



Preliminary Program

Thursday 6 September (FCT-UNL, Room 204, Building IV (E.IV))		
8:30-9:00	Opening	Reception
9:00-9:10	Organizers	Opening Ceremony
Plenary Session	Chair: <i>Brombin Chiara</i>	
9:10- 9:50	Prof. Benoit Liquet	A Unified Regularized Group PLS Algorithm Scalable to Big Data. Application on genomics data
Session A	Chair: <i>Andrea Bracciali</i>	Machine explanation – Interpretation of Machine Learning Models for Medicine and Bioinformatics
9:50-10:10	Raul V. Casana-Eslava, Ian H. Jarman, Sandra Ortega-Martorell, Paulo J. Lisboa and José D. Martínez-Guerrero.	#2. Structure finding stabilization and optimization with the PC algorithm
10:10-10:30	Ahsan Bilal, Alfredo Vellido and Vicent Ribas.	#12. Enabling interpretation of the outcome of a human obesity prediction machine learning analysis from genomic data
10:30-10:50	Fernando Luis-Ferreira, Daniel Rodrigues, João Sarraipa and Ricardo Goncalves	#41. Smartwatch Based Fall Detection System for Elders' Surveillance
10:50-11:10		Coffee Break
Session B	Chair:	Computational Intelligence Methods for Bioinformatics and Biostatistics – I
11:10 -11:30	Marco Frasca, Maryam Sepehri, Alessandro Petrini, Giuliano Grossi and Giorgio Valentini	#5. Committee-based Active Learning to Select Negative Examples for Predicting Protein Functions
11:30 -11:50	Vanessa D'Amario, Gabriele Arnulfo, Lino Nobili and Annalisa Barla	#6. Classification of epileptic activity through temporal and spatial characterization of intracranial recordings
11:50 -12:10	Vincenzo Bonnici, Simone Caligola, Antonino Aparo and Rosalba Giugno.	#11. Centrality speeds the subgraph isomorphism search up in target aware contexts
12:10-12:30	Catarina Delfino and Quirina Ferreira	#42. Real-time adsorption of a Co-octaethylporphyrin monitored with scanning tunneling microscopy
12:30-14:00		Lunch
Session C	Chair:	Fast and Efficient Solutions for Computational Intelligence Methods in Bioinformatics, Systems and Computational Biology
14:00- 14:20	Stefano Beretta, Mauro Castelli, Ivo Gonçalves and Daniele Ramazzotti.	#15. A quantitative assessment of the effect of different algorithmic schemes to the task of learning the structure of Bayesian Networks
14:20- 14:40	Andrea Tangherloni, Simone Spolaor, Leonardo Rundo, Marco S. Nobile, Paolo Cazzaniga, Giancarlo Mauri, Pietro Lio, Daniela Besozzi and Ivan Merelli.	#27. GENHAP: Evolutionary Computation for Haplotype Assembly
14:40- 15:00	Stefano Beretta, Paola Bonizzoni and Ivan Merelli.	#37. HaploVir: Inferring Viral Haplotypes from Deep Sequencing of a Mixture of Strains using a Path Decomposition Algorithm
15:00-15:20	Hassan Pazira	#19. Improved Predictor-Corrector Algorithm
15:20-15:40	Jade Hind, Abir Hussain, Dhiya Al-Jumeily, Casimiro Aday Curbelo Montañez, Basma Abdulaimma, Carl Chalmers and Paulo Lisboa	#24. Association Analysis Shift Regularisation: A Proposed Methodology for Epistasis Interaction in Genomic Studies
15:40 -16:00		Coffee Break
Session D	Chair:	Engineering Bio-Interfaces and Rudimentary Cells as a Way to Develop Synthetic Biology
16:00- 16:20	Mónica Machado and Quirina Ferreira	#43. Drug Delivery Films for Ocular Diseases Treatment
16:20-16:40	João Pereira Da Silva , Paulo Morgado Zagalo, Paulo A. Ribeiro and Maria Raposo.	#34. Adsorption of Triclosan on sensors based on PAH/PAZO thin-films: the effect of pH
16:40-17:00	Filipa Pires , Bárbara Rodrigues, Gonçalo Magalhães-Mota, Paulo António Ribeiro and Maria Raposo	#22. Effect of epigallocatechin-3-gallate on DMPC oxidation revealed by infrared spectroscopy
17:00-17:20	Thais Pivetta , Filipa Pires and Maria Raposo.	#29. Effect of EGCG on the DNA in presence of UV Radiation
17:20-17:40	Sara Pereira , Érica Pinto, Paulo Ribeiro and Susana Sério	#31. Non-Thermal Atmospheric pressure Plasmas: Generation, Sources and Applications
17:40-18:00	Gonçalo Magalhães-Mota , Filipa Pires, Paulo António Ribeiro and Maria Raposo.	#54. Detection of Triclosan Dioxins After UV Irradiation – A Preliminary Study

18:00-18:20	Telma Marques , Sam Eden, Małgorzata A. Śmiałek, Ilko Bald, Maria Raposo and Nigel J. Mason.	#47. Enhanced degradation of laser-irradiated DNA using Gold Nanoparticles
Friday 7 September (FCT-UNL, Room 204, Building IV (E.IV))		
Plenary Session	Chair: Paulo Lisboa	
9:00- 9:40	Prof. Alberto Paccanaro	Answering questions in biology and medicine by making inferences on networks
Session E	Chair:	Soft Computing Methods for Characterizing Diseases from Omics Data
9:40- 10:00	Antonino Fiannaca, Massimo La Rosa, Laura La Paglia, Alfonso Urso, Riccardo Rizzo and Giosue' Lo Bosco.	#52. Identification of Key miRNAs in regulation of PPI Networks
10:00- 10:20	Domenico Amato, Mattia Di Gangi, Giosue' Lo Bosco and Riccardo Rizzo.	#45. Recurrent Deep Neural Networks for Nucleosome Classification
10:20-10:40	Angelo Ciaramella, Davide Nardone and Antonino Staiano	#49. Compressive Sensing and Hierarchical Clustering for Microarray Data with Missing Values.
10:40-11:00		Coffee Break
Session F	Chair:	Computational Methods for Neuroimaging Analysis
11:00-11:20	Max Garagnani, Evgeniya Kirilina and Friedemann Pulvermüller.	#16. Perception-action circuits for word learning and semantic grounding: a neurocomputational model and neuroimaging study
11:20-11:40	Angela Serra, Antonio Della Pietra, Marcus Herdener, Roberto Tagliaferri and Fabrizio Esposito.	#1. Automatic discrimination of auditory stimuli perceived by the human brain
11:40-12:00	Simeon Spasov, Olaf Hauk and Seyedeh-Rezvan Farahibozorg.	#23. Decoding Semantic Word Categories from Electro- and Magnetoencephalography data
12:00-12:20	Tiago Fernandes, João Pereira, Bruno Direito, Alexandre Sayal and Miguel Castelo-Branco.	#36. Statistical validation of State-Space Granger Causality with Time- Reverse Surrogate and its boundaries in fMRI data
12:20-12:40	Razvan E. Kusztos, Giovanna Maria Dimitri and Pietro Liò	#13. Neural Models for Brain Networks Connectivity Analysis
12:40-14:00		Lunch
Plenary Session	Chair:	
14:00- 14:40	Prof. Alexandra Carvalho	Model selection for temporal biomedical data
Session G	Chair:	Networking biostatistics and bioinformatics
14:40- 15:00	Monica Chiogna, Vera Djordjilovic, Chiara Romualdi and Elisa Salviato	#4. Searching for the Source of Difference: a Graphical Model Approach
15:00- 15:20	Federica Cugnata and Paola M.V. Rancoita	#56. Improving Sensitivity and Specificity Calculation from Myocardial Imaging Data
15:20- 15:40	Luca Del Core, Eugenio Montini, Clelia Di Serio and Andrea Calabria	#55. Longitudinal Studies and Integrative Biology with Heterogeneous data: an approach using rarefaction
15:40- 16:00	Mahdi Shafiee Kamalabad and Marco Grzegorzczuk.	#3. A new partially Coupled Piece-Wise linear Regression Model for statistical network Structure Inference
16:00 -16:20		Coffee Break
Session H	Chair:	Computational Intelligence Methods for Bioinformatics and Biostatistics –III
16:20-16:40	Carlos Cano	#21. Computational Annotation of Genetic Biomarkers using Topologically Associating Domains
16:40-17:00	João Villa-Brito, Marta B. Lopes, Alexandra M. Carvalho and Susana Vinga	#40. Unravelling breast and prostate common gene signatures by Bayesian network learning
17:00-17:20	Pedro Ferreira, Alexandra Carvalho and Susana Vinga	#39. Variational inference in probabilistic single-cell RNA-seq models
17:20-17:40	Bozidar Popovic.	#51. New method for getting probability distributions with application
17:40-18:00	Laxmi Parida and Filippo Utro	#8. PiXora: Simultaneous Phasing of Multiple Polyploids
18:00-18:40	Chair: Roberto Tagliaferri	CIBB 2019 Meeting
19:00-22:30		Social Dinner
Saturday 8 September (FCT-UNL, Room 204, Building IV (E.IV))		
Plenary Session	Chair:	
9:00- 9:40	Prof. Fernando Luís Ferreira	Ethics and our moral in research, let's think about it!
Session I	Chair:	Computational Intelligence Methods for Bioinformatics and Biostatistics –IV
9:40- 10:00	Marta Lovino, Gianvito Urgese, Enrico Macii, Santa Di Cataldo and Elisa Ficarra	#14. Predicting the Oncogenic Potential of Gene Fusions using Convolutional Neural Networks
10:00-10:20	Ivan Olier, Philippa Grace McCabe, Disha Agarwal and Sandra Ortega-Martorell	#38. Benchmarking Multitask Learning for QSARS
10:20-10:40	Sebastian Daberdaku	#10. Paratope identification by classification of local antibody surface patches enriched with eight physicochemical properties
10:40-11:00	Pietro Lio and Andrea Bracciali	#58. Computational Intelligence to explore the link between diabetes and arthritis
11:00-11:20		Coffee Break
Session J	Chair:	Modeling and Simulation Methods for System Biology and System Medicine

11:20-11:30	Chiara Damiani, Dario Pescini and Marco S. Nobile	#26. Global Sensitivity Analysis of Constraint-based Metabolic Models
11:30-11:50	Ahmad Husein Alkaff, Mutiara Saragih, Mochammad Arfin Fardiansyah Nasution and Usman Sumo Friend Tambunan	#9. Inhibition of Primed Ebola Virus Glycoprotein by Peptide Compound Conjugated to HIV-1 Tat Peptide Through a Virtual Screening Approach
11:50-12:10	Niccolò Totis, Andrea Tangherloni, Marco Beccuti, Paolo Cazzaniga, Marco Nobile, Daniela Besozzi, Marzio Pennisi and Francesco Pappalardo	#44. GPU Powered Parameter Estimation of a large-Scale Kinetic Metabolic Model
12:10-12:30	Mochammad Arfin Fardiansyah Nasution, Ahmad Husein Alkaff, Ilmi Fadhilah Rizki and Usman Sumo Friend Tambunan.	#33. Pharmacophore Modelling, Virtual Screening, and Molecular Docking Simulations of Natural Product Compounds as Potential Inhibitors of Ebola Virus Nucleoprotein
12:30-14:00		Lunch
Session K	Chair: Marco Masseroli	Machine Learning in Health Informatics and Biological Systems
14:00- 14:20	Davide Castaldi, Ilaria Giordani, Antonio Candelieri, Francesco Archetti and Roberto Mattina.	#48. The Scourge of Anti-microbial Resistance: A Machine learning Approach for prescription Patterns Analytics
14:20- 14:40	Fabrizio Frasca, Matteo Matteucci, Marco Morelli and Marco Masseroli.	#32. Unveiling Gene Expression Histonic Regulative Patterns by Hyperplanes Clustering
14:40-15:00	Arif Canakoglu, Luca Nanni, Artur Sokolovsky and Stefano Ceri.	#46. Designing and Evaluating Deep Learning Methods for Cancer Classification on Gene Expression Data
15:00-15:20	Hugo Martiniano, Muhammad Asif, Astrid Vicente and Luís Correia.	#25. A Semi-supervised Learning Approach to the Identification and Prioritization of Genes Associated with Autism Spectrum Disorder
15:20-15:40	Joana Moreira, Mariana Moreira, Nuno Pombo and Nuno Garcia.	#50. Identification of real and imaginary movements in EEG using Machine Learning models
15:40 -16:00		Coffee Break
Session L	Chair:	Computational Intelligence Methods for Bioinformatics and Biostatistics –V
16:00 -16:20	Alessio Mancini, Claudio Angione, Pietro Liò and Sandra Pucciarelli.	#57. The ciliates as complex eukaryotic single cell models for studying molecular communication: an insight on the evolution of signaling molecules also involved in human brain metabolism.
16:20 -16:40	Leif Peterson and Tomothy Thompson	#61. In Silico ADME and Toxicity Prediction Using N-grams for Chemical Fingerprinting
16:40 -17:00	Cheick Tidiane Ba, Elena Casiraghi, Marco Frasca, Jessica GlioZZo, Giuliano Grossi, Marco Mesiti, Marco Notaro, Paolo Perlasca, Alessandro Petrini, Matteo Re and Giorgio Valentini	#35. A Graphical Tool for the Exploration and Visual Analysis of Biomolecular Networks
17:00-17:20	Manuela Ferrario, Alice Cambiaghi, Eliandre de Olivera and Roberta Pastorelli	#17. An innovative approach to integrate proteomics and metabolomics data in severe septic shock
17:20-17:40	Casimiro Aday Curbelo Montañez, Paul Fergus, Carl Chalmers and Jade Hind.	#30. Analysis of Extremely Obese Individuals Using Deep Learning Stacked Autoencoders and Genome-Wide Genetic Data
17:40-18:00	Organizers & CIBB2019 Organizers	End of Meeting & Farewell