

POSTERS' LIST

Table of Contents

Precision Medicine: harnessing big data for cancer and other complex diseases.....	1
Proteins in Proteins in 3D: the dynamics of protein structures and their interactions.....	3
Single-cell approaches: dissecting cellular heterogeneity across multiple modalities.....	4
Dynamics of immune processes: from responses to pathogens to immunotherapy.....	7
Machine Learning algorithms for advancing spatial biology.....	8
Other.....	9
Deciphering ecology and evolution with creative genomics approaches.....	10

Precision Medicine: harnessing big data for cancer and other complex diseases

Poster session 1: Tuesday 12 September, 15:30 – 17:00

N°	Poster Title	Presenter's first name	Presenter's last name
A1*	Identifying Functional, Non-Coding Somatic Single Nucleotide Variants through the REMIND-Cancer Bioinformatics Pipeline	Nicholas	Abad
A3	Network-Based Clustering of Pan-Cancer Data Accounting for Clinical Covariates	Fritz	Bayer
A5	The BioRef Infrastructure: A Framework for Personalized Reference Intervals	Tobias Ueli	Blatter
A7	Multi-Omics Analysis of Multifocal Hepatocellular Carcinoma	Gina	Boot
A9	Machine learning for extraction of biochemical reactions from the scientific literature	Blanca	Cabrera Gil
A11	An automated, low-cost library preparation protocol for low-coverage whole genome sequencing-based genotype imputation	pietro	Cattaneo

N°	Poster Title	Presenter's first name	Presenter's last name
B3	TCR specificity predictions with the state-of-the-art approach TCRpcDist	Marta Andreia	Da Silva Perez Gomes
B5	Characterising the replicability of RNA-Seq downstream analysis results	Peter Methys	Degen
B7	Flexible multi-omics data integration using autoencoders by a versatile PyTorch-based toolbox	Jan	Ewald
B9	Computational approaches to deconvolve the tumor micro-environment using ATAC-Seq data.	Aur�lie	Gabriel
B11	A novel bootstrap approach for gene-set enrichment analysis on a multi-omics level with data from studies on Spinal Muscular Atrophy	Shamini	Hemandhar kumar
C1	Adipose tissue acquires an epigenetic memory during obesity that persists after weight loss	Laura Catharina	Hinte
C3	Decoding the collective impact of cancer genomic alterations	Arvind	Iyer
C5	Signature Informed Sampling for Transcriptomics Data	Nikita	Janakarajan
C7	Tumors derived from PROCR-positive mammary stem cells give rise to claudin-low breast cancer with poor prognosis	Michal	Kloc
C11	Swiss-PO and its upcoming updates	Fanny	Krebs
D1	Identification of cancer cells from de novo SNVs calls in single-cell transcriptomes	Val�rie	Marot-Lassauzaie
D3	Gene Ontology Causal Activity Models (GO-CAMs) for human biology	Patrick	Masson
D5	Comprehensive comparison of tools for fitting mutational signatures	Mat�š	Medo
D7	Enhancing interoperability for a more reusable bioinformatics knowledge base	Tarcisio	Mendes de Farias
D9	Exploring the rules of T-cell receptor generation: Insights from a data-driven analysis of V(D)J recombination	Dana	Moreno
D11	CREMA: Inference of gene regulatory networks from a cromatin state dynamics.	Mikhail	Pachkov
E5	Multi-layered genetic approaches to identify approved drug targets	Marie	Sadler
E3	Curation and integration of cancer single-cell RNA-seq data for meta-analysis	Petr	Taus
E1*	Recent key developments in SwissDrugDesign for effective support of drug discovery	Antoine	Daina

N°	Poster Title	Presenter's first name	Presenter's last name
E7	Charting the Heterogeneity of Colorectal Cancer Consensus Molecular Subtypes using Spatial Transcriptomics	Alberto	Valdeolivas
E9	MR-link-2: a pleiotropy robust cis MR method to identify the cause of GWAS loci	Adriaan	van der Graaf
E11	Somatic short tandem repeat mutations may regulate gene expression in colorectal cancer	Max	Verbiest
F5	Highly configurable query tool for a FAIR access to curated, standardized, and processed public transcriptomics datasets	Julien	Wollbrett
F3	Characterization of Microsatellite Deletion and Insertion in Colorectal Cancer	Feifei	Xia

*interactive screen

Proteins in 3D: the dynamics of protein structures and their interactions

Poster session 1: Tuesday 12 September, 15:30 – 17:00

N°	Poster Title	Presenter's first name	Presenter's last name
F1*	SwissParam 2023: an improved web-based tool for efficient ligand parameterization	Marine	Bugnon
F7	Structural and functional control of proteins through phosphorylation	Miguel	Correa Marrero
F9	Annotation of biologically relevant ligands in UniProtKB using ChEBI	Elisabeth	Coudert
F11**	Modelling disease progression in metastasised breast cancer using Continuous-Time Markov Chains	Marc	Vaisband
G1	Closing the loop: combining Bayesian optimization with sequence- or structure-based method for optimization of peptide-protein binding	Jerome	Eberhardt
G3	An open-source pipeline for conformational state recognition applied to the PDB archive	Joseph	Ellaway
G5	Challenging the current view on protein prenylation in T helper cells using experimental data and information on protein 3D structures	Jana	Koch
G9	Structural modelling of thousands of T Cell Receptors to be encoded into 1D fingerprints	Francesca	Mayol Rullan
G11	Embedding-based alignment: combining protein language models and alignment approaches to detect structural similarities in twilight-zone	Lorenzo	Pantolini

N°	Poster Title	Presenter's first name	Presenter's last name
G7*	Disrupting dimeric β -amyloid by electric fields	Pablo Andres	Vargas Rosales
H1	AlphaFold-based discovery of novel protein interaction interfaces	Chop	Lee
H3	Targeting Allosteric Sites of PDK-1 and PLK-1 With Natural Compounds From Daucus Carota as a Potential Therapeutic for Triple-Negative Breast Cancer.	Kayode	Raheem
H5	Automated benchmarking of protein-ligand complex prediction	Xavier	Robin
H7	Attracting Cavities 2.0: Improving the Flexibility and Robustness for Small-Molecule Docking	Ute	Roehrig
H9*	Drug repurposing: Enol-pyruvyltransferase as a novel target for Mycobacterium tuberculosis	Shivani	Singh
H11	Making computed structure models reusable and accessible with SWISS-MODEL and ModelArchive	Gerardo	Tauriello

* Interactive screen

** On Wednesday exchange poster location with F8

Single-cell approaches: dissecting cellular heterogeneity across multiple modalities

Poster session 1: Tuesday 12 September, 15:30 – 17:00

N°	Poster Title	Presenter's first name	Presenter's last name
I1	Reconstructing spatiotemporal gene expression and enhancer activity in Drosophila embryos using scRNA-Seq and optimal transport	Baptiste	Alberti
I3	Standardization of single-cell metadata: scFAIR, an Open Research Data initiative	Frederic	Bastian
I5	Landscape of cellular interactions in hepatocellular carcinoma associated with chronic HCV infection and fatty liver disease	Andrej	Benjak
I7	scAmpi & gExcite - A start-to-end framework for single-cell gene expression and antibody analysis	Anne	Bertolini
I9	Metacells untangle large and complex single-cell transcriptome networks	Mariia	Bilous
I11	A general approach for modelling time-course data	Eva	Brombacher
K1*	Unchaining the full potential of public single-cell RNA-Seq data for drug discovery	Constance	Ciaudo Beyer

N°	Poster Title	Presenter's first name	Presenter's last name
J3	From cells, to targets, to patients: using single-cell and spatial transcriptomics technologies for target identification in cancer	Slavica	Dimitrieva
J5	Navigating the fast-evolving single-cell field: curated information about single-cell RNA-seq protocols	Sagane	Dind
J7	The effect of freezing tissue samples on single-cell RNA-sequencing outputs	Athimed	El Taher
J9	Accounting for low transcript sampling rates in scRNA-seq using the Good-Turing estimator	Martin	Fahrenberger
J11	Deep exponential families for single-cell data analysis	Pedro	Falé Ferreira
J1	Metacells facilitate the analysis of single-cell multiomics data	Léonard	Hérault
K3	CZ CELLxGENE Discover is an online analytical platform and the largest repository of standardized single-cell data	Jason	Hilton
K5	To hash or not to hash: can sample multiplexing work without cell tagging?	Robert	Ivanek
K7	Single-Cell Full-Length Isoform Sequencing of patient-derived organoid cells of Pancreas Ductal Adeno Carcinoma	Tülay	Karakulak
K9	Activation state of synovial macrophages differs across chronic inflammatory joint diseases	Aleksandra	Khmelevskaia
K11	A hybrid population model enables the study of single-cell heterogeneity in an epigenetic memory system.	Viviane	Klingel
L1	Disentangling biological fluctuations from measurement noise in time-course data of cell growth and fluorescence	Björn	Kscheschinski
L3	A probabilistic framework for parametrizing RNA velocity fields with manifold-consistent cell cycle dynamics	Alex	Lederer
L5	Benchmarking computational methods for single-cell chromatin data analysis	Siyuan	Luo
M3	omnibenchmark: open continuous collaborative benchmarking of computational biology methods	Almut	Lütge
M5	Functional antibody screening based on single cell transcriptomic readouts	Xiaoli	Ma

N°	Poster Title	Presenter's first name	Presenter's last name
M1*	CellFromSpace: A versatile tool for spatial transcriptomic data analysis through reference-free deconvolution and guided cell type/activity annotation	Antonin	Marchais
N1	Adjustments to reference dataset design improve cell type label transfer	Carla	Mölbart
N3	Modeling chromatin accessibility in single cells in terms of transcription factor activities	Sarah	Morillo Leonardo
N5	Find the Optimal Flow: How FloVelo Pushes RNA Velocity Boundaries to Infer Splicing Dynamics in scRNA-seq Data	Julia	Naas
O1	Multi-modal integration in human breast cancer and deconvolution reveals spatial relationship of immune and tumor subclasses	Patrick	Rölli
O3	How to identify cells in G0 quiescent state in single cell experiments?	Julien	Roux
O5	Learning cell type-specific transcription factor binding sites based on cooperativity and cell type similarity	Emanuel	Sonder
P1	Bio-Express Workbench: A big data platform for large-scale analysis of biological data	WANGHO	SONG
P3	Coarse-graining of Spatial Transcriptomics data into metaspots	Matei	Teleman
P5	Molecular mechanisms reconstruction from single-cell multi-omics data with HuMMuS	Rémi	Trimbour
Q1	Generalizing fate mapping to multi-view single-cell data	Philipp	Weiler
Q3	Comparison of single cell RNA sequencing using short read and long read sequencing: quality evaluation of the new MAS-ISO-seq approach	Natalia	Zajac
Q5	Bayesian phylogenetic inference using single-cell lineage tracing data	Antoine	Zwaans

*interactive
screen

Dynamics of immune processes: from responses to pathogens to immunotherapy

Poster session 2: Wednesday 12 September, 14:15 - 15:45

N°	Poster Title	Presenter's first name	Presenter's last name
A2	Uncovering the dynamics of cellular responses triggered by iron-carbohydrate complexes in human macrophages using quantitative proteomics and phosphoproteomics	Jonas	Bossart
A4	Unravelling of tumor microbiome and its implication for oncogenic signalling	Linh	Dang
A6	Transcriptome-based classifier identifies tumor CD8 T cell immunophenotype and predicts clinical outcome	Iakov	Davydov
A10	Tumor immune cell composition predicting response to treatment	Christian	Halter
B2	Unconventional binding modes of HLA-I ligands	Yan	Liu
B4	Identifying common elements in breast cancer signaling pathways, gene expression and protein interaction network	Mohamadreza	Mahmoodvand
B6	Clinical sepsis diagnostics: Next generation sequencing in combination with Big Data and machine learning as a diagnostic tool for sepsis	Jan	Müller
A12*	High-resolution spatial and temporal immunity scores based on vaccination, recoveries and accounting for immunity waning	Ferdous	Nasri
B10	Modeling the regulatory network underlying Retinoic Acid resistance in Acute Promyelocytic Leukaemia	José Antonio	Sánchez Villanueva
B12	Clonotype and transcriptome analysis of adoptive TIL products allows insight into T cell behaviour to improve future processing approaches	Michael	Sandholzer
C2	Myeloid-T cell interplay, cell state transitions and checkpoint inhibitor response in melanoma	Petra	Schwalie
C4	Characterization of the chromatin and transcriptional landscapes of intratumoral NK cells using single cell multiomics	Clara	Serger
C6	Molecular profiling reveals features of clinical immunity and immunosuppression in asymptomatic P. falciparum malaria	Stephanie	Studniberg
C8	Robust predictions of binding specificities for rare MHC-I alleles	Daniel	Tadros

N°	Poster Title	Presenter's first name	Presenter's last name
C10	Can immunotherapy biomarkers also predict response to neoadjuvant chemoradiotherapy in locally advanced rectal cancer?	Ramon	Torreglosa do Carmo
C12	Delineation of signaling networks that underlie distinct macrophage phenotypic states	Tiberiu	Totu
D2	GeneSelectR: A Machine Learning-Based R Package for Enhanced Feature Selection and Biological Assessment in RNAseq Analysis of Complex Biological Datasets	Damir	Zhakparov

Machine Learning algorithms for advancing spatial biology

Poster session 2: Wednesday 12 September, 14:15 - 15:45

N°	Poster Title	Presenter's first name	Presenter's last name
D4	Biomachine Learning: the dimensionality reduction and feature selection using Categorical gradient boosted trees paradigm	Athanasios	Angelakis
D6	Detecting Single Cell Blasts in Acute Myeloid Leukaemia using an Auto-Encoder	Alice	Driessen
D8	Bayesian rank-based clustering via Mallows mixtures with covariates for cancer subtyping	Emilie	Eliseussen
D10	Learning and predicting single-cell drug responses of progressed melanoma patients.	Gabriele	Gut
E12*	Exploring the phenotypic landscape of colorectal tumor buds and their environment: an analysis pipeline for seqIF images	Mauro Bruno	Gwerder
E2	Empowering Early Cancer Detection and Therapy Optimization: LIToSeek's Synergistic Integration of Next Generation Sequencing Liquid Biopsy and AI Technologies	Noushin	Hadadi
E4	Mr	Flurin	Hidber
E6	Spatial distribution patterns and metabolic division of labour in social insects	Helder	Hugo
E8	Improving the production process of Mesenchymal Stromal Cells by predicting the cell confluence with AI models based on image and impedance data	Max	Joas
D12	Deep learning methods with interpretability to improve clinical CRC classification systems	Inbar	Leaf

N°	Poster Title	Presenter's first name	Presenter's last name
F8**	Challenging Evaluation Standards for Machine Learning Models in Drug Discovery	Adriano	Martinelli
F12*	Digital synthesis of multiplexed stains using unpaired image-to-image translation*	Adriano	Martinelli
F10	Prediction of cellular neighbourhoods in 3D spatial transcriptomics data using graph neural networks	Enes	Senel
F2	SwissTumorScreen: Genome-wide screenings to improve variant interpretation and to guide personalized oncology.	Debora	Sesia
F4	Deep Learning based analysis infers degnon motifs for human N-termini	Susmitha	Shankar
F6	Topological encoding of relations in data from multiplex immunohistochemistry images	Bernadette	Stolz
G2	Cross-cohort prognosis of levodopa-induced dyskinesia in Parkinson's disease	Rebecca Loo	Ting Jiin
G4	Unveiling tissue compartments through dimensionality reduction and archetypal analysis with Chrysalis	Demeter	Túrós
H6	Combining evolution and protein language models for cancer driver mutation prediction with D2D	Konstantina	Tzavella

* Interactive screen ** Exchange poster location with F11 on Wed. 13

Other

Poster session 2: Wednesday 12 September, 14:15 - 15:45

N°	Poster Title	Presenter's first name	Presenter's last name
G8	Canine Staphylococcaceae circulating in a Kenyan animal shelter	Hatice	Akarsu Egger
G10	Analyses of chemical and biological contexts of the molecular replacements provided by the SwissBioisostere database for drug discovery.	Alessandro	Cuozzo Vilá
G12	The FAIR Cookbook - the essential resource for and by FAIR doers	Vassilios	Ioannidis
H2	BioMedIT: Switzerland's secure infrastructure for analysing biomedical data	Shubham	Kapoor
H4	The de.NBI Industrial Forum fosters the connection between academia and industry	Nils-Christian	Lübke
I12*	Spatial transcriptomics support in scdrake package	Lucie	Pfeiferova
H6	Annotation of metabolic reactions in UniProtKB	Nevila	Nouspikel
G6*	IMPTOX: AI-driven characterization of microplastics to better understand their effects on health.	Carlos Andrés	Pena

H8	Continuous Benchmarking of Bioinformatics Methods with the LEM-style frameworks	Mathieu	Seppy
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*Interactive screen

Deciphering ecology and evolution with creative genomics approaches

Poster session 2: Wednesday 12 September, 14:15 - 15:45

N°	Poster Title	Presenter's first name	Presenter's last name
I2	A novel approach to the Bgee method to detect actively expressed genes in RNA-Seq samples: detection of reference non-expressed genes, and statistical treatment over multiple samples	Alessandro	Brandulas Cammarata
I4	Causes and consequences of extremely genomic high diversity of European amphioxus wild populations	Marina	Brasó-Vives
I6	Inter-genotype gene expression variability across multiple organs in ray-finned fishes	Christabel Floi	Bucaó
I8	Gene expression variability shows signal of evolutionary conservation across mammals	Christabel Floi	Bucaó
I10	Quantitative genetics and population genomics goes wild: Short term evolutionary response to climate change in the barn owl (<i>tyto alba</i>)	Tristan	Cumer
K12*	The Swiss Pathogen Surveillance Platform – a nationwide One-health sequencing data platform	Adrian	Egli
J4	Effective bet-hedging through growth rate dependent stability	Daan Hugo	de Groot
J6	Holistic non-invasive biodiversity analysis using selective nanopore sequencing	Amit	Fenn
J8	A complete draft human gene functionome from large-scale evolutionary modeling and experimental Gene Ontology annotations	Marc	Feuermann
J10	GuaCAMOLE: fragment GC bias-aware abundance estimation from metagenomic data increases accuracy and replicability	Laurenz	Holcik
J12	V-pipe enables surveillance of SARS-CoV-2 variants in Swiss wastewater	Anika	John
K2	Comparative transcriptomic analysis of land plants	Irene	Julca
K4	Inter- and intra-strain dynamics of freshwater microbial communities in aquacultures – a metagenomics approach	Adamandia	Kapopoulou

N°	Poster Title	Presenter's first name	Presenter's last name
K6	Comparative gene expression analysis of moulting in Insect and Crustacean lineages	Kenneth	Kim
K8	HaploBlocks: Efficient Detection of Positive Selection in Large Population Genomic Datasets	Benedikt	Kirsch-Gerweck
K10	Orthology inference at scale with FastOMA	Sina	Majidian
L2	Community conservatism is present in all investigated microbial phyla	Lukas	Malferttheiner
L3	BUSCOv5: Assessing Genomic Data of Eukaryotes, Prokaryotes and Viruses	Matthew R	Berkeley
M2	The evolution of ant crop milk proteins over independent gains of a social transfer behavior	Marie-Pierre	Meurville
M6*	Scoary2: Rapid association of phenotypic multi-omics data with microbial pan-genomes	Thomas	Roder
M4	Large scale orthology inference and phylostratigraphy of birds (Aves)	Yannis	Nevers
N2	Deep Generative Methods to Drive Phage Genetic Edition	Carlos Andrés	Pena
N4	Deciphering the dynamics of genome replication using whole-population DNA abundance data	Florian	Pflug
N6	PanGraph: scalable bacterial pan-genome graph construction	Marco	Molari
O2	Squiggle Analysis for Metagenomic Viability Inference	Harika	Urel
O4	Characterisation of Ancestral Gene Repertoires – Ancestral Gene Ontology Enrichment Analyses	Alex	Warwick Vesztröcy
O6	Independent Benchmarking of Short Reads Metagenomics Pipelines	Jeferyd	Yepes García

* Interactive screen