**ABSTRACT**

A genetic predisposition or susceptibility to Autism Spectrum Disorder (ASD) is an increased likelihood of developing it based on the genetic makeup of a person. The multiple variants found in each gene have their own probability of associated risk and so the major problem lies in the systematic evaluation of their functional significance to ASD. Hence it is essential to develop methods for quantitative evaluation of ASD candidate genes with co-occurring mutations which will provide a clear understanding of their relevance to ASD. This research work deals with the development of a discriminative model for prioritization of candidate genes considering mutations in them and to classify them based on their predisposition to the disorder. The model for gene susceptibility prediction is built by integrating the combined potential of substantiation for each ASD linked gene and the related mutations. In this research work gene susceptibility prediction is modelled as a pattern classification problem and deep learning techniques are employed to build the models. The performance evaluation of these models proves that Long Short Term Memory (LSTM) based gene susceptibility prediction model has shown better performance.