**Concepts and Main Aspects of RNA-Seq**

**25th, 28th and 29th April 2016**

**Wellcome Trust Centre for Human Genetics, Seminar Rooms A/B**

**Monday 25th April**

Introducing general principles of NGS and RNA-Seq in particular.

***Lectures***

9:30-10:00 Introduction to NGS (high-throughput sequencing, millions of short fragments)

10:00-10:45 Experimental design (choice of technology, replicates, sequencing depth, batch effects etc)

*10:45- 11:15 Morning Break (tea, coffee and biscuits will be provided)*

*11:15-12:00 Course discussion*

**Thursday 28th April** *full day (7h)*

Introducing bioinformatic analysis of RNA-Seq data.

Differential gene expression and pathway analysis.

***Lectures***

09:00-09:45 Introduction to RNA-Seq (capturing different types of RNA; polyA+ vs rRNA depletion; CAGE/SAGE; biases in RNA data (GC, length, sequencability bias; bias in different abundances). Quality control (fastqc, picard)

09:45-10:15 Alignment (split-read aligner vs DNA aligner; unique/probabilistic mappings; TopHat)

10:15-10:45 Transcript quantification. Data normalisation and QC.

*10:45-11:15 Morning Break (tea, coffee and biscuits will be provided)*

11:15-12:00 Differential gene expression analysis

12:00-12:45 Pathway analysis for biological interpretation, including practical demonstration

*12:45-13:30 Lunch break (note lunch is not provided but hot food/sandwiches are available on site)*

***Practicals***

13:30-15:30 Data QC and differential expression analysis using edgeR

*15:30-15:45 Afternoon Break*

15.45-16:30 Optional session to finish practical

**Friday 29th April**

Data visualisation, further RNA-Seq applications and new techniques.

***Lectures***

09:00-09:45 Visualization (UCSC, IGV; wiggle/bigwig/bed/bigbed files), including practical demonstration

09.45-10:30 Splicing analysis

10:30-10:45 *Morning Break (tea, coffee and biscuits will be provided)*

10:45-11:30 Cutting edge technologies

*10.45-10.55 Nanopore technology*

*10.55-11.05 Single cell technology*

*11.05-11.15 DropSeq*

*11.15-11.30 Q&A*

11:30-12:30 Single cell RNA sequencing

*11.30-12.00 Using single cell transcriptomics to understand cellular identity in iPSC-derived cortical neurons*

*12.00-12.30 Evaluating quality of single cell data*

12:30-13:30 *Lunch break (note lunch is not provided but hot food/sandwiches are available on site)*

Course organisers available for Q&A session

***Practicals***

13:30-15:30 Quality control (raw data and processed/cleaned data) and alignment.

*15:30-15:45 Afternoon Break*

15:45-16:30 Optional session to finish practical