RNA sequencing analysis) is a powerful technique used to study the transcriptome—the complete set of RNA transcripts produced by the genome under specific conditions. Here's a concise definition:

RNA-seq Analysis

RNA-seq analysis refers to the bioinformatic and statistical processing of RNA sequencing data to quantify, compare, and interpret gene expression levels across samples.

It involves:

Sequencing RNA transcripts (usually after converting to cDNA)

Mapping the reads to a reference genome or transcriptome

Quantifying expression levels of genes or transcripts

Detecting differentially expressed genes (DEGs) between conditions

Exploring alternative splicing, fusion transcripts, non-coding RNAs, and allele-specific expression

This method allows researchers to:

Identify genes involved in disease

Compare expression between cell types or treatments

Discover novel transcripts

1)

Tags: transcriptomics, gene expression, NGS, bioinformatics, differential expression

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1) RNA-seq is widely used in cancer biology, developmental studies, and personalized medicine

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Last update: **2025/07/06 16:51**