LIVER FIBROSIS DETECTION USING ENSEMBLE MODEL OF SUPPORT VECTOR MACHINE AND DECISION TREE

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ABSTRACT

Liver fibrosis is a progressive condition identified by the excessive formation of extracellular proteins matrix, resulting in scarring and impaired the liver functions. A prompt and precise diagnosis is essential for efficient treatment and disease management because delays in treatment can develop into cirrhosis or liver failure. Traditional diagnostic methods often face problems when there is a variable progression of the complex nature of fibrosis development and variations in the clinical data. Futhermore, these diagnostic methods show data inconsistencies, and the complexity of underlying patterns usually limit their diagnostic dependability. To avoid these isues, aggregation of several learning models helps to lower variation and bias, thereby improving predicted accuracy by means of ensemble approaches. In this study, an approach of machine learning techniques called ensemble model of support vector machine (SVM) and decision tree (DT) were proposed to diagnose liver fibrosis. The methodology includes multiple phases: dataset acquisition, a pre-processing layer (comprising one-hot encoding, data visualization, and data cleaning), feature extraction and selection utilizing machine learning algorithms, and partitioning the data into training and testing sets. Furthermore, cross-validation and evaluation metrics were utilized to evaluate model performance, including accuracy, precision, recall, and F1-score to evaluate the proposed model. The results found that the proposed ensemble model shows quite outstanding performance with the accuracy of 99.46%, a precision of 100%, a recall of 95.96%, and an F1-score of 97.87%, compared to SVM and DT classifiers achieving accuracy rates of 96.79% and 98.03%, respectively.

Keywords: Liver Fibrosis Detection; Hepatitis C Virus (HCV); Machine Learning; Ensemble Learning (EL); Support Vector Machine (SVM), Decision Tree (DT)

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1. INTRODUCTION

Liver Fibrosis is a major and rising global health concern in the initial stage of chronic liver disease. Liver Fibrosis originated from the inflammation and damage of the liver caused by hepatitis C virus (HCV). The HCV infection afflicters millions of people globally and usually causes severe diseases including cirrhosis and
hepatocellular cancer [1]. In Addition, the complicated pathophysiology of liver fibrosis is caused in part by many elements, including genetic predisposition, excessive alcohol consumption, metabolic problems and chronic hepatic damage [2]. HCV elements start a sequence of biochemical events that builds up fibrotic tissue.

Gradually, this accumulation reduces liver capacity and sets off a chronic wound-healing reaction. Early diagnosis greatly increases survival rates and clinical outcomes; thus, liver fibrosis must be diagnosis correctly and quickly. Furthermore, Liver Fibrosis can affect underline that a number of etiologies, including steatosis, viral infections, drug abuse, and genetic disease. Whatever the underlying cause either toxic, autoimmune, or viral, chronic liver damage starts a fibro genic process linked mostly to metabolic abnormalities. An accurate diagnosis becomes even more crucial considering the contributing factors and the possibility of disease progress. Stress the need of early, accurate diagnosis and treatment in greatly affecting the course of liver fibrosis. Still, traditional diagnosis techniques typically rely mostly on the subjective, time-consuming, inconsistent judgment of medical professionals [3]. Modern technological solutions like Artificial Intelligence (AI) approach, are being used by healthcare systems to overcome these constraints and raise diagnosis outcomes. In order to improve disease detection, maximize treatment

planning, and enable continuous patient monitoring—all of which lower human error and diagnostic delays, AI is being increasingly applied in healthcare environments. Particularly, a subfield of AI called machine learning (ML) has become rather important for medical diagnosis. For challenging tasks like liver fibrosis detection, algorithms such as SVM and DT particularly appeal because of their ability to manage high-dimensional clinical data and prevent overfitting. Nevertheless, the promising outcomes, these models may still lack generalizability and prediction accuracy in various clinical environments [4].

ML techniques have been developed to address these limitations in diagnostic systems [5]. ML-based approaches enhance performance by improving accuracy, robustness, and stability in disease prediction [6]. In particular, EL methods, which combine the strengths of multiple models, have consistently outperformed individual conventional models in various medical applications, including the diagnosis of liver fibrosis [7-8].
The main contribution of this work is developing ML framework for liver fibrosis detection. Combining advanced ML algorithms with EL techniques in this paper methodology raises diagnostic accuracy. The paper especially shows that predictive performance is much improved by combining SVM with DT models. Moreover, a thorough assessment of the models is done applying performance criteria including accuracy, F1-score, recall, and precision.

The rest of the paper is structured as follows. Heading 2 summarizes the related works. Next, heading 3 presents the proposed methodology for the detection of liver fibrosis. Then, heading 0 provides the results and discussion. Finally, the last section (heading 0) concludes the paper and outlines future directions.

2. RELATED WORKS

In recent years, ML has been applied to the medical field for diagnosis liver fibrosis, categorization, and forecasting, including the ability to determine the stage of liver fibrosis. To predict and distinguish between the various stages of liver fibrosis in patients infected with the hepatitis B virus, a number of researchers employed machine learning techniques. ML is essentially a computational method that uses knowledge or historical data to produce predictions.

Modhugu and Ponnusamy (2024) [9] performed a comparative examination of SVM, and DT algorithms for predicting liver disease utilizing a dataset obtained from Kaggle. Their research demonstrated that SVM attained the best accuracy at 85%, at 82% and DT at 79%. After analysis of the results, it highlights SVM proficiency in managing high-dimensional data and intricate boundary conditions, rendering it appropriate for medical diagnostics. Nonetheless, the "black-box" characteristic of SVM presents obstacles to clinical interpretability, which is essential for medical decision-making. Furthermore, DT provide a more interpretable model framework, enabling doctors to trace the decision-making process. Zhang et al. (2023) [10] employed hierarchical decision rules through DT, offering an interpretable option for the classification of liver illness. Nonetheless, their research underscored the vulnerability of DT to overfitting, particularly when utilized on imbalanced medical datasets. Ensemble approaches have been proposed to improve model resilience and predictive performance.

Additionally, it creates complex problems of overfitting, despite their interpretability, especially when used to unbalanced medical datasets [11]. Ensemble methods have emerged as effective strategies for surmounting these individual limitations. To enhance prediction performance, techniques like as RF, GBM, and XGBoost integrate many models. An XGBoost model trained on post-cholecystectomy patient data surpassed standalone models in identifying liver fibrosis, as demonstrated by Liu et al. (2023) [11], achieving a balanced accuracy of 93.16%.

Bernal et al. (2023) [12] demonstrated that ensemble approaches produced the greatest accuracy and generalizability in datasets of highly obese patients with non-alcoholic fatty liver disease (NAFLD). They used the radiological prediction of microvascular invasion (MVI) in hepatocellular carcinoma (HCC) for treatment planning; however, the clinical implementation of predictive models is constrained by issues of interpretability and generalizability. Additionally, created and validated an ensemble-based MVI prediction model utilizing data from 2,096 patients across three distinct cohorts. A 3D-ResNet network was initially trained on a primary dataset and subsequently improved using an expert-informed training method, resulting in a substantial increase in the model AUC from 0.54 to 0.83. Acknowledging the constraints of single-model deployment in varied clinical environments, researcher employed EL methodologies through three deployment strategies: direct model application, fine-tuning based on data sharing, and an innovative skeleton sharing architecture. The ensemble-enhanced skeleton sharing model consistently delivered strong predictive performance, achieving an AUC of 0.85 in the second patient cohort. A similar pattern was observed in the third cohort, where it continued to outperform both the original and traditional data-sharing models. These findings highlight the practical value of the skeleton sharing approach, emphasizing how EL not only improves predictive accuracy across different datasets but also enhances clinical flexibility and interpretability—key factors for real-world application.

In a 2024 study, Zhang et al. [13] further validated the advantages of ensemble methods in liver fibrosis prediction. Their research demonstrated that ensemble models consistently outperformed individual machine learning algorithms across various datasets, showing higher scores in AUC, sensitivity, and specificity. These results underscore the power of ensemble techniques in addressing complex clinical classification problems. However, the study also pointed out a common critique of ensemble models—their often-large computational requirements and complexity—which can be a limiting factor for clinical use.

In another relevant study focused on chronic hepatitis B (CHB), researchers conducted a retrospective analysis of 618 patients from Zhejiang Provincial People's Hospital. Their goal was to develop a machine learning model capable of accurately staging liver fibrosis. This effort highlights the growing momentum behind applying advanced ML strategies to improve the precision of liver disease diagnosis and staging, especially in chronic conditions like hepatitis B.

The DT model proved to be the superior classifier through resampling strategies, Additionally, utilizing use the serological marker for fibrosis stages F0-1, F2, F3, and F4 in the training cohort were 0.898, 0.891, 0.907, and 0.944, respectively. Validation on an independent external cohort of 571 patients produced comparably high AUCs of 0.906, 0.876, 0.931, and 0.933, respectively. Moreover, the model's risk classification was highly correlated with pathological diagnoses, highlighting its clinical relevance. Collectively highlight the increasing efficacy of ensemble and tree-based machine learning methods in the management of liver disease. They not only improve predictive accuracy but, when combined with hybrid approaches, they provide the interpretability essential for incorporation into clinical workflows.

Another research study, Shankar et al. (2024) [14] presented an interpretable ensemble model that harmonizes clinical applicability with precision in predicting cirrhosis in hepatitis C patients. Individuals with cirrhosis may also suffer from neurological impairment and gastrointestinal bleeding. The management of cirrhosis aims to avert further advancement of the condition. Early detection of cirrhosis is essential to prevent complications.ML has demonstrated efficacy in delivering precise and reliable information for the diagnosis of various diseases. Nonetheless, no research to date has employed machine learning to identify cirrhosis in individuals with hepatitis C. This research acquired a dataset comprising 28 variables from 2038 Egyptian patients sourced from the ML Repository at the University of California, Irvine. The Extra Trees model surpassed the other models, with an accuracy of 96.92%, a recall of 94.00%, a precision of 99.81%, and an area under the receiver operating characteristic curve of 96%, utilizing only 16 of the 28 features.

Moreover, Soni and Rai (2021) [15] performed a comparative analysis of multiple classification methods for diagnosing liver illness utilizing the Indian Liver Patient Dataset (ILPD). Their research evaluated the classification performance of DT, k-nearest neighbors (KNN), random forest (RF), and logistic regression (LR) methods. The KNN model attained the best diagnostic accuracy at 72.04%, succeeded by LR at 70.15%, RF at 65.00%, and DT at 63.46%. While KNN exhibited enhanced efficacy in this context, the study focus was confined to the fundamental classification of liver disease existence and did not encompass predictions regarding disease progression or severity. This underscored a significant constraint in practical implementation, particularly considering the necessity of early detection and staging for prompt intervention.

Conversely, Emu et al. (2020) [16] progressed the discipline by concentrating on hepatic fibrosis staging in patients with hepatitis C. Researchers assessed the efficacy of ML models, predicting the degree of liver fibrosis using a dataset of 1,385 Egyptian patients. Both the entire feature set and an optimized subset from feature selection were employed to train the models. Five-fold cross-validation results showed that the MLP model with the entire feature set was superior to other methods and attained the highest predicted accuracy of 97.831%. A DT classifier was 97.45% correct and generated 28 understandable rules.". The importance of high-performing as well as explainable models for the purpose of therapy was highlighted by this work in order to capitalize on the same data set of 1,385 hepatitis C Egyptian patients.

Ghazal et al. (2021) [17] developed a predictive model named Hep-Pred to predict advanced levels of liver fibrosis. To limit the parameter space, their method used a SVM model with feature selection optimization and utilized 29 clinical features. Using five-fold cross-validation, Hep-Pred was stunning at a 97.9% accuracy, outperforming the existing models such as the DT classifier that had an accuracy of 84.8%. This performance is an example of the flexibility and capacity of SVM to suit hard classification tasks in clinical data sets, particularly when employed in conjunction with suitable feature selection methods. The study demonstrates how accurate machine learning models can enhance liver fibrosis early detection and staging, which plays a pivotal role in successful hepatitis C treatment regimens.

For enhancing liver fibrosis diagnosis precision, Suárez et al. (2023) [18] developed an EL framework on different classifiers. They considered their model to be more sensitive and specific compared to other single-model approaches, providing an equilibrated diagnostic performance. For evaluating significant liver fibrosis in patients of chronic hepatitis B, Jiang et al. (2025) [19] focused on designing noninvasive diagnostic models. The RF model gave the highest area under the receiver operating characteristic curve (AUC) of 0.819, according to their comparison of six machine learning methods. The paper demonstrates the effectiveness of ensemble methods like RF, where diagnosis is improved through combining many decision trees' decisions. Another publication developed an AI-driven, platelet-independent noninvasive liver fibrosis test. This screening is particularly beneficial for patients whose platelet count can be a poor estimator. With an AUC of 0.886 in the detection of severe fibrosis (≥ F2), SVM was superior to the logistic regression and XGBoost models out of the models used. This shows how SVM can be utilized to develop noninvasive diagnostic tools that are sensitive and specific. In order to identify liver steatosis and fibrosis in their early stages, the FibrAIm project employed machine learning techniques on normalized screening data. The model successfully identified individuals who were at risk, proving the value of early identification and the efficacy of EL for population-level screening approaches.

Lastly, Alotaibi et al. in (2023) [20] extensively reviewed different machine learning methods for predicting advanced fibrosis and stages of cirrhosis. The study revealed that ensemble models such as widely utilized XGBoost performed better for the most part compared to individual algorithms. The study addressed a significant issue with adopting machine learning advancements in actual clinical practice by utilizing explainable artificial intelligence (XAI) techniques to enhance the clinical interpretability of the models. All these findings support the general view that EL techniques, especially when supplemented with interpretability frameworks, are a strong and reliable method to push the diagnosis of noninvasive liver disease. The Fuzzy Fibrosis Decision Support System (F2DS), which employs fuzzy logic and machine

learning to address the issue of predicting the stages of liver fibrosis, was also presented in a study in 2025 Alotaibi et al. in (2025) [21].

The latest advancements in machine learning techniques, namely SVM, DT, and ensembles, have proven highly promising for improving the identification and staging of liver fibrosis in patients with hepatitis. According to a comprehensive review of literature, SVM and DT complement one another to classify liver fibrosis: Although DT provides interpretable decision paths through their hierarchical branch structure, SVM has good classification performance by detecting optimal hyperplane separations in high-dimensional feature spaces.

This paper proposes an ensemble method that combines SVM and DT create a more reliable diagnostic framework for liver fibrosis assessment. Moreover. integration between SVM classification accuracy and DT effectively addressing the limitations of each individual model while preserving their respective strengths. This study strengthens previous research and underscores the medical significance of EL, emphasizing its potential as an established technique in liver disease.

3. METHODOLOGY

The theoretical framework for this study is developed to address gaps identified in the literature, particularly those related to the detection and classification of liver fibrosis and hepatitis C through and feature engineering methods. For that reason, this comprehensive framework is designed to operational the process and enhance the accuracy and reliability of our classification models, ultimately contributing significant insights to the field. **Figure 1** shows that methodology encompasses with the following phases only, Dataset Acquisition, Pre-Processing layer (One hot encoding, Data Visualization, Data cleaning), Feature Extraction and Selection using the ML algorithms, the splitting the data between training and testing, and utilizing cross validation and evaluation results to measure the performance of the model. By following the structured approach, seek to improve the accuracy and reliability of detecting and classifying liver fibrosis in hepatitis C.

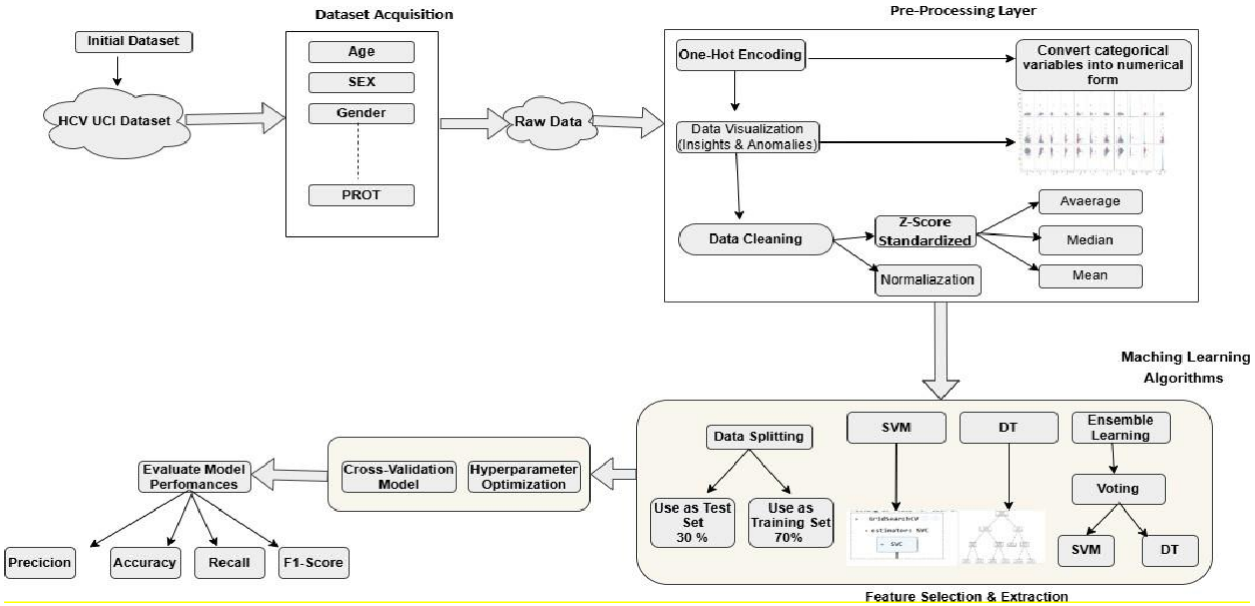

Figure 1. Proposed Framework of Methodology

3.1 Environmental Setup

The proposed model is created in the Jupyter environment using Python for the experiments. Additionally, used Jupyter Lab a web-based interactive tool, to organize and configure various aspects of data science, such as scientific computing, computational journalism, and machine learning. **Figure 1** shows the Proposed Framework of methodology. The methodology focuses on improving the accuracy of predicting liver fibrosis disease in hepatitis C patients, assessing the severity of the disease, and developing a patient recommendation system.

In this study, HCV UCI dataset utilized to comprising 615 records with 14 attributes. The dataset includes laboratory reports from both blood donors and non-blood donors diagnosed with Hepatitis C, along with demographic information such as age and sex. The response variable for classification is categorical, distinguishing between healthy individuals (blood donors) and patients with liver disease (non-blood donors). The dataset further categorizes liver disease into four stages, including Hepatitis C, fibrosis, and cirrhosis. Specifically, the dataset contains 540 records for blood donors, 24 for Hepatitis patients, 21 for fibrosis patients, and 30 for cirrhosis patients.

3.2 Pre-Processing Layer

The dataset comprises 14 attributes, including Age, Sex, Albumin (ALB), Alkaline Phosphatase (ALP), Bilirubin (BIL), Choline Esterase (CHE), Gamma-Glutamyl Transferase (GGT), Aspartate Aminotransferase (AST), Alanine Aminotransferase (ALT), Creatinine (CREA), Total Protein (PROT), and Cholesterol (CHOL). Among these, the variables sex and outcome are categorical, while age is continuous. The preprocessing steps applied to the dataset include scaling, encoding, and handling numeric data. **Table 1** provides a detailed description of the attributes, their preprocessing steps, and the feature names with corresponding values. This representation clarifies the role of each attribute in model training and documents the preprocessing steps to support reproducibility. It also shows how categorical and continuous variables were handled consistently to maintain uniformity throughout the modeling pipeline.

Table 1. Description of Attributes

Sr No	Features Name	Values	Pre- processing	Description
1	Age	Continuous	Scaling	The age of the patient
2	Sex	Binary	Encoding	The sex of the patient
3	ALB	Numeric	Scaling	Albumin quantity in the blood
4	ALP	Numeric	Scaling	Alkaline phosphatase in the blood
5	ALT	Numeric	Scaling	Alanine aminotransferase (liver damage status)
6	AST	Numeric	Scaling	Aspartate aminotransferase in the liver
7	BIL	Numeric	Scaling	Bilirubin test value in the blood
8	CHE	Numeric	Scaling	Serum cholinesterase (liver function)
9	CHOL	Numeric	Scaling	Cholesterol in the blood
10	CREA	Numeric	Scaling	Creatinine in the blood
11	GGT	Numeric	Scaling	Creatinine in the blood

12	PROT	Numeric	Scaling	Protein test
13	Category	Multi-Class	Encoding	Class Label

Missing data is a common issue in applications of data science. For that purpose, initially, researcher have been evaluated dataset to identify feature categories such as numeric, multiclass, binary and continuous and in the preprocessing layer scaling and encoding. Subsequently, target variable in a multi-class classification problem is a categorical feature spanning more than two classes. The target variable in a multi-class classification issue is a categorical feature that has more than two classes. Class labels are transformed into a numerical format appropriate for ML algorithms using encoding approaches like label encoding in order to get this dataset ready for training and testing. Following encoding, continuous numerical features are scaled to ensure constant value ranges for the best model performance, and binary and multi-class categorical values are suitably converted.

3.4 Data Cleansing

Dataset preparation is a crucial step in EL methods of ML algorithms to ensure accurate prediction of liver fibrosis detection. For that purpose, feature scaling and feature encoding process are included. Therefore, one-hot encoding was used for feature encoding process to converting categorical data into binary vectors in the integer format for enhancing the correct detection of Liver Fibrosis. As a result, converting each category into a binary vector where the index corresponding to the integer is set to '1' and all other indices are set to '0'. Additionally, reducing the impact of attributes with higher values predominating while computing distance was achieved via Z-score standardization. By means of this formula, the dataset is normalized into a conventional normal distribution with a mean of 0 and a standard deviation of 1. [22].

$$z = (x - \mu) / \sigma \quad (1)$$

where x represents the data point, μ is the mean of the dataset, σ is the standard deviation of the dataset.

After applying the Z-Score formula, **Figure 2** highlights the statistics of the features such as mean, median, standard deviation. Therefore, modification promotes outlier detection and improves comprehension of data distribution [23]. To make sure the central tendency is aligned, the dataset's mean was recalculated to confirm it is zero by computing the z-scores. In addition, the median was examined to ensure consistency as a measure of central tendency, despite the fact that it is not directly impacted by z-scores. As a result, standard deviation computation confirmed the data dispersion around the mean, However, the data point count offered a thorough grasp of the dataset size [24]. Thereafter, dataset is normalized, a comprehensive standardization procedure shows the statistical analysis to improves the accuracy and training of ML models such as SVM, DT and EL, as shown in **Table 2**.

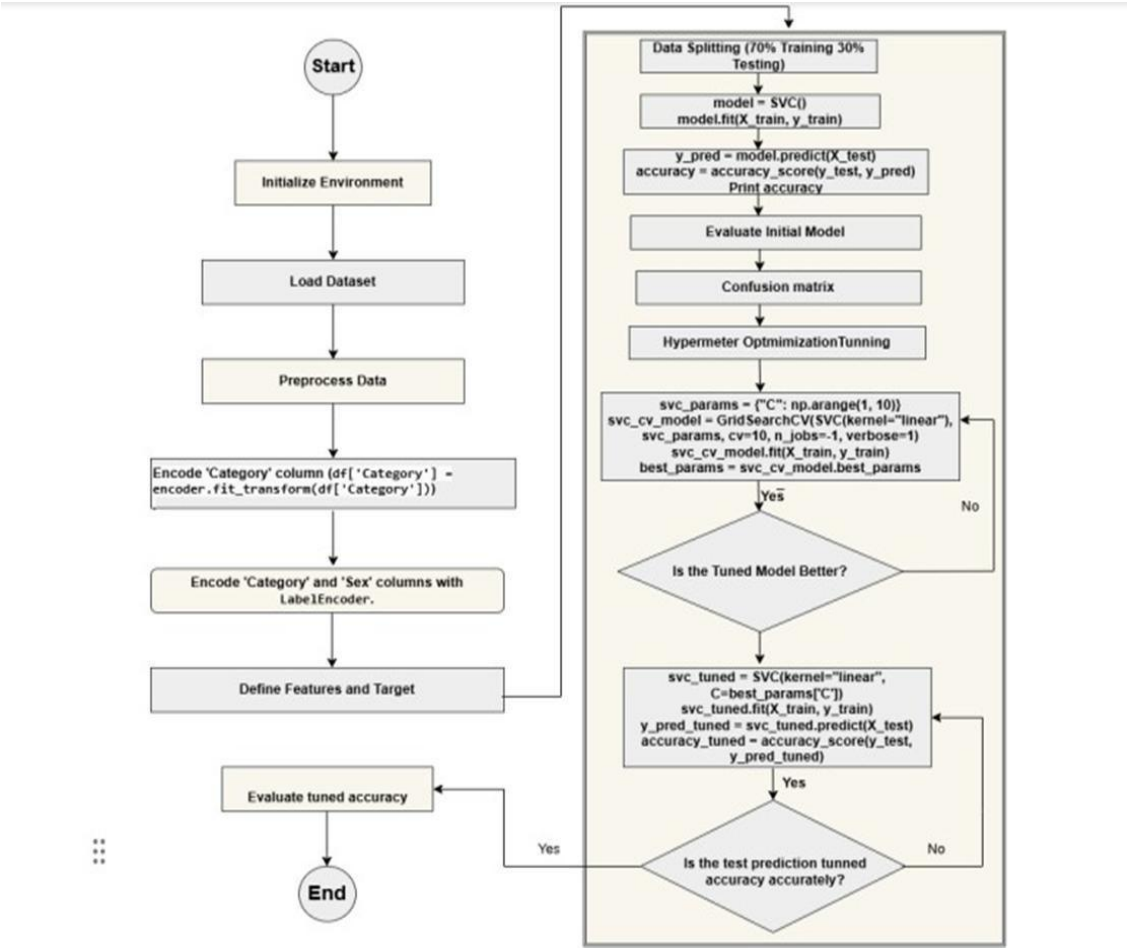

Figure 2. Flowchart of the Support Vector Machine

Table 2. Z-Score Standardized

	Age	Sex	ALB	ALP	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
Count	615.0	615.0	615.0	615.0	615.0	615.0	615.0	615.0	615.0	615.0	615.0	615.0
Mean	47.408	0.487	41.155	66.285	28.045	34.786	11.397	8.14	5.281	81.288	39.533	71.927
Std	10.405	0.487	6.148	28.112	25.475	30.097	19.673	2.206	1.313	49.756	54.646	6.13
Min	19.0	0.0	20.0	0.0	0.0	10.6	0.8	1.42	2.0	0.0	4.5	50.0
25%	39.0	0.0	38.8	51.7	16.4	21.6	5.3	6.935	4.458	67.0	20.3	69.3
50%	47.0	1.0	41.7	65.3	25.9	25.9	7.3	8.52	5.29	77.0	33.0	72.2
75%	54.0	1.0	44.3	79.3	35.3	32.1	12.1	9.55	6.055	88.0	47.8	75.4
max	77.0	1.0	82.0	416.0	325.3	324.0	254.0	16.41	9.67	1079.1	650.9	90.0

4. DEVELOPMENTS OF THE MODELS

In the constantly changing field of ML, creating robust models is crucial to detecting insightful results from complex datasets. In order to revolutionize data classification and predictive analytics, this study employed three primary methodologies: SVM, DT and EL. Each technique has unique benefits, making them all highly effective in identifying liver fibrosis and hepatitis C.

The **"Development of the Models"** section placed more emphasis on DT, which limited the discussion of SVM and ensemble approaches. In the revised version, the coverage of SVM has been expanded to emphasize its strength in handling high-dimensional medical datasets and its relevance in liver disease prediction. The DT discussion has been condensed to maintain balance, while new references on ensemble learning—particularly the Voting Classifier—have been added to illustrate its role in improving diagnostic accuracy. These updates ensure a more comprehensive and balanced presentation of SVM, DT, and ensemble methods within the methodological framework.

4.1 Support Vector Machines (SVM)

SVM was developed by Vladimir Vapnik and Alexey Chervonenkis in the 1960s It is defined is a supervised machine learning algorithm used for classification and regression tasks [25]. Additionally, finds the ideal hyperplane in a high-dimensional space that divides data points of several classes most effectively. Working with high-dimensional data [26], SVM are resilient against overfitting and SVM studies clinical data and biomarkers to improve liver fibrosis detection accuracy. **Figure 2** shows the SVM flowchart, which comprises feature engineering and preprocessing meant to raise model performance. Once noise has been removed, SVM is used to identify relevant features. Examining the dataset, filling in missing variables, and using data visualization help one to understand changing relationships. Following data distribution into training and test sets, an initial SVM model is trained and evaluated. GridSearch CV hyperparameter adjustment helps to improve the model even more. These planned work flows guarantee strong SVM model development for liver fibrosis detection in Hepatitis C.

While SVMs are typically less prone to overfitting, we addressed potential risks by applying GridSearch-based hyperparameter tuning combined with stratified cross-validation to ensure balanced generalization. To avoid dependence on a single model, SVM was evaluated alongside DTs and then combined in a Voting Classifier. The close agreement between training and testing accuracies, together with confusion matrix results, confirmed that overfitting had no significant impact on our findings**DECISION** TREE (DT)

DT are great for detecting liver fibrosis in people with Hepatitis C because they can handle both number and categorical data and are easy to understand. Studies including those by Maimone et al. (2018) [27] and Nitta et al. (2019) [28] show how well decision trees classify fibrosis phases using a range of biomarkers and clinical data. Emphasizing how they might be used with non-invasive testing to increase accuracy, Wang et al. (2021) [29] and Kim et al. (2020) [30] The dataset is investigated to ascertain its structure, missing values are evaluated, and data preparation is performed before applying decision trees in this work. After categorical variable encoding for numerical input, **Figure 3** shows how the dataset is split in training and testing sets in a 70-30 ratio. An initial DT model trained with the Gini criteria, which evaluates node impurity, helps one to make predictions. The model decision-making process helps one to grasp its working mechanism Liu et al. (2022) [31]. Moreover, a Gini-based model is compared with a DT model developed using the Entropy criterion measuring information gain.

While larger datasets are preferable, our dataset of 615 records and 14 attributes reflect common clinical constraints and to mitigate risks of bias or overfitting we applied cross-validation, hyperparameter tuning, and EL. We acknowledge that a larger dataset would strengthen the conclusions and have noted this in the Limitations and Future Work section. Regarding model choice, SVM, though often applied to high-dimensional data, is also effective in medium-sized medical datasets with nonlinear patterns and was selected for its robustness and complementarity to DT. DTs, although best suited for categorical data, also perform well on continuous attributes when guided by appropriate splitting criteria; in this study, their interpretability complemented SVM's margin-based learning. By integrating both in a Voting Classifier, the ensemble balanced their strengths, mitigated individual weaknesses, and achieved superior generalizability. These justifications and acknowledgments have been incorporated into the revised manuscript.

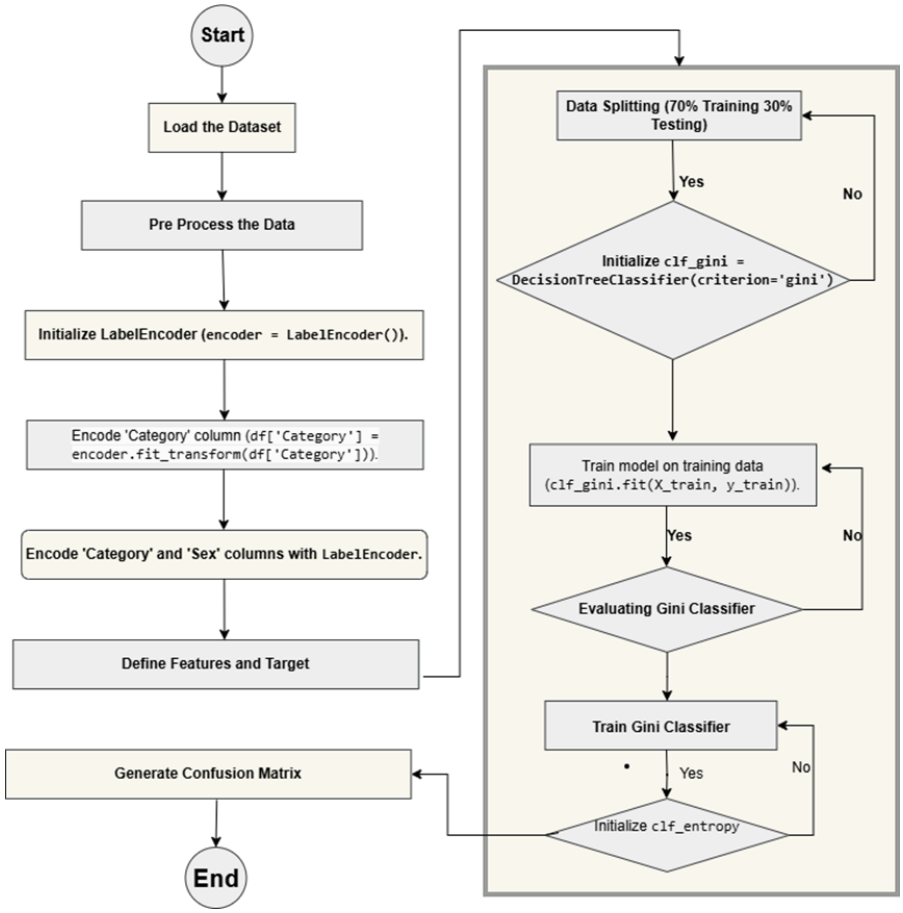

Figure 3. Flowcharts of the decision tree

5. ENSEMBLE LEARNING

Ensemble learning (EL) is a type of machine learning that takes results from several different models, like SVM and DT, and combines them to make a stronger, more accurate, and more general model. Often times, ensemble methods beat single-model approaches by using the strengths and offsetting the shortcomings of every individual model. A powerful meta-machine learning method, EL aggregates predictions from many models to improve accuracy. Leveraging the benefits of both, this work aggregates SVM with DT. As demonstrated in **Figure 4**, the ensemble framework begins with developing individual models, which are subsequently integrated into a voting classifier. After that. hyper-parameter is used and train the model. Finally, researcher have been used the evaluation metrics such as accuracy, precision, recall, and F1-score; a confusion matrix to measures the performance of models. Finally, EL approach guarantees strong and consistent liver fibrosis detection, therefore proving the effectiveness of ensemble methods in managing complex medical diagnostics and improving prediction outcomes.

While SVMs are robust for high-dimensional data, they are sensitive to parameter selection, less effective with categorical variables, and vulnerable to noise or class imbalance, whereas Decision Trees, though interpretable, are prone to overfitting and performance variability depending on the splitting criterion. By integrating SVM and DT within a soft Voting Classifier, the ensemble offsets these weaknesses—leveraging the interpretability of DTs and the margin maximization of SVMs—thereby reducing variance, improving

robustness, and consistently achieving higher test accuracy than individual models. This discussion has now been incorporated into the revised *Discussion* section to justify the adoption of the ensemble framework.

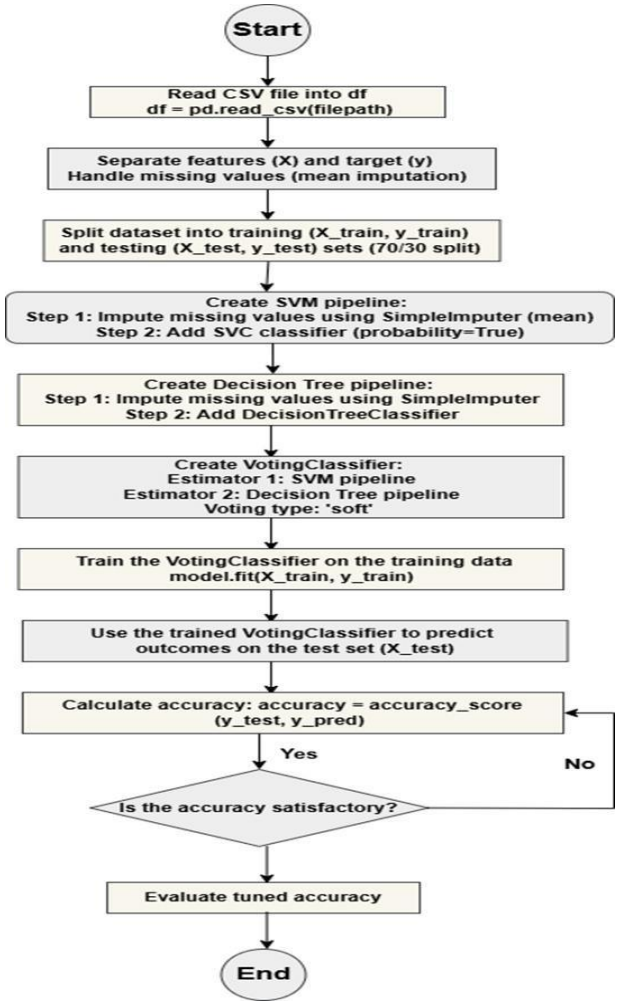

Figure 4. Flowcharts of the Ensemble learning

Diagrams specify that ≥80% accuracy was considered satisfactory, consistent with prior clinical decision support literature where 70–80% is deemed useful and ≥80% indicates stronger reliability. In addition to accuracy, we evaluated sensitivity, specificity, precision, and recall via the confusion matrix to ensure clinical relevance, and we clarified in the flowchart that "satisfactory accuracy" refers to ≥80% accuracy with balanced performance across metrics. These additions enhance clarity, reproducibility, and transparency for future replication.

6. RESULTS AND DISCUSSIONS

SVM, DT, and EL are among the models that are assessed. After 10-fold cross-validation, SVM models initial Sklearn accuracy score of 91.53% increased to 95.48%. The SVM model computed metrics include 96.79% accuracy, 100% precision, 96.79% recall, and 98.36% F1 score. With an accuracy of 98.03%, precision of 100%, recall of 97.69%, and F1 score of 98.83%, DT model performed marginally better. With a 99.46% model accuracy, the EL model performed better than the others. The average precision of 100%, average recall of 95.96%, and average F1 score of 97.87% are the overall metrics for the multiclass

confusion matrix. Moreover, the evaluation metrics used to assess the performance of the ML models include accuracy, precision, recall, and F1 score. Accuracy is calculated as the ratio of correctly predicted observations to the total observations. It is given by the formula:

$$\text{Accuracy} = (\text{TP} + \text{TN}) / (\text{TP} + \text{TN} + \text{FP} + \text{FN}) \quad (2)$$

Precision is defined as the ratio of true positive predictions to the total predicted positives. It indicates the model's ability to avoid false positives:

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

Recall (also known as sensitivity or the true positive rate) measures the model's ability to identify all relevant instances:

$$\text{Recall} = \text{TP} / (\text{TP} + \text{FN}) \quad (4)$$

F1 Score provides a balance between precision and recall. It is the harmonic mean of the two and is calculated as:

$$\text{F1 Score} = 2 \times (\text{Precision} \times \text{Recall}) / (\text{Precision} + \text{Recall}) \quad (5)$$

These metrics together provide a comprehensive view of model performance, especially in imbalanced dataset. **Table 3** highlights the Performance Comparison of SVM, DT, and EL Models while **Figure 5** shows its comparison graph

Table 3. Performance Comparison of SVM, DT, and Ensemble Learning Models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1 Score (%)
SVM (10-fold CV)	95.48	100.00	96.79	98.36
Decision Tree (DT)	98.03	100.00	97.69	98.83
Ensemble Learning (EL)	99.46	100.00	95.96	97.87

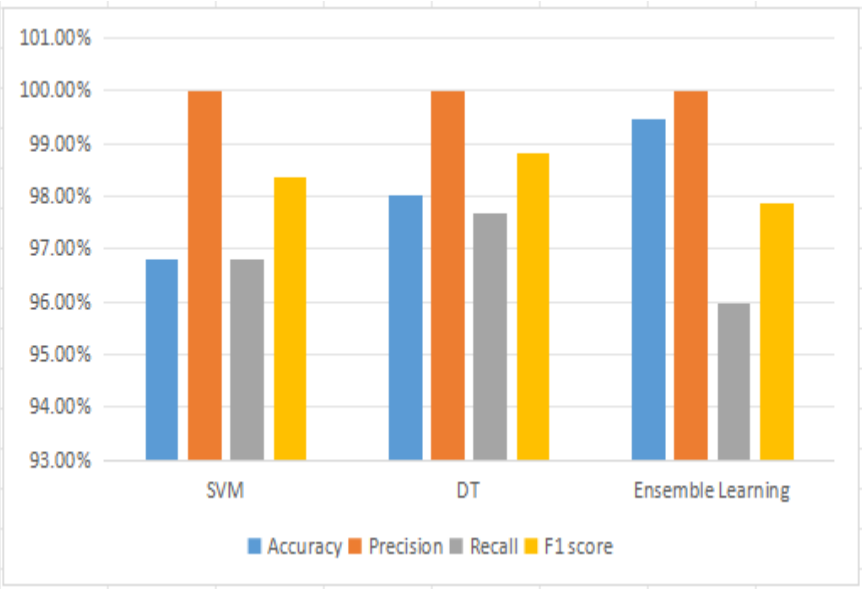

Figure 5. Model Matrix Graph

Figure 5 illustrates the comparative performance of SVM, DT, and the EL model (Voting Classifier) across four evaluation metrics: Accuracy, Precision, Recall, and F1-score. The SVM attained approximately 96.8% accuracy, 100% precision, 96.8% recall, and 98.6% F1-score. The Ensemble model recorded the highest accuracy (around 99%), while also maintaining 100% precision, 96% recall, and 97.8% F1-score, reflecting the complementary strengths of SVM and DT.

These outcomes highlight how reliable and effective the machine learning methods used were. The EL Model in particular performed the best overall, demonstrating its capacity to combine the advantages of several models to produce high reliable and accurate predictions. These results are consistent with previous studies that demonstrate the advantages of ensemble approaches for enhancing prediction performance. The high metrics across accuracy, precision, recall, and F1 scores for the EL model demonstrate how ensemble methods are known to achieve superior accuracy and balanced performance.

7. CONCLUSION

In recent years, the hepatitis C virus (HCV) infection has afflicted many people worldwide and led to severe liver diseases like hepatocellular carcinoma and fibrous disorders. Given patient data, it is challenging to classify liver fibrosis in HCV patients. Conventional diagnostic methods, depending on clinical opinion, are time-consuming and prone inhuman mistake, which often delays diagnosis. Therefore, it is imperative to design a model that enhances accuracy and timeliness of diagnosis. This paper investigates the possibility of machine learning techniques including EL, decision trees, and SVM to raise diagnostic accuracy and efficiency. Data preparation which included carefully deleting noisy and null data as well as imputation of missing values, it was an absolutely vital initial step. This procedure assured that the dataset which comprised 615 entries from the HCV UCI repository with 14 attributes, was correct and comprehensive. Feature encoding, scaling, and thorough data visualization were applied to prepare the data for study and to understand the relationships between variables.

Every machine learning model has special benefits. SVM is resistant to overfitting and manages high-dimensional data well. Decision trees help predict the stage of liver fibrosis accurately because they can handle both numerical and categorical data. To get the best results, EL combines the predictions of several models, such as SVM and DT. Metrics like accuracy, precision, recall, and F1 score were used to thoroughly

assess the models' performance. The SVM model's accuracy was 96.79%, while its precision and recall were 100% and 96.79%, respectively. With an accuracy of 98.03% and an F1 score of 98.83%, the DT model did marginally better. With an accuracy of 99.46%, precision of 100%, recall of 95.96%, and F1 score of 97.87%, the EL model outperformed the others. These findings demonstrate the potency and efficacy of machine learning techniques, especially ensemble methods, in enhancing liver fibrosis diagnosis prediction performance. The ability of EL to combine several models to lower bias and variance was very helpful. The study supports earlier findings and shows how machine learning can revolutionize medical diagnostics. By incorporating these cutting-edge techniques into clinical practice, diagnostic results can become more accurate, reliable, and consistent, which will ultimately improve patient care. To improve early detection and treatment of liver fibrosis in HCV patients, future studies should improve these models, integrate bigger and more varied datasets, and investigate how to integrate them into clinical decision-making systems.

8.1 Future Directions

Although the proposed EL framework demonstrated encouraging results in detecting liver fibrosis among Hepatitis C patients, several avenues remain for future investigation. Validation on larger and more heterogeneous datasets, preferably collected from multiple clinical centers, is necessary to improve generalizability and robustness. Moreover, advanced ensemble methods such as stacking, bagging, and boosting (e.g., XGBoost, LightGBM, Random Forests) could be explored to further strengthen predictive accuracy.

Given the suitability of SVM for high-dimensional data, future studies may extend the model to include genomic, proteomic, and imaging variables, thereby supporting multi-modal prediction of fibrosis progression. Addressing class imbalance through synthetic resampling techniques such as SMOTE may also enhance classification performance across fibrosis stages.

For clinical application, incorporating explainable machine learning approaches such as SHAP or LIME will be important to improve interpretability and physician confidence in the predictions. Additionally, longitudinal modeling to capture disease progression over time, along with integration into clinical decision support systems (CDSS) connected to electronic health records (EHRs), represents a crucial step toward real-world implementation.

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