

RNA-Seq Data Analysis

26th – 27th November 2018

Organised by
WHG Bioinformatics Core

Helen Lockstone

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Course Tutors



Helen Lockstone



Santiago Revale

Many combined years experience with sequencing data and particularly transcriptomics – we and the rest of the team assist WHG researchers in a variety of ways



Eshita Sharma



Ben Wright

Bioinformatics Core Group

<http://www.well.ox.ac.uk/bioinformatics-statistical-genetics>

Course Format & Housekeeping

- Running as part of teaching for WHG's DPhil programme in Genomic Medicine & Statistics, opened out to other researchers at WHG and Medical Sciences Division
- 2-day course with theory followed by practical sessions on each key topic
- Informal and interactive - please ask questions!
- Register(s) to sign please
- Tea/coffee arriving at 11am, lunch break at around 12.30. We'll stick approximately to the outlined schedule, but adjust timings if needed
- If the fire alarm sounds, please heed and leave the building by the main entrance
- If you are not familiar with the building, toilets are located first corridor on your left as you walk back towards Reception

- Introducing RNA-Seq as a technique, steps and tools for processing and analysing the data, important considerations for experimental design and dealing with the resulting data
- Provide orientation and context to techniques, tools and developments in this diverse field
- Strong focus on practical aspects of dealing with data generated by an RNA-Seq experiment
 - Alignment and data formats
 - Checking data quality and characteristics
 - Understanding how to use analysis packages appropriately

What will you gain?

- Works at different levels:
 - A broad overview and introduction to sequencing and RNA-Seq to provide insight and information
 - Starting point for working with your own RNA-Seq data
 - Developing bioinformatics/computational biology skills, perhaps as part of DPhil or for new career opportunities
 - Skills in high demand – considerable investment of time and effort if coming from non-computational background but likely to be worthwhile
- How to get the most from this course (this will vary depending on background knowledge and experience):
 - It may be a lot of information to take in if you are new to this area
 - Extract the broader messages of each session, and don't worry too much about the details of commands and code
 - Remember Bioinformatics Core can run at least some of the steps for you
 - For bioinformaticians, ability to analyse a new type of data, useful refresher or augmenting knowledge