Transcriptomic analysis is the comprehensive study of all messenger RNA (mRNA) molecules transcribed from DNA in a cell or tissue at a specific time — collectively known as the transcriptome.

 Key Concepts Transcriptome: The full set of RNA transcripts (mainly mRNA) expressed by the genome under specific conditions.

Purpose: To understand gene expression patterns, identify disease markers, alternative splicing events, non-coding RNAs, or responses to treatments or environmental stimuli.

 Common Techniques RNA sequencing (RNA-seq): High-throughput sequencing of RNA to quantify gene expression levels.

Microarrays: Older method using hybridization to measure RNA abundance.

qRT-PCR: Quantitative real-time PCR used for targeted validation.

 Applications Cancer research: Identify oncogenes, tumor suppressor activity, or therapy targets.

Neuroscience: Understand cell-type-specific expression in brain regions.

Developmental biology: Track gene activity over time.

Pharmacogenomics: Study how drugs influence gene expression.

⚠ Limitations Sensitive to RNA quality and degradation.

Requires robust bioinformatics pipelines.

Interpretation may be confounded by cellular heterogeneity.

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