

A Review of Effective Gene Selection Methods for Cancer Classification Using Microarray Gene Expression Profile

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Abstract : Cancer is one of the dreadful diseases, which causes considerable death rate in humans. DNA microarray-based gene expression profiling has been emerged as an efficient technique for cancer classification, as well as for diagnosis, prognosis, and treatment purposes. In recent years, a DNA microarray technique has gained more attraction in both scientific and in industrial fields. It is important to determine the informative genes that cause cancer to improve early cancer diagnosis and to give effective chemotherapy treatment. In order to gain deep insight into the cancer classification problem, it is necessary to take a closer look at the proposed gene selection methods. We believe that they should be an integral preprocessing step for cancer classification. Furthermore, finding an accurate gene selection method is a very significant issue in a cancer classification area because it reduces the dimensionality of microarray dataset and selects informative genes. In this paper, we classify and review the state-of-art gene selection methods. We proceed by evaluating the performance of each gene selection approach based on their classification accuracy and number of informative genes. In our evaluation, we will use four benchmark microarray datasets for the cancer diagnosis (leukemia, colon, lung, and prostate). In addition, we compare the performance of gene selection method to investigate the effective gene selection method that has the ability to identify a small set of marker genes, and ensure high cancer classification accuracy. To the best of our knowledge, this is the first attempt to compare gene selection approaches for cancer classification using microarray gene expression profile.

Keywords : gene selection, feature selection, cancer classification, microarray, gene expression profile

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