

## **A GRAPH CLUSTERING APPROACH TO IDENTIFY KEY GENES FROM MICROARRAY GENE EXPRESSION DATA**

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### **ABSTRACT**

To identify genes that play an important role in a disease is an important task. In this paper we proposed a method to identify key genes. For this first we analyze the genes based on their expression values using statistical technique and sort then in ascending order of their p-value. Then we construct gene regulatory network from microarray gene expression profile using correlation technique. In gene regulatory network construction, we take only those genes whose p-value is less than 0.01 and have the gene name. Thereafter we download the expression values of these genes in different samples. These expression values are further modified by applying Singular Value decomposition. The gene regulatory network is generated calculating interaction between genes using modified expression values. The interaction between filtered genes is calculated using correlation. Thereafter the graph is clustered by using Markov Cluster Algorithm and the gene corresponding to nodes of maximum degree for different value of parameter  $r$  is identified as key genes. Finally, validation of the result is done using existing literature.

**KEYWORDS:** Microarray Gene Expression, Gene Regulatory Network, Singular Value Decomposition, Latent Semantic Analysis, Markov Cluster Algorithm