

BBCC2026

Bioinformatics and Computational Biology Conference

21-23 October, 2026

Chioostro San Francesco, Via Luca Giordano, 2, Naples, Italy



ABSTRACT BOOK

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BBCC2026 Conference Program

Day 1 - October 21

13:30 *Registration Desk Opens*

14:15 *Conference Opening – Welcome and Introduction*

Invited lecture

14:30 **Prof. Diego Di Bernardo**, Dept. of Chemical, Materials and Industrial Engineering, University of Naples “Federico II”, Italy & Telethon Institute of Genetics and Medicine.
Engineering Gene Circuits to advance therapy of Rare Genetic Disorders: from mathematical modelling to experimental implementation

15:20 Lorenzo Bertolini Agnoletto
Mapping the operating regime of in-context learning in Evo 2: matched natural and synthetic sequences isolate length and scale as the limits of performance

15:40 Heshmat Borhani
Small Signature, Full Picture: A 50-Gene Classifier Resolves Unclassified Colorectal Cancers

16:00 Marialuisa Lusito
Rethinking the Denominator: Deep Learning Segmentation Rescues Mitochondrial Activity from Confluency Artifacts

16:20 *Coffee Break and Posters*

17:00 Domenico Palladino
Unexpected Intestinal Inflammation in Eosinophilic Esophagitis Revealed by Cytokine Profiling and Bioinformatic Analysis

17:20 Riccardo De Luca
Supporting Reactome LLM Curator Tool with Domain-Specific Models and Semantic Partitioning

17:40 Carla Pollastro
An Integrated Statistical–Bioinformatic Patient-Level Workflow for Exploratory Genomic Characterization of Rare Neoplasms Using Tumor–Normal Whole-Exome Sequencing

18:00 Francesco Nascimben
Enhancing Missense Variant Pathogenicity Prediction through Local Graph Modelling

18:20 Dhruv C. Rathod
From Knowledge Graph to Molecular Mechanism: Mapping Heme-TLR4 Inflammatory Signaling Using Computational and Experimental Approaches

18:40 *Closing remarks and communications*

Day 2 - October 22

9:00	Opening of the Second Day
	Carmen Di Giovanni
9:00	Molecular Insights into Cr(VI)-Induced Disruption of Sperm Chromatin
	Lucrezia Pierfederici
9:20	Temporal transcriptomic signature of Oropouche virus infection in human vaginal epithelium
	Noemi Scala
9:40	The phosphomannomutase axis in medulloblastoma: an integrative computational perspective
	Invited lecture
10:00	Prof. Dr. Manja Marz , Faculty of Mathematics and Computer Science, Friedrich-Schiller-University Jena, Jena, Germany. Full genome alignments with RNA secondary structures of RNA viruses
10:50	Coffee Break and Posters
	Evgenia V Kriventseva
11:30	Scaling orthology to pangenomic and metagenomic data: the OrthoDB and BUSCO ecosystem
	Paulina Hladki
11:50	Not All RNA Motifs Speak the Same Sequence Language
	Alfredo Iacoangeli
12:10	Beyond Disease Risk: Using Large-scale Human Genomics to Deconstruct ALS
	Martina Terrusa
12:30	Leishmania infantum infection associated with reduced A-to-I RNA editing in human neutrophils
	Marika D'Avanzo
	From Sequences to Strategies: AI-Based Early Detection of SARS-CoV-2 Variants and Their Impact on Hospitalizations
12:50	
13:00	Break – Lunch buffet
	Invited lecture
14:00	Dr. Alessandro Pandini , Department of Computer Science, Brunel University of London, UK. Decoding Protein Molecular Dynamics with Graph Models, Residue Coevolution and Machine Learning
	Francesca Cuturello
14:50	Learning Protein–Protein Interaction Interfaces from Multimodal Representations
	Guido Barducci
	ProbJanusDDG: A Protein Stability Change Predictor with Calibrated Uncertainty Intervals for Individual Mutations
15:10	
	Otho Mantegazza
15:30	Evo 2's Perception of Single Nucleotide Substitutions in the Genes of Two Plant Model Organisms
	Matteo Manfredi
	Alpha&ESMhFolds: An updated database for the comparison and functional annotation of predicted structural models for the human proteome
15:50	
	Rino Ragno
	db.3d-qsar.com. A Unique Free and Interactive Database of Ligand- and Structure- and AI-Based (3D) QSAR Models
16:10	
16:30	Coffee Break and Posters
17:10	Network Tools and Applications in Biology (NETTAB) Invited lecture Dr Martina Stella , Algorithmiq, Milano, Italy. Redefining computation: quantum computing for real-world impact today
18:00	Closing remarks and communications
20:00	<i>Social dinner (reserved for participants who have booked their participation)</i>

9:00	Opening of the Third Day Martina Palummo Systematic prediction of drug responsiveness across cancer cell lines based on machine learning from DNA methylation profiles
9:00	Cinzia Pizzi AquaSei: A Deep Learning Framework for Functional Prediction of Non-Coding Variants across Multiple Aquaculture Species
9:20	Alessandra Robello Computational Framework for the Design of Second-Generation Pharmacochaperones Targeting Allosteric Pockets
10:00	Invited lecture Prof. Irina Moreira , Faculty of Sciences and Technology, University of Coimbra, Portugal. Structural Biology in the Age of AI: Integrating Bioinformatics and Translational Research
10:50	Coffee Break and Posters Thi Kim Hue Nguyen Coupled Autoencoder for multi-omics data integration
11:30	Simone Bonora Structure-Based Characterization of Rare Germline Variants in Lung Cancer Susceptibility
11:50	Maria Chiara Langella Navigating omics opportunities and bottlenecks: why FAIRification and scientist responsibility matter
12:10	Prof. Richard Röttger , Dept. of Mathematics and Computer Science (IMADA) University of Southern Denmark (SDU), Odense M, Denmark. Collaborative Data Science – From Real Estate to Spatial Transcriptomics”
12:30	
13:00	Closing ceremony and announcements
13:10	Lunch buffet

Tutorials

	Tutorial no. 1	Tutorial no. 2	Tutorial no. 3
Title	From Omics Data and Metadata to Clinical Meaning: Bioinformatics in Cancer and Rare Disease	Introduction to Biological Network Analysis and Robustness Assessment	Hello, nf-core!
When	October 21 – 9:00 – 13:00	October 21 – 9:00 – 13:00	October 23 – 14:30 – 17:30
Where	Info mailed to participants	Conference Room	Conference Room
Instructors	Francesco Cecere, Senior Bioinformatic Researcher, and Eva Luna Tarallo, Junior Bioinformatic Researcher (UOS Laboratori di Ricerca e Biobanca AORN Santobono-Pausilipon IRCCS, Naples, Italy).	Annamaria Carissimo, Senior Researcher, Istituto per le Applicazione del Calcolo “M.Picone”, National Research Council of Italy, Naples, Italy; and Valeria Policastro, Junior Assistant Professor Dep. of Political Science, Univ. of Naples “Federico II”, Naples, Italy	Margherita Mutarelli, staff researcher, Institute of Applies Sciences and Intelligent Systems “Eduardo Caianiello”, Pozzuoli, Italy

Sponsors and Supporting Institutions



Institute of Food Sciences of the National Research Council of Italy



Department of Chemistry and Biology "A. Zambelli", University of Salerno, Italy



University of Salerno, Italy

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