BBCC2024

Bioinformatics and Computational Biology Conference

November 27-29, 2024

Aula Magna Facolta di Biotecnologie

Università di Napoli Federico II

Via Tommaso de Amicis 95

Naples, Italy

and

pre-conference training activities November 27-29, 2024 Area di Ricerca del CNR, via Castellino 111 Naples, Italy

PROGRAM

BBCC2024 Conference Chairs

Dr. Angelo Facchiano – National Research Council, Institute of Food Sciences, Avellino, Italy (Chair and Coordination of the BBCC Conference Series) Prof. Mario Guarracino – University of Cassino and Southern Lazio, Cassino, Italy. Dr. Ilaria Granata – National Research Council, Institute for High-Performance Computing and Networking, Naples, Italy Dr. Lucia Maddalena – National Research Council, Institute for High-Performance Computing and Networking, Naples, Italy Prof. Anna Marabotti – University of Salerno, Italy

Scientific Committee

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Dipartimento di Chimica e Biologia "A. Zambelli", University of Salerno, Italy



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BBCC2024 is as an Affiliated Conference of ISCB since 2017



Bioinformatics Italian Society patronizes BBCC conferences since 2006



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BBCC2024 Main Conference Program

November 27		
9:30	Opening the Registration Desk	
10:30	Conference Opening – Welcome and Introduction	
	Session: Structural Bioinformatics	
10:50	Invited lecture	
	Marta Szachniuk	
	Frontiers in computational prediction of RNA structure	
	Francesca Ferrero	
11:40	Relevance of DNA tridimensional shape in RNA:DNA:DNA triple helix formation Carmen Biancaniello	
	Probing Structural Dynamics of Human Prion Protein and T183A Variant through NMR-Restrained MD	
12:00	Simulations	
	Nancy D'Arminio	
12:20	MDaRes: a R-driven tool for MD Data through structural alphabet approaches	
12:40	Karol Wróblewski Exploring Protein Flexibility and Peptide Structure Prediction with CABS-flex	
13:00	Break – Lunch buffet Serena Rosignoli	
14:40	Developing Tools for Structural Bioinformatics: from Python to Bedside	
	Maria Milanesi	
15:00	Design and Validation of Broad-Spectrum Antiviral Compounds Against SARS-CoV-2	
	Simone Pirone	
15:20	Exploring Phosphomannomutase Evolution Through Structural and Sequence-Based Phylogenetics: Implications for Brain Hypoxia Response	
10.20	Sebastian Kmiecik	
15:40	Advancing Protein-Peptide Docking: New Applications of ESMFold and CABS-dock Methods	
16:00	Coffee Break and Poster session	
	Session: Databases of biological information	
16:30	Invited lecture	
	Marco Beccuti	
	IT Infrastructure and Computational Services in the PNRR IR SUS-MIRRI.IT Project to support the	
	Italian Microbial Research	
17:20	Elisa Mauriello Collating marine metagenomics resources	
17.20	Ivan Fruggiero	
17:40	An interactive genetic fingerprinting database for chestnut genotyping	
18:00	Closing remarks of first day	

November 28

9:00	Session: Omics and disease Bruno Giovanni Galuzzi
9:00	Identification of miRNA Biomarkers for Inflammatory Bowel Disease Using Machine Learning
	Carmen Marino
9:20	Metabolomic approach to investigating Nusinersen neurometabolic effects
9:40	Francesco Reggiani Data Fusion applications for cancer genomics data analysis
2.10	Mattia Fanelli
9:50	Combined MERFISH and bulk-RNA seq analysis on PDAC Spheroids infected with oncolytic virus SG33
	Francesco Massaini Spatial Duofilino of the Trunov Microauxinounant: A companison of tools for the extraction of features
10:00	Spatial Profiling of the Tumor Microenvironment: A comparison of tools for the extraction of features predictive of therapy response
10:10	Invited lecture
	Enrico Glaab
	Comprehensive blood metabolomics profiling analysis of Parkinson's disease
11:00	Coffee Break and Poster session
	Session: Bioinformatics development and applications
11:30	Vincenzo Bonnici PanDelos-plus: A parallel algorithm for computing genetic sequence homology in pangenomic analysis
11.50	Gregory Butler
11:50	Feature Engineering for Protein Sequence Analysis
	Maurizio Giordano
12:10	Context-specific Essential Genes Identification and Prediction by Learning Multi-Omics and Network Data Rodolfo Tolloi
12:30	NaStrO: an ultra-rapid, open-source computing pipeline for Nanopore data
10 -	Ludovica Celli
12:50	scVAR: a tool for the integration of genomics and transcriptomics from single cell RNA-sequencing data
13:10	Break – Lunch buffet
14:20	Special session: Collaborative Advancements in Bioinformatics: Integrating Infrastructure and Industrial Solutions
	Francesca De Leo
14:20	ELIXIR Infrastructure
	Roberta Bosotti
14:40	<i>The National Facility for Data Handling and Analysis at Human Technopole: supporting the Italian research community</i>
11.10	Sara Riccardo
15:00	Empowering discovery: advancing life sciences through accessible genomic innovation
4 - 4 -	Paolo Bianco – Marco Fiorletta
15:15	<i>Empowering Scientific Research: Customized HPC Solutions for Optimal Performance and Efficiency</i> <i>Michelangelo Sofo – Giuseppe Labianca</i>
15:30	DietAdhoc - A decision support system for nutrition specialists
	Laura Casalino
15 45	OASI Biobank: Advancing Asplenia Research through Integrated Bioinformatics and Collaborative
15:45	Infrastructure
16:00	Coffee Break and Poster session

16:30 Session: Novel and challenging methodologies and big data analysis

16:30	Invited lecture
	Jack Tuszyński
	Investigations of metabolic changes in cancer cells resulting from pharmacological agents and low- intensity electromagnetic fields
	Leili Shahriyari
	Personalized Cancer Care through Digital Twin Technology: Integrating Patient-Specific Data with
17:20	Quantitative Systems Pharmacology
	Carmine Fruggiero
17:40	inDAGO: a user-friendly graphical interface for dual RNA-seq data analysis
18:00	Closing remarks of second day
20:00	Social dinner (upon reservation)

November 29

9:00	Session: Novel and challenging methodologies and big data analysis (continued)
	Antonella Prisco
9:00	Modeling Variations in Antibody Response Magnitude and Longevity
	Roberta Esposito
	Metagenomic analyses identify biosynthetic gene clusters of Mediterranean sponges leading to bioactive
9:20	products
	Aleksandra Swiercz
9:40	Quality of semi-automated de novo genome assembly
10:00	End of session and communications
	Session: Statistics and Artificial Intelligence in Data Analytics
10:10	Invited lecture
	Audronė Jakaitienė
	Predictive Analytics in Medicine and Biology
11:00	Coffee Break and Posters
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14:30	Session: Systems biology
	Giovanni Scala
14:30	Multi-omics data integration methods for cancer-subtyping, drug discovery and tumor-model alignment
	Debora Dallera
	Integrative analysis of heterogeneous high-throughput transcriptomic data for promoter selection in bacterial
14:50	genomes to support microbial synthetic biology
	Silvia Giulia Galfrè
15:10	Machine learning and explainable AI for transcriptomic analysis in Multiple Sclerosis
	Chiara Cimolato
15:30	Mathematical Modeling of Phage-Mediated CRISPRi System for Inhibiting Antibiotic Resistance
	Special session: Funding opportunities for young scientists
15:50	Organized by youngBITS, young-infolife, and ISCB RGS-Italy groups
	Ermanno Rizzi - Italian Cystic Fibrosis Research Foundation (FFC Ricerca)
	"Funding initiatives for young researchers: the experience of the Italian Cystic Fibrosis Research Foundation
	(FFC Ricerca)".
	Daniela Guidone - Telethon Institute of Genetics and Medicine (TIGEM) and "Gianni Mastella Research
	Fellowship 2024"
16:00	Airway surface as a battleground against bacteria
	Michele Genovese - Telethon Institute of Genetics and Medicine (TIGEM) and "Gianni Mastella Starting
	Grant 2024"
16:10	"Alternative therapeutic target to restore the mucociliary clearance in CF"
	Round table with the session speakers and representatives of the youngBITS, young-infolife, and RGS-Italy
16:50	ISCB groups
16:50	Announcements: best oral and poster presentation awards – Future works

17:00 Closing of the Conference

Pre-Conference Training Activities

Two training activities are held at:

Consiglio Nazionale delle Ricerche (CNR), Via Pietro Castellino 111, Naples, Italy Each activity is restricted to a maximum number of 15 participants, selected on the basis of demand.

November 25

One-day training activity From raw matrices to differential expression/methylation patterns: a functional genomics approach to detect molecular insights

Instructors and Organizers: Dr. Luca Ambrosino and Dr. Francesco Cecere Institute of Genetics and Biophysics "Adriano Buzzati-Traverso" Consiglio Nazionale delle Ricerche, Naples, Italy

November 26

One-day training activity Software Environments, Containers, and Notebooks (for Bioinformatics and Computational Biology)

Instructor Dr. Raoul Bonnal, IFOM - Research Computing & Data Science Manager Helpers Dr. Riccardo Lorenzo Rossi, Bioinformatics scientist, and Dr. Cristiano Petrini, Bioinformatics engineer - IFOM-ETS, Research Computing & Data Science

Organisers

Prof. Anna Marabotti, University of Salerno, ELIXIR-IT, Italy Prof. Allegra Via, University of Rome "La Sapienza", ELIXIR-IT, Italy Dr. Angelo Facchiano, CNR-ISA, Avellino, Italy Dr. Ilaria Granata, CNR-ICAR, Naples, Italy Dr. Lucia Maddalena, CNR-ICAR, Naples, Italy

This training is organized by the ELIXIR-IT Training Platform