

Simplifying RNA-seq with cloud computing approach

Abstract

The explosion of high-throughput RNA sequencing (RNA-seq) technologies has transformed our ability to investigate gene expression and regulatory mechanisms with unprecedented depth. However, the computational intensity and complexity of RNA-seq data analysis pose significant hurdles, particularly for researchers with limited access to powerful computational resources. In this presentation, we introduce a streamlined approach to RNA-seq analysis using cloud computing platforms like AWS. We demonstrate how cloud-based tools and services, such as FastQC, STAR, and DESeq2, can be seamlessly integrated to perform comprehensive RNA-seq data analysis, from initial quality control and alignment to differential expression analysis and visualization. This approach not only ensures high performance and reproducibility but also democratizes access to advanced computational resources.