

Abstract

RNA Binding Proteins (RBPs) are essential players in the realm of RNA interactions, holding a pivotal role in genetic regulation and biological processes. They exhibit the remarkable ability to bind diverse RNA types, including messenger RNA (mRNA), ribosomal RNA (rRNA), and noncoding RNA, thereby influencing gene expression, RNA stability, and cellular functions. Investigating RBPs is paramount for a comprehensive understanding of gene regulation, RNA stability, and the nuanced functions of RNA within cells. RBP serves as linchpins in orchestrating gene expression, genetic messaging, and RNA stability, with their involvement spanning key cellular processes like transcription, translation, splicing, and RNA modulation. The effectiveness of RBPs is paramount for the proper execution of various biological functions, encompassing development, regulation, and overall cellular activity. The Convolutional Neural Networks (CNN) architecture optimization is used to perform RBP classification method. CNN is a type of artificial neural network architecture specifically designed for processing two dimensional data. Experimental results unveil that employing a dense layer size of 32 yields the highest validation accuracy when compared to other dense layer sizes. Consequently, the utilization of a dense layer size of 32 emerges as the optimal choice for achieving peak performance in the context of the classification task under consideration in this experiment.