

09:30-10:30

BIOINF Main Track 1

Aula Magna

Chair: Davide Chicco

09:30-09:45	An Enhanced Pipeline for Multi-Omic Integration Based on Topological Data Analysis Veronica Paparozzi · Anna Plaksienko · Marco Pedicini · Christine Nardini
09:45-10:00	Analysis of biological networks using Krylov subspace trajectories H. Robert Frost
10:00-10:15	Evaluating SMT-Based Formal Inference for GRN Synthesis: From Data Density to Structural Rules Ofri Caspi · Michal Greenberg · Eitan Tannenbaum · Hillel Kugler
10:15-10:30	A Pipeline for Predicting Variant Associations with Complex Disorders via Functional Annotations Francesco Gualdi · Zeno Darani · Daniele Malpetti · Marco Scutari · Francesca Mangili