

HOME	CALLS	PROGRAM	SESSIONS	KEYNOTE	REGISTRATION	ORGANISATION	EVENTS	TRAVEL
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Provisional program

September 4, Wednesday		September 5, Thursday		September 6, Friday	
8:30 - 9:30	Registration	9:00 - 10:00	Keynote Speaker: Prof. Uzey Kaymak	9:00 - 10:00	Keynote Speaker: Prof. M. Luz Calle Rosignara
9:30 - 9:40	Opening	10:00 - 10:30	Coffee break	10:00 - 10:30	Coffee break
9:40 - 10:40	Keynote Speaker: Dr. Ana Cvejic	10:30 - 12:40	SPECIAL SESSION: Machine Learning in Healthcare Informatics and Medical Biology (Papers 19, 24, 27, 38, 17, 21, 22)*	10:30 - 12:40	SPECIAL SESSION: Modeling and Simulation Methods for Computational Biology and Systems Medicine (Papers 5, 36, 39, 41, 42, 48, 51)*
10:40 - 11:10	Coffee break	12:40 - 14:00	Lunch	12:40 - 14:00	Lunch
11:10 - 12:40	MAIN TRACK SESSION 1 (Papers 46, 45, 37, 34, 50)*	14:00 - 14:50	Invited Speaker: Prof. Marco Masierotti	14:00 - 16:20	SPECIAL SESSION: Algebraic and Computational Methods for the Study of RNA Behaviour (Papers 6, 9, 40, 47, 40, 46, 43)*
12:40 - 14:00	Lunch	14:50 - 16:20	SPECIAL SESSION: Machine Learning in Healthcare Informatics and Medical Biology (Papers 30, 25, 2, 31, 44)*	16:20 - 16:50	Coffee break
14:00 - 14:30	CIBB Meeting	16:20 - 16:50	Coffee break	16:50 - 18:00	MAIN TRACK SESSION 4 (Papers 28, 56, 33, 35)*
14:30 - 16:20	SPECIAL SESSION: Intelligence methods for molecular characterization and dynamics in translational medicine (Papers 62, 63, 65, 46, 59, 20)*	16:50 - 18:40	MAIN TRACK SESSION 3 (Papers 49, 58, 10, 18, 57, 29)*	18:00 - 18:15	Farewell
16:20 - 16:50	Coffee break				
16:50 - 18:40	MAIN TRACK SESSION 2 (Papers 11, 7, 32, 15, 43, 50)*	20:00 -	Social Dinner		*paper number refers to EasyChair ID

The detailed version of the program can be downloaded [here](#)

LIST OF ACCEPTED PAPERS

Main track

- Maria Raposo. **Computational Intelligence Methods as tools to develop Sensors of Molecular Traces in Complex Systems**
- The Tien Mai, Leiv Ronneberg, Zhi Zhao, Manuela Zucknick and Jukka Corander. **Composite local low-rank structure in learning drug sensitivity**
- Angela Serra, Antonio Federico and Dario Greco. **Integrative analysis with regularised random forest for toxicity prediction**
- Eleonora Cappelli, Emanuel Weitschek and Fabio Cumbo. **Extending knowledge on genomic data and metadata of cancer by exploiting taxonomy-based relaxed queries on domain-specific ontologies**
- Alberto Dennuzio, Enrico Formenti, Luciano Margara, Valentin Montmirail and Sara Riva. **Solving Equations on Discrete Dynamical Systems**
- André Veríssimo, Marta Lopes, Eunice Carrasquinha and Susana Vinga. **Random sample consensus for the robust identification of outliers in cancer data**
- Işıksoy Ekşioğlu and Mehmet Tan. **Prediction of Drug Synergy by Ensemble Learning**
- Ryan Mitchell, David Cairns, Kevin Pollock and Carron Shankland. **Effective use of evolutionary computation to parameterise an epidemiological model**
- Thais Priscilla Pivetta, Carlota J.F. Conceição, Filipa Pires, Paulo A. Ribeiro and Maria Raposo. **Liposomes as a drug delivery system for a novel class of anticarcinogenic agents**
- Manuel Anacleto, Susana Vinga and Alexandra M Carvalho. **MSAX: Multivariate symbolic aggregate approximation for time series classification**
- Mohammad Mehdi Hosseinzadeh, Riccardo Dondi, Giancarlo Mauri and Italo Zoppis. **A New Heuristic to Find Overlapping Dense Subgraphs in Biological Networks**
- Moritz Kulesa, Eneldo Loza Mencía and Johannes Fürnkranz. **Improving the Fusion of Outbreak Detection Methods with Supervised Learning**
- Simone Spolaor. **Hybrid modeling of biological systems with FuzzX**
- Guillaume Fertin, Matthieu David, Dominique Tessier and Hélène Rogniaux. **MS/MS spectra interpretation and the interest of SpecFit for identifying uncommon modifications**
- Meysam Roodi, Zahra Lak and Andreas Moshovos. **Skip-Pass: Accelerating BWA-MEM Aligner**
- Isis Bonet, Alejandro Peña, Christian Lochmuller, Héctor Alejandro Patiño and Mario Gongora. **Deep Clustering for Metagenomics**
- Meysam Roodi. **SW+: On Accelerating Smith-Waterman Execution of GATK HaplotypeCaller**

NEWS

August 21, 2020: [the BMC Medical Informatics supplement of the special session on Machine Learning in Healthcare Informatics and Medical Biology](#) has been published

July 12, 2019: [List of accepted papers](#)

July 10, 2019: [Early Bird Registration Deadline Extension: 22 July 2019](#)

May 16, 2019: [Final Deadline Extension: 9 June 2019](#)

May 11, 2019: [Registration is now open](#)

April 29, 2019: [Deadline Extended: 15 May 2019](#)

April 1, 2019: [Submission of papers is now open](#)

March 8, 2019: [List of keynote speakers](#)

March 4, 2019: [List of accepted special sessions](#)

October 1, 2018: [Call for special sessions and tutorials available](#)

PAST CONFERENCES

CIBB 2018
CIBB 2017
CIBB 2016
Wikipedia page

- Daniele D'Agostino, Ivan Merelli, Marco Aldinucci and Pietro Liò. **NeoHiC: a web application for the analysis of Hi-C data**
- Lucrezia Patruno, Edoardo Galimberti, Daniele Ramazzotti, Giulio Caravagna, Luca De Sano, Marco Antoniotti and Alex Graudenzi. **cyTRON and cyTRON/JS: two Cytoscape-based applications for the inference of cancer evolution models**
- Guillaume Zamora, Caro Fuchs, Aurélie Degeneffe, Pieter Kubben and Uzay Kaymak. **A clinical decision support system by using wrist-worn smartphone tremor measurements**
- Changhee Han, Leonardo Rundo, Kohei Murao, Zoltán Ádám Milacski, Kazuki Umemoto, Hideki Nakayama and Shin'Ichi Satoh. **GAN-based Multiple Adjacent Brain MRI Slice Reconstruction for Unsupervised Alzheimer's Disease Diagnosis**

Special Session: Modeling and Simulation Methods for Computational Biology and Systems Medicine

- Paola Lecca and Angela Re. **Analysis of Observability of Bacterial Growth Models**
- Eric Nisoli, Marco S Nobile, Thalia Vlachou, Pier Giuseppe Pelicci and Paolo Cazzaniga. **GPU-powered investigation of cell proliferation**
- Mattia Rovetta, Daniela Besozzi and Renata Tisi. **Modeling calcium signaling in *S. cerevisiae* cells in response to hypotonic shock**
- Marzio Pennisi, Giulia Russo, Giuseppe Sgroi, Giuseppe Alessandro Parasiliti Palumbo and Francesco Pappalardo. **In Silico simulation of Daclizumab effects using Agent Based Models**
- Nicola Bombieri, Simone Caligola, Antonio Mastrandrea, Silvia Scaffeo, Tommaso Carlucci, Franco Fummi, Carlo Laudanna, Gabriela Constantin and Rosalba Giugno. **Modelling, Simulation, and Tuning of Metabolic Networks Through Electronic Design Automation**
- Giulia Paiardi, Chiara Urbinati, Paola Chiodelli, Alessandro Orro, Matteo Uggeri, Luciano Milanese, Marco Rusnati and Pasqualina D'Ursi. **Implementation of an incremental docking method to study long-sugar chains interactions with proteins**
- Simone Pernice, Marco Beccuti, Greta Romano, Marzio Pennisi, Alessandro Maglione, Santina Cutrupi, Francesco Pappalardo, Lorenzo Capra, Giuliana Franceschinis, Massimiliano De Pierro, Gianfranco Balbo, Francesca Cordero and Raffaele Calogero. **Multiple Sclerosis disease: a computational approach for investigating its drug interactions**

Special session: Machine Learning in Healthcare Informatics and Medical Biology

- Giuseppe Agapito, Mario Cannataro, Pietro Hiram Guzzi and Marianna Milano. **Learning Weighted Association Rules in Human Phenotype Ontology**
- Rohit Pardasani, Rupanjali Chaudhuri, Sushma Maya, Sheetal Chaurasia and Navchetan Awasthi. **Quantitative Assessment of Respiratory Distress using CNN for Multivariate Time Series Segmentation**
- Gaia Ceddia, Sara Pidò and Marco Masseroli. **Computational analysis and comparison of gene networks from TCGA normal and cancer data**
- Erica Tavazzi, Sebastian Daberdaku, Alessandro Zandonà, Rosario Vasta, Andrea Calvo, Adriano Chiò and Barbara Di Camillo. **An Adaptive K-Nearest Neighbours Algorithm for the Imputation of Static and Dynamic Mixed-Type Clinical Data**
- Davide Chicco, Augustin Toma, Pingzhao Hu and Patrick R. Lawler. **Machine learning driven prediction of heart failure from gene expressions of patients with ST segment elevation myocardial infarction (STEMI)**
- Steffen Albrecht, Miguel A. Andrade-Navarro and Jean-Fred Fontaine. **Machine learning application to assess the quality of early stage next-generation sequencing data**
- Francisco Cristovao, Arif Canakoglu, Mark Carman, Silvia Cascianelli, Luca Nanni, Pietro Pinoli and Marco Masseroli. **Comparing classic, deep and semi-supervised learning for whole-transcriptome breast cancer subtyping**
- Alberto Pinheira, Camila Nascimento, Rodrigo Dias and Inês Dutra. **Characterizing the profile of bipolar disorder-associated single nucleotide polymorphisms in a large UK cohort**
- Mafalda Falcão Ferreira, Rui Camacho and Luis Teixeira. **Autoencoders as Weight Initialization of Deep Classification Networks for Cancer vs. Cancer Studies**
- Pierre Michel, Nicolas Ngo, Jean-François Pons, Stéphane Delliaux and Roch Giorgi. **A filter approach for feature selection in classification: application to atrial fibrillation detection in ECG recordings**
- Eunice Carrasquinha, João Santinha, Alexander Mongolin, Maria Lisitskiya, Joana Ribeiro, Fátima Cardoso, Leonardo Vanneschi and Nickolas Papanikolaou. **Regularization techniques in Radiomics: A case study on the prediction of pCR in Breast Tumours and the Axilla**
- Federico Cabitza and Andrea Seveso. **Ordinal Labels in Machine Learning: A User-centered Approach to Improve Data Validity in Medical Settings**

- Bruno Galuzzi, Mirko Gaslini, Antonio Candelieri, Ilaria Giordani, Gaia Arosio and Francesco Archetti. **A Tool for Anomaly Detection in ECG Signals to support health medical Decisions**

Special session: Algebraic and Computational Methods for the Study of RNA Behaviour

- Semyon Grigorev, Yuliya Susanina and Anna Yaveyn. **Modification of Valiant's Parsing Algorithm for String-searching Problem**
- Maria Waldl, Sebastian Will, Michael Wolfinger, Ivo Hofacker and Peter F. Stadler. **Bi-alignments as Models of Incongruent Evolution of RNA Sequence and Structure**
- Semyon Grigorev and Polina Lunina. **On Secondary Structure Analysis by using Formal Grammars and Artificial Neural Networks**
- Stefano Maestri and Emanuela Merelli. **Process-based Modelling of Non-coding RNA Functions**
- Michela Quadrini, Emanuela Merelli and Riccardo Piergallini. **Label Core for Understanding RNA-RNA Interactions**
- Alessio Mancini and Sandra Pucciarelli. **Innovative Computational Approaches for the Comprehension of mRNA Intron Retention**
- Gianvito Grasso, Filip Stojceski and Andrea Danani. **Coarse-Grained Molecular Simulations to Investigate the Supramolecular Properties of Polycations-RNA Binding Dynamics**

Special Session: Intelligence methods for molecular characterization and dynamics in translational medicine

- Marilisa Montemurro, Elena Grassi, Gianvito Urgese, Emanuele Parisi, Carmelo Gabriele Pizzino, Andrea Bertotti and Elisa Ficarra. **Single-cell DNA Sequencing Data: A Pipeline for Multi-sample Analysis**
- Davide Maspero, Marzia Di Filippo, Dario Pescini, Giancarlo Mauri, Marco Vanoni, Alex Graudenzi and Chiara Damiani. **Integration of Single-cell RNA-sequencing Data into Flux Balance Cellular Automata**
- Serena Scala, Luca Basso-Ricci, Francesca Dionisio, Danilo Pellin, Stefania Giannelli, Federica Andrea Salerio, Maria Pia Cicalese, Francesca Ferrua, Alessandro Aiuti and Luca Biasco. **In vivo tracking of hematopoietic progenitors in humans unveils resilience of hematopoietic stem cells and long-term survival of lymphoid precursors.**
- Adriano De Marino, Andrea Calabria, Fabrizio Benedicenti, Marco Antoniotti and Eugenio Montini. **ISwap: a bioinformatics tool for index switching detection in vector integration site studies**
- Maryam Omrani, Andrea Calabria and Alessandro Aiuti. **Toward better understanding of alignment artifacts in viral vector integration sites identification**
- Luca Del Core, Andrea Calabria, Daniela Cesana, Eugenio Montini, Ernst Wit and Marco Grzegorzczak. **A Bayesian regression for clonal diversity in Gene Therapy safety studies**

CONTACT

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