

Workshop Proposal for the 11th IEEE International Conference on Healthcare Informatics (IEEE ICHI 2023).

Title: "Network and Pathway Analysis in Health Informatics"

Organizers:

- Mario Cannataro, University Magna Graecia of Catanzaro
- Pietro Cinaglia, University Magna Graecia of Catanzaro
- Marianna Milano, University Magna Graecia of Catanzaro
- Giuseppe Agapito, University Magna Graecia of Catanzaro

Mario Cannataro is a full professor of computer engineering and the director of the Data Analytics research center at the University "Magna Græcia" of Catanzaro, Italy. His current research interests include bioinformatics, health informatics, artificial intelligence, data mining, parallel computing. He has published 6 books and more than 300 papers in international journals and conference proceedings. Mario Cannataro is Editor-in-Chief of the Encyclopedia of Bioinformatics and Computational Biology 2nd Ed., and Associate Editor of Briefings in Bioinformatics and IEEE/ACM Transactions on Computational Biology and Bioinformatics journals. He is a Senior Member of ACM, ACM SIGBio, IEEE, IEEE Computer Society, BITS (Bioinformatics Italian Society) and SIBIM (Italian Society of Biomedical Informatics). He regularly co-organizes international workshops on bioinformatics and high- performance computing in primary conferences such as ACM-BCB, IEEE-BIBM and ICCS.

Pietro Cinaglia is research fellow at University "Magna Græcia" of Catanzaro. His current research interests focus on bioinformatics: data processing and analysis, network analysis, and artificial intelligence. He is serving as a reviewer for several scientific journals, as well as for national and international conferences.

Marianna Milano is an assistant professor and a senior research scientist in the field of Omics and Biological Networks data Analysis at the University Magna Græcia, of Catanzaro, Italy. Her research interests are focused on the development of innovative algorithms for the analysis of clinical and omic data through the application of biological knowledge formalized in ontologies; the extraction of knowledge from biological and biomedical data; use of formal knowledge representation tools in the field of computational biology; development of algorithms for the analysis of biological and biomedical networks through the application of graph theory. She is a Member of BITS (Bioinformatics Italian Society). She is serving as a reviewer for several scientific journals as well as for national and international conferences, and as a chair and program committee member of several national and international conferences, managing many special issues.

Giuseppe Agapito is an assistant professor and a senior research scientist in the field of Parallel and Distributed Computing, Machine Learning, Omics and Biological Networks data Analysis at the University Magna Græcia, of Catanzaro, Italy. His research interests are focused on the study of machine learning methods that can be used to take advantage of the vast amount of data that are

produced nowadays. In particular, the research focuses on the development, implementation, and application of computational intelligence techniques for addressing complex real-world problems in different domains, especially in the field of biology and omics sciences. From 2017 to today He co-organized and chaired the International Workshop "Bioinformatics' Challenges to Computer Science" (BBC), in conjunctions with the International Conference on Computational Science (ICCS). From 2018 to today He co-organized and chaired the International Workshop "Parallel and Cloud-based Bioinformatics and Biomedicine" (ParBio), in conjunctions with the ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB). He co-organized and co-chaired the "1st International Workshop on Novel Data Mining Methods for the Analysis of High-Throughput Biological Data (DM-HT-D)", in conjunction with the 20th IEEE International Conference on Data Mining IEEE ICDM 2020. He organized and chaired the International Special Track "Biological Network Analysis in Computational Biology and Biomedicine" in conjunctions with IEEE International Symposium on Computer-Based Medical Systems (CBMS), 2017. He is serving as a reviewer for several scientific journals as well as for national and international conferences, and as a chair and program committee member of several national and international conferences, managing many special issues.

Organization/Editorial activities:

Workshop/Track chair:

- Workshop on High Performance Bioinformatics and Biomedicine (HiBB), held in the past at the IEEE BIBM Conference (2015-2022) and Euro-Par Conference (2010-2014).
- Workshop on Bioinformatics' Challenges to Computer Science, held at ICCS Conference (2008-2022).
- Workshop on Parallel and Cloud-based Bioinformatics and Biomedicine (ParBio), held at ACM-BCB Conference (2012-2022)

Editorial Board Member:

- Editor-in-Chief of the Encyclopedia of Bioinformatics and Computational Biology 2nd Ed.
- Encyclopedia of Bioinformatics and Computational Biology, Elsevier (2016-now)
- Briefings in Bioinformatics (2012-now)
- High-Throughput (ISSN 2571-5135), MDPI (2017-now)
- Future Generation Computer Systems, Elsevier (2012-2016)
- The Open Proteomics Journal, BENTHAM OPEN (2009, 2010, 2011, 2012-now)
- The Open Medical Informatics Journal, BENTHAM OPEN (2009, 2010, 2011, 2012-now)
- The International Journal of Web Portals, IGI Global (2011, 2012-now)

List of PC Members will be defined as soon as possible.

CALL FOR PAPERS

This Workshop discusses the advantages provided from novel solutions in Health Informatics for data modeling and knowledge extraction, by focusing the attention on network and pathway analysis. Genomics data are usually acquired from massive parallel sequencing technologies (e.g., Next Generation Sequencing - NGS) applied to DNA- and RNA- sequencing (DNA-seq and RNA-seq). It is investigated, e.g., in Genome-Wide Association Studies (GWAS) to provide a deep insight into

biological systems. In the last decade, novel methodologies in Health Informatics have been applied to encode biological functions at molecular, cellular, and tissue system levels. In this context, the pathway and network analysis are important research targets to give meaning to high-throughput biological data, to investigate genome-wide genetic markers and their breeding value, or to extract knowledge from multi-omics data; to give a practical example, the pathway analysis is a well-known methodology in personalized oncology. Therefore, both are relevant topics in health informatics (e.g., genomics and precision medicine).

Papers focused on health informatics, molecular and systems biology, including reviews of software tools and methods, are considered relevant to the topic under discussion. The Workshop will discuss the use of novel technologies, architectures and models in Health Informatics, e.g., to develop novel high-performance and/or parallel networks-based applications (e.g., algorithms, software tools, methodologies) for biological and -omics data processing, by bringing together scientists in the fields of bioinformatics, data science, and health informatics, as well as scientists working in application-related fields (e.g., biology and medicine).

Topics of interest

The workshop will consider articles describing novel computational algorithms and software tools, data models, as well as novel methodologies based on artificial intelligence and systems biology. Papers must focus on original research contributions related to scientific knowledge currently published in literature, and/or formal assessments of software tools and methodologies for the following topics of interest (but are not limited to):

- Networks-based applications for healthcare;
- Pathway analysis in Health Informatics;
- Networks Analysis (e.g., alignment, motif discovery);
- Data representation and analysis in healthcare;
- Graph representation learning for visualizing and interpreting medical data;
- Complex network models for structure and function analysis in health informatics;
- Artificial intelligence in healthcare;
- Non- conventional architectures (e.g., GPUs, FPGAs) for network and pathway analysis.