|  | ID | session | title |
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| 27june-1 | 597 | Algorithms for Bioinformatics | Predicting genetic variants impact on transcription factor binding sites using k-mer-based motif models |
| 27june-2 | 614 | Algorithms for Bioinformatics | Detection of endogenous CAG instability through Nanopore sequencing of the Huntingtin Exon1 |
| 27june-3 | 497 | Algorithms for Bioinformatics | Prediction of Metabolic Profiles from Transcriptomics Data in Human Cancer Cell Lines |
| 27june-4 | 500 | Algorithms for Bioinformatics | CREDO: a friendly Customizable, REproducible, DOcker file generator. |
| 27june-5 | 501 | Algorithms for Bioinformatics | A new methodology for the modelling, analysis and visualization of COVID-19 data: COVID-19 Community Temporal Visualization. |
| 27june-6 | 510 | Algorithms for Bioinformatics | Detecting C-to-U RNA editing by direct RNA sequencing |
| 27june-7 | 522 | Algorithms for Bioinformatics | Unravelling the instability of mutational signatures extraction via Archetypal Analysis |
| 27june-8 | 553 | Algorithms for Bioinformatics | Delivering REDItools in Galaxy |
| 27june-9 | 549 | Algorithms for Bioinformatics | FunTaxIS-Lite: a simple and light solution to investigate the functional taxonomy. |
| 27june-10 | 550 | Algorithms for Bioinformatics | PLANTOGEN-A, an easy-to-use de novo assembly pipeline |
| 27june-11 | 599 | Sequencing and genotyping technologies | Long amplicon-based protocol for SARS-CoV-2 characterization |
| 27june-12 | 517 | Sequencing and genotyping technologies | Towards pocket-sized genomic analyses: cross-platform benchmark of multi-organism genomic data indexing and alignment |
| 27june-13 | 525 | Sequencing and genotyping technologies | Development of a workflow for the identification of mito-nuclear variants in Amyotrophic Lateral Sclerosis patients from Exome Sequencing data |
| 27june-14 | 536 | Sequencing and genotyping technologies | Assessing potential feasibility of Nanopore Sequencing platform for the detection of Ribonucleotides in DNA molecules |
| 27june-15 | 574 | Sequencing and genotyping technologies | An integrated, scalable framework for identification and quantification of tandem duplications in DNA sequencing data |
| 27june-16 | 556 | Personal genome analysis | Human genetic diversity alters therapeutic gene editing off-target outcomes |
| 27june-17 | 587 | Biological Networks | Analysis of molecular interactions and pathways to assess the similarity of biomarkers: a case study on autism spectrum disorders. |
| 27june-18 | 613 | Biological Networks | Network analysis revealed potential keystone taxa of microbiome in soil- and soilless-cultivated tomatoes |
| 27june-19 | 560 | Biological Networks | A world without B cells: |
| 27june-20 | 507 | Personal medicine | Cancer signatures for reproducible gene expression analysis data: the computational way to achieve precision medicine |
| 27june-21 | 600 | Protein structure and function | Exploration of LRIG2 homodimerization and dimerization impact by the deletion of LRIG2 Ig-1 domain, p.R550C, and p.S523R mutations |
| 27june-22 | 602 | Protein structure and function | In silico investigations reveal the molecular mechanism of HIV-1 matrix protein p17 variants in lymphoma pathogenesis |
| 27june-23 | 607 | Protein structure and function | UV-C EXPOSURE SUGGESTS A SARS-CoV-2 SPIKE PROTEIN ANTIVIRAL STRATEGY BASED ON REDUCING AGENTS |
| 27june-24 | 555 | Protein structure and function | Handling proteins. Tangible models in soft rubber allow composition of complex structures. |
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| 28june-1 | 581 | Metagenomics | Uncover a microbiota signature of upper respiratory tract in patients with SARS-CoV-2+ |

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| 28june-2 | 596 | Metagenomics | MetaPhage: an automated pipeline for analyzing, annotating, and classifying bacteriophages in metagenomics sequencing data. |
| 28june-3 | 504 | Metagenomics | hgtseq: a standard pipeline to study horizonal gene transfer |
| 28june-4 | 558 | Metagenomics | Computational analysis of shotgun metagenomics data from Parkinson patients highlights the presence of specific molecular pathways enriched in unknown species |
| 28june-5 | 565 | Metagenomics | Spectral segments as bacterial biomarkers |
| 28june-6 | 584 | Multi-omics data analysis and integration | Polympact: exploring functional relations among common human genetic variants |
| 28june-7 | 609 | Multi-omics data analysis and integration | Recent achievements of the EOSC-Life project |
| 28june-8 | 505 | Multi-omics data analysis and integration | A comprehensive investigation of histotype-specific microRNA and their variants in early stage ovarian cancer |
| 28june-9 | 520 | Multi-omics data analysis and integration | OneData for biobank data federation |
| 28june-10 | 539 | Multi-omics data analysis and integration | Unravelling microenvironment heterogeneity of ovarian cancer: a portray of innate and acquired platinum chemoresistance |
| 28june-11 | 561 | Multi-omics data analysis and integration | A multi-omics machine learning approach to find reliable signatures for TNBC patients' prognosis prediction |
| 28june-12 | 498 | Pangenomics | Chromosome communities in the human pangenome |
| 28june-13 | 577 | Single-cell data analysis | SINGLE CELL RNA SEQUENCING OF IMMUNOSUPPRESSIVE NEUTROPHILS FROM G-CSF TREATED DONORS |
| 28june-14 | 578 | Single-cell data analysis | LACE 2.0: an interactive tool for longitudinal cancer evolution |
| 28june-15 | 588 | Single-cell data analysis | CIA inspector: A Cluster Independent Annotation method to investigate cell identities in scRNA-seq data |
| 28june-16 | 592 | Single-cell data analysis | Harmonizing annotation of single cells with the Cell Marker Accordion |
| 28june-17 | 527 | Single-cell data analysis | Differential cellular communication analysis from single cell RNA sequencing data with scSeqComm |
| 28june-18 | 572 | Single-cell data analysis | Cell-cell communication analysis from single-cell data: comparison of approaches using datasets of normal mammary gland and breast cancer |
| 28june-19 | 583 | Spatial transcriptomics | Tissue transcriptomic on pancreatic cancer: different approaches |
| 28june-19 | 518 | Gene regulation, transcriptomics and epigenomics | A microRNA regulatory network driven by the epigenetic factor LSD1 in Glioblastoma |
| 28june-19 | 534 | Gene regulation, transcriptomics and epigenomics | EpiStatProfiler: a new R package for the qualitative analysis of DNA methylation. |
| 28june-19 | 535 | Gene regulation, transcriptomics and epigenomics | MC profiling: a novel approach to dissect DNA methylation heterogeneity from genome-wide bisulfite sequencing data |
| 28june-19 | 554 | Gene regulation, transcriptomics and epigenomics | Deregulated lncRNAs in Alzheimers Disease inferred by weighted gene co-expression network analysis |
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| 29june-1 | 521 | Bioimaging | Artificial intelligence to detect patients affected by COVID-19 |
| 29june-2 | 590 | Biological data management | Submission to European Genome-phenome Archive (EGA): from months to hours. |
| 29june-3 | 593 | Biological data management | Processing MALDI/ToF spectra for differential peptidomics in a clinical asset |
| 29june-4 | 603 | Biological data management | expressyouRcell: shooting for space-time changes in gene expression in cells |
| 29june-5 | 566 | Biological data management | BIOCHAIN-AI: a platform for securely sharing and analysing microbiological data. |
| 29june-6 | 568 | Biological data management | Developing of a Molecular Tumor Registry of a National Cancer Center on 1988 NGS solid tumor profiles |

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| 29june-7 | 589 | Biological Databases | Design and implementation of the MBDS-DB federated database for the Sardinian Microbial Culture Collections |
| 29june-8 | 541 | Biological Databases | UTRdb 3.0 a comprehensive, expert curated catalog of eukaryotic mRNAs untranslated regions |
| 29june-9 | 579 | Machine Learning in Bioinformatics | SVMyr: a new web server predicting co- and post-translational myristoylation in proteins |
| 29june-10 | 580 | Machine Learning in Bioinformatics | Embedding of protein sequence and function improves the prediction of human pathogenic variants. |
| 29june-11 | 604 | Machine Learning in Bioinformatics | Dimensionality reduction of single cell atlases with deep learning approaches |
| 29june-12 | 610 | Machine Learning in Bioinformatics | Bioinformatics in Italy: the students perspective |
| 29june-13 | 611 | Machine Learning in Bioinformatics | Enhancing Biomolecular Simulations With Hybrid Potentials Incorporating NMR Data |
| 29june-14 | 503 | Machine Learning in Bioinformatics | Comparison of early integration approaches for cancer survival prediction |
| 29june-15 | 552 | Machine Learning in Bioinformatics | We can make it better  improving the performances of AI-based predictors of protein structures |
| 29june-16 | 519 | Machine Learning in Bioinformatics | A novel feature selection method applied to microarray data classification |
| 29june-17 | 546 | Machine Learning in Bioinformatics | Integrated quality control of allele-specific copy numbers, mutations and tumour purity from cancer whole genome sequencing assays |
| 29june-18 | 547 | Machine Learning in Bioinformatics | Novelty Detection of cancer metabolites based on 2D NMR TOCSY Spectra |
| 29june-19 | 548 | Machine Learning in Bioinformatics | Argot3.0: a genome-wide automatic protein function prediction exploiting neural networks |
| 29june-20 | 515 | Systems Biology | A biochemical model accurately simulates discontinuous transcription and replication of SARS-CoV-2 genome |
| 29june-21 | 530 | Systems Biology | Implementation of a Python simulator for microbial communities evolution via agent-based modeling |
| 29june-22 | 538 | Systems Biology | A Graphical Framework for extended Reaction Systems |
| 29june-23 | 576 | Systems Biology | A new modeling paradigm to integrate metabolic networks and dynamic models using GreatMod framework. |
| 29june-24 | 591 | Translational medicine | Xenturion: a biobank to unleash the full potential of metastatic colorectal cancer preclinical models. |