Programme BioSB 2026

Tuesday May 12

12-13 May
BioSB
2026
Hosted by Maastricht University

08:30-10:00	**REGISTRATION** (and poster set-up)			REGISTRATION DESK
10:00-10:15	**OPENING** by conference chairs Michiel Adriaens, Martina Summer-Kutmon and Susan Steinbusch-Coort			LEGIOENZAAL
10:15-11:00	**KEYNOTE: Ines Thiele, University of Galway, Ireland** *Digital metabolic twins for accelerated diagnosis of rare diseases*			LEGIOENZAAL
11:00-11:15	**COFFEE BREAK** (and poster set-up)			LEGIOENZAAL
PARALLEL	ROOM: NAPOLEON	ROOM: MAAS	ROOM: DE VERLICHTING	
11:15-12:45	**S1: Mechanistic modelling - Part A**	**S2: Single-cell and spatial omics**	**S3: Building and Running AI in the Life Sciences Industry**	
	11:15 **Fabian Ormersbach** *Microtubule Mysteries: Particles, Barriers, and the Cell Wall*	11:15 **Gustavo S. Jeuken** *CycleVI: Isolating cell cycle variation with an interpretable deep generative model*	11:15 **Wouter Touw** *From Molecules to Manufacturing: Setting the Pace with AI at dsm-firmenich*	
	11:37 **Griffin Kutler Dodd** *Eco-evolutionary design finds effective broadly neutralizing HIV-1 antibodies*	11:37 **Ewald van Dyk** *ISFaN: Normalizing single cell proteomics data with accurate covariance estimates between protein pairs*	11:30 **Guizela Huelsz Prince** *Our cBioPortal Copilot Experience (SE4BIO)*	
	12:00 **Jelle Bonthuis** *GPRimproved: converting gene expression to enzymatic capacity*	12:00 **Valentijn Tromp** *scHLAseq: A Tool for Allele-Specific HLA Class II Expression Analysis at Single-Cell Resolution*	11:45 **Geo Velikkakam James** *Applications of language models in industrial setup (Rijk Zwaan)*	
	12:22 **Ruth Großeholz** *Plant development across scales: from nodule formation to source-sink dynamics*	12:22 **Federico Bocci** *Navigating the attractor landscape of single cells*	12:00 **Henk-Jan van den Ham** *Applications of language models in data democratisation (The Hyve)*	
			12:15 **Panel discussion and audience Q&A**	
12:45-13:30	**LUNCH** (and open poster session)			LEGIOENZAAL
PARALLEL	ROOM: NAPOLEON	ROOM: MAAS	ROOM: DE VERLICHTING	
13:13-15:00	**S4: Graphs & Networks**	**S5: Genomics**	**S6: Tools and Infrastructure (co-hosted by ELIXIR-NL)**	
	13:30 **Dries Heylen** *Using Knowledge Graphs for Post-COVID-19 Drug Repurposing*	13:30 **Mina Shahisavandi** *Genetic Architecture of Perinatal Depression: Disentangling perinatal-specific and general depression pathways*	13:30 **Ana Mendes** *bio.tools: a community-driven registry for research software in the life sciences*	
	13:52 **Niccolò Bianchi** *Semantically-valid negative samples integration techniques for scalable semi-automated drug repurposing prediction pipelines in rare disease research*	13:52 **Nienke Mekkes** *Neuropathology-anchored genomics refines cross-disorder genetic architecture of brain disorders*	13:52 **Rodrigo García Valiente** *AbSolution: an interactive tool for feature-based analysis of AIRR-seq data enabling automation and computational reproducibility*	
	14:15 **Marvin Martens** *A reusable transcriptomic-to-AOP workflow: Integrating web-based RNA-seq analysis and molecular AOP tools for platinum-induced kidney toxicity*	14:15 **Vivek Bhardwaj** *Computational tools to study epigenetic regulation in single cells*	14:15 **Denise Slenter** *Plant Metabolic Pathways Wiki: The Linked Open Data service for querying and analyzing plant pathway knowledge*	
	14:37 **Hendrik Marks** *Gene expression noise in development: genome-wide dynamics*	14:37 **Hanneke van Deutekom** *Clinical Implications and Challenges of Illumina TruPath Genome; combining high-accuracy short-read sequencing with long range information*	14:37 **Leon Mei** *A FAIRworkflow community: beyond Galaxy-NL to support harmonized workflow development, infrastructure and education*	
15:00 - 15:30	**COFFEE BREAK**			LEGIOENZAAL
15:30 - 16:00	**DEMO PITCHES**			LEGIOENZAAL
16:00 - 16:45	**KEYNOTE: Kirsten ten Tusscher, Utrecht University** *Computing Roots*			LEGIOENZAAL
16:45-17:30	**BREAK**			
17:30-18:30	**POSTER / DEMO SESSION 1: Even numbers presented - Drinks & Snacks**			LEGIOENZAAL
18:30-19:30	**POSTER / DEMO SESSION 2: Odd numbers presented - Drinks & Snacks**			LEGIOENZAAL
19:30-21:30	**CONFERENCE DINNER** - Campfire			CASTLE COURTYARD
21:30 - 01:00	**PARTY**			THE CHAPEL

Wednesday May 13

07:00-08:00	Morning run with Peter-Bram			
08:00-08:45	**REGISTRATION**			REGISTRATION DESK
08:45-08:50	**OPENING** by conference chairs Michiel Adriaens, Martina Summer-Kutmon and Susan Steinbusch-Coort			LEGIOENZAAL
08:50-09:30	**BioSB YIA 2026 Ernestina Hauptfeld, Utrecht University** *Nature's Clean-up Crew: Bioremediation through a Metagenomic Lens*			LEGIOENZAAL
09:30-09:45	**COFFEE BREAK**			LEGIOENZAAL
PARALLEL	ROOM: NAPOLEON	ROOM: MAAS		
09:45-11:15	**S7: Multi-omics data integration**	**S8: Proteomics and structural bioinformatics**		
	9:45 **Sadegh Rizi** *Comprehensive Metabolite Ratio QTL Mapping Using Summary Statistics Reveals Novel Enzyme Biology and Disease Mechanisms*	9:45 **Cunliang Geng** *Scaling SwiftMHC Training: A 100× Speedup Through Systematic Pipeline Optimisation*		
	10:07 **Bram Pronk** *A multi-omic model for minimally-invasive tumour load quantification from blood plasma*	10:07 **Farzaneh Parizi** *Peptide Distance Metrics for T Cell–Informed Antigenic Mapping: Tracking Virus Evolution for Pandemic Preparedness*		
	10:30 **Kayle Boessen** *Identifying Post-COVID Syndrome Patient Clusters using Multi-Modal Meta Similarity Network Fusion*	10:30 **Jan van Eck** *PLM-eXplain: Divide and Conquer the Protein Embedding Space*		
	10:52 **Timothy Ebbels** *Metabolomics-Focussed Pathway-Aware Multi-omic Data Fusion*	10:52 **Charlotte Adang** *The when, the why and the how: phylogenetic reconstruction of the J-domain protein family reveals specialisation preceding generalisation*		
11:15-13:00	**LUNCH** (and open poster session)			LEGIOENZAAL
11:30-12:30	**BREAKOUT** (BioSB education session)			MAAS
11:30-12:45	**BREAKOUT** (Meet your future employer)			NAPOLEON
PARALLEL	ROOM: NAPOLEON	ROOM: MAAS	ROOM: DE VERLICHTING	
13:00-14:30	**S9: Machine Learning**	**S10: Mechanistic modelling - Part B**	**S11: Microbiology (co-hosted by KNVM)**	
	13:00 **Stavros Makrodimitris** *A new classification loss to maximize clinical utility of machine learning models*	13:00 **Max de Rooij** *Modelling fast and slow: using mixture models to find latent class parameter trajectories in biological ODE models with TemporalMixtureModels.jl*	13:30 **Anna Sheehy** *Deep Longitudinal Phenotyping of a Single Individual Enables Host–Microbiome Metabolic Modelling Over 3.6 Years*	
	13:22 **Aniek Eijpe** *From Black Box to Biology: Explainable Multimodal Cancer Survival Prediction*	13:22 **Laurence Nickel** *Mechanistic PBPK Modeling of Indoxyl Sulfate Effects on OAT1/3-Mediated Furosemide Pharmacokinetics in Chronic Kidney Disease*	13:22 **Can Dedekoy** *Reducing Heterogeneity in Cross-Study Microbiome ML with Data Attribution*	
	13:45 **Daniyal Selani** *Mind the Gap: Rethinking Temporal Modeling in Clinical Transformers*	13:45 **Ricco Zeegelaar** *A 3D Multiscale, Multicellular, Mechanistic Cardioid digital twin to predict differentiation and organisation outcomes*	13:45 **Auke Haver** *Wastewater-Based Genomic Surveillance: What did we learn from the COVID-19 pandemic?*	
	14:07 **Yongsoo Kim** *Statescope: An integrative Bayesian deconvolution framework for discovering cell states in tumors*	14:07 **Marian Breuer** *Metabolic networks inferred from RNA-seq expression binarization indicate unexpected basic similarity across diverse human cell types*	14:07 **Petra Matyskova** *Robust microbial representation to predict plant root colonization*	
14:30-15:00	**COFFEE BREAK**			LEGIOENZAAL
15:00-15:45	**KEYNOTE: David Shorthouse, University College London, UK** *Adaptive Machine Learning for Discovery in the Biosciences*			LEGIOENZAAL
15:45-16:00	**AWARDS AND CLOSING**			LEGIOENZAAL