Oxford Genomics CENTRE

UNIVERSITY OF OXFORD

RNA-Seq Data Analysis

7th - 8th June 2018

Organised by

WHG Bioinformatics Core

Helen Lockstone

Santiago Revale

Dr Eshita Sharma

Dr Ben Wright

wellcome centre human genetics

Course Format

- 2-day course with mixture of theory and practical sessions
- Previously run as taught module for the DPhil programme in Genomic Medicine and Statistics at WHG (opened out to Medical Sciences Division)
- High interest within WHG and good opportunity to initiate new interactions between researchers and Bioinformatics Core team – tell us about what you are working on!

Course Tutors

Helen Lockstone

Santiago Revale

Eshita Sharma

Ben Wright

Bioinformatics Core Group
http://www.well.ox.ac.uk/bioinformatics-statistical-genetics

Many years experience with sequencing data and particularly transcriptomics

Course Aims

- Introduce key steps of RNA-Seq analysis from raw data to biological interpretation of results
- Provide orientation and context to techniques, tools and developments in this diverse field
- Focus on practical aspects of dealing with data generated by an RNA-Seq experiment
  - Alignment and data formats
  - Checking data quality and characteristics
  - Understand how to use analysis packages appropriately

Course Outcomes

- Insight into RNA-Seq experiments and dealing with the data they generate
- Depending on background, may be a lot of new information to take in
  - Think of the broader messages of each session
  - Remember Bioinformatics Core can run any or all of the steps for you and help you get to the biological interpretation stage
  - Often helpful anyway for the early processing steps which are computationally intensive
- Some may be keen to develop computational biology skills, perhaps as part of DPhil or for new career opportunities
  - Be aware that is a considerable investment of time and effort if coming from non-computational background (but many benefits)
  - Once data processed to gene counts, can analyse using R on a laptop
- For those who are bioinformaticians themselves, gaining further knowledge and ability to analyse a new type of data