

MONDAY 31 AUGUST • PARALLEL SESSION 1 • 13:30 –14:30

ROOM AD	ROOM BC	ROOM EF
GENOMICS, EPIGENOMICS AND GENOME EDITING From Signals to Risk: Scalable Genotyping and Genetic Inference. Session Chairs: Shilpa Garg, Knut Reinert Leveraging ONT move table values for signal-aware variant calling (P)¹ Xian Yu • <i>University of Hong Kong, China</i> GUANinE v1.1 Reveals Complementarity of Supervised and Genomic Language Models (P) Eyes Robson • <i>UC Berkeley, USA</i> Locityper enables biobank-scale genotyping of structurally complex loci (H) Timofey Prodanov • <i>Heinrich Heine University Düsseldorf, Germany</i>	PROTEINS AND STRUCTURAL BIOLOGY Protein–Protein Interactions: Discovery, Stoichiometry & Affinity Session Chairs: Emmanuel Levy, Basile Wicky Stoic: Fast and accurate protein stoichiometry prediction (P) Daniil Litvinov • <i>University of Basel & SIB, Switzerland</i> Rapid Proteome-Wide Discovery of Protein–Protein Interactions with ppIRIS (H) Luiz Felipe Piochi • <i>INRIA, France</i> PreFold-dG: Estimating binding affinity of protein–protein interactions from intermediate representations of protein folding models (P) Sungjoon Park • <i>LG AI Research, South Korea</i>	BIODIVERSITY, SUSTAINABILITY AND ENVIRONMENTAL BIOINFORMATICS Advances in Gut Microbiota Analysis, linking microbiota to health Session Chairs: Avidan Neumann; Lucas Paoli A Spectrum of Gut Microbiota Signatures Predicts Long-Term Health Status (P) Himmi Lindgren • <i>University of Turku, Finland</i> Improving metagenome binning by integrating intrinsic features and taxonomy (H) Simon Rasmussen • <i>University of Copenhagen, Denmark</i> Exploring functional insights into the human gut microbiome via the structural proteome (H) Yu Li • <i>The Chinese University of Hong Kong, China</i>

¹ P = Proceedings paper (peer-reviewed paper published in the ECCB 2026 Proceedings)

H = Highlight presentation

MONDAY 31 AUGUST • PARALLEL SESSION 2 • 14:45–15:45

ROOM AD	ROOM BC	ROOM 8
SYSTEMS BIOLOGY, MULTI-OMICS INTEGRATION AND MODELLING Systems Biology: Diseases: from detection to drugs Session Chairs: Maria Rodriguez Martinez; Valentina Boeva Multimodal contrastive learning for integrating molecular representations and cellular phenotypes in drug–target interaction prediction (P)² Yu-Chiao Chiu • <i>University of Pittsburgh, USA</i> Large-scale simulation of coverage and error rate trade-offs for cancer detection in cell-free DNA whole-genome sequencing (P) Li-Ting Chen • <i>University Medical Center Utrecht, Netherlands</i> A linear interpretable model for drug target prediction (P) Santiago Ferreyra • <i>Fundação Getulio Vargas, Brazil</i>	GENOMICS, EPIGENOMICS, AND GENOME EDITING Sequence Data structures and search Session Chairs: Maria Anisimova, Knut Reinert, RSHash: A fast and space-efficient hash table for k-mers (P) Jonas Schulte-Mattler • <i>Heinrich Heine University Düsseldorf, Germany</i> Ultrafast and accurate sequence alignment and clustering of viral genomes (H) Adam Gudyś • <i>Silesian University of Technology, Poland</i> k-mer manifold approximation and projection for visualizing DNA sequences (H) Lu Cheng • <i>University of Eastern Finland, Finland</i>	BIODIVERSITY, SUSTAINABILITY, AND ENVIRONMENTAL BIOINFORMATICS Metagenomic Sequence Analysis (Cleanup, Invertion Detection, and Alignment Visualisation) Session Chairs: Lucas Paoli, Katja Bärenfaller TheBIGbam: Compression and interactive exploration of large-scale sequencing alignments with circular mapping support (P) Martin Boutroux • <i>EPFL, Switzerland</i> Cleanifier: Contamination removal from microbial sequences using spaced seeds of a human pangenome index (H) Jens Zentgraf • <i>Saarland University, Germany</i> TPMM: Three-component posterior mixture model enables robust invertion detection in low-depth metagenomes and suggests potential viral invertions (P) Yi Lu • <i>City University of Hong Kong, China</i>

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MONDAY 31 AUGUST • PARALLEL SESSION 3 • 16:15–17:15

ROOM AD	ROOM BC	ROOM EF
SYSTEMS BIOLOGY, MULTI-OMICS INTEGRATION AND MODELLING Systems Biology: Single-Cell Session Chairs: Maria Rodriguez Martinez; Valentina Boeva Shortcomings of silhouette in single-cell integration benchmarking (H)³ Pia Rautenstrauch • Charité – Universitätsmedizin Berlin, Germany Discovering reference-missing cell types from bulk transcriptomics (P) Yimin Fan • The Chinese University of Hong Kong, China Charting spatial ligand–target activity using Renoir (H) Hamim Zafar • Indian Institute of Technology Kanpur, India	TRANSCRIPTOMICS AND GENE REGULATION Methods for spatial omics Session Chairs: Raphaëlle Luisier, Ozgur Tastan SlotDeconv: Spatial Transcriptomics Deconvolution via Diversity-Constrained Prototype Learning and Spatial Refinement (P) Zhi Wie • New Jersey Institute of Technology, USA SPIDER: Spatially Integrated Denoising via Embedding Regularization with Single-Cell Supervision (P) Md Istiaq Ansari • University of Central Florida, USA DESpace2: Detection of differential spatial patterns in spatial omics data (P) Peiying Cai • University of Zurich & SIB, Switzerland	PROTEINS AND STRUCTURAL BIOLOGY Applied Structural Biology: Proteomics, Evolution & Interactions Session Chairs: Ivet Bahar, Basile Wicky From transporter to motor: Evolutionary and structural insights into the emergence of prestin's area-motor activity in mammals (H) Raul Araya-Secchi • Universidad San Sebastián, Chile usiGrabber: Automating the curation of proteomics spectra data at scale, making large datasets ready for use in machine learning systems (P) Konstantin Ketterer • Hasso Plattner Institute, Germany Structure-Conditioned Self-Supervised Learning of Residue Interaction Constraints in Protein Kinases for Variant Interpretation (P) Shakiba Fadaei • University of Lausanne & SIB, Switzerland

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TUESDAY 1 SEPTEMBER • PARALLEL SESSION 4 • 10:30 – 11:30

ROOM AD	ROOM BC	ROOM EF
SYSTEMS BIOLOGY, MULTI-OMICS INTEGRATION AND MODELLING Systems Biology: Agents & Spatial Session Chairs: Anaïs Baudot; Valentina Boeva Unifying non-Markovian dynamics and agent heterogeneity in scalable stochastic networks (H)⁴ Maria Rodriguez Martinez • <i>Yale University, USA</i> ARCADIA Reveals Spatially Dependent Transcriptional Programs through Integration of scRNA-seq and Spatial Proteomics (P) Kevin Hoffer-Hawlik • <i>Columbia University, USA</i> Informing agent-based models with spatial data using convolutional autoencoders (P) Bi-Rong Wang • <i>Eindhoven University of Technology, Netherlands</i>	PROTEINS AND STRUCTURAL BIOLOGY Immune molecule design Session Chairs: Emmanuel Levy, Basile Wicky De Novo Epitope-Specific Antibody Design via Time-Dependent Guidance (P) Yunji Kim • <i>Seoul National University, South Korea</i> ImmunoMatch learns and predicts cognate pairing of heavy and light immunoglobulin chains (H) Joseph Ng • <i>University College London, UK</i> Mitigating Goodhart's Law in Epitope-Conditioned TCR Generation Using Plug-and-Play Reward Designs (P) Fredo Guan • <i>Arizona State University, USA</i>	BIODIVERSITY, SUSTAINABILITY, AND ENVIRONMENTAL BIOINFORMATICS LLM and Agent Based Modelling (in Health and Protein-Protein Interactions) Session Chairs: Katja Bärenfaller, Lucas Paoli Agent-based modelling identifies multiple paths to inflammation resolution (P) Hermès Desgrez Dautet • <i>Institut RESTORE, France</i> ProteomeLM: A proteome-scale language model enables accurate and rapid prediction of protein-protein interactions and gene essentiality across taxa (H) Cyril Malbranke • <i>EPFL & SIB, Switzerland</i> Relation Extraction for Diet, Non-Communicable Disease and Biomarker Associations (RECoDe): A CoDiet study (P) Donghee Choi • <i>Imperial College London, UK & Pusan National University, South Korea</i>

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TUESDAY 1 SEPTEMBER • PARALLEL SESSION 5 • 11: 45 – 12:45

ROOM AD	ROOM BC	ROOM EF
GENOMICS, EPIGENOMICS, AND GENOME EDITING RNA regulation and chromatin context Session Chairs: Maria Anisimova, Knut Reinert Improved RNA–DNA interaction calling suggests RNA-based gene regulation of phenotypic transitions (H)⁵ Timothy Warwick • <i>Goethe University Frankfurt, Germany</i> From transcripts to cells: Dissecting sensitivity, signal contamination, and specificity in Xenium spatial transcriptomics (H) Mariia Bilous • <i>CHUV & SIB, Switzerland</i> CREsted: Modeling genomic and synthetic cell-type-specific enhancers across tissues and species (H) Niklas Kempynck • <i>VIB-KU Leuven, Belgium</i>	TRANSCRIPTOMICS AND GENE REGULATION RNA genomics: from basic mechanism to medical application Session Chairs: Uwe Ohler, Chair TBC Prognostic RNA-splicing archetypes in breast cancer identified by extended pre-training of histopathology foundation models (H) Lisa Fournier • <i>University of Geneva, EPFL, University of Bern & SIB, Switzerland</i> ExoShorkie: Predicting RNA-seq coverage of exogenous genomes in yeast by transfer learning (P) Jonathan Mandl • <i>Bar-Ilan University, Israel</i> miRBind2 enables sequence-only prediction of miRNA binding and transcript repression (P) David Čechák • <i>Central European Institute of Technology, Czechia</i>	PROTEINS AND STRUCTURAL BIOLOGY Generative & Predictive Deep Learning for Protein & RNA Session Chairs: Ivet Bahar, Basile Wicky Optimizing protein design through uncertainty-weighted steering of protein language models (P) Byung-Jun Yoon • <i>Texas A&M University, USA</i> PI-Mamba: Linear-time protein backbone generation via spectrally initialized flow matching (P) Tianyu Wu • <i>University of Illinois Urbana–Champaign, USA</i> RIBEX: Predicting and explaining RNA binding across structured and intrinsically disordered region (IDR)-rich proteins (P) Samuele Firmani • <i>Helmholtz Munich, Germany</i>

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TUESDAY 1 SEPTEMBER • PARALLEL SESSION 6 • 15:15 – 16:15

ROOM AD	ROOM BC	ROOM EF
GENOMICS, EPIGENOMICS, AND GENOME EDITING Cancer Biomarkers and Immune targets Session Chairs: Maria Anisimova, Shilpa Garg Liquid biopsies reveal dual compartments of cancer risk from tumor- and host-derived mutations (P)⁶ Federica Malighetti • <i>enGenome, Italy</i> Micropeptides encoded by lncRNAs associated with cancer progression reveal novel immunogenic epitopes (P) Stav Zok • <i>The Hebrew University of Jerusalem, Israel</i> Modeling time-varying genetic effects on binary disease risk via functional Mendelian randomization (P) Nicole Fontana • <i>Politecnico di Milano & Human Technopole, Italy</i>	SYSTEMS BIOLOGY, MULTI-OMICS INTEGRATION AND MODELLING Systems Biology: Metabolism Session Chairs: Maria Rodriguez Martinez; Valentina Boeva Machine learning and data-driven inverse modeling of metabolomics unveil key processes of active aging (H) Jiahang Li • <i>Nankai University, China</i> Reusable generative models for mechanistic studies of metabolic dynamics (H) Ljubisa Miskovic • <i>EPFL, Switzerland</i> MAAMOUL: Metabolic network-based discovery of microbiome–metabolome shifts in disease (P) Efrat Muller • <i>Tel Aviv University, Israel</i>	TRANSCRIPTOMICS AND GENE REGULATION Networks - from 3D interactions to protein/protein Session Chairs: Uwe Ohler, Ozgur Tastan Chiron3D: An interpretable deep learning framework for understanding the DNA code of chromatin looping (P) Sebastian Hönig • <i>ETH Zurich, Switzerland</i> Network-based stratification of allele-specific expression reveals patient subgroups in Huntington's disease (P) Aishwarya Iye • <i>Maastricht University, Netherlands</i> An end-to-end computational framework for "Record-seq" transcriptional recording data (P) Florian Hugi • <i>ETH Zurich, Switzerland</i>

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WEDNESDAY 2 SEPTEMBER • PARALLEL SESSION 7 • 09:00 – 10:00

ROOM AD	ROOM BC	ROOM EF
TRANSCRIPTOMICS AND GENE REGULATION Transcription regulation: from data to predictive models Session Chairs: Raphaëlle Luisier, TBC Unexpectedly high intrinsic sequence specificity and complex DNA binding of human transcription factors (H)⁷ Hamed Najafabadi • <i>McGill University, Canada</i> STAN: A computational framework for inferring spatially informed transcription factor activity (H) Hatice Ulku Osmanbeyoglu • <i>University of Pittsburgh, USA</i> From enhancer scale to locus scale: Modelling gene regulation with sequence-to-function models (H) Casper H. Blaauw • <i>VIB.AI & KU Leuven, Belgium; Hubrecht Institute, Netherlands</i>	SYSTEMS BIOLOGY, MULTI-OMICS INTEGRATION AND MODELLING Systems Biology: Network-based approaches to Diseases Session Chairs: Anaïs Baudot; Alfonso Valencia PatientProfiler, from multi-omic data to clinical insight: Patient-specific models to derive signalling-based biomarkers (H) Veronica Lombardi • <i>Sapienza University of Rome, Italy</i> A novel ILP framework to identify compensatory pathways in genetic interaction networks with GIDEON (P) Jocelyn Garcia • <i>Tufts University, USA</i> Decoding non-coding SNPs: Systems genomics modelling dissects the heterogeneity of IBD (H) Dezso Modos • <i>Imperial College London, UK</i>	PROTEINS AND STRUCTURAL BIOLOGY Biomolecular Dynamics, Conformational Sampling & Structural Variant Analysis Session Chairs: Basile Wicky; Emmanuel Levy Reconstructing atomistic biomolecular dynamics from high-speed atomic force microscopy data (H) Florence Tama • <i>RIKEN & Nagoya University, Japan</i> Efficient sampling of large-scale transition pathways and intermediate conformations in sub-mesoscopic protein complexes (H) Domenico Scaramozzino • <i>Karolinska Institutet, Sweden</i> Accurate identification and mechanistic evaluation of pathogenic missense variants with Rhapsody-2 (H) Ivet Bahar • <i>Stony Brook University, USA</i>

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WEDNESDAY 2 SEPTEMBER • PARALLEL SESSION 8 • 10:30 – 11:30

ROOM AD	ROOM BC	ROOM EF
SYSTEMS BIOLOGY, MULTI-OMICS INTEGRATION AND MODELLING Systems Biology: Advanced Modeling and Machine Learning Session Chairs: Anaïs Baudot, Alfonso Valencia Universal differential equations for quantifying NF-κB–p53 signalling crosstalk (P)⁸ Umur Kaya • <i>Freie Universität Berlin, Germany</i> SELFFormerMM: Multimodal molecular representation learning via SELFIES, structure, text, and knowledge graph integration (P) Erva Ulusoy • <i>Hacettepe University, Turkey</i> Semi-supervised learning for automated perineural invasion detection in multi-organ H&E whole-slide images (P) Ahmad Alkhan • <i>University of Limerick, Ireland</i>	GENOMICS, EPIGENOMICS, AND GENOME EDITING Interpretable genomics and model trust Session Chairs: Shilpa Garg, Knut Reinert BaGGLS: A Bayesian shrinkage framework for interpretable modelling of interactions in high-dimensional biological data (P) Marta Lemanczyk • <i>Hasso Plattner Institute, Germany</i> PRISM-G: An interpretable privacy scoring framework for assessing risk in synthetic human genome data (P) Alejandro Correa Rojo • <i>KU Leuven, Belgium</i> Knowledge-guided learning with curated prior genetic biomarkers for robust model interpretation (P) Beomsu Baek • <i>University of Nevada, Las Vegas, USA</i>	BIODIVERSITY, SUSTAINABILITY, AND ENVIRONMENTAL BIOINFORMATICS Diving into Virus Host Prediction and Coral Microbiome Diversity Session Chairs: Avidan Neumann, Katja Bärenfaller Coral microbiomes as reservoirs of unknown genomic and biosynthetic diversity (H) Lucas Paoli • <i>EPFL, Switzerland</i> GiantHost: A domain-adaptive and uncertainty-aware framework for giant virus host prediction (P) Fuchuan Qu • <i>City University of Hong Kong, China</i> ViralQC: A tool for assessing completeness and contamination of predicted viral contigs (P) Cheng Peng • <i>City University of Hong Kong, China</i>

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WEDNESDAY 2 SEPTEMBER • PARALLEL SESSION 9 • 13:15 – 14:15

ROOM AD	ROOM BC	ROOM EF
TRANSCRIPTOMICS AND GENE REGULATION Single cell - cell types to trajectories Session Chairs: Raphaëlle Luisier, Uwe Ohler scTimeBench: A streamlined benchmarking platform for single-cell time-series analysis (P⁹) Eric Haoran Huang • <i>McGill University, Canada</i> CellTypeAI: Automated cell identification for scRNA-seq using local generative AI (P) Rufus Daw • <i>University of Manchester, UK</i> Sensitivity analysis of cell fate trajectories from single-cell transcriptomics (P) Abdullah Al Noman • <i>Virginia Tech, USA</i>	GENOMICS, EPIGENOMICS, AND GENOME EDITING Evolutionary graphs and Biosynthetic Inference Session Chairs: Maria Anisimova, Shilpa Garg Nerpa 2: Probabilistic linking of biosynthetic gene clusters to nonribosomal peptides (P) Ilia Olkhovskii • <i>Helmholtz Institute for Pharmaceutical Research Saarland (HIPS), Germany</i> Episode clustering in phylogenetic networks (P) Pawel Gorecki • <i>University of Warsaw, Poland</i> ARGformer: Learning on ancestral recombination graphs with transformers (P) David Bonet • <i>University of California, Santa Cruz, USA</i>	PROTEINS AND STRUCTURAL BIOLOGY Structure-Based Drug Discovery & Binding Pocket Analysis Session Chairs: Ivet Bahar, Basile Wicky Attracting Cavities 3.0: Faster and more versatile molecular docking for the SwissDock webserver (P) Ute F. Röhrig • <i>SIB, Switzerland</i> PepGen: Conditional generation of peptides for MHC binding (P) Dani Korpela • <i>Aalto University, Finland & Broad Institute of MIT and Harvard, USA</i> Pocket-PROTACs: An interpretable pocket-aware deep learning framework for predicting PROTAC-induced protein degradation (P) Kai Chen • <i>Central South University, China</i>

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