CIBB 2026

Version 11 - updated September 12, 2026

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

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

Opening	Wed 2 Sep, 09:15-09:30 - Opening Remarks; 16:45 - Opening Scientific Introduction
Poster sessions	Aula Gini
Social programme	Thu 3 Sep, from 18:00 - Social Event + Social Dinner
Closing	Fri 4 Sep, 17:30-17:45 - Closing Remarks, Aula Magna

Programme by Room and Day

Room-oriented timetable for quick on-site consultation.

Wednesday, September 2

Aula Magna

Time	Session	Chair	Paper / Talk	Authors
09:30-09:45	BIOINF Main Track 1	Davide Chicco	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	BIOINF Main Track 1	Davide Chicco	Analysis of biological networks using Krylov subspace trajectories	H. Robert Frost
10:00-10:15	BIOINF Main Track 1	Davide Chicco	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	BIOINF Main Track 1	Davide Chicco	A Pipeline for Predicting Variant Associations with Complex Disorders via Functional Annotations	Francesco Gualdi, Zeno Darani, Daniele Malpetti, Marco Scutari and Francesca Mangili
14:15-14:30	BIOINF Main Track 2	Graziano Pesole	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	BIOINF Main Track 2	Graziano Pesole	LLM-Guided Integer Linear Programming for Antibody Library Design	Mikel Landajuela Larma
14:45-15:00	BIOINF Main Track 2	Graziano Pesole	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	BIOINF Main Track 2	Graziano Pesole	OmicsGPT: Multi-Agent Bioinformatics Orchestration for Evidence-Grounded RNA-seq Interpretation	Patrick Roney and James Li
15:45-16:00	BIOINF Main Track 2	Graziano Pesole	Identifying functional drivers of Hepatoblastoma outcomes via agent-based modeling and transcriptomics	Alessandro Ravoni, Yuanhua Liu, Stefano Cairo, Filippo Castiglione and Christine Nardini
16:00-16:45	**Keynote — Francesco Asnicar**			
08:45-09:15	**Opening Remarks**			
09:15-09:30	**Opening Scientific Introduction**			
12:00-12:15	SS10: Computational tools for the effective design of mRNA-based therapeutics	Francesco Branda	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

Time	Session	Chair	Paper / Talk	Authors
12:15-12:30	SS10: Computational tools for the effective design of mRNA-based therapeutics	Duccio Medini, Giuseppe Maccari	Secondary structure design for efficient translation initiation	Tobias von der Haar and Corina Keller
12:30-12:45	SS10: Computational tools for the effective design of mRNA-based therapeutics	Duccio Medini, Giuseppe Maccari	Manufacturability of mRNA Therapeutics: Native vs. N-1-Methyl-Pseudouridine	Roland Huber, Kuo Chieh Liao and Yue Wan
12:45-13:00	SS10: Computational tools for the effective design of mRNA-based therapeutics	Duccio Medini, Giuseppe Maccari	Optimizing RNA yield using deep neural networks coupled to massively parallel screening	Adrien Villain
13:00-13:15	SS10: Computational tools for the effective design of mRNA-based therapeutics	Duccio Medini, Giuseppe Maccari	MAP-Net: An Interpretable Deep Learning Framework for Universal mRNA Manufacturability	Giorgio Ciano
11:00-11:15	SS11: GPU-accelerated analysis of single-cell and spatial omics	Duccio Medini, Giuseppe Maccari	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
11:15-11:30	SS11: GPU-accelerated analysis of single-cell and spatial omics	Dario Righelli	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
11:30-11:45	SS11: GPU-accelerated analysis of single-cell and spatial omics	Dario Righelli	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
11:45-12:00	SS11: GPU-accelerated analysis of single-cell and spatial omics	Dario Righelli	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

Wednesday, September 2

Aula Gini

Time	Session	Chair	Paper / Talk	Authors
11:00-11:15	**SS1: AI and Computational Methods for Medical Informatics - Part I**			
11:15-11:30	SS1: AI and Computational Methods for Medical Informatics - Part I	Francesco Branda	Diagnosing Rejection Collapse via Uncertainty Decomposition	Walter Endrizzi, Flavio Ragni, Stefano Bovo, Monica Moroni, Giuseppe Jurman and Venet Osmani
11:30-11:45	SS1: AI and Computational Methods for Medical Informatics - Part I	Francesco Branda	ClinRAG-BiLSTM: An Agentic Cloud AI Framework for Explainable and Traceable Breast Cancer Decision Support	Adaleta Gicic and Dženana Đonko
11:45-12:00	SS1: AI and Computational Methods for Medical Informatics - Part I	Francesco Branda	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 Tavolato
12:00-12:15	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	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
12:15-12:30	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	Ontology-Aware Candidate Reranking for SNOMED CT Entity Linking in Clinical Notes	Luka Blašković, Nikola Tanković and Ivo Ipšić
12:30-12:45	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	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
12:45-13:00	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	Decoding HIV-1 Antibody Escape with Interpretable Protein Language Models	Fahsai Nakarin, Pawin Taechoyotin and Kayla G. Sprenger
13:00-13:15	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	AutoEncoder based approach for the identification of genomic regions responsible for poorly described oligo-patient disorders	Joanna Szyda

Wednesday, September 2

Aula III

Time	Session	Chair	Paper / Talk	Authors
12:00-12:15	BIOSTAT Main Track 1	Graziano Pesole	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
12:15-12:30	BIOSTAT Main Track 1	Antonello Maruotti	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
12:30-12:45	BIOSTAT Main Track 1	Antonello Maruotti	Multivariate Model-Based Landmarking Approach in Mixture Cure Models to Dynamic Prediction	Bianca Ferraro, Marco Alfò and Marta Cipriani
12:45-13:00	BIOSTAT Main Track 1	Antonello Maruotti	Functional Fuzzy Clustering of Longitudinal biological marker's trajectories	Silvia D'Elia, Valeria Paggi, Marco Alfò and Maria Brigida Ferraro
13:00-13:15	BIOSTAT Main Track 1	Antonello Maruotti	Reducing the Size of Breastfeeding Reference Arms in Infant Nutrition Studies Using Prognostic Covariate Adjustment	Luca Lavalle
11:00-11:15	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	Dario Righelli	A topological object-proposal pipeline for cellular fiber segmentation	Riccardo Ceccaroni, Valerio Reffo, Camilla Pezzini, Roberta Sartori, Marco Sandri, Pierpaolo Brutti and Davide Risso
11:15-11:30	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	Annamaria Carissimo	Quantum Machine Learning for Missense Variant Pathogenicity Prediction in the KCNQ Gene Family	Markel Garcia, Sara Capponi, Aitor Bergara and Aritz Leonardo
11:30-11:45	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	Annamaria Carissimo	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
11:45-12:00	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	Annamaria Carissimo	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

Wednesday, September 2

Museo dell'Arte Classica

Time	Session	Chair	Paper / Talk	Authors
16:45-19:00	**Poster Session A / Coffee Break**	Davide Chicco	**ELIXIR-IT: the Italian Research Infrastructure for Big Data in Life Sciences**	Graziano Pesole

Wednesday, September 2

Terrazza del Rettorato

Time	Session	Chair	Paper / Talk	Authors
10:30-11:00	Coffee Break	Antonello Maruotti	A Dependent Dirichlet Process Approach to Population Size Estimation	Lucia Gallucci
13:15-14:15	**Lunch**		**Computational metagenomics to unravel person-to-person microbiome transmission**	Francesco Asnicar
19:00-20:00	Welcome Cocktail + MUSA Jazz Concert	Annamaria Carissimo	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 Cristofoletti, Maria Grazia Narducci and Roberta Tarallo

Thursday, September 3

Aula Magna

Time	Session	Chair	Paper / Talk	Authors
15:35-15:50	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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
09:30-10:15	**Keynote — Marianna Rapsomaniki**		**Building predictive models for precision oncology across scales, modalities and perturbations**	Marianna Rapsomaniki
08:45-09:00	MEDINF Main Track 1	Elisabetta Ferretti	Soft-GLCM: Stabilizing Differentiable Texture Analysis through Soft Quantization	Haoyue Chen, Giuseppe Salvaggio, Albert Comelli and Anthony Yezzi
09:00-09:15	MEDINF Main Track 1	Elisabetta Ferretti	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	MEDINF Main Track 1	Elisabetta Ferretti	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
13:30-13:45	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	Silvia Cascianelli and Marco Masseroli	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	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	Silvia Cascianelli and Marco Masseroli	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	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	Silvia Cascianelli and Marco Masseroli	SpatialJEPA: JEPA-inspired graph-context distillation for spatially aware multiomics integration	Dylan Mann-Krzisnik and Yue Li
14:15-14:30	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	Silvia Cascianelli and Marco Masseroli	Benchmarking a Spatial-Aware Foundation Model: An Empirical Evaluation of CellPLM in Transcriptomics	Juha Im, Haiping Liu and Hongpeng Zhou
14:30-14:45	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part I	Elisabetta Sciacca; Lorenzo Martini	FLoRe: Fingerprint-based Long-Read Overlap Reconstruction	Manuel Sica, Rocco Zaccagnino and Rosalba Zizza
14:45-15:00	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part I	Elisabetta Sciacca; Lorenzo Martini	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
17:05-17:20	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	ChloroGuide: prediction of subplastid localization using protein language model	Filip Pietluch and Przemyslaw Gagat
15:20-15:35	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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
15:50-16:05	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	Privacy-preserving federated batch effect correction in omics data with ComBatFed	Yuliya Burankova, Mohammad Mahdi Kazemi, Linda Baumbach and Jan Baumbach

Time	Session	Chair	Paper / Talk	Authors
16:05-16:20	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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
16:35-16:50	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	rSignificativity: an R package to compute significativity indexes for agreement values	Roberto Pagliarini and Alberto Casagrande

Thursday, September 3

Aula Gini

Time	Session	Chair	Paper / Talk	Authors
15:20-15:35	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	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
15:35-15:50	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	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
15:50-16:05	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	Integration of Large Language Models and Retrieval-Augmented Generation for Clinical Decision Support in Inflammatory Bowel Disease	Gabriele Rumi, Andrea Mazzei, Daniele Napolitano, Franco Scaldaferri, Giuseppe Cattaneo and Antonio Gasbarrini
16:05-16:20	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	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
16:20-16:35	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	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
16:35-16:50	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	NanoMambaNet: A Linear-Time CNN-Mamba Hybrid Architecture for Basecalling-Free Nanopore Pathogen Classification	Chayanika Bhattacharjee, Kolin Paul and Niranjan Sarode
16:50-17:05	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	SOPHYSM: More Steps towards Digital Twins of Solid Tumours	Diego Cividini and Marco Antoniotti
13:30-13:45	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	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
13:45-14:00	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	Hybrid Quantum-Classical Convolutional Neural Network for Genomic Sequence Classification	Giovanni Acampora, Angela Chiatto and Roberto Schiattarella
14:45-15:00	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	Temporal quantum feature maps for longitudinal biomedical data	Maria Demidik, Filippo Utro, Alexey Galda, Daniel Blankenberg, Karl Jansen and Laxmi Parida
14:15-14:30	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	Quantum Kernel Estimation for the Discovery of Early Lung Cancer Detection	Hamed Javidi, Alex Zajichek, Hakan Doga, Laxmi Parida, Filippo Utro and Peter Mazzone
14:30-14:45	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	Quantum-Assisted Clinical Risk Factor Selection for Diabetes Readmission Prediction	Floriano Caprio, Matteo Tortora, Paolo Soda and Sunil Gentyala

Time	Session	Chair	Paper / Talk	Authors
14:00-14:15	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	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, September 3

Aula III

Time	Session	Chair	Paper / Talk	Authors
14:15-14:30	SS13: Modern Bayesian Factor Models for Complex Biological Data	Pantelis Samartsidis; Lorenzo Schiavon; Alejandra Avalos-Pacheco	A Sparse Rotationally Invariant Integrative Factor Model	Alejandra Avalos-Pacheco
14:30-14:45	SS13: Modern Bayesian Factor Models for Complex Biological Data	Pantelis Samartsidis; Lorenzo Schiavon; Alejandra Avalos-Pacheco	Tensor decompositions for Bayesian factor models with dynamic loadings: an application to causal inference	Pantelis Samartsidis
14:45-15:00	SS13: Modern Bayesian Factor Models for Complex Biological Data	Pantelis Samartsidis; Lorenzo Schiavon; Alejandra Avalos-Pacheco	Informed Sparse Factorization for Psychometric Construct Recognition	Lorenzo Schiavon
13:30-13:45	SS7: Computational Intelligence for Integrative Host–Microbe Genomics: From Single-Cell Regulation to Population-Scale Pangenomes	Antonello Maruotti	An entropy based method for mapping mixed lineage next generation sequencing data	Gregory Fonseca
13:45-14:00	SS7: Computational Intelligence for Integrative Host–Microbe Genomics: From Single-Cell Regulation to Population-Scale Pangenomes	Antonello Maruotti	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
14:00-14:15	SS7: Computational Intelligence for Integrative Host–Microbe Genomics: From Single-Cell Regulation to Population-Scale Pangenomes	Antonello Maruotti	Learned Indexing for Genome Exact Mapping: A Comparative Study	Zeinab Hassaan, Eman Hassan, Baker Mohammad and Lobna Said
15:20-15:35	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	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
15:35-15:50	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Modeling Overdispersed Zero-Inflated Longitudinal Count Data: A Beta-Binomial Mixed-Effects Approach	John Barrera, Ana Arribas-Gil, Dae-Jin Lee and Cristian Meza
15:50-16:05	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Longitudinal Microbiome Analysis in R: Review and Selection Pipeline	Irene Creus-Martí and Francisco José Santonja Gómez
16:05-16:20	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	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
16:20-16:35	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Machine learning identifies candidate microbiome features associated with rheumatoid arthritis risk despite limited external predictive performance	Raissa Silva, Rachel Audo, Axel Finckh, Claire Immediato Daien and Zubeyir Salis
16:35-16:50	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Leveraging hologenomic data for phenotypic prediction: potential and pitfalls	Solène Pety, Ingrid David, Andrea Rau and Mahendra Mariadassou
16:50-17:05	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	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

Time	Session	Chair	Paper / Talk	Authors
17:05-17:20	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Supervised NMF to unravel signature-class associations in microbiome composition: application to microbial signature of downy mildew epidemology in vineyards.	Alioune-Badara Diouf, Paola Fournier, Jean-Marc Frigerio, Corinne Vacher and Simon Labarthe

Thursday, September 3

Museo dell'Arte Classica

Time	Session	Chair	Paper / Talk	Authors
10:15-12:30	**Poster Session B / Coffee Break**			

Thursday, September 3

Meeting point / Rome city centre

Time	Session	Chair	Paper / Talk	Authors
18:00-	**Social Event + Social Dinner**			

Thursday, September 3

Terrazza del Rettorato

Time	Session	Chair	Paper / Talk	Authors
12:30-13:30	**Lunch**			

Thursday, September 3

Terrazza del Rettorato + Aula II

Time	Session	Chair	Paper / Talk	Authors
15:00-15:20	**Coffee Break**			

Friday, September 4

Aula Magna

Time	Session	Chair	Paper / Talk	Authors
14:45-15:00	BIOINF Main Track 4	Monica Ballarino	How Much Architecture Does a Protein Transformer Need to Self-Discover?	Giansalvo Cirrincione, Elisa Ficarra and Marta Lovino
15:00-15:15	BIOINF Main Track 4	Monica Ballarino	Incorporating Biologically Informed Masking into Protein Language Models for Pocket Identification	Luiza Gomes Ferreira
15:15-15:30	BIOINF Main Track 4	Monica Ballarino	EXTRARNAS: A Framework for Extracting RNA Structures with Multiple Tools	Federico Di Petta, Piermichele Rosati, Piero Hierro Canchari, Michela Quadrini and Luca Tesei
15:30-15:45	BIOINF Main Track 4	Monica Ballarino	FusFun: a tool for the functional evaluation of gene fusions in RNA-seq–data	Francesca Miccolis, Martina Filieri, Elisa Ficarra and Marta Lovino
16:15-16:30	BIOINF Main Track 5	Cinzia Pizzi	PRIMA: a bidirectional state-space architecture and training approach for modelling protein-protein interactions	Arturo Fiorellini-Bernardis, Sebastien Boyer, Jean Quentin, Ghassene Jebali and Oliver Bent
16:45-17:00	BIOINF Main Track 5	Cinzia Pizzi	iPerturb: An interpretable framework for predicting gene expression changes under perturbations	Khang Ta Gia and Linh Huynh Viet
16:30-16:45	BIOINF Main Track 5	Cinzia Pizzi	PANDORA: a multiparametric framework for sensitive detection of insertional mutagenesis	Riccardo Pizzichemi
17:00-17:15	BIOINF Main Track 5	Cinzia Pizzi	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
17:15-17:30	BIOINF Main Track 5	Cinzia Pizzi	An XAI-Driven Transformer for Non-Canonical Splice-Site Prediction	Ahmed Negm, Nahla Belal and Mohamed Khedr
08:45-09:00	BIOSTAT Main Track 2	Marco Alfo'	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	BIOSTAT Main Track 2	Marco Alfo'	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	BIOSTAT Main Track 2	Marco Alfo'	Bootstrap-Aggregated Method-of-Moments Estimation of Copula Correlation Under Generalized Gamma Dependent Censoring	Hyun-Soo Zhang and Chung Mo Nam
17:30-17:45	**Closing Remarks**			
13:15-14:00	**Invited Talk — Pavel Pevzner**	Marco Beccuti	**Will AI replace Professors?**	Pavel Pevzner
09:30-10:15	**Keynote — Andrea Rau**	Marco Alfo'	**Leveraging biological priors in Bayesian genomic prediction models for complex traits**	Andrea Rau
14:00-14:15	SS6: Chemoinformatics and computational chemistry for drug discovery and prediction of chemical properties and activities	Davide Chicco	Bridging Generative AI and Synthesis-on-Demand Chemical Spaces for Structure-based De Novo Drug Design	Cosmin Ichim, Viet-Khoa Tran-Nguyen and Pedro Ballester
14:15-14:30	SS6: Chemoinformatics and computational chemistry for drug discovery and prediction of chemical properties and activities	Davide Chicco	A Framework for Diversity Constrained Design of Natural Product like Molecules	Aditi Vijil and Pin-Yu Chen

Time	Session	Chair	Paper / Talk	Authors
14:30-14:45	SS6: Chemoinformatics and computational chemistry for drug discovery and prediction of chemical properties and activities	Davide Chicco	Identification of Allosteric Binding Pockets and Ligand-Induced Network Rewiring in PHF6	Lisia Peqini, Alessio Ferrini, Lan Phan Bach Tun, Jacopo Miotto, Massimo Bellanda and Damiano Piovesan

Friday, September 4

Aula Gini

Time	Session	Chair	Paper / Talk	Authors
14:45-15:00	BIOINF Main Track 3	Chiara Parrillo	Reinforcement Learning for Antibody Sequence Infilling	Chak Shing Lee, Conor F. Hayes, Denis Vashchenko and Mikel Landajuela Larma
15:00-15:15	BIOINF Main Track 3	Chiara Parrillo	Reinforcement Learning-Based Control Strategy for Boolean Gene Regulatory Networks	Michal Shoob, Hila Glazz, Avraham Raviv and Hillel Kugler
15:15-15:30	BIOINF Main Track 3	Chiara Parrillo	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
15:30-15:45	BIOINF Main Track 3	Chiara Parrillo	A Neural Factorization Machine Approach to Drug–Target Interaction with Global Features	Mirco Perna and Simona Ester Rombo
10:45-11:00	MEDINF Main Track 2	Marco Masseroli	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
11:00-11:15	MEDINF Main Track 2	Marco Masseroli	Lexical and Embedding Similarity for ICD to Hetionet Disease Alignment: A Controlled Multi-View Study	Amani Braham and Insaf Tnazefti
11:15-11:30	MEDINF Main Track 2	Marco Masseroli	Expert Knowledge & Machine Understanding: Bridging Reactome’s Ontology with LLM Semantic Embeddings	Susanna Bravi, Riccardo De Luca, Rosa Sicilia, Christine Nardini and Mario Santoro
11:30-11:45	MEDINF Main Track 2	Marco Masseroli	Radiomics-Based Thyroid Nodule Classification with Label-Conditional Conformal Prediction	Laura Testa, Umberto Ferraro Petrillo and Pierpaolo Brutti
11:45-12:00	MEDINF Main Track 2	Marco Masseroli	Thyroid Nodule Segmentation in Ultrasound Images with Conformal Uncertainty Estimation	Francesco Teodori, Umberto Ferraro and Pierpaolo Brutti
14:00-14:15	MEDINF Main Track 3	Nikolas Petsas	Reliability-Aware Benchmarking of Self-Supervised Learning in Histopathology Under 1-10% Label Regimes	Alicem Koyun, Pranjali Changadeo Pingale, Sachin Mote and Gianluca Pizzuti
14:15-14:30	MEDINF Main Track 3	Nikolas Petsas	NoduleFlow: Automatic 3D Longitudinal Lung Nodule Detection and Segmentation	Giulia Romoli, Filippo Ruffini, Francesco Di Feola, Valerio Guarrasi, Matteo Tortora and Paolo Soda
14:30-14:45	MEDINF Main Track 3	Nikolas Petsas	Federated vs. Centralized Learning: A Comparative Prediction Analysis for Hospitalization Cost	Shinto Pulickal Thomas, Jiregna Olani Kedida, Thierry Bossy, Juan Ramon Troncoso-Pastoriza, Alessandro Desideria, Dario Gregori and Corrado Lanera

Friday, September 4

Aula III

Time	Session	Chair	Paper / Talk	Authors
10:45-11:00	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	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
11:00-11:15	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	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
11:15-11:30	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	Pixel-Wise Nuclei Localization in Cervical Cytology with Hierarchical Feature Representations	Ciro Russo, Alessandro Bria and Claudio Marrocco
11:30-11:45	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	Estimating Oocyte Biological Age: An Explainable Deep Learning Approach for Assisted Reproduction	Andrea Piermartini, Donatella Firmani, Francesco Leotta, Claudio Manna and Silvia Raffi
11:45-12:00	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	GLD-VAE: A Guided Latent Diffusion Variational Autoencoder for Class Imbalance in Multi-Omics Data	Durga Parkhi, Srijay Deshpande and Animesh Acharjee
12:00-12:15	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	LLMs Fail at Protein Sequence Annotation and Localization: A Comparative Study against a Tool-Augmented Agentic solution	Asia Leuzzi, Elisa Ficarra and Marta Lovino
14:00-14:15	SS3: Bayesian Causal Inference for Public Health	Lucia Gallucci	Causal Effects on Latent Structures via Bayesian Nonparametric Factor Models	Roberta De Vito, Giovanni Parmigiani and Dafne Zorzetto
14:15-14:30	SS3: Bayesian Causal Inference for Public Health	Lucia Gallucci	Discovering Heterogeneous Treatment Effects: A Bayesian Spike-and-Slab Approach	Dafne Zorzetto, Roberta De Vito and Falco J. Bargagli-Stoffi
14:30-14:45	SS3: Bayesian Causal Inference for Public Health	Lucia Gallucci	Network-based modelling of categorical data for personalized causal inference	Federico Castelletti and Laura Ferrini
14:45-15:00	SS3: Bayesian Causal Inference for Public Health	Lucia Gallucci	Transporting principal causal effects across strata: A Bayesian causal inference approach	Veronica Ballerini, Falco Joannes Bargagli Stoffi and Francesca Dominici
15:00-15:15	SS9: Computational Methods for Mental Health and Well-Being	Francesca Gasparini	A study on the use of learning techniques and explainability methods on TMS-EEG data	Sara Nocco, Eleonora Arrigoni, Diego Corna, Francesca Gasparini, Alberto Pisoni, Leonor Josefina Romero Lauro and Aurora Saibene
15:15-15:30	SS9: Computational Methods for Mental Health and Well-Being	Francesca Gasparini	Identifying relevant Facial Action Units associated with Depression for Generating Synthetic Images using LLMs	Jona Maximilian Kao and Michael Gertz
15:30-15:45	SS9: Computational Methods for Mental Health and Well-Being	Francesca Gasparini	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, September 4

Aula II

Time	Session	Chair	Paper / Talk	Authors
10:45-11:00	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	DirHopGNN: an efficient approach to k-hop GNNs	Francesco Madeddu and Mario Santoro
11:00-11:15	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	Assessing Community Stability in Weighted Single-Cell Networks	Valeria Policastro, Domenico Sgambato, Dario Righelli, Vincenzo della Gatta, Luisa Cutillo and Annamaria Carissimo
11:15-11:30	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine		Katz Kernel Based Stratification of Breast Cancer Patients	Francesco Cellitti, Lorenzo Di Rocco, Livia Perfetto, Veronica Lombardi and Umberto Ferraro Petrillo
11:30-11:45	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	A Multilayer Graph Diffusion Model for Spatial Transcriptomics Reveals Cell-Cell Propagation Dynamics.	Caterina Francesca Perri, Annamaria Defilippo, Federico Manuel Giorgi, Pietro Hiram Guzzi and Pierangelo Veltri
11:45-12:00	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	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
12:00-12:15	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	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, September 4

Terrazza del Rettorato

Time	Session	Chair	Paper / Talk	Authors
10:15-10:45	Coffee Break			
15:45-16:15	Coffee Break			
12:15-13:15	Lunch			

Wednesday, September 2

Time	Room	Session	Chair	Paper title	Authors
09:30-09:45	Aula Magna	BIOINF Main Track 1	Davide Chicco	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	BIOINF Main Track 1	Davide Chicco	Analysis of biological networks using Krylov subspace trajectories	H. Robert Frost
10:00-10:15	Aula Magna	BIOINF Main Track 1	Davide Chicco	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	BIOINF Main Track 1	Davide Chicco	A Pipeline for Predicting Variant Associations with Complex Disorders via Functional Annotations	Francesco Gualdi, Zeno Darani, Daniele Malpetti, Marco Scutari and Francesca Mangili
14:15-14:30	Aula Magna	BIOINF Main Track 2	Graziano Pesole	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	BIOINF Main Track 2	Graziano Pesole	LLM-Guided Integer Linear Programming for Antibody Library Design	Mikel Landajuela Larma
14:45-15:00	Aula Magna	BIOINF Main Track 2	Graziano Pesole	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	BIOINF Main Track 2	Graziano Pesole	OmicsGPT: Multi-Agent Bioinformatics Orchestration for Evidence-Grounded RNA-seq Interpretation	Patrick Roney and James Li
15:45-16:00	Aula Magna	BIOINF Main Track 2	Graziano Pesole	Identifying functional drivers of Hepatoblastoma outcomes via agent-based modeling and transcriptomics	Alessandro Ravoni, Yuanhua Liu, Stefano Cairo, Filippo Castiglione and Christine Nardini
12:00-12:15	Aula III	BIOSTAT Main Track 1	Graziano Pesole	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
12:15-12:30	Aula III	BIOSTAT Main Track 1	Antonello Maruotti	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
12:30-12:45	Aula III	BIOSTAT Main Track 1	Antonello Maruotti	Multivariate Model-Based Landmarking Approach in Mixture Cure Models to Dynamic Prediction	Bianca Ferraro, Marco Alfò and Marta Cipriani
12:45-13:00	Aula III	BIOSTAT Main Track 1	Antonello Maruotti	Functional Fuzzy Clustering of Longitudinal biological marker's trajectories	Silvia D'Elia, Valeria Paggi, Marco Alfò and Maria Brigida Ferraro
13:00-13:15	Aula III	BIOSTAT Main Track 1	Antonello Maruotti	Reducing the Size of Breastfeeding Reference Arms in Infant Nutrition Studies Using Prognostic Covariate Adjustment	Luca Lavalle
10:30-11:00	Terrazza del Rettorato	Coffee Break	Antonello Maruotti	A Dependent Dirichlet Process Approach to Population Size Estimation	Lucia Gallucci
16:00-16:45	**Aula Magna**	**Keynote — Francesco Asnicar**			
13:15-14:15	**Terrazza del Rettorato**	**Lunch**		**Computational metagenomics to unravel person-to-person microbiome transmission**	**Francesco Asnicar**
08:45-09:15	**Aula Magna**	**Opening Remarks**			
09:15-09:30	**Aula Magna**	**Opening Scientific Introduction**			
16:45-19:00	**Museo dell'Arte Classica**	**Poster Session A / Coffee Break**	Davide Chicco	**ELIXIR-IT: the Italian Research Infrastructure for Big Data in Life Sciences**	**Graziano Pesole**

Time	Room	Session	Chair	Paper title	Authors
11:00-11:15	**Aula Gini**	**SS1: AI and Computational Methods for Medical Informatics - Part I**			
11:15-11:30	Aula Gini	SS1: AI and Computational Methods for Medical Informatics - Part I	Francesco Branda	Diagnosing Rejection Collapse via Uncertainty Decomposition	Walter Endrizzi, Flavio Ragni, Stefano Bovo, Monica Moroni, Giuseppe Jurman and Venet Osmani
11:30-11:45	Aula Gini	SS1: AI and Computational Methods for Medical Informatics - Part I	Francesco Branda	ClinRAG-BiLSTM: An Agentic Cloud AI Framework for Explainable and Traceable Breast Cancer Decision Support	Adaleta Gicic and Dženana Đonko
11:45-12:00	Aula Gini	SS1: AI and Computational Methods for Medical Informatics - Part I	Francesco Branda	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 Tavolato
12:00-12:15	Aula Gini	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	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
12:15-12:30	Aula Gini	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	Ontology-Aware Candidate Reranking for SNOMED CT Entity Linking in Clinical Notes	Luka Blašković, Nikola Tanković and Ivo Ipšić
12:30-12:45	Aula Gini	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	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
12:45-13:00	Aula Gini	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	Decoding HIV-1 Antibody Escape with Interpretable Protein Language Models	Fahsai Nakarin, Pawin Taechoyotin and Kayla G. Sprenger
13:00-13:15	Aula Gini	SS1: AI and Computational Methods for Medical Informatics - Part II	Francesco Branda	AutoEncoder based approach for the identification of genomic regions responsible for poorly described oligo-patient disorders	Joanna Szyda
12:00-12:15	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	Francesco Branda	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
12:15-12:30	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	Duccio Medini, Giuseppe Maccari	Secondary structure design for efficient translation initiation	Tobias von der Haar and Corina Keller
12:30-12:45	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	Duccio Medini, Giuseppe Maccari	Manufacturability of mRNA Therapeutics: Native vs. N-1-Methyl-Pseudouridine	Roland Huber, Kuo Chieh Liao and Yue Wan
12:45-13:00	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	Duccio Medini, Giuseppe Maccari	Optimizing RNA yield using deep neural networks coupled to massively parallel screening	Adrien Villain
13:00-13:15	Aula Magna	SS10: Computational tools for the effective design of mRNA-based therapeutics	Duccio Medini, Giuseppe Maccari	MAP-Net: An Interpretable Deep Learning Framework for Universal mRNA Manufacturability	Giorgio Ciano
11:00-11:15	Aula Magna	SS11: GPU-accelerated analysis of single-cell and spatial omics	Duccio Medini, Giuseppe Maccari	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
11:15-11:30	Aula Magna	SS11: GPU-accelerated analysis of single-cell and spatial omics	Dario Righelli	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

Time	Room	Session	Chair	Paper title	Authors
11:30-11:45	Aula Magna	SS11: GPU-accelerated analysis of single-cell and spatial omics	Dario Righelli	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
11:45-12:00	Aula Magna	SS11: GPU-accelerated analysis of single-cell and spatial omics	Dario Righelli	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
11:00-11:15	Aula III	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	Dario Righelli	A topological object-proposal pipeline for cellular fiber segmentation	Riccardo Ceccaroni, Valerio Reffo, Camilla Pezzini, Roberta Sartori, Marco Sandri, Pierpaolo Brutti and Davide Risso
11:15-11:30	Aula III	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	Annamaria Carissimo	Quantum Machine Learning for Missense Variant Pathogenicity Prediction in the KCNQ Gene Family	Markel Garcia, Sara Capponi, Aitor Bergara and Aritz Leonardo
11:30-11:45	Aula III	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	Annamaria Carissimo	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
11:45-12:00	Aula III	SS5: Biostatistical and Artificial Intelligence Methods for Personalized Medicine and Health	Annamaria Carissimo	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
19:00-20:00	Terrazza del Rettorato	Welcome Cocktail + MUSA Jazz Concert	Annamaria Carissimo	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 Cristofoletti, Maria Grazia Narducci and Roberta Tarallo

Thursday, September 3

Time	Room	Session	Chair	Paper title	Authors
15:35-15:50	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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
15:00-15:20	**Terrazza del Rettorato + Aula II**	**Coffee Break**			
09:30-10:15	**Aula Magna**	**Keynote — Marianna Rapsomaniki**		**Building predictive models for precision oncology across scales, modalities and perturbations**	**Marianna Rapsomaniki**
12:30-13:30	**Terrazza del Rettorato**	**Lunch**			
08:45-09:00	Aula Magna	MEDINF Main Track 1	Elisabetta Ferretti	Soft-GLCM: Stabilizing Differentiable Texture Analysis through Soft Quantization	Haoyue Chen, Giuseppe Salvaggio, Albert Comelli and Anthony Yezzi
09:00-09:15	Aula Magna	MEDINF Main Track 1	Elisabetta Ferretti	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	MEDINF Main Track 1	Elisabetta Ferretti	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
10:15-12:30	**Museo dell'Arte Classica**	**Poster Session B / Coffee Break**			
18:00-	**Meeting point / Rome city centre**	**Social Event + Social Dinner**			
15:20-15:35	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	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
15:35-15:50	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	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
15:50-16:05	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	Integration of Large Language Models and Retrieval-Augmented Generation for Clinical Decision Support in Inflammatory Bowel Disease	Gabriele Rumi, Andrea Mazzei, Daniele Napolitano, Franco Scaldaferri, Giuseppe Cattaneo and Antonio Gasbarrini
16:05-16:20	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	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
16:20-16:35	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	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
16:35-16:50	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	NanoMambaNet: A Linear-Time CNN-Mamba Hybrid Architecture for Basecalling-Free Nanopore Pathogen Classification	Chayanika Bhattacharjee, Kolin Paul and Niranjan Sarode

Time	Room	Session	Chair	Paper title	Authors
16:50-17:05	Aula Gini	SS12: Machine learning for structured data in clinical informatics and medical biology	Davide Chicco	SOPHYSM: More Steps towards Digital Twins of Solid Tumours	Diego Cividini and Marco Antoniotti
14:15-14:30	Aula III	SS13: Modern Bayesian Factor Models for Complex Biological Data	Pantelis Samartsidis; Lorenzo Schiavon; Alejandra Avalos-Pacheco	A Sparse Rotationally Invariant Integrative Factor Model	Alejandra Avalos-Pacheco
14:30-14:45	Aula III	SS13: Modern Bayesian Factor Models for Complex Biological Data	Pantelis Samartsidis; Lorenzo Schiavon; Alejandra Avalos-Pacheco	Tensor decompositions for Bayesian factor models with dynamic loadings: an application to causal inference	Pantelis Samartsidis
14:45-15:00	Aula III	SS13: Modern Bayesian Factor Models for Complex Biological Data	Pantelis Samartsidis; Lorenzo Schiavon; Alejandra Avalos-Pacheco	Informed Sparse Factorization for Psychometric Construct Recognition	Lorenzo Schiavon
13:30-13:45	Aula Magna	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	Silvia Cascianelli and Marco Masseroli	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 Magna	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	Silvia Cascianelli and Marco Masseroli	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 Magna	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	Silvia Cascianelli and Marco Masseroli	SpatialJEPA: JEPA-inspired graph-context distillation for spatially aware multiomics integration	Dylan Mann-Krzisnik and Yue Li
14:15-14:30	Aula Magna	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications	Silvia Cascianelli and Marco Masseroli	Benchmarking a Spatial-Aware Foundation Model: An Empirical Evaluation of CellPLM in Transcriptomics	Juha Im, Haiping Liu and Hongpeng Zhou
13:30-13:45	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	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
13:45-14:00	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	Hybrid Quantum-Classical Convolutional Neural Network for Genomic Sequence Classification	Giovanni Acampora, Angela Chiatto and Roberto Schiattarella
14:45-15:00	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	Temporal quantum feature maps for longitudinal biomedical data	Maria Demidik, Filippo Utro, Alexey Galda, Daniel Blankenberg, Karl Jansen and Laxmi Parida
14:15-14:30	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	Quantum Kernel Estimation for the Discovery of Early Lung Cancer Detection	Hamed Javidi, Alex Zajichek, Hakan Doga, Laxmi Parida, Filippo Utro and Peter Mazzone
14:30-14:45	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	Quantum-Assisted Clinical Risk Factor Selection for Diabetes Readmission Prediction	Floriano Caprio, Matteo Tortora, Paolo Soda and Sunil Gentyala
14:00-14:15	Aula Gini	SS16: Quantum Artificial Intelligence for Bioinformatics and Biostatistics: Theory, Algorithms, and Applications	Roberto Schiattarella	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
14:30-14:45	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part I	Elisabetta Sciacca; Lorenzo Martini	FLoRe: Fingerprint-based Long-Read Overlap Reconstruction	Manuel Sica, Rocco Zaccagnino and Rosalba Zizza
14:45-15:00	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part I	Elisabetta Sciacca; Lorenzo Martini	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
17:05-17:20	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	ChloroGuide: prediction of subplastid localization using protein language model	Filip Pietluch and Przemyslaw Gagat
15:20-15:35	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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	Chair	Paper title	Authors
15:50-16:05	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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 Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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 Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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
16:35-16:50	Aula Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	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 Magna	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II	Elisabetta Sciacca; Lorenzo Martini	rSignificativity: an R package to compute significativity indexes for agreement values	Roberto Pagliarini and Alberto Casagrande
13:30-13:45	Aula III	SS7: Computational Intelligence for Integrative Host–Microbe Genomics: From Single-Cell Regulation to Population-Scale Pangenomes	Antonello Maruotti	An entropy based method for mapping mixed lineage next generation sequencing data	Gregory Fonseca
13:45-14:00	Aula III	SS7: Computational Intelligence for Integrative Host–Microbe Genomics: From Single-Cell Regulation to Population-Scale Pangenomes	Antonello Maruotti	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
14:00-14:15	Aula III	SS7: Computational Intelligence for Integrative Host–Microbe Genomics: From Single-Cell Regulation to Population-Scale Pangenomes	Antonello Maruotti	Learned Indexing for Genome Exact Mapping: A Comparative Study	Zeinab Hassaan, Eman Hassan, Baker Mohammad and Lobna Said
15:20-15:35	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	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
15:35-15:50	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Modeling Overdispersed Zero-Inflated Longitudinal Count Data: A Beta-Binomial Mixed-Effects Approach	John Barrera, Ana Arribas-Gil, Dae-Jin Lee and Cristian Meza
15:50-16:05	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Longitudinal Microbiome Analysis in R: Review and Selection Pipeline	Irene Creus-Martí and Francisco José Santonja Gómez
16:05-16:20	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	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
16:20-16:35	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Machine learning identifies candidate microbiome features associated with rheumatoid arthritis risk despite limited external predictive performance	Raissa Silva, Rachel Audo, Axel Finckh, Claire Immediato Daien and Zubeyir Salis
16:35-16:50	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Leveraging hologenomic data for phenotypic prediction: potential and pitfalls	Solène Pety, Ingrid David, Andrea Rau and Mahendra Mariadassou
16:50-17:05	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	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
17:05-17:20	Aula III	SS8: Computational Intelligence Methods for Complex, Compositional, and Longitudinal Microbiome Data in One Health	Marta Avalos Fernandez	Supervised NMF to unravel signature-class associations in microbiome composition: application to microbial signature of downy mildew epidemology in vineyards.	Alioune-Badara Diouf, Paola Fournier, Jean-Marc Frigerio, Corinne Vacher and Simon Labarthe

Friday, September 4

Time	Room	Session	Chair	Paper title	Authors
14:45-15:00	Aula Gini	BIOINF Main Track 3	Chiara Parrillo	Reinforcement Learning for Antibody Sequence Infilling	Chak Shing Lee, Conor F. Hayes, Denis Vashchenko and Mikel Landajuela Larma
15:00-15:15	Aula Gini	BIOINF Main Track 3	Chiara Parrillo	Reinforcement Learning-Based Control Strategy for Boolean Gene Regulatory Networks	Michal Shoob, Hila Glazz, Avraham Raviv and Hillel Kugler
15:15-15:30	Aula Gini	BIOINF Main Track 3	Chiara Parrillo	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
15:30-15:45	Aula Gini	BIOINF Main Track 3	Chiara Parrillo	A Neural Factorization Machine Approach to Drug–Target Interaction with Global Features	Mirco Perna and Simona Ester Rombo
14:45-15:00	Aula Magna	BIOINF Main Track 4	Monica Ballarino	How Much Architecture Does a Protein Transformer Need to Self-Discover?	Giansalvo Cirrincione, Elisa Ficarra and Marta Lovino
15:00-15:15	Aula Magna	BIOINF Main Track 4	Monica Ballarino	Incorporating Biologically Informed Masking into Protein Language Models for Pocket Identification	Luiza Gomes Ferreira
15:15-15:30	Aula Magna	BIOINF Main Track 4	Monica Ballarino	EXTRARNAS: A Framework for Extracting RNA Structures with Multiple Tools	Federico Di Petta, Piermichele Rosati, Piero Hierro Canchari, Michela Quadrini and Luca Tesei
15:30-15:45	Aula Magna	BIOINF Main Track 4	Monica Ballarino	FusFun: a tool for the functional evaluation of gene fusions in RNA-seq–data	Francesca Miccolis, Martina Filieri, Elisa Ficarra and Marta Lovino
16:15-16:30	Aula Magna	BIOINF Main Track 5	Cinzia Pizzi	PRIMA: a bidirectional state-space architecture and training approach for modelling protein-protein interactions	Arturo Fiorellini-Bernardis, Sebastien Boyer, Jean Quentin, Ghassene Jebali and Oliver Bent
16:45-17:00	Aula Magna	BIOINF Main Track 5	Cinzia Pizzi	iPerturb: An interpretable framework for predicting gene expression changes under perturbations	Khang Ta Gia and Linh Huynh Viet
16:30-16:45	Aula Magna	BIOINF Main Track 5	Cinzia Pizzi	PANDORA: a multiparametric framework for sensitive detection of insertional mutagenesis	Riccardo Pizzichemi
17:00-17:15	Aula Magna	BIOINF Main Track 5	Cinzia Pizzi	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
17:15-17:30	Aula Magna	BIOINF Main Track 5	Cinzia Pizzi	An XAI-Driven Transformer for Non-Canonical Splice-Site Prediction	Ahmed Negm, Nahla Belal and Mohamed Khedr
08:45-09:00	Aula Magna	BIOSTAT Main Track 2	Marco Alfo'	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	BIOSTAT Main Track 2	Marco Alfo'	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	BIOSTAT Main Track 2	Marco Alfo'	Bootstrap-Aggregated Method-of-Moments Estimation of Copula Correlation Under Generalized Gamma Dependent Censoring	Hyun-Soo Zhang and Chung Mo Nam
17:30-17:45	**Aula Magna**	**Closing Remarks**			
10:15-10:45	**Terrazza del Rettorato**	**Coffee Break**			
15:45-16:15	**Terrazza del Rettorato**	**Coffee Break**			
13:15-14:00	**Aula Magna**	**Invited Talk — Pavel Pevzner**	Marco Beccuti	**Will AI replace Professors?**	**Pavel Pevzner**

Time	Room	Session	Chair	Paper title	Authors
09:30-10:15	**Aula Magna**	**Keynote — Andrea Rau**	Marco Alfo'	**Leveraging biological priors in Bayesian genomic prediction models for complex traits**	**Andrea Rau**
12:15-13:15	**Terrazza del Rettorato**	**Lunch**			
10:45-11:00	Aula Gini	MEDINF Main Track 2	Marco Masseroli	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
11:00-11:15	Aula Gini	MEDINF Main Track 2	Marco Masseroli	Lexical and Embedding Similarity for ICD to Hetionet Disease Alignment: A Controlled Multi-View Study	Amani Braham and Insaf Tnazefti
11:15-11:30	Aula Gini	MEDINF Main Track 2	Marco Masseroli	Expert Knowledge & Machine Understanding: Bridging Reactome's Ontology with LLM Semantic Embeddings	Susanna Bravi, Riccardo De Luca, Rosa Sicilia, Christine Nardini and Mario Santoro
11:30-11:45	Aula Gini	MEDINF Main Track 2	Marco Masseroli	Radiomics-Based Thyroid Nodule Classification with Label-Conditional Conformal Prediction	Laura Testa, Umberto Ferraro Petrillo and Pierpaolo Brutti
11:45-12:00	Aula Gini	MEDINF Main Track 2	Marco Masseroli	Thyroid Nodule Segmentation in Ultrasound Images with Conformal Uncertainty Estimation	Francesco Teodori, Umberto Ferraro and Pierpaolo Brutti
14:00-14:15	Aula Gini	MEDINF Main Track 3	Nikolas Petsas	Reliability-Aware Benchmarking of Self-Supervised Learning in Histopathology Under 1-10% Label Regimes	Alicem Koyun, Pranjali Changadeo Pingale, Sachin Mote and Gianluca Pizzuti
14:15-14:30	Aula Gini	MEDINF Main Track 3	Nikolas Petsas	NoduleFlow: Automatic 3D Longitudinal Lung Nodule Detection and Segmentation	Giulia Romoli, Filippo Ruffini, Francesco Di Feola, Valerio Guarrasi, Matteo Tortora and Paolo Soda
14:30-14:45	Aula Gini	MEDINF Main Track 3	Nikolas Petsas	Federated vs. Centralized Learning: A Comparative Prediction Analysis for Hospitalization Cost	Shinto Pulickal Thomas, Jiregna Olani Kedida, Thierry Bossy, Juan Ramon Troncoso-Pastoriza, Alessandro Desideria, Dario Gregori and Corrado Lanera
10:45-11:00	Aula II	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	DirHopGNN: an efficient approach to k-hop GNNs	Francesco Madeddu and Mario Santoro
11:00-11:15	Aula II	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	Assessing Community Stability in Weighted Single-Cell Networks	Valeria Policastro, Domenico Sgambato, Dario Righelli, Vincenzo della Gatta, Luisa Cutillo and Annamaria Carissimo
11:15-11:30	Aula II	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine		Katz Kernel Based Stratification of Breast Cancer Patients	Francesco Cellitti, Lorenzo Di Rocco, Livia Perfetto, Veronica Lombardi and Umberto Ferraro Petrillo
11:30-11:45	Aula II	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	A Multilayer Graph Diffusion Model for Spatial Transcriptomics Reveals Cell-Cell Propagation Dynamics.	Caterina Francesca Perri, Annamaria Defilippo, Federico Manuel Giorgi, Pietro Hiram Guzzi and Pierangelo Veltri
11:45-12:00	Aula II	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	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
12:00-12:15	Aula II	SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine	Annamaria Defilippo	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
10:45-11:00	Aula III	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	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
11:00-11:15	Aula III	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	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

Time	Room	Session	Chair	Paper title	Authors
11:15-11:30	Aula III	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	Pixel-Wise Nuclei Localization in Cervical Cytology with Hierarchical Feature Representations	Ciro Russo, Alessandro Bria and Claudio Marrocco
11:30-11:45	Aula III	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	Estimating Oocyte Biological Age: An Explainable Deep Learning Approach for Assisted Reproduction	Andrea Piermartini, Donatella Firmani, Francesco Leotta, Claudio Manna and Silvia Raffi
11:45-12:00	Aula III	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	GLD-VAE: A Guided Latent Diffusion Variational Autoencoder for Class Imbalance in Multi-Omics Data	Durga Parkhi, Srijay Deshpande and Animesh Acharjee
12:00-12:15	Aula III	SS2: AI2 in Healthcare: Artificial Intelligence Empowering Augmented Intelligence	Paolo Soda	LLMs Fail at Protein Sequence Annotation and Localization: A Comparative Study against a Tool-Augmented Agentic solution	Asia Leuzzi, Elisa Ficarra and Marta Lovino
14:00-14:15	Aula III	SS3: Bayesian Causal Inference for Public Health	Lucia Gallucci	Causal Effects on Latent Structures via Bayesian Nonparametric Factor Models	Roberta De Vito, Giovanni Parmigiani and Dafne Zorzetto
14:15-14:30	Aula III	SS3: Bayesian Causal Inference for Public Health	Lucia Gallucci	Discovering Heterogeneous Treatment Effects: A Bayesian Spike-and-Slab Approach	Dafne Zorzetto, Roberta De Vito and Falco J. Bargagli-Stoffi
14:30-14:45	Aula III	SS3: Bayesian Causal Inference for Public Health	Lucia Gallucci	Network-based modelling of categorical data for personalized causal inference	Federico Castelletti and Laura Ferrini
14:45-15:00	Aula III	SS3: Bayesian Causal Inference for Public Health	Lucia Gallucci	Transporting principal causal effects across strata: A Bayesian causal inference approach	Veronica Ballerini, Falco Joannes Bargagli Stoffi and Francesca Dominici
14:00-14:15	Aula Magna	SS6: Chemoinformatics and computational chemistry for drug discovery and prediction of chemical properties and activities	Davide Chicco	Bridging Generative AI and Synthesis-on-Demand Chemical Spaces for Structure-based De Novo Drug Design	Cosmin Ichim, Viet-Khoa Tran-Nguyen and Pedro Ballester
14:15-14:30	Aula Magna	SS6: Chemoinformatics and computational chemistry for drug discovery and prediction of chemical properties and activities	Davide Chicco	A Framework for Diversity Constrained Design of Natural Product like Molecules	Aditi Vijil and Pin-Yu Chen
14:30-14:45	Aula Magna	SS6: Chemoinformatics and computational chemistry for drug discovery and prediction of chemical properties and activities	Davide Chicco	Identification of Allosteric Binding Pockets and Ligand-Induced Network Rewiring in PHF6	Lisia Peqini, Alessio Ferrini, Lan Phan Bach Tun, Jacopo Miotto, Massimo Bellanda and Damiano Piovesan
15:00-15:15	Aula III	SS9: Computational Methods for Mental Health and Well-Being	Francesca Gasparini	A study on the use of learning techniques and explainability methods on TMS-EEG data	Sara Nocco, Eleonora Arrigoni, Diego Corna, Francesca Gasparini, Alberto Pisoni, Leonor Josefina Romero Lauro and Aurora Saibene
15:15-15:30	Aula III	SS9: Computational Methods for Mental Health and Well-Being	Francesca Gasparini	Identifying relevant Facial Action Units associated with Depression for Generating Synthetic Images using LLMs	Jona Maximilian Kao and Michael Gertz
15:30-15:45	Aula III	SS9: Computational Methods for Mental Health and Well-Being	Francesca Gasparini	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

Paper Index

Sorted alphabetically by paper title. Search this page or the whole PDF by title or author.

Paper title	Authors	Day	Time	Room
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	Thursday	13:30-13:45	Aula Gini
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	Thursday	15:20-15:35	Aula Gini
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
A Dependent Dirichlet Process Approach to Population Size Estimation	Lucia Gallucci	Wednesday	10:30-11:00	Terrazza del Rettorato
A Framework for Diversity Constrained Design of Natural Product like Molecules	Aditi Vijil and Pin-Yu Chen	Friday	14:15-14:30	Aula Magna
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	Wednesday	11:45-12:00	Aula III
A Multilayer Graph Diffusion Model for Spatial Transcriptomics Reveals Cell-Cell Propagation Dynamics.	Caterina Francesca Perri, Annamaria Defilippo, Federico Manuel Giorgi, Pietro Hiram Guzzi and Pierangelo Veltri	Friday	11:30-11:45	Aula II
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
A Pipeline for Predicting Variant Associations with Complex Disorders via Functional Annotations	Francesco Gualdi, Zeno Darani, Daniele Malpetti, Marco Scutari and Francesca Mangili	Wednesday	10:15-10:30	Aula Magna
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	14:00-14:15	Aula Gini
A Sparse Rotationally Invariant Integrative Factor Model	Alejandra Avalos-Pacheco	Thursday	14:15-14:30	Aula III
A study on the use of learning techniques and explainability methods on TMS-EEG data	Sara Nocco, Eleonora Arrigoni, Diego Corna, Francesca Gasparini, Alberto Pisoni, Leonor Josefina Romero Lauro and Aurora Saibene	Friday	15:00-15:15	Aula III
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	11:00-11:15	Aula III
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	Thursday	09:00-09:15	Aula Magna
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 Cristofoletti, Maria Grazia Narducci and Roberta Tarallo	Wednesday	19:00-20:00	Terrazza del Rettorato
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	Thursday	09:15-09:30	Aula Magna
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
An entropy based method for mapping mixed lineage next generation sequencing data	Gregory Fonseca	Thursday	13:30-13:45	Aula III
An XAI-Driven Transformer for Non-Canonical Splice-Site Prediction	Ahmed Negm, Nahla Belal and Mohamed Khedr	Friday	17:15-17:30	Aula Magna
Analysis of biological networks using Krylov subspace trajectories	H. Robert Frost	Wednesday	09:45-10:00	Aula Magna
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 II
AutoEncoder based approach for the identification of genomic regions responsible for poorly described oligo-patient disorders	Joanna Szyda	Wednesday	13:00-13:15	Aula Gini

Paper title	Authors	Day	Time	Room
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
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	Thursday	15:20-15:35	Aula III
Bootstrap-Aggregated Method-of-Moments Estimation of Copula Correlation Under Generalized Gamma Dependent Censoring	Hyun-Soo Zhang and Chung Mo Nam	Friday	09:15-09:30	Aula Magna
Bridging Generative AI and Synthesis-on-Demand Chemical Spaces for Structure-based De Novo Drug Design	Cosmin Ichim, Viet-Khoa Tran-Nguyen and Pedro Ballester	Friday	14:00-14:15	Aula Magna
Causal Effects on Latent Structures via Bayesian Nonparametric Factor Models	Roberta De Vito, Giovanni Parmigiani and Dafne Zorzetto	Friday	14:00-14:15	Aula III
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	Wednesday	14:45-15:00	Aula Magna
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	12:00-12:15	Aula III
ChloroGuide: prediction of subplastid localization using protein language model	Filip Pietluch and Przemyslaw Gagat	Thursday	17:05-17:20	Aula Magna
ClinRAG-BiLSTM: An Agentic Cloud AI Framework for Explainable and Traceable Breast Cancer Decision Support	Adaleta Gicic and Dženana Đonko	Wednesday	11:30-11:45	Aula Gini
Comparative analysis of unsupervised multi-omics integration for pancreatic cancer subtype discovery	Gonçalo Costa-Ferreira, Marta B. Lopes and Eunice Carrasquinha	Friday	08:45-09:00	Aula Magna
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	11:30-11:45	Aula Magna
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
Decoding HIV-1 Antibody Escape with Interpretable Protein Language Models	Fahsai Nakarin, Pawin Taechoyotin and Kayla G. Sprenger	Wednesday	12:45-13:00	Aula Gini
Diagnosing Rejection Collapse via Uncertainty Decomposition	Walter Endrizzi, Flavio Ragni, Stefano Bovo, Monica Moroni, Giuseppe Jurman and Venet Osmani	Wednesday	11:15-11:30	Aula Gini
DirHopGNN: an efficient approach to k-hop GNNs	Francesco Madeddu and Mario Santoro	Friday	10:45-11:00	Aula II
Discovering Heterogeneous Treatment Effects: A Bayesian Spike-and-Slab Approach	Dafne Zorzetto, Roberta De Vito and Falco J. Bargagli-Stoffi	Friday	14:15-14:30	Aula III
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
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	Wednesday	11:45-12:00	Aula Magna
Estimating Oocyte Biological Age: An Explainable Deep Learning Approach for Assisted Reproduction	Andrea Piermartini, Donatella Firmani, Francesco Leotta, Claudio Manna and Silvia Raffi	Friday	11:30-11:45	Aula III
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	12:15-12:30	Aula III
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	Wednesday	12:30-12:45	Aula Gini
Evaluating SMT-Based Formal Inference for GRN Synthesis: From Data Density to Structural Rules	Ofri Caspi, Michal Greenberg, Eitan Tannenbaum and Hillel Kugler	Wednesday	10:00-10:15	Aula Magna
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
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	Thursday	16:35-16:50	Aula Magna
EXTRARNAS: A Framework for Extracting RNA Structures with Multiple Tools	Federico Di Petta, Piermichele Rosati, Piero Hierro Canchari, Michela Quadrini and Luca Tesei	Friday	15:15-15:30	Aula Magna
Federated vs. Centralized Learning: A Comparative Prediction Analysis for Hospitalization Cost	Shinto Pulickal Thomas, Jiregna Olani Kedida, Thierry Bossy, Juan Ramon Troncoso-Pastoriza, Alessandro Desideria, Dario Gregori and Corrado Lanera	Friday	14:30-14:45	Aula Gini

Paper title	Authors	Day	Time	Room
FLoRe: Fingerprint-based Long-Read Overlap Reconstruction	Manuel Sica, Rocco Zaccagnino and Rosalba Zizza	Thursday	14:30-14:45	Aula Magna
Functional Fuzzy Clustering of Longitudinal biological marker's trajectories	Silvia D'Elia, Valeria Paggi, Marco Alfò and Maria Brigida Ferraro	Wednesday	12:45-13:00	Aula III
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
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	Thursday	14:45-15:00	Aula Magna
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
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	11:15-11:30	Aula Magna
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	Thursday	16:20-16:35	Aula Magna
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
How Much Architecture Does a Protein Transformer Need to Self-Discover?	Giansalvo Cirrincione, Elisa Ficarra and Marta Lovino	Friday	14:45-15:00	Aula Magna
Hybrid Quantum-Classical Convolutional Neural Network for Genomic Sequence Classification	Giovanni Acampora, Angela Chiatto and Roberto Schiattarella	Thursday	13:45-14:00	Aula Gini
Identification of Allosteric Binding Pockets and Ligand-Induced Network Rewiring in PHF6	Lisia Peqini, Alessio Ferrini, Lan Phan Bach Tun, Jacopo Miotto, Massimo Bellanda and Damiano Piovesan	Friday	14:30-14:45	Aula Magna
Identifying functional drivers of Hepatoblastoma outcomes via agent-based modeling and transcriptomics	Alessandro Ravoni, Yuanhua Liu, Stefano Cairo, Filippo Castiglione and Christine Nardini	Wednesday	15:45-16:00	Aula Magna
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
Incorporating Biologically Informed Masking into Protein Language Models for Pocket Identification	Luiza Gomes Ferreira	Friday	15:00-15:15	Aula Magna
Informed Sparse Factorization for Psychometric Construct Recognition	Lorenzo Schiavon	Thursday	14:45-15:00	Aula III
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 II
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 II
Integration of Large Language Models and Retrieval-Augmented Generation for Clinical Decision Support in Inflammatory Bowel Disease	Gabriele Rumi, Andrea Mazzei, Daniele Napolitano, Franco Scaldaferri, Giuseppe Cattaneo and Antonio Gasbarrini	Thursday	15:50-16:05	Aula Gini
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
iPerturb: An interpretable framework for predicting gene expression changes under perturbations	Khang Ta Gia and Linh Huynh Viet	Friday	16:45-17:00	Aula Magna
Katz Kernel Based Stratification of Breast Cancer Patients	Francesco Cellitti, Lorenzo Di Rocco, Livia Perfetto, Veronica Lombardi and Umberto Ferraro Petrillo	Friday	11:15-11:30	Aula II
Learned Indexing for Genome Exact Mapping: A Comparative Study	Zeinab Hassaan, Eman Hassan, Baker Mohammad and Lobna Said	Thursday	14:00-14:15	Aula III
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	15:20-15:35	Aula Magna
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
Lexical and Embedding Similarity for ICD to Hetionet Disease Alignment: A Controlled Multi-View Study	Amani Braham and Insaf Tnazefti	Friday	11:00-11:15	Aula Gini
LLM-Guided Integer Linear Programming for Antibody Library Design	Mikel Landajuela Larma	Wednesday	14:30-14:45	Aula Magna
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
Longitudinal Microbiome Analysis in R: Review and Selection Pipeline	Irene Creus-Martí and Francisco José Santonja Gómez	Thursday	15:50-16:05	Aula III

Paper title	Authors	Day	Time	Room
Machine learning identifies candidate microbiome features associated with rheumatoid arthritis risk despite limited external predictive performance	Raissa Silva, Rachel Audo, Axel Finckh, Claire Immediato Daien and Zubeyir Salis	Thursday	16:20-16:35	Aula III
Manufacturability of mRNA Therapeutics: Native vs. N-1-Methyl-Pseudouridine	Roland Huber, Kuo Chieh Liao and Yue Wan	Wednesday	12:30-12:45	Aula Magna
MAP-Net: An Interpretable Deep Learning Framework for Universal mRNA Manufacturability	Giorgio Ciano	Wednesday	13:00-13:15	Aula Magna
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	Thursday	13:45-14:00	Aula III
Microbial Community Structure and Immune Integration in Lung Adenocarcinoma	Chiara Napoli, Francesco Bardozzo, Luigi Liguori, Claudio Angione, Annalisa Occhipinti and Roberto Tagliaferri	Thursday	13:30-13:45	Aula Magna
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
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	Thursday	16:05-16:20	Aula III
Modeling Overdispersed Zero-Inflated Longitudinal Count Data: A Beta-Binomial Mixed-Effects Approach	John Barrera, Ana Arribas-Gil, Dae-Jin Lee and Cristian Meza	Thursday	15:35-15:50	Aula III
Multivariate Model-Based Landmarking Approach in Mixture Cure Models to Dynamic Prediction	Bianca Ferraro, Marco Alfò and Marta Cipriani	Wednesday	12:30-12:45	Aula III
NanoMambaNet: A Linear-Time CNN-Mamba Hybrid Architecture for Basecalling-Free Nanopore Pathogen Classification	Chayanika Bhattacharjee, Kolin Paul and Niranjan Sarode	Thursday	16:35-16:50	Aula Gini
Network-based modelling of categorical data for personalized causal inference	Federico Castelletti and Laura Ferrini	Friday	14:30-14:45	Aula III
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
OmicsGPT: Multi-Agent Bioinformatics Orchestration for Evidence-Grounded RNA-seq Interpretation	Patrick Roney and James Li	Wednesday	15:00-15:15	Aula Magna
Ontology-Aware Candidate Reranking for SNOMED CT Entity Linking in Clinical Notes	Luka Blašković, Nikola Tanković and Ivo Ipšić	Wednesday	12:15-12:30	Aula Gini
Optimizing RNA yield using deep neural networks coupled to massively parallel screening	Adrien Villain	Wednesday	12:45-13:00	Aula Magna
PANDORA: a multiparametric framework for sensitive detection of insertional mutagenesis	Riccardo Pizzichemi	Friday	16:30-16:45	Aula Magna
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	Friday	11:00-11:15	Aula III
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
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	Wednesday	12:00-12:15	Aula Gini
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	12:00-12:15	Aula Magna
PRIMA: a bidirectional state-space architecture and training approach for modelling protein-protein interactions	Arturo Fiorellini-Bernardis, Sebastien Boyer, Jean Quentin, Ghassene Jebali and Oliver Bent	Friday	16:15-16:30	Aula Magna
Privacy-preserving federated batch effect correction in omics data with ComBatFed	Yuliya Burankova, Mohammad Mahdi Kazemi, Linda Baumbach and Jan Baumbach	Thursday	15:50-16:05	Aula Magna
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	Thursday	16:20-16:35	Aula Gini
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
Quantum Machine Learning for Missense Variant Pathogenicity Prediction in the KCNQ Gene Family	Markel Garcia, Sara Capponi, Aitor Bergara and Aritz Leonardo	Wednesday	11:15-11:30	Aula III

Paper title	Authors	Day	Time	Room
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
Radiomics-Based Thyroid Nodule Classification with Label-Conditional Conformal Prediction	Laura Testa, Umberto Ferraro Petrillo and Pierpaolo Brutti	Friday	11:30-11:45	Aula Gini
Reducing the Size of Breastfeeding Reference Arms in Infant Nutrition Studies Using Prognostic Covariate Adjustment	Luca Lavalle	Wednesday	13:00-13:15	Aula III
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
Reinforcement Learning-Based Control Strategy for Boolean Gene Regulatory Networks	Michal Shoob, Hila Glazz, Avraham Raviv and Hillel Kugler	Friday	15:00-15:15	Aula Gini
Reliability-Aware Benchmarking of Self-Supervised Learning in Histopathology Under 1-10% Label Regimes	Alicem Koyun, Pranjali Changadeo Pingale, Sachin Mote and Gianluca Pizzuti	Friday	14:00-14:15	Aula Gini
rSignificativity: an R package to compute significativity indexes for agreement values	Roberto Pagliarini and Alberto Casagrande	Thursday	16:50-17:05	Aula Magna
Secondary structure design for efficient translation initiation	Tobias von der Haar and Corina Keller	Wednesday	12:15-12:30	Aula Magna
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	Friday	10:45-11:00	Aula Gini
Sequence-Derived Physicochemical Features and Stacked Learning for SUMOylation-Site Prediction	Junyan Li, Qiaobin Yao, Danda Rawat, Jiang Li and Shaolei Teng	Wednesday	14:15-14:30	Aula Magna
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	Thursday	15:35-15:50	Aula Magna
Soft-GLCM: Stabilizing Differentiable Texture Analysis through Soft Quantization	Haoyue Chen, Giuseppe Salvaggio, Albert Comelli and Anthony Yezzi	Thursday	08:45-09:00	Aula Magna
SOPHYSM: More Steps towards Digital Twins of Solid Tumours	Diego Cividini and Marco Antoniotti	Thursday	16:50-17:05	Aula Gini
SpatialJEPA: JEPA-inspired graph-context distillation for spatially aware multiomics integration	Dylan Mann-Krzisnik and Yue Li	Thursday	14:00-14:15	Aula Magna
Supervised NMF to unravel signature-class associations in microbiome composition: application to microbial signature of downy mildew epidemology in vineyards.	Alioune-Badara Diouf, Paola Fournier, Jean-Marc Frigerio, Corinne Vacher and Simon Labarthe	Thursday	17:05-17:20	Aula III
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	Thursday	13:45-14:00	Aula Magna
Temporal quantum feature maps for longitudinal biomedical data	Maria Demidik, Filippo Utro, Alexey Galda, Daniel Blankenberg, Karl Jansen and Laxmi Parida	Thursday	14:45-15:00	Aula Gini
Tensor decompositions for Bayesian factor models with dynamic loadings: an application to causal inference	Pantelis Samartsidis	Thursday	14:30-14:45	Aula III
Thyroid Nodule Segmentation in Ultrasound Images with Conformal Uncertainty Estimation	Francesco Teodori, Umberto Ferraro and Pierpaolo Brutti	Friday	11:45-12:00	Aula Gini
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	Thursday	15:35-15:50	Aula Gini
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	11:00-11:15	Aula Magna
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	17:00-17:15	Aula Magna
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 Tavolato	Wednesday	11:45-12:00	Aula Gini
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
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	Friday	09:00-09:15	Aula Magna
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	Wednesday	11:30-11:45	Aula III