

Monday, July 5, 2021 — Virtual Postersession 1

14:00-15:30 CEST | UMT+2

Single cell applications in health and disease I

ID	Presenter	Title	Time
15	Neeraj Sinha	Comprehensive analysis of changes in tissue spatial architecture in colitis associated cancer development using imaging mass cytometry	14:00
27	Lorenz Adlung	Cell-to-cell variability in JAK2/STAT5 pathway components and cytoplasmic volumes define survival threshold in erythroid progenitor cells	14:05
42	Akihisa Yamamoto	Alteration of Spatio-Temporal Pattern of Deformation and Migration of Human Gastric Cells Induced by Cancer Progression	14:10
43	Arik Horne	Synthetic Embryo structures: a new model for early embryonic diseases?	14:15

Multidimensional data from population cohorts

ID	Presenter	Title	Time
18	Álvaro Fernández Ochoa	The role of Metabolomics in MSTARs (Multimodal clinical mass Spectrometry to TArget treatment ReSistance). A preliminary study focused on HNSCC.	14:00
29	Lorenzo Bonaguro	Natural human variation in multi-layered cohorts predicts the function of CRELD1: a novel regulator of immune homeostasis in mouse and human	14:05
37	Olga Lazareva	BiCoN: Network-constrained biclustering of patients and omics data	14:10
41	Piotr Nyczka	Cohortizer — A tool for generating stylized transcriptome profiles of disease cohorts with tunable signal strength	14:15

(Multi)-omics

ID	Presenter	Title	Time
20	Juan Henao	Stratification in preterm infants with chronic lung disease by a multi-omics integration approach	14:00
28	Matthias Becker	A new computational architecture for genomics	14:05
46	Matti Hoch	Inference of phenotypes and drug targets from large-scale disease maps	14:10
55	Thomas Ulas	hCocena: A network-based approach for omics data integration	14:15
57	Lisa Holsten	A favorable clinical outcome of influenza infection in neonates is linked to reprogramming of monocytes towards a less inflammatory phenotype	14:20

Modelling in drug research

ID	Presenter	Title	Time
10	Maxim Karnetzki	Plasmodium falciparum phospholipid metabolism. Development of a comprehensive ODE model for potential drug target identification.	14:00
52	Undine Falkenhagen	Reducing systems biology models to derive mechanism-based drug effect models	14:05
58	Benedict Wolf	Emulating target trials to estimate the additional average treatment effect of treatment recommender systems	14:10

Modelling I

ID	Presenter	Title	Time
36	Ben Illigens	Application of a mechanistic model to design RTI prophylaxis trials	14:00
39	Tara Hameed	Diagnosing data sparsity as a bottleneck for mechanistic model development	14:05
40	Judith Thoma	Theoretical Modelling of Dynamic Phenotypes of Human HSC Affected by Clinical Agent	14:10
56	Simon Merkt	A cell cycle dependent population dynamics model with parameter inference from scRNA-seq data	14:15

Tuesday, July 6, 2021 — Virtual Postersession 2

14:00-15:30 CEST | UMT+2

Single cell applications in health and disease II

ID	Presenter	Title	Time
3	Karoline Barbosa	Massive Parallel Single-Cell RNA-Sequencing: a systematic review	14:00
14	Jorin Diemer	Modeling the regulation of major ion species in the intra-erythrocytic malaria parasite Plasmodium falciparum	14:05
22	Erika Dudkin	Distribution-free differential expression analysis for scRNA-seq data across patient groups	14:10
23	Jens Hansen	Identification of cell-type specific pathway-networks from multi-omic datasets in the Kidney Precision Medicine Project using MBCO	14:15

Machine learning based models

ID	Presenter	Title	Time
12	Cyrrillus Tan	Structured decomposition improves systems serology prediction and interpretation	14:00
35	Stefanie Warnat-Herresthal	Swarm Learning for decentralized and confidential clinical machine learning	14:05
50	Tim Daniel Rose	Identifying specific molecular signatures from heterogeneous omics data for patient stratification and disease subtyping	14:10
53	Dongheon Lee	Hybrid Data-driven Mechanistic Modeling Approach to Describe Uncertain Intracellular Signaling Pathways	14:15
59	Martina Prugger	Unsupervised logic-based mechanism inference for network-driven biological processes	14:20

COVID-19 research

ID	Presenter	Title	Time
25	Jonas Schulte-Schrepping	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment	14:00
31	Rainer Knoll	Persistent natural killer cell dysfunction in severe COVID-19	14:05
32	Nico Reusch	Neutrophils in COVID-19	14:10
33	Elena De Domenico	Optimized workflow for handling of clinical samples for single-cell transcriptomics on infectious diseases including COVID-19	14:15
38	Anna Aschenbrenner	Disease severity-specific neutrophil signatures in blood transcriptomes stratify COVID-19 patients	14:20
49	Avidan Neumann	Viral and Immunological Multidimensional Correlates of COVID-19 Severity and Mortality	14:25

Cancer research

ID	Presenter	Title	Time
7	Bernard Staumont	Tumor secretome and VEGF-C induce opposite transcriptomic changes in lymphatic endothelial cells	14:00
11	Kiran Vanaja	Computational modeling predicts PTEN as a feedback loop of the PI3K/Akt/mTOR pathway mediates the emergence of resistance to PI3K pathway inhibitors.	14:05
13	Karina Biskup	Sialic acid linkage analysis refines the diagnosis of ovarian cancer	14:10
54	Roman Kurilov	Expression signatures for stratifying pancreatic cancer patients into Gemcitabine- and Oxaliplatin-based treatment arms	14:15

Modelling II

ID	Presenter	Title	Time
1	Noah Chicoine	Extension of the Human Blood Coagulation Model to Understand the Role of C1-Inhibitor in Hereditary Angioedema	14:00
4	Matthias Fischer	Mathematical modelling of colon epithelium population dynamics reveals conditions for maintaining tissue homoeostasis	14:05
44	Sophie Bekisz	IN SILICO LYMPHANGIOGENESIS: From a simple mathematical model of receptor trafficking in LECs to the experimentally characterized influence of uPARAP	14:10
45	Anna Stalkerich	Cell Homeostasis or Cell Death - The balancing act between autophagy and apoptosis caused by steatosis induced ER stress	14:15