

Poster	session	title	authors
1	Algorithms for Bioinformatics	An automated method for biological marker segmentation, quantification, and co-localization, from histochemical and immunohistochemical images.	Casiraghi E., Vergani B., Villa A.
2	Algorithms for Bioinformatics	Speeding up Node Label Learning in Unbalanced Biomolecular Networks through a Parallel and Sparse GPU-based Hopfield Model	A. Petrini, M. Notaro, J. Gliozzo, G. Valentini, G. Grossi, M. Frasca
3	Algorithms for Bioinformatics	Analysis of sequence and secondary structure motifs in RNA molecules: method and applications	Adinolfi M, Pietrosanto M, Ausiello G, Helmer-Citterich M
4	Algorithms for Bioinformatics	Pre-processing of high-throughput sequencing data	Manconi A, Moscatelli M, Gnocchi M and Milanese L
5	Algorithms for Bioinformatics	Metagenomic analysis by bacterial short reads classification with deep network model	Fiannaca A, La Paglia L, LA Rosa M, Lo Bosco G, Rizzo R, Gaglio S, Urso A
6	Algorithms for Bioinformatics	cuRnet: an R package for the single-source shortest paths analysis on GPUs	Vincenzo Bonnici, Federico Busato, Murodzhon Akhmedov, Simone Caligola, Franco Fummi, Nicola Bombieri, Ivo Kwee, Rosalba Giugno
7	Biological Databases	Development of an Android application for study and research in pharmacology	Zammarchi G, Pisanu C
8	Biological Databases	Docking and Molecular dynamics protocol for ligand binding characterization of Nuclear Receptors	D Ursi P, Uggeri M, Rovida E, Fossa P, Milanese L, Orro A
9	Biological Databases	Human non-coding RNA networks construction and interpretation	Vincenzo Bonnici, Giorgio De Caro, Sabino Liuni, Domenica D Elia, Nicola Bombieri, Rosalba Giugno, Flavio Liciulli
10	Biological Databases	The ITSoneDB upgrade: a resource expanding its view from Fungi to the entire Eukaryotic domain	Ilaria Larini, Bruno Fosso, Monica Santamaria, Flavio Liciulli, Sabino Liuni and Graziano Pesole
11	Comparative Genomics	Statistical modelling of CG interdistance across multiple organisms	Merlotti A., Faria do Valle I., Remondini D., Castellani G.
12	Database and Big Data application in Bioinformatics	Genomic and pharmacogenomic correlation in different cell line data collection for the detection of predictors of drug response	Di Bella S, Carapezza G, Isacchi A and Bosotti R
13	Database and Big Data application in Bioinformatics	The PhenoMeNal Cloud Research Environment for Metabolomics	The PhenoMeNal Consortium, Rosato A
14	Database and Big Data application in Bioinformatics	Onassis: Ontology Annotation and Semantic Similarity Software	Galeota E, Pelizzola M
15	Database and Big Data application in Bioinformatics	REDIdb 3.0: a comprehensive collection of RNA editing events in plant organellar genomes	Lo Giudice C, Pesole G, Picardi E
16	Database and Big Data application in Bioinformatics	REDIportal: a comprehensive database of A-to-I RNA editing events in humans	Picardi E, Flati T, Gioiosa S, D Erchia AM, Lo Giudice C, Castrignanò T, Chillemi G, Pesole G
17	Database and Big Data application in Bioinformatics	A Infrastructure for Precision Medicine through analysis of Big Data	Moscatelli M, Gnocchi M, Manconi A, Pessina M, Fellegara G, Rampoldi S, Milanese L, Casasco A

18	Database and Big Data application in Bioinformatics	HmtDB 2017: data update, a better performing query system and human mitochondrial DNA haplogroup predictor	Preste R, Clima R, Calabrese C, Diroma MA, Santorsola M, Scioscia G, Simone D, Shen L, Gasparre G, Attimonelli M
19	Database and Big Data application in Bioinformatics	A new web portal for exploring inter- and intra-cellular interactions in muscle regeneration	Palma A, Perfetto L, Calderone A, Castagnoli L, Cesareni G
20	Database and Big Data application in Bioinformatics	WEB INFRASTRUCTURE FOR THE MANAGEMENT OF THE BBMRI.IT ITALIAN BIOBANK NETWORK	Gnocchi M., Moscatelli M., Manconi A., Milanese L.
21	Database and Big Data application in Bioinformatics	Pi/4 -Rotation Method for Feature Subset Selection	Neumann U, Heider D
22	Epigenetics	Inter-individual variability of methylated CpGs in blood samples of healthy individuals	Palumbo D, Affinito O, Monticelli A, Cocozza S
23	Epigenetics	Analysis of regular regions in nucleosome profiles	Pezzini F , Scharf D. , Brakhage A. , Shelest E.
24	Gene Network	A Web Graphical Tool for the Integration of Unbalanced Biomolecular Networks	P. Perlasca , M. Mesiti , M. Notaro , A. Petri , J. Gliozzo , G. Valentini , M. Frasca
25	Genome 3D: Bioinformatics, computing infrastructure and opportunities for Chroma	TAD-AH: a computational tool for refinement of TAD prediction and differential analysis	Nicoletti C, Bicciato S, Forcato M
26	Genome 3D: Bioinformatics, computing infrastructure and opportunities for Chroma	NuchaRt: a tool for Hi-C data analysis and multi-omic data integration	Fabio Tordini, Zakaria Benmounah, Luciano Milanese, Pietro Liò, Marco Aldinucci, Ivan Merelli
27	Genome variations and their impact on biomedicine	A Web-accessible database for Galactosemia-related proteins	Scafuri B, d'Acerno A, Facchiano A, Marabotti A
28	Genome variations and their impact on biomedicine	Analysis of recurrent nucleotide variants reveals possible inconsistencies of the human reference genome	Bertoldi L, Ferrarini M, De Pascale F, Valle G
29	Genomics of Disease	WES variants prioritization in a case of complex disease: an integrative approach	Guido Baselli, Alessandro Pietrelli, Serena Pelusi, Marica Meroni, Anna Ludovica Fracanzani, Giorgio Soardo, Elisabetta Bugianesi, Renato Romagnoli, Salvatore Petta, Luca Miele, Silvia Fargion, Paola Dongiovanni, Luca Valenti
30	Genomics of Disease	Exome sequencing to identify denovo and germline rare variants in neuroblastoma family trios	Vito Alessandro Lasorsa, Daniela Formicola, Piero Pignataro, Alessandro Testori, Marcella Pantile, Carlo Zanon, Maria Rosaria Esposito, Gian Paolo Tonini, Mario Capasso
31	Genomics of Disease	Modeling biomolecular profiles in a graph-structured sample space for clinical outcome prediction with melanoma and ovarian cancer patients.	J. Gliozzo, M. Notaro, A. Petri, P. Perlasca, M. Mesiti, E. Casiraghi, G. Grossi, M. Re, A. Paccanaro, G. Valentini
32	Molecular Evolution	A preliminary classification of Microbial Transglutaminases	Deborah Giordano, Angelo Facchiano
33	Next Generation Sequencing	myVCF: a desktop application for high-throughput mutations data management	Pietrelli A, Valenti L
34	Next Generation Sequencing	A tool suite for CNV analysis from whole exome sequencing data in Galaxy	Zonnedda B, Medda R, Onano S, Atzeni R, Cuccuru G, Fotia G, Uva P
35	Next Generation Sequencing	Whole-exome sequencing of breast cancer initiating cells and paired primary tumors: the impact of variant callers and filtering strategies.	Noemi Di Nanni, Valentina Appierto, Cinzia De Marco, Valentina Angeloni, Maria Grazia Daidone, Luciano Milanese, Ettore Mosca
36	Next Generation Sequencing	TiCoRse: Time Course RNA-Seq Analysis Tool	Righelli Dario, Angelini Claudia

37	Next Generation Sequencing	Analysis of miRNA and piRNA biogenesis in breast cancer cells	Memoli D, Rinaldi A, Giurato G., Salvati A, Rizzo F, and Weisz A
38	Next Generation Sequencing	Somatic Mutations in Cancer: A Comprehensive Pipeline for Detection and Annotation of Variations using DNA- and RNA-Seq Data	Giurato G, Ravo M, Rizzo F and Weisz A
39	Next Generation Sequencing	Integration, processing, and data analysis in the operational support of a large scale NGS core facility	Atzeni R, Cuccuru G, Lianas L, Medda R, Pireddu L, Uva P, Zara I, Zanetti G, Fotia G
40	Next Generation Sequencing	Impact of sample size in variant identification from exome sequencing data	Uva P, Cuccuru G, Atzeni R, Zanetti G, Fotia G
41	Next Generation Sequencing	Pushing the limits of the "clinical exome" (TruSight One) Next Generation Sequencing on MiSeq for the analysis of clinical cancer samples	Cusi C, Carapezza G, Di Bella S, Lupi R, Rizzo E, Ferlito G, Somaschini A, Radrizzani L, Leone A, Memeo L, Isacchi A and Bosotti R
42	Pharmacogenomics	Automatic selection of informative genes for an improved prediction of drug response in cancer cell lines	Pepe G, Parca L, Pietrosanto M, Ausiello G, Helmer Citterich M.
43	Pharmacogenomics	Integrated analysis of converging genome-wide genotyping and transcriptomic data to identify genes associated with lithium response in bipolar disorder	Pisanu C, Congiu D, Costa M, Chillotti C, Arda R, Severino G, Angius A, Heilbronner U, Hou L, McMahon FJ, Schulze TG, Del Zompo M, Squassina A
44	Precision Medicine	BROWSer - Bioinformatics Resource for Omics Wide Services: Railway to Precision Medicine	Clima R, Santorsola M, Preste R, Avelluto M, Berardi M, Calabrese C, Contu A, Gasparre G, Porcelli AM, Silvestris F, Simone D, Attimonelli M
45	Predictive modeling of diseases and Personalized Medicine	Analysing the relations among genes and polygenic diseases with eDGAR	Babbi G, Martelli PL, Profiti G, Bovo S, Savojardo C, Casadio R.
46	Protein structure and function	Conformational analysis of T384S EGFR mutant by molecular dynamics simulations	Polo A, Costantini S
47	Protein structure and function	The mechanisms of protein kinases inhibiting by pyrrol derivatives.	Hurmach V., Kuznietsova H., Rybalchenko V.
48	Protein structure and function	A bioinformatic tool for the investigation of HGD mutations responsible for Alkaptonuria	Cicaloni V, Bernini A, Santucci A, Spiga O.
49	Protein structure and function	From in Silico to in Vitro: a trip to reveal Flavonoid Binding on Kir6.1	Alfonso Trezza, Vittoria Cicaloni, Piera Porciatti, Francesco Pettini, Andrea Langella, Fabio Fusi, Simona Saponara and Ottavia Spiga
50	Proteomics	A web-based tool for serum degradation analysis	Romano P, Profumo A
51	Systems Biology	Natural-bioactive compounds study by means of bioinformatics approaches	S. Dotolo and A. Facchiano
52	Systems Biology	Lessons from Electronic Design Automation for Modeling and Simulation of Biological Systems	Simone Caligola, Nicola Bombieri, Rosalba Giugno
53	Trascriptomics, RNA-Seq, Chip-Seq, mRNA, piRNA	Cancer CRISPr-like reverse-engineering: mining gene signatures from copy number aberrations with ICARo	Pallocca M, Fanciulli M
54	Trascriptomics, RNA-Seq, Chip-Seq, mRNA, piRNA	WoPPER: Webserver for Position Related data analysis of gene Expression in Prokaryotes	Puccio S & Grillo G, Licciulli F, Severgnini M, Liuni, Bicciato, De Bellis G, Ferrari F & Peano S
55	Trascriptomics, RNA-Seq, Chip-Seq, mRNA, piRNA	Bioinformatics approaches for RNA editing detection: a comparative study of state of the art software	Diroma MA, Ciaccia L, Pesole G, Picardi E
56	Trascriptomics, RNA-Seq, Chip-Seq, mRNA, piRNA	Involvement of PIWI-interacting RNAs in different molecular and clinicopathological subclasses of colon cancer	Rinaldi A, Rizzo F, Sellitto A, Memoli D, Trapani D, Sahnane N, Furlan D, Giurato G and Weisz A
57	Trascriptomics, RNA-Seq, Chip-Seq, mRNA, piRNA	Evaluation of Differential Expression Analysis Methods for Single-Cell RNA-Sequencing	Dal Molin A, Baruzzo G, Di Camillo B