

08:30	<i>Registration</i>
09:00	<i>Opening</i>
09:20:00 Leslie Smith	Keynote talk: Prof. Natalio Krasnogor , School of Computing Science, Newcastle University "Accelerating Synthetic Biology via Software and Hardware Advances"
10:20	<i>Engineering Bio-interfaces And Rudimentary Cells As A Way To Develop Synthetic Biology</i> 10:20 Maria Raposo: Artificial Nanosystems To Decode Natural Antioxidants-cellular Membrane Interactions 10:40 Quirina Ferreira: Nanostructured Drug Delivery Films For Brimonidine Controlled Release
11:00	<i>Coffee Break</i>
11:40:00 Francesco Masulli	11:40 Riccardo Rizzo: A Deep Learning Neural Network For Nucleosome Identification 11:58 Alexandru Floares: Exploring The Functional Redundancy Of miRNA In Cancer With Computational Intelligence 12:16 Antonio Eleuteri: The Analysis Of Lupus Nephritis Disease Dynamics Under A Markov Assumption With Use Of Biomarker Data 12:34 Javier Palarea: Some Robust Tools For The Detection Of Low-quality And Outlying Maldi-tof Mass Spectra 12:52 Daniele Pepe: PLS-SEM Mediation Analysis Of Gene-expression Data For The Evaluation Of A Drug Effect
13:10	<i>Lunch Break</i>
14:30:00 Elia Biganzoli	Keynote talk: Prof. Mark Beaumont , School of Biological Sciences, Bristol University "Population genetic inference using Expectation Propagation"
15:30	15:30 Franco Masulli: Semantic Clustering In Spectral Space For Characterizing Functional Protein Communities 15:50 Mohammad Kagdi: Evolution Of Dendritic Morphologies For Pattern Recognition In Passive Neuron Model 16:10 Andrew Schaumberg: Deepscope: Nonintrusive Whole Slide Saliency Annotation And Prediction From Pathologists At The Microscope
16:30	<i>Coffee Break</i>
17:00:00 Paolo Cazzaniga	17:00 Leif Peterson: Statistical Randomization Test For Inferring Order Of Somatic Mutations In Cancer <i>Modeling And Simulation Methods for Systems Biology and Systems Medicine</i> 17:20 Dario Pescini: Approximate Simulation Of Chemical Reaction Systems With Micro, Meso And Macro-scales 17:40 Paolo Cazzaniga: COSYS: Computational Systems Biology Infrastructure 18:00 Riccardo Colombo: Ensembles Of Parametrizations To Investigate The Crabtree Phenotype By Constraining Mechanism-based Simulations 18:20 Erin Scott: Process Algebra With Layers: A Language For Multi-scale Integration Modelling, Illustrated By A Cell Cycle And DNA Damage Case Study
18:40	<i>End of day</i>

08:30	<i>Registration</i>
09:00:00 Giulio Caravagna	Keynote talk: Dr. Guido Sanguinetti , School of Informatics, University of Edinburgh "Exploiting spatial features in the analysis of ChIP- and BS-Seq data"
10:00	10:00 Kevin Burke: Non-proportional Hazards Modelling Via Multi-parameter Regression 10:20 Daniela Coca: Statistical Texture-based Mapping Of Cell Differentiation Under Microfluidic Flow 10:40 Gilbert MacKenzie: A Critique Of Lasso-based Methods In Sparse Contingency Tables
11:00	<i>Coffee Break</i>
11:40 Roberto Tagliaferri	<i>Statistical Inference In Mechanistic Models Of Biological Systems</i> 11:40 Mu Niu: Parameter Inference In Differential Equation Models Of Biopathways Using Time Warped Gradient Matching 11:58 Umberto Noe: Inference In A Partial Differential Equations Model Of Pulmonary Arterial And Venous Blood Circulation Using Statistical Emulation
12:15	12:16 Ivan Merelli: A Logistic Model Tree Based Approach For eQTL Data Prediction Integration 12:34 Esmail Nouriani: Multi Task Learning For Pathogen-host Protein-protein Interaction Prediction 12:52 Anna Paola Carrieri: Dimension Reduction Of Metagenome Data Using Rodeo Improves Phenotype Prediction
13:10	<i>Lunch Break</i>
14:30 Andrea Bracciali	Keynote talk: Prof. Bud Mishra , Courant Inst., Tandon School of Engg & NYU SoM "(Cancer) Genomics via (Sub)Optical Mapping"
15:30 Fabio Tordini	High-performance Computing And Deep Learning Methods For Genomic Data Analysis 15:30 Zakaria Benmounah: A Novel Algorithm For CpG Island Detection In Human Genome Based On Clustering And Chaotic Particle Swarm Optimization 15:50 Kamel Zelti: An Efficient Compound Classification Technique Based On Multiple Kernel Learning For Virtual Screening
	16:10 NVIDIA Guest talk - Alison Lowndes
16:30	<i>Coffee Break</i>
17:00 David Gilbert	17:00 Kristy Hassall: Multiple Testing Correction Within A Model Selection Framework 17:20 Federico Andreis: An Adaptive Strategy To Oversample Rare And Clustered Traits 17:40 Sanja Brdar: Ensemble Approaches For Stable Assessment Of Clusters In Microbiome Samples 18:00 Daniele Pepe: SEM Significant Shortest Paths For The Characterization Of Gene Expression Data 18:20 Roberto Tagliaferri: A Machine Learning Approach To Investigate Multi-omic Regulatory Circuits In Bacterial Metabolic Pathways
18:40	<i>End of day</i>

SOCIAL DINNER

The old bridge Inn - Bridge of Allan

08:30	<i>Registration</i>
09:00 Clelia Di Serio	Keynote talk :Prof. Antonietta Mira , IDIDS, Università della Svizzera Italiana "Statistical inference on large-scale gene duplication networks"
10:00	10:00 Hiroshi Noborio: GPU-based Omnidirectional Shortest Distance Algorithm And Its Evaluation By Changing GPU Cores 10:20 Veronica Biga: Information-theoretic Active Contour Model For Microscopy Image Segmentation Using Texture 10:40 Igor Saggese: STABLE: A Novel Approach To Denovo Assembly Of RNA-seq Data
11:00	<i>Coffee Break</i>
11:30 Marco Bonetti	Modeling Dependence In Survival Analysis: Methodological Issues And Biomedical Implications 11:30 Chiara Brombin: Assessing The Impact Of An Emotion Recognition Task On Heart Rate Variability 11:48 Marco Bonetti: Comparing Discrete Time Multistate Models Using Dissimilarities 12:04 Chiara Gigliarano: Retrospective Study Of The Effect Of The Number Of Removed Lymph Nodes On Prostate Cancer Recurrence 12:22 Andrea Giussani: Modeling Dependence In Bivariate Multi-state Processes: A Frailty Approach 12:40 Elia Biganzoli: Modeling The Covariates Effects On The Hazard Function By Piecewise Exponential Artificial Neural Networks: An Application To A Controlled Clinical Trial On Renal Carcinoma 12:58 Clelia Di Serio: Comparing Frailty Models In Tumor Dormancy Frameworks
13:10	<i>Lunch Break</i>
14:30 Andrea Bracciali	Keynote talk: Dr. Daniela Paolotti , Institute for Scientific Interchange, Turin "Unsupervised extraction of latent syndromes from self-reported influenza-like illness symptoms"
15:30	15:30 Vladimir Rogojin: NetControl4BioMed - Automatic discovery of combined drug therapy 15:50 Davide Sardina: Correlation Between Proteomic Network Inference And Protein-protein Interaction Networks 16:10 Susanna Conde: Causal Effect Of Body Mass Index On Metabolites: Multiple Instruments
16:30	<i>Coffee Break</i>
17:00:00 Giosue' Lo Bosco	Biocuration And Integration Of Biomedical Databases 17:00 Riccardo Rizzo: Using The Gremlin Language To Solve Biological Tasks: A Case Study On BioGraphDB 17:20 Fabio Cumbo: IRIS-TCGA: An Information Retrieval And Integration System For Cancer Genomic Data 17:40 Simona Rombo (Giosue' LoBosco): Integration Of Biological Data Sources To Build Complex Functional Networks 18:00 Davide Sardina: A web interface to query and filter data from ArrayExpress 18:20 Kevin Heffernan: Complex Network Data And Document Stratification For Comorbidity Analysis
18:40	End of CIBB2016