

09:00 – 10:15 Parallel Working Group Sessions

- I. Assay Standards and Quality Control
Martin Hirst (BCGSC)
- II. Bioethics
Yann Joly (McGill)

*10:15 – 10:45 Coffee break***10:45 – 12:00 Parallel Working Group Sessions**

- III. Data Eco-system & Integrative Analysis
Paul Flicek (EMBL-EBI) & Guillaume Bourque (McGill)
- IV. Communication
Stephanie Weber (Eurice)

*12:00 – 13:00 Lunch***13:00 – 13:15 Welcome & General Remarks**

Eric Marcotte (Chair of IHEC Executive Committee, CIHR)

Country Updates

- 13:15 – 13:35 CANADA – Paul Lasko (CIHR), Martin Hirst (BCGSC)
- 13:35 – 14:00 EU – Tomasz Dylag (EC), Philip Rosenstiel (IKMB/SYSCID), Maja Jagodic (KI/MultipleMS)
- 14:00 – 14:05 GERMANY – Jörn Walter (Saarland University)
- 14:05 – 14:15 HONG KONG – Danny Leung (HKUST)
- 14:15 – 14:20 JAPAN – Toshikazu Ushijima (NCC)
- 14:20 – 14:35 SINGAPORE – Shyam Prabhakar (GIS)
- 14:35 – 14:40 SOUTH KOREA – Suman Lee (KNIH)
- 14:40 – 14:45 USA – John Satterlee (NIH)
- 14:45 – 15:00 USA 4D Nucleome – Lisa Chadwick (NIH)
- 15:00 – 15:15 USA ENCODE – Mike Pazin (NIH)
- 15:15 – 15:30 Global Alliance for Genomics and Health – Paul Flicek (EMBL-EBI)

*15:30 – 15:40 Photo session**15:40 – 16:10 Coffee break***Working Group Updates**

- 16:10 – 16:20 Assay Standards and Quality Control – Martin Hirst (BCGSC)
- 16:20 – 16:30 Bioethics – Yann Joly (McGill)
- 16:30 – 16:40 Data Eco-system – Paul Flicek (EMBL-EBI)
- 16:40 – 16:50 Integrative Analysis – Guillaume Bourque (McGill)
- 16:50 – 17:00 Communication – Stephanie Weber (Eurice)
- 17:00 – 18:00 **Future of IHEC** – Eric Marcotte (CIHR), Martin Hirst (BCGSC)
Human Cell Atlas (John Marioni, EMBL-EBI), HubMAP (Ananda Roy, NIH)

18:00 – 19:00 ISSC**09:00 – 09:15 Opening Remarks**

IHEC (Eric Marcotte, Chair of IHEC Executive Committee, CIHR, Canada)
DEEP (Jörn Walter, Coordinator of DEEP, Saarland University)

09:15 – 10:30 Single Cell Analysis

Reversing Epigenetic Silencing
Amanda Fisher, Imperial College London, UK
Mammalian DNA methylation landscapes and human cancers
Alexander Meissner, MPI for Molecular Genetics, DE
Towards single cell sequencing of whole animals
Nikolaus Rajewsky, MDC Berlin, DE

*10:30 – 11:00 Coffee break***11:00 – 11:50 Computational Epigenetics**

Transposable elements in normal and cancer epigenome
Ting Wang, Washington University, US
Single cell epigenomics
Amos Tanay, Weizmann Institute, IS

11:50 – 12:05 Selected Short Talk

Systematic mapping of chromatin state landscapes during mouse embryonic development
David Gorkin, UCSD, US

12:05 – 12:35 Rapid Fire Talks

DNA methylation as epigenetic marker of normal and malignant cell differentiation in BLOOD
Angelika Merkel, CNAG-CRG, ES

Understanding developmental programming using tissue-level transcriptome combinatorics and single-cell RNA-seq
Peng He, Caltech, US

Sex-specific gene regulation in immune cells
Daniel Rico, Newcastle University, UK

Cohesin loss eliminates all loop domains, leading to links among superenhancers and downregulation of nearby genes
Suhay Rao, Stanford University, US

Integrative analysis defines gene-specific regulatory elements
Florian Schmidt, Saarland University, DE

Comparative analysis of DNaseI, ATAC, and NOMe-seq experiments reveals DNA sequence and structure-specific biases
Marcel Schulz, Saarland University, DE

SCIENCE DAY 1

Friday, October 13, 2017

12:35 – 14:30 Lunch & Poster session**14:30 – 15:20 Computational Epigenetics***Cell-type heterogeneity and deconvolution algorithms in EWAS*

Andrew E. Teschendorff, UCL London, UK

Epigenetic networks and recognition of regulatory elements

Martin Vingron, MPI for Molecular Genetics, DE

15:20 – 16:00 Coffee break**16:00 – 17:45 Epigenomics in Biology & Medicine***Personal Regulome Navigation*

Howard Y. Chang, Stanford University, US

Understanding circulating DNA through epigenomics

Yuk Ming Dennis Lo, CUHK, CN

Epigenetic signatures of chronic inflammation: lessons from the intestinal barrier

Philip Rosenstiel, IKMB, DE

The challenge of harmonizing data access agreements for IHEC

Yann Joly, McGill University, CA

17:45 – 18:45 EXEC**20:00** Conference dinner

SCIENCE DAY 2

Saturday, October 14, 2017

09:00 – 10:15 Epigenomics in Biology & Medicine*Insights into the role of the chromatin associated factor ATRX*

Doug Higgs, University of Oxford, UK

Autoimmune disease gene discovery by integrated analysis of genetic and epigenetic data

Chris Cotsapas, YSM, US

Personalized and cell-specific network-based pathway analysis of multiple sclerosis associated genomic regions

Sergio E. Baranzini, UCSF, US

Shaping chromatin in the nucleus, the bricks and the architects

Geneviève Almouzni, Curie Institute, FR

10:15 – 10:45 Coffee break

SCIENCE DAY 2

Saturday, October 14, 2017

10:45 – 12:00 Spatial Organisation of the Genome*Genome Architecture Mapping: discovering chromatin contacts in rare cell types*

Ana Pombo, MDC Berlin, DE

3-D genome reconfiguration in brain development and disease

Jennifer Phillips-Cremins, Penn, US

High-resolution TADs reveal DNA sequences underlying genome organization in flies

Fidel Ramírez, MPI of Immunobiology and Epigenetics, DE

12:00 – 12:30 Selected Short Talks*IHEC Data Portal 2017 update*

David Bujold, McGill University, CA

Histone Acetylome-Wide Association Study of Host Response to Tuberculosis

Shyam Prabhakar, Genome Institute of Singapore, SG

12:30 – 12:45 Rapid Fire Talks*Integrative analysis of single cell expression data reveals distinct regulatory states in bidirectional promoters*

Fatemeh Behjati, Saarland University, DE

Discovery of two identities of neuroblastoma cells via the analysis of super-enhancer landscapes

Valentina Boeva, Inserm, FR

Genome-wide Identification of Cardiac-specific Enhancers and Regulatory Variants in Heart Failure

Eleanor Wong, Genome Institute of Singapore, SG

12:45 – 14:30 Lunch & Poster session**14:30 – 15:45 Functional Epigenomics***Defining neocortical cell types and enabling genetic access to them through single cell transcriptomics and epigenetics*

Bosiljka Tasic, Allen Institute, US

Linking epigenetic identity changes to metabolic adaptation in breast cancer

Mathieu Lupien, Princess Margaret Cancer Centre, CA

Epigenomic analysis identifies an altered function of AGXT in non-alcoholic fatty liver disease (NAFLD) and a link to kidney stone disease

Cristina Cadenas, IfADO, DE

15:45 – 16:15 Coffee break**16:15 – 17:05 Functional Epigenomics***Dissecting cancer biology with reprogramming technology*

Yasuhiro Yamada, CiRA, JP

DEEP analysis of human epigenomes

Jörn Walter, Saarland University, DE

17:05 – 18:00 Conclusions & End of Meeting