

SEPTEMBER 4, 2019 – WEDNESDAY

8:30 - 9:30	REGISTRATION	
9:30 – 9:40	OPENING	
9:40 – 10:40	KEYNOTE SPEAKER: Dr. Ana Cvejic	
10:40 – 11:10	COFFEE BREAK	
11:10 – 12:40	MAIN TRACK SESSION 1	
	Chair: Riccardo Dondi	
11:10 – 11:28	Maria Raposo	Computational Intelligence Methods as tools to develop Sensors of Molecular Traces in Complex Systems
11:28 – 11:46	Isis Bonet, Alejandro Peña, Christian Lochmuller, Héctor Alejandro Patiño and Mario Gongora	Deep Clustering for Metagenomics
11:46 – 12:04	Guillaume Fertin, Matthieu David, Dominique Tessier and Hélène Rogniaux	MS/MS spectra interpretation and the interest of SpecFit for identifying uncommon modifications
12:04 – 12:22	Moritz Kulessa, Eneldo Loza Mencía and Johannes Fürnkranz	Improving the Fusion of Outbreak Detection Methods with Supervised Learning
12:22 – 12:40	Işıksu Ekşioğlu and Mehmet Tan	Prediction of Drug Synergy by Ensemble Learning
12:40 - 14:00	LUNCH	
14:00 - 14:30	CIBB MEETING	
14:30 - 16:20	SPECIAL SESSION: Intelligence methods for molecular characterization and dynamics in translational medicine	
	Chairs: Andrea Calabria, Daniela Cesana, Chiara Damiani	
14:30 - 14:48	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.
14:48 - 15:06	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
15:06 - 15:24	Luca Del Core, Andrea Calabria, Daniela Cesana, Eugenio Montini, Ernst Wit and Marco Grzegorzczuk	A Bayesian regression for clonal diversity in Gene Therapy safety studies

15:24 - 15:42	Maryam Omrani, Andrea Calabria and Alessandro Aiuti	Toward better understanding of alignment artifacts in viral vector integration sites identification
15:42 - 16:00	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
16:00 - 16:20	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
16:20 - 16:50	COFFEE BREAK	
16:50 - 18:40	MAIN TRACK SESSION 2	
	Chair: Stefano Beretta	
16:50 - 17:08	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
17:08 - 17:26	The Tien Mai, Leiv Ronneberg, Zhi Zhao, Manuela Zucknick and Jukka Corander	Composite local low-rank structure in learning drug sensitivity
17:26 - 17:44	Manuel Anacleto, Susana Vinga and Alexandra M Carvalho	MSAX: Multivariate symbolic aggregate approximation for time series classification
17:44 - 18:02	Alberto Dennuzio, Enrico Formenti, Luciano Margara, Valentin Montmirail and Sara Riva	Solving Equations on Discrete Dynamical Systems
18:02 - 18:20	Meysam Roodi, Zahra Lak and Andreas Moshovos	Skip-Pass: Accelerating BWA-MEM Aligner
18:20 - 18:40	Daniele D'Agostino, Ivan Merelli, Marco Aldinucci and Pietro Liò	NeoHiC: a web application for the analysis of Hi-C data

SEPTEMBER 5, 2019 – THURSDAY

9:00 – 10:00	KEYNOTE SPEAKER: Prof. Uzay Kaymak	
10:00 – 10:30	COFFEE BREAK	
10:30 - 12:40	SPECIAL SESSION: Machine Learning in Healthcare Informatics and Medical Biology	
	Chair: Davide Chicco	
10:30 - 10:48	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
10:48 - 11:06	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
11:06 - 11:24	Mafalda Falcão Ferreira, Rui Camacho and Luis Teixeira	Autoencoders as Weight Initialization of Deep Classification Networks for Cancer vs. Cancer Studies
11:24 - 11:42	Federico Cabitza and Andrea Seveso	Ordinal labels in machine learning: a user-centered approach to improve data validity in medical settings
11:42 - 12:00	Gaia Ceddia, Sara Pidò and Marco Masseroli	Computational analysis and comparison of gene networks from TCGA normal and cancer data
12:00 - 12:18	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
12:18 - 12:40	Steffen Albrecht, Miguel A. Andrade-Navarro and Jean-Fred Fontaine	Machine learning application to assess the quality of early stage next-generation sequencing data
12:40 - 14:00	LUNCH	
14:00 - 14:50	INVITED SPEAKER: Prof. Marco Masseroli	
14:50 - 16:20	SPECIAL SESSION: Machine Learning in Healthcare Informatics and Medical Biology	
	Chair: Angela Serra	
14:50 - 15:08	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
15:08 - 15:26	Alberto Pinheira, Camila Nascimento, Rodrigo Dias and Inês Dutra	Characterizing the profile of bipolar disorder-associated single nucleotide polymorphisms in a large UK cohort

15:26 - 15:44	Giuseppe Agapito, Mario Cannataro, Pietro Hiram Guzzi and Marianna Milano	Learning Weighted Association Rules in Human Phenotype Ontology
15:44 - 16:02	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)
16:02 - 16:20	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
16:20 - 16:50	COFFEE BREAK	
16:50 - 18:40	MAIN TRACK SESSION 3	
	Chair: Simone Spolaor	
16:50 - 17:08	Meysam Roodi	SW+: On Accelerating Smith-Waterman Execution of GATK HaplotypeCaller
17:08 - 17:26	Changhee Han, Leonardo Rundo, Kohei Muraio, 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
17:26 - 17:44	Angela Serra, Antonio Federico and Dario Greco	Integrative analysis with regularised random forest for toxicity prediction
17:44 - 18:02	André Veríssimo, Marta Lopes, Eunice Carrasquinha and Susana Vinga	Random sample consensus for the robust identification of outliers in cancer data
18:02 - 18:20	Guillaume Zamora, Caro Fuchs, Aurélie Degeneffe, Pieter Kubben and Uzay Kaymak	A clinical decision support system by using wrist-worn smartphone tremor measurements
18:20 - 18:40	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

SEPTEMBER 6, 2019 – FRIDAY

9:00 – 10:00	KEYNOTE SPEAKER: Prof. M. Luz Calle Rosingana	
10:00 – 10:30	COFFEE BREAK	
10:30 - 12:40	Special session: Modeling and Simulation Methods for Computational Biology and Systems Medicine	
	Chair: Marco Beccuti	
10:30 - 10:48	Paola Lecca and Angela Re	Analysis of observability of bacterial growth models
10:48 - 11:06	Eric Nisoli, Marco S Nobile, Thalia Vlachou, Pier Giuseppe Pelicci and Paolo Cazzaniga	GPU-powered investigation of cell proliferation
11:06 - 11:24	Mattia Rovetta, Daniela Besozzi and Renata Tisi	Modeling calcium signaling in <i>S. cerevisiae</i> cells in response to hypotonic shock
11:24 - 11:42	Marzio Pennisi, Giulia Russo, Giuseppe Sgroi, Giuseppe Alessandro Parasiliti Palumbo and Francesco Pappalardo	In Silico simulation of Daclizumab effects using Agent Based Models
11:42 - 12:00	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
12:00 - 12:18	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.
12:18 - 12:40	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.
12:40 - 14:00	LUNCH	
14:00 - 16:20	Special session: Algebraic and Computational Methods for the Study of RNA Behaviour	
	Chair: Emanuela Merelli	
14:00 - 14:20	Semyon Grigorev, Yuliya Susanina and Anna Yaveyn	Modification of valiant's parsing algorithm for string-searching problem
14:20 - 14:40	Maria Waldl, Sebastian Will, Michael Wolfinger, Ivo Hofacker and Peter F. Stadler	Bi-alignments as models of incongruent evolution of RNA sequence and structure

14:40 - 15:00	Semyon Grigorev and Polina Lunina	On secondary structure analysis by using formal grammars and artificial neural networks
15:00 - 15:20	Michela Quadrini, Emanuela Merelli and Riccardo Piergallini	Label Core for Understanding RNA-RNA Interactions
15:20 - 15:40	Alessio Mancini and Sandra Pucciarelli	Innovative Computational Approaches for the Comprehension of mRNA Intron Retention
15:40 - 16:00	Stefano Maestri and Emanuela Merelli	Process-based modelling of non-coding RNA functions
16:00 - 16:20	Gianvito Grasso, Filip Stojceski and Andrea Danani	Coarse-Grained Molecular Simulations to Investigate the Supramolecular Properties of Polycations-RNA Binding Dynamics
16:20 - 16:50	COFFEE BREAK	
16:50 - 18:00	MAIN TRACK SESSION 4	
	Chair: Marco S. Nobile	
16:50 - 17:08	Ryan Mitchell, David Cairns, Kevin Pollock and Carron Shankland	Effective use of evolutionary computation to parameterise an epidemiological model
17:08 - 17:26	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
17:26 - 17:44	Mohammad Mehdi Hosseinzadeh, Riccardo Dondi, Giancarlo Mauri and Italo Zoppis	A New Heuristic to Find Overlapping Dense Subgraphs in Biological Networks
17:44 - 18:00	Simone Spolaor	Hybrid modeling of biological systems with FuzzX
18:00 - 18:15	FAREWELL	