

Monday, October 19th

13.00	Registration (onwards)
14.15 - 14.30	Welcome & Introductory Remarks
Session:	Dynamics of genomes and genetic variation I Chairs: Rosanna Verde, Sandro Banfi
14.30 - 15.20	KN1 - Peter Van Loo (The Francis Crick Institute, UK) "Molecular Archaeology of Cancer"
15.20 - 15.35	01 - Emanuel Weitschek (IASI-CNR, Italy) "Extraction of multiple rule-based models to classify RNA-seq cancer data"
15.35 - 15.50	02 - Leny Bravo (Universidad Privada San Juan Bautista, Escuela de Medicina Humana, Peru) "Repeated observation of immune gene sets enrichment in women with non-small cell lung cancer"
15.50 - 16.30	<i>Coffee break</i>
Session:	Dynamics of genomes and genetic variation II
16.30 - 16.45	03 - Marianna Cerasuolo (University of Portsmouth, Department of Mathematics, UK) "Neuroendocrine Trans-differentiation in Human Prostate Cancer Cells: a Strange Case of Dr. Jekyll and Mr. Hyde"
16.45 - 17.00	04 - Audrone Jakaitiene (Department of Human and Medical Genetics, Vilnius University) "Detection of Rare Mutations using Beta-Binomial model in Next-Generation Sequencing Experiments"
17.00 - 17.15	05 - Francesca Taranto (CRA-ORT, Italy) "High throughput SNP discovery and population structure in Pepper (C.Annum) using genotype-by-sequencing"
17.15 - 17.30	06 - Paolo Anagnostou (Dipartimento di Biologia Ambientale, Sapienza University of Rome, Italy) "The emerging complexity of genomic architecture in human population isolates"
17.30 - 17.45	07 - M.G. Notarangelo, E. Signori (IAC-CNR, IFT-CNR, Italy) "Biology and Mathematics for anti-tumoral vaccines"
17.45	<i>Welcome reception at Aula Magna Partenope</i>

Tuesday, October 20th

Session:	Dynamics of motifs Chair: Lucia Maddalena	15.20 - 15.35	015 - Alberto Maria Bersani (Sapienza University of Rome, Italy) "Theoretical foundations of the total quasi-steady state approximation in enzyme kinetics"
09.30 - 10.20	KN2 - Sebastiaan H. Meijnsing (Max Planck Institute for Molecular Genetics, Germany) "Transcriptional regulation: When $1 + 1 \neq 2$ "	15.35 - 15.50	016 - Maria Pia Saccomani (University of Padova, Italy) "Parameter Identifiability of ODE Models in Systems Biology"
10.20 - 10.35	08 - Adane Mamuye (University of Camerino, Italy) "Characterization of RNA interaction network with persistent homology and group theory"	15.50 - 16.30	<i>Coffee Break</i>
10.35 - 10.50	09 - Marco Salvemini (University of Naples Federico II, Italy) "Bioinformatics and transcriptomics to uncover the sex determination in the sand fly species <i>Phlebotomus perniciosus</i> , a major Old World vector of <i>Leishmania infantum</i> "	Session:	Dynamics of biological networks III Chair: Antonio Irpino
10.50 - 11.05	010 - Kumar Parijat Tripathi (ICAR-CNR, Italy) "A simple computational protocol to detect and functionally interpret circular RNA in RNA-seq experiments"	16.30 - 16.45	017 - Elijah Lowe (Stazione Zoologica Anton Dohrn, Naples, Italy) "A transcriptomic approach to developmental Gene Regulatory Networks"
11.05 - 11.45	<i>Coffee break</i>	16.45 - 17.00	018 - Marina Piccirillo (ICAR-CNR, Italy) "Reconstructing a Genetic Network from Gene Perturbations in Secretory Pathway of Cancer Cell Lines"
Session:	Dynamics of biological networks I Chair: Paola Festa	17.00 - 17.15	019 - Daniele Ferone (University of Naples Federico II, Italy) "Combinatorial optimization approaches for biclustering of gene expression data"
11.45 - 12.35	KN3 - Giuseppe Jurman (Fondazione Bruno Kessler, Italy) "Differential network analysis and graph classification: a glocal approach"	17.15 - 17.30	020 - Jennifer Dodd (University of Sheffield, UK) "Identifying translomes for defining neuroprotective therapies against widespread RNA dysregulation in neurodegeneration"
12.35 - 12.50	011 - Alessandro Zandonà (Fondazione Bruno Kessler, Italy) "Complex networks for the analysis of microbiome structures"	17.30 - 17.45	021 - Sara Mancinelli (IGB-CNR, Italy) "Design of Experiments implementation in a transfection protocol fine-tuning: Design of Transfections (DoT)"
12.50 - 13.05	012 - Ettore Mosca (ITB-CNR, Italy) "Network analysis of genetic variations in Autism Spectrum Disorders"	17.45 - 18.00	022 - Roberto Croce (ETH Zürich, Switzerland) "A quantitative Turing model validation for the simulation of lung branching morphogenesis"
13.05 - 13.20	013 - Seetharaman Parashuraman (IBP-CNR, Italy) "Unravelling druggable signalling networks that control F508del-CFTR proteostasis"	20.00	<i>Social Dinner</i>
13.20 - 14.15	<i>Lunch</i>		
Session:	Dynamics of biological networks II Chair: Gerardo Toraldo		
14.15 - 15.05	KN4 - Panos M. Pardalos (University of Florida, USA) "Optimization-Based Data Mining Approaches in Neuroscience Research"		
15.05 - 15.20	014 - Elisabeth Remy (I2M/AMU/CNRS, France) "Discrete dynamics of embedded regulatory circuits"		

Wednesday, October 21st

Session: Dynamics of pattern recognition
Chair: **Angelo Facchiano**

09.30 - 10.20 KN5 - **Morgane Thomas-Chollier** (Ecole Normale Supérieure, France)
"Motifs search and discovery from genome scale experiments"

10.20 - 10.35 O23 - **Giulia Fison** (Sapienza University of Rome, Italy)
"Searching for equivalent compact solutions to classification problems for genomic sequences"

10.35 - 10.50 O24 - **Ilaria Granata** (ICAR-CNR, Italy)
"DecontaMiner: a pipeline for the detection and analysis of contaminating sequences in human NGS sequencing data"

10.50 - 11.05 O25 - **Sonali Chavan** (IBP-CNR, Italy)
"Dissecting the functions of secretory pathway by transcriptional profiling"

11.05 - 11.45 *Coffee break*

Session: Dynamics of genomes and genetic variation
Chair: **Marco Salvemini**

11.45 - 12.35 KN6 - **Marco Cosentino Lagomarsino** (Université Pierre et Marie Curie, France)
"Quantitative laws in gene-family evolution"

12.35 - 12.50 O26 - **Mariella Ferrante** (Stazione Zoologica Anton Dohrn, Italy)
"Genome-enabled exploration of a toxic marine diatom"

12.50 - 13.05 O27 - **Mariano Avino** (ICAR-CNR, Italy)
"A web resource on skeletal muscle tissue specific transcriptome of Primates order"

13.05 - 13.20 O28 - **Irma Terracciano** (CRA-ORT, Italy)
"Sequence capture and target re-sequencing approaches to dissect naturally occurring allelic variation at candidate genes controlling carotenoid biosynthesis in tomato"

13.20 *Concluding Ceremony*

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Organizing Secretariat

YES MEET

Via San Nicola, 4 - 80067 Sorrento (Na) ITALY

Tel. +39 0818770604

Fax +39 0818770258

info@bmtl.it

info@yesmeet.it

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Bringing Maths  to Life

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Centro Congressi Federico II

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PROGRAM