

Presentation title: Differential Expression Analysis RNA-Seq of Experiments

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Abstract

As the cost of sequencing continues to decrease, RNA-Seq becomes an ever more attractive platform for studying gene expression. A common goal is the discovery of genes that are differentially expressed between experimental conditions. The scale and nature of RNA-Seq data makes for many statistical challenges. We will discuss statistical approaches to rigorous DE analysis of RNA-Seq data to analyse multifactor RNA-Seq experiments while accounting for biological variation.