

Transcriptomics consists of the mathematical, statistical and computing methods that aim to solve biological problems using nucleotides and amino acid sequences and related information. Transcriptomics is about searching biological databases, comparing sequences, looking at protein structure and more generally, asking biological question with a computer. Biological or genetic information is the fundamental concept of Transcriptomics. Transcriptomics, a genome-wide measurement of mRNA expression levels based on DNA microarray technology is one of the prominent fields of study. This is the term given to the set of all transcripts or messenger RNA (mRNA) molecules produced in cells. It can also be applied to the specific subset of transcripts present in a particular cell or the total set of transcripts in organism. **KEY FEATURES:** • Theoretical approaches, large number of examples and references. • Real application scenarios, such as transcriptome project that require the use of a whole set of drug design tools. • Illustrations help readers understand the research methodology easily. • Lists of Web resources of important research centers, institutes, and other sources of information.



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