



Fuzzy Mining Approach for Gene Clustering and Gene Function Prediction

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Abstract— Microarray technology helps biologists for monitoring expression of thousands of genes in a single experiment on a small chip. Microarray is also called as DNA chip, gene chip, or biochip is used to analyze the gene expression profiles. After genome sequencing, DNA microarray analysis has become the most widely used functional genomics approach in the bioinformatics field. Biologists are vastly overwhelmed by the enormous amount of unique qualities of genome-wide data produced by the DNA Microarray experiment. Clustering is the process of grouping data objects into set of disjoint classes called clusters so that objects within a class are highly other classes. Generating high-quality gene clusters and identifying the underlying biological mechanism of the gene clusters are the important goals of clustering gene expression analysis. It is presently the far most used method for gene expression analysis which provides a Fuzzy mining strategy to extract meaningful information from expression profile. In this paper we have used a fuzzy mining approach for Gene Clustering with using different membership function and dividing the available gene expression data for each type of experimental value with four variables for better accuracy. This approach can effectively capture heterogeneity in expression data for pattern discovery. Based on these patterns, it can make accurate Gene Function Predictions and these predictions can be made in such a way that each gene can be allowed to belong to more than one functional class with different degrees of membership.

Keywords— Microarray; Fuzzy Mining; Gene Function Clustering; Gene function Prediction

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