BBCC2025
Bioinformatics and
Computational Biology Conference
December 1-4, 2025
20th annual edition

Programme

BBCC2025 Conference Chairs

Dr. Angelo Facchiano – National Research Council, Institute of Food Sciences, Avellino, Italy (Chair and Coordination of the BBCC Conference Series)
Prof. Michele Caraglia – University of Campania "L. Vanvitelli", Naples, Italy.
Prof. Anna Marabotti – University of Salerno, Italy
Prof. Silvia Zappavigna – University of Campania "L. Vanvitelli", Naples, Italy

Scientific Committee
Dr. Claudia Angelini – National Research Council, Institute for Applied Mathematics "M. Picone", Italy
Prof. Karine Audouze – University Paris Cité, Paris, France
Prof. Pantelis Bagos – University of Thessaly, Greece
Prof. Maria Luisa Chiusano – University of Naples "Federico II", Naples, Italy
Prof. Paola Festa – University of Naples "Federico II", Italy
Prof. Christoph Friedrich – University of Applied Science and Arts Dortmund, Germany
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. Bruno Hay Mele – University of Naples "Federico II", Naples, Italy
Prof. Dominik Heider – Director of the Institute for Medical Informatics, University of Münster, Germany
Dr. Lucia Maddalena – National Research Council, Institute for High-Performance Computing and Networking, Naples, Italy
Prof. Irina Moreira, Faculty of Sciences and Technology, Coimbra University, Portugal
Dr. Vera Pancaldi, INSERM, Centre de Recherches en Cancérologie de Toulouse, France
Prof. Alessandro Pandini – Brunel University London, UK
Prof. Roberto Tagliaferri – University of Salerno, Italy
Prof. Ozlem Tastan Bishop – Rhodes University, South Africa

BBCC2025 is organized with the following Partners and Sponsors:

Institute of Food Sciences of the National Research Council of Italy (ISA-CNR)

BBCC is as an Affiliated Conference of ISCB since 2017

Bioinformatics Italian Society patronizes BBCC conferences since 2006

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Conference Programme

December 1, 2025

9:30	Opening of the Registration Desk
10:30	Conference Opening – Welcome and Introduction
10:40	**Invited Lecture** **Prof. Yayoi Natsume-Kitatani** ***Data-Driven Approaches to Medical and Omics Data for Advancing Drug Discovery***
11:30	Marcelo Hurtado *CellTFusion: A novel approach to unravel cell states via cell type deconvolution and TF activity estimated from bulk RNAseq data identifies clinically relevant cell niches*
11:50	Maria Chiara Langella *Computational approaches to identify programmed cell death-regulating natural compounds in cancer research*
12:10	Aleksandar Anžel *Enhancing Biomedical Time Series Analysis and Visualization through Interactive Summary Polar Diagrams*
12:30	Chiara Fiorentino *An RNAseq alone approach to quantify skewed X chromosome inactivation from bulk RNAseq data*
12:50	Communications from the organizing committee
13:00	Break – Lunch buffet and Posters
14:20	Luigi Di Costanzo *The Protein Design Archive (PDA) and the PDBx/mmCIF Transition: Tools and Standards for the Future of Structural Biology*
14:40	Carmen Biancaniello *Integrative NMR and ML-Driven MD Reveal PKA Phosphorylation of a High-Energy State of RKIP*
15:00	Gabriele Tomé *ProTN: a comprehensive workflow to match proteomics with computational analysis at high resolution*
15:20	Michela Quadrini *STAlign: A Proximity-Based Framework for Comparing RNA and Protein 3D Structures*
15:40	Coffee Break and Posters
16:00	**Invited Lecture** **Prof. Tomasz Żok** ***When bases break the rules – taming the non-canonical nucleic acids***
16:50	Stefano Marino *RnaEnsembleFold, a pseudo-SHAPE generative RNA secondary structure predictive algorithm*

17:10	Margherita A.G. Matarrese *Identification of RNA Triple Helices from Sequence and Secondary Structure*
17:30	Closing remarks for the first day
18:00	Social Activity for BBCC Participants
20:00	Social Dinner (reserved for participants who have booked their participation)

December 2, 2025

8:45	Opening of the Registration desk
9:00	Andre Jatmiko Wijaya *Genomic Data Representation for Horizontal Gene Transfer Detection*
9:20	Gabriele Leoni *Are Genomic Language Models Learning the Molecular Logic of Translation?*
9:40	**Invited Lecture** **Prof. Barbara Di Camillo** ***From Single Cells to Multicellular Information Systems Analysis***
10.30	Round Table: **NETwork Tools and Applications in Biology (NETTAB): what are the next frontiers for bioinformatics** Discussion with current and former members of the Scientific Committee, invited speakers, and all conference participants
11:00	Coffee Break and Posters
11:30	Vasuk Gautam *Unraveling ASCVD Risk in HIV through Multi-Omics Integration: Linking Gut Microbiome Dysbiosis and Triglyceride Alterations*
11:50	Francesca Calanca *Omics2Surv From Penalized Models to Deep Learning: An R Package for Multi-Omics Survival Analysis*
12:10	Dramane Dagnogo *Brain-Blood Transcriptional Multi-tissue Analysis Reveals Shared Inflammatory Signatures*
12:30	Tiziana Castrignanò *Software Tools for the Development of de novo Transcriptome Assembly Resources*
12:50	Emine Sumeyra Turali Emre *Automated Screening of Antibacterial Nanoparticle Literature: Dataset Curation and Model Evaluation*
13:10	Break – Lunch buffet and Posters
14:20	Elie Maza *A stable combination of non-stable genes outperforms standard reference genes for RT-qPCR data normalization*

14:40	Francesco Cecere *scGraphVerse: An R package for Inferring and Integrating Single-Cell Gene Regulatory Networks*
15:00	Agostino Aiezzo *Early Sepsis Prediction using Time-Series Machine Learning: A Multi-Dataset Analysis and Dynamic Risk Stratification*
15:20	Amalia Chiariello *GenePrior: a modular R workflow for tier-based variant prioritization and automated reanalysis of exome data*
15:40	Giorgia Bucciarelli *RNA binding and modification multiomics decode the role of YBX1 in limiting cutaneous squamous cell carcinoma invasion*
16:00	Antonio Colaprico *Multi-Omics profiling of neuroblastoma identifies immunological biomarkers associated with higher risk of relapse: results from the MICCHADO study*
16:20	**Invited Lecture** **Prof. Sean Holden** ***Optimal Transport in Bioinformatics with an Application to Spatial Omics Data***
17:10	Announcements, awards, future works
17:30	Closing of the Conference

Training activities

Activity no. 1: Tutorial in R on bulk RNA-seq analysis: from raw counts to biological interpretation

December 3 – 9:00 – 14:00

This practical tutorial covers the analysis of bulk RNA-seq data using R and Bioconductor packages. We'll use DESeq2 for differential expression analysis, which is one of the most popular and robust methods for RNA-seq analysis.

Instructions to register for this activity will be given to registered participants to the BBCC2025 Conference. If places are still available, consideration will be given to opening registration to individuals who are not registered for the conference.

Activity no. 2: Spatial Transcriptomics Analysis in R

December 3 – 9:00 – 14:00

Spatial transcriptomics enhances traditional RNA sequencing by preserving tissue architecture, allowing gene expression analysis in its spatial context. This technology is transforming fields like developmental biology, neuroscience, and cancer research by providing insights into tissue organization and cell interactions. This course offers a comprehensive introduction to spatial transcriptomics data analysis using R, covering key topics such as technological platforms, preprocessing, quality control, normalization, clustering, differential analysis, spatially variable genes, and tissue microenvironment analysis.

Activity no.3: Train-the-Trainer

December 3 and 4 – full day

This course is part of the ELIXIR-GOBLET Train the Trainer (TtT) programme. TtT courses aim to give new instructors and teachers tools and tips for providing an enriching learning experience to trainees, irrespective of topic, and to include best-practice guidance on course and training material development.