Special Sessions

MODELING AND SIMULATION METHODS FOR COMPUTATIONAL BIOLOGY AND SYSTEMS MEDICINE

Aims and scope:
Computational Biology deals with the analysis of biological systems at different scales of complexity, by means of proper modeling frameworks and computational methods. Given that Computational Biology approaches are becoming well established, the challenge is now to apply the developed techniques towards the definition of personalized models in order to identify individually tailored drugs and treatments; i.e. to realize the Personalized Medicine paradigm. The scope of this special session is to bring together researchers involved in the development of methods applied to the fields of Computational Biology and Systems Medicine.

Topics of interest include but are not limited to:

- analysis of robustness of cellular networks
- biomedical model parameterization
- cancer progression models
- epidemiological models
- clinical image analysis
- emergent properties in complex biological systems
- flux balance analysis
- metabolic engineering
- metabolic pathway analysis
- model verification and refinement methods
- models of neural activity
- multiscale modelling and simulation of biological systems
- parameter estimation methods
- personalized models
- reverse engineering of reaction networks
- software tools for computational biology
- space-temporal modelling and simulation of biological systems

Organizers:

NEWS

July 12, 2019:
List of accepted papers

July 10, 2019:
Early Bird Registration
Deadline Extension: 22
2019

May 16, 2019:
Final Deadline Extensio
June 2019

May 11, 2019:
Registration is now ope

April 29, 2019:
Deadline Extended: 15
2019

April 1, 2019:
Submission of papers is
open

March 8, 2019:
List of keynote speaker

March 4, 2019:
List of accepted special

October 1, 2018:
Call for special sessions
tutorials available

PAST CONFERENC

CIBB 2018

CIBB 2017

CIBB 2016

Wikipedia page

- Rosalba Giugno, Dept. of Computer Science, University of Verona, Italy
- Marco Beccuti, Dept. of Computer Science, Univ. of Turin, Italy
- Marzio Pennisi, Dept. of Mathematics & Computer Science, Univ. of Catania, Italy
- Pietro Liò, Dept. of Computer Science and Technology, Univ. of Cambridge, UK
- Marco S. Nobile, Dept. of Computer Science, Systems and Communication, Univ. of Milano-Bicocca, Italy

MACHINE LEARNING AND COMPUTATIONAL INTELLIGENCE IN MULTI-OMICS AND MEDICAL IMAGE ANALYSIS

Aims and scope:
There is an increasing need for the application of Machine Learning (ML) and Computational Intelligence (CI) techniques that can effectively perform image processing operations such as segmentation, co-registration, classification, and dimensionality reduction in the fields of neuroimaging and oncological imaging. Although the manual approach often remains the golden standard in some tasks (e.g., segmentation), ML can be exploited to automate and facilitate the work of researchers and clinicians. Frequently used techniques include Support Vector Machines (SVMs) for classification problems, graph-based methods, and Artificial Neural Networks (ANNs). More recently, deep ANNs have shown to be very successful in computer vision tasks owing to the ability to automatically extract hierarchical descriptive features from input images. It has also been used in the oncological and neuroimaging domains for automatic disease diagnosis, tissue segmentation, and even synthetic image generation. The main issue, however, remains the relative sample paucity in typical imaging datasets that leads to a poor generalisation of the employed deep ANNs, considering the high number of required parameters. Consequently, parameter-efficient design paradigms specifically tailored to medical applications ought to be devised, also by exploiting CI-based techniques (e.g., neuroevolution).
In this context, these advanced ML techniques can be suitably exploited to combine heterogeneous sources of information, allowing for multi-omics data integration. Such a kind of analyses may represent a significant step towards personalised medicine.

Topics of interest include but are not limited to:

- Machine Learning techniques for segmentation, co-registration, classification, or dimensionality reduction of medical images
- Deep Learning for neuroimaging and oncological imaging analysis
- Integration of multi-omics data
- Brain network analysis
- Application of graph theory to MRI and fMRI data
- Application of machine learning methodologies for neurodegenerative disease studies
- Computational modelling and analysis of neuroimaging
- Methods of analysis for structural or functional connectivity
- Development of new neuroimaging tools
- Radiomic analyses for tumour phenotypes
- Radiogenomics for intra- and inter-tumoural heterogeneity evaluation
- Generative adversarial models for data augmentation
- Computational Intelligence methods for optimizing medical image analysis tasks

Organizers:

- Giovanna Maria Dimitri, Computer Laboratory, University of Cambridge, Cambridge, UK
- Tiago Azevedo, Computer Laboratory, University of Cambridge, Cambridge, UK
- Leonardo Rundo, Department of Radiology, University of Cambridge, Cambridge, UK
- Andrea Tangherloni, Department of Haematology, University of Cambridge, Cambridge, UK
- Jin Zhu, Computer Laboratory, University of Cambridge, Cambridge, UK

MACHINE LEARNING IN HEALTHCARE INFORMATICS AND MEDICAL BIOLOGY

Aims and scope:
Machine learning has become a pivotal tool to analyze biomedical and biological datasets, especially in the Big Data era. In fact, machine learning algorithms can identify hidden relationships and structures in health care data, and even take advantage of them to make accurate predictions about similar or future data instances. For example, machine learning software has been able to predict the diagnosis of tumor patients just by processing

patients' clinical features, allowing scientists to save time and money compared to wet lab experiments.
Computational researchers have also exploited machine learning to infer knowledge about patients by analyzing biological datasets, especially the ones featuring genetics and epigenomic traits. Data mining approaches applied to such datasets, in fact, can lead to relevant discoveries both to understand molecular biology and to gain new knowledge about patients' diseases.
Our special session on "Machine Learning in Healthcare Informatics and Medical Biology" aims at boosting these scientific fields, calling for researchers able to show the potential and the advance of machine learning algorithms to make accurate computational predictions in health care datasets and in patient-oriented biological datasets.

Topics in this special session include:

- Machine learning methods applied to health care and biomedical datasets;
- Machine learning methods applied to genetics, and epigenomics datasets, aimed at better understanding the conditions of healthy individuals (controls) and/or sick patients;
- Machine learning methods applied to biological datasets, aimed at better understanding the underlying biomolecular scenario;
- Machine learning software and tools in the healthcare and biological domain;
- Statistical models to analyze healthcare, biomedical, and biological datasets;
- Data mining applications in the healthcare and biological domain.

Organizers:

- Davide Chicco, Peter Munk Cardiac Centre, Toronto, Ontario, Canada
- Anne-Christin Hauschild, Philipps-Universität Marburg, Marburg, Germany
- Mickael Mendez, University of Toronto, Toronto, Ontario, Canada
- Giuseppe Jurman, Fondazione Bruno Kessler, Trento, Italy
- Joao Ribeiro Pinto, Instituto de Engenharia de Sistemas e Computadores Tecnologia e Ciencia, Porto, Portugal

Special session website:
https://davidechicco.github.io/cibb2019specialsession/

ALGEBRAIC AND COMPUTATIONAL METHODS FOR THE STUDY OF RNA BEHAVIOUR

Aims and Scope:
The study of RNA molecules has given rise to a wide range of open problems, from the prediction of spatial conformations to the comprehension of the relation between their structures and functions. A deeper understanding of these issues has great scientific relevance and paves the way for novel applications in medicine and pharmacology. Such a huge potential has attracted interest from different disciplines, theoretical and applied as well as computational and experimental. Nevertheless, achieving any real advancesin this field requires the effort to pull together methodologies and expertise from all these even distant approaches.
The aims of our special session are to gather scientists (from various disciplinary background) whose studies address RNA molecules, and facilitate the integration of different research areas. We encourage the presentation of main objectives and preliminary results of active studies and surveys.
In recent years, emerging techniques have come into play alongside the more "traditional" ones. Formal languages, process algebras, computational topology, quantum information processing, and learning algorithms were found to be decisive in facing the complexity of RNA modeling. The main goal of our special session is to highlight the advantages and limitations of these alternative points of view, to show how they can steer RNA modeling towards new directions. We want to promote the interplay of such different disciplines to widen our ability to understand RNA behaviour, also from a computational point of view.

Topics of interest include, but are not limited to:

- RNA structure and functions entangled relation
- Higher order RNA properties
- RNA 2D and 3D structure analysis and prediction
- RNA-RNA/RNA-protein interactions
- RNA structures comparison
- RNA kinetics
- Long non-coding RNAs (lncRNA)
- RNA pattern recognition, clustering and classification
- RNA force fields and simulation
- RNA inverse folding

- RNA-nanoparticles interaction
- Nanoparticles for RNA delivery

Organizers:

- Emanuela Merelli, University of Camerino, Italy
- Stefano Maestri, University of Camerino, Italy
- Michela Quadrini, University of Camerino, Italy

Special session website:
http://www.emanuelamerelli.eu/bigdata/algebraicrna

ENGINEERING BIO-INTERFACES AND RUDIMENTARY CELLS AS A WAY TO DEVELOP SYNTHETIC BIOLOGY

Aims and scope:
The bioengineering has been fundamental in both regenerate medicine and the understanding of biochemical mechanisms involved in life appearance and maintenance. The aim of this special session is to bring together theoretical researchers interested in cutting-edge methods to address the challenges posed by the huge amount of data produced in omics sciences and in application to systems and synthetic biology and experimental researchers with interests on develop experimentally new approaches of synthetic biology for biomedical and biotechnological applications like implants, artificial organs, advanced medical systems, drug delivery systems and sensors. The track of this SS aims to present latest experimental advancements concerning synthetic biology.

Relevant topics within this context include, but are not limited to:

- physical interactions between biological molecules,
- effect of radiation and plasma in biological tissues,
- cell-nanomaterials interactions,
- molecular aspects of membrane assembly and transport,
- communication between cells,
- biosensors at micro and nanoscales,
- drug delivery systems,
- liposomes and encapsulation of molecules,
- synaptic transmission,
- artificial organs and contractile systems.

Organizers:

- Maria Raposo, Universidade Nova de Lisboa, Portugal
- Quirina Ferreira, Universidade de Lisboa, Portugal
- Paulo A. Ribeiro, Universidade Nova de Lisboa, Portugal
- Susana Sério, Universidade Nova de Lisboa, Portugal
- Filipa Pires, Universidade Nova de Lisboa, Portugal
- Cláudia Lage, Universidade Federal do rio de janeiro, Brazil

INTELLIGENCE METHODS FOR MOLECULAR CHARACTERIZATION AND DYNAMICS IN TRANSLATIONAL MEDICINE

Aims and scope:
The growth of single cell technologies combined with high throughput sequencing opened new frontiers in translational medicine and basic biology by shedding lights on the behavior of the cells in their environment, like the tissue, over time and providing deeper view of functional genomics at single cell resolution. In cancer research field, for example, the mutational profile of an expanded clone in an infiltrated tissue can be tracked over time dissecting the functional role of the acquired mutations and characterizing its evolution. In gene therapy, clonal tracking by retroviral vector integration site analysis directly supported the assessment of safety and long term efficacy of the treatment and became a requirement in the monitoring procedures for commercialized medical products by regulatory authorities. Moreover, the *in vivo* characterization of the dynamics of vector marked clones over time and tissues revealed biological insights of stem cells activity in several clinical and preclinical gene therapy applications. Clonal studies at molecular level are also important in other translational research fields such as immunotherapies or HIV-1.

The emerging research interest in the molecular characterization of clones over time required novel Bioinformatics methodologies, covering different disciplines and topics from mathematical modeling to population based statistics, somatic mutation search and profiling, clonal evolution and phylogenetic reconstruction. This special session is focused on the bioinformatics procedures related to clonal tracking and dynamics, and single cell applications to translational biomedicine with the aim of presenting novel methodological approaches and their applications.

Relevant topics within this context include, but are not limited to:

- Clonal tracking and clonal dynamics in vivo
- Patient characterization by molecular analysis
- Single cell technologies for translational research
- Statistical methods for clonal dynamics
- Mathematical modeling of patient clones over time
- Ecological and population based studies applied to clonal characterization
- Functional characterization of clonal repertoire
- Bioinformatics for genome editing and precision medicine
- Computational technologies for NGS data handling

Organizers:

- Andrea Calabria, San Raffaele Telethon Institute for Gene Therapy, Italy

SOFT COMPUTING METHODS FOR CHARACTERIZING DISEASES FROM OMICS DATA

Aims and scope:
In modern biomedical research, high-throughput technologies, such as the next generation sequencing, produces huge data sets. High-throughput data are collected in the broad context of genomics, epigenomics, transcriptomics and proteomics. From these data, it is possible to explain the pathogenesis or predict the predisposition and/or the clinical outcome of several human diseases, among which psychiatric, cardiovascular, obesity, aetiology of a number of diseases such as cancer, schizophrenia, and Alzheimer, just to name a few. The identification of new strategies for processing and analyzing such kind of data is becoming more and more necessary since their large amount of data can sometimes represent a real obstacle to effectively identify the most relevant patterns and to build comprehensive models capable of explaining complex biological phenotypes. The aim of the special session is to host original papers and reviews on recent research advances and the state-of-the-art methods in the fields of Soft Computing, Machine Learning and Data Mining methodologies concerning with the processing of omics data in order to shed light about the relationship between genotype and disease-related phenotype.

Relevant topics within this context include, but are not limited to:

- Machine learning
- Sparse Coding
- Data Mining
- Fuzzy and Neuro-Fuzzy Systems
- Probabilistic and statistical modelling
- OMICs in the context of genomics, epigenomics, transcriptomics anroteomics
- Evaluation of protein folding and/or protein-ligand interactions (wher ligands are proteins, DNA, RNA and small molecules), also in the context of genetic variation
- Identification of potential gene regulatory elements (i.e., binding oranscription factors, miRNAs, etc.)
- Analysis of common genetic variants (i.e., SNPs, HLA genotypesicrosatellites)
- Analysis of experimental data from next-generation sequencing
- Analysis of gene expression data
- Biomedical applications

Organizers:

- Angelo Ciaramella, University of Napoli Parthenope, Italy
- Giosuè Lo Bosco, University of Palermo, Italy
- Alberto Paccanaro, Royal Holloway University of London, United Kingdom
- Umberto Ferraro Petrillo, Università di Roma - La Sapienza, Italy

- Antonino Staiano, University of Napoli Parthenope, Italy
- Giorgio Valentini, Università degli Studi di Milano, Italy

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