

Aula Magna

08:45-09:30 **BIOSTAT Main Track 2**

Chair: Marco Alfo'

08:45-09:00 **Comparative analysis of unsupervised multi-omics integration for pancreatic cancer subtype discovery**

Gonçalo Costa-Ferreira · Marta B. Lopes · Eunice Carrasquinha

09:00-09:15 **Treatment persistence drives estimator performance in longitudinal causal inference based on observational data: A simulation study**

Sergio Gaiotti · Sara Poletto · Enrico Longato · Erica Tavazzi · Martina Vettoretti

09:15-09:30 **Bootstrap-Aggregated Method-of-Moments Estimation of Copula Correlation Under Generalized Gamma Dependent Censoring**

Hyun-Soo Zhang · Chung Mo Nam

09:30-10:15 **Keynote — Per Kragh Andersen**

Chair: Marco Alfo'

09:30-10:15 **Multi-state models for recurrent events**

Per Kragh Andersen

10:15-10:45 **Coffee Break**

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10:45-12:15 **SS14: Networks and Graph Neural Networks for Bridging Bioinformatics and Medicine**

Chair: Annamaria Defilippo

10:45-11:00 **DirHopGNN: an efficient approach to k-hop GNNs**

Francesco Madeddu · Mario Santoro

11:00-11:15 **Assessing Community Stability in Weighted Single-Cell Networks**

Valeria Policastro · Domenico Sgambato · Dario Righelli · Vincenzo della Gatta · Luisa Cutillo · Annamaria Carissimo

11:15-11:30 **Bio-RL-GRN: Prior-Guided Reinforcement Learning for Gene Regulatory Network Inference**

Tshepo Kitso Gobonamang · Okaile Marumo · Mavuna Sebapalo · Mpoeleng Dimane

11:30-11:45 **A Multilayer Graph Diffusion Model for Spatial Transcriptomics Reveals Cell-Cell Propagation Dynamics.**

Caterina Francesca Perri · Annamaria Defilippo · Federico Manuel Giorgi · Pietro Hiram Guzzi · Pierangelo Veltri

11:45-12:00 **Integrating Genomic Annotations and Traits Dependencies for single-nucleotide polymorphisms Prioritization with Causally Reliable Concept Bottleneck Models**

Francesco De Santis · Daniele Malpetti · Francesco Gualdi · Francesca Mangili

12:00-12:15 **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 · Michał Grochowski

12:15-13:15 **Lunch**

12:15-13:15 **Lunch**

13:15-14:00 Invited Talk — Pavel Pevzner

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14:00-14:45 **SS6: Chemoinformatics and computational chemistry for drug discovery and prediction of chemical properties and activities**
Chair: Davide Chicco

14:00-14:15 **Bridging Generative AI and Synthesis-on-Demand Chemical Spaces for Structure-based De Novo Drug Design**
Cosmin Ichim · Viet-Khoa Tran-Nguyen · Pedro Ballester

14:15-14:30 **A Framework for Diversity Constrained Design of Natural Product like Molecules**
Aditi Vijil · Pin-Yu Chen

14:30-14:45 **Identification of Allosteric Binding Pockets and Ligand-Induced Network Rewiring in PHF6**
Lisia Pegini · Alessio Ferrini · Lan Phan Bach Tun · Jacopo Miotto · Massimo Bellanda · Damiano Piovesan

14:45-15:45 BIOINF Main Track 4

14:45-15:00 **How Much Architecture Does a Protein Transformer Need to Self-Discover?**
Giansalvo Cirrincione · Elisa Ficarra · Marta Lovino

15:00-15:15 **Incorporating Biologically Informed Masking into Protein Language Models for Pocket Identification**
Luiza Gomes Ferreira

15:15-15:30 **EXTRARNAS: A Framework for Extracting RNA Structures with Multiple Tools**
Federico Di Petta · Piermichele Rosati · Piero Hierro Canchari · Michela Quadrini · Luca Tesei

15:30-15:45 **FusFun: a tool for the functional evaluation of gene fusions in RNA-seq-data**
Francesca Miccolis · Martina Filieri · Elisa Ficarra · Marta Lovino

15:45-16:15 Coffee Break

15:45-16:15 **Coffee Break**

16:15-17:45	BIOINF Main Track 5
16:15-16:30	PRIMA: a bidirectional state-space architecture and training approach for modelling protein-protein interactions Arturo Fiorellini-Bernardis · Sebastien Boyer · Jean Quentin · Ghassene Jebali · Oliver Bent
16:30-16:45	iPerturb: An interpretable framework for predicting gene expression changes under perturbations Khang Ta Gia · Linh Huynh Viet
16:45-17:00	Katz Kernel Based Stratification of Breast Cancer Patients Francesco Cellitti · Lorenzo Di Rocco · Livia Perfetto · Veronica Lombardi · Umberto Ferraro Petrillo
17:00-17:15	PANDORA: a multiparametric framework for sensitive detection of insertional mutagenesis Riccardo Pizzichemi
17:15-17:30	Towards a unified framework: a data structures benchmark for representing genomic information Matteo Tommaso Ungaro · Mauricio Orantes Bonilla · Francesca Querques · Evelyne Tassone · Simona Giunta
17:30-17:45	An XAI-Driven Transformer for Non-Canonical Splice-Site Prediction Ahmed Negm
17:45-18:00	Closing Remarks
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