

Bulk **transcriptomes** refer to the collective **gene expression** profile of a population of **cells**, which is typically obtained through **RNA sequencing** (RNA-seq) analysis of a sample containing many thousands or even millions of cells. Bulk transcriptome analysis is a commonly used technique in **molecular biology** and **genetics** research to study the overall **gene expression** patterns and biological processes in a particular tissue or cell population.

The advantage of bulk transcriptome analysis is that it can provide a comprehensive view of the gene expression landscape within a specific cell type or tissue, and can identify differentially expressed genes and pathways associated with particular biological processes or disease states. However, it is important to note that bulk transcriptome analysis does not provide information on individual cell states or subpopulations, and may mask important heterogeneity within the cell population being studied.

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