

DDLS Annual Conference 2023

November 15-16, 2023



POSTER

1	Integrative Data Processing Pipeline for PROseq Uncovers Mechanisms of Transcription across Functional Genomic Regions Serhat Aktay, KTH Royal Institute of Technology
2	FunCoup 5: Functional Association Networks in All Domains of Life, Supporting Directed Links and Tissue-Specificity Davide Buzzao, Stockholm University
3	Deciphering sex differences in human immunity using systems immunology Camila Consiglio, Lund University
4	Understanding the microbial diversity in the healthy vagina Gabriella Edfeldt, Karolinska Institutet
5	REFSTRA (Reference-Free Single-cell Transcriptome Autotyping) for deconvolution of paired Spatial Transcriptomics data Alper Eroglu, SciLifeLab
6	CoolBeans: user-friendly workflow for identifying multi-metabolite signatures of exposure. Núria Estanyol-Torres, Chalmers University of Technology
7	Processing spatial networks through UMI David Fernandez Bonet, KTH Royal Institute of Technology
8	Revealing the RBP regulome in hepatocellular carcinoma via consensus GRN inference Mateusz Garbulowski, SciLifeLab/ Stockholm University
9	Utilizing large-scale genomic data to explore variable disease penetrance Sanna Gudmundsson, SciLifeLab/KTH
10	U-FISH: a universal deep learning approach for accurate FISH spot detection across diverse datasets Weize Xu, AI Cell Lab, KTH
11	Model based DNA basecallers Joakim Jaldén, KTH Royal Institute of Technology
12	Detecting resin wood in Scots pine with laboratory-bespoke X-ray computed tomography imaging Sheng Joevenller, Luleå University of Technology
13	Inferring dissipation from cell-membrane fluctuations Sreekanth K Manikandan, Department of Chemistry, Stanford University
14	An Advanced Deep Learning Pipeline for Genome-Wide Imaging Screen Analysis Uncovering Cell Death Regulators Salma Kazemi Rashed, Lund University
15	Beam search decoder for enhancing sequence decoding speed in single-molecule peptide sequencing data Javier Kipen, KTH Royal Institute of Technology
16	BIIF - Support on BioImage Analysis in Sweden Anna Klemm, SciLifeLab
17	Single-cell RNA sequencing-based program-polygenic risk scores associated with pancreatic cancer risks in the UK Biobank cohort Yelin Zhao, Karolinska Institutet
18	Deep Learning with Big Data for Genetic Epidemiology Max Kovalenko, Uppsala University

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| 19 | Spatial transcriptomics and GWAS data identify putative causal tissue structures for complex traits
Linda Kvastad, SciLifeLab/KTH |
| 20 | Bacterial vaginosis: Understanding the effect of antibiotic-free treatment on the vaginal microbiome
Emilia Lahtinen, Karolinska Institutet |
| 21 | SciCommander Track provenance of any shell command
Samuel Lampa, Karolinska University Hospital |
| 22 | Kidney automatic segmentation and cystic renal occupying lesions classification system based on the Deep Learning.
Hui Li, Chalmers University of Technology |
| 23 | Metagenomics of insect bulkDNA for population genetics
Samantha López Clinton, Swedish Museum of Natural History |
| 24 | Multimodal signal recordings in neuroscience: modeling strategies
Melisa Maidana Capitan, Linköping University |
| 25 | National Genomics Infrastructure (NGI) Next Generation Sequencing and Genotyping for Swedish Research
Tom Martin, National Genomics Infrastructure (NGI) |
| 26 | Multi-metabolic signature of controlled modification of dietary carbohydrate quality
Cecilia Martinez Escobedo, Chalmers University of Technology |
| 27 | From Genes to Causal Maps: A Benchmark for Gene Regulatory Network Inference
Mariia Minaeva, KTH Royal Institute of Technology |
| 28 | Identification of metabolomic networks linked with incident heart failure.
Jakub Morze, SGMK Copernicus University / Chalmers University of Technology |
| 29 | Predicting Protein-Protein Interactions using Machine Learning
Sarah Narowe Danielsson, SciLifeLab/ Stockholm University |
| 30 | Recalibrating differential gene expression analysis by variance in gene dosage
Philipp Rentzsch, SciLifeLab |
| 31 | Mapping the genetic architecture of sarcoidosis across populations
Natalia Rivera, Karolinska Institutet |
| 32 | The Swedish Childhood Tumor Biobank
Johanna Sandgren, Karolinska Institutet |
| 33 | Targeted Proteomics of Blood Plasma from the hPOP Cohort
Thanadol Sutantiwanichkul, KTH Royal Institute of Technology |
| 34 | Barcode-free prediction of cell lineages from scRNA-seq datasets
Marcel Tarbier, SciLifeLab/KI |
| 35 | Deep Learning for Time Series Classification of Parkinsons Disease Eye Tracking Data
Gonzalo Uribarri, SciLifeLab/KTH |
| 36 | Benchmarking orthologous clustering programs for proteins a case study in Pseudomonas aeruginosa
Virág Varga, Chalmers University of Technology |

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| 37 | Predicting plastic-degrading potential of the Baltic Sea: a data-driven approach with taxonomic information
Máté Vass, Chalmers University of Technology |
| 38 | Predicting Preterm Birth Using Machine Learning
Nicole Wagner, Karolinska Institutet |
| 39 | Navigating the Toolbox: A Comparative Analysis of Metagenomic Tools for Taxonomic and Resistance Gene Identification
Marcus Wenne, Chalmers University of Technology |
| 40 | SciLifeLab Data Platform
Liane Hughes, SciLifeLab/UU |
| 41 | SciLifeLab Serve - enabling sharing of machine learning models and applications
Arnold Kochari, SciLifeLab |
| 42 | Services and support from SciLifeLab Data Centre
Katarina Öjefors Stark, SciLifeLab Data Centre |