	Teaching assistant and student project assistant at the course of Natural computing, master degree in Bioinformatics and medical Biotechnologies, Department of Biotechnologies, University of Verona.
2013 – 2014	Laboratory tutor at the course Algorithms for bioinformatics, Bachelor’s degree in Bioinformatics and medical Biotechnologies, Department of Biotechnologies, University of Verona.
2013 – 2014	Laboratory tutor course of Programming Laboratory I, Bachelor’s degree in Bioinformatics and medical Biotechnologies, Department of Biotechnologies, University of Verona.
2012 – 2013	Laboratory tutor. Course of Programming Laboratory, bachelor’s degree in Applied Mathematics, Department of Computer Science, University di Verona.
2012 – 2013	Laboratory tutor course Algorithms bachelor’s degree in Computer Science, Department of Computer Science, University of Verona.
Dal 2010	Co-advisor of bachelor and master thesis in Bioinformatics, graph theory and parallel computing.

Third mission

This section reports the activities regarding the third mission of the University, namely the activity in which the university interacts with the society, beside the classical of education and research.

2025	Invited speaker. Round table “Il potenziamento dell’ecosistema bioinformatico toscano: costruire opportunità per nuove connessioni tra gruppi, e tra università e imprese”. BIOINFORMATIHA 12 - Dodicesima Edizione della Giornata Toscana di Bioinformatica e Systems Biology, 15-16 September 2025, Fondazione Pisana per la Scienza, San Giuliano Terme, Italy.
2025	Invited speaker. “Intelligenza artificiale: evoluzione o rivoluzione?” June 8th, 2025. Bardi, Italy.

2025	Organizer of the informative event “Sfida l’algoritmo” at “Notte europea delle ricercatrice e dei ricercatori”. September 26th 2025. Parma
2024	Organizer of the informative event “Sfida l’algoritmo” at “Notte europea delle ricercatrice e dei ricercatori”. September 27th 2024. Parma
2023	Mentor at “Startup Weekend Parma - Innovating for Sustainability”. November 24-26, 2023, Parma.
2023	Organizer of the informative event “Sfida l’algoritmo” at “Notte europea delle ricercatrice e dei ricercatori”. September 29th 2023. Parma.
2023	Speaker. Computer Science Day. University of Parma. 9 May 2023.
2022	Organizer of the informative event “Sfida l’algoritmo” at “Notte europea delle ricercatrice e dei ricercatori”. September 30th 2022. Parma.
2022	Speaker at #piday (International Day of Mathematics). University of Parma. Talk tile “Characterization of random sequences”. 11th March 2022, Parma.
2021	Juryman for the event Premio Scuola Digitale (MIR) of Provincia di Verona. 15th April 2020, Verona.
2020	Talk “Bioinformatica: il coding della vita” at the award day of Premio Scuola Digitale (MIUR) of Provincia di Verona. 20th February 2020, Verona.
2020	Juryman for the event Premio Scuola Digitale (MIUR) of Provincia di Verona. 20th February 2020, Verona.
2020	Talk at the University open days for the bachelor’s degree in Bioinformatics. 21th January 2020, Verona.

Scientific publications

Books

[B1] Manca V. and Bonnici V.. “Infogenomics: The Informational Analysis of Genomes”. Cham: Springer Nature Switzerland, 2023.

Journal articles

[R34] Giovanni Micale, Antonio Di Maria, Roberto Grasso, Vincenzo Bonnici, Alfredo Ferro, Dennis Shasha, Rosalba Giugno, and Alfredo Pulvirenti.
MultiGraphMatch: a subgraph matching algorithm for multigraphs.
ACM Trans. Knowl. Discov. Data (2025).
https://doi.org/10.1145/3728361

[R33] Aparo, A., Avesani, S., Parmigiani, L., Napoli, S., Bertoni, F., Bonnici, V., Cascione, L. and Giugno, R.
EasyCircR: Detection and reconstruction of circular RNAs post-transcriptional regulatory interaction networks.
Computers in Biology and Medicine, 188, p.109846. 2025.
https://doi.org/10.1016/j.compbiomed.2025.109846

[R32] Bonnici V..
A Maximum Value for the Kullback–Leibler Divergence between Quantized Distributions.
Information 2024, 15(9), 547; https://doi.org/10.3390/info15090547.

[R31] Bonnici V., Chicco D.
Seven quick tips for gene-focused computational pangenomic analysis.
BioData Mining 17, 28 (2024). https://doi.org/10.1186/s13040-024-00380-2.

[R30] Bonnici V., Grasso R., Micale G., di Maria A., Shasha D., Pulvirenti A., Giugno R.
ArcMatch: high-performance subgraph matching for labeled graphs by exploiting edge domains.
Data mining and knowledge discovery. DOI: 1007/s10618-024-01061-8.

[R29] Aparo A., Bonnici V., Avesani S, Cascione L, Giugno R.
DiGAS: Differential gene allele spectrum as a descriptor in genetic studies.
Computers in Biology and Medicine.
https://doi.org/10.1016/j.compbiomed.2024.108924

[R28] Bonnici, V, Mengoni, C, Mangoni, M, Franco, G, Giugno, R.
PanDelos-frags: A methodology for discovering pangenomic content of incomplete microbial assemblies.
JOURNAL OF BIOMEDICAL INFORMATICS, vol. 148, ISSN: 1532-0464, doi: 10.1016/j.jbi.2023.104552

[R27] Avesani, S., Viesi, E., Alessandrì, L., Motterle, G., Bonnici, V., Beccuti, M., Calogero, R. and Giugno, R.
Stardust: improving spatial transcriptomics data analysis through space aware modularity optimization based clustering.
GigaScience, Volume 11, 2022, giac075, https://doi.org/10.1093/gigascience/giac075

[R26] Bonnici V, Cicceri G, Distefano S, Galletta L, Polignano M, Scaffidi C.
Covid19/IT the digital side of Covid19: A picture from Italy with clustering and taxonomy.
PloS one. 2022 Jun 9;17(6):e0269687. https://doi.org/10.1371/journal.pone.0269687

[R25] Bonnici, V. Giugno, R.
PANPROVA: PANgenomic PROkaryotic eVolution of full Assemblies.
Bioinformatics. 2022. 10.1093/bioinformatics/btac158

[R24] Aparo, A., Sala P., Bonnici V., Giugno R.
TEDAR: Temporal dynamic signal detection of adverse reactions
Artificial Intelligence in Medicine Volume 122, December 2021, 102212.
doi.org/10.1016/j.artmed.2021.102212

[R23] Tognon, M., Bonnici, V., Garrison, E., Giugno, R., Pinello, L.
GRAFIMO: variant and haplotype aware motif scanning on pangenome graphs.
PLOS computational biology. 2021. https://doi.org/10.1371/journal.pcbi.1009444

[R22] Bonnici, V., Franco, G., Manca, V.
Spectral concepts in genome informational analysis.
Theoretical Computer Science. 2021. https://doi.org/10.1016/j.tcs.2021.06.039

[R21] Bonnici, V., Cicceri, G., Distefano, S., Galletta, L., Polignano, M. and Scaffidi, C..
IT-Covid19-IT: la risposta della comunità informatica italiana alla pandemia. Mondo Digitale, p.2, 2021

[R20] Licheri, N., Bonnici, V., Beccuti, M. and Giugno, R.
GRAPES-DD: exploiting decision diagrams for index-driven search in biological graph databases.
BMC bioinformatics, 22(1), pp.1-24, 2021. Doi: 10.1186/s12859-021-04129-0

[R19] Bonnici V., Maresi M., Giugno R.
Challenges in gene-oriented approaches for pangenome content discovery.
Briefings in Bioinformatics, 1-11, 09-2020. doi: 10.1093/bib/bbaa198

[R18] Aparo A., Bonnici V., Micale G., Ferro E., Shasha D., Pulvirenti A., Giugno R.
Fast Subgraph Matching Strategies based on Pattern-only Heuristics
Interdisciplinary Sciences: Computational Life Sciences, 11(1), 21-32, 2019. doi: 10.1007/s12539-019-00323-0.

[R17] Bonnici, V., Manca, V.
An informational test for random finite strings.

Entropy, 20(12), 934 (2019). doi:10.3390/e20120934

[R16] Bonnici V., Giurgno R., Manca V.
PanDelos: a dictionary-based method for pan-genome content discovery.
BMC Bioinformatics 19 (15), 48-59. (2019). doi:10.1186/s12859-018-2417-6

[R15] Bonnici, V., De Caro, G., Constantino, G., Liuni, S., D'Elia, D., Bombieri, N., Licciulli, F., Giugno, R.
Arena-Idb: a platform to build human non-coding RNA interaction networks
BMC bioinformatics 19.10 (2018): 231. doi: 10.1186/s12859-018-2298-8

[R14] Bonnici, V., Busato, F., Aldegheri, S., Akhmedov, M., Cascione, L., Carmena, A.A., Bertoni, F., Bombieri, N., Kwee, I., Giugno, R.
cuRnet: an R package for graph traversing on GPU
BMC bioinformatics 19.10 (2018): 221. doi: 10.1186/s12859-018-2310-3

[R13] F. Russo, S. Di Bella, F. Vannini, G. Berti, F. Scoyni, H. Cook, A. Santos, G. Nigita, V. Bonnici, A. Laganà, F. Geraci, A. Pulvirenti, R. Giugno, F. De Masi, K. Belling, L. Jensen, S. Brunak, M. Pellegrini, A. Ferro.
miRandola 2017: a curated knowledge base of non-invasive biomarkers.
Nucleic acids research 46, no. D1 (2017): D354-D359. doi: 10.1093/nar/gkx854.

[R12] V. Bonnici, R. Giugno.
On the variable ordering in subgraph isomorphism algorithms.
IEEE/ACM Transaction on Computational Biology and Bioinformatics. 01/2017.
doi:10.1109/TCBB.2016.2515595.

[R11] V. Bonnici, V. Manca.
Informational laws of genome structures.
Scientific Reports (6), 06/2016. doi:10.1038/srep28840

[R10] V. Bonnici, F. Busato, G. Micale, N. Bombieri, A. Pulvirenti, R. Giugno.
APPAGATO: an Approximate Parallel and stochastic GrAph querying Tool for biological networks.
Bioinformatics, 04/2016. doi:10.1093/bioinformatics/btw223

[R9] V. Bonnici, V. Manca.
Recurrence distance distributions in computational genomics.
American Journal of Bioinformatics and Computational Biology (3), 10/2015.
doi:10.7726/ajbcb.2015.1002;

[R8] V. Bonnici, V. Manca.
Infogenomics tools: A computational suite for informational analysis of genomes.
Journal of Bioinformatics and Proteomics Review (1), 06/2015. doi: 10.15436/2381-0793.15.002.

[R7] F. Rinnone, G. Micale, V. Bonnici, G.D. Bader, D. Shasha, A. Ferro, A. Pulvirenti, R. Giugno.
NetMatchStar: an enhanced Cytoscape network querying app.
F1000Research (4), 11/2015. doi:10.12688/f1000research.6656.2

[R6] S. Alaimo, V. Bonnici, D. Cangemi, A. Ferro, R. Giugno, A. Pulvirenti.
DTWeb: a web-based application for Drug-Target interaction prediction through domain-tuned network-based inference .
BMC System Biology (9), 06/2015. doi:10.1186/1752-0509-9-S3-S4

[R5] V. Bonnici, F. Russo, N. Bombieri, A. Pulvirenti and R. Giugno
Comprehensive reconstruction and visualization of non-coding regulatory networks in human.
Frontiers in Bioengineering and Biotechnology. - Bioinformatics and Computational Biology, 12/2014. doi:10.3389/fbioe.2014.00069

[R4] F. Russo, S. Di Bella, V. Bonnici, A. Laganà, G. Rainaldi, M. Pellegrini, A. Pulvirenti, R. Giugno, A. Ferro.
A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs.
BMC Genomics (15), 05/2014. doi:10.1186/1471-2164-15-S3-S4

[R3] V. Bonnici, R. Giugno, A. Pulvirenti, D. Shasha, A. Ferro.
A subgraph isomorphism algorithm and its application to biochemical data.
BMC Bioinformatics (14). 04/2013. doi:10.1186/1471-2105-14-S7-S13

[R2] R. Giugno, V. Bonnici, N. Bombieri, A. Pulvirenti, A. Ferro, D. Shasha.
GRAPES: A Software for Parallel Searching on Biological Graphs Targeting Multi-Core Architectures.
PLoS ONE (8), 10/2013. doi:10.1371/journal.pone.0076911

[R1] V. Bonnici, A. Ferro, R. Giugno, A. Pulvirenti, D. Shasha.
Enhancing Graph Database Indexing By Suffix Tree Structure.
Lecture Notes in Computer Science. Volume 6282 LNBI, 2010, Pages 195-203.
doi.org/10.1007/978-3-642-16001-1_17

Book chapters

[C3] V. Bonnici, A. Cracco, G. Franco
A k-mer Based Sequence Similarity for Pangenomic Analyses.
In: Machine Learning, Optimization, and Data Science, 7th International Conference, LOD 2021, Grasmere, UK, October 4–8, 2021, Revised Selected Papers, Part II. DOI: 10.1007/978-3-030-95470-3_3

[C2] A. Mensi, V. Bonnici, S. Caligola, R. Giugno.
Construction and Analysis of miRNA Regulatory Networks.
In: Laganà A. (eds) MicroRNA Target Identification. Methods in Molecular Biology, vol 1970. Humana Press, New York, NY. Print ISBN 978-1-4939-9206-5. Online ISBN 978-1-4939-9207-2. Doi doi.org/10.1007/978-1-4939-9207-2_9.

[C1] F. Scoyni, V. Bonnici, A. Pulvirenti, R. Giugno.
Genetic alteration of miRNA affecting cancer pathways.
In: Cancer and Noncoding RNAs, Translational Epigenetics, Elsevier, 2018.
ISBN 978-0-12-811022.5. doi: 10.1016/B978-0-12-811022-5.00015-2.

Conference papers, abstracts, and posters

[A32] Nnadi, G. O., Bonnici, V., Avesani, S., Viesi, E., & Giugno, R.
Leveraging Graph Information for Spatially Informed Patient Data Analysis with GIST.
In 2025 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB) (pp. 1-8). IEEE. Tainan, Taiwan August 20-22, 2025.
10.1109/CIBCB66090.2025.11177089

[A31] A. Levante, L. Troiani, V. Pierdomenico, A. Dal Palù, E. Neviani, V. Bernini, V. Bonnici, C. Lazzi. Exploring the biodiversity of a targeted microbial core of lactic acid bacteria: connecting experimental datasets with predictive models. 28th International ICFMH Conference FOOD MICRO 2024. July 8-11, 2024, Burgos, Spain.

[A30] Boldini, G., Diana, A., Arceri, V., Bonnici, V., Bagnara, R. (2024). A Machine Learning Approach for Source Code Similarity via Graph-Focused Features. In: Nicosia, G., Ojha, V., La Malfa, E., La Malfa, G., Pardalos, P.M., Umeton, R. (eds) Machine Learning, Optimization, and Data Science. LOD 2023. Lecture Notes in Computer Science, vol 14505. Springer, Cham. https://doi.org/10.1007/978-3-031-53969-5_5

[A29] V. Bonnici, V. Arceri, A. Diana, F. Bertini, E. Neviani, A. Levante, V. Berinini, E. Neviani, A. Dal Palù
BIOCHAIN: towards a platform for securely sharing microbiological data
In Proceedings of the 27th International Database Engineered Applications Symposium (IDEAS '23). Association for Computing Machinery, New York, NY, USA, 59–63. https://doi.org/10.1145/3589462.3589501

[A28] S. Astorino, V. Bonnici and G. Franco.
An Investigation to Test Spectral Segments as Bacterial Biomarkers.
UCNC 2023: 20th International Conference on Unconventional Computation and Natural Computation. March 13 - 17, 2023. University of North Florida, Jacksonville, Florida, USA. https://doi.org/10.1007/978-3-031-34034-5_1

[A27] Avesani S, Viesi e, Alessandrì L, Motterle G, Bonnici V, Beccuti M, Calogero R, Giugno R.
A new space-based method for downstream analysis of spatial transcriptomics data.
18th annual Meeting of the Bioinformatics Italian Society, 27-29 June 2022, Verona, Italy.

[A26] Bonnici V, Mangoni M, Franco G and Giugno R.
A systematic evaluation of computational tools for gene-oriented pangenome detection in fragmented genomes.
18th annual Meeting of the Bioinformatics Italian Society, 27-29 June 2022, Verona, Italy.

[A25] Astorino A, Bonnici V, Franco G.
Spectral segments as bacterial biomarkers.
18th annual Meeting of the Bioinformatics Italian Society, 27-29 June 2022, Verona, Italy.

[A24] Bonnici V, Arceri V, Bertini F, Iotti E, Dal Palù A.
BIOCHAIN-AI: a platform for securely sharing and analysing microbiological data.
18th annual Meeting of the Bioinformatics Italian Society, 27-29 June 2022, Verona, Italy.

[A23] Licheri, N., Amparore, E., Bonnici, V., Giugno, R., & Beccuti, M.
An entropy heuristic to optimize decision diagrams for index-driven search in biological graph databases.
Proceedings of the CIKM 2021 Workshops co-located with 30th ACM International Conference on Information and Knowledge Management (CIKM 2021). Gold Coast, Queensland, Australia, November 1-5, 2021.

[A22] M. Tognon, V. Bonnici, E. Garrison, R. Giugno and L. Pinello.
Variant and haplotype aware motif scanning on genome variation graphs.
RECOMB 2021. 25th international conference on research in computational molecular biology. Aug 29 – sep 1- 2021. online.

[A21] Bonnici V., Motterle G., Franco G., Giugno R.
A methodology for capturing pangenomic content among incomplete genomes.
Annual meeting of the Bioinformatics Italian Society,
1-2 July 2021, online.

[A20] Tognon M., Bonnici V., Garrison E., Giugno R., Pinello L.
GRAFIMO: variant and haplotype aware motif scanning on pangenome graphs.
Annual meeting of the Bioinformatics Italian Society,
1-2 July 2021, online.

[A19] Motterle G., Alessandrì L., Viesi E., Bonnici V., Cordero F., Beccuti M., Calogero R. and Rosalba G.
Stardust: spatial tranScripTomics data analysis through space awARe modularity optimization baseD clUSTering.
Annual meeting of the Bioinformatics Italian Society,
1-2 July 2021, online.

[A18] Bonnici V.
A maximum value for the the Kullback-Leibler divergence.
IEEE International Symposium on Information Theory
12-20 July 2021, online.

[A17] Licheri N., Bonnici V., Beccuti M., Giugno R.

Decision diagrams-based indexing for searching in biomedical graphs.
WEPA 2020 - Fourth International Workshop on Enumeration Problems and Applications. Online.

[A16] Bonnici V., Caligola S, Fiorini G., Giudice L., Giugno R.
LErNet: characterization of lncRNAs via context-aware network expansion and enrichment analysis.
16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology 9-11 Luglio 2019. Certosa di Pontignano, Siena, Italy. Doi: 10.1109/CIBCB.2019.8791487

[A15] Bombieri N., Bonnici V., Giugno R.
Parallel Searching on Biological Networks.
Euromicro International Conference on Parallel, Distributed, and Network-Based Processing PDP2019. Pavia Febbrario 13-15, 2019, pp. 1-12.

[A14] Bonnici V., Giugno R., Bombieri N.
An Efficient Implementation of a Subgraph Isomorphism Algorithm for GPUs.
2018 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Madrid, Spain, Dicember 3-6, 2018, pp. 2674-2681. doi:10.1109/BIBM.2018.8621444

[A13] A. Aparo, V. Bonnici, G. Micale, A. Ferro, D. Shasha, A. Pulvirenti, R. Giugno.
Simple Pattern-only Heuristics Lead To Fast Subgraph Matching Strategies on Very Large Networks.
PACBB'18: 12th International Conference on Practical Applications of Computational Biology & Bioinformatics. Toledo (Spain). 20-22 Giugno, 2018. doi: 10.1007/978-3-319-98702-6_16

[A12] Bonnici V., Caligola S., Aparo A., Giugno R.
Centrality Speeds the Subgraph Isomorphism Search Up in Target Aware Contexts.
InComputational Intelligence Methods for Bioinformatics and Biostatistics. CIBB 2018. 5-8 September 2018, Caparica, Portogallo. Lecture Notes in Computer Science, vol 11925. Springer, Cham. Dpi: https://doi.org/10.1007/978-3-030-34585-3_3.

[A11] F. Scoyni, T.B. Hansen, R. Giugno, V. Bonnici, G. Fiorini, A. Simonelli, L. Cheng, A. Hill, H. de Vries, K. Kanninen, J. Kjems, T. Malm.
Deregulated expression of Cirs-7 circular RNA in transgenic Alzheimer disease mouse model.
The non-coding Genome, EMBO\EMBL Conference, EMBL. September 13 – 16, 2017, Heidelberg, Germany.

[A10] V. Bonnici, F. Busati, M. Akhmedov, S. Caligola, L. Cascione, R. Montemanni, F. Fummi, F. Bertoni, N. Bombieri, I. Kwee, R. Giugno.
cuRnet: an R package for the single-source shortest paths analysis on GPUs.
Bioinformatics Italian Society (BITS) Annual Meeting 2017. Luglio 5-7, 2017, Cagliari, Italy.

[A9] V. Bonnici, G. De Caro, S. Luini, D. D'Elia, N. Bombieri, R. Giugno, F. Liciuli.
Human non-coding RNA networks construction and interpretation.
Bioinformatics Italian Society (BITS) Annual Meeting 2017. Luglio 5-7, 2017, Cagliari, Italy.

[A8] V. Bonnici, G. De Caro, S. Luini, D. D'Elia, N. Bombieri, R. Giugno, F. Liciuli.
Database of human non-coding RNA interactions.
Bioinformatics Italian Society (BITS) Annual Meeting 2016. Giugno 15-17, 2016, Salerno, Italy.

[A7] V. Bonnici, G. Franco, N. Bombieri, R. Giugno.
A scoring methodology for an integrated network of non-coding RNAs and genetic diseases.
Bioinformatics Italian Society (BITS) Annual Meeting 2015. Giugno 3-5, 2015, Milano, Italy.

[A6] F. Russo, S. Di Bella, V. Bonnici, A. Laganà, R. D'Aurizio, M. Pellegrini, A. Pulvirenti, R. Giugno, A. Ferro.
Biological network annotation tool with cellular and extracellular miRNA data.
10th Annual Network Biology Symposium & Cytoscape Workshop, Institut Pasteur, Ottobre 10, 2013, Parigi, Francia.

[A5] S. Di Bella, F. Russo, V. Bonnici, A. Pulvirenti, R. Giugno, A. Ferro.
Cellular and extracellular microRNAs: a systematic comparison of expression profiles and the role of drugs in circulating miRNA levels.
Bioinformatics Italian Society (BITS) Annual Meeting 2013. Maggio 21-23, 2013, Trieste, Italy.

[A4] Pulvirenti A, Giugno R, Di Bella S, Nigita G, Macca V, Giummarra A, Garofalo D, Caruso G, Bonnici V, Ferro A.
An integrated system for mining relations among microRNAs, drugs and phenotypes.
EMBNET NEWS, vol. 18, ISSN: 2226-6089. 2012.

[A3] Bonnici V, Giugno R, Pulvirenti A, Shasha D, Ferro A.
Core algorithms to search in biological structured data .
EMBNET NEWS, vol. 18, ISSN: 2226-6089. 2012.

[A2] V. Bonnici, A. Ferro, R. Giugno, A. Pulvirenti, D. Shasha.
RelaxGrep: approximate graph searching by query relaxation.
Proceeding on 5th IAPR International Conference on Pattern Recognition in Bioinformatic. Lecture Notes in Bioinformatics, Springer. 22-24 September 2010, Nijmegen, The Netherlands. 2010.

[A1] V. Bonnici, A. Ferro, R. Giugno, A. Pulvirenti, D. Shasha.
Enhancing Graph Database Indexing By Suffix Tree Structure.
Proceeding on 5th IAPR International Conference on Pattern Recognition in Bioinformatic Lecture Notes in Bioinformatics, Springer. 22-24 September 2010, Nijmegen, The Netherlands. 2010.

Research computational tools

Software and computational platforms that has been released and that are currently maintained. The date of the first release is reported.

since 2024 — ArcMatch: high-performance subgraph matching for labeled graphs by exploiting edge domains.
A subgraph isomorphism algorithm which exploits edges domains.
https://github.com/vbonnici/ArcMatch

since 2022 — PANPROVA: PANgenomic PROkaryotic eVolution of full Assemblies.
A methodology to simulate evolution of bacterial populations in agreement with pangenomic features.
https://github.com/InfOmics/PANPROVA

since 2021 — PanDelos-fragments
A software for retrieving the pangemoic content in collections of complete and draft genomes of bacteria.
https://github.com/InfOmics/PanDelos-fragments

since 2021 — PanDelos-Ord
A parallel software for retrieving the pangemoic content in collections of bacteria.
https://github.com/vbonnici/PanDelos

since 2019 — LErNet
An R packet for characterizing lncRNAs via network analysis by means of genomic and system-level data.
https://github.com/InfOmics/LErNet

since 2019 GRASS
A parallel algorithm for searching subgraphs. C++/CUDA for GP-GPU architectures.
https://github.com/InfOmics/GRASS

since 2018 PanDelos
A software for retrieving the pangemoic content in collections of bacteria.
https://github.com/InfOmics/PanDelos

since 2018 Arena-Idb
Integration and visualization of biological networks of non-coding RNA in human.
http://arenaidb.ba.itb.cnr.it

since 2018 cuRnet
A framework for GPGPU architecture for graph analysis provided via R.
https://bitbucket.org/curnet/

since 2015 InfoGenomicsTools
A computational suite for the informational analysis of genomic sequences developed in Java. It provides a framework with efficient building-blocks algorithms and data structures, a graphical interface and a command line interface to them.
https://bitbucket.org/infogenomics/igtools

since 2015 NetMatchStar
A Cytoscape 3.0 plug-in for searching subgraphs in biological networks and for computing their statistical significance.
http://alpha.dmi.unict.it/netmatchstar/netmatchstar.html
http://apps.cytoscape.org/apps/netmatchstar

since 2015 APPAGATO
A GPGPU tool for the approximate, stochastic search of subgraphs in biological networks, developed in C++ and CUDA.
http://profs.scienze.univr.it/~bombieri/APPAGATO/

since 2014 ncRNA-DB e ncINetView
Integration and visualization of non-coding-RNA centered regulation networks in Homo sapiens. It provides a database of ncRNA interactions, an API to interface with it, a command line interface and a Cytoscape 3.0 plug-in. It is developed in Java on top of the NoSQL OrientDB DBMS.
http://ncrnadb.scienze.univr.it/ncrnadb/

since 2013 GRAPES
A parallel application ofr SMP (symmetric MultiProcessor) architectures for the efficient search of sugraphs within big graphs. The tool is developed on C++ and POSIX threads.
https://github.com/InfOmics/GRAPES

since 2013 Integration of the RI and RI-DS algorithms into the framework SNAP (
Stanford Network Analysis Platform) provide by the Stanford University, California (USA).
https://github.com/snap-stanford/snap/tree/master/contrib/unict_univr-risnap

since 2013 RI and RI-DS
Two efficient algorithms for searching subgraphs.
https://github.com/InfOmics/RI
https://github.com/InfOmics/RI-DS

since 2010 GraphGrepSX.
Indexing and subgraph searching for collection of graphs.
https://github.com/InfOmics/GraphGrepSX
https://github.com/InfOmics/GraphGrepSXIE

Attended courses and certificates

Certificates	Coursera license 3GNSZ2SZHE. “Introduction to Genomic Technologies”. Provided by Bloomberg School of Public Health, Johns Hopkins University. 2015.
	Coursera license XUC26F9JVR. “Genomic Data Science with Galaxy”. Provided by Bloomberg School of Public Health, Johns Hopkins University. 2015.
	Coursera license 99DMDSX7GW. “Python for Genomic Data Science”. Provided by Bloomberg School of Public Health, Johns Hopkins University. 2015.
	Coursera license 7VPYH25FVZ. “Command Line Tools for Genomic Data Science”. Provided by Bloomberg School of Public Health, Johns Hopkins University. 2015.
	Coursera license Y2ZVWV6P3Q. “Algorithms for DNA Sequencing”. Provided by Bloomberg School of Public Health, Johns Hopkins University. 2015.
	Coursera license A8HBDUXY7P. “Bioconductor for Genomic Data Science”. Provided by Bloomberg School of Public Health, Johns Hopkins University. 2015.
	Coursera license F32S87FD9S. “Statistics for Genomic Data Science”. Provided by Bloomberg School of Public Health, Johns Hopkins University. 2015.
Summer school	Summer school in Bioinformatics and Computational Biology. “Computational Genomics and Personalized Medice”. J.T. Schwartz International School for Scientific Research. Lipari (Italy), 2014.
	Summer school in Computational Social Science. “Modelling Spatio-Temporal Reasoning in Complex Social Systems”. J.T. Schwartz International School for Scientific Research. Lipari (Italy), 2014.
	Summer school in Bioinformatics and Computational Biology. “Computational Network Biology”. J.T. Schwartz International School for Scientific Research. Lipari (Italy), 2013.
	Summer school in Computational Social Science. “Big data”. J.T. Schwartz International School for Scientific Research. Lipari (Italy), 2013.
	Summer school in Bioinformatics and Computational Biology. “Computational Network Biology”. J.T. Schwartz International School for Scientific Research. Lipari (Italy), 2013.
	Summer school in Computational Complex Systems. “Dynamic Network and Social Behaviour”. J.T. Schwartz International School for Scientific Research. Lipari (Italy), 2012.
	Summer school in Bioinformatics and Computational Biology. “Pharmacogenomics”. J.T. Schwartz International School for Scientific Research. Lipari (Italy), 2012.
	Summer school in Computational Complex Systems. “Data mining and modelling of complex techno-socio-economic systems”.

J.T. Schwartz International School for Scientific Research. Lipari (Italy), 2012.

Other courses

Course: Research Project Writing “Absolute Beginners”. University of Verona, 11-25 June 2019.

Conference: “Dall’esoma per tutti al genoma di tutti”. 19 April 2017. University of Verona.

Training day: “La gestione dei diritti: il diritto d’autore nel mondo analogico, digitale e in quello Open Access”. 1st February 2013. University of Verona.

Doctoral course: “Mixed-effects models: Fondamenti teorici e applicazioni in R”. University of Verona. 2013.

Doctoral course:: “A formal framework for processes inspired by the functioning of living cells”. University of Verona. 2012.

Doctoral course:: “Algorithmic Graph Theory”. University of Verona. 2012.

Traning: “Next generation sequencing data analysis with Chipster”.
CSC – IT center for science LTD. Espoo (Finland). 2012.

Working experiences

2013 – 2014

Translation reviewer for the project “Italian MSDN Translation Wiki”.
Employer: Dynamic Contract Solutions, 6A Partnership Court, Park Street, DUNDALK, Co. Louth Ireland. Customer: Microsoft.

2012

Translation reviewer for the project “Italian MSDN Translation Wiki”.
Employer: Dynamic Contract Solutions, 6A Partnership Court, Park Street, DUNDALK, Co. Louth Ireland. Customer: Microsoft.

2010 – 2012

Consultant for design and developing a distributed system at Network Consulting Engineering s.r.l. Via Etnea n. 52, 95028 Valverde (CT).

2010

Design and development of a Java application for documental storage and Apache Lucene-based search engine.
Employer: Network Consulting Engineering s.r.l. Via Etnea n. 52, 95028 Valverde (CT).

Technical skills

Computer languages

C (excellent), C++ (excellent), Bash scripting (excellent) , Java SE (excellent), R (excellent), Python (excellent), Matlab (excellent), Latex (excellent), XML (excellent), XSLT (excellent), JavaScript (excellent), XHTML (excellent), HTML (excellent), CSS (good), PHP (excellent), JSP (good), PERL (good), TCL (good), Modula2 (good), CUDA (good), OpenCL (good).

Environments

Eclipse, Visual Studio, NetBeans, QT-creator.

Operating systems

Windows, Linux, Unix, BSD, MAC OSX.

Databases

MySQL, IBM DB2, Oracle, PostgreSQL, OrientDB, Neo4J.

Frameworks and other tools	UML, Latex, CVS, Ant, Maven, Eclipse SDK, OSGi, Apache Web Server, Java EE, Apache Tomcat, JBoss, Intel CUDA, OpenCL, OpenCV, Apache Hibernate, Apache Lucene, Apache Solr, Apache Tika, SWING, SWT, JFace, Joomla, JQuery, TinkerPop.
Creative instruments	Microsoft Office, Adobe CS, Gimp, Inkscape.
Framework and applications for bioinformatics	FASTX-Toolkit, SAM-tools, Picard-tools, BEDtools, Bioconductor, bioPython, bioPerl, BALL (Biochemical Algoritms Library), BWA, Bowtie2, NovoAlign, SOAP, Masai, TopHat, Control-FreeC, TakeABreak, BreakDancer, OncoScan, ShatterProf, BLAST, HMMER, GATB, GATK, SeqAn, Galaxy, Cytoscape.

In witness

Parma, October 7th, 2025