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Leveraging Machine Learning for Early Risk Prediction in Cirrhosis Outcome Patients

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Abstract

Millions of individuals worldwide suffer from liver cirrhosis, which is one of the primary causes of mortality. Healthcare professionals may have more opportunities to treat cirrhosis patients effectively if early death prediction is made and it is postulated that death in this cohort would be correlated with laboratory test findings and other relevant diagnoses. In this study five machine learning models, including Logistic Regression (LR), Naive Bayes (NB) and K-Nearest Neighbors (K-NN), XGBoost, and AdaBoost, are implemented and evaluated. The preprocessing steps included feature selection, categorical data encoding, and data balancing using SVMSMOTE. The XGBoost model demonstrated superior performance, achieving 89.55% accuracy, 89.69% precision, 89.55% recall, and an F1-score of 89.59% after balancing. These findings highlight the potential of machine learning models in accurate risk detection in patients with cirrhosis and providing valuable support in clinical decision-making and improving patient treatment.

Keyword: Cirrhosis Prediction, Clinical Decision Support, Machine learning, Medical Data, XGBoost

1. INTRODUCTION

Machine learning (ML) methods have transformed clinical research by enabling the discovery of hidden patterns in patient data, leading to predictive models for diagnosis and prognosis support [1]. Previous research efforts have explored the use of ML in liver disease, including cirrhosis, which remains a major global cause of mortality. Despite promising advances, challenges in handling heterogeneous clinical data, class imbalance, and feature relevance persist, limiting the practical implementation of predictive models in healthcare settings [2] [3]. Efforts to predict mortality among end-stage liver disease (ESLD) patients and liver transplant outcomes have utilized models like Logistic Regression, Naive Bayes, and K-Nearest Neighbors [4] [5]. The study conducted by Rahman et al. [6] utilized Logistic Regression (LR), Naive Bayes (NB) and K-Nearest Neighbors (K-NN) models to determine that logistic regression delivered 85% accuracy. Research in [7] demonstrated the combination of feature extraction methods that resulted in 88.10% accuracy and an F1 score of 88.68% by using classifiers such as LR, Random Forest (RF), K-NN, Support Vector Machine (SVM), Multi-Layer Perceptron (MLP) and ensemble methods. The combination of SVM with adjusted Particle Swarm Optimization (PSO) led to improved heart and liver dataset classification accuracy according to Behera et al. [8]. XGBoost resulted in 76% accuracy and 78% AUC value for liver cirrhosis development prediction in patients with Wilson disease according to Ali et al. [9].

The study of Anıl Utku et al. [10] developed an MLP deep learning model that provided superior performance to conventional methods (NB, K-NN, LR, RF, SVM, DT) by reaching 85.71% precision with 80.48% accuracy. Oguzhan et al. [11] conducted classifier evaluation to discover that Decision Tree (DT) provided the best accuracy level of 87.75%. XGBoost showed better performance outcomes compared to LightGBM in the study by Prakash et al. [12] as XGBoost delivered 75% while LightGBM reached 67%. yet they often faced difficulties with sample bias or limited feature optimization. These studies emphasize that even minor variations in algorithm performance can significantly affect liver disease classification. Despite these advancements achieving optimal accuracy in cirrhosis classification remains a challenge, particularly in managing imbalanced datasets and selecting the most effective models.

Given these limitations, there is a critical need for robust machine learning pipelines that can accurately predict cirrhosis outcomes while effectively managing clinical data complexity. This study addresses these gaps by implementing a comprehensive approach that includes feature selection, categorical data encoding, and data balancing using SVMSMOTE. We evaluate the performance of five machine learning models Logistic Regression, Support Vector Machine, XGBoost, AdaBoost, and K-Nearest Neighbors across multiple metrics to identify the most effective classifier for cirrhosis outcome prediction.

The main contribution of this study is the development of a data-driven predictive framework that significantly improves cirrhosis outcome classification accuracy. By integrating SVMSMOTE for data balancing and identifying key clinical features such as hepatomegaly and bilirubin, the study offers valuable insights into early risk prediction strategies and clinical decision support. The findings not only advance machine learning applications in hepatology but also propose practical methodologies for future predictive healthcare research. The consistent sections of the paper are structured as follows: Section 2 presents the research material and method. Section 3 details the result and discussion. The final section presents the conclusion and suggests directions for future research.

2. MATERIAL AND METHOD

Figure 1 shows the main steps of the proposal for cirrhosis outcome prediction. This research procedure includes acquisition dataset, pre-processing, encoding categorical data, feature importance, balancing data, dividing data, classification models and performance metrics.

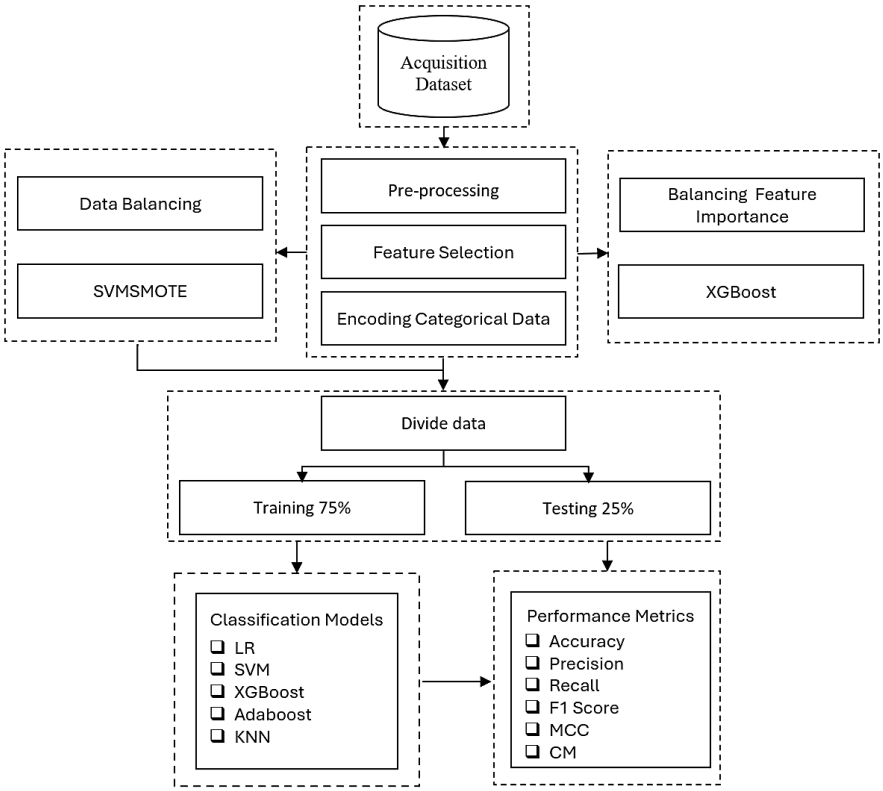

Figure 1. The Proposal for Cirrhosis Outcome Prediction

2.1. Acquisition Dataset

The research was conducted on a publicly available dataset collected from Kaggle, an open-access repository for research in several domains. The link is to the dataset [13]. This study utilized the dataset to detect cirrhosis and analyze health results related to liver illnesses. Table 1 defines number, variable name, role, type, and description.

Table 1. Dataset Information

No	Variable Name	Role	Type	Description
1	ID	ID	Integer	Unique identifier
2	N_Days	Other	Integer	Number of days between registration and the earlier of death, transplantation, or study analysis time in July 1986

No	Variable Name	Role	Type	Description
3	Status	Target	Categorical	Status of the patient: C (censored), CL (censored due to liver tx), or D (death)
4	Drug	Feature	Categorical	Type of drug: D-penicillamine or placebo
5	Age	Feature	Integer	Age
6	Sex	Feature	Categorical	M (male) or F (female)
7	Ascites	Feature	Categorical	Presence of ascites: N (No) or Y (Yes)
8	Hepatomegaly	Feature	Categorical	Presence of hepatomegaly: N (No) or Y (Yes)
9	Spiders	Feature	Categorical	Presence of spiders: N (No) or Y (Yes)
10	Edema	Feature	Categorical	Presence of edema: N (no edema and no diuretic therapy), S (edema present without diuretics or resolved by diuretics), Y (edema despite diuretics)
11	Bilirubin	Feature	Continuous	Serum bilirubin
12	Cholesterol	Feature	Integer	Serum cholesterol
13	Albumin	Feature	Continuous	Albumin
14	Copper	Feature	Integer	Urine copper
15	Alk_Phos	Feature	Continuous	Alkaline phosphatase
16	SGOT	Feature	Continuous	SGOT
17	Tryglicerides	Feature	Integer	Triglycerides
18	Platelets	Feature	Integer	Platelets per cubic
19	Prothrombin	Feature	Continuous	Prothrombin time
20	Stage	Feature	Categorical	Histological stage of disease (1, 2, 3, or 4)

2.2. Pre-processing Data

Data preparation includes preparing raw data to a logical and understood structure. Data preprocessing is crucial for optimizing ML models and improving diagnostic accuracy. Our suggested system includes the subsequent data processing steps:

2.2.1. Feature Selection

Feature selection is an important information preprocessing method in the domains of pattern detection and machine learning. The benefits of feature selection include improved decreased computational time needed for the prediction model and improved data quality through an effective data gathering method [14]. We employed manual feature selection techniques in this study to drop this column, the N_Days.

2.2.2. Encoding Categorical Data

Converting categorical variables from textual data to numerical values is crucial for machine learning algorithms to accurately anticipate correlations. Most machine learning models evaluate numerical data, not text [15]. The label coding approach was utilized in this research to turn category data into numerical values. Each categorical value in the features is assigned a separate integer. Our dataset included 7 categorical variables; for instance, the "Hepatomegaly" feature is defined by the presence of hepatomegaly as 0 (No) or 1 (Yes).

2.2.3. Data Balancing

This study's dataset for cirrhosis outcome prediction is asymmetric, which affects the prediction results. Classifiers may be biased towards the class with more data if there is an important discrepancy between them. This condition is usually referred to as "imbalanced data" [16]. We used SVMSMOTE, a method that generates synthetic samples from smaller classes to prevent overfitting. Overfitting is the reason the model performs well on the training set but falls short on the testing set [17].

We selected 7905 samples from the above reference due to the predominant category in these data being the censored due to liver tx of cirrhosis in a significant percentage, which is dispersed throughout each stage, and Figure 2 (A, B) depicts the count before and after the SVMSMOTE technique. Table 2 shows the total number of samples for each stage of cirrhosis in the dataset before and after using the SVMSMOTE technique.

Table 2. Shows the number of class instances before and after data balance.

Class	Before SVMSMOTE	After SVMSMOTE
Censored (C)	4965	4965
Death (D)	2665	4965
Censored due to Liver tx (CL)	275	4965

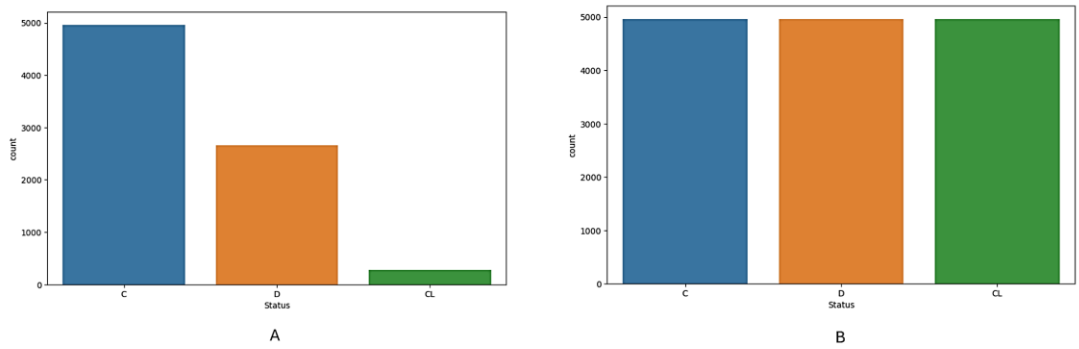

Figure 2. (A, B) Before and After Applied SVMSMOTE

2.3. Feature Importance

To identify the relevant clinical features contributing to cirrhosis patient outcomes, we applied the extreme gradient boosting algorithm, a powerful tree-based ensemble learning method known for its ability to handle heterogeneous data effectively.

2.4. Divide Data

The dataset is divided into two split-up sets: training and test sets. Classifiers are learned using a training set containing 85% of the dataset. The model of accuracy and performance on previously unseen data is explicitly evaluated on applying the testing dataset, which accounts for 15% of the dataset.

2.5. Classification Models

The classification is a crucial step in supervised learning that uses their knowledge from the training dataset to determine the target features in the testing dataset. The classifiers, which include LR, SVM, XGBoost, AdaBoost, and K-NN, were chosen and proceeded following and were applied in this study and are discussed below.

2.5.1. Logistic Regression (LR)

The statistical method known as logistic regression is used to examine the validity of data when the variable of interest is influenced by one or more explanatory variables and a dichotomous variable, which has only two possible answers, is represented by a metric, which is an ordered quantitative variable [18].

$$P(y = 1|x) = \sigma(w^T x + b) = 1 / (1 + e\hat{}(-(w^T x + b))) \quad (1)$$

2.5.2. Support Vector Machine (SVM)

SVM is a powerful and widely used method that falls under the category of supervised learning techniques and can be used in both classification and regression; the algorithm then selects the hyperplane that defines the largest margin between the two classes [19].

$$f(x) = w^T x + b \quad (2)$$

2.5.3. Extreme Gradient Boosting (XGBoost)

Feature The XGBoost method is a gradient-boosting technique that utilizes decision trees to imitate the connections between variables and the target variable. Iteratively creates a decision tree ensemble model and reduces the loss function via gradient descent [20].

$$Obj(\theta) = \Sigma_i \, l(y_i, \hat{y}_i) + \Sigma_k \, \Omega(f_k) \quad (3)$$

2.5.4. Adaptive Boosting (AdaBoost)

Feature AdaB is the abbreviation for Adaptive Boosting, a machine learning meta-algorithm. The approach works in conjunction with a variety of learning algorithms to improve their performance outcomes. Many methods of learning generate output, which is then merged into weighted values to create the boosted classifier output [21].

$$F(x) = \Sigma_m \, \alpha_m \, h_m(x) \quad (4)$$

2.5.5. K-nearest neighbors (K-NN)

K-NN is a very effective approach for classification and regression that is used and executed in a procedure of dividing data based on a specific distance measure of points inside the feature space known as k-neighbor. This classification technique is essentially a voting mechanism for neighbors; a sample is categorized based on a majority vote of the nearest neighbors [22].

$$d(x, x_i) = \sqrt{\Sigma_j (x_j - x_{ij})^2} \quad (5)$$

2.6. Performance Metrics

In this study, various metrics were used to test the efficacy of the models, inclusive of accuracy, precision, recall, F1-score, Matthews correlation coefficient, and confusion matrix, as shown in the specifics below.

1. Accuracy: This measures the proportion of correctly classified instances out of the total number of predictions. Equation 1 is expressed as:

$$\text{Accracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (6)$$

2. Precision: The precision measures the proportion of correctly classified positive observations to the total classified positives. Equation 2 is expressed as:

$$\text{Precision} = \frac{TP}{TP + FP} \quad (7)$$

3. Recall: The recall quantifies the model is ability to identify all relevant positive cases. Equation 3 is expressed as:

$$\text{Recall} = \frac{TP}{TP+FP} \quad (8)$$

4. F1-Score: This is the harmonic means of precision and recall, assuming a balance between the two. Equation 4 is expressed as:

$$F1 - \text{score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (9)$$

5. Matthews Correlation Coefficient : stands as a strong metric that evaluates both correct and incorrect positive and negative matches while keeping its balance across unbalanced datasets. Equation 5 is expressed as:

$$\text{MCC} = \frac{(TP \times TN) - (FP \times FN)}{\sqrt{(TP \times FP)(TP+FN)(TN+FP)(TN+FN)}} \quad (10)$$

6. Confusion Matrix: is uses a tabular format to display prediction outcomes so professionals can understand how a classification model functions. Equation 6 is expressed as:

$$\text{Confusion Matrix} = \begin{bmatrix} TP & FN \\ FP & TN \end{bmatrix} \quad (11)$$

3. RESULTS AND DISCUSION

This section presents the final results from tests with all implemented classification methods. The study relied on LR, SVM, XGBoost, Adaboost, and K-NN classification models to conduct the analysis with feature selection techniques such as XGBoost. Furthermore, the evaluation of the testing set data showed how well the models operated, including their effectiveness and efficiency. A set of metrics, including accuracy, precision, recall, F1 score, MCC and CM, served for the model evaluation. We implemented several experiments.

3.1. Feature Importance Analysis

In this study, the model was trained on the preprocessed clinical dataset, and feature importance was extracted based on the model's internal gain-based scoring mechanism. This approach evaluates each feature's contribution to reducing the loss function across all decision trees in the model. As illustrated in Figure 3, hepatomegaly demonstrated the highest importance score (0.1933), making it the most influential feature in predicting patient outcomes. Bilirubin (0.1324) and cholesterol (0.1209) followed as the next most significant contributors, reflecting their well-established roles in liver function assessment. Additional features such as

edema, stage, and prothrombin also showed meaningful importance values, indicating their involvement in disease progression.

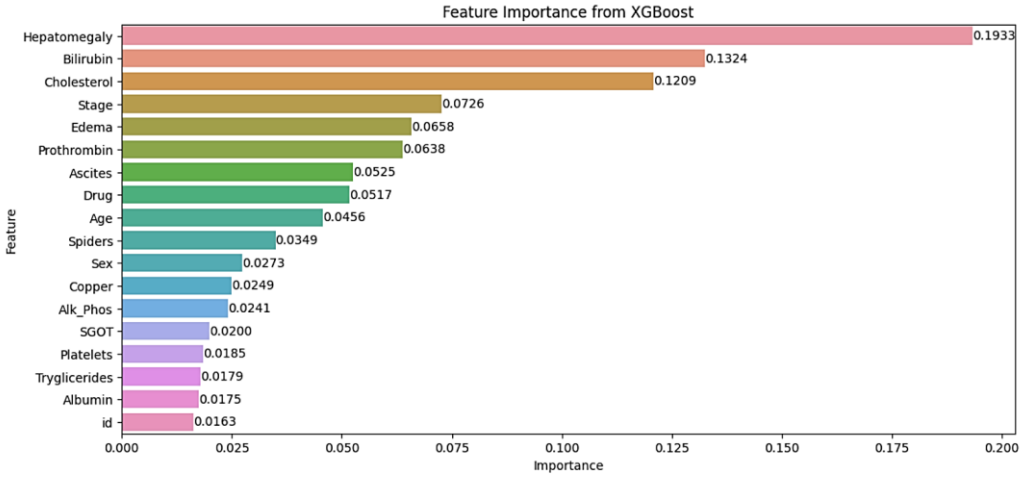

Figure 3. Feature Importance XGBoost

3.2. Model Performance Analysis

In this experiment we processed their data through techniques to make the information suitable for model prediction. The original dataset contained 7905 samples along with all its features (19) when we trained our models prior to balancing the data. XGBoost classifier displayed advanced performance than its competitors as it achieved 81.49% accuracy along with 80.25% precision, 81.49% recall, 80.32% F1-Score as well as 62.66% MCC. The dataset presents an asymmetrical structure which causes a significant difference in the number of observations denoted by censored (C), censored due to liver tx (CL), or death (D). The dataset received balance through SVMSMOTE to make two separate datasets. The dataset contains 75% training samples which belong to the first category while the remaining 25% constitute the testing samples. The evaluation of the training -testing split approach applied to the balanced feature-set 19 produced maximum results for the ET model with accuracy of 89.55% precision 89.69% recall 89.55%, F1 score of 89.59%, and MCC of 84.37%. Table 3 amd Table 4 shows the XGBoost results before and after the performance of the SVMSMOTE technique.

Table 3. Before SVMSMOTE

Evaluation Metrics	LR	SVM	XGBoost	AdaBoost	K-NN
Accuracy	74.81	62.62	81.49	79.92	66.46
Precision	71.69	56.82	80.25	78.69	63.88
Recall	74.81	62.62	81.49	79.92	66.46
F1-score	72.04	52.91	80.32	78.91	63.94
MCC	45.39	08.67	60.99	57.75	26.15

Table 4. After SVMSMOTE

Evaluation Metrics	LR	SVM	XGBoost	AdaBoost	K-NN
Accuracy	71.70	63.59	89.55	81.63	77.50
Precision	72.16	69.16	89.69	81.78	77.04
Recall	71.70	63.59	89.55	81.63	77.50
F1-score	71.71	64.55	89.59	81.65	77.21
MCC	57.71	46.08	84.37	72.51	66.30

3.3. Confusion Matrix Analysis

An examination of confusion matrices allowed for better understanding of the machine learning algorithms applied to classification tasks. Each matrix contains information about true positives and false positives and true negatives and false negatives for the three different classes: censored (C), censored due to Liver tx (CL), and death (D).The five classifiers including XGBoost, K-Nearest Neighbors, Logistic Regression, AdaBoost, and Support Vector Machine presented their results through confusion matrices as displayed in Figure 4. The XGBoost and K-NN achieved high predictive accuracy for classifying class 1 (CL) where XGBoost maintained almost flawless classification for all classes. The misclassification rates of Logistic Regression and SVM reached higher levels during the classification of class 2 (D) because the imbalance needed better pre-SMOTE handling. AdaBoost managed to achieve balanced prediction results on all classes

while causing less extreme misclassification than both Logistic Regression and SVM. The data presentation matrices illustrate the varying ability of algorithms to handle imbalanced along with multiclass data which supports later implementation of SVMSMOTE to minimize mistakes and enhance performance results.

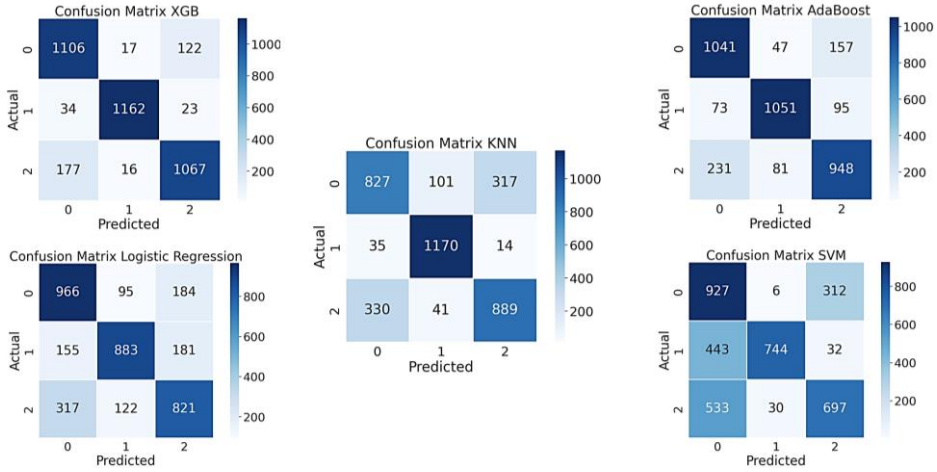

Figure 4. Confusion Matrix All Models

3.4. Comparative Analysis

A data evaluation involved 2,235 instances that were split into three distinct classes C (censored), D (death) and CL (censored due to liver tx). Multiple classifiers reached different performance levels based on their calculated average accuracy, precision and recall alongside F1-score according to Table 5. XGBoost stands out from other tested classifiers through its superior performance as it demonstrated an average accuracy rate of 90% in processing complex multiclass datasets. The performance results placed AdaBoost after XGBoost with an average accuracy of 83% and K-NN right behind them at 78%. The accuracy values obtained from LR and SVM models were 72% and 63% respectively as shewon Figure 5. performance metrics average accuracy. The models XGBoost and AdaBoost show better capabilities for medical data management by delivering balanced accurate predictions to all classes.

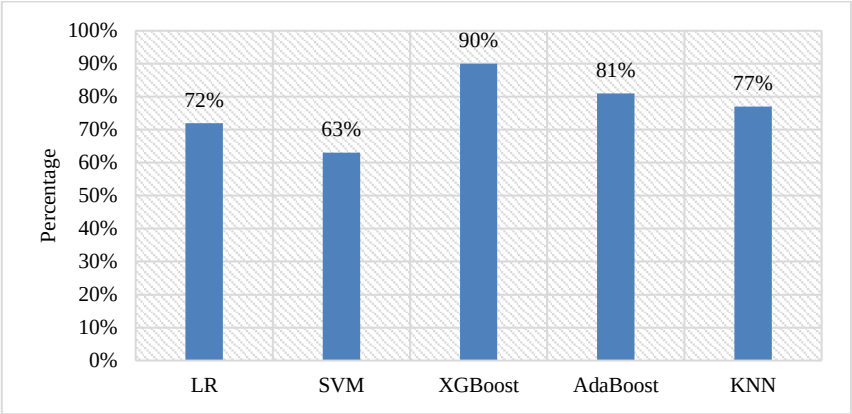

Figure 5. Performance Metrics Average Accuracy

Table 5. Classification Report

Method	Class	Precision	Recall	F1-Score	Support	Average Accuracy
LR	C	67%	78%	72%	1245	72%
	D	80%	72%	76%	1219	
	CL	69%	65%	67%	1260	
SVM	C	49%	74%	59%	1245	63%
	D	95%	61%	74%	1219	
	CL	67%	55%	61%	1260	
XGBoost	C	84%	89%	86%	1245	90%
	D	97%	95%	96%	1219	
	CL	88%	85%	86%	1260	
AdaBoost	C	77%	84%	80%	1245	81%

Method	Class	Precision	Recall	F1-Score	Support	Average Accuracy
	D	89%	86%	88%	1219	
	CL	79%	75%	77%	1260	
	C	69%	66%	68%	1245	
K-NN	D	89%	96%	92%	1219	77%
	CL	73%	71%	72%	1260	

3. DISCUSSION

The research examined how machine learning models forecast cirrhosis patient clinical outcomes by implementing the SVMSMOTE technique to manage unbalanced data distribution. XGBoost yielded the best results from model evaluation with accuracy at 89.55% and precision at 89.69% and recall at 89.55% along with an F1-score of 89.59%. The study demonstrates that improving class balance provides important benefits to model reliability within clinical data which contains vital information in minority classes. The most important features according to the analysis proved to be hepatomegaly and bilirubin and cholesterol levels which support existing medical knowledge about liver disease evolution. The model demonstrates validity through these results which supports its use for early clinical decision support. When compared to prior studies, the findings demonstrate an improvement summarizing the studies and results table 6. Overall, the study confirms that machine learning, particularly ensemble approaches like SVMSMOTE with XGBoost combined with proper data preprocessing, holds strong potential for improving early prediction and clinical management of cirrhosis outcomes.

Table 6. Summarizing the studies and results

Study	Model	Result
Rahman et al. [6]	LR, NB,K-NN	Logistic Regression: 85% accuracy
Research [7]	LR, RF, K-NN, SVM, MLP, Ensemble methods	88.10% accuracy, 88.68% F1 score
Behera et al. [8]	SVM with PSO	Improved accuracy for heart and liver dataset classification
Ali et al. [9]	XGBoost	76% accuracy, 78% AUC value for liver cirrhosis prediction
Anıl Utku et al. [10]	MLP deep learning model	85.71% precision, 80.48% accuracy
Oguzhan et al. [11]	DT	Best accuracy: 87.75%
Prakash et al. [12]	XGBoost, LightGBM	XGBoost: 75%, LightGBM: 67%
Our study	LR, SVM, XGBoost, AdaBoost ,K-NN	SVMSMOTE with XGBoost : 90.00%

4. CONCLUSION

In The research utilized machine learning models to predict cirrhosis outcomes while resolve problem associated with uneven and diverse clinical information.The XGBoost became the optimal classifier because it delivered superior accuracy through SVMSMOTE based data balancing and Hepatomegaly along with bilirubin levels functioned as primary indicators which medical experts have identified as important clinical markers. The research outcomes show how machine learning strengthens both risk evaluation and treatment outcome prediction for cirrhosis patients through better care resource planning and improved therapy preparation. Future research could explore larger datasets and additional ML algorithms to further refine predictive accuracy and generalize findings across diverse patient populations. The integration of these models into clinical practice may significantly improve patient outcomes and support healthcare decision-making.

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