

Current Trends in Long Read Sequencing and Bioinformatics Analysis

3rd October 2024

Room HERGE, Campus Gasthuisberg, UZ Leuven

Introduction - Principles of Long Read Sequencing

- 8:30–9:00 **Registration**
- 9:00–9:10 **Welcome** - *Joris Vermeesch, KU Leuven*
- 9:10–9:50 **Long read sequencing: technology and applications**
Wouter Bossuyt, Genomics Core Leuven
- 9:50–10:20 **Introduction to long read data analysis**
Enora Ghelain and Alvaro Cortés, Genomics Core Leuven
- 10:20–10:50 **Analysis long read data at the Flemish Super Computer**
Erika Souche, KU Leuven and Alexander Vapirev, VSC

Structural Variation

- 11:00 - 11:40 **Keynote - Towards the detection of all classes of structural variation**
David Porubsky, University of Washington
- 11:40–11:55 **Structural variation I** - *Piet Maes, KU Leuven*
- 11:55–12:10 **S-Locus pear denovo assembly** – *Hanne Claessen, KU Leuven*

Biomedical applications

- 13:00–13:40 **Keynote - Long-read sequencing in rare disease**
Lars Feuk, Uppsala University
- 14:00–14:15 **Tandem repeats** - *Dale Annear, Antwerp U.*
- 14:15–14:30 **Tandem repeat expansions in frontotemporal dementia**- *Wouter De Coster, Antwerp U.*
- 14:30–14:45 **Episignature in patients with developmental disorders**
Benjamin Huremagic, KU Leuven

Long Read Transcriptomes

- 15:00 – 15:40 **Keynote - Long read transcriptomics** - *Júlia Faura Llorens, Antwerp U.*
- 15:40 – 15:55 **Mapping the transcriptional architecture of bacterial viruses with ONT-cappable-seq** - *Maarten Boon, KU Leuven*
- 16:00 – 16:15 **Capturing short RNA molecules with long RNA sequencing technologies** - *Eva Novoa, U. Pompeu Fabra*
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- 16:15 – 16:30 **Your long read project. Questions and final words**
Genomics Core Team