

Aula Magna

08:45-09:30	MEDINF Main Track 1
08:45-09:00	Soft-GLCM: Stabilizing Differentiable Texture Analysis through Soft Quantization Haoyue Chen · Giuseppe Salvaggio · Albert Comelli · Anthony Yezzi
09:00-09:15	A Unified Framework for Bipartite Network Projection and Backbone Extraction, with an Application to Gene-Disease Associations Panagiota Kontou · Ioannis Charatsiaris · Efstathios Voulgaris · Pantelis Bagos
09:15-09:30	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 · Andja Srebro
09:30-10:15	Keynote — Marianna Rapsomaniki
09:30-10:15	Building predictive models for precision oncology across scales, modalities and perturbations Marianna Rapsomaniki
12:30-13:30	Lunch
12:30-13:30	Lunch
13:30-14:30	SS15: Spatial Omics Analysis and Integration: Models, Methods, and Applications Chair: Roberto Schiattarella
13:30-13:45	Microbial Community Structure and Immune Integration in Lung Adenocarcinoma Chiara Napoli · Francesco Bardozzo · Luigi Liguori · Claudio Angione · Annalisa Occhipinti · Roberto Tagliaferri
13:45-14:00	SVC-Probe: A Framework for Evaluating Perturbation Generalization in Spatial Foundation-Model Embeddings Jake Y. Chen · Huu Phong Nguyen · Fuad Al Abir · Ehsan Saghapour
14:00-14:15	SpatialJEPA: JEPA-inspired graph-context distillation for spatially aware multiomics integration Dylan Mann-Krzisnik · Yue Li
14:15-14:30	Benchmarking a Spatial-Aware Foundation Model: An Empirical Evaluation of CellPLM in Transcriptomics Juha Im · Haiping Liu · Hongpeng Zhou
14:30-15:00	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part I Chair: Elisabetta Sciacca; Lorenzo Martini
14:30-14:45	FLoRe: Fingerprint-based Long-Read Overlap Reconstruction Manuel Sica · Rocco Zaccagnino · Rosalba Zizza
14:45-15:00	Genomic Centromere Profiling Tool using Centeny Maps for Centromere Characterization Across Genomes Mauricio Orantes Bonilla · Matteo Tommaso Ungaro · Luca Corda · Andreas Giannis · Simona Giunta

15:00-15:20	Coffee Break
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15:20-17:05	SS4: Better Tools for Better Biology: Bioinformatics Software Advances - Part II Chair: Elisabetta Sciacca; Lorenzo Martini
15:20-15:35	ChloroGuide: prediction of subplastid localization using protein language model Filip Pietluch · Przemyslaw Gagat
15:35-15:50	LeProteine: Resource-Aware Protein Binder Design Pipelines on Blackwell GPU Al Hamna Asif · Rana Abu Bakar · Filippo Cugini · Juan Jose Vegas Olmos · Amna Younus
15:50-16:05	Privacy-preserving federated batch effect correction in omics data with ComBatFed Yuliya Burankova · Mohammad Mahdi Kazemi · Linda Baumbach · Jan Baumbach
16:05-16:20	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 · Jan Baumbach
16:20-16:35	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 · Francesca Cordero
16:35-16:50	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 · Simone Pernice
16:50-17:05	rSignificativity: an R package to compute significativity indexes for agreement values Roberto Pagliarini · Alberto Casagrande