

Long-Read Sequencing

April 3-4 2019; BMC Uppsala

Preliminary program

Day 1 April 3

April 3rd (*BMC lecture halls B8 and B10*)

8:30 – 8:55 Registration. **B10.**

Symposium in **B8:**

9:00 – 9:05 Welcome note.

9:05 – 9:25 What is the latest in Long-Read Sequencing technologies at NGI?

SESSION 1 – INTRODUCTION to technologies and research highlights. **B8.**

9:25 – 9:50 Company presentation: **10X Genomics.**

9:50 – 10:15 Company presentation: **Oxford Nanopore.**

10:15 - 10:40 Company presentation: **PacBio.**

10:40 – 11:00 Coffee break, **B10**

SESSION 1, continued: INTRODUCTION to technologies and research highlights. **B8.**

11:00 – 11:30 KEYNOTE SPEAKER - **Sonja Vernes**, Max Planck. *The Bat1K Project: Bat Genomes, Biology, and Implications.*

11:30 – 11:50 **Mohamed Zouine**, INRA/ENSAT. *Long DNA molecule sequencing: from de novo assembly to chromosome level scaffolding of the tomato and melon genomes.*

11:50 – 12:10 **Lucia Cavalier**, Uppsala University - Uppsala Academic Hospital. *Long read sequencing in clinical applications.*

12:10 - 13:15 LUNCH in **B10.**

SESSION 2: Human genomics & medicine, **B8**

13:15 – 13:45 KEYNOTE SPEAKER - **Alexander Hoischen**, Radboud UMC. *Medical genetics: Identification of hidden structural variants with long-read sequencing.*

13:45 – 14:05 **Yahya Anvar**, Leiden University Medical Center. *Long-reads paving the way to personalized therapeutics.*

14:05 – 14:25 **Ida Höijer**, UU. *New approaches for long-read targeted sequencing.*

14:25 – 14:45 **Wigard Kloosterman**, UM Utrecht. *Unraveling human genome structure using long-read Nanopore sequencing.*

14:45 – 15:15 Coffee, company booths open for presentations. **B10**.

SESSION 3: Non-model organisms & biodiversity, B8

15:15 – 15:45 KEYNOTE SPEAKER -**Kerstin Howe**, Sanger. *Sequencing the Tree of Life: The Sanger Darwin Project*

15:45 - 16:05 **Matt Webster**, Uppsala University. *A chromosome-level hybrid assembly of the honeybee genome.*

16:05 – 16:25 **Niklas Mähler**, Umeå University. *Long-read assembly of Norway spruce and Scots pine.*

16:25 – 16:45 **Åsa Sjöling**, KI. *SMRT analysis of plasmid gene content and methylation profiles within clonal lineages of enterotoxigenic Escherichia coli (ETEC).*

16:45 - 17:00 Closing statement

17:00 - 18:30 Mingle and bar. **B10**.

Day 2

April 4th (*Trippelrummet at Navet*)

9:00 – 9:05 Introduction to Day2 workshops.

Workshop 1: General analysis of Long-read data, company presentations

9:05 - 9:25 **Oxford Nanopore**, TBA

9:25 - 9:55 **PacBio**, **Armin Töpfer**

9:55 - 10:15 **10x**, TBA

10:15 - 10:35 Coffee break, Navet

Workshop 2: De novo assembly with long reads

10:35 - 11:05 KEYNOTE: **Kerstin Howe**, Sanger Institute. *Genome Assembly Validation: Common Assembly Issues and Strategies for Improvements.*

11:05-11:20 **SciLifeLab**, TBA. *Hybrid assembly of long-read data.*

11:20 - 11:35 **Academic presentation**, TBA

11:35 - 12:20 Panel discussion

12:20 - 13:20 Lunch and informal mingle

Workshop 3: Structural variation

13:20 - 13:50 KEYNOTE: **Alexander Hoischen**, Radboud UMC. *Application of long-read data for structural variation studies.*

13:50 - 14:05 **Academic presentation**, TBA

14:05 - 14:20 **SciLifeLab**, TBA.

14:20 - 15:00 Panel discussion.

15:00 - 15:10 Closing the event.