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*Statistical Analysis of RNA-Seq Data: A Comparison of Three R Packages*

Next generation sequencing of RNA (RNA-Seq) is a new tool which can be used for analysis of differential expression of genes. A number of R/Bioconductor packages have been developed in recent years to deal with such data. In this project we examine the performance of three widely used packages (DESeq, edgeR and DEGseq) on two datasets with biological replication and show that a Poisson model as used in DEGseq is not appropriate in the presence of biological replicates and that there is a lack of consistency between the other two methods even though their overall performance is similar.