BBCC2017

LIST OF POSTERS

First group – posters presented on Monday 18th (afternoon) and Tuesday 19th (morning) sessions

Session: Molecular Simulations

Poster no. 1
Can force fields currently used in molecular dynamics simulations reproduce the fine structure of proteins?
Nicole Balasco, Luciana Esposito, Luigi Vitagliano

Poster no. 2
Structural basis for mutations of human aquaporins associated to genetic diseases Luisa Calvanese, Gabriella D'Auria, Lucia Falcigno, Romina Oliva

Poster no. 3
Computational analysis of the interactions between arginine and GALT enzyme to rationalize the activity of a putative chaperon on the protein stability
Lucrezia Catapano, Anna Marabotti

Poster no. 4
What can bioinformatics due for rare diseases? An example from Fabry disease
Valentina Citro, Chiara Cimmaruta, Ludovica Liguori, Maria Monticelli, Gaetano Viscido, Giuseppina Andreotti and Maria Vittoria Cubellis

Poster no. 5
Comparative analysis of molecular motions in SIRTUIN2 proteins
S. Dotolo, A. Facchiano and A. Pandini

Poster no. 6
Hotspot residues involved in potency and selectivity of the ligand binding in Nuclear Receptors
D'Ursi P, Uggeri M, Rovida E, Fossa P, Milanesi L,Orro A

Poster no. 7
The variability of backbone geometry as a new tool for protein structure validation
Luciana Esposito, Nicole Balasco, Amarinder Singh Thind, Mario R. Guarracino, Luigi Vitagliano

Poster no. 8
Homology modelling based study of structural properties of Microbial Transglutaminases Deborah Giordano, Angelo Facchiano

Poster no. 9
Electrostatic fingerprints in avian influenza hemagglutinins
Irene Righetto, Alireza Heidari, Francesco Filippini

Poster no. 10
Prediction of the effects of amino acid mutations on protein stability: an analysis of available tools and their reliability
Bernardina Scafuri, Angelo Facchiano, Anna Marabotti

SESSIONS: APPLICATIONS IN GENOMICS AND APPLICATIONS IN MEDICINE

Poster no. 11
Improvement of the Ion Torrent PGM sequencing workflow of a gene panel for next generation sequencing of DNA samples from patients
Giancarlo Castellano, Eva Gonzalez, Alba Roset, Eva Fernandez, Ricard Isanta, Wladimiro Jimenez Pedro Jares

Poster no. 12
ClusterScan: a tool to discover and annotate genomic clusters
Massimiliano Volpe, Marco Miralto, Stefano Gustincich, Remo Sanges

Poster no. 13
Integration of transcriptomic data in genome scale metabolic networks: a computational approach to study complex diseases
Ilaria Granata, Enrico Troiano, Mara Sangiovanni, and Mario R. Guarracino

Poster no. 14
Circulating microRNAs expression profiles are associated with childhood obesity: results of the I.Family Study

Giuseppe Iacomino, Paola Russo, Pasquale Marena, Fabio Lauria, Antonella Venezia, Pasquale De Luca, Wolfgang Ahrens, Ronja Foraita, Kathrin Günther, Stefaan De Henauw, Lauren Lissner, Dénes Molnár, Luis A Moreno, Michael Tornaritis, Toomas Veidebaum, and Alfonso Siani

Poster no. 15
A Genome-Wide Association Study identifies new loci associated with sweet and fat preferences: results from the I.Family study
Fabio Lauria, Marco Miele, Stefaan De Henauw, Carmen Dering, Antje Hebestreit, Monica Hunsberger, Hannah Jilani, Jaakko Kaprio, Dénes Molnár, Luis A. Moreno, Teemu Palviainen, Toomas Veidebaum, Alfonso Siani, Paola Russo

Second group – posters presented on Tuesday 19ᵗʰ (afternoon) and Wednesday 20ᵗʰ (morning) sessions

SESSION: METAGENOMICS

Poster no. 16
Going deeper in deep sequencing: looking for recombinants molecules
Chiara Colantuono, Stefano Mazzoleni, Maria Luisa Chiusano

Poster no. 17
Metagenomic and metatranscriptomic analysis of bacteria from acid mine ecosystem
Jakub Ridl, Lukas Falteisek, Jan Paces, Hynek Strnad, Ivan Cepicka, Cestmir Vlcek

Poster no. 18
Metagenomic approaches to unravel the microbiome of deep-sea loriciferans
Michael Tangherlini, Alfonso Esposito, Roberto Danovaro, Maria Luisa Chiusano.

Poster no. 19
GLOSSARY: the GLobal Ocean 16S Subunit web Accessible Resource
Tangherlini M., Miralto M., Dell'Anno A., Corinaldesi C., Danovaro R., Chiusano M.L.

SESSION: OMICS AND MULTI-OMICS

Poster no. 20
Using deep learning for supervised feature selection in ovarian cancer detection A. d'Acierno, F. Nazzaro

Poster no. 21
Multiomic statistical approach to celiac disease
Eugenio Del Prete, Angelo Facchiano, Pietro Liò

Poster no. 22
HiCeekR: a novel Shiny app for the analysis of Hi-C data
Lucio Di Filippo, Miriam Gagliardi Maria Rosaria Matarazzo, Claudia Angelini

Poster no. 23
Characterization of epithelial-mesenchymal transition intermediate/hybrid phenotypes associated to resistance to EGFR inhibitors in non-small cell lung cancer cell lines
Valentina Fustaino, Dario Presutti, Teresa Colombo, Beatrice Cardinali, Giuliana Papoff, Rossella Brandi, Paola Bertolazzi, Giovanni Felici, Giovina Ruberti

Poster no. 24
A bioinformatics framework to identify cell subpopulations from bulk gene expression data of cancer samples.
Andrea Grilli, Sara Castellano, Cristina Battaglia, Silvio Bicciato

Poster no. 25
Single-sample transcriptional classification of colorectal cancer
Claudio Isella, Jessica Giordano, Enzo Medico

Poster no. 26
miRTissue: a web service for characterizing the type of miRNA-target interaction in specific tissues
Antonino Fiannaca, Massimo La Rosa, Laura La Paglia, Alfonso Urso

Poster no. 27
The ciliate Tetrahymena thermophila as a case study for the construction of a meta-model multi compartment resource and the analysis of free-living ciliate metabolism.
Alessio Mancini, Filmon Eyassu, Maxwell Conway, Annalisa Occhipinti, Sandra Pucciarelli, Claudio Angione , Pietro Liò

Poster no. 28
A Sparse Learning-Based Approach for class-specific feature selection
Ornella Affinito, Angelo Ciaramella, Sergio Cocozza, Gennaro Miele, Antonella Monticelli, Davide Nardone, Domenico Palumbo, Antonino Staiano

Poster no. 29
A Bioinformatic Framework to Assess the Transcriptomic Response of Species to Environmental Toxins
Siavash Nazari, Mehrdad Hajibabaei

Poster no. 30
A strategy combining a single variant and gene-based approach in multiplex family to detect rare variants associated with Rheumatoid Arthritis
Maëva Veyssiere, Javier Perea, Laetitia Michou, Anne Boland-Auge, Vincent Meyer, Jean-François Deleuze, François Cornelis, Elisabeth Petit-Teixeira, Valérie Chaudru

Poster no. 31
A Comparison Study between Filter Feature Selection Algorithms for Protein sequences Classification
Naoual Guannoni, Faouzi Mhamdi, Mourad Elloumi