

Abstract

Cancer is a condition of abnormal cell growth, leading to uncontrolled cell growth and invasion of body tissues. Its effects include attacks on normal cells and organs, causing a variety of symptoms. In 2022, the United States reported 1,918,030 cases of cancer were reported with 609,360 deaths. This research focuses on predicting the bioactivity of PLK1 inhibitors as anti-cancer using the Cuckoo Search-Ensemble method. Cuckoo Search Algorithm (CSA) is used for feature selection, while ensemble learning combines models such as Random Forest, Adaptive Boost, and XGBoost to improve prediction accuracy. This study aims to the development of machine learning for PLK1 bioactivity prediction, with the potential for model improvement to achieve more accurate results in the context of anti-cancer. Based on the results, the model is effective in predicting the model of PLK1 inhibitor bioactivity. XGBoost produced R^2 and CC values of 0.57 and 0.80, respectively. These results show that the combination of ensemble learning, and CSA could significantly enhance the accuracy and reliability of bioactivity predictions for PLK1 inhibitors, opening up a promising new direction for the creation of cancer treatments.

Keywords: Cancer, PLK1 Bioactivity Inhibitors, Cuckoo Search Algorithm, Ensemble Learning, Machine Learning