**ABSTRACT**

The objective of this work is to use deep learning Convolutional Neural Network (CNN) to predict drug resistance and drug sensitivity in tuberculosis based on the genomic data. The existing techniques for determining drug resistance in tuberculosis strains are laborious and include growing bacteria in the presence of drugs. Getting the outcomes of this can take a long time. These techniques can also produce false positives or false negatives and are not always accurate. The proposed work intends to address these shortcomings by offering a quicker and more precise way to determine drug resistance in strains of tuberculosis. In terms of prediction performance, the proposed approach attained 97.27% accuracy. This model may be applied in clinical applications to diagnose tuberculosis drug resistance more quickly and accurately, improving patient outcomes after treatment.