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Abstract

Microarray technology allows for the simultaneously monitor of expression levels for thousands of genes or entire genomes. Diseases are often controlled by groups of genes, rather than individual ones. Association rule mining technique in data mining plays a vital role in the field of bioinformatics. In this paper, it has been proposed a novel approach for analysis of microarray gene expression profiling data. It discovers frequent patterns, expressions profiles using transcript expression intervals and extract significant relations among microarray genes. It is important to get efficient and important patterns to reveal fatal and crucial reasons for diseases. It provides improving prediction for diseases and treatment decisions for cancer

patients.

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Computer Science

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Keywords

Data Mining Gene Expression Analysis Frequent Pattern Mining Gene Expression Analysis Using Gene Intervals.