

# DRAFT PROGRAM | THURSDAY 13 FEBRUARY

08:45 - 09:10 Registration & coffee

09:10 - 09:15 Welcome

## Session 1

### MICROBIAL & PLANT GENOMICS: FROM SIMPLE TO COMPLEX

Chair: TBD

09:15 - 09:20 Introduction by session chair

09:20 - 09:55 Strain tracking with metagenomics to understand pathogen transmission  
**Nick Loman**, *Institute of Microbiology and Infection, University of Birmingham, UK*

09:55 - 10:30 The origin of complex cells  
**Thijs Ettema**, *Wageningen University, NL*

10:30 - 11:00 Coffee break

11:00 - 11:35 Confounder-aware systems medical approaches  
**Sofia Forslund**, *Experimental and Clinical Research Centre (ECRC, a joint venture of the Max Delbrück Center for Molecular Medicine and the Charité University Hospital), DE*

11:35 - 12:10 The genomes of human civilization  
**Klaus Mayer**, *Plant Genome and Systems Biology, Helmholtz Center Munich, DE*

12:10 - 12:45 Linking sequence and variation in large graphical pangenomes  
**Erik Garrison**, *University of California, Santa Cruz, US*

12:45 - 13:30 Lunch

13:30 - 14:30 Poster Session

## Session 2

### PROTEIN BIOINFORMATICS

Chair: TBD

14:30 - 14:35 Introduction by session chair

14:35 - 15:10 Charge regulation in intrinsically disordered proteins  
**Rohit Pappu**, *Washington University in St. Louis, US*

15:10 - 15:45 Studies of context-specific cell signalling  
**Evangelia Petsalaki**, *EMBL-EBI, UK*

15:45 - 16:00 *Selected Talk:* Title  
**Speaker selected from abstracts 1**, *Affiliation*

16:00 - 16:30 Coffee break

16:30 - 17:05 Statistical methods for mass spectrometry and proteomics  
**Olga Vitek**, *Northeastern University, US*

17:05 - 17:40 Probabilistic mapping of the sub-cellular proteome  
**Laurent Gatto**, *De Duve Institute – UC Louvain, BE*

17:40 - 18:15 Extending the small molecule similarity principle to all levels of biology  
**Patrick Aloy**, *the Structural Bioinformatics and Network Biology lab, IRB Barcelona, ES*

18:15 - 19:00 Reception

19:00 - 19:45 Guided tour to the conference restaurant

20:00 - 22:30 Conference dinner

08:45 - 09:15 Welcome coffee

## Session 3

### DATA INTEGRATION, MACHINE LEARNING AND NETWORKS

Chair: TBD

- 09:15 - 09:20 Introduction by session chair
- 09:20 - 09:55 Ontologies in the wild  
**Helen Parkinson**, *EMBL-EBI, UK*
- 09:55 - 10:30 Regulatory network dynamics in developmental and evolutionary lineages  
**Sushmita Roy**, *Dept. of Biostatistics and Medical Informatics, Wisconsin Institute for Discovery, University of Wisconsin, US*
- 10:30 - 11:00 Coffee break
- 11:00 - 11:35 Matrix Factorization approaches for data integration. Towards better gene set and pathway analysis  
**Aedin Culhane**, *Dana-Farber Cancer Institute & Harvard TH Chan School of Public Health, US*
- 11:35 - 12:10 Interpretable machine learning approaches for understanding functional genomics in the human brain  
**Daifeng Wang**, *University of Wisconsin-Madison, US*
- 12:10 - 12:25 *Selected Talk: Title*  
**Speaker selected from abstracts 2**, *Affiliation, Country*
- 12:25 - 13:15 Lunch
- 13:15 - 14:15 Poster Session

## Session 4

### SINGLE CELL ANALYSIS BIOINFORMATICS

Chair: TBD

- 14:15 - 14:20 Introduction by session chair
- 14:20 - 14:55 The female reproductive atlas: one cell at a time  
**Roser Vento**, *Sanger Institute, UK*
- 14:55 - 15:30 Spatial and temporal transcriptomics reveal microglia-astroglia crosstalk in the amyloid- $\beta$  plaque cell niche of Alzheimer's disease  
**Ashley Lu**, *VIB-KU Leuven Center for Brain & Disease Research, BE*
- 15:30 - 15:45 *Selected Talk: Title*  
**Speaker selected from abstracts 3**, *Affiliation, Country*
- 15:45 - 16:15 Coffee break
- 16:15 - 16:30 *Selected Talk: Title*  
**Speaker selected from abstracts 4**, *Affiliation, Country*
- 16:30 - 17:05 Single-cell proteomics: From data, through models to understanding  
**Nikolai Slavov**, *Northeastern University, US*
- 17:05 - 17:15 Closing remarks