

Introduction to RNA-Seq Analysis with R and Bioconductor

Abstract

Starting with raw sequencing data (FASTQ files), we will transform them into gene-level counts by aligning reads to a reference transcriptome and quantifying gene expression levels. We shall then perform exploratory data analysis to assess data quality and uncover relationships between samples. Finally we perform differential gene expression analysis to identify key genes and visualize the results effectively. All analyses shall be done using R and Bioconductor packages.