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# An ensembling approach to predict hepatitis in patients with liver disease using machine learning

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## Abstract

With a 3.5% mortality rate, liver disease is one of the worst diseases in existence. The world is targeting this major health issue from several perspectives, to improve prevention, diagnosis, and treatment due to having the highest incidence of liver disorders. For liver problem disease, also known as HEP C is now the most prevalent disease in the world. This is due to the rapid progression of HEP C, which can only be stopped by early diagnosis. If not, it progresses to the last stage of HEP C cirrhosis, which has no other treatment options besides liver transplantation. One and only machine learning algorithms like LR, RF, KNN, XGBoost and K-Means can be used to predict liver illness utilizing modern methods like artificial intelligence. Data is gathered from Kaggle and subjected to several machine learning algorithms after pre processing in order to quickly diagnose liver disease. In this work, liver disease is predicted early on using pre-processing, feature extraction, and classification techniques. Recall, precision, and F1 score metrics are used to compare the accuracy of the six algorithms, and these algorithms are then combined to provide the most accurate diagnosis of liver disease. Additionally, to improve accuracy, all of these algorithms are ensemble, and accuracy was 78.96%, along with precision, recall, and F1 score.

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## 1 Introduction

Over 70 million individuals worldwide are infected with hepatitis C (HEP C), which is contagious and kills 0.4 million people per year. Electronic health records (EHRs) of patients can be used by doctors to more fully comprehend this condition and its prognosis because they contain information that computer-based approaches based on statistics and computational intelligence can process to reveal novel discoveries and trends that would otherwise go unnoticed by medical professionals.

Chronic liver disease is the leading cause of death worldwide and significantly negatively affects the vast majority of people. This condition is brought on by a number of variables that have an impact on the liver. It is vital to evaluate the effectiveness of various machine learning algorithms in order to lower the high cost of predicting the presence of chronic liver disease. The performance of different classifying algorithms was evaluated using a variety of measurement methodologies, such as accuracy, precision, recall, F1 score, and specificity. Accuracy was 75%, 74%, 69%, 64%, 62%, and 53%, respectively, for logistic regression (LR), random forest (RF), decision tree (DT), support vector machine (SVM), K-Nearest Neighbors (KNN), and Naive Bayes (NB). [1] showed that the LR has the greatest degree of accuracy.

Early diagnosis is essential for the treatment and management of liver disease. Particularly in the realm of medicine, decision tree algorithms are frequently used. The DT algorithms J48, logistic model tree (LMT), RF, Random Tree (RT), REPTree, Decision Stump, and Hoeffding Tree are a few examples. According to the data, Decision Stump has the highest accuracy when compared to other tactics. The management of people's health will be aided by the use of decision trees to predict liver disease. See, [2] and references cited therein for details.

The signs of a disease can be hazy and readily mistaken for those of other medical conditions, and liver illnesses can be challenging to identify. The approximately a hundred different forms of liver illnesses have a wide range of symptoms. Sometimes a person may not exhibit any symptoms, yet their liver may already be seriously damaged. Using conventional methods, it is difficult to reliably detect liver illnesses in their early stages; new methods and approaches have been presented in recent years. Because there are many different liver illnesses, up until late-stage liver disease and liver failure, each disease's symptoms are typically unique. [3] compare the diagnostic efficiency of various classification techniques offered by the SAS software package, including Neural Network, Auto Neural, High Performance (HP) SVM, HP Forest, HP Tree (Decision Tree), and HP Neural. The maximum accuracy rate is achieved by neural networks, while HP Forest has the lowest accuracy rate. Therefore, software-based methods may help with early detection, increasing the likelihood that a patient will receive therapy. It seems improbable that liver disease diagnoses are consistently correct.

Computer-Aided Diagnosis (CAD) is a dynamic, quickly expanding field of study in medical imaging. Due to the potential for potentially misleading medical treatments caused by faults in medical diagnostic systems, major efforts have been made in recent years to improve computer-aided diagnostics applications. In computer assisted diagnosis, machine learning is crucial. The assessment field is now inundated with statistical estimating algorithms that cannot deliver accurate performance outcomes. Large data points, missing values, and categorical data are all problems that statistical models struggle to handle. These and other factors highlight the value of MLT. Many applications, including image detection, data mining, natural language processing, and illness diagnostics, rely heavily on machine learning. ML suggests potential answers for each of these fields. These tools offer the chance for a better decision-making process and are highly helpful for the examination of such issues, see [4].

A significant amount of the cost of healthcare worldwide is caused by chronic illnesses (CIs). These disorders require lifetime treatment for patients. Predictive models are now commonly used in the diagnosis and prognosis of various illnesses. Modern researchers assert that some ML models are compromised by growing confined datasets with malicious material, which can have serious repercussions. As a result, choosing the appropriate approaches to use or selecting the appropriate models is a necessity to making perfect selections, see [5]. The machine learning predictive models can offer proof for great approaches to suggest for the diagnosis of chronic diseases.

Fatty liver disease is thought to be the most prevalent form of chronic liver disease worldwide (FLD). Early detection is crucial for fatty liver disease care and the prevention of serious health effects. According to accuracy, sensitivity, specificity, positive predictive value, and negative predictive value, the performances were graded. The logistic regression technique performs better than all other algorithms when accuracy is compared (accuracy 76.30%, sensitivity 74.10%, and specificity 64.90%). [6] demonstrates that machine learning algorithms, especially the logistic regression model, provide a more precise prediction for fatty liver diseases based on medical data from electronic medical records. This model could be a very useful tool for clinical decision-making.

The research papers from various academic conferences and journals are categorized; these articles used data mining approaches to classify and diagnose diseases using publicly available medical information and were published between 2007 and 2019. The findings of the [7] showed a sharp increase in the use of data mining techniques for disease classification in recent years. The results also showed that little attention was paid to creating procedures that used incremental data mining techniques. Researchers can create medical decision support systems with insights into cutting-edge development approaches thanks to the helpful knowledge about various data mining techniques and their usage in disease detection. On the similar lines of [8], this paper is then extended to diagnose that patient is able to donate blood or not and also predict the categories of HEP C.

The rest of the paper is as follows: In Section 2, literature review is presented. The applied methodology is discussed in Sections 3. In Section **??**, the results and discussion is given. Finally, Section **??** summarizes the main findings and concludes the paper.

## 2 Literature Review

Machine learning algorithms have recently gained significant importance in the medical field, particularly for using medical databases to diagnose diseases. These methods are used by numerous businesses to improve medical diagnostics and predict diseases early. NB, LR, SVM, KNN, K-Means clustering, DT's, and RF's are just a few of the machine learning techniques that are used to identify and predict numerous diseases. The medical industry has used machine learning to provide tools and analyses data relating to diseases. As a result, machine learning algorithms are crucial to the early detection of diseases, see [9] for more details.

Data mining is significantly used in the automated diagnosis and prognosis of diseases. Data mining techniques and technologies are used to analyses medical data. The prevalence of liver disorders has substantially increased recently, and they are now among the most fatal illnesses in many countries. the categorization of liver illness utilizing J48, multi-layer perceptron (MLP), SVM, RF, and Bayes networks. These algorithms generate a variety of results using the PSO feature selection paradigm. [10] noted that the J48 and Bayes net classification algorithms outperform other classification techniques.

The problem of liver disease has become more widespread in the twenty-first century. The mortality toll from liver disease has increased by about 2 million per year worldwide, according to the most recent survey study, 3.5% of deaths globally are attributable to liver disease. Because chronic liver disease is one of the most fatal illnesses, it is easily reversible with early diagnosis and treatment. A patient who has Chronic Liver Disease (CLD) in its early stages can live longer because to the quick development of artificial intelligence (AI), which includes numerous machine learning algorithms. To accurately determine the outcome of liver illnesses, prediction is used. A historical database of liver diseases is used to identify and extract the hidden knowledge of liver illness, see [11] and the references cited therein.

Medical data sources have been widely mined using data mining techniques to obtain insights. Classification is a supervised learning method that can be used in data mining to build models that define important data classes. As Nearest Neighbor is the most popular, powerful, and straightforward pattern recognition technique. KNN is a straightforward classifier that classifies samples according to the class of their nearest neighbors. High volume exists in medical data bases. A less accurate classification outcome may be obtained if the data collection comprises duplicated and unnecessary attributes. The prediction model aids the doctors in efficiently diagnosing heart disease while requiring less attributes. [12] showed that in India and Andhra Pradesh, heart disease is the leading cause of death. The mortality rate from heart disease will decrease with the identification of key risk factors, the creation of decision support systems, and efficient control strategies.

The standard procedure in hospitals is to obtain the data needed for a diabetic diagnosis by a variety of tests, and based on that diagnosis, the proper therapy is given, see [13]. In the healthcare sector, big data analytics is crucial. Large databases are used by the healthcare sector. With the use of big data analytics, one may examine enormous datasets and uncover hidden details and patterns that can be used to derive knowledge from the data and forecast results appropriately. The dataset has been subjected to a variety of machine learning techniques, with the classification being carried out using the LR approach, which has the highest accuracy (96%). AdaBoost classifier was the best model, with a pipeline application yielding a 98.8% accuracy rate.

The likelihood of these diseases being fatally diagnosed early may reduce this risk. Using machine learning models, an effective automated disease diagnosis model is created. diabetes, heart disease, and the coronavirus are three serious illnesses. An android app receives the data, analyses it using a machine learning model that has already been trained on the same dataset and deployed on firebase, and then displays the results of the sickness detection. To do computation for prediction, logistic regression is used. Coronavirus, heart disease, and diabetes risk can all be identified with the aid of early detection. [14] showed that the suggested approach can assist clinicians in dispensing treatment-related drugs at the appropriate time. According to the comparison analysis, the proposed model beats the competitor models in terms of a variety of performance metrics among the already used models. Additionally, the suggested model regularly outperforms other models with lower levels of uncertainty, notably when compared to LR, J48, KNN, ANN, RF, GB, and ANFIS.

Practical software-based solutions are successfully implemented. A significant amount of diagnostic information on various sorts of ailments and diseases is produced every day as part of routine diagnosis. Data mining and analytics techniques and solutions play a crucial part in the knowledge discovery process from this diagnostic data because they automatically uncover linkages in vast amounts of data. There are many data mining techniques that can be used to predict diseases, including clustering, classification, association rules, and regression. [15] study is focused on evaluating the effectiveness of various classifiers for the detection of liver diseases because classifiers, which are data mining tools that take a lot of data representing things to be classified and try to predict which class the new data belongs to, have attracted a lot of attention for disease diagnosis.

Extraction of knowledge from sizable databases is the aim of data mining. A database may be viewed as a sizable search space for extracting this knowledge, and a mining algorithm as a search method. An exhaustive search is generally impractical since a search space has a vast number of components. As a result, effective search techniques are crucial. Numerous applications have successfully used search techniques based on genetic-based algorithms. There are several applications where genetic algorithms play an evolutionary role with data mining techniques, and these applications are described in [16].

Heart disease is the most common ailment on the planet. The ability to identify whether a patient has heart disease or not using clinical data is crucial since early detection of cardiac problems will increase survival rates. This will hasten the diagnosing procedure. The KNN, Naive Bayes, and SVM supervised machine learning algorithms are put to the test on the heart diseases dataset. [17] showed, the test results unambiguously demonstrate that the Nave Bayes algorithm has a prediction accuracy of 86.6% for heart disease. The performance of Naive Bayes and other classification techniques, such as random forest and decision trees, can be compared in the future.

Neural networks are used to create a prediction system for cardiac risk level. The results of [18] obtained demonstrate that the developed diagnostic system can accurately predict the risk level of cardiac illnesses.

One of the biggest health challenges is identifying the precursors to diabetes in a person. a formula for estimating the danger of type 2 diabetes. Six machine learning classification techniques were used by [13], and a variety of statistical indicators were used to assess the results. Tests were run on a dataset made up of 18 questions on diabetes that were gathered through online and offline surveys. The PIMA database also used these methods. The experimental results showed that RF had the best overall performance, with an accuracy rate of 94.10% for our dataset. The highest accuracy is also provided by RF for the PIMA dataset.

The dataset was put through a number of machine learning approaches, with the classification being done using the LR method, which has the highest accuracy (96%). The best model was the AdaBoost classifier, which had a 98.8% accuracy rate in a pipeline application, see [13] for details. Using various datasets, we compared the accuracy of two different machine learning techniques. It is clear from this dataset's comparison to the prior dataset that the model's diabetes prediction accuracy and precision have increased. The risk that non-diabetics may develop diabetes in the following years can be ascertained by continuing this research.

## 3 Methodology

This research focuses on the disorder and prediction of liver disease. The steps for predicting liver disease using machine learning are as follows.

### 3.1 Data set for analysis

The data under consideration is labeled, requiring the application of supervised machine learning for its analysis. 583's clinical information patients are gathered from the Kaggle database, which is basically a data-set of patients' blood sample. This data set contains 416 liver patient records and 167 non liver patient records collected from North East of Andhra Pradesh, India. The "Dataset" column is a class label used to divide groups into liver patient (liver disease) or not (no disease). This data set contains 441 male patient records and 142 female patient records. This data may be found at *https://www.kaggle.com/datasets/uciml/indian-liver-patient-records*. The description of the dataset are given as follows:

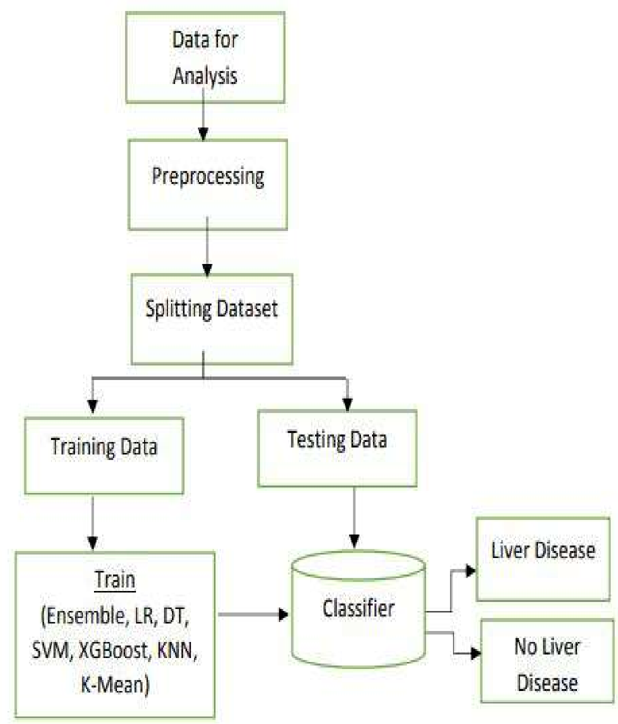


**Figure 1.** Data pre-processing

Here, response variable is patient have liver disease or not. The actual input data consists of lab test findings relating to healthy blood donors and liver infection-related illness. Whether the patient has liver disease or not is predicted by the output variable or dependent variable. Machine learning, a subset of computer science, is the subject that is most in the news right now. The world's date is hooded and is produced swiftly every day.

**Table 1.** Description of Data Set

| Attribute | Meaning | Measurement Unit |
|---|---|---|
| Age | Age of patient | year |
| Total Bilirubin | Total bilirubin in blood | mg/dL |
| Direct Bilirubin | Direct bilirubin in blood | mg/dL |
| Alkaline Phosphotase | Alkaline phosphatase level in the blood | IU/L |
| Alamine Aminotransferase | Alamine aminotransferase level in blood | IU/L |
| Aminotransferase | Aminotransferase in blood | IU/L |
| Total Proteins | Total protein level in blood | g/L |
| Albumin | Albumin level in the blood | g/L |
| Albumin and Globulin Ratio | Albumin and globulin ratio in blood | g/dL |
| Gender | 1: Male, 0: Female | Binary |
| Target | 1: Liver disease, 0: No liver disease | Binary |

### 3.2 Data processing

The method of cleaning up a dataset is applied to get rid of errors, noise, and missing data. In this data collection, the missing values are eliminated by using average values in their place. The gender attribute is converted into binary digits in advance. Additionally, categories are created from the dependent or output characteristic to predict liver illness, train and propose a machine learning model.

### 3.3 Splitting data

The training and testing phase of machine learning is crucial for the classification of biological datasets. The entire data collection is divided into two sets. One dataset is used for training, and the other one is used for testing. 25% of the data are in the testing data set and 75% are in the training data set, which were selected at random. After testing and training using data, algorithms are predicted.

### 3.4 Classifier

A labelled training dataset is used in supervised machine learning techniques to impart the underlying algorithm. The trained system then divides the unlabeled test dataset into related categories using the unlabeled test dataset. Using metrics like accuracy, precision, recall, and F1 score, this step assesses the effectiveness of every method. Using these performance criteria, the machine learning algorithms are contrasted. The classifier applied on this data are: *Enseble*, *LR*, *RF*, *KNN*, *K-Mean*, *SVM* and *XGBoost*. These ML algorithms applied on this data and then compare their accuracies by using different performance metrics with existing algorithms.

### 3.5 Prediction liver disease

The values of the patients' test results are an input that the proposed ML algorithm uses for evaluation. After receiving input from the user, the ML algorithm makes a prediction on whether the patient has liver disease or not.

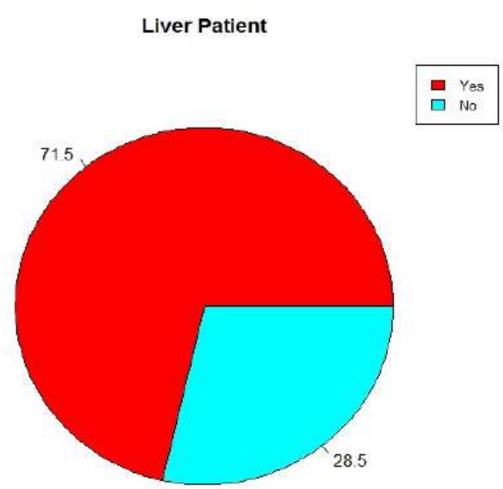


**Figure 2.** Patients with lever disease

## 4 Results

For this study the data actually used is labeled data so for labeled data classification is to be used. Different techniques for classifying data, including RF, LR, SVM, XGBoost, KNN, and K-Means, have accuracy ratings of 74.34%, 74.17%, 73.98%, 72.92%, 71.03%, and 69.60%, respectively. These algorithms are then combined to increase accuracy to 78.96%. It is simple to create publication-quality graphs using mathematical symbols and calculations with *R*, which is one of its benefits. Although the user has full freedom, carefully selected defaults have been made for tiny design decisions in graphics.

**Table 2.** Comparison between existing and proposed ensemble algorithm

| | Algorithms | | |
|---|---|---|---|
| **Parameter** | **2013** | **2018** | **Proposed** |
| Accuracy | 73.27 | 70.67 | 78.96 |
| Precision | 73.21 | 49.90 | 95.87 |
| Recall | 71.50 | 70.70 | 99.00 |
| Success ratio | 00.73 | 00.70 | 00.78 |

In Table 2, we have compared [19], [2] and [20] with our proposed ensemble model.

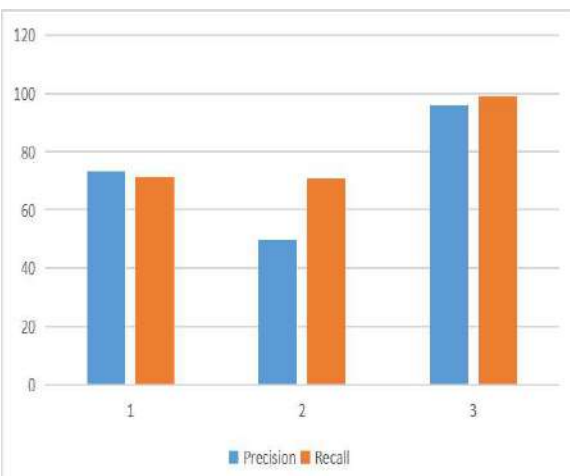


**Figure 3.** Precision-Recall of existing and proposed algorithm

## 4.1 Accuracy

Accuracy is expressed as the total number of values or points that were correctly categorized after all other values were added together and multiplied by 100. In other words, accuracy was found to be 73.27% after applying the current algorithm, while accuracy in the suggested work was 78.96%. From the confusion matrix, the accuracy may be calculated as:

$$\text{Accuracy} = (TP + TN)/(TP+TN+FN+TN)$$

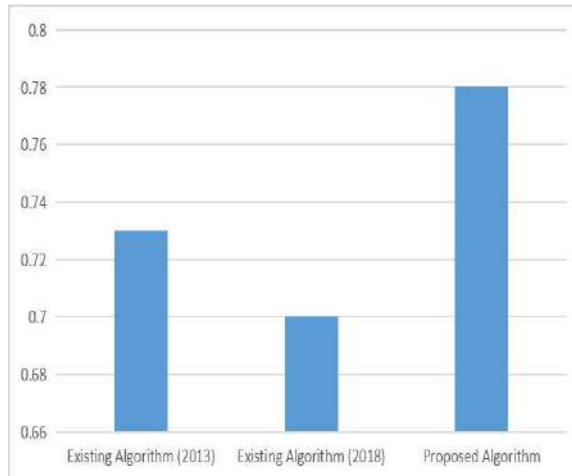


**Figure 4.** Success ratio of existing and proposed algorithm

where TP, FP, TN and FN are denoted as true positive, false positive, true negative and false negative, respectively.

**Table 3.** Comparison between proposed algorithm with accuracy in percentage

| **Algorithm** | **Accuracy** |
|---|---|
| Ensemble | 78.96 |
| RF | 74.34 |
| LR | 74.17 |
| SVM | 73.98 |
| XGBoost | 72.92 |
| KNN | 71.03 |
| K-Means | 69.60 |

The accuracy of different classification models is given as follows.

## 4.2 Precision, Recall and F1 score

Actually the performances of classification algorithms are mostly related to Precision, Recall and F1 score.

Precision is actually determined that how much precise is model in each class. From confusion matrix, the precision is calculated as:

Precision = TP/(TP+FP)

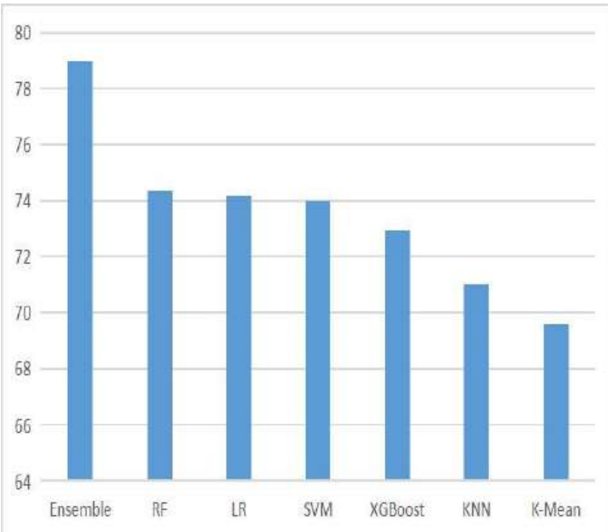


**Figure 5.** Accuracy of ensemble and different existing algorithms

It can be seen that ensembling classification has highest than all other algorithms. The accuracy and other parameters like precision, recall and F1 score are compared with existing study.

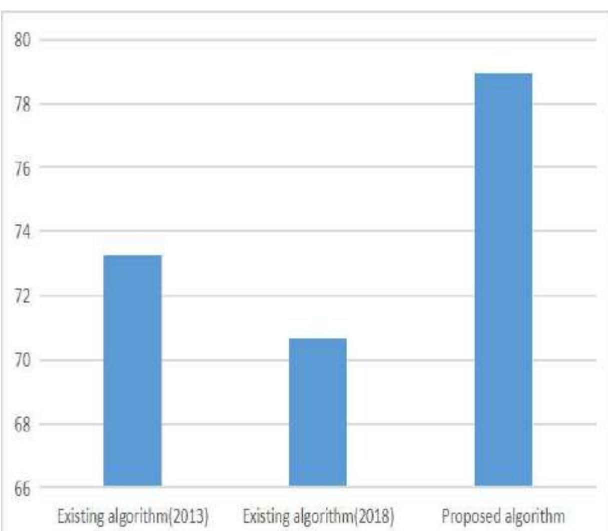


**Figure 6.** Accuracy of existing and proposed algorithm

**Table 4.** Comparison between existing and proposed ensemble algorithm with precision, recall and F1 score in percentage

| Algorithm | Precision | Recall | F1 Score |
|---|---|---|---|
| Ensemble | 95.87 | 99.00 | 84.00 |
| RF | 75.58 | 85.99 | 80.40 |
| LR | 71.61 | 99.90 | 84.00 |
| SVM | 71.37 | 99.99 | 83.19 |
| XGBoost | 54.00 | 76.00 | 82.00 |
| KNN | 94.17 | 73.48 | 82.54 |
| K-Mean | 97.30 | 70.90 | 81.92 |

Low FP rate and high precision are related. Which algorithm performs the best for the dataset of blood samples is suggested by precision. More accuracy and precision are achieved by the algorithm the higher the precision. As a result, ensemble technique has the highest accuracy of any algorithm because it has the highest precision value.

A general assessment is provided by the recall. The ratio of examples that are correctly classified to all of the cases in a set is another name for it. The algorithm functions well if the expected accuracy is high. In all of these algorithms, ensemble technique has a recall rate of 99%, which is greater than the recall rates of all other algorithms combined. Therefore, compared to other methods, ensemble technique is more accurate. Due to its higher recall, ensemble technique produces a higher percentage of examples that are correctly identified when compared to all the cases in the collection. Ensemble technique hence has a greater prediction accuracy.

Recall = TP/(TP+FN)

The F1 score represents the harmonic average of recall and precision. The F1 score is based on the recall and precision rates. The F1 score increases with increasing precision and recall. An algorithm's accuracy increases with the F1 score. The ensemble algorithm outperformed all other algorithms in this situation with a F1 score of 84%. Consequently, an ensemble technique has greater accuracy than any other algorithms. The precision and recall of proposed algorithm are more than existing studies.

The success ratio is also obtained. The ratio of the number of points that were correctly categorized to all of the points can be used to illustrate success ratio. Success rate equals number of correctly classified points/total number.

## 5 Comparative Study

In this section, we compared the proposed and existing algorithms in terms of accuracy. In the following table, we compared [19], [2], [21] and [20] with our proposed ensemble model.

**Table 5.** Comparison between existing and proposed ensemble algorithm with accuracy in percentage

| Algorithm | Year | Accuracy |
|---|---|---|
| Proposed | 2023 | 78.96 |
| [19] | 2013 | 73.27 |
| [2] | 2018 | 70.67 |
| [21] | 2021 | 70.54 |
| [20] | 2022 | 75.00 |

F1 = (2*Precision*Recall)/(Precision + Recall)


**Figure 7.** Precision, Recall and F1 score of different algorithms

In Table 5, we can clearly see that our proposed algorithm performed well compared in terms of accuracy which is 78.96, higher than existing studies used in this paper.

## 6 Discussion and Conclusions

The primary objective of this study is to assess and compare the ability of the classification algorithms to determine using the *R* programming language whether or not a patient has liver disease. The study's data set is freely accessible on Kaggle. Several classification techniques, including LR, RF, SVM, and XGBoost, were employed to evaluate performance. From Table 2, it can be seen that our proposed model outperformed in terms of accuracy, precision, recall and F1 score than the existing model, i.e., all the values of evaluation metrics are greater than the existing model used in this study. It can also be seen that the existing study has an accuracy of 78.96%, precision of 95.87%, recall of 99%, and F1 score of 84% which are obtained by an ensemble algorithm that is greater than existing models. In contrast to intrusive approaches, which are both costly and hazardous to the body, the suggested methodology will assist medical practitioners in accurately classifying HEP C or liver disease patients in a non-invasive and less expensive manner. In future, by applying other ML algorithm with ensemble, one can improve the predication capability of liver disease.

## Author Contributions

**Muhammad Arif**: Conceptualization, Methodology, Software **Mohsin Abbas**: Data curation, Writing- Original draft preparation. **Muhammad Ahmed Shehzad**: Visualization, Investigation.: **Zakia Batool**: Software, Validation. **Mahwish Rabia**: Reviewing and Editing. **Abdul Majid Soomro**: Writing- Reviewing and Editing

## Compliance with Ethical Standards

It is declare that all authors don't have any conflict of interest. It is also declare that this article does not contain any studies with human participants or animals performed by any of the authors. Furthermore, informed consent was obtained from all individual participants included in the study.

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