

TUESDAY, APRIL 2

	ROOM EUROPA	ROOM AZIE	ROOM AFRIKA	ROOM AMERIKA	ROOM 1+2	
8:30	CONFERENCE REGISTRATION					CENTRAL HALL
9:30	OPENING					ROOM EUROPA
9:45	KEYNOTE: Mustafa Khammash , ETH Zürich <i>Circuits and devices for robust multicellular control</i>					
10:30	COFFEE BREAK WITH EXHIBITORS					
	GENOMICS & GENOME BIOINFORMATICS	METABOLISM	3D BIOINFORMATICS & FUNCTIONAL PREDICTION	ELIXIR-NL: WORKING WITH DATA RESOURCES		
11:15	Joris van de Haar (NKI) <i>Identifying epistasis in cancer genomes: a delicate affair</i>	Maurien Olsthoorn (DSM) (INVITED) <i>Omics to Steer Industrial Metabolic Pathway and Product Development</i>	Miguel Correa Marrero (WUR) <i>Simultaneous unsupervised inference of protein-protein contacts and interactions</i>	Friederike Ehrhart (Maastricht University) (CHAIR) <i>History of rare disease and their genetic causes - a data driven approach</i>		
11:40	Shauna O'Donovan (Maastricht University) <i>Use of deep learning methods to translate drug-induced gene expression changes from hepatocyte exposed in vitro to in vivo.</i>	Marian Breuer (Maastricht University) <i>Essential Metabolism for a Minimal Cell</i>	Juami van Gils (VU) <i>To fold or not to fold?</i>	Marc Maurits (LUMC) <i>A Big-Data Approach to Electronic Health Record Data - Using dimensionality reduction and clustering techniques to study longitudinal relationships between diseases</i>		
12:00	Mehmet Akdel (Wageningen University) <i>Assembling genome maps from optical signals</i>	Athanasios Litsios (University of Groningen) <i>Metabolic oscillations cause START by promoting cell-size-independent pulses in Cln3 production</i>	Janani Durairaj (WUR) <i>Structure-based Prediction of Terpene Synthase Product Specificity</i>	Renaud Tissier (VUmc) <i>Integration of several omic sources in prediction models using network-based approaches</i>		
12:20	Patrick Deelen (UMC Groningen) (CHAIR) <i>Using public RNA-seq data to predict gene functions and disease relevance</i>	Martin Pabst (TU Delft) (CHAIR) <i>Exploring the phylogenetic diversity of the nine-carbon sugar metabolism by mass spectrometry</i>	Hanka Venselaar (Radboudumc) (CHAIR) <i>Lost in translation - Experiences from a Structural Biologist</i>	Marvin Martens (Maastricht University) <i>Expanding Adverse Outcome Pathway knowledge by creating AOP-Wiki RDF with semantic annotations to facilitate risk assessment of chemicals</i>		
12:45	LUNCH: Exhibitors and Poster viewing					CENTRAL HALL
	BioSB MEMBER ASSEMBLY					ROOM AZIE
14:00	GROUP PHOTO					ROOM EUROPA
	MEDICAL BIOLOGY (I)	MODELING HUMAN METABOLISM WITH METABOLOMICS DATA (NMC)	SINGLE CELL BIOLOGY	ELIXIR-NL: TOOLS & RESOURCES	IMMUNOLOGY	
14:15	João Belo (AMC) (INVITED) <i>Interaction Mapping: improved biological analysis with domain knowledge incorporation</i>	Peter-Bram 't Hoen (Radboudumc) <i>Search for early pancreatic cancer blood biomarkers in five European prospective population biobanks using metabolomics</i>	Lude Franke (INVITED) <i>Towards personalised cell-type specific directed gene networks through single-cell eQTL analysis</i>	Chris van Run (Prinses Maxima Centrum) <i>Building a research subject registry based on diagnostic data: how not to miss out on rare subjects</i>	Jurjen Tel (TUE) (INVITED) <i>Single cell analysis reveals functional heterogeneity within plasmacytoid dendritic cells and identifies environmental cues that drive type 1 IFN production</i>	
14:40	Zandra Félix Garza (TUE) <i>Systems medicine of psoriasis: The journey towards blue light-based personalized treatment</i>	Ronan Fleming (Leiden University) <i>Mechanistic model-driven exometabolomic characterisation of human dopaminergic neuronal metabolism</i>	Phillipp Schmidt (VU) <i>When and how to switch? – Studying gene expression at single cell level in Baker's yeast</i>	Chaitra Sarathy (Maastricht University) <i>An integrative workflow to visualize Elementary Flux Modes in genome-scale metabolic models</i>	Peter de Greef (Utrecht University) <i>The naive T-cell receptor repertoire has an extremely broad distribution of clone sizes</i>	
15:00	Rurika Oka (Princess Máxima Center) <i>Mutational landscapes in normal hematopoiesis and paediatric AML</i>	Fianne Sips (TUE) <i>Dynamic modeling of time-series metabolomics reveals physiological differences in intestinal bile acid handling between healthy men</i>	Johan van Heerden (VU) <i>Integrated biphasic growth rate, gene expression and size homeostasis behaviour of single B. subtilis cells</i>	Justin J.J. van der Hoof (Wageningen University) <i>Integrated metabolome mining and annotation workflow accelerates specialised metabolite discovery</i>	Nila Servaas (UMC Utrecht) <i>Orphan Receptors in an Orphan Disease: Identification of the NR4A Family as Key Players of Dendritic Cell Dysregulation in Systemic Sclerosis</i>	
15:20	Evgeni Levin (AMC) (CHAIR) <i>Intelligible models for cardiometabolic domain</i>	Panel discussion <i>Which data do we need to advance the field?</i>	Ahmed Mahfouz (LUMC) (CHAIR) <i>Untangling Single Cell Data: Interaction, Identification, and Integration</i>	Mateusz Kuzak (DTL/ELIXIR-NL) <i>On the Road to Research Software Sustainability</i>	Aridaman Pandit (UMC Utrecht) <i>Integration of transcriptomic and epigenetic profiling reveals that CXCL4 modulates dendritic cell differentiation and induces fibrosis</i>	
15:45	COFFEE BREAK WITH EXHIBITORS					CENTRAL HALL
	HOT TOPIC SESSION					ROOM EUROPA
16:30	Gabriel Bucur , Radboud University <i>Large-Scale Gene Network Causal Inference with Bayes Factors of Covariance Structures (BFCS)</i>					
16:55	Bas Teusink , Vrije Universiteit <i>Compartment-specific proteome constraints drive changes in yeast metabolism</i>					
17:20	Harmen Bussemaker , Columbia University <i>From millions of DNA reads to mechanistic insight into transcription factor function</i>					
17:45	POSTER & DEMO SESSION I (INCL. DRINKS)					CENTRAL HALL
19:30	CONFERENCE DINNER					RESTAURANT
21:00	PUB QUIZ (ORGANIZED BY: YoungCB)					BAR
22:30	LIVE MUSIC (Blazing Harrows)					CENTRAL HALL



WEDNESDAY, APRIL 3

	ROOM EUROPA	ROOM AZIE	ROOM AFRIKA	ROOM AMERIKA	ROOM 1+2
7:00	MORNING RUN				
8:30	CONFERENCE REGISTRATION				CENTRAL HALL
9:30	OPENING CONFERENCE				
9:45	KEYNOTE: Michal Linial , Hebrew University of Jerusalem <i>Not all proteins are born alike: Evolution solutions in translational control</i>				
10:30	COFFEE BREAK WITH EXHIBITORS				
	MEDICAL BIOLOGY (2)	DATA INTEGRATION & NETWORK BIOLOGY	METAGENOMICS	ELIXIR-NL: EDUCATION	
			CHAIR: Bas Dutilh, UU		
11:15	Marleen Nieboer, UMC Utrecht <i>Prioritization of non-coding genomic structural variants in cancer</i>	Michiel Adriaens, Maastricht University <i>A network based approach for interpreting allelic imbalance in dilated cardiomyopathy</i>	Nina Dombrowski, NIOZ (INVITED) <i>Using genomics approaches to illuminate the deep roots and evolution of archaea</i>	Tsjerk Wassenaar, Hanze UAS <i>Data Science for Life Sciences at Hanze UAS</i>	
11:40	Thies Gehrmann, LUMC <i>Nutrient challenge exposes transcriptomic shift by lifestyle intervention in healthy participants</i>	Edoardo Saccenti, Wageningen University <i>Simulation and reconstruction of metabolite-metabolite association networks using a metabolic dynamic model and correlation based-algorithms</i>	Victoria Pascal Andreu, WUR <i>gutSMASH: a software package that facilitates systematic analysis of the metabolic potential of anaerobic bacteria</i>	Adrien Melquiond, Utrecht University <i>Education in the cloud for applied bioinformatics in Life Sciences</i>	
12:00	Jens Schouten, TUE <i>Accurate classification of blood cells in a small acute lymphoblastic leukemia dataset using convolutional neural networks</i>	Abhinandan Devaprasad, UMC Utrecht <i>Discovering progenitor plasticity and cell specific regulatory networks from meta-analysis of the hematopoietic stem cell tree</i>	Alex Salazar, TU Delft <i>Evolution of genome architecture in bacteriophages during host-adaptation</i>	Mateusz Kuzak, DTL/ELIXIR-NL <i>Lesson development for Open Source Software best practices adoption</i>	
12:20	Sanne Abeln, VU (CHAIR) <i>Bioinformatics for biomedicine - like looking for a needle in a haystack?</i>	Martina Kutmon, Maastricht University (CHAIR) <i>Beyond Pathway Analysis: Identification of Active Subnetworks in Rett Syndrome</i>	Daniel Garza, UU (INVITED) <i>Interpreting microbes in their environments with metabolic models</i>	Celia van Gelder, DTL/ELIXIR-NL (Chair) <i>Capacity building in FAIR data stewardship in the Netherlands</i>	
12:45	LUNCH POSTER & DEMO SESSION II				CENTRAL HALL
14:00	BREAKOUT SESSIONS:	Metagenomics for business (BIUP)	Predicting biophysical characteristics of proteins from their sequence	Practical FAIR research data management	SPARQLing Biology; a beginners course
15:30	COFFEE BREAK WITH EXHIBITORS				CENTRAL HALL
16:00	BIO SB YOUNG INVESTIGATOR AWARD 2019: Eva Brinkman, Karolinska Institute, Scifilab <i>Quantitative assessment of genome editing</i>				ROOM EUROPA
16:45	KEYNOTE: Eran Segal , Weizmann Institute of Science <i>Personalizing treatments using microbiome and clinical data</i>				ROOM EUROPA
17:30	AWARDS & CLOSING REMARKS				ROOM EUROPA
17:45	END OF THE PROGRAM				