Abstract

Diagnosis of cancer is one of the most emerging clinical applications in microarray gene expression data. However, cancer classification on microarray gene expression data still remains a difficult problem. The main reason for this is the significantly large number of genes present relatively compared to the number of available training samples. In this paper, a novel approach to feature extraction combining the statistical t-test and absolute scoring is proposed for achieving better classification rate. Suitable classification approaches using the linear Support Vector Machines, the Proximal Support Vector Machines and the Newton Support Vector Machines is also discussed. A comparative analysis on the different techniques for feature extraction is also presented. Microarray cancer data based on Adenoma and Carcinoma with 7086 and 7457 genes of 4 and 18 patients respectively is used for this study. Increase in the classification rate of the proposed new method is clearly demonstrated in the results.

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