Gene Regulation and Novel Tools for Transcriptional Profiling

Leuven, 9 May 2017

Scientific committee
Stefaan Derveaux (VIB Nucleomics Core Facility)
Matthew Holt (VIB-KU Leuven Center for Brain and Disease Research)
Bernard Thienpont (VIB-KU Leuven Center for Cancer Biology)
Mark Veugelers (VIB Technology Watch team)

09h30-09h35 Welcome

SESSION 1: TOPIC 1: TRANSCRIPTION FACTOR NETWORKS

09h35-10h10 Zeynep Kalender Atak, VIB-KU Leuven Center for Brain and Disease Research, BE
Suggested title: i-cisTarget: cis-regulatory enrichment analysis in human, mouse and fly

10h10-10h45 Pieter De Bleser, VIB-UGent Center for Inflammation Research, BE
Suggested title: RSAT (Regulatory Sequence Analysis Tools)

10h50-11h15 Coffee

SESSION 2: TOPIC 2: EPIGENETICS

11h15-11h50 Dieter Weichenhan, Div. of Epigenomics and Cancer Risk Factors, DKFZ, Heidelberg, DE
The pros and cons of DNA methylome analysis methods

11h50-12h25 Simon Andrews, Babraham Institute, GB
BS-Seq data processing, visualization and exploration

12h25-13h30 Lunch

SESSION 3: TOPIC 3: (POST)TRANSCRIPTIONAL REGULATION

13h30-14h05 Frederik Coppens, VIB-UGent Center for Plant Systems Biology, BE
Suggested title: General overview of RNA-Seq and transcriptional landscape

14h05-14h40 Christoph Koenig, Pacific Biosciences, US
Suggested title: Iso-seq or RNA-seq: Analysis of intronic and exonic reads in RNA-seq data characterizes transcriptional and post-transcriptional regulation

14h40-15h15 Marco-Antonio Mendoza-Parra, IGBMC, FR
Exploring chromatin regulation by ChIP-Sequencing: From datasets quality assessment, enrichment patterns identification and multi-profiles integration, to the reconstitution of gene regulatory wires describing biological systems behavior

15h15-15h45 Coffee

SESSION 4: TOPIC 4: SINGLE-CELL GENE EXPRESSION

15h45-16h20 Joakim Lundeberg, SciLife, SE
Spatial Single-Cell Transcriptomics

16h20-16h55 Juozas Nainys, Institute of Biotechnology, Vilnius University, Vilnius, LT
High throughput single-cell RNAseq using droplet microfluidics