

TUESDAY, MAY 15

	ROOM EUROPA	ROOM AZIE	ROOM AFRIKA	ROOM AMERIKA	ROOM 4&5	
8:30	CONFERENCE REGISTRATION					Central Hall
9:30	OPENING					ROOM EUROPA
9:45	KEYNOTE Chiara Dalla Man , University of Padova <i>Modeling as a Tool to Understand Glucose Regulatory System in Humans</i>					
10:30	COFFEE BREAK WITH EXHIBITORS					
	GENOMICS	METABOLIC MODELLING	RNA & PROTEIN DIVERSITY	ELIXIR-NL: FAIR DATA I	TOOLS & RESOURCES	
11:00	Marleen Balvert (INVITED) <i>An image representation based convolutional network for DNA classification</i>	Michael Lenz (INVITED) <i>Modelling the influence of adipose tissue free fatty acid and amino acid metabolism on plasma glucose regulation</i>	Simon van Heeringen (INVITED) <i>Regulatory remodeling in the allo-tetraploid frog <i>Xenopus laevis</i></i>	Jaap Heringa ELIXIR-NL	Martina Kutmon (INVITED) <i>Understanding molecular mechanisms using biological pathway and network analysis</i>	
11:25	Leen Stougie <i>Full-length de novo viral quasispecies assembly through variation graph construction</i>	Linda Thijssen <i>A physiology based glucose-insulin-GLP-1 model: explaining changes observed after Roux-en-Y gastric bypass</i>	Aridaman Pandit <i>Clusters of T cell clones persist spatially and temporally in immune responses</i>	Saskia Hiltemann <i>myFAIR Analysis: Personal FAIR Data Management and Analysis</i>	Peter van 't Hof <i>Fast and complex genomics variant analysis using Apache Spark to enable digenic inheritance discoveries</i>	
11:45	Patrick Deelen <i>Improving diagnostic yield of exome-sequencing through prioritization of genes with predicted HPO assignments</i>	Nhung Pham <i>Genome-scale constraint-based metabolic modeling and analysis of <i>Cryptococcus curvatus</i></i>	Malgorzata Komor <i>Proteogenomic analysis of alternative splicing: Protein isoforms as biomarkers for early detection of colorectal cancer</i>	Hindrik Kerstens <i>Towards a FAIR biobanking and genomics eco-system for both diagnostic and research purposes</i>	Mihai Lefter <i>Enabling HGVS Standardisation on a Genomic Scale</i>	
12:05	Dick de Ridder (CHAIR) <i>Practical pangenomics for plants</i>	Bas Teusink (CHAIR) <i>Understanding the regulation of yeast metabolism under dynamic conditions</i>	Martijn Huynen (CHAIR) <i>Systematic alignment and comparison of complexome profiles to uncover remodeling of mitochondrial complexes in congenital disease</i>	Wasin Poncheewin <i>NG-Tax 2.0: 16S rRNA amplicons analysis through semantic framework using FAIR principles</i>	Andrew Stubbs (CHAIR) <i>Scalable OMICS Analysis & Reporting (SOAR): An open and FAIR framework for translational and clinical research</i>	
12:30	LUNCH: Exhibitors and Poster viewing					CENTRAL HALL
	BioSB MEMBER ASSEMBLY					ROOM AZIE
	YoungCB ASSEMBLY					ROOM AFRIKA
	HotTopics: SINGLE MOLECULE SEQUENCING					ROOM EUROPA
13:30	Christian Gilissen (INVITED) , RUMC <i>Long-read sequencing – for detecting clinically relevant structural variation</i>					
14:00	Jasper Linthorst (INVITED) , VUMC / TU Delft <i>Graph-based comparison of multiple de-novo assembled genomes</i>					
14:15	Natasja de Groot (INVITED) , Biomedical Primate Research Center <i>PacBio SMRT sequencing of multigene families MHC and KIR</i>					
14:30	Alexander Wittenberg (INVITED) , KeyGene <i>Nanopore sequencing accelerating crop innovation</i>					
	GENETIC VARIANTS & POPULATION GENETICS	INTEGRATION OF OMICS DATA	REGULATION & SIGNALLING	ELIXIR-NL: FAIR DATA II		
14:45	Rob ter Horst (INVITED) <i>Intra-individual and inter-individual variation in immune responses</i>	Martijn van den Heuvel (INVITED) <i>Principles of wiring of the human connectome</i>	Federica Eduati (INVITED) <i>Combining microfluidics and mathematical modelling for prioritisation of personalised cancer treatments from patient biopsies</i>	Friederike Ehrhart <i>The method and added value of integrating genetic variation data for rare diseases from multiple databases</i>		
15:10	Kyoko Watanabe <i>A global view of genetic architecture and pleiotropy in human complex traits</i>	Dieter Stoker <i>Bayesian data integration to predict novel genes involved in the MHC pathway</i>	Olga Ivanova <i>A framework for exhaustive simulation of epistatic patterns using Petri net models</i>	Jasper Koehorst <i>SAPP: functional genome annotation and analysis through a semantic framework using FAIR principles</i>		
15:30	Ehsan Motazed <i>Family based haplotype estimation using DNA sequence reads</i>	Nanne Aben <i>iTOP: inferring topologies between omics data</i>	Bram Thijssen <i>Delineating signaling activity using feedback-Inference of Signaling Activity</i>	Niels Zondervan <i>FAIR Data Management in Life-Sciences</i>		
15:50	Sara Pulit (CHAIR) <i>Large-scale genome-wide association studies and fine-mapping in obesity and fat distribution traits</i>	Michiel Adriaens (CHAIR) <i>Multi-omics from single omics: putting the squeeze on RNA-seq data</i>	Vera van Noort (CHAIR) <i>Understanding Post-translational modifications</i>	Marc Galland <i>Building a community of practice in scientific programming for life scientists</i>		
16:15	COFFEE BREAK WITH EXHIBITORS					CENTRAL HALL
16:45	KEYNOTE: Martin Kircher , Berlin Institute of Health <i>Interpretation of human genetic variation across the genome</i>					ROOM EUROPA
17:30	GROUP PHOTO (Main Entrance De Wereld)					
17:45	POSTER & DEMO SESSION I (INCL. DRINKS)					CENTRAL HALL
19:15	BioSB CONFERENCE DINNER					RESTAURANT
21:00	PUB QUIZ (ORGANIZED BY: YoungCB)					BAR
22:30	LIVE MUSCI (Blazing Harrows)					BAR

WEDNESDAY, MAY 16

	ROOM EUROPA	ROOM AZIE	ROOM AFRIKA	ROOM AMERIKA	ROOM 4&5
7:00	MORNING RUN				
9:00	CONFERENCE REGISTRATION				
9:30	KEYNOTE: Jason Locasale , DUKE University <i>Quantitative approaches to understanding metabolism in cancer</i>				
10:15	COFFEE BREAK WITH EXHIBITORS				
	PERSONALIZED MEDICINE	NETWORK BIOLOGY	METABOLOMICS (NETHERLANDS METABOLOMICS CENTER) CHAIR: Merlijn van Rijswijk	ELIXIR-NL: AGRIFOOD DATA CONCEPTS & APPLICATIONS CHAIR: Willem-Jan Knibbe	MICROBIOME & ECOSYSTEMS
10:45	Rianne de Vries (INVITED) <i>BreathCloud: Exhaled breath analysis as a companion diagnostic for therapy stratification</i>	Janine Post (INVITED) <i>Network modeling in cartilage disease</i>	Tim Ebbels (INVITED) <i>Integrating Metabolomics and Other Omics Data: Chemometric and Network Tools</i>	Sjaak Wolfert <i>DATA-FAIR – value creation by data sharing in agri-food business</i>	Bas Dutilh (INVITED) <i>Viral metagenomics</i>
11:10	Agnieszka Wegrzyn <i>Phenylketonuria: modeling cerebral amino acid and neurotransmitter metabolism</i>	Thierry Mondeel <i>ChIP-exo analysis highlights Fkh1 and Fkh2 transcription factors as hubs that integrate multi-scale networks in budding yeast</i>	Erik van den Akker <i>BBMRI-NL: a vast resource of 1H-NMR metabolomics data and algorithms for approaches in personalized medicine</i>	Jan Top <i>Handling the complexity of personalised dietary guidance</i>	Bastiaan von Meijefeldt <i>Robust taxonomic classification of 'dark' microbial sequences and bins with CAT and BAT</i>
11:30	Evert Bosdriesz <i>Comparative network reconstruction to identify selective anti-cancer drug combinations</i>	Samar Tareen <i>Modelling Cellular Metabolic Flexibility</i>	Huub Hoefsloot (INVITED) <i>The statistical analysis of metabolomics time-series data</i>	Martijn Derks <i>Balancing selection for lethal recessives in pigs</i>	Johan van Heerden <i>Bacterial growth rate is disturbed by cell division and restored by adaptive resource management</i>
11:50	Anke-Hilse Maitland-van der Zee (CHAIR) <i>Personalized Medicine, optimizing health care for the individual patient</i>	Joana Gonçalves (CHAIR) <i>Deciphering gene regulation from temporal response and perturbation data</i>	Folkert Kuipers (INVITED) <i>TBD</i>	Frits van Evert <i>Combining data and models for decisions in precision agriculture</i>	Sasha Zhernakova (CHAIR) <i>Gut metagenomics: population studies</i>
12:15	LUNCH				
	POSTER & DEMO SESSION II				
13:30	BIUP INDUSTRY MEETING: COMMERCIAL APPLICATIONS OF DEEP LEARNING	PHENOTYPE DATA CAPTURE	QUANTITATIVE IMMUNOLOGY	MODELS OF LIFE: ISBE IN ACTION	60-MINUTE FAIRification OF A DATASET
	HotTopics: SINGLE CELL OMICS				
14:30	Stein Aerts (INVITED) , KU Leuven <i>Single-cell Gene Regulatory Networks</i>				
15:00	Monique van der Wijst , UMC Groningen <i>Personalized co-expression networks reveal genetic risk factors that change the regulatory wiring of cells</i>				
15:15	Marc Jan Bonder , EMBL-EBI <i>Genetic and epigenetic determinants of splicing variability in single cells</i>				
15:30	Philip Lijnzaad , Princess Máxima Center for Pediatric Oncology <i>Understanding pediatric oncology one cell at a time</i>				
15:45	COFFEE BREAK WITH EXHIBITORS				
16:15	YOUNG INVESTIGATOR AWARD 2018: Bram Thijssen , Netherlands Cancer Institute <i>Bayesian statistics for integrative, knowledge-based models of biological systems</i>				
16:15	KEYNOTE: Alexander van Oudenaarden , Hubrecht Institute-KNAW / UMC Utrecht / Utrecht University <i>Whole-organism clone-tracing using single-cell sequencing</i>				
17:30	AWARDS & CLOSING REMARKS				
17:45	END OF THE PROGRAM				

Up-to-date information available on the conference app