

2019 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology

Monday, July 8th

20:00-22:30 Dinner

Tuesday, July 9th

8:45-9:00 – Opening
SESSION 1 – ROOM: SALA BRACCI – Chairs: Luca Mesin and James Hughes
9:00-10:00 – Keynote Talk: " <i>Deep Learning for Biomedical Data</i> ", <u>Pierre Baldi</u> , University of California, Irvine, USA.
10:00-10:20 Sara Moccia, <u>Lucia Migliorelli</u> , Rocco Pietrini and Emanuele Frontoni. <i>Preterm infants' limb-pose estimation from depth images using convolutional neural networks</i>
10:20-10:40 Juraj Kacur, Jaroslav Polec, <u>Filip Csoka</u> and Eva Smolejova. <i>GMM Based Detection of Schizophrenia Using Eye Tracking</i>
10:40-11:00 <u>Pierangela Bruno</u> and Francesco Calimeri. <i>Using Heatmaps for Deep Learning based Disease Classification</i>
11:00-11:30 Coffee break
11:30-11:50 Andrea Bizzego, <u>Nicole Bussola</u> , Damiana Salvalai, Marco Chierici, Valerio Maggio, Giuseppe Jurman and Cesare Furlanello. <i>Integrating deep and radiomics features in cancer bioimaging</i>
11:50-12:10 <u>Marica Muffoletto</u> , Xiao Fu, Aditi Roy, Marta Varela, Paul Bates and Oleg Aslanidi. <i>Development of a Deep Learning Method to Predict Optimal Ablation Patterns for Atrial Fibrillation</i>
12:10-12:30 Thomas Clifford, Justin Bruce and <u>John Matta</u> . <i>Using Node-Based Resilience Clustering to Predict and Analyze Medical Data</i>
12:30-12:50 Giovanni Cugliari, <u>Silvia Benevenuta</u> , Simonetta Guarrera, Carlotta Sacerdote, Rosario Tumino, Salvatore Panico, Vittorio Krogh, Paolo Vineis, Giuseppe Matullo and Piero Fariselli. <i>Improving the prediction of cardiovascular risk with machine-learning and DNA methylation data</i>
12:50-13:10 <u>Eleftheria Polychronidou</u> , Ilias Kalamaras, Konstantinos Votis and Dimitrios Tzovaras. <i>HealthVision: An interactive web based platform for healthcare data analysis and visualisation</i>
13:10-13:30 <u>Thomas Clifford</u> , Justin Bruce, Tayo Obafemi-Ajayi and John Matta. <i>Comparative Analysis of Feature Selection Methods to Identify Biomarkers in a Stroke-Related Dataset</i>

13:30-15:00 Lunch Break

PARALLEL SESSIONS	
SESSION 2 – ROOM: SALA BRACCI – Chair: Eleftheria Polychronidou	SESSION 2 – ROOM: SALA VERANDA – Chair: Marco Masseroli
15:00-15:20 Tahmina Zebin and Thierry Chausalet. <i>A deep learning approach for length of stay prediction in clinical settings from medical records</i>	15:00-15:20 Linlin Zhao, Nima Abedpour, Christopher Blum, Petra Kolkhof, Mathias Beller, Markus Kollmann and Emidio Capriotti. <i>Predicting gene expression level in E. coli from mRNA sequence information</i>
15:20-15:40 Tahmina Zebin and Thierry Chausalet. <i>Design and implementation of a deep recurrent model for prediction of readmission in urgent care using electronic health records</i>	15:20-15:40 Bence Bruncsics and Peter Antal. <i>A multi-trait evaluation of network propagation for GWAS results</i>
15:40-16:00 Abdul Haleem Butt, Carne Zambrana, Sebastian Idelsohn-Zielonka, Mireia Claramunt-Molet, Amaia Ugartemendia-Etxarri, Erika Rovini, Alessandra Moschetti, Eloy Opisso Salleras, Filippo Cavallo, Carlos Molleja and Cristina Martin. <i>Assessment of Purposeful Movements for Post-Stroke Patients in Activities of Daily Living with Wearable Sensor Device</i>	15:40-16:00 Aristidis Vrahatis, Georgios Dimitrakopoulos, Sotiris Tasoulis and Vassilis Plagianakos. <i>A single-cell Systems Biology approach for disease-specific subpathway extraction</i>
16:00-16:20 Jeffrey Dale, Zhao Junya and Tayo Obafemi-Ajayi. <i>Multi-objective Optimization Approach to Find Biclusters in Gene Expression Data</i>	16:00-16:20 Aristidis Vrahatis, Sotiris Tasoulis, Georgios Dimitrakopoulos and Vassilis Plagianakos. <i>Visualizing High-Dimensional Single-Cell RNA-seq Data via Random Projections and Geodesic Distances</i>
16:20-16:40 Gaurav Sharma and Shubhajit Roy Chowdhury. <i>Enhancement in Focality of Non-Invasive Brain Stimulation through High Definition (HD) Anodal Transcranial Direct Current Stimulation (tDCS) Techniques</i>	16:20-16:40 Hisham Al-Mubaid. <i>Analysis of Gene Variants for Functional Annotations</i>
16:40 – 17:00 Marta Pinto, Mário Pereira and Diana Raposo. <i>GameAAL - AAL solution based on Gamification and Machine Learning Techniques</i>	16:40 – 17:00 Abirami Mahadevan, Anagha Vishnuvajjala, Naman Dosi and Shrisha Rao. <i>A Predictive Model for Drug-Drug Interaction Using a Similarity Measure</i>

17:00-17:30 Coffee break

17:30 – 19:30 Tutorial - ROOM: SALA BRACCI: “Bioinformatics tools for investigating the tumor-immune cell interface”. <u>F. Finotello</u>, Biocenter - Innsbruck Medical University, Austria	
19:30-20:15 - Short Poster Presentations (5 minutes each) – ROOM: SALA BRACCI	19:30-20:30 : BBTC meeting – ROOM: SALA VERANDA
Dieter Langosch, Yao Xiao, Bo Zeng, Nicola Brenner, <u>Dmitrij Frishman</u> and Marc Teese. <i>Experimental determination and data-driven prediction of homotypic transmembrane domain interfaces</i>	
<u>Luca Zanella</u> , Pina Fusco, Maria Rosaria Esposito, Pierantonio Facco, Fabrizio Bezzo and Elisa Cimetta, <i>A Data-Driven Approach to Assess the Role of Neuroblastoma-Derived Exosomes in Cancer Dissemination</i>	
<u>Quan Gu</u> and Jonathan Lim. <i>A Bi-clustering of metabolic data and an R package for metabolic bicluster analysis</i>	
<u>Antonio Pallotti</u> , Emanuela Tagliente and Leandro Lucangeli. <i>A 5G monitoring system through wearable sensors and machine learning for personalized medicine</i>	
<u>Regina-Veronicka Kalaydina</u> , Alexandra Wojaczek, Mohammed Gasmallah, Hedi Zhou, Dr. Farhana Zulkernine and Dr. Myron Szewczuk. <i>Image Object Detection Facilitates the Study of Fucosylation in Multicellular Tumour Spheroids</i>	
<u>Pasquale Fedele</u> , Chiara Fedele, Fabio Giannini and Alessandra Rufa. <i>A platform for biofeedback signals analysis</i>	
<u>Muhammad Shoaib Farooq</u> and Fajar Arshad. <i>A convolutional neural network approach for predicting oncogenes using sequence statistical moments into PseAAC</i>	
<u>Akil Loumani</u> , Brahem Chaouch Wafa, Larbi Ahmed Amine, Mediani Ahmed, Bensoltane Ahmed. and Bekada Ahmed Mohamed Ali. <i>Rep PCR Characterization of lactic acid bacteria isolated from sheep’s milk in Algeria and assessment their potential probiotics</i>	

20:30-22:30 Dinner & Poster Session

Wednesday, July 10th

SESSION 3 – ROOM: SALA BRACCI – Chairs: John Matta and Emidio Capriotti

8:40-9:40 Keynote Talk: "Data integration strategies to support clinical research", Riccardo Bellazzi, University of Pavia, Pavia, Italy

9:40 – 10:00 Michael Dubé, Sheridan Houghten and Daniel Ashlock. *Pandemic: A Graph Evolution Story*

10:00-10:20 James Hughes, Sheridan Houghten and Joseph Brown. *Descriptive Symbolic Models of Gaits from Parkinson's Disease Patients*

10:20-10:40 Daniel Ashlock, Wendy Ashlock and James Montgomery. *Implementing Phenotypic Plasticity with an Adaptive Generative Representation*

10:40-11:00 Lukas Pfannschmidt, Christina Göpfert, Ursula Neumann, Dominik Heider and Barbara Hammer. *FRI - Feature Relevance Intervals for Interpretable and Interactive Data Exploration*

11:00-11:30 Coffee break & group photo in the main cloister near the well

11:30-11:50 Sheridan Houghten, Angelo Romualdo, Tyler Collins and Joseph Alexander Brown. *Compression of Biological Networks using a Genetic Algorithm with Localized Merge*

11:50-12:10 Daniel Ashlock, Sierra Gillis, Amanda Saunders and Andrew Riley. *Large Block Matching Characters for Dehydrin Classification*

12:10-12:30 Martin Prodel, Ludovic Lamarsalle and Vincent Augusto. *ATLAS: a Robust Algorithm for Temporal Sequence Alignment of Treatment Lines using Claim Databases*

12:30-12:50 Luca Mesin, Forough Mokabberi and Christian Francesco Carlino. *Identification of optimal surgical intervention for Chiari I malformation*

12:50-13:10 Luca Mesin, Massimo Valerio and Giorgio Capizzi. *Detection and Assessment of Encephalitis from EEG*

13:10-14:40 Lunch break

14:40-15:00 Swati Vipsita, Ankita Shreya and Santos Kumar Baliarsingh. *Cancer Classification using improved Extreme Learning Machine*

15:00-15:20 Nada Almugrm and Hala Alshamlan. *FF SVM: New FireFly based Gene Selection Algorithm for Microarray Cancer Classification*

15:30-23:00 Social Tour & Dinner

*Social Tour in Siena: Tour of a Contrada "La Selva" & Dinner (at 19:30 in Contrada)
Address of Contrada "La Selva": Via Vallepiatta, 53100 Siena.*

Thursday, July 11th

SESSION 4 – ROOM: SALA BRACCI – Chair: Peter Antal
8:40-9:40 Keynote Talk: "Facilitating the discovery and analysis of genomic data via standardized APIs" <u>Cristina Yenyx Gonzalez Garcia, EMBL-EBI, Cambridge, UK</u>
9:40 – 10:00 Luca Becchetti, Michele Gentili, Lorenzo Farina, <u>Leonardo Martini</u> and Manuela Petti. <i>Biological Random Walks: integrating heterogeneous data in disease gene prioritization</i>
10:00-10:20 Zhao Junya, Thy Nguyen, Donald Adjeroh, Perry Koob, Jonathan Kopel and <u>Tayo Obafemi-Ajavi</u> . <i>Genotype Combinations Linked to Phenotype Subgroups in Autism Spectrum Disorders</i>
10:20-10:40 <u>Gaia Ceddia</u> , Pietro Pinoli, Stefano Ceri and Marco Masseroli. <i>Non-negative Matrix Tri-Factorization for Data Integration and Network-based Drug Repositioning.</i>
10:40-11:00 Patrick Echtenbruck, <u>Michael Emmerich</u> and Boris Naujoks. <i>A Multiobjective Approach to Classification in Drug Discovery</i>
11:00-11:30 Coffee break
11:30-11:50 <u>Vincenzo Bonnici</u> , Simone Caligola, Giulia Fiorini, Luca Giudice and Rosalba Giugno. <i>LErNet: characterization of lncRNAs via context-aware network expansion and enrichment analysis.</i>
11:50-12:10 <u>Michael Saint-Antoine</u> and Abhyudai Singh. <i>Evaluating Pruning Methods in Gene Network Inference</i>
12:10-12:30 <u>Nuriye Özlem Özcan Şimşek</u> , Arzucan Özgür and Fikret Gürgen, <i>Statistical Representation Models for Mutation Information within Genomic Data</i>
12:30-12:50 <u>Behrooz Abbaszadeh</u> and M.C.E. Yagoub. <i>Optimum Window Size and Overlapping for Efficient Seizure Prediction</i>
12:50-13:10 <u>Hisham Al-Mubaid</u> . <i>Gene Mutation Analysis for Functional Annotations Using Graph Heuristics</i>

13:10-14:40 Lunch break

SESSION 5 – ROOM: SALA BRACCI – Chairs: Emanuele Giordano and Simone Furini	
14:40-15:00 “Data Science for Vaccines R&D” Duccio Medini, PhD, Head Data Science and Clinical Systems GSK Vaccines R&D	
PARALLEL SESSIONS	
SESSION 5 – ROOM: SALA BRACCI – Chair: Emanuele Giordano	SESSION 5 – ROOM: SALA VERANDA– Chair: Simone Furini
15:00-15:20 <u>David Gomez-Cabeza</u> , Lucia Bandiera, Eva Balsa-Canto and Filippo Menolascina. <i>Information content analysis reveals desirable aspects of in vivo experiments of a synthetic circuit</i>	15:00-15:20 <u>Lys Sanz Moreta</u> , Ahmad Salim Al-Sibahi, Thomas Hamelryck, Douglas Theobald, Basile Nicolas Rommes, William Bullock and Andreas Manoukian. <i>A Probabilistic Programming Approach to Protein Structure Superposition</i>

15:20-15:40 Marco S. Nobile , Thalia Vlachou, Simone Spolaor, Paolo Cazzaniga, Giancarlo Mauri, Pier Giuseppe Pelicci and Daniela Besozzi. <i>ProCell: Investigating cell proliferation with Swarm Intelligence</i>	15:20-15:40 Kamal Taha . <i>Predicting the Functions of Proteins from their Co-occurrences with Implicit and Explicit Functional Terms in Texts</i>
15:40-16:00 Simone Caligola , Tommaso Carlucci, Franco Fummi, Carlo Laudanna, Gabriela Constantin, Nicola Bombieri and Rosalba Giugno. <i>Automatic parameterization of the purine metabolism pathway through discrete event-based simulation</i>	15:40-16:00 Qanita Bani Baker and Manar K Al-Bataineh. <i>Genetic Algorithm for Optimizing Global Alignment of Protein-Protein Interaction Network</i>
16:00-16:20 Roberto Pagliarini and Alessandra Boletta. <i>In silico simulations reveal a causative link between increased glycolysis and metabolic reprogramming in autosomal dominant polycystic kidney disease</i>	16:00-6:20 Paolo Valdez, Jerome Cary Beltran and Prospero Naval Jr. <i>Predicting Protein-Protein Interactions based on Biological Information using Extreme Gradient Boosting</i>
16:20-16:50 Coffee break	
16:50-17:10 Angela Re and Paola Lecca. <i>Determining structural parameter identifiability in biological dynamical models by analysing the statistical properties of the likelihood behavior</i>	16:50-17:10 Feng-Chi Chen, Pin-Shen Lee, Yun-Yu Huang, Huang-Chi Wu and Hsuan-Yu Lin . <i>Interactions between Inter Partes Review and Hatch-Waxman Litigations</i>
17:10-17:30 Arindam Chakraborty, Mahendra Kumar Gohil , Savitha Govardhan and Bhaskar Dasgupta. <i>Volumetric Representation of Biomolecules Using Cell Decomposition and Robotics</i>	17:10-17:30 Long Ma and Yan Wang. <i>Constructing a Semantic Graph with Depression Symptoms Extracted from Twitter</i>
17:30-17:50 Mahendra Kumar Gohil , Arindam Chakraborty, Savitha Govardhan and Bhaskar Dasgupta. <i>Structural Prediction of RNA Loops by Simulated Annealing</i>	17:30-17:50 Talha Ali Khan , Khawaja Zain-Ul-Abideen and Steve Ling. <i>A Modified Particle Swarm Optimization Algorithm Used for Feature Selection of UCI Biomedical Data Sets</i>
ROOM: SALA BRACCI	
18:00 Best paper award announcement & closing	

18:15-20:00 Free time

20:00-22:00 Dinner