

Draft Programme for the BioGeMT Symposium

Time	Session	Speaker	Format
13:30– 13:40	Opening remarks	Panagiotis Alexiou	In person
13:40– 13:50	Capturing RNA metabolism dynamics with machine learning and direct RNA nanopore sequencing of nucleotide analogs	Emmanouil Maragkakis	Online
13:50– 14:00	From Phage Selection to Sequence Space: Profiling Recombinant Antibody Diversity via Nanopore Reads	David Saliba	In person
14:00– 14:10	Cracking the Genetic Code of Osteoporosis	Marichela Schembri	In person
14:10– 14:20	AtlasMSI: Autoencoder-Based Representation Learning and Segmentation for MALDI-MSI	Max Stróżyk	Online
14:20– 14:30	Pseudogene-derived artifacts in PKD1: Evidence from third generation HTS and ParaDISM a pseudogene-aware bioinformatics pipeline	Rosienne Farrugia	In person
14:30– 14:40	Discriminative Learning of Substitution Matrices and Gap Penalties	Michał Startek	In person
14:40– 14:50	An SQL database for TargetMI multilayered and multiomic data	Stephanie Bezzina Wettinger	Online
14:50– 15:00	Profiling the ageing monocyte before the insult to characterize a pre-sepsis innate immune state	Brendon Scicluna	In person
15:00– 15:10	Genomic Benchmarks QC: Quality-curated genomic benchmarks for fair and reproducible ML evaluation	Katarina Gresova	Online
15:10– 15:20	Closing remarks	Jean-Paul Ebejer	In person