



Development of a Machine Learning Model for Predicting Survival Outcomes in AIDS Patients Using Feature Selection Techniques

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Abstract

Acquired immunodeficiency syndrome (AIDS) continues to pose a significant global health challenge, affecting millions worldwide. This study focuses on developing and evaluating machine learning models to predict the survival probabilities of AIDS patients while estimating their remaining lifespan based on clinical data using Classification Learner software in MATLAB2024b. The research utilizes the AIDS Clinical Trials Group Study 175 dataset, an open-source dataset obtained from Kaggle, comprising 23 predictive variables, including demographic factors, clinical indicators, and treatment histories. The dataset was randomly split into training (80%) and testing (20%) subsets, allowing the evaluation of 34 different machine learning models. The Boosted Tree model demonstrated the highest accuracy, achieving 87.86%. Further assessments were conducted to compare model performance using the test set. Additionally, feature selection techniques were applied to identify the most critical predictors while minimizing the number of features required for effective classification. The study concluded that the Linear Support Vector Machine (SVM) model achieved optimal performance, delivering an accuracy of 85.0% when utilizing a reduced set of five to six key features: (1) time, (2) CD4 count at 20 weeks (cd420), (3) Karnofsky score (karnof), (4) baseline CD4 count (cd40), (5) prior 30-day zidovudine use (z30), and (6) treatment strategy (str2).

Keywords: AIDS, classification algorithms, artificial intelligence, classification learner, feature selection, HIV, machine learning