Curriculum Vitae et Studiorum
of
Vincenzo Bonnici

Personal information

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	Italian National Scientific Qualification as Associate Professor, sector 01/B1, valid from 29/04/2021 to 29/04/2030

Current position

since 2019	Temporary Assistant Professor of Computer Science at the Department of Computer Science, University of Verona, Italy.
since 2018	Teacher in charge of the course Discrete Biological Models, Bachelor degree in Bioinformatics, Department of Computer Science, University of Verona, Italy.

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: 110/100. 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 this 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. [R18,R12,R10,R7,R3,R2,R1,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. These studies have been published on journal such as Briefings in Bioinformatics and BMC bioinformatics. [R19,R17,R16,R11,R9,R8,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. [R15,R13,R6,R5,R4,C2,C1,A16,A11,A9,A8,A6,A5,A4]

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

I have also been advisor and co-advisor of several bachelor and master thesis Computer Science and Bioinformatics. I am currently teacher in charge of the course Discrete Biological Models of the bachelor degree in Bioinformatics provided by the Department of Computer Science of the University of Verona, and I have been teacher for four years for the course of Programming Laboratory I at the bachelor degree in Computer Science. I am currently member of the Didactic College and Ph.D. board of the Department of Computer science.

Research assignments

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.

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	Scientific responsibility of the 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 identificare 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 activities.

Prof. Alfredo Ferro, University of Catania, Italy	Graph theory, data mining and their application in bioinformatics. a.
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.
Dr. 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

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

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

Member in organizations

GRIN: GRuppo di INformatica
Junior Member – IEEE Computer Society Technical Committee on Computational Life Sciences (TCCLS)
BITS (Bioinformatics Italian Society)
GNCS (Gruppo Nazionale per il Calcolo Scientifico) – IndAM
InfoLife Laboratory – CINI (Consorzio Interuniversitario Nazionale per l'Informatica)
InfOmics laboratoy, University of Verona.

Organization of scientific conferences

2021	Techincal 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.
2018-2019	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

2021-	Editorial board member for the journal "Healthcare analytics", ISSN 2772-4425, ELSEVIER.
2020-2022	Editorial board member for the journal "Computational Biology and Bioinformatics (CBB)", ISSN print 2330-8256, ISSN online 2330-8281, Science Publishing Group.
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 Bioinformatics, Oxford Academic BMC Bioinformatics, Springer Nature Briefings in Bioinformatics, Oxford University Press Computational and Structural Biotechnology Journal, Elsevier DATABASE, Oxford University Press Data Mining and Knowledge Discovery, Springer Discrete Applied Mathematics, Elsevier Evolutionary Bioinformatics, SAGE 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 Genetics, section Bioinformatics and Computational Biology Frontiers in Plant Science, section Bioinformatics and Computational Biology Future Internet, MDPI Genomics, Elsevier Information Systems, Elsevier International Journal of Data Science and Analytics, Springer Journal of Computational Science, Elsevier Journal of Theoretical Biology, Elsevier Knowledge and Information Systems, Springer Pattern Recognition, Elsevier PLOS ONE, Public Library of Science Transactions on Computational Biology and Bioinformatics, IEEE/ACM Wiley Interdisciplinary Reviews: Systems Biology and Medicine
Conferences	LOD2020. The Sixth International Conference on Machine Learning, Optimization, and Data Science – July 19-23, 2020 – Certosa di Pontignano, Siena – Tuscany, Italy

Collegial bodies

since 2020	Member of the PhD board in Computer Science, Department of Computer Science, University of Verona.
since 2015	Member of the Didactic College, Department of Computer Science, University of Verona.

Teaching activities

2021	Teacher in charge of the course 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 course 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.

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

Journals

[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

Impact factor: 3.73; Cite score: 4.08; Quartili: Q1; Citazioni Scopus|GoogleScholar: 17|23

[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

[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 and abstracts

[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 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 nclNetView 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

Verona,5 May 2021