

BBCC2024
Bioinformatics and Computational Biology Conference
November 27-29, 2024

Overview Program

November 25

One-day training activity

From raw matrices to differential expression/methylation patterns: a functional genomics approach to detect molecular insights

(participation limited to 15 attendees)

November 26

One-day training activity

Software Environments, Containers, and Notebooks (for Bioinformatics and Computational Biology)

(participation limited to 15 attendees)

November 27-29

BBCC2024 Main Conference

BBCC2024 Main Conference Program

November 27

9:30 Opening the Registration Desk

10:30 Conference Opening – Welcome and Introduction

Session: Structural Bioinformatics

10:40 Invited lecture

Marta Szachniuk

Frontiers in computational prediction of RNA structure

Francesca Ferrero

11:30 *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

11:50 *Simulations*

Nancy D'Arminio

12:10 *MDaRes: a R-driven tool for MD Data through structural alphabet approaches*

Karol Wróblewski

12:30 *Exploring Protein Flexibility and Peptide Structure Prediction with CABS-flex*

12:50 **To be confirmed**

13:10 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

Exploring Phosphomannomutase Evolution Through Structural and Sequence-Based Phylogenetics:

15:20 *Implications for Brain Hypoxia Response*

Sebastian Kmiecik

15:40 *Advancing Protein-Peptide Docking: New Applications of ESMFold and CABS-dock Methods*

16:00 Coffee Break and Posters

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

Elisa Mauriello

17:20 *Collating marine metagenomics resources*

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*

Francesco Reggiani

9:40 *Data Fusion applications for cancer genomics data analysis*

Mattia Fanelli

9:50 *Combined MERFISH and bulk-RNA seq analysis on PDAC Spheroids infected with oncolytic virus SG33*

Francesco Massaini

Spatial Profiling of the Tumor Microenvironment: A comparison of tools for the extraction of features

10:00 *predictive of therapy response*

10:10 **Invited lecture**

Enrico Glaab

Comprehensive blood metabolomics profiling analysis of Parkinson's disease

11:00 **Coffee Break and Posters**

Session: Bioinformatics development and applications

Vincenzo Bonnici

11:30 *PanDelos-plus: A parallel algorithm for computing genetic sequence homology in pangenomic analysis*

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*

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**

Special session: Collaborative Advancements in Bioinformatics: Integrating Infrastructure and Industrial Solutions

Francesca De Leo

14:20 *ELIXIR Infrastructure*

Roberta Bosotti

The National Facility for Data Handling and Analysis at Human Technopole: supporting the Italian research community

14:40 *Sara Riccardo*

15:00 *Empowering discovery: advancing life sciences through accessible genomic innovation*

Paolo Bianco – Marco Fiorletta

15:15 *Empowering Scientific Research: Customized HPC Solutions for Optimal Performance and Efficiency*

Michelangelo Sofo – Giuseppe Labianca

15:30 *DietAdhoc® a decision support system nutrition specialists*

Laura Casalino

OASI Biobank: Advancing Asplenia Research through Integrated Bioinformatics and Collaborative

15:45 *Infrastructure*

16:00 *Concluding remarks on the session, with questions and answers to all speakers*

16:10 Coffee Break and Posters

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

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 products

9:20

Aleksandra Swiercz

9:40 *Quality of semi-automated de novo genome assembly*

10:00 *To be confirmed (short presentation)*

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

Krzysztof Pysz

11:30 *Deep discriminative models in the detection of amyloid signaling motifs*

Marco Benedetto

11:50 *AI-Driven Antibiotic Resistance Prediction in Hospital and Clinic Settings*

Alessandro Esposito

Classification and biochemical evaluation via Raman and Surface-enhanced Raman scattering spectroscopy of breast cancer cell lines expressing different levels of HER2

12:10

Francesca Cuturello

Enhancing predictions of protein stability changes induced by single mutations using MSA-based language models

12:30

12:50 *To be confirmed*

13:10	Break –Lunch buffet
14:30	Session: Systems biology <i>Giovanni Scala</i>
14:30	<i>Multi-omics data integration methods for cancer-subtyping, drug discovery and tumor-model alignment</i> <i>Debora Dallera</i>
14:50	<i>Integrative analysis of heterogeneous high-throughput transcriptomic data for promoter selection in bacterial genomes to support microbial synthetic biology</i> <i>Silvia Giulia Galfrè</i>
15:10	<i>Machine learning and explainable AI for transcriptomic analysis in Multiple Sclerosis</i> <i>Chiara Cimolato</i>
15:30	<i>Mathematical Modeling of Phage-Mediated CRISPRi System for Inhibiting Antibiotic Resistance</i>
15:50	Round Table - Young-BITS and Young-InfoLife members and funding opportunities
16:50	<i>Announcements: best oral and poster presentation awards – Future works</i>
17:00	<i>Closing of the Conference</i>