Abstract

Recent advances in the DNA microarray technology have provided the ability to examine and measure the expression levels of thousands of genes simultaneously in an organism. In this technology each gene is recorded under different conditions or each gene is evaluated under a single environment but in different types of tissues. In the first case it is used in identification of functionally related genes whereas the second type of technology is helpful in classification of different types of tissues and identification of those genes whose expression levels are good diagnostic indicators. Different approaches have been applied to classify different datasets. However, the main challenges in this task is the availability of a smaller number of samples compared to a huge number of genes and the noisy nature of biological data. This paper review on different techniques used to classify the genes and improved efficiency of biomarker identification due to these classifications.

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