TUESDAY, MAY 15

ROOM EUROPA

8:30 CONFERENCE REGISTRATION

9:30 OPENING

9:45 KEYNOTE: Chiara Dalla Man, University of Padova

Modeling as a Tool to Understand Glucose Regulatory System in Humans

10:30 COFFEE BREAK WITH EXHIBITORS

11:00 GENOMICS

Marleen Balvert (INVITED)
An image representation based convolutional network for DNA classification

Michael Lens (INVITED)
Modeling the influence of adipose tissue free fatty acid and amino acid metabolism on plasma glucose regulation

Simon van Heeringen (INVITED)
Regulatory remodeling in the allo-tetraploid frog Xenopus laevis

Jaap Herenga
ELIXIR-NL

Saskia Hiltemann
myFAIR Analysis: Personal FAIR Data Management and Analysis

Martina Kutmon (INVITED)
Understanding molecular mechanisms using biological pathway and network analysis

11:25 Leen Stougie
Full-length de novo viral quasispecies assembly through variation graph construction

Linda Thijssen
A physiology based glucose-insulin-GLP-1 model: explaining changes observed after Roux-en-Y gastric bypass

Aridaman Pandit
Clusters of T cell clones persist spatially and temporally in immune responses

Saskia Hiltemann
myFAIR Analysis: Personal FAIR Data Management and Analysis

Peter van ‘t Hof
Fast and complex genomics variant analysis using Apache Spark to enable aligicentric inheritance discoveries

11:45 Patrick Deelen
Improving diagnostic yield of exome-sequencing by prioritization of genes with predicted HPO assignments

Nhung Pham
Genome-scale constraint-based metabolic modeling and analysis of Cryptococcus curvatus

Malgorzata Komor
Proteogenomic analysis of alternative splicing: Protein isoforms as biomarkers for early detection of colorectal cancer

Hindrik Kerstens
Towards a FAIR biobanking and genomics eco-system for both diagnostic and research purposes

Mihai Lefter
Enabling HEVS Standardisation on a Genomic Scale

12:05 Dick de Ridder (CHAIR)
Practical pangenomics for plants

Bas Teusink (CHAIR)
Understanding the regulation of yeast metabolism under dynamic conditions

Martijn Huynen (CHAIR)
Systematic alignment and comparison of complexome profiles to uncover remodeling of mitochondrial complexes in congenital disease

Wasin Poncheewin
NG-Tag 2.0: 16S rRNA amplicons analysis through semantic framework using FAIR principles

Andrew Stubbs (CHAIR)
Scalable OMICS Analysis & Reporting (SOAR): An open and FAIR framework for translational and clinical research

12:30 LUNCH: Exhibitors and Poster viewing

13:00 HotTopics: SINGLE MOLECULE SEQUENCING

13:10 Christian Gilsen (INVITED), UMC
gap-cloning for life-science applications

13:40 Jasper Lintinhorst (INVITED), VUMC / TU Delft
Graph-based comparison of multiple de novo assembled genomes

14:15 Natasha de Groot (INVITED), Biomedical Primate Research Center
PacBio SMRT sequencing of multigene families MHC and KIR

14:30 Alexander Wittenberg (INVITED), KeyGene
Nanoarray sequencing accelerating crop innovation

14:45 GENETIC VARIANTS & POPULATION GENETICS

Rob ter Horst (INVITED)
Intra-individual and inter-individual variation in immune responses

Martin van den Heuvel (INVITED)
Principles of wiring of the human connectome

Takuma Kohto
Drift in allelic expression of SNPs

Elke Ravnik
The method and added value of integrating genetic variation data for rare diseases from multiple databases

15:10 Kyoko Watanabe
A global view of genetic architecture and pleiotropy in human complex traits

Dieter Stoker
Bayesian data integration to predict novel genes involved in the MHC pathway

Olga Ivanova
A framework for exhaustive simulation of epistatic patterns using Petri net models

Jasper Koehorst
SAPP: functional genome annotation and analysis through a semantic framework using FAIR principles

15:30 Elsien Motazed
Family based haplotype estimation using DNA sequence reads

Nanne Aben
IOTP: inferring topologies between omics data

Bram Thijssen
Delineating signaling activity using feedback-Inference of Signaling Activity

Niels Zonderman
FAIR Data Management in Life-Sciences

15:50 Sara Pult (CHAIR)
Large-scale genome-wide association studies and fine-mapping in obesity and fat distribution traits

Michiel Adriaens (CHAIR)
Multi-omics from single omics: putting the squeeze on RNA-seq data

Vera van Noort (CHAIR)
Understanding Post-translational modifications

Marc Galland
Building a community of practice in scientific programming for life scientists

16:15 COFFEE BREAK WITH EXHIBITORS

16:45 KEYNOTE: Martin Kircher, Berlin Institute of Health
Interpretation of human genetic variation across the genome

17:30 GROUP PHOTO (Main Entrance De Wereld)

18:00 POSTER & PUBLICATIONS RECEPTION (HOT DRINKS)

19:15 BioSB CONFERENCE DINNER

21:00 PUB QUIZ (ORGANIZED BY: YoungCB)

22:30 LIVE MUSIC (Blazing Harrows)

Up-to-date information available on the conference app
### Room Europa, May 16

#### 7:00
- **Morning Run**

#### 9:00
- **Conference Registration**
  - Central Hall
  - Room Europa

#### 9:30
- **Keynote:** Jason Locasale, Duke University
  - Quantitative approaches to understanding metabolism in cancer

#### 10:15
- **Coffee Break with Exhibitors**

#### 10:45
- **Personalized Medicine**
  - Rianne de Vries (Invited)
  - BreathCloud: Exhaled breath analysis as a companion diagnostic for therapy stratification

- **Network Biology**
  - Janine Post (Invited)
  - Network modeling in cartilage disease

- **Metabolomics**
  - Tim Ebbels (Invited)
  - Integrating Metabolomics and Other Omics Data: Chemometric and Network Tools

- **Elixir-NL: AgriFood Data Concepts & Applications**
  - Sjaak Wolfert
  - DATA-FAIR – value creation by data sharing in agri-food business

- **Microbiome & Ecosystems**
  - Bas Dutilh (Invited)
  - Viral metagenomics

#### 11:10
- **Phenylketonuria**
  - Janine Post (Invited)
  - Network modeling in cartilage disease

- **Network Modeling**
  - Thierry Mondeel
  - ChIP-exo analysis highlights Fkh1 and Fkh2 transcription factors as hubs that integrate multi-scale networks in budding yeast

- **ELIXIR-NL:**
  - Erik van den Akker
  - BBMRI-NL: a vast resource of 1H-NMR metabolomics data and algorithms for approaches in personalized medicine

- **Microbiome & Ecosystems**
  - Jan Top
  - Handling the complexity of personalized dietary guidance

- **ELIXIR-NL:**
  - Bastiaan van Meijenfeldt
  - Robust taxonomic classification of ‘dark’ microbial sequences and bins with CAT and BAT

#### 11:30
- **Rianne de Vries (Invited)**
  - BreathCloud: Exhaled breath analysis as a companion diagnostic for therapy stratification

- **Samar Tareen**
  - Comparative network reconstruction to identify selective anti-cancer drug combinations

- **Joanna Goñalves (Chair)**
  - Deciphering gene regulation from temporal response and perturbation data

- **Frits van Evert**
  - Combining data and models for decisions in precision agriculture

- **Martijn Derks**
  - Balancing selection for lethal recessives in pigs

- **Folkert Kuipers (Invited)**
  - The statistical analysis of metabolomics time-series data

- **Sasha Zhernakova (Chair)**
  - Gut metagenomics: population studies

- **Evert Bosdriesz**
  - Comparative network reconstruction to identify selective anti-cancer drug combinations

- **Sjoaak Wolfert**
  - DATA-FAIR – value creation by data sharing in agri-food business

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- **Johan van Heerden**
  - Bacterial growth rate is disturbed by cell division and restored by adaptive resource management

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  - Gut metagenomics: population studies

#### 11:50
- **Anke-Hilse Maitland-van der Zee (Chair)**
  - Personalized Medicine, optimizing health care for the individual patient

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  - Deciphering gene regulation from temporal response and perturbation data

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#### 12:15
- **Lunch**

#### 13:30
- **Bioup Industry Meeting: Commercial Applications of Deep Learning**

- **Phenotype Data Capture**

- **Quantitative Immunology**

- **Models of Life: iSBE in Action**

- **60-Minute Fairification of a Dataset**

#### 14:30
- **Stein Aerts (Invited), KU Leuven**
  - Single-cell Gene Regulatory Networks

- **Monique van der Wijst, UMC Groningen**
  - Personalized co-expression networks reveal genetic risk factors that change the regulatory wiring of cells

- **Marc Jan Bonder, EMBL-EBI**
  - Genetic and epigenetic determinants of splicing variability in single cells

- **Philip Lijnzaad, Princess Maxima Center for Pediatric Oncology**
  - Understanding pediatric oncology one cell at a time

#### 15:45
- **Coffee Break with Exhibitors**

#### 16:15
- **Young Investigator Award 2018:** Bram Thijssen, Netherlands Cancer Institute
  - Bayesian statistics for integrative, knowledge-based models of biological systems

- **Keynote:** Alexander van Oudenaarden, Hubrecht Institute-KNAW / UMC Utrecht / Utrecht University
  - Whole-organism clone-tracing using single-cell sequencing

#### 17:30
- **Awards & Closing Remarks**

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*Up-to-date information available on the conference app*