

Detailed programme BioSB 2023



Tuesday May 9

08:30 - 09:30	CONFERENCE REGISTRATION			REGISTRATION DESK / LOUNGE 1
09:30 - 09:45	OPENING			LAMORAAL
09:45 - 10:30	KEYNOTE: Johannes Söding, MaxPlanck Institute for Biophysical Chemistry, Germany <i>New tools for protein structure and sequence searching and metagenome assembly</i>			LAMORAAL
10:30 - 11:00	EDUCATIONAL PLENARY: Jessica Lindvall, Head of Training SciLifeLab Training Hub, Stockholm University / Deputy Head of Node, ELIXIR-SE			LAMORAAL
11:00 - 11:30	COFFEE BREAK WITH EXHIBITORS			LOUNGE 1 + ROOM 525
PARALLEL	LAMORAAL	ABDIJ	ROOM 558	ROOM 559
11:30 - 13:00	S1: ARTIFICIAL INTELLIGENCE	S2: COMPUTATIONAL METABOLOMICS	S3: EVOLUTIONARY SYSTEMS BIOLOGY & BIOINFORMATICS	S4: ELIXIR-NL: FAIR DATA & PROVENANCE
11:30	Kirti Biharie, TU Delft <i>Cell type matching across species using protein embeddings and transfer learning</i>	11:30 Alessia Vignoli, University of Florence <i>Metabolomics of Ageing: a personalized NMR-based approach to predict Alzheimer's disease evolution</i>	11:30 Bram van Dijk, Max Planck Institute for Evolutionary Biology <i>Identifying and tracking mobile elements in evolving compost communities yields insights into the nanobiome</i>	11:30 Martin Brandt, SURFsara <i>SURF Research Cloud as compute platform for sensitive data</i>
11:53	Swier Garst, TU Delft <i>A comprehensive comparison between federated learning against centralized learning shows robustness to various data-level challenges</i>	11:53 Denise N. Slenker, Maastricht University <i>Discovering life's directed metabolic (sub) paths to interpret biochemical markers using the DSMN</i>	11:53 Aysun Urhan, TU Delft <i>SAP: Synteny-aware gene function prediction for bacteria using protein embeddings</i>	11:53 Jeaphianne van Rijn, Maastricht University <i>The semantic landscape: an ever growing, publicly available overview of nanosafety knowledge</i>
12:16	Paul van Lent, TU Delft <i>Simulated Design-Build-Test-Learn Cycles for Evaluating Machine Learning and Automated Recommendation in Metabolic Engineering</i>	12:16 Duygu Dede Sener, Maastricht University <i>An R-shiny application for functional analysis and visualization of transcriptomic and metabolomic data</i>	12:16 Meike Wortel, University of Amsterdam <i>Ecological effects on the evolution of cefotaxime resistance in Escherichia coli</i>	12:16 Junda Huang, Radboud UMC <i>Targeted FDP-querying of FAIRified multi-omics data, a X-omics/TWOC demonstrator</i>
12:39	Aalt-Jan van Dijk, Wageningen UR <i>Artificial intelligence Plant and animal research Structural biology/bioinformatics</i>	12:39 Justin van der Hooft, Wageningen UR <i>Breaking Bonds & Barriers: Computational Metabolomics Strategies to Organize, Prioritize, and Annotate Metabolites in Mass Spectrometry Profiles</i>	12:39 Anne Kupczok, Wageningen UR <i>Co-transfer of functionally interdependent genes contributes to genome mosaicism in lambdoid phages</i>	12:39 Jasper Koehorst, Wageningen UR <i>FAIR Data Station</i>
13:00 - 14:15	LUNCH WITH EXHIBITORS			LOUNGE 1 + ROOM 525
13:20 - 14:05	EDUCATIONAL SESSION			LAMORAAL
PARALLEL	LAMORAAL	ABDIJ	ROOM 558	ROOM 559
14:15 - 15:45	S5: CANCER RESEARCH	S6: MECHANISTIC & MULTISCALE MODELING	S7: ELIXIR-NL: RESOURCES & COMMUNITIES	
14:15	Jurriaan Janssen, Amsterdam UMC/VU Amsterdam <i>oncoBLADE: a Bayesian deconvolution method tailored for solid tumor application by integrating DNA-seq data</i>	14:15 Johannes Odendaal, UMC Groningen <i>Personalised computational modelling of mitochondrial β-oxidation using MCADD patient proteomics as a tool for risk stratification</i>	14:15 Duong Vu, Westerdijk Fungal Biodiversity Institute <i>The Westerdijk fungal data resources for bioinformatics and biology</i>	
14:38	Youri Hoogstrate, Erasmus MC, Cancer Institute <i>Transcriptome analysis reveals tumor microenvironment changes in glioblastoma</i>	14:38 Robert Smith, Wageningen UR <i>The art of war: How bacterial SPARTan armies overpower invaders</i>	14:38 Rob Hooft, Health-RI <i>The "Genomic Data Infrastructure" project realizes a million human genomes dream</i>	
15:01	Evert Bosdriesz, VU Amsterdam <i>Understanding cell state dependent drug response using comparative network reconstruction</i>	15:01 Sara Moreno-Paz, Wageningen UR <i>Kinetic modeling to understand and improve curcuminoid production in Pseudomonas putida</i>	15:01 Vitor Martins dos Santos, Wageningen UR <i>Fostering synergies: The ELIXIR Microbial Biotechnology & Systems Biology Communities</i>	
15:25	Alberto Nakauma, Erasmus MC <i>Driver hotspot mutations in whole-genomes of APOBEC-enriched bladder cancers</i>	15:25 Kirsten ten Tusscher, Utrecht University <i>Multi-scale modeling in plant root development and adaptation</i>	15:25 Helena Rasche, Erasmus MC <i>The Galaxy Community update</i>	
15:45 - 16:30	COFFEE BREAK WITH EXHIBITORS			LOUNGE 1 + ROOM 525
16:30 - 17:15	BIOSB YOUNG INVESTIGATOR AWARD 2023: Soufiane Mourragui, Alexander van Oudenaarden Group at the Hubrecht Institute (Utrecht) <i>Computational models for clinical drug response prediction</i>			LAMORAAL
17:15 - 17:30	GROUP PHOTO			LAMORAAL
17:30 - 19:30	POSTER & DEMO SESSION I (EVEN NUMBERS) - INCL. DRINKS			LOUNGE 1 + ROOM 525
19:30 - 21:00	CONFERENCE DINNER			RITZ
21:00 - 24:00	BAR & POPPUZZLE LIVE & THE COLLECTORS BAND			O'Donnell's Pub

Wednesday May 10

07:00 - 08:00	MORNING RUN			GATHER IN FRONT OF VENUE
08:00 - 09:00	MEET THE PI			LOUNGE 1
08:30 - 09:30	CONFERENCE REGISTRATION			REGISTRATION DESK / LOUNGE 1
09:30 - 09:45	OPENING			LAMORAAL
09:45 - 10:30	KEYNOTE: Dagmar Iber, Department of Biosystems Science and Engineering, ETH Zürich, Switzerland <i>Principles of development: how to develop complex shapes & functionalities from single cells</i>			LAMORAAL
10:30 - 11:00	COFFEE BREAK WITH EXHIBITORS			LOUNGE 1 + ROOM 525
PARALLEL	LAMORAAL	ABDU	ROOM 558	ROOM 559
11:00 - 12:30	S8: HEALTH RESEARCH	S9: HIGH-THROUGHPUT PHENOTYPING	S10: MICROBIAL COMMUNITIES (KNVM)	S11: STRUCTURAL BIOLOGY
11:00	Daniele Bizzarri, Leiden University Medical Center <i>1H-NMR metabolomics guided methylation mortality predictors</i>	11:00 Matti Gralka, VU Amsterdam <i>Fundamental metabolic strategies of heterotrophic bacteria</i>	11:00 Roel van der Ploeg, University of Amsterdam <i>High-level integration of longitudinal oral microbiome and metabolome data finds pathways important to induced gingivitis</i>	11:00 David Poole, VU Amsterdam <i>Displacement docking: A novel approach for broad spectrum and multi-species inhibitors</i>
11:23	Jeppe Severens, Leiden University Medical Center <i>Transcriptomic classification, risk stratification and therapy selection in AML</i>	11:23 Sarah Mehrem, University of Utrecht <i>Using multi-omics and high-throughput imaging to understand plant genetics in lettuce</i>	11:23 Ernestina Hauptfeld, Utrecht University <i>Unravelling the identity and potential for hydrocarbon degradation of the elusive Grifpark bacterium</i>	11:23 Juami van Gils, UMC Groningen <i>Disordered flanks slow down the growth of amyloid fibrils in neurodegenerative disease</i>
11:46	Freek Relouw, Eindhoven University of Technology <i>Development and Validation of a Mathematical Model for Acute and Prolonged Inflammatory Responses to Lipopolysaccharide in Humans by Modelling mRNA Expression in Monocytes</i>	11:46 Katarina Smolenová, Wageningen UR <i>Digital tomato twins</i>	11:46 Sara Benito-Vaquerizo, Wageningen UR <i>Model-driven design of bacterial communities for utilization of CO₂, CO and H₂ gas mixtures</i>	11:46 Fabian Schuhmann, Carl von Ossietzky University Oldenburg <i>ALISE: An Improved And Automated Virtual Drug Screening Procedure</i>
12:09	Edoardo Saccenti, Wageningen UR <i>Integrated systems approaches to understand Necrotizing Soft Tissue Infections: the INFECT-PERAID-PERMIT projects 2012-2023</i>	12:09 Rick van de Zedde & Sven Warris, Wageningen UR <i>Lessons-learned and new insights on data storage, data processing and information extraction at the Netherlands Plant Eco-phenotyping Centre (NPEC)</i>	12:09 Jos Boekhorst, Wageningen UR <i>ADHD symptom reduction after dietary intervention is associated with gut microbiome composition</i>	12:09 Anton Feenstra, VU Amsterdam <i>Ten Tips for Protein Property Prediction – Common Challenges and Best Practices</i>
12:30 - 13:30	POSTER & DEMO SESSION II (ODD NUMBERS) - INCL. LUNCH			LOUNGE 1 + ROOM 525
PARALLEL	LAMORAAL	ABDU	ROOM 558	ROOM 559
13:30 - 15:00	S12: AI IN HEALTH RESEARCH	S13: SINGLE CELL TECHNIQUES	S14: MICROBIAL GENOMICS	S15: ALGORITHMS FOR GENOMICS
13:30	Marc Pagès-Gallego, UMC Utrecht, Oncode Institute <i>Ultra-fast deep-learned pediatric CNS tumor classification during surgery</i>	13:30 Maryna Korschewnik, University Medical Center Groningen, University of Groningen <i>Identification of genetic variants that impact gene co-expression relationships using large-scale single-cell data</i>	13:30 Jasper van Bemmelen, TU Delft <i>AmpliVar: an optimized amplicon sequencing approach to estimating lineage abundances in viral metagenomes</i>	13:30 Soufyan Lakbir, VU Amsterdam <i>CIBRA: Computational Identification of Biologically Relevant Alterations</i>
13:53	Fleur Wallis, Prinses Máxima Centrum M&M: An RNA-seq based Pan-Cancer Classifier for Pediatric Malignancies	13:53 Bram Thijssen, Netherlands Cancer Institute <i>Inferring single-cell protein levels and cell cycle behavior in heterogeneous cell populations</i>	13:53 William Scott, Wageningen UR <i>A Structured Evaluation of Genome-Scale Constraint-Based Modeling Tools for Microbial Consortia</i>	13:53 Roy Straver, UMC Utrecht <i>Missing k-mer imputation for nanopore base modification models</i>
14:16	Siqi Wei, AstraZeneca and Vrije University Amsterdam <i>Representation of small molecules for drug discovery using machine learning</i>	14:16 Gerard Bouland, TU Delft <i>Single-cell RNA sequencing reveals a rewiring of transcriptional relationships in Alzheimer's Disease associated with risk variants</i>	14:16 Ling-Yi Wu, Utrecht University <i>Benchmarking Virus Identification Tools Using Real Metagenomic Data</i>	14:16 Rick Beeloo, Utrecht University <i>GRAPHITE: Longest Maximum Exact Matches in large sequence collections</i>
14:39	Yongsoo Kim, Amsterdam UMC <i>Computational genomics to unravel tumor heterogeneity and microenvironment</i>	14:39 Miao-Ping Chien, Erasmus MC <i>Microscopy-based functional and spatial single cell sequencing</i>	14:39 Daniel Tamarit, Utrecht University <i>Inference and reconstruction of the heimdallarchaeal ancestry of eukaryotes</i>	14:39 Jasmijn Baajens, TU Delft <i>Algorithms for viral lineage abundance estimation from wastewater sequencing data</i>
15:00 - 15:30	COFFEE BREAK WITH EXHIBITORS			LOUNGE 1 + ROOM 525
15:30 - 16:15	KEYNOTE: Alexandre Bonvin, Bonvin Lab, Utrecht University, Netherlands <i>Solving 3D puzzles of biomolecular interactions by integrative modelling</i>			LAMORAAL
16:15 - 16:30	POSTER PRIZE WINNER & CLOSING			LAMORAAL
17:00 - 17:30	POSTER PICKUP			