

Conference Programme

Wednesday		May 2
13.00	14.00	Registration and poster hang-up
14.00	14.20	Welcome and Introduction
14.20	15.10	Keynote Lecture (Dulbecco Lecture) <i>Dr. Ileana Zucchi</i> Renato Dulbecco: genes, cancer and epigenomics
15.10	16.10	Session 1 (first part): Next Generation Sequencing, Pharmacogenomics
15.10	15.30	<i>Giugno R, Abate F, Bombieri N, Delledonne M, <u>Ferrarini A</u>, Ficarra E, Pulvirenti A, Acquaviva A</i> Integrated cloud environment for characterization of genotype specific transcriptome from next generation sequencing data
15.30	15.50	<i>Pozzoli U</i> Next Generation Programming: software tools for NGS tertiary analysis
15.50	16.10	<i>D'Antonio M, D'Onorio De Meo P, Pesole G, <u>Castrignanò T</u></i> Building an optimized pipeline for whole-exome sequencing
16.10	16.30	Coffee Break
16.30	17.30	Session 1 (second part): Next Generation Sequencing, Pharmacogenomics
16.30	16.50	<i>Castellana S, <u>Mazza T</u></i> On the impact of short-reads quality on variants detection
16.50	17.10	<i>Conte I, Migliore C, Merella S, Avellino R, Marco-Ferreres R, Carrella S, Emmett W, Sanges R, Bockett N, Van Heel D, Meroni G, Bovolenta P, Banfi S, <u>Stupka E</u></i> An RNA-seq-based approach highlights a role of miR-204 in axon guidance in vertebrates
17.10	17.30	<i>Visconti A, <u>Cordero F</u>, Calogero RA</i> Improving biomarker discovering for chemosensitivity prediction using an integrated approach
17.30	20.00	BITS General Assembly
Thursday		May 3
8.30	9.00	Poster hang-up
9.00	9.50	Keynote Lecture (G. Preparata Lecture) <i>Prof. Eugene W. Myers</i> On bioimage informatics and decoding genomes
9.50	10.50	Coffee Break and Poster Session
10.50	12.50	Session 2: System Biology, Molecular Evolution
10.50	11.10	<i>Beka S, <u>te Boekhorst I</u>, Abnizova I</i> The location of T1 diabetes associated SNPs in regulatory regions
11.10	11.30	<i>Calviello L, Stano P, Mavelli F, Luisi PL, Marangoni R</i> Quasi-cellular Systems: stochastic simulation analysis at nanoscale range
11.30	11.50	<i>Cordero F, Gribaudo M, Manini D</i> An analytical spatially-based approach to study cancer cell population evolutions

11.50	12.10	<i>Gherardini PE, Sacco F, Paoluzi S, Saez-Rodriguez J, Helmer-Citterich M, Ragnini-Wilson A, Castagnoli L, Cesareni G</i> A combined computational/experimental strategy to map phosphatases on growth pathways
12.10	12.30	<i>Pendino V, Ciccarelli FD</i> microRNAs regulate the dosage of duplicated genes
12.30	12.50	<i>Re M, Mesiti M, Valentini G</i> Drug repositioning through pharmacological spaces integration based on networks projections
12.50	13.10	<i>Guzzi PH, Cannataro M</i> Cyto-Sevis: semantic similarity-based visualisation of protein interaction networks
13.10	14.10	<i>Lunch Break</i>
14.10	16.10	Session 3: Genomics, Transcriptomics, Proteins Structure and Function
14.10	14.30	<i>Carrara M, Calogero R</i> Digging in the RNA-seq garbage: evaluating the characteristics of unmapped RNA-seq reads in normal tissues
14.30	14.50	<i>Colantoni A, Ferrè F, Helmer-Citterich M</i> Alternative splicing as regulator of protein-protein interactions
14.50	15.10	<i>Grützmann K, Szafranski K, Pohl M, Voigt K, Petzold A, Schuster S</i> Fungal alternative splicing associates with higher cellular complexity and virulence
15.10	15.30	<i>Romano C, Buffa P, Pandini A, Massimino M, Tirrò E, Manzella L, Fraternali F, Vigneri P</i> Computational and experimental characterization of critical amino acidic residues in the BCR-ABL kinase domain explaining TKIS resistance in patients with chronic myeloid leukemia
15.30	15.50	<i>Sinha S, Iannelli F, Collino A, Ghisletti S, Natoli G, Ciccarelli FD</i> CNV analysis of inflammation driven hepatocellular carcinoma
15.50	16.10	<i>Testori A, Caizzi L, Cutrupi S, Friard O, De Bortoli M, Corà D, Caselle M</i> The role of transposable elements in shaping the combinatorial interaction of transcription factors
16.10	19.30	Social Tour of Catania
19.30	23.00	Social Dinner

Friday		May 4
8.15	8.30	<i>Poster hang-up</i>
8.30	9.20	Keynote Lecture <i>Prof. Charles E. Lawrence</i> Statistical inference in high dimensional spaces of genomics: an RNA structural example
9.20	10.20	Session 4 (first part): Algorithms for Bioinformatics, Metagenomics
9.20	9.40	<i>Cangelosi D, Muselli M, Blengio F, Versteeg R, Eggert A, Schramm A, Garaventa A, Gambini C, Varesio L</i> Translation of a robust, biology-driven, prognostic classifier of cancer patients outcome into clinically relevant rules

9.40	10.00	<i>Frasca M, Bertoni A, Valentini G</i> Regularized network-based algorithm for predicting gene functions with high-imbalanced data
10.00	10.20	<i>Pio G, Ceci M, D'Elia D, Loglisci C, Malerba D</i> A novel biclustering algorithm for the discovery of meaningful biological correlations between miRNAs and mRNAs
10.20	11.20	<i>Coffee Break and Poster Session</i>
11.20	12.40	Session 4 (second part): Algorithms for Bioinformatics, Metagenomics
11.20	11.40	<i>Malagoli Tagliazucchi G, Miccio A, Cavazza A Poletti V, Peano C, De Bellis G, Mavilio F, Biccato S</i> A bioinformatics framework for the identification of active regulatory elements through the integrative analysis of high-throughput genomic data
11.40	12.00	<i>Micale G, Pulvirenti A, Giugno R, Ferro A</i> A greedy and stochastic algorithm for multiple local alignment of interaction networks
12.00	12.20	<i>Policriti A, Scalabrin S, Vezzi F, Vicedomini R</i> GAM: Genomic Assemblies Merger
12.20	12.40	<i>D'Antonio M, Paoletti D, Santamaria M, Castrignanò T, Pesole G</i> SARMA: a web resource for species assignment of high-throughput sequencing reads from metagenomics analysis
12.40	13.40	<i>Lunch Break</i>
13.40	15.00	Session 5: Biobanks and Biological Databases
13.40	14.00	<i>Di Domenico T, Walsh I, Martin A, Tosatto S</i> MobiDB: a comprehensive database of intrinsic protein disorder annotations
14.00	14.20	<i>Canakoglu A, Gangi P, Gennaro S, Masseroli M</i> Identification of gene annotations and interactions and protein-protein interaction associated disorders through data integration
14.20	14.40	<i>Liberti S, Calderone A, Sacco F, Perfetto L, Iannuccelli M, Panni S, Santonico E, Palma A, Nardoza AP, Castagnoli L, Cesareni G</i> HUPHO: the human phosphatase portal
14.40	15.00	<i>Pappalardo AM, Guarino F, Messina A, Pulvirenti A, Giugno R, Ferro A, De Pinto V</i> A knowledge base for fish and fishery products
15.00	15.45	Session 6: Technological track
15.00	15.15	<i>Guzzi PH, Cannataro M</i> Micro-Analyzer: a tool for automatic pre-processing of multiple affymetrix arrays
15.15	15.30	<i>Gaido L, Bencivenni M, Cesini D, Donvito G, Veronesi P</i> IGI grid services for the bioinformatics community
15.30	15.45	<i>Falciano F, Rossi E</i> FERMI: the most powerful computational resource for Italian scientists
15.45	16.00	Presentation of BITS 2013 and Farewell
16:00	17:00	Tutorial
16.00	17.00	<i>Micale G.</i> Biological Network Alignment