**ABSTRACT**

Gene expression profiling by microarray technique has been effectively utilized for classification and diagnostic guessing of cancer nodules. Several machine learning and data mining techniques are presently applied for identifying cancer using gene expression data. Though, these techniques have not been proposed to deal with the particular needs of gene microarray examination. Initially, microarray data is featured by a high-dimensional feature space repeatedly surpassing the sample space dimensionality by a factor of 100 or higher. Additionally, microarray data contains a high degree of noise. The majority of the existing techniques do not sufficiently deal with the drawbacks like dimensionality and noise. Gene ranking method is later introduced to overcome those problems. Some of the widely used Gene ranking techniques are T-Score, ANOVA, etc. But those techniques will sometimes wrongly predict the rank when large database is used. To overcome these issues, this paper proposes a technique called Enrichment Score for ranking purpose. The classifier used in the proposed technique is Support Vector Machine (SVM). The experiment is performed on lymphoma data set and the result shows the better accuracy of classification when compared to the conventional method.