

CIBB 2026

Version 2 - updated August 18, 2026

Detailed Program - September 2-4, 2026 - Sapienza University of Rome

Use PDF search (Ctrl/Cmd+F) to find an EasyChair ID, paper title, or author. A compact paper index is included at the end.

Opening	Wed 2 Sep, 08:45 - Opening Remarks; 09:15 - Opening Scientific Introduction
Poster sessions	Museo dell'Arte Classica
Welcome event	Wed 2 Sep, 19:00 - Welcome Cocktail + MUSA Jazz Concert
Social programme	Thu 3 Sep, from 18:00 - Social Event + Social Dinner
Closing	Fri 4 Sep, 17:45 - Closing Remarks, Aula Magna

Wednesday, September 2

Time	Room	Session	ID	Paper title	Authors
08:45–09:10	Aula Magna	Opening Remarks			
09:15–09:30	Aula Magna	Opening Scientific Introduction		ELIXIR-IT: the Italian Research Infrastructure for Big Data in Life Sciences	Graziano Pesole
09:30–09:45	Aula Magna	Bioinformatics Main Track 1	8929	An Enhanced Pipeline for Multi-Omic Integration Based on Topological Data Analysis	Veronica Paparozzi, Anna Plaksienko, Marco Pedicini and Christine Nardini
09:45–10:00	Aula Magna	Bioinformatics Main Track 1	4302	Analysis of biological networks using Krylov subspace trajectories	H. Robert Frost
10:00–10:15	Aula Magna	Bioinformatics Main Track 1	2693	Evaluating SMT-Based Formal Inference for GRN Synthesis: From Data Density to Structural Rules	Ofri Caspi, Michal Greenberg, Eitan Tannenbaum and Hillel Kugler
10:15–10:30	Aula Magna	Bioinformatics Main Track 1	2493	A Pipeline for Predicting Variant Associations with Complex Disorders via Functional Annotations	Francesco Gualdi, Zeno Darani, Daniele Malpetti, Marco Scutari and Francesca Mangili
10:30–11:00	All rooms	Coffee Break			
11:00–11:15	Aula Gini	SS1: AI and Computational Methods for Medical Informatics — Part I	1619	Diagnosing Rejection Collapse via Uncertainty Decomposition	Walter Endrizzi, Flavio Ragni, Stefano Bovo, Monica Moroni, Giuseppe Jurman and Venet Osmani
11:00–11:15	Aula III	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	6217	Quantum Machine Learning for Missense Variant Pathogenicity Prediction in the KCNQ Gene Family	Markel Garcia, Sara Capponi, Aitor Bergara and Aritz Leonardo
11:00–11:15	Aula Magna	SS11: GPU-accelerated analysis of single-cell and spatial omics	7261	GPU-accelerated single-cell and spatial transcriptomics on NVIDIA DGX H100: a systematic benchmark of speed, scalability, and biological concordance	Luca Vedovelli, Corrado Lanera, Daniele Sabbatini and Dario Gregori
11:15–11:30	Aula Gini	SS1: AI and Computational Methods for Medical Informatics — Part I	3868	ClinRAG-BiLSTM: An Agentic Cloud AI Framework for Explainable and Traceable Breast Cancer Decision Support	Adaleta Gicic and Dženana Đonko
11:15–11:30	Aula III	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	1942	Zero-shot phenotype prediction and screening of engineered immune receptor variants using contrastive learning-based workflow	Jie Shi, Yenho Chen, Kyle Daniels, Shangying Wang and Sara Capponi
11:15–11:30	Aula Magna	SS11: GPU-accelerated analysis of single-cell and spatial omics	7861	CudaMon: An R Package to Monitor NVIDIA GPUs, Showcased by Monitoring a GPU-accelerated Single-cell Analysis Workflow in R	Mohammad Amin Zadenoori, Riccardo Ceccaroni, Davide Risso and Gabriele Sales
11:30–11:45	Aula Gini	SS1: AI and Computational Methods for Medical Informatics — Part I	8082	Towards Federated and Explainable Quantum Machine Learning for Possible Epileptic Seizure Detection	Francesco Mercaldo, Hubert Schölnast, Oliver Eigner, Marta Petyk, Antonella Santone, Mario Cesarelli, Fabio Martinelli and Paul Tavalato
11:30–11:45	Aula III	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	1095	A Landmarked Penalised Weibull Framework for Time-Updated Survival Modelling of Heterogeneous Clinical Outcomes in Multiple Sclerosis	Francisco José Aparicio Serrano, Ariadna Masot-Llima, Agustín Pappolla, Susana Otero-Romero, René Carvajal, Álvaro Cobo-Calvo, Manel Alberich, María Jesús Arévalo, Georgina Arrambide, Cristina Auger, Joaquín Castillo, Manuel Comabella, Ingrid Galán, Daniel Hernández, Carlos Nos, Jordi Río, Breogán Rodríguez-Acevedo, Jaume Sastre-Garriga, Ángela Vidal-Jordana, Ana Zabalza, Àlex Rovira, Xavier Montalban, Mar Tintoré, Marco Lorenzi, Deborah Pareto and Carmen Tur
11:30–11:45	Aula Magna	SS11: GPU-accelerated analysis of single-cell and spatial omics	1377	DualBioGraph: Patient-Held-Out Tumor--Normal Classification Using Dual Graph Neural Networks	Al Hamna Asif, Rana Abubakar, Amna Younus, Juan Jose Vegas Olmos and Filippo Cugini

Time	Room	Session	ID	Paper title	Authors
11:45-12:00	Aula Gini	SS1: AI and Computational Methods for Medical Informatics — Part I	4010	Predicting Alzheimer's Progression Over Time Using Sheaf Neural Networks and Brain Graphs	Annamaria Defilippo, Giulia Avolio, Pierangelo Veltri, Pietro Liò and Pietro Hiram Guzzi
11:45-12:00	Aula III	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	1964	AI-assisted Single-Cell transcriptomics reveals persistent malignant CD4+ activity in Sézary Syndrome patient	Domenico Palumbo, Viola Melone, Luigi Palo, Carlo Ferravante, Giulia Salvatore, Cristina Cristofolletti, Maria Grazia Narducci and Roberta Tarallo
11:45-12:00	Aula Magna	SS11: GPU-accelerated analysis of single-cell and spatial omics	7472	A topological object-proposal pipeline for cellular fiber segmentation	Riccardo Ceccaroni, Valerio Reffo, Camilla Pezzini, Roberta Sartori, Marco Sandri, Pierpaolo Brutti and Davide Risso
12:00-12:15	Aula Gini	SS1: AI and Computational Methods for Medical Informatics — Part II	6112	Ontology-Aware Candidate Reranking for SNOMED CT Entity Linking in Clinical Notes	Luka Blašković, Nikola Tanković and Ivo Ipšić
12:00-12:15	Aula III	Biostatistics Main Track	7999	Evaluating in-context learning with prompting regimes for transformer-based synthetic health tabular data generation	Amanda Bertgren, Fredrik Öhberg, Paolo Soda, Ulf Näslund, Patrik Wennberg and Christer Grönlund
12:00-12:15	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	8123	Secondary structure design for efficient translation initiation	Tobias von der Haar and Corina Keller
12:15-12:30	Aula Gini	SS1: AI and Computational Methods for Medical Informatics — Part II	5226	Evaluating Locally-Deployable Large Language Models on Free-Text Data in an Italian Obstetric Context	Pierluigi Reali, Giulio Steyde, Gianluca Carta, Mark James Carman and Maria Gabriella Signorini
12:15-12:30	Aula III	Biostatistics Main Track	3151	Multivariate Model-Based Landmarking Approach in Mixture Cure Models to Dynamic Prediction	Bianca Ferraro, Marco Alfò and Marta Cipriani
12:15-12:30	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	3825	Manufacturability of mRNA Therapeutics: Native vs. N-1-Methyl-Pseudouridine	Roland Huber, Kuo Chieh Liao and Yue Wan
12:30-12:45	Aula Gini	SS1: AI and Computational Methods for Medical Informatics — Part II	4267	Decoding HIV-1 Antibody Escape with Interpretable Protein Language Models	Fahsai Nakarin, Pawin Taechoyotin and Kayla G. Sprenger
12:30-12:45	Aula III	Biostatistics Main Track	7447	Functional Fuzzy Clustering of Longitudinal biological marker's trajectories	Silvia D'Elia, Valeria Paggi, Marco Alfò and Maria Brigida Ferraro
12:30-12:45	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	7526	Optimizing RNA yield using deep neural networks coupled to massively parallel screening	Adrien Villain
12:45-13:00	Aula Gini	SS1: AI and Computational Methods for Medical Informatics — Part II	3189	AutoEncoder based approach for the identification of genomic regions responsible for poorly described oligo-patient disorders	Joanna Szyda
12:45-13:00	Aula III	Biostatistics Main Track	4469	Reducing the Size of Breastfeeding Reference Arms in Infant Nutrition Studies Using Prognostic Covariate Adjustment	Luca Lavalle
12:45-13:00	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	4170	MAP-Net: An Interpretable Deep Learning Framework for Universal mRNA Manufacturability	Giorgio Ciano
13:00-13:15	Aula Gini	SS1: AI and Computational Methods for Medical Informatics — Part II	7478	Prediction of treatment response in Multiple Sclerosis with Machine Learning models	Ariadna Masot-Llima, Francisco Aparicio-Serrano, Agustín Pappolla, Susana Otero-Romero, René Carvajal, Álvaro Cobo-Calvo, Manel Alberich, María Jesús Arévalo, Georgina Arrambide, Cristina Auger, Joaquín Castillo, Manuel Comabella, Ingrid Galán, Daniel Hernández, Carlos Nos, Jordi Río, Breogán Rodríguez-Acevedo, Jaume Sastre-Garriga, Àngela Vidal-Jordana, Ana Zabalza, Àlex Rovira, Xavier Montalban, Mar Tintoré, Xavier Lladó, Deborah Pareto and Carmen Tur

Time	Room	Session	ID	Paper title	Authors
13:00–13:15	Aula III	Biostatistics Main Track	0193	A Dependent Dirichlet Process Approach to Population Size Estimation	Lucia Gallucci
13:00–13:15	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	5527	Toward Simulation-Informed Lipid Nanoparticle Design with Martini Coarse-Grained Models	Mariana Valério, Pablo Cardona Perez, Salma Maaquili, Mariia Borbuliak and Paulo C. T. Souza
13:15–14:15	All rooms	Lunch			
14:15–14:30	Aula Magna	Bioinformatics Main Track 2	2019	Sequence-Derived Physicochemical Features and Stacked Learning for SUMOylation-Site Prediction	Junyan Li, Qiaobin Yao, Danda Rawat, Jiang Li and Shaolei Teng
14:30–14:45	Aula Magna	Bioinformatics Main Track 2	8294	LLM-Guided Integer Linear Programming for Antibody Library Design	Mikel Landajuela Larma
14:45–15:00	Aula Magna	Bioinformatics Main Track 2	3485	Cell Senescence Identification Using Single-Cell Transcriptomics Foundation Model	Yongqi Zhao, Fan Tong, Xiangwen Zheng, Yuanyuan Ma, Huajian Mao, Yuting Zhou, Peixiang Yang and Dongsheng Zhao
15:00–15:15	Aula Magna	Bioinformatics Main Track 2	2325	OmicsGPT: Multi-Agent Bioinformatics Orchestration for Evidence-Grounded RNA-seq Interpretation	Patrick Roney and James Li
15:15–15:30	Aula Magna	Bioinformatics Main Track 2	8670	Single-cell characterization of HERV-K transcriptional landscapes in acute and chronic HIV infection	Lucrezia Pierfederici, Elisabetta Lazzari, Gabriella Rozera, Lavinia Fabeni, Flavia Smoquina, Giulia Berno, Federica Forbici, Valentina Mazzotta, Andrea Antinori, Daniele Pietrucci, Daniele Maria Papetti, Fabrizio Maggi, Isabella Abbate and Giovanni Chillemi
15:30–15:45	Aula Magna	Bioinformatics Main Track 2	8886	Identifying functional drivers of Hepatoblastoma outcomes via agent-based modeling and transcriptomics	Alessandro Ravoni, Yuanhua Liu, Stefano Cairo, Filippo Castiglione and Christine Nardini
15:45–16:00	Aula Magna	Bioinformatics Main Track 2	6161	CellChat Hotspot: A Focused Lens on Tumor Microenvironment Communication	Dario Monaco, Mirea Dioguardi, Maria Dipalma, Eliseo Mattioli, Francesco Alfredo Zito, Francesco Giovannelli, Angela Ricco, Oronzo Brunetti, Antonella Argentiero and Simona De Summa
16:00–16:45	Aula Magna	Keynote — Nicola Segata		Computational metagenomics to unravel person-to-person microbiome transmission	Nicola Segata
16:45–19:00	Museo dell'Arte Classica	Poster Session A / Coffee Break			
19:00–20:00	Museo dell'Arte Classica	Welcome Cocktail + MUSA Jazz Concert			

Thursday, September 3

Time	Room	Session	ID	Paper title	Authors
08:45–09:00	Aula Magna	Medical Informatics Main Track 1	2797	Soft-GLCM: Stabilizing Differentiable Texture Analysis through Soft Quantization	Haoyue Chen, Giuseppe Salvaggio, Albert Comelli and Anthony Yezzi
09:00–09:15	Aula Magna	Medical Informatics Main Track 1	2624	A Unified Framework for Bipartite Network Projection and Backbone Extraction, with an Application to Gene–Disease Associations	Panagiota Kontou, Ioannis Charatsiaris, Efstathios Voulgaris and Pantelis Bagos
09:15–09:30	Aula Magna	Medical Informatics Main Track 1	5158	All Biases Are Not Equal: Implications for Equity in Emergency Department AI through a Gender Lens	Marta Avalos, Nadia Elorga-Castagnet, Lucía Gallego-Andrés, Cédric Gil-Jardiné, Ariel Guerra-Adames, Emilie Lesaine, Yamina Meziani, Marie Peyronnet and Andja Srebro
09:30–10:15	Aula Magna	Keynote — Marianna Rapsomaniki		Building predictive models for precision oncology across scales, modalities and perturbations	Marianna Rapsomaniki
10:15–12:30	Museo dell'Arte Classica	Poster Session B / Coffee Break			
12:30–13:30	All rooms	Lunch			
13:30–13:45	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	3483	A Block Decomposed QUBO Workflow for Chromosome-Y Phylogeny Reconstruction	Giuliana Siddi Moreau, Riccardo Berutti, Manuela Profir, Lorenzo Pisani, Maria Laura Clemente and Lidia Leoni
13:30–13:45	Aula III	SS7: Computational Intelligence for Integrative Host–Microbe Genomics: From Single-Cell Regulation to Population-Scale Pangenomes	0628	An entropy based method for mapping mixed lineage next generation sequencing data	Gregory Fonseca
13:30–13:45	Aula Magna	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	5147	Microbial Community Structure and Immune Integration in Lung Adenocarcinoma	Chiara Napoli, Francesco Bardozzo, Luigi Liguori, Claudio Angione, Annalisa Occhipinti and Roberto Tagliaferri
13:45–14:00	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	1799	Hybrid Quantum-Classical Convolutional Neural Network for Genomic Sequence Classification	Giovanni Acampora, Angela Chiatto and Roberto Schiattarella
13:45–14:00	Aula III	SS7: Computational Intelligence for Integrative Host–Microbe Genomics: From Single-Cell Regulation to Population-Scale Pangenomes	2827	MethylAging: A HiFi Long-Read Epigenetic Clock for Biological Age Prediction in an Emirati Blood Cohort Using Promoter-Aggregated Methylation Features	Dalia Barayan, Layan Hattab, Hoor Nadhari, Amna Ahmed, Mauricio Paton, Michael Olbrich, Antonello Maruotti, Mira Mousa, Habiba Alsafar and Andre Barreiros
13:45–14:00	Aula Magna	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	5257	SVC-Probe: A Framework for Evaluating Perturbation Generalization in Spatial Foundation-Model Embeddings	Jake Y. Chen, Huu Phong Nguyen, Fuad Al Abir and Ehsan Saghapour
14:00–14:15	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	7611	Temporal quantum feature maps for longitudinal biomedical data	Maria Demidik, Filippo Utro, Alexey Galda, Daniel Blankenberg, Karl Jansen and Laxmi Parida
14:00–14:15	Aula III	SS7: Computational Intelligence for Integrative Host–Microbe Genomics: From Single-Cell Regulation to Population-Scale Pangenomes	0430	Learned Indexing for Genome Exact Mapping: A Comparative Study	Zeinab Hassaan, Eman Hassan, Baker Mohammad and Lobna Said
14:00–14:15	Aula Magna	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	1202	SpatialJEPa: JEPa-inspired graph-context distillation for spatially aware multiomics integration	Dylan Mann-Krzisnik and Yue Li

Time	Room	Session	ID	Paper title	Authors
14:15–14:30	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	6572	Quantum Kernel Estimation for the Discovery of Early Lung Cancer Detection	Hamed Javidi, Alex Zajichek, Hakan Doga, Laxmi Parida, Filippo Utro and Peter Mazzone
14:15–14:30	Aula III	SS13: Modern Bayesian Factor Models for Complex Biological Data	0047	A Sparse Rotationally Invariant Integrative Factor Model	Alejandra Avalos-Pacheco
14:15–14:30	Aula Magna	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	6407	Benchmarking a Spatial-Aware Foundation Model: An Empirical Evaluation of CellPLM in Transcriptomics	Juha Im, Haiping Liu and Hongpeng Zhou
14:30–14:45	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	6884	Quantum-Assisted Clinical Risk Factor Selection for Diabetes Readmission Prediction	Floriano Caprio, Matteo Tortora, Paolo Soda and Sunil Gentyala
14:30–14:45	Aula III	SS13: Modern Bayesian Factor Models for Complex Biological Data	0112	Tensor decompositions for Bayesian factor models with dynamic loadings: an application to causal inference	Pantelis Samartsidis
14:30–14:45	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances — Part I	1918	FLoRe: Fingerprint-based Long-Read Overlap Reconstruction	Manuel Sica, Rocco Zaccagnino and Rosalba Zizza
14:45–15:00	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	6561	A quantum generative model for in silico clinical trials using scarce training datasets	Olatz Sanz, Reza Dastbasteh, Mikel Hernaez, Roberto Sanchez-Navarro, Maria Diez-Campelo, Felipe Prosper, Ana Alfonso-Pierola, Sara Capponi, Pedro Crespo Bofill and Josu Etxezarreta Martinez
14:45–15:00	Aula III	SS13: Modern Bayesian Factor Models for Complex Biological Data	5335	Informed Sparse Factorization for Psychometric Construct Recognition	Lorenzo Schiavon
14:45–15:00	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances — Part I	4158	Genomic Centromere Profiling Tool using Centeny Maps for Centromere Characterization Across Genomes	Mauricio Orantes Bonilla, Matteo Tommaso Ungaro, Luca Corda, Andreas Giannis and Simona Giunta
15:00–15:20	All rooms	Coffee Break			
15:20–15:35	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	4237	A comparative knowledge- and data-driven machine learning analysis for H-CPAP failure prediction	Keying Qiao, Marco Masseroli, Luca Novelli, Matteo Bertoli, Roberto Cosentini, Eugenia Belotti, Isabelle Piazza, Chiara Baroni, Matteo Stenico, Fabiano Di Marco, Michele Capelli and Silvia Cascianelli
15:20–15:35	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	0901	Benchmarking differential abundance methods in respiratory microbiome: evaluating the impact of confounder adjustment	Céline Hosteins, John Barrera, Cristian Meza, Raphaël Enaud, Laurence Delhaes and Marta Avalos
15:20–15:35	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances — Part II	5684	ChloroGuide: prediction of subplastid localization using protein language model	Filip Pietluch and Przemyslaw Gagat
15:35–15:50	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	5123	Toward Personalized Diabetic Retinopathy Screening: Deep Learning Fundus Image Analysis and Clinical Risk Factors	Flavio Ragni, Paolo Bresolin, Stefano Bovo, Madalina Cocu, Sandro Inchiostro, Federica Romanelli, Giulia Malfatti, Monica Moroni and Giuseppe Jurman
15:35–15:50	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	2364	Modeling Overdispersed Zero-Inflated Longitudinal Count Data: A Beta-Binomial Mixed-Effects Approach	John Barrera, Ana Arribas-Gil, Dae-Jin Lee and Cristian Meza
15:35–15:50	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances — Part II	6177	LeProteine: Resource-Aware Protein Binder Design Pipelines on Blackwell GPU	Al Hamna Asif, Rana Abu Bakar, Filippo Cugini, Juan Jose Vegas Olmos and Amna Younus

Time	Room	Session	ID	Paper title	Authors
15:50–16:05	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	9989	Integration of Large Language Models and Retrieval-Augmented Generation for Clinical Decision Support in Inflammatory Bowel Disease	Gabriele Rumi, Andrea Mazzei, Daniele Napolitano, Franco Scaldaferrì, Giuseppe Cattaneo and Antonio Gasbarrini
15:50–16:05	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	5862	Longitudinal Microbiome Analysis in R: Review and Selection Pipeline	Irene Creus-Martí and Francisco José Santonja Gómez
15:50–16:05	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances — Part II	1823	Privacy-preserving federated batch effect correction in omics data with ComBatFed	Yuliya Burankova, Mohammad Mahdi Kazemi, Linda Baumbach and Jan Baumbach
16:05–16:20	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	6006	Disease Classification from raw metagenomic data through Large Language Model embedding of DNA sequences	Gaspar Roy, Eugeni Belda, Yann Chevaleyre, Edi Prifti and Jean-Daniel Zucker
16:05–16:20	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	3673	MicroEnsemble: A Patient-Anchor and Label-Anchor Contrastive Ensemble for Longitudinal Microbiome Classification	Amr Doma, Ahmed Wesal, Youssef Ellakany, Ghada El-Boghdady, Sama Mohamed, Yara Elshamy, Peter Salah and Tamer Basha
16:05–16:20	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances — Part II	7334	CyChat: a conversational Cytoscape app for no-code, reproducible network analysis	Jeanine Liebold, Merle Stahl, Jan-Ole Schulze, Mohammad Mehdi Razavi, Gary D. Bader, Stefan Kurtz and Jan Baumbach
16:20–16:35	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	4286	Project-Aware Edited Nearest Neighbours for Label-Noise Filtering in SNP-Based Biogeographical Ancestry Inference	Cosimo Grazzini, Stefania Morelli, Elena Pilli, Giulia Cereda and Daniele Castellana
16:20–16:35	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances — Part II	0853	GreatORCA: a framework for biological laboratory data analysis and integration for computational modelling	Dora Tortarolo, Simone Pernice, Lorenzo Pace, Sandro Gepiro Contaldo, Giulia Burrone, Fabiana Clapero, Donatella Valdembri, Guido Serini, Federica Riccardo, Lidia Tarone, Marco Beccuti and Francesca Cordero
16:20–16:35	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	1762	Machine learning identifies candidate microbiome features associated with rheumatoid arthritis risk despite limited external predictive performance	Raissa Silva, Rachel Audo, Axel Finckh, Claire Immediato Daïen and Zubeyir Salis
16:35–16:50	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	2170	NanoMambaNet: A Linear-Time CNN-Mamba Hybrid Architecture for Basecalling-Free Nanopore Pathogen Classification	Chayanika Bhattacharjee, Kolin Paul and Niranjana Sarode
16:35–16:50	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	5619	Leveraging hologenomic data for phenotypic prediction: potential and pitfalls	Solène Pety, Ingrid David, Andrea Rau and Mahendra Mariadassou
16:35–16:50	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances — Part II	0829	Extending Forge4Flame with Integrated Visualization and Customizable Airborne and Contact Transmission for Agent-Based Epidemic Simulations	Daniele Baccega, Irene Terrone, Matteo Costantino, Domiziana Porporato, Elisa Feyles, Irene Arduino, Rachele Francese, Manuela Donalisio, Marco Beccuti and Simone Pernice
16:50–17:05	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	4425	SOPHYSM: More Steps towards Digital Twins of Solid Tumours	Diego Cividini and Marco Antoniotti
16:50–17:05	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	5966	Microbiomes Under Human Pressure: An Integrated One Health Data Analysis Pipeline	Omar Orellana-Díaz, Gautier Chauvin, Luis Marti, Raphaël Enaud, Laurence Delhaes and Marta Avalos

Time	Room	Session	ID	Paper title	Authors
16:50-17:05	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances — Part II	4281	rSignificativity: an R package to compute significativity indexes for agreement values	Roberto Pagliarini and Alberto Casagrande
17:05-17:20	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	5467	Supervised NMF to unravel signature-class associations in microbiome composition: application to microbial signature of downy mildew epidemiology in vineyards.	Alioune-Badara Diouf, Paola Fournier, Jean-Marc Frigerio, Corinne Vacher and Simon Labarthe
18:00-	Meeting point / Rome city centre	Social Event + Social Dinner			

Friday, September 4

Time	Room	Session	ID	Paper title	Authors
08:45–09:00	Aula Magna	Biostatistics Main Track — Plenary	2968	Comparative analysis of unsupervised multi-omics integration for pancreatic cancer subtype discovery	Gonçalo Costa-Ferreira, Marta B. Lopes and Eunice Carrasquinha
09:00–09:15	Aula Magna	Biostatistics Main Track — Plenary	4773	Treatment persistence drives estimator performance in longitudinal causal inference based on observational data: A simulation study	Sergio Gaiotti, Sara Poletto, Enrico Longato, Erica Tavazzi and Martina Vettoretti
09:15–09:30	Aula Magna	Biostatistics Main Track — Plenary	2648	Bootstrap-Aggregated Method-of-Moments Estimation of Copula Correlation Under Generalized Gamma Dependent Censoring	Hyun-Soo Zhang and Chung Mo Nam
09:30–10:15	Aula Magna	Keynote — Per Kragh Andersen		Multi-state models for recurrent events	Per Kragh Andersen
10:15–10:45	All rooms	Coffee Break			
10:45–11:00	Aula Gini	Medical Informatics Main Track 3	7409	Self-Supervised Cytoplasmic Wave Detection Framework for In Vitro Fertilisation Embryo Time-Lapse	Attilio Di Vicino, Emanuel Di Nardo, Mario Cimmino, Riccardo Talevi, Sergio Chirico, Michele Di Capua and Angelo Ciaramella
10:45–11:00	Aula III	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	8881	Growth-Aware CT Image Synthesis via Volume-Conditioned Diffusion Models	Francesco Di Feola, Lorenzo Carusone, Giulia Romoli, Filippo Ruffini, Massimiliano Mantegna, Valerio Guarrasi, Matteo Tortora and Paolo Soda
10:45–11:00	Aula Magna	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	0944	DirHopGNN: an efficient approach to k-hop GNNs	Francesco Madeddu and Mario Santoro
11:00–11:15	Aula Gini	Medical Informatics Main Track 2	0650	Lexical and Embedding Similarity for ICD to Hetionet Disease Alignment: A Controlled Multi-View Study	Amani Braham and Insaf Tnazefti
11:00–11:15	Aula III	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	5009	Paraffinity - Semisynthetic Supervision for Automated Tissue Embedding Quality Control	Andrea Mazzei, Giorgia Sparapassi, Fabio Berrettoni, Davide Timperi, Dario Branco, Francesco Merolla, Stefania Staibano, Giuseppe Cattaneo and Gian Marco Di Domenico
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11:30–11:45	Aula Gini	Medical Informatics Main Track 2	0528	Radiomics-Based Thyroid Nodule Classification with Label-Conditional Conformal Prediction	Laura Testa, Umberto Ferraro Petrillo and Pierpaolo Brutti
11:30–11:45	Aula III	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	1526	Estimating Oocyte Biological Age: An Explainable Deep Learning Approach for Assisted Reproduction	Andrea Piermartini, Donatella Firmani, Francesco Leotta, Claudio Manna and Silvia Raffi

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11:45-12:00	Aula Gini	Medical Informatics Main Track 2	6982	Thyroid Nodule Segmentation in Ultrasound Images with Conformal Uncertainty Estimation	Francesco Teodori, Umberto Ferraro and Pierpaolo Brutti
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14:15-14:30	Aula Gini	Medical Informatics Main Track 3	5662	NoduleFlow: Automatic 3D Longitudinal Lung Nodule Detection and Segmentation	Giulia Romoli, Filippo Ruffini, Francesco Di Feola, Valerio Guarrasi, Matteo Tortora and Paolo Soda
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14:30-14:45	Aula III	SS3: Bayesian Causal Inference for Public Health	2887	Network-based modelling of categorical data for personalized causal inference	Federico Castelletti and Laura Ferrini

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16:45-17:00	Aula Magna	Bioinformatics Main Track 5	4454	Katz Kernel Based Stratification of Breast Cancer Patients	Francesco Cellitti, Lorenzo Di Rocco, Livia Perfetto, Veronica Lombardi and Umberto Ferraro Petrillo
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5335	Informed Sparse Factorization for Psychometric Construct Recognition	Lorenzo Schiavon	Thursday	14:45-15:00	Aula III
5467	Supervised NMF to unravel signature-class associations in microbiome composition: application to microbial signature of downy mildew epidemiology in vineyards.	Alioune-Badara Diouf, Paola Fournier, Jean-Marc Frigerio, Corinne Vacher and Simon Labarthe	Thursday	17:05-17:20	Aula III
5527	Toward Simulation-Informed Lipid Nanoparticle Design with Martini Coarse-Grained Models	Mariana Valério, Pablo Cardona Perez, Salma Maaquili, Mariia Borbuliak and Paulo C. T. Souza	Wednesday	13:00-13:15	Aula Magna
5619	Leveraging hologenomic data for phenotypic prediction: potential and pitfalls	Solène Pety, Ingrid David, Andrea Rau and Mahendra Mariadassou	Thursday	16:35-16:50	Aula III
5662	NoduleFlow: Automatic 3D Longitudinal Lung Nodule Detection and Segmentation	Giulia Romoli, Filippo Ruffini, Francesco Di Feola, Valerio Guarrasi, Matteo Tortora and Paolo Soda	Friday	14:15-14:30	Aula Gini
5684	ChloroGuide: prediction of subplastid localization using protein language model	Filip Pietluch and Przemyslaw Gagat	Thursday	15:20-15:35	Aula Magna
5759	Assessing Community Stability in Weighted Single-Cell Networks	Valeria Policastro, Domenico Sgambato, Dario Righelli, Vincenzo della Gatta, Luisa Cutillo and Annamaria Carissimo	Friday	11:00-11:15	Aula Magna
5862	Longitudinal Microbiome Analysis in R: Review and Selection Pipeline	Irene Creus-Martí and Francisco José Santonja Gómez	Thursday	15:50-16:05	Aula III
5966	Microbiomes Under Human Pressure: An Integrated One Health Data Analysis Pipeline	Omar Orellana-Diaz, Gautier Chauvin, Luis Marti, Raphaël Enaud, Laurence Delhaes and Marta Avalos	Thursday	16:50-17:05	Aula III
6006	Disease Classification from raw metagenomic data through Large Language Model embedding of DNA sequences	Gaspar Roy, Eugeni Belda, Yann Chevaleyre, Edi Prifti and Jean-Daniel Zucker	Thursday	16:05-16:20	Aula Gini
6112	Ontology-Aware Candidate Reranking for SNOMED CT Entity Linking in Clinical Notes	Luka Blašković, Nikola Tanković and Ivo Ipšić	Wednesday	12:00-12:15	Aula Gini

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6161	CellChat Hotspot: A Focused Lens on Tumor Microenvironment Communication	Dario Monaco, Mirea Dioguardi, Maria Dipalma, Eliseo Mattioli, Francesco Alfredo Zito, Francesco Giovannelli, Angela Ricco, Oronzo Brunetti, Antonella Argentiero and Simona De Summa	Wednesday	15:45-16:00	Aula Magna
6177	LeProteine: Resource-Aware Protein Binder Design Pipelines on Blackwell GPU	Al Hamna Asif, Rana Abu Bakar, Filippo Cugini, Juan Jose Vegas Olmos and Amna Younus	Thursday	15:35-15:50	Aula Magna
6187	Reinforcement Learning for Antibody Sequence Infilling	Chak Shing Lee, Conor F. Hayes, Denis Vashchenko and Mikel Landajuela Larma	Friday	14:45-15:00	Aula Gini
6217	Quantum Machine Learning for Missense Variant Pathogenicity Prediction in the KCNQ Gene Family	Markel Garcia, Sara Capponi, Aitor Bergara and Aritz Leonardo	Wednesday	11:00-11:15	Aula III
6305	Pixel-Wise Nuclei Localization in Cervical Cytology with Hierarchical Feature Representations	Ciro Russo, Alessandro Bria and Claudio Marrocco	Friday	11:15-11:30	Aula III
6407	Benchmarking a Spatial-Aware Foundation Model: An Empirical Evaluation of CellPLM in Transcriptomics	Juha Im, Haiping Liu and Hongpeng Zhou	Thursday	14:15-14:30	Aula Magna
6561	A quantum generative model for in silico clinical trials using scarce training datasets	Olatz Sanz, Reza Dastbasteh, Mikel Hernaez, Roberto Sanchez-Navarro, Maria Diez-Campelo, Felipe Prosper, Ana Alfonso-Pierola, Sara Capponi, Pedro Crespo Bofill and Josu Etxezarreta Martinez	Thursday	14:45-15:00	Aula Gini
6572	Quantum Kernel Estimation for the Discovery of Early Lung Cancer Detection	Hamed Javidi, Alex Zajichek, Hakan Doga, Laxmi Parida, Filippo Utro and Peter Mazzone	Thursday	14:15-14:30	Aula Gini
6752	Towards a unified framework: a data structures benchmark for representing genomic information	Matteo Tommaso Ungaro, Mauricio Orantes Bonilla, Francesca Querques, Evelyne Tassone and Simona Giunta	Friday	17:15-17:30	Aula Magna
6884	Quantum-Assisted Clinical Risk Factor Selection for Diabetes Readmission Prediction	Floriano Caprio, Matteo Tortora, Paolo Soda and Sunil Gentyala	Thursday	14:30-14:45	Aula Gini
6956	FusFun: a tool for the functional evaluation of gene fusions in RNA-seq-data	Francesca Miccolis, Martina Filieri, Elisa Ficarra and Marta Lovino	Friday	15:30-15:45	Aula Magna
6982	Thyroid Nodule Segmentation in Ultrasound Images with Conformal Uncertainty Estimation	Francesco Teodori, Umberto Ferraro and Pierpaolo Brutti	Friday	11:45-12:00	Aula Gini
7182	Bio-RL-GRN: Prior-Guided Reinforcement Learning for Gene Regulatory Network Inference	Tshepo Kitso Gobonamang, Okaile Marumo, Mavuna Sebalalo and Mpoeleng Dimane	Friday	11:15-11:30	Aula Magna
7261	GPU-accelerated single-cell and spatial transcriptomics on NVIDIA DGX H100: a systematic benchmark of speed, scalability, and biological concordance	Luca Vedovelli, Corrado Lanera, Daniele Sabbatini and Dario Gregori	Wednesday	11:00-11:15	Aula Magna
7334	CyChat: a conversational Cytoscape app for no-code, reproducible network analysis	Jeanine Liebold, Merle Stahl, Jan-Ole Schulze, Mohammad Mehdi Razavi, Gary D. Bader, Stefan Kurtz and Jan Baumbach	Thursday	16:05-16:20	Aula Magna
7409	Self-Supervised Cytoplasmic Wave Detection Framework for In Vitro Fertilisation Embryo Time-Lapse	Attilio Di Vicino, Emanuel Di Nardo, Mario Cimmino, Riccardo Talevi, Sergio Chirico, Michele Di Capua and Angelo Ciarrella	Friday	10:45-11:00	Aula Gini
7434	An XAI-Driven Transformer for Non-Canonical Splice-Site Prediction	Ahmed Negm	Friday	17:30-17:45	Aula Magna
7447	Functional Fuzzy Clustering of Longitudinal biological marker's trajectories	Silvia D'Elia, Valeria Paggi, Marco Alfò and Maria Brigida Ferraro	Wednesday	12:30-12:45	Aula III
7472	A topological object-proposal pipeline for cellular fiber segmentation	Riccardo Ceccaroni, Valerio Reffo, Camilla Pezzini, Roberta Sartori, Marco Sandri, Pierpaolo Brutti and Davide Risso	Wednesday	11:45-12:00	Aula Magna

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7478	Prediction of treatment response in Multiple Sclerosis with Machine Learning models	Ariadna Masot-Llima, Francisco Aparicio-Serrano, Agustín Pappolla, Susana Otero-Romero, René Carvajal, Álvaro Cobo-Calvo, Manel Alberich, María Jesús Arévalo, Georgina Arrambide, Cristina Auger, Joaquín Castillo, Manuel Comabella, Ingrid Galán, Daniel Hernández, Carlos Nos, Jordi Río, Breogán Rodríguez-Acevedo, Jaume Sastre-Garriga, Ángela Vidal-Jordana, Ana Zabalza, Àlex Rovira, Xavier Montalban, Mar Tintoré, Xavier Lladó, Deborah Pareto and Carmen Tur	Wednesday	13:00-13:15	Aula Gini
7526	Optimizing RNA yield using deep neural networks coupled to massively parallel screening	Adrien Villain	Wednesday	12:30-12:45	Aula Magna
7592	Integrating Implicit and Explicit Relational Biases through Graph-Based Multiple Instance Learning: A Case Study in Skin Lesion Diagnosis	Rafał Buler, Jakub Buler, Maciej Bobowicz and Michał Grochowski	Friday	12:00-12:15	Aula Magna
7611	Temporal quantum feature maps for longitudinal biomedical data	Maria Demidik, Filippo Utro, Alexey Galda, Daniel Blankenberg, Karl Jansen and Laxmi Parida	Thursday	14:00-14:15	Aula Gini
7861	CudaMon: An R Package to Monitor NVIDIA GPUs, Showcased by Monitoring a GPU-accelerated Single-cell Analysis Workflow in R	Mohammad Amin Zadenoori, Riccardo Ceccaroni, Davide Risso and Gabriele Sales	Wednesday	11:15-11:30	Aula Magna
7994	Reliability-Aware Benchmarking of Self-Supervised Learning in Histopathology Under 1-10% Label Regimes	Alicem Koyun, Pranjali Changadeo Pingale and Sachin Mote	Friday	14:00-14:15	Aula Gini
7999	Evaluating in-context learning with prompting regimes for transformer-based synthetic health tabular data generation	Amanda Bertgren, Fredrik Öhberg, Paolo Soda, Ulf Näslund, Patrik Wennberg and Christer Grönlund	Wednesday	12:00-12:15	Aula III
8082	Towards Federated and Explainable Quantum Machine Learning for Possible Epileptic Seizure Detection	Francesco Mercaldo, Hubert Schölnast, Oliver Eigner, Marta Petyx, Antonella Santone, Mario Cesarelli, Fabio Martinelli and Paul Tavalato	Wednesday	11:30-11:45	Aula Gini
8109	Integrating Genomic Annotations and Traits Dependencies for single-nucleotide polymorphisms Prioritization with Causally Reliable Concept Bottleneck Models	Francesco De Santis, Daniele Malpetti, Francesco Gualdi and Francesca Mangili	Friday	11:45-12:00	Aula Magna
8123	Secondary structure design for efficient translation initiation	Tobias von der Haar and Corina Keller	Wednesday	12:00-12:15	Aula Magna
8198	Expert Knowledge & Machine Understanding: Bridging Reactome's Ontology with LLM Semantic Embeddings	Susanna Bravi, Riccardo De Luca, Rosa Sicilia, Christine Nardini and Mario Santoro	Friday	11:15-11:30	Aula Gini
8294	LLM-Guided Integer Linear Programming for Antibody Library Design	Mikel Landajuela Larma	Wednesday	14:30-14:45	Aula Magna
8398	iPerturb: An interpretable framework for predicting gene expression changes under perturbations	Khang Ta Gia and Linh Huynh Viet	Friday	16:30-16:45	Aula Magna
8413	Identifying relevant Facial Action Units associated with Depression for Generating Synthetic Images using LLMs	Jona Maximilian Kao and Michael Gertz	Friday	15:15-15:30	Aula III
8670	Single-cell characterization of HERV-K transcriptional landscapes in acute and chronic HIV infection	Lucrezia Pierfederici, Elisabetta Lazzari, Gabriella Rozera, Lavinia Fabeni, Flavia Smoquina, Giulia Berno, Federica Forbici, Valentina Mazzotta, Andrea Antinori, Daniele Pietrucci, Daniele Maria Papetti, Fabrizio Maggi, Isabella Abbate and Giovanni Chillemi	Wednesday	15:15-15:30	Aula Magna
8697	Incorporating Biologically Informed Masking into Protein Language Models for Pocket Identification	Luiza Gomes Ferreira	Friday	15:00-15:15	Aula Magna
8729	A Neural Factorization Machine Approach to Drug-Target Interaction with Global Features	Mirco Perna and Simona Ester Rombo	Friday	15:30-15:45	Aula Gini
8881	Growth-Aware CT Image Synthesis via Volume-Conditioned Diffusion Models	Francesco Di Feola, Lorenzo Carusone, Giulia Romoli, Filippo Ruffini, Massimiliano Mantegna, Valerio Guarrasi, Matteo Tortora and Paolo Soda	Friday	10:45-11:00	Aula III
8886	Identifying functional drivers of Hepatoblastoma outcomes via agent-based modeling and transcriptomics	Alessandro Ravoni, Yuanhua Liu, Stefano Cairo, Filippo Castiglione and Christine Nardini	Wednesday	15:30-15:45	Aula Magna

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8929	An Enhanced Pipeline for Multi-Omic Integration Based on Topological Data Analysis	Veronica Paparozzi, Anna Plaksienko, Marco Pedicini and Christine Nardini	Wednesday	09:30-09:45	Aula Magna
9152	A Computational Ethical Framework for Financial Digital Phenotyping for Mental Health	Oluwadara Adedeji, Michael Mayowa Farayola, Jeff Brozena, Irina Tal, Regina Connolly and Mark Matthews	Friday	15:30-15:45	Aula III
9167	Transporting principal causal effects across strata: A Bayesian causal inference approach	Veronica Ballerini, Falco Joannes Bargagli Stoffi and Francesca Dominici	Friday	14:45-15:00	Aula III
9177	Identification of Allosteric Binding Pockets and Ligand-Induced Network Rewiring in PHF6	Lisia Pegini, Alessio Ferrini, Lan Phan Bach Tun, Jacopo Miotto, Massimo Bellanda and Damiano Piovesan	Friday	14:30-14:45	Aula Magna
9410	LLMs Fail at Protein Sequence Annotation and Localization: A Comparative Study against a Tool-Augmented Agentic solution	Asia Leuzzi, Elisa Ficarra and Marta Lovino	Friday	12:00-12:15	Aula III
9658	GLD-VAE: A Guided Latent Diffusion Variational Autoencoder for Class Imbalance in Multi-Omics Data	Durga Parkhi, Srijay Deshpande and Animesh Acharjee	Friday	11:45-12:00	Aula III
9844	Interpretable Convolutional Neural Networks Reveal Sequence Determinants of SF3B1-Mutant Susceptible Cryptic Splice Junctions in Cancer	Luca Faretra, Francesco Napolitano, Massimo Pancione and Luigi Cerulo	Friday	15:15-15:30	Aula Gini
9989	Integration of Large Language Models and Retrieval-Augmented Generation for Clinical Decision Support in Inflammatory Bowel Disease	Gabriele Rumi, Andrea Mazzei, Daniele Napolitano, Franco Scaldaferrì, Giuseppe Cattaneo and Antonio Gasbarrini	Thursday	15:50-16:05	Aula Gini