

Presentation title: Analysing RNA-seq: from reads to results

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Abstract

High-throughput sequencing of the transcriptome leads to the production of millions of short reads which need to be analysed in order to make biological inference. RNA-seq data are complex and the analysis involves a series of steps for which research is ongoing. However the choice of analysis methodology can have a major impact on the findings of an experiment. In this talk I will outline the major steps involved in analysing an RNA-seq dataset. I will discuss and compare the available strategies for each stage of the pipeline. I will also point out several areas in RNA-seq data analysis which require further research in order for the full potential of the technology to be realised.