

RNA-Seq Data Analysis 27-28 November, 2017

Taught module for DPhil programme in
Genomic Medicine and Statistics

Organised by Bioinformatics Core at WHG:

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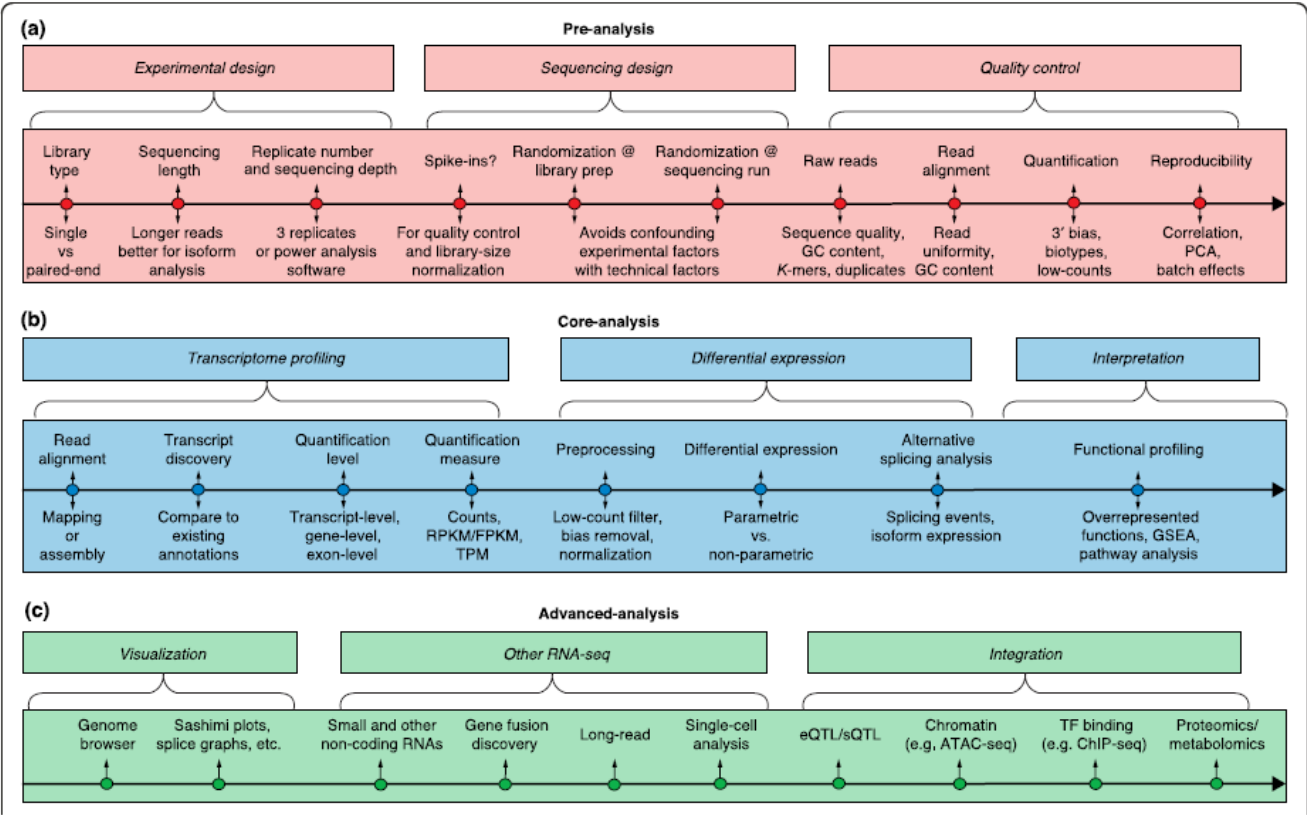


- Taught module for the DPhil programme in Genomic Medicine and Statistics, based at WHG
- 10 places advertised through MSDTC and 5 additional internal places (max 20)
 - Morning refreshments provided!
- New 2-day format with strong practical focus



A survey of best practices for RNA-seq data analysis

Ana Conesa^{1,2*}, Pedro Madrigal^{3,4*}, Sonia Tarazona^{2,5}, David Gomez-Cabrero^{6,7,8,9}, Alejandra Cervera¹⁰, Andrew McPherson¹¹, Michał Wojciech Szczesiak¹², Daniel J. Gaffney³, Laura L. Elo¹³, Xuegong Zhang^{14,15} and Ali Mortazavi^{16,17*}



- Introduce key steps of RNA-Seq analysis from raw data to biological interpretation of results
- Orientate attendees to resources, tools and developments in the 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

Any sensible pipeline will produce reasonable results

- Gene expression data are descriptive and require human decision-making to take the information further
 - What genes/pathways to focus follow-up experiments on?
 - Different researchers could easily identify quite different themes from the same results
 - Much of the data may end up un-used
- This step is highly subjective and probably far more variable than choice of tools for different processing steps!