

POSTER SESSION 2

WEDNESDAY 10 SEPTEMBER, 14:45 – 16:00

COMPUTATIONAL METHODS FOR SINGLE-CELL AND SPATIAL OMICS (Boards A - G)

N°	PRESENTER	TITLE
A2	Matei Teleman	SuperSpot: coarse graining spatial transcriptomics data into metaspots
A4	Arber Qoku	Prismo: A Unifying Factor Model Framework for Domain-informed Multi-omics Data Integration
A6*	Jiayi Wang	Expression biomarkers for aldosterone-producing adenomas: genotyping individual cells using long-read single-cell transcriptomic data
A8	Pierre Bost	Next generation pipeline for next generation spatial transcriptomic data
A10	Reto Gerber	Enhancing Imaging Mass Cytometry Analysis through Improved Marker Aggregation
A12	Veera Timonen	Blood Cell Painting enables large-scale genotype-phenotype discovery in immune cells
B2	Mathias Ramm Haugland	Learning a transparent representation of genes and their functions in single cells.
B4	Nadezhda Azbukina	Perturbation screens reveal a spectrum of cell type-specific signal transduction response in human organoids
B6*	Daan de Groot	Bonsai: How trees unlock the potential of single-cell omics data
B8	Lars Bosshard	Evaluating Network-Based Simulations of Single-Cell RNA-Seq Data for Robust Gene Co-Expression Analysis
B10	Nylsa Chammartin	Development of predictive models assessing the effects of SARS-CoV-2 drugs and their combinations on 3D tissue and mice research models, leveraging single-cell RNA sequencing
B12	Izaskun Mallona	Omnibenchmark: well-defined, reproducible, extensible, and continuous benchmarking for computational biology
C2	Lisa Fournier	Automated identification of molecularly defined breast cancer tumor domains from histopathology

C4	Eugenia Galeota	CIA: A Clustering-Independent Annotation Tool for Accurate and Efficient Cell Type Identification in Single-Cell RNA Sequencing Data
C6*	Arsham Mikaeili	Multimodal integration of gene expression and alternative splicing in single-cell and spatial tr
C8	Jack Kuipers	Single-cell copy number calling and event history reconstruction
C10	Melissa Ensmenger	Application and Evaluation of Current Approaches for Spatially Resolved Omics Prediction from Histology Images
C12	Karolina Zielinska	Single-cell transcriptomic analysis of the bone marrow stromal networks during chemotherapy
D2	Marina Esteban-Medina	Predicting cancer drug sensitivity across scales: From cell lines to single-cells with machinel learning and mechanistic models
D4	Valeria Ranzani	lRescue: uncertainty-aware quantification of transposable elements expression at single cell level
D6	Emanuel Sonder	A platform for obtaining cell type-specific TF binding predictions
D8	Pavel Kos	Scalable and Reproducible Analysis of H&E-Stained Slides Using Machine Learning
D10	Sarah Morillo Leonardo	Modeling chromatin accessibility in single cells in terms of tran- scription factor activities
D12	Lovro Rabuzin	GRASS-MIL: Graph-based Representation and Analysis of Spatial Structures with Multiple Instance Learning
E2	Ekta Shah	BaM-SVA improves batch correction for better scRNA transcriptomics data integration
E4	Josep Garnica	When there is no ground truth: assessing consistency of transcriptomics-based cell type classifications using internal validation metrics
E6	Aur�lie Gabriel	Annotating scATAC-Seq data using reliable chromatin accessibility signatures
E8	Mariia Bilous	Enhancing Single-Cell Spatial Transcriptomics Analysis: Unraveling Bias, Variability and Correction Strategies Through Large-Scale Evaluation
E10	Siyuan Luo	On metrics for subpopulation detection in single-cell and spatial omics data
E12	Emanuela Kerschbamer	Spatial transcriptomics analysis of tuberculosis vaccination route in the mouse lung
F2	Frederic Bastian	Comparative single-cell transcriptomics in dozens of species
F4	Antoine Zwaans	Modelling incomplete sequencing of lineage tracing barcodes for robust single-cell phylogenetic inference
F6	Aryan Kamal	Transcriptional regulation of cell fate plasticity in hematopoiesis
F8	Valeriia Dragan	Harmonizing immune receptor–epitope interactions into an extensible knowledge graph
F10	Jing Lu	Uncovering Cellular Senescence Through Machine Learning: Overcoming Marker Limitations with Integrated Transcriptomic and Interaction Analysis

F12	Theophile Bouiller	Benchmarking Foundation Models for in-silico Gene Perturbation Using scRNA-seq Data
G2	Hilal Kazan	SCITUNA: Single-Cell data integration tool using network alignment

*Interactive screen

PROTEIN DESIGN AND MODELING MOLECULAR ASSEMBLIES (Boards G - K)

N°	PRESENTER	TITLE
G4	Serena Francisco	Structural consequences of a IAHP-associated R-to-P substitution in an α -helix of Alsin
G6	Saubashya Sur	ADMET profiling, molecular docking, and simulation analysis help identify appropriate natural products as inhibitors of isocitrate lyase in <i>Mycobacterium abscessus</i>
G8	Marine Bugnon	Generating tailored high-quality datasets for evaluating structure-based computational drug design tools
G10	Gerardo Tauriello	Working with Computational Models in the AlphaFold Era using SWISS-MODEL and ModelArchive
G12	Océane Follonier	From bytes to binders: design, score and optimize
H2	Marco Malatesta	Integrating complementary functional association signals uncovers a novel partner in Coenzyme Q biosynthesis
H4	Janani Durairaj	Protein-Ligand Complex Prediction - Are we there yet?
H6	Ute Roehrig	Attracting Cavities 2.1: Accelerating High-Confidence Docking with the SwissDock Webserver
H10	Thomas Minotto	Exploring homology detection via k-means clustering of proteins embedded with a large language model
H12	Rok Breznikar	Accurate Small-Molecule Conformer Prediction and Its Transferability to Protein-Environment Conformations
I2	Deepak Yadav	Training graph neural network to classify SNARE proteins structures
I6	Jakob Steuer	Understanding Molecular Switches in Bacterial Gene Regulation
I4	Ali Hariri	Graph rewiring for long range-aware protein learning
J2	Wei Wei	Astromime: Graph-Based Learning for the Detection of Protein Local Surface Mimicry
J4	Mostafa Kalhor	Prosit-XL: Accurate Fragment Intensity Prediction and Enhanced Cross-Linked Peptide Identification for Protein Structural and Interaction Studies

J6*	Luciano Andres Abriata	molecularARweb tools for molecular graphics and modeling in web-based augmented and virtual reality --as easy as browsing a webpage!
K2	Anissa Benabbas	Engineering brighter fluorescent proteins with DropSynth and machine learning methods
K4	Daniil Litvinov	Enhancing PPI prediction and interpretability with deep learning
K6*	Mehdi Mirzaie	Unrevealing Protein Evolution Through Energy Landscapes: A computational Approach

*Interactive screen

INTEGRATIVE BIOINFORMATICS FOR EVOLUTIONARY AND ENVIRONMENTAL PROCESSES

N°	PRESENTER	TITLE
L2	Marco Molari	Quantifying the Evolutionary Dynamics of Structure and Content in Closely Related E. coli Genomes
L4	Jan Baumbach	Fake it till you make it - High-order epistasis detection with quantum computing
L6*	Nadia Neuner-Jehle	Phylogenetic Analysis of Non-Polio Enteroviruses to Develop a Scalable Nomenclature System
M2	Jolien D'aes	Genome database mining-derived unique genetic fingerprints allow genome-edited rice identification
M4	jian fu	A Multi-Omics Framework for Decoding Disease Mechanisms: Insights from Methylmalonic Aciduria
M6	Marc Feuermann	A compendium of human gene functions derived from evolutionary modelling
N2	Laura Voittl	Identifying Genetic Variants for a Mendelian Trait using Long Read Sequencing in Three Domestic Animal Species
N4	Leander Goldbach	Alternative RNA hydrogen-bonding schemes and their effect on the evolution of RNA structure.
N6	Davide Corà	A computational pipeline for the analysis of the role of proteins from unknown species in shotgun metagenomics data: application to the study of gut microbiota in a mouse model of Alzheimer's disease
O2	Jeferyd Yepes García	Fine-tuning Large Language Models for lignocellulose-related sequence annotation in a metagenomics context and comparison against specialized classical tools
O4	Michele Leone	Machine Learning integration of taxonomic sources to leverage genomic and biodiversity data
O6	Rodrigo Hernández Velázquez	ViromeXplore: integrative workflows for complete and reproducible viral characterization

P2	Jacob Riina	Lightning-Fast Simulations on Large Fitness Landscapes
P4	Tamara Bojanić	Evolution of the gene regulatory network within closely related bacterial strains
P6	Jacopo Pasqualini	Genome context interpretation of dark protein functions in the human gut microbiome
Q2	Sneha Sundar	Diversity of F-like plasmid transfer genes in livestock-associated E.coli
Q4	Alessandro Brandulas Cammarata	Robust Data-driven gene expression inference for RNA-seq using intergenic regions as estimation of background noise
Q6	Nikolai Romashchenko	OMAmer 2: Improved protein (sub-)family classification with sequence and structural data
R2	Silvia Prieto	Harnessing ancestral gene order reconstruction to refine gene loss inference in a domesticated crop
R4	Robert Waterhouse	From literature to biodiversity data: mining arthropod organismal and ecological traits with machine learning
R6	David Presby	Supporting Shaky Foundations: Manually Derived Image Features Complement Foundation Models for Genetic Associations and Disease Predictions
S2	Victor Rossier	Improving Varroa resistance in Apis mellifera using short- and long-read metagenomics

*Interactive screen

OTHER (Boards S - V)

N°	PRESENTER	TITLE
S6	Julian van Gerwen	Predicting cellular functions of human phosphosites
S8	Camilla Righetti	Single-Cell RNA and TCR sequencing suggests a key role for tissue-infiltrating EOMES+Tr1-like cells and their circulating precursors in autoimmune diseases
S10	Paul van Rijen	Cell-Triage: Using Domain-Specific Language Models for Full-Text Triage in Cell Line Biocuration
S12	Séverine Duvaud	The semantic web community at SIB Swiss Institute of Bioinformatics
T2	Monique Zahn	How does SIB support open software and databases?
T4	Patrick Masson	Modeling Human Functional Networks with Gene Ontology Causal Activity Models (GO-CAMs)
T6	Shakiba Fadaei	Novel universal protein classification method
T8	Elisabeth Coudert	Rhea, a FAIR resource of expert curated biochemical and transport reactions

T10	Arthur Babey	MOOSE-FS: Multiple-Objective Optimization for Ensemble Feature Selection
T12	Alex SMITH	Developmentally-corrected Omics Time Course Analysis in C. elegans
U2	Edouard de Castro	LitSABER: An Integrated System for Literature Curation
U4	Alexandra Graf	Stratification of Microbiome Metadata Using Machine Learning Techniques
U6	Geert van Geest	SIB promotes open and FAIR educational materials in bioinformatics
U8	Hubert Rehrauer	GEO Uploader: Simplifying the data deposition in the GEO repository
U10	Sacha Bors	Interpreting Visual Transformer RETFound in Retinal Phenotyping: Insights from Temporal Angle Predictions
U12	ALEXANDRE PASCHOAL	Generative AI improves the mirtrons classification
V2	Lucille Pourcel	Enzyme and transporter annotation in UniProtKB using Rhea and ChEBI
V4	Marion Nyamari	Comparison of genome alignment and transcriptome mapping for non-model species
V6	Ahmed Moustafa	Comparing CNN and BERT Models for 16S rRNA Taxonomic Classification
V8	Kenneth Agbo	Novel Protocols for Negative Peptide Generation and Feature Selection for Training Robust ML-based Peptide Classifiers
V10	Marius Meylan	Genes, poop, and plaque and other stories in the Light of Evolution
V12	Qingyao Huang	Fostering Sustainability and Environmental Awareness at Work

CLINICAL DATA SCIENCE*

*relocated from Poster Session 1 to Poster Session 2 at the authors' request

N°	PRESENTER	TITLE
H8	András Hatos	OncoBoard: Aiding molecular tumor boards to improve variant interpretation
S4*	Hugo Armando Guillen Ramirez	Advancing Multilingual Medical Terminology Analysis in Healthcare