

From RNA-Seq data to bioinformatics analysis using Nanopore sequencers



Oxford

NANOPORE

Technologies



FRANCE GÉNOMIQUE

ASTER - Algorithms and software for third generation RNA sequencing

- Bonsai, CRIStAL, Lille
- Erable, LBBE, Lyon
- Institut Pasteur de Lille
- R&D Bioseq, Genoscope



10:45 - 11:30 James Platt (Oxford Nanopore), *Full length transcript sequencing of RNA and cDNA with Oxford Nanopore*

11:30 - 12:00 Jean-Marc Aury (Genoscope), *RNA sequencing with the MinION at Genoscope*

12:00 - 12:45 Laurent Jourdren and Sophie Lemoine (IBENS Paris), *One year of developments and collaborations around the MinION on the Genomic facility of the IBENS*

12:45 - 14:00 Lunch and open discussions

14:00 - 14:30 Quentin Carradec (Genoscope), *MinION on board of the Tara expedition*

14:30 - 15:00 Rayan Chikhi (CNRS, CRISAL, Lille) and Leandro Lima (ERABLE, Lyon), *A first look at error-correction tools on Nanopore RNA-seq data*

15:00 - 15:45 Hagen Tilgner (BRMI, Weill Cornell), *What genes are saying, not how much they talk*

15:45-16:30 Coffee break

16:30- 17:00 Vincent Lacroix (ERABLE, Lyon), *Identification and quantification of isoforms in RNAseq data: deep short reads Vs shallow long reads: initial answers and open questions*

17:00- 17:30 Camille Marchet (IRISA Rennes), *De novo Clustering of Gene Expressed Variants in Transcriptomic Long Reads Data Sets*