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** - *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*

16:15 – 16:30	**Your long read project. Questions and final words** *Genomics Core Team*