Bulk RNA-seq analysis using python (pyrpipe) and R (Rsubread)

Abstract

Bulk RNA sequencing analysis is a powerful technique for studying gene expression at the transcriptome level, allowing for the identification of differentially expressed genes between different conditions. This analysis typically involves several key steps: quality control, read alignment, quantification of gene expression, and differential expression analysis. Here, we present a comprehensive workflow for conducting bulk RNA-seq analysis using the pyrpipe library in Python and the Rsubread package in R.