

Hepatitis C prediction using SVM, logistic regression and decision tree

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Abstract

Hepatitis C is an infection of the liver brought on by the HCV virus. In this condition, early diagnosis is challenging because of the delayed onset of symptoms. Predicting well enough can spare patients from permanent liver damage. The primary goal of this work is to use several machine learning methods to forecast this disease based on widely available and reasonably priced blood test data in order to diagnose and treat patients early on. Three machine learning techniques support vector machine (SVM), logistic regression, decision tree, has been applied on one dataset in this work. To find a suitable approach for illness prediction, the confusion matrix, precision, recall, F1 score, accuracy, receiver operating characteristics (ROC), performances of different strategies have been assessed. The SVM model's overall accuracy is 0.92, the highest among the three models.

Keywords: Machine Learning Techniques; Hepatitis C Virus; Data Mining; Decision Tree; HCV; Performance Measurements; ROC.

1. Introduction

The liver is found in the upper section of the human gastrointestinal system, weighing approximately 1400-1800 g in males and 1200-1400 g in women. It has crucial activities such as digestion, metabolism, toxin release, immunisation, and nutrition storage. That is why some liver illnesses can be fatal [1, 2].

Liver illnesses are classified according to their aetiology and effects on the liver. Infection, damage, exposure to medications or toxic chemicals, a process, or a genetic defect (such as hemochromatosis) are all possible causes. The aforementioned reasons can result in hepatitis, cirrhosis, and stones that can grow and cause blockages, fatty infiltration, and, in rare circumstances, liver cancer. Genetic disorders can also interfere with important liver activities, causing the deposition and accumulation of toxic components such as iron or copper [3,4,5].

Non-alcoholic fatty liver disease (NAFLD) is one of the most common liver illnesses, characterised by lipid buildup. The term "non-alcoholic steatohepatitis" refers to inflammation and harm to liver cells. Cirrhosis is also among the most dangerous liver illnesses. This illness replaces healthy tissue with scar tissue. As a result, the liver is permanently damaged and incapable of functioning normally. The leading causes of liver cirrhosis include drinking, non-alcoholic fatty liver disease, chronic hepatitis C, and chronic hepatitis B [7].

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Hepatitis is classified into two types: acute hepatitis [8], in which the liver is rapidly inflamed, and chronic hepatitis [9], in which the liver is gradually inflamed and damaged over time. Although any of the aforementioned factors might induce hepatitis, it is most commonly caused by infection with a virus belonging to the hepatitis virus group. These viruses are known as hepatitis A, B, C, D, and E, in the sequence in which they were identified [10].

Hepatitis C is a Ribonucleic acid (RNA) virus with multiple genotypes located in the Hepacivirus genus from the Flaviviridae family [11]. It is a factor that causes hepatitis C disease, chronic liver disease, liver cirrhosis, hepatocellular carcinoma. For these reasons, Hepatitis C virus (HCV) is one of the most important global health problems in the world. Worldwide, 350,000 people out of 185 million patients infected with HCV die from diseases caused by HCV [12].

The prevalence of HCV infection in the world is around 1.6%. The prevalence of HCV is decreasing in developed countries, and there are several reasons for this decrease. It was achieved through the use of the HCV test and the development of new recombinant coagulation factors. Before the discovery of HIV in 1989, HCV transmission was increasing due to 2%–10% HCV-infected blood products. For this reason, it is one of the reasons for the high morbidity and mortality in the elderly population. The prevalence of HCV in Northern Europe is below 1%, and the high prevalence is in Asia and Africa. The highest prevalence is in Egypt. The prevalence is in the USA with 1.8%, in Germany with 0.6%, in Canada with 0.8%, in France with 1.1%, in Japan with 1.5–2.3%, in China with 3.2%, and the prevalence in Egypt is approximately 15%–20%. It is estimated that there are 185 million hepatitis C patients in the world, 3–4 million people are infected with HCV every year and 350 thousand of them die from diseases that develop after HCV infection [13].

Serological and molecular diagnostic methods are used in the diagnosis of HCV infection. Serological tests are used for diagnosis and screening of the disease; virological tests are necessary to confirm the infection, to evaluate the treatment response, and to diagnose immunosuppressive patients in whom anti-HCV is not detected. HCV infection is one of the most important causes of chronic liver disease worldwide. There are approximately 71 million individuals infected with HCV in the world [1], [2].

2. Literature Review

Traditionally, health professionals make a medical report concerning a patient's condition based on histopathological exams. With the advances in information and communication technologies, especially in artificial intelligence (AI) and machine learning (ML), efficient data collection, processing, and visualization methods have arisen. Clinicians combining the outcomes of AI and ML models with the findings of clinical methods can further improve their decisions on disease detection. Undoubtedly, ML techniques have significantly contributed to the early prediction of breast cancer [20], disease complications in diabetes (handling it as a classification problem [21,22] or regression task for the short-term glucose prediction [23,24], heart disease [25], lung diseases [26-34] chronic obstructive pulmonary disease (COPD) [35], stroke [36], chronic kidney disease (CKD) [37], lung cancer [38] etc. ML is used in cloud computing and high-performance computing [48- 54].

Hepatitis C has been predicted and diagnosed in several studies using machine learning algorithms. Ma et al. [39] developed a number of classification models and determined that the XGBoost method achieved the highest accuracy (91.56%). Three machine learning methods were used by Ahammed et al. [40], and the greatest accuracy (94.40%) was obtained using KNN. In their investigation, Nandipati et al. [41] discovered that binary class labels performed better than multiclass labels, and they used the RF model to obtain an accuracy of 54.56%. Among the four machine learning models created by Mamdouh et al. [42], the RF model achieved an accuracy of 94.06% without hyperparameter adjustment and 94.88% with tuning. Using multiple-classifier models, El-Salam et al. [43] obtained accuracy rates between 65.6% and 68.9%. Applying a number of machine learning techniques, Hashem et al. [44] discovered an accuracy range of 66.3% to 84.4% for predicting advanced chronic hepatitis C. Neural networks had the best accuracy (95.12%) among the algorithms tested by Syafa'ah et al. [45]. With four machine learning methods, Oleiwi et al. [46] determined that the decision tree approach classified and diagnosed hepatitis C with the highest accuracy (93.44%). This work attempts to choose the optimal algorithms using frequent and low-cost blood test data for hepatitis C prediction.

3. Materials and Methods

Here, we have provided the description of the dataset we relied on and the main steps of the adopted methodology for liver disease risk prediction, namely, class balancing and features' ranking in the balanced data. Finally, we note the ML models we based on for the experimental results.

3.1. Dataset Description

The UCI dataset contains data from 615 individuals, was, created by Lichtinghagen et al. [47], and came from the Center for Machine Learning and Intelligent Systems at the University of California, Irvine (UCI). For each individual, a record that includes thirteen features, which are age, gender, blood levels of ALB, ALP, ALT, AST, bilirubin (BIL), CHE, CHOL, GGT, PROT, CREA, and the target feature categorizes individuals as either blood donors or those with hepatitis C, including its progression to fibrosis and cirrhosis. .

3.2. Features Analysis

Fig.1 shows the top 10 features selected by the SelectKBest method using the ANOVA F-value (f_{classif}) as the score function. AST (Aspartate Aminotransferase), BIL (Bilirubin), GGT (Gamma-Glutamyl Transferase), ALB (Albumin), CHE (Cholinesterase), ALT (Alanine Aminotransferase), PROT (Proteins), ALP (Alkaline Phosphatase), CHOL (Cholesterol), CREA (Creatinine) are the top 10 attributes. The feature "AST" has the highest score, suggesting it may be the most significant predictor of the target variable among the selected features. This implies a strong statistical relationship between AST levels and the target variable.

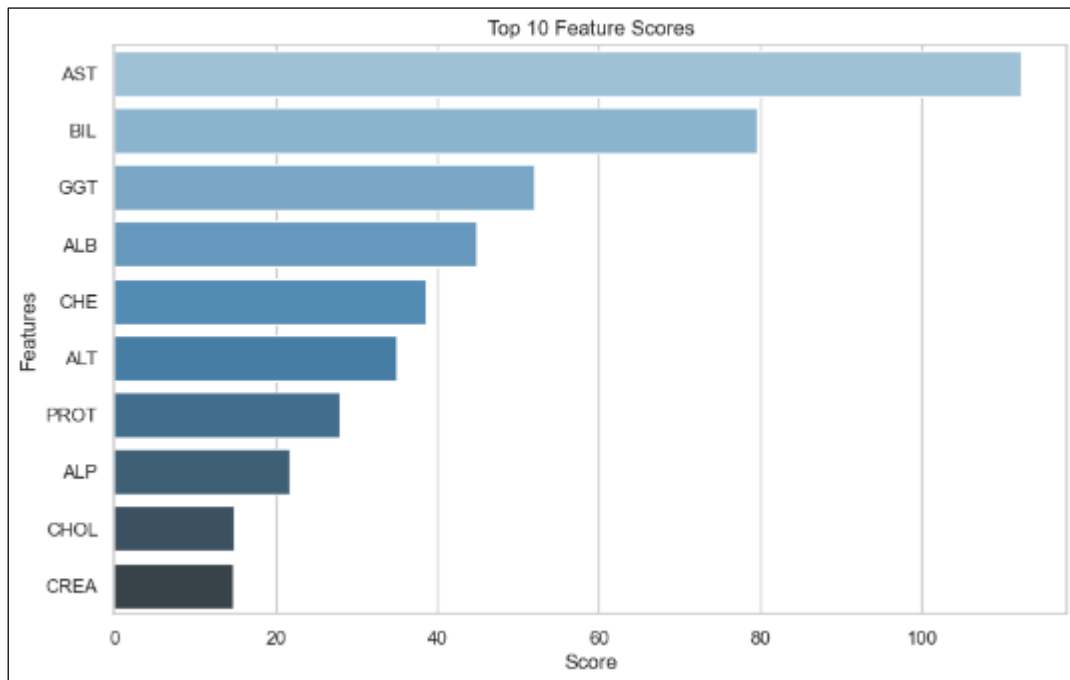


Figure 1 Top 10 features using SelectKBest method

3.3. Machine Learning Models

In this research article, we have experimented with various ML models to uncover which one outperforms the others by evaluating their prediction performance. Specifically, we have focused on Decision tree and Logistic Regression models, which are probabilistic classifiers. In addition, we have used the well-known kernel-based (linear, RBF, Polynomial) classifier Support Vector Machine (SVM).

3.4. Evaluation Metrics

To evaluate the ML models' performance, we have utilized the most commonly used metrics in the relevant literature, such as Accuracy, Precision, Recall, F-score. The confusion matrix consists of the elements true positive (TP), true negative (TN), false positive (FP) and false negative (FN). The metrics are defined as follows.

Accuracy: summarizes the performance of the classification task and measures the number of correctly predicted instances out of all the data instances.

$$Accuracy = \frac{TN+TP}{TN+TP+FN+FP} \quad (1)$$

Recall: corresponds to the proportion of participants who were diagnosed with LD and were correctly classified as positive, concerning all positive participants.

$$Recall = \frac{TP}{TP+FN} \quad (2)$$

Precision: indicates how many of those who were identified as LD belong to this class.

$$Precision = \frac{TP}{TP+FP} \quad (3)$$

F-Score: is the harmonic mean of the Precision and Recall and sums up the predictive performance of a model. The desired metrics will be calculated with the help of the Confusion matrix.

$$F - Score = \frac{2*Precision*Recall}{Precision+Recall} \quad (4)$$

4. Results

In this section, the experiment settings and the acquired outcomes will be described. For the evaluation of our proposed ML models, we have relied on the Jupyter Notebook in Python environment. In addition, the experiments were performed on a computer system with the following specifications: 11th generation Intel(R) Core(TM) i5-13400 @ 2.50 GHz, RAM 16 GB, Windows 11 Education, 64-bit OS and x64 processor. Various ML models, such as SVM, LR, and DT has been assessed in terms of Accuracy, Precision, Recall, F-Measure.

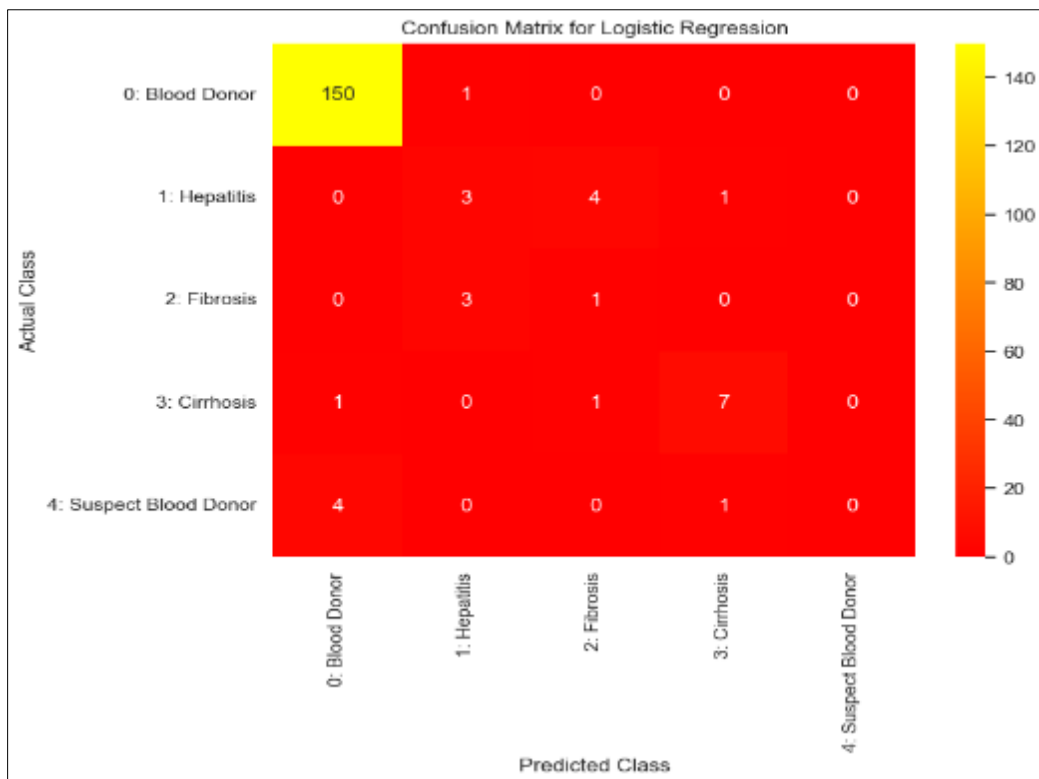


Figure 2 Confusion Matrix for Logistic Regression

Figure 2 and 3 describes the confusion matrix for Logistic Regression and Decision Tree. Figure 4 and 5 ROC curve for Decision Tree and Logistic regression, respectively.

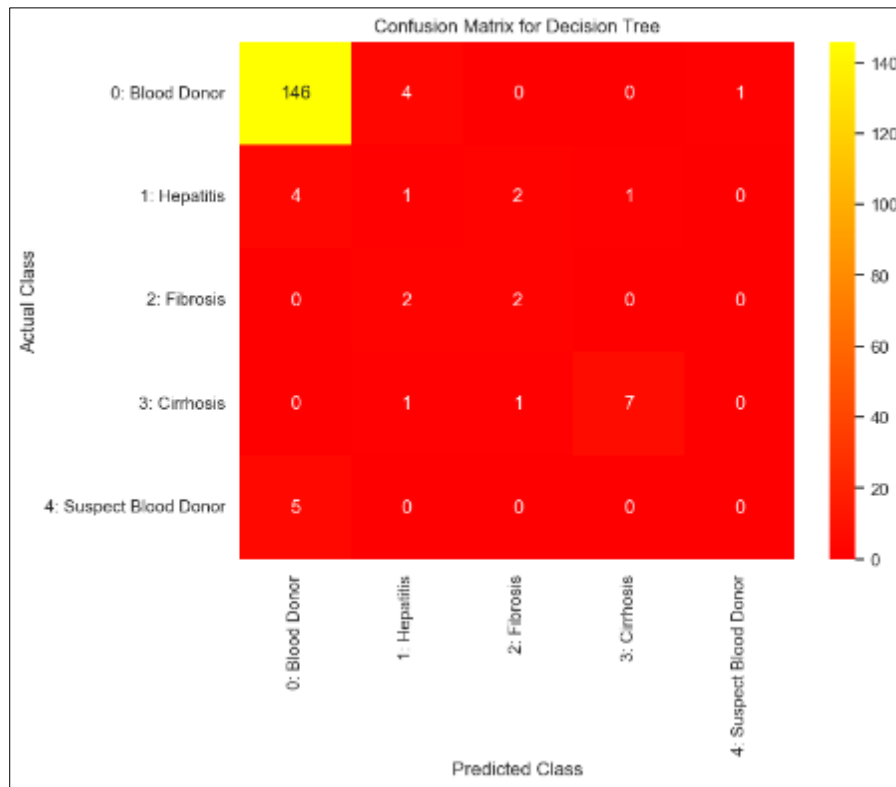


Figure 3 Confusion Matrix for Decision Tree

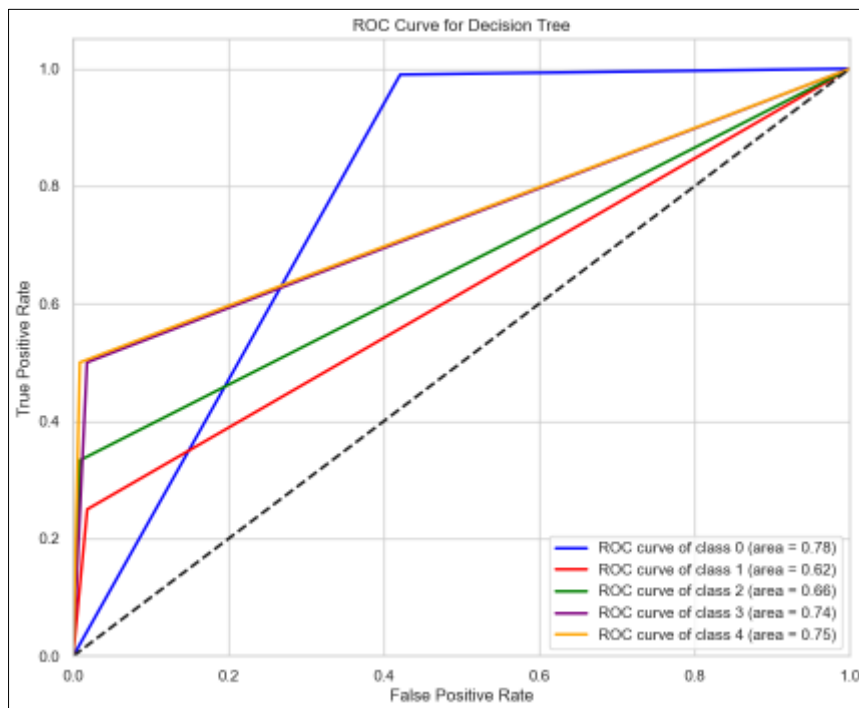


Figure 4 ROC curve for Decision Tree

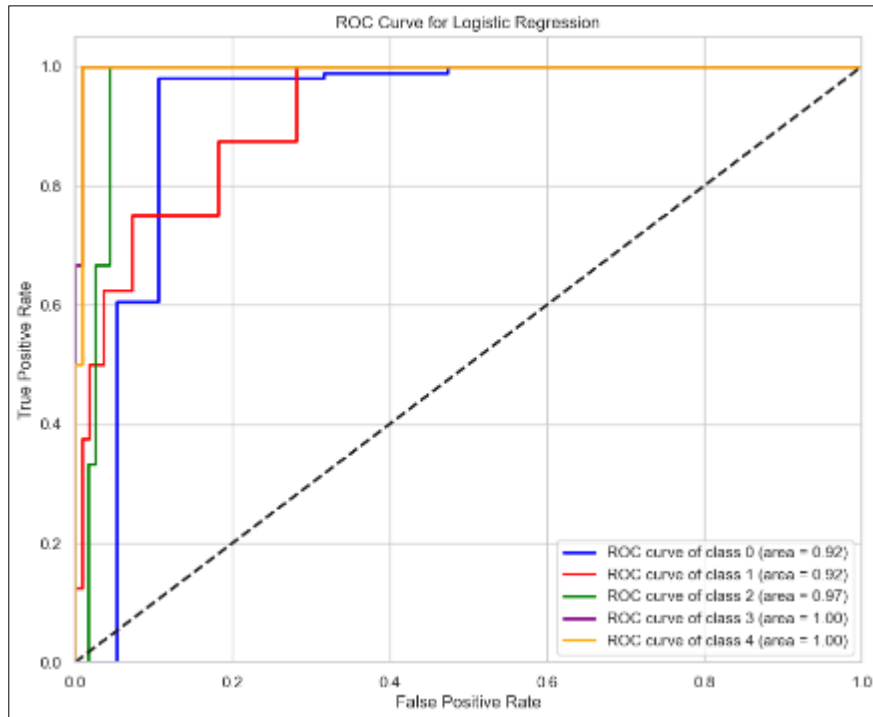


Figure 5 ROC curve for Logistic Regression

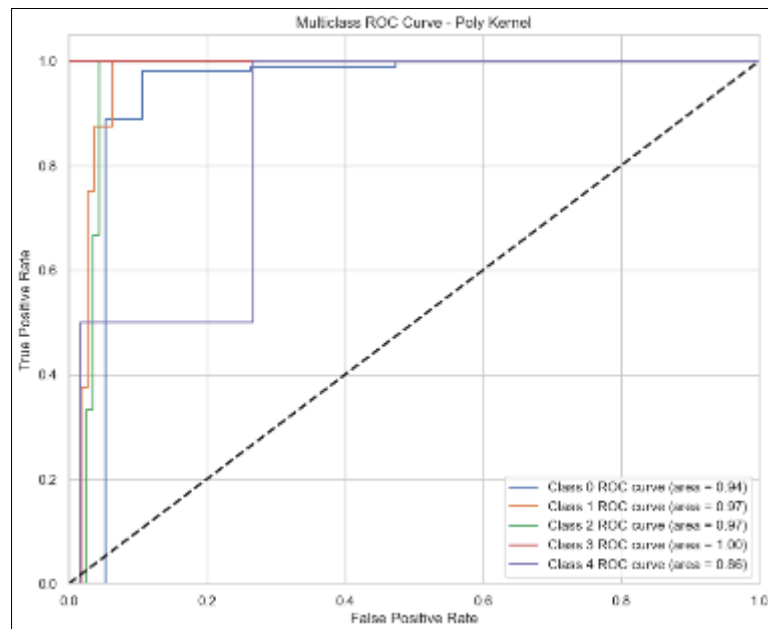


Figure 6 ROC curve for SVM (Polynomial Kernel)

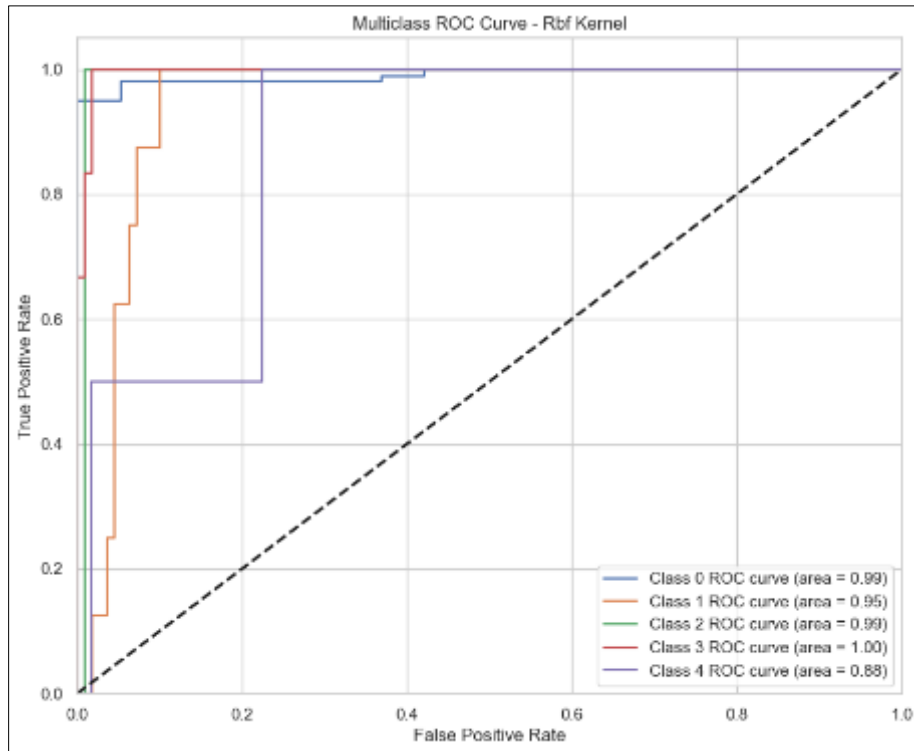


Figure 7 ROC curve for SVM (RBF Kernel)

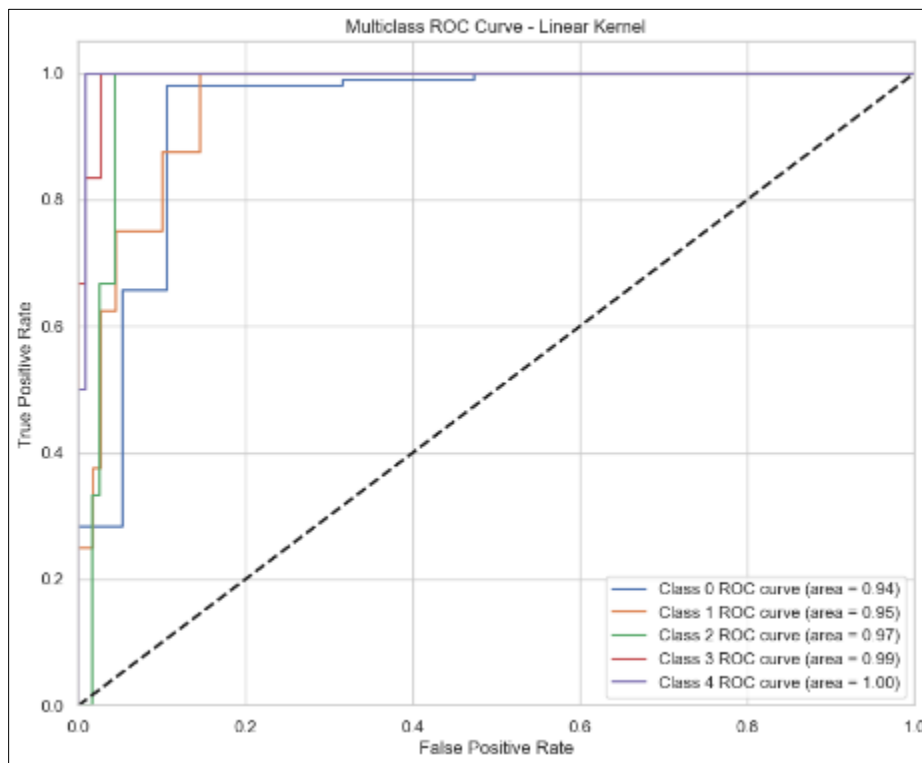


Figure 7 ROC curve for SVM (Linear Kernel)

Table 1 Performance of ML Models

| Model | Class | Precision | Recall | F1-Score | Accuracy |
|---------------------|-------|-----------|--------|----------|----------|
| Logistic Regression | 0 | 0.97 | 0.99 | 0.98 | 0.91 |
| | 1 | 0.43 | 0.38 | 0.40 | |
| | 2 | 0.17 | 0.25 | 0.20 | |
| | 3 | 0.78 | 0.78 | 0.78 | |
| | 4 | 0.00 | 0.00 | 0.00 | |
| Decision Tree | 0 | 0.94 | 0.97 | 0.95 | 0.88 |
| | 1 | 0.12 | 0.12 | 0.12 | |
| | 2 | 0.40 | 0.50 | 0.44 | |
| | 3 | 0.88 | 0.78 | 0.82 | |
| | 4 | 0.00 | 0.00 | 0.00 | |
| SVM (RBF Kernel) | 0 | 0.98 | 0.99 | 0.99 | 0.92 |
| | 1 | 0.00 | 0.00 | 0.00 | |
| | 2 | 0.30 | 0.75 | 0.43 | |
| | 3 | 0.82 | 1.00 | 0.90 | |
| | 4 | 0.00 | 0.00 | 0.00 | |

Table 1 compares the performance of three different machine learning models: Logistic Regression, Decision Tree, and SVM (RBF Kernel) based on several metrics—Precision, Recall, F1-Score, and Accuracy. Each model's performance is evaluated for different classes labeled from 0 to 4.

For Logistic Regression:

- Class 0 has high Precision, Recall, and F1-Score.
- Class 1 and 2 show much lower values across the metrics.
- Class 3 has a good balance of Precision and Recall.
- Class 4 has zero values across all metrics, indicating poor or no prediction.
- Overall accuracy of the Logistic Regression model is 0.91.

For the Decision Tree:

- Class 0 again performs well.
- Class 1 and 2 have lower scores, with class 1 performing particularly poorly.
- Class 3 has good metrics, notably in Precision and F1-Score.
- Class 4, similar to the logistic regression, shows zero in all metrics.

The total accuracy for the Decision Tree is 0.88.

For SVM with RBF Kernel:

- Class 0 has excellent metrics nearly perfect.
- Class 1 and 4 again show zero values, indicating failure in predicting these classes.
- Class 2 and 3 have variable performance, with class 3 performing exceptionally well in Recall and F1-Score.

The SVM model's overall accuracy is 0.92, the highest among the three models.

5. Conclusion

In conclusion, our study aimed to employ various machine learning techniques to predict hepatitis C based on routine and affordable blood test data. Our results demonstrated that the SVM and Logistic regression techniques are effective in diagnosing hepatitis C in its early stages with high accuracy. However, our study has some limitations, including the use of limited datasets, the lack of clinical data, and the absence of a clinical trial. In future work, we aim to incorporate additional features related to hepatitis C to develop more reliable and efficient machine learning techniques. Moreover, we recommend conducting a clinical trial to validate the performance of these techniques in real-world scenarios. Overall, our study provides promising results for the early detection and diagnosis of hepatitis C using machine learning techniques, which could ultimately improve patient outcomes and save lives.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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