Abstract

The recognizing and pre-detecting process of genetic mutation becomes an important issue for research. There are various techniques that may help in detecting diseases, cancer and tumors. Microarray is considered as type of representation for gene expression that may help in detection process. M microarrays are considered as a representation for samples that contains gene expression. These gene expressions are used in analyzing samples that may be normal or affected, and help in diagnosis. To utilize the benefit of microarrays, machine learning algorithms and gene selection methods must be used to facilitate processing on microarrays and to overcome some challenges that may face microarrays. From these challenges that may face Microarrays; high dimensional data problem which is considered an important challenges that rise in different datasets. It suffers from redundant, irrelevant and noisy data. Solving this
problem requires a method that simplifies this representation. Feature selection process can be a solution that may solve this important problem, and to reduce the number of features to be used in clustering and classification. The problem can be defined as a selection of a small subset of genes from a set of gene expression data, recorded on DNA micro-arrays for classification. This survey observes some various techniques of classification, and gene selection methods such as filters and wrappers methods. To determine the suitable hybrid method or the powerful model that combine different techniques for detecting new or difficult mutated disease. And also introduces different emerging swarm intelligence techniques that prove its challenging ability in feature selection and classification in microarrays. These emerged techniques proved that there are upcoming approaches that can be used in detecting cancer. Swarm intelligence techniques proved that it can be hybridized with any mathematical or statistical techniques to gain better results.

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Index Terms

Computer Science

Information Sciences

Keywords

Microarray, Machine learning, Swarm intelligence, Feature selection, Classification