**ABSTRACT**

Pathogenic gene identification is an important research problem in biomedical domain. The genetic cause of ASD, which is a multifaceted developmental disability is hard to research. Hence, there is a critical need for inventive approaches to further portray the genetic basis of ASD which will enable better filtering and specific therapies. This paper adopts machine learning techniques to classify gene sequences which are the significant drivers of syndromic and asyndromic ASD. The synthetic dataset with 150 sequences of six different categories of genes were prepared and coding measures of gene sequences were taken as attributes for gene identification. Pattern learning algorithms like support vector machine, decision tree and Multiplayer perceptron were used to train the model. The model was evaluated using 10 fold cross validation and the results are reported. The study reveals that Decision trees outperform other classifiers with an accuracy of 97.33%