POSTER SESSION 1

TUESDAY 9 SEPTEMBER, 15:15 – 16:30

INFECTIOUS DISEASES (Boards A -C)

N°	PRESENTER	TITLE
A1	Simon Tang	Bulk and single-cell transcriptomic insights into treatment-induced changes in tuberculosis patients from Tanzania
A3	Lisa Pagani	Cross-scale effect of microbiome dynamics on resistance
A5	Hesham ElAbd	Decoding immune repertoires by integrating immune sequencing techniques and large-scale functional antibody repertoire profiling methods
A7	Javier Alejandro Delgado Nungaray	In silico analysis of the endogenous CRISPR-Cas system in Pseudomonas aeruginosa PAO1
A9	Philippe Le Mercier	Extending viral protein annotation with structural modeling: AlphaFold3 sheds light on reoviral capsid structures
A11	Benjamin Heiniger	Proteogenomics identifies conserved and lineage-specific novel small proteins in clinical Mycobacterium tuberculosis reference strains
B1	Nosihle Msomi	Deciphering Seasonal Human Coronaviruses: Linking Viral Evolution, Immune Exposure, and Global Surveillance
B3	Valeriia Timonina	Clonal Hematopoiesis in People Living With HIV: Association With Aging and Inflammation
B5	Carlos Ramirez Alvarez	Defining an interferon-clock: a precise description of the interferon response kinetic
B9	Srinithi Purushothaman	Screening for rectal colonization with multidrug-resistant pathogens: usage of rapid metagenomic long-read technology
B11	Mariam Ait Oumelloul	Integrating genetics and metabolomics: A genome-wide association study of plasma metabolite profiles in people living with HIV
C1	Luca Sesta	Detecting epistasis from SARS-CoV-2 genomic data
C3	José Luis Ruiz Rodríguez	Microbiota and mosquito-borne diseases: A meta-transcriptomics workflow for the taxonomic and functional profiling of these unexpected guests
C5	Ashley Rooney	Swab comparison for ease-of-use assessment and oral microbiota characterization

C7	Matija Trickovic	Human gut microbiota subspecies carry implicit information for in-depth microbiome research
C9	Concetta Guerra	AB-RELIEVE: an AI-designed next-generation antibody therapy resilient to SARS-CoV-2 variants
C11*	Thomas Roder	Assembly Curator: rapid and interactive consensus assembly generation for bacterial genomes

*Interactive screen

CLINICAL DATA SCIENCE (Boards D - H)

N°	PRESENTER	TITLE
D1	Linda Grob	KidsCan_01: In depth tumor profiling for children with high-risk, progressive & relapsed malignancies
D3	Oriol Canal Pujol	Targeted-CNV-Learner: A Machine Learning Framework for CNV Detection in Targeted Sequencing
D5	Gregor Sturm	Data Science Operations (DSO) - A command line helper bringing DevOps principles to data analysis projects
D7	Marchi Okawa	Identification of genes associated with X chromosome inactivation using tensor decomposition.
D9	Eline Meijer	Batch effects and data representation in Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry (MALDI-TOF MS) data for machine learning driven identification of microorganisms
D11	Matthias Lienhard	Genetic Contributions to Non-Hereditary Acute Aortic Syndrome and Aneurysm: Towards Improved Risk Prediction
E1	Helena Jambor	Enhancing Oncology Care with Visual Treatment Timelines
E3	Cassandra Litchfield	Integrating FFPE derived Whole Genome Sequencing into Routine Molecular Pathology: Validation and Establishment of a Bioinformatics Workflow
E5	Aya Galal	Machine Learning-Based Identification of a Proteomic Panel for Parkinson’s Disease Diagnosis
E7	Jan-Niklas Runge	Real-world performance of AI-based tumor cell content quantification
E9	Y-h. Taguchi	Tensor Decomposition based unsupervised feature extraction applied to Bioinformatics

E11	Olga Trofimova	Deep learning aging marker from retinal images unveils sex-specific genetic and clinical signatures
F1	Dennis Bontempi	Genetic and Prognostic Insights from Deep Learning Segmentation of Carotid Lumen Diameter
F3	Leah Böttger	Sex-specific disease associations and genetic architecture of retinal phenotypes
F5	Arthur Babey	HES-XPLAIN - An open platform for accelerating the development of eXplainable AI systems
F7	Cécile Trottet	Deep Hierarchical Subtyping of Multi-Organ Systemic Sclerosis Trajectories
F9	Anne Hoffmann	Exploring Obesity Variability through Machine Learning-Driven Patient Segmentation
F11	Julien Roux	Rapid and long-lasting remodelling of the blood transcriptome following bariatric surgery
G1	Alexander Blume	Cardiovascular disease biomarkers derived from circulating cell-free DNA methylation
G3	Ivo Kwee	Combining multi-omics factorization methods for robust biomarker identification
G5	Luca Stickley	Microbiome as a predictor of long-term pulmonary outcomes in severe SARS-CoV-2 survivors
G7	Falko Noé	Multiomics Integration for Exercise Personalisation: Insights from the ACTIBATE Trial on Brown Adipose Tissue Activation
G9	Maria Boulougouri	END-TO-END INTERPRETABLE GRAPH LEARNING FOR PATIENT CLASSIFICATION
G11	Dennis Gankin	Predicting Genetic Risk with Biologically Interpretable Neural Networks at the Scale of the UK Biobank
H1	Silvano Coletti	The Multiscale Phenotypic Interactome: An HPC-Accelerated ST-GNN Approach for Real-Time, Multimodal Health Monitoring
H3	Lidia Reznik	Multimodal generative AI assistant for all cancer modalities

OTHER (Board H)

N°	PRESENTER	TITLE
H5	Irena Maus	ELEAD: Increasing women’s leadership, visibility, and impact in ELIXIR

H7	Filip Stefaniak	Machine Learning and Explainable Artificial Intelligence for prediction and understanding of RNA-small molecule interactions.
H9*	Aparna Pandey	KeggMapWizard: interactive and versatile biochemical pathway maps

*Interactive screen

CANCER RESEARCH (Boards I - U)

N°	PRESENTER	TITLE
I1	Sergio Vazquez Montes de Oca	Predicting Immunotherapy Response in Advanced Bladder Cancer: A Meta-Analysis of Six Independent Poster √
I3	Olivier Dennler	Evaluating Sequence and Structural Similarity Metrics for Predicting Shared Paralog Functions
I5	Yan Liu	Unraveling the molecular basis of cross-reactivity in TCR epitope recognition
J1	Elisa Mariella	Targeting oxidative metabolic vulnerabilities in sotorasib-tolerant lung cancer cells
J3*	Fabiana Rodrigues de Goes	From Data to Discovery: Exploring Microprotein for Cancer AI-Driven Analysis
J5	Aparajita Karmakar	Developing an Explainable AI Framework to Predict siRNA Gene Knockdown Efficacy
K1	Eva Romanovsky	CG>TG mutation frequency as negative predictor of homologous recombination deficiency in ovarian and breast cancer
K3*	Luis Heriberto Vazquez Mendoza	Multicomplex-based Pharmacophore Modeling Targeting the Estrogen Receptor β. Towards the search for breast cancer drugs
K5	Christian Peralta Viteri	Revisiting the Reverse Paradigm: A Deep Learning Approach for Targeted Cancer Therapy Efficacy Prediction
L1	Halimat Atanda	Associating cancer-specific single nucleotide variants with methylation changes using models based on convolutional neural networks
L3*	Alexander Kel	Druggable master regulators of "orphan" death pathways
L5	Coralie Capron	Integrated Multi-Omics Analysis Unveils a Functional Vulnerability Signature and New Therapeutic Targets to Eradicate Intestinal Cancer Stem Cells

M1	Katiane Tostes	Metabolic Gene Signatures as Predictive Biomarkers of Response to Immune Checkpoint Inhibitors in NSCLC
M3	Laura Collesano	Predicting the antigenic peptidome
M5	Paolo Angelino	Toward Personalized Treatment: A Gene Signature to Predict nCRT Response in Rectal Cancer
N1	Ali Saadat Varnosfaderanii	From Mutation to Degradation: Predicting Nonsense-Mediated Decay with NMDEP
N3	Martin Lukačišin	Prediction of drug interactions using isogrowth profiling
N5	Polina Shichkova	Identification of predictive and monitoring biomarkers with plasma proteomics in NSCLC patients
O1	Karolina Zielinska	Genomic and Transcriptomic Insights into the Pathogenesis of Therapy-related Acute Myeloid Leukemia from TP53-mutant Clonal Hematopoiesis
O3	Anissa El Marrahi	An Integrated Portrait of Prostate Cancer Progression
O5	Sara Costa	Tumor mutational signature dynamics at single-cell resolution
P1	Dana Lea Moreno	MixTCRclean: a tool to improve TCR data quality by detecting and correcting errors in TCR sequences
P3	Peter Leary	MARMOT A Multifaceted R Pipeline for Analysing Spectral Flow Cytometry Data
P5	Caroline Sophie Wandinger	Sparse Canonical Correlation Analysis as an Unbiased Approach to Explore Gene Expression Co-Regulation Across Cell Types
Q1	Paul Gueguen	Single-cell and Spatial multi-omics identifies distinct central memory phenotypes in CTCL
Q3	Mechthild Lütge	Single-Sample Tumor Archetype Assignment for Clinical and Early-Phase Drug Development Applications
Q5	Giorgia Gandolfi	nf-core/tumourevo: A Robust Bioinformatics and Machine Learning Pipeline for Analyzing Tumor Evolution from Whole-Genome Sequencing Data
R1	Alessandro Cuozzo Vilá	CytoxPred: efficient prediction of cancer cell lines targeted by cytotoxic small molecules
R3	Daniyar Karabayev	Cell-free DNA methylation profiling for diffuse large B-cell lymphoma subtyping via whole-genome enzymatic methyl sequencing
R5	Marta Perez Gomes	TCRpcDist: In Silico Tool for Advancing Cancer Immunotherapies
S1	Andrea Mock	Predicting therapy response in breast cancer patients using spatial proteomics of metastatic lymph nodes

S3	Alen Stambolliu	Deciphering Retrotransposable Elements dynamics in tumor-infiltrating lymphocytes through combination of short- and long-read single-cell RNA sequencing
S5	Theo Maffei	Interpretable Graph Representation Learning on Spatial Omics
S7	Carlotta Schieler	Integrative Multi-Omics Profiling Unveils Enhanced Antibody Responses in Cancer Patients Post-Influenza Vaccination
S9	Aakanksha Singh	Evaluating the impact of experimental factors on deconvolution accuracy in multimodal transcriptional data: A benchmarking study
S11	Jacob Hanimann	The Spatially Resolved Transcriptional Landscape of Tumor Budding in Colorectal Cancer
T1	Christian Halter	Benchmarking tools for population-level exploratory single-cell data analysis
T3	Natacha Koenig	Multiomics investigation of the action of CDK12/13 inhibitors in prostate cancer.
T5	Daniel Marbach	Generalizable AI predicts immunotherapy outcomes across cancers and treatments
T7	Agnieszka Kraft	Resolving malignant cell heterogeneity in tumor bulk RNA-seq data with CDState
T9	Evi Vlachou	Human Bone Marrow Niche Remodelling After Allogeneic Hematopoietic Cell Transplantation
T11	Abdullah Kahraman	Heterogeneous and novel transcript expression in single cells of patient-derived ccRCC organoids
U1	Asim Bikas Das	Artificial intelligence and network medicine-based framework to support subtype-specific precision therapy for gliomas

*Interactive screen