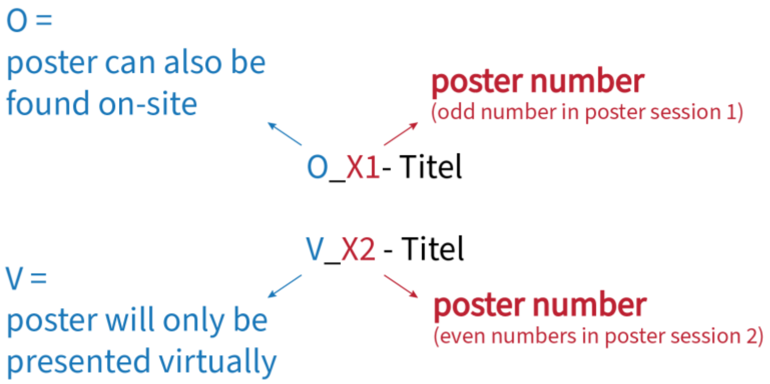
POSTER SESSION 1 & 2

POSTER OVERVIEW

A few notes on the numbering:



O =
poster can also be found on-site

poster number
(odd number in poster session 1)

O_X1- Titel

V_X2 - Titel

V =
poster will only be presented virtually

poster number
(even numbers in poster session 2)

Schedule:

Poster session 1: Tuesday, 14 September, 15:30 – 17:00, Foyer
Poster session 2: Wednesday, 15 September, 13:45 – 15:15, Foyer

Artificial intelligence, machine learning and computer vision: expanding the bioinformatics toolkit

TUESDAY ON-SITE (O)

- ***O_A1 – Estimating the Normalizing Constant in Bayesian Networks***
  Fritz Bayer

- ***O_A3 – Interpretable deep learning approach enables detection of phosphorylated peptides based on their tandem mass spectra***
  Tom Altenburg

- ***O_A5 – Mapping high-resolution cell states in single-cell RNA-seq data***
  Pascal Grobecker

- ***O_A7 – Large-scale assessment of reverse screening methodology for predicting protein targets of druglike molecules***
  Antoine Daina

- ***O_A9 – Improving Cancer Survival Prediction With Multitask Neural Networks***
  Daniel Rowson

- ***O_A11 – A morphometric framework for the embryo-wide quantification of tissue organisation at single cell resolution***
  Max Brambach

- ***O_A13 – Tool for automatic selection of antibody phage display candidates from large NGS datasets***
  Miguel Antunes

- ***O_A15 – Motif in T cells for the prediction of interactions***
  Giancarlo Croce

- ***O_A17 – DEPICTION: an interpretability toolbox for computational biologists***
  An-phi Nguyen

- ***O_19 – Genome-Wide Association Studies of retinal vessel tortuosity identify 173 novel loci, capturing genes and pathways associated with disease and vascular tissue pathomechanics***
  Mattia Tomasoni

- ***O_A14 – Profiling Of Protein Clusters Using Over Representation Analysis***
  Maria d'Errico
  change of time: will now be presented on Tuesday in Poster session 1

TUESDAY VIRTUALLY (V)

- ***V_A1– MET exon 14 skipping: a case study for the detection of genetic variants in cancer driver genes by deep learning.***
  Vladimir Nosi

- ***V_A3 – COMPARATIVE GENOMICS OF PROTEINS INVOLVED IN THE ELECTRICAL GENERATION OF PROKARYOTES AND ARCHAEA***
  Anastasia Tsareva

WEDNESDAY ON-SITE

- ***O_A2 – Discovering Novel Cell Types across Heterogeneous Single-cell Experiments***
  Maria Brbic

- ***O_A4 – CREMA: Automated modelling of genome-wide chromatin state in terms of local constellations of regulatory sites.***
  Mikhail Pachkov

- ***O_A6 – iMOKA: k-mer based software to analyze large collections of sequencing data***
  Claudio Lorenzi

- ***O_A8 – Recognition of Proteins by Random Forest based on Nanopore Sensing Data***
  Stéphane Hess

- ***O_A10 – Creation of a Pan-allele HLA class I predictor***
  Simon Eggenschwiler

- ***O_A12 – Comparison of deep learning embeddings of protein sequences for predicting protein-protein interactions***
  Marco Anteghini

- ***O_A16 – Secure and versatile data and computing platforms for cutting-edge data science in biomedical research***
  Priyasma Bhoumik

- ***O_A18 – SwissBioisostere 2021: new developments and updates***
  Alessandro Cuozzo Vila

- ***O_A20 – Interpretable T-cell receptor binding prediction using Feature-wise Additive Networks***
  An-phi Nguyen

WEDNESDAY VIRTUALLY (V)

- ***V_A2 – An essential powerful new tool in the In Silico Drug Discovery Toolbox - The InfoCodex Knowledge Discovery Engine***
  Beat Meyer

Cancer biology and precision medicine: deepening our understanding towards tailored treatments

TUESDAY ON-SITE (O)

- ***O_B1 – protti: an R package for comprehensive analysis of peptide- and protein-centric bottom-up proteomics data***
  Jan-Philipp Quast

- ***O_B3 – Estrogen signature and gene coexpression network for breast cancer stratification and survival analysis***
  Carlos Henrique Venturi Ronchi

- ***O_B5 – Morphometric analysis of epithelial bladder cancer progression***
  Franziska Lampart

- ***O_B7 – PREDICTION OF POSTOPERATIVE PAIN SCORES IN PATIENTS UNDERGOING MAJOR BREAST SURGERY***
  Shathish Kumar

- ***O_B9 – Benchmarking joint multi-omics dimensionalityreduction approaches for the study of cancer***
  Laura Cantini

- ***O_B11 – CanIsoNet v1.0: Database to dissect the functional impact of isoform switching events in cancer***
  Tülay Karakulak

- ***O_B13 – Identification of deleterious Variants of Uncertain Significance in BRCA2 BRC4 repeat through molecular dynamics simulations***
  Siddharth Sinha

WEDNESDAY ON-SITE (O)

- ***O_B4 – The molecular underpinnings of wild-type Von Hippel-Lindau clear cell renal cell carcinomas***

Aashil Batavia

- ***O_B8 – DNA damage repair proteins synergistically affect the cancer prognosis and resistance***
  Meetal Sharma

- ***O_B10 – Integration of single cell RNA-sequencing data across tissues and cancer types reveals pathways leading to dendritic cell activation***
  Bhavesh Soni

- ***O_B12 – The landscape of poly(A) site usage in cancer***
  Dominik Burri

- ***O_B14 – CIViCutils - a Python module for matching and downstream processing of CIViC variant information***
  Lourdes Rosano Gonzalez

Evolutionary dynamics and ecology: where organisms, time and space interplay

TUESDAY ON-SITE (O)

- ***O_C1 – Imputation of ancient genomes***
  Barbara Mota

- ***O_C3 – Comparative genomics to predict cancer protecting alleles***
  Lamis Naddaf

- ***O_C5 – Comparative genomics of platyhelminths sheds light on adaptation to parasitism***
  Natalia Zajac

- ***O_C7 – A flexible snakemake pipeline to map ancient DNA data***
  Samuel Neuenschwander

- ***O_C9 – BUSCO v5: assessing genomic data of eukaryotic, prokaryotic and viral species***
  Mose Manni

TUESDAY VIRTUALLY (V)

- ***V_C1 – A theoretical investigation of artificial community selection methods***
  Björn Vessman

WEDNESDAY ON-SITE (O)

- ***O_C2 – Investigating the relationship between expression variability and tissue specificity in the northern pike***
  Christabel Bucao

- ***O_C4 – Does mistranslation help or hinder evolution on adaptive landscapes?***
  Michael Schmutzer

- ***O_C6 – DeepDive: deep learning estimation of palaeodiversity from fossil data***
  Rebecca Brown Cooper

- ***O_C8 – A long-lived population of stem cells under neutral competition shapes the clonal composition of cerebral organoids***
  Florian Pflug

- ***O_C10 – New models for the spatial distribution of fossil taxa demonstrate size-dependent dispersal and cooling-driven extinction of carnivores***
  Torsten Hauffe

Population genomics in human health: connecting genotypes to phenotypes

TUESDAY ON-SITE (O)

- ***O_D1 – Stratification of Schizophrenia patients using transfer learning on OMICS data***
  Daria Doncevic

- ***O_D3 – PhaseRE: Identifying recombination location per sample using long reads***
  Sina Majidian

TUESDAY VIRTUALLY (V)

- ***V_D1 – eQTL Catalogue: a compendium of uniformly processed human gene expression and splicing QTLs***
  Nurlan Kerimov

WEDNESDAY ON-SITE (O)

- ***O_D2 – A comprehensive framework for low-coverage whole genome sequencing imputation across human populations***
  Simone Rubinacci

- ***O_D4 – Estimation of age-specific marker effects for time-to-diagnosis traits***
  Sven Erik Ojavee

- ***O_D6 – Parent-of-origin inference for biobank scale datasets***
  Robin J. Hofmeister

- ***O_D8 – Genotype data compression a glimpse of tomorrow's data***
  Rick Wertenbroek

- ***O_D5 – Investigating scenarios regulating gene expression in the immune system***
  Diana Avalos
  change of time: will be presented on Wednesday in Poster session 2

Spatiotemporal gene expression dynamics and single-cell approaches: zooming in to better scale up

TUESDAY ON-SITE (O)

- ***O_E1 – Inferring single-cell trees alongside cell-state transitions from lineage tracing and RNAseq data***
  Sophie Seidel

- ***O_E3 – Model-based robustness and bistability analysis for methylation-based, epigenetic memory systems***
  Viviane Klingel

- ***O_E5 – Inferring gene regulatory networks in D. rerio***
  Dorde Relic

- ***O_E7 – Latenta: unified, probabilistic and interpretable modelling of single-cell omics data***
  Wouter Saelens

- ***O_E9 – scROSHI - single cell robust supervised hierarchical identification of cell types***
  Michael Prummer

WEDNESDAY ON-SITE (O)

- ***O_E2 – Embryo multiplexing enables quantitative investigation of global chemokine-scavenger interactions***
  Marvin Albert

- ***O_E4 – Super-cells untangle large and complex single-cell transcriptome networks***
  Mariia Bilous

- ***O_E6 – Optimal Transport improves cell-cell similarity inference in single-cell omics data***
  Geert-Jan Huizing

- ***O_E8 – Integration of single-cell with bulk RNA-Seq to provide a unified view of gene expression and analysis tools in Bgee***
  Tarcisio Mendes de Farias

Pathogens, immune systems and host-pathogen interactions: an arms race with infectious agents

TUESDAY ON-SITE (O)

- ***O_F1 – Genome-to-genome analysis identifies hepatitis B virus escape mutations induced by NTCP variation and HLA class I restriction***
  Zhi Ming Xu

- ***O_F3 – Deep generative selection models of T and B cell receptor repertoires with soNNia***
  Giulio Isacchini

- ***O_F5 – Dengue infection leaves on the antibody repertoire a serotype-specific immune fingerprint that includes rare clones with strong neutralizing activity***
  Eriberto Natali

- ***O_F7 – Deciphering the landscape of phosphorylated HLA-II ligands***
  Marthe Solleder

- ***O_F9 – Determinants of SARS-CoV-2 transmission to guide vaccination strategy in a European urban area***
  Sarah Brüningk

WEDNESDAY ON-SITE (O)

- ***O_F2 – Phylogenomic Analysis of the Tuberculosis Epidemic in Dar es Salaam***
  Michaela Zwyer

- ***O_F4 – Effects of the mutational spectrum of SARS-CoV-2 on its past, ongoing and future molecular evolution***
  Konstantin Popadin

- ***O_F6 – A 3R infection model and genome-wide approach to characterize novel anti-mycobacterial compounds and to decipher their mode of action***
  Jahn Nitschke

- ***O_F8 – metaGCcorrect: Correcting GC Bias Improves Accuracy and Comparability in Metagenomic Abundance Estimation***
  Laurenz Holcik

WEDNESDAY VIRTUALLY (V)

- ***V_F2 – Benchmarking algorithms for B-cell receptor reconstruction using single cell RNA-seq data***
  Tommaso Andreani

Others:
topics beyond the main sessions

TUESDAY ON-SITE (O)

- ***O_G1 – OpenGenomeBrowser: A dynamic and scalable web platform for comparative genomics***
  Thomas Roder

- ***O_G3 – lincRNA sequences are biased to counteract translation***
  Anneke Brümmer

- ***O_G5 – Emphasis on numbers is not enough: why addressing Equality, Diversity and Inclusion at the SIB Swiss Institute of Bioinformatics matters***
  Aitana Lebrand

- ***O_G7 – Updated Version of SwissSimilarity, a Web Tool for High Throughput Ligand-Based Virtual Screening***
  Maiia E. Bragina

- ***O_G9 – Supporting new developments of structure prediction methods with Continuous Automated Model EvaluatiOn (CAMEO)***
  Xavier Robin

- ***O_G11 – Hematological changes from conception to childbirth: an indicator for major pregnancy complications.***
  Marion Patxot Bertran

WEDNESDAY ON-SITE (O)

- ***O_G2 – Enabling structure-guided life science research with SWISS-MODEL***
  Gerardo Tauriello

- ***O_G4 – ZARP: RNA-Seq analysis made easy***
  Christina Herrmann

- ***O_G6 – sciCORE: scientific computing platform for life sciences and biomedicine***
  Lorenza Bordoli

- ***O_G8 – A proteomics benchmark study: Making an informed decision about the ideal proteomics data analysis workflow***
  Eva Brombacher

- ***O_G10 – Association Plots reveal cluster-specific genes from high-dimensional transcriptome data***
  Elzbieta Gralinska

- ***O_G12 – RCRUNCH: a flexible workflow for completely automated analysis of CLIP data***
  Maria Katsantoni