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Enhancing Liver Disease Classification Using Support Vector Machine with IQR-Based Outlier Handling

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Abstrak

Penyakit hati merupakan masalah kesehatan yang signifikan dan memerlukan diagnosis dini serta akurat untuk mencegah komplikasi serius. Dalam penelitian ini, kami mengusulkan pendekatan penyaringan outlier menggunakan metode *Interquartile Range* (IQR) untuk meningkatkan kinerja algoritma *Support Vector Machine* (SVM) dalam klasifikasi penyakit hati. Dataset penyakit hati yang tersedia secara publik, terdiri dari 1.700 data pasien dengan berbagai atribut klinis, digunakan dalam penelitian ini. Metode IQR diterapkan untuk mendeteksi dan menghapus nilai-nilai ekstrem sebelum proses pelatihan model. Model SVM menggunakan kernel *Radial Basis Function* (RBF) untuk menangkap hubungan nonlinier dalam data. Klasifikasi dievaluasi dalam dua kondisi: tanpa dan dengan penghapusan outlier berbasis IQR. Metode evaluasi kinerja meliputi akurasi, presisi, *recall*, skor F1, dan ROC-AUC. Hasil eksperimen menunjukkan bahwa pra-pemrosesan menggunakan IQR meningkatkan kinerja model, dengan akurasi meningkat dari 84,41% menjadi 84,74% dan skor ROC-AUC naik dari 92,08% menjadi 93,28%. Secara khusus, *recall* untuk kelas negatif meningkat dari 84,31% menjadi 89,76%, yang menunjukkan peningkatan deteksi pasien sehat. Temuan ini menunjukkan bahwa penanganan outlier menggunakan IQR dapat memberikan kontribusi terhadap hasil klasifikasi yang lebih stabil dan akurat, terutama untuk model yang sensitif terhadap ketidakteraturan data seperti SVM.

Kata Kunci: *Support Vector Machine*, IQR, Penyaringan Outlier, Klasifikasi Penyakit Hati, *Machine Learning*

Abstract

Liver disease is a significant health issue that requires early and accurate diagnosis to prevent serious complications. In this study, we propose an outlier filtering approach using the Interquartile Range (IQR) to enhance the performance of the Support Vector Machine (SVM) algorithm in liver disease classification. A publicly available liver dataset consisting of 1,700 patient records with various clinical attributes was used, and the IQR method was applied to detect and remove extreme values before model training. The SVM model employed the Radial Basis Function (RBF) kernel to capture nonlinear relationships in the data. The classifier was evaluated under two conditions: without and with IQR-based outlier removal. Performance metrics including accuracy, precision, recall, F1-score, and ROC-AUC were used to assess the model. The experimental results showed that the IQR-based preprocessing improved model performance, with the accuracy increasing from 84.41% to 84.74% and the ROC-AUC score rising from 92.08% to 93.28%. Notably, the recall for the negative class improved from 84.31% to 89.76%, indicating enhanced detection of healthy patients. These findings demonstrate that outlier handling using IQR can contribute to more stable and accurate classification outcomes, especially for models that are sensitive to data irregularities such as SVM.

Keywords*: Support Vector Machine, IQR, Outlier Filtering, Liver Disease Classification, Machine Learning*

1. INTRODUCTION

Liver disease is a serious global health concern with increasing prevalence and significant mortality rates. According to the World Health Organization (WHO), liver-related illnesses are responsible for approximately 2 million deaths annually, positioning them among the top eleven causes of death worldwide [1]. A substantial proportion of these deaths result from cirrhosis, liver cancer, and complications arising from chronic hepatitis infections. The Global Burden of Disease Study also reports a steady rise in liver disease cases over the past decade, particularly in low- and middle-income countries [2]. In regions such as Southeast Asia, including

Indonesia, early diagnosis remains a challenge. It is estimated that more than 60% of liver disease cases are identified only at advanced stages, reducing the likelihood of effective intervention [3].

Machine learning has emerged as a promising approach to support the early classification of liver disease cases. Compared to traditional diagnostic procedures, machine learning-based models can provide faster and more cost-effective predictions while minimizing the dependence on specialized clinical expertise [4]. Among available algorithms, classical models such as Logistic Regression, Decision Tree, K-Nearest Neighbor, and Support Vector Machine (SVM) are widely used due to their interpretability, computational efficiency, and suitability for limited datasets. In contrast to ensemble or deep learning approaches that often require large-scale data and substantial computational resources, classical models offer greater transparency and are easier to integrate into clinical decision-support systems [5]. The effectiveness of SVM in handling medical classification problems is also demonstrated in heart disease prediction. There is a study reporting that SVM achieved 91.8% accuracy in heart disease classification, outperforming K-Nearest Neighbor (88%) and Logistic Regression (83%) [6]. This result reinforces the robustness of SVM in handling medical datasets with nonlinear patterns and supports its selection as the sole algorithm in this study, given its balance of accuracy, computational efficiency, and adaptability to limited clinical data.

Several studies have applied classical machine learning algorithms to liver disease classification. One study implemented a pruned Decision Tree and achieved an accuracy of 73.76%, yet did not address outlier presence [7]. Another work used K-Nearest Neighbor with elbow-based optimization and reported an accuracy of approximately 75%, though performance inconsistency suggested the need for better preprocessing [8]. Logistic Regression, Naive Bayes, and KNN have also been tested for predicting liver cirrhosis, with Logistic Regression achieving 85% accuracy but without any specific data cleaning [9]. Naive Bayes was evaluated with cross-validation and obtained 64.3% accuracy, further emphasizing the variability of performance when data quality is not optimized [10]. Most of these studies did not explicitly incorporate outlier handling techniques, which are crucial to improving generalization and fairness in classification tasks.

This study proposes an approach to improve the performance of Support Vector Machine (SVM) in liver disease classification by applying outlier filtering using the Interquartile Range (IQR) method. SVM has a strong ability to construct an optimal hyperplane that separates classes with the maximum margin and demonstrates excellent performance when dealing with high-dimensional and complex data [11]. Despite these advantages, SVM is highly sensitive to data irregularities such as outliers [12]. Outliers can distort the decision boundary and significantly reduce model accuracy. IQR is a statistical technique that identifies and removes extreme values lying outside the interquartile range, thereby reducing noise and improving the representativeness of the data used for model training [13]. Unlike scaling techniques such as RobustScaler, which reduce the influence of outliers without removing them, IQR-based filtering actively excludes such values, which can be particularly beneficial for sensitive algorithms like SVM [14].

The main contribution of this research is the implementation and evaluation of IQR-based outlier removal as a preprocessing step to optimize SVM performance in classifying liver disease. This study compares the performance of SVM models trained on raw data with those trained on data processed through IQR filtering. The effectiveness of the proposed approach is evaluated using metrics such as accuracy, precision, recall, F1-score, and ROC-AUC.

2. METHODS

The development of a liver disease classification model using the Support Vector Machine (SVM) algorithm and the Interquartile Range (IQR) outlier handling method was carried out through a series of systematic and structured stages. Each step in the research process is carefully designed not only to ensure the reproducibility of the proposed approach across implementations, but also to provide conceptual and procedural clarity that allows other researchers to understand, replicate, and potentially extend the methodology in similar future studies [15]. The overall research process is illustrated in Figure 1.

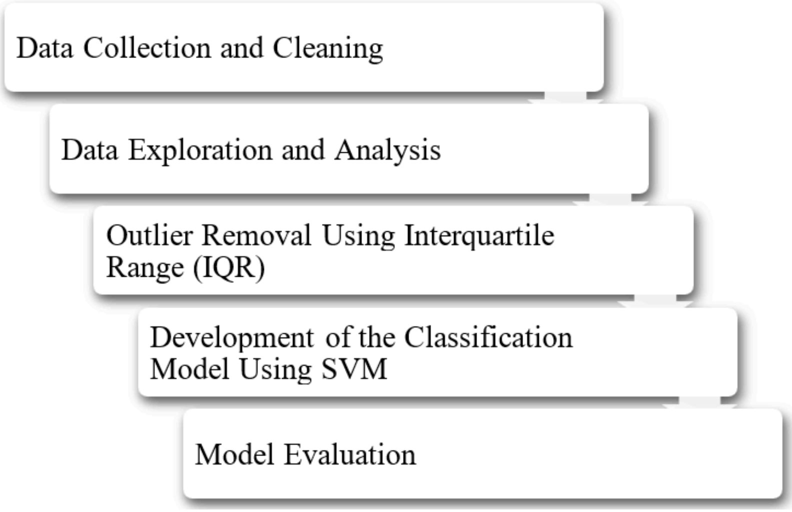


Figure 1. Research Procedure

Referring to Figure 1, each stage carried out is explained in detail as follows.

2.1. Data Collection and Cleaning

The dataset used in this study was obtained from a publicly available source titled "Liver Disease Dataset" [16]. It contains medical records of 1,700 patients and includes various clinical attributes such as Age, BMI, Alcohol Consumption, Smoking, Genetic Risk, and Liver Function Test results. The target variable is labeled as *Diagnosis*, indicating whether a patient is diagnosed with liver disease (1) or not (0). Prior to modeling, data cleaning was conducted, which included the removal of missing values and the conversion of all features to numerical format. This step ensured data quality and consistency, forming a strong basis for further analysis.

2.2. Data Exploration and Analysis

An initial exploratory data analysis was performed to understand the overall characteristics of the dataset. Descriptive statistics and visualization tools such as histograms, boxplots, and correlation heatmaps were employed to observe feature distributions, assess the relationships between variables, and detect potential outliers. This analysis revealed that several features contained extreme values, which could potentially distort the learning process of the model. Based on these findings, the application of outlier filtering using IQR was considered essential for improving model robustness.

2.3. Outlier Removal Using Interquartile Range (IQR)

The IQR method was applied to remove extreme values from each feature. IQR is a statistical measure calculated as the difference between the third quartile (Q_3) and the first quartile (Q_1), as shown in Equation (1).

$$IQR = Q_3 - Q_1 \tag{1}$$

A data point x is considered an outlier if it is outside the range of values based on equation (2).

$$x < Q_1 - 1.5 \times IQR \text{ or } x > Q_3 + 1.5 \times IQR \tag{2}$$

This method was applied independently to each numerical feature [17]. Observations identified as outliers were removed from the dataset. By excluding such extreme values, the data became more representative of the true population distribution [18]. This step aimed to reduce noise and improve the learning performance of the SVM classifier, which is known to be sensitive to outliers.

2.4. Development of the Classification Model Using SVM

Support Vector Machine (SVM) is a supervised classification algorithm that aims to find the optimal hyperplane separating two classes with the maximum margin [19]. In this study, the Radial Basis Function

(RBF) kernel was used, as it allows the model to handle nonlinear relationships among features effectively. SVM solves a convex optimization problem, as shown in Equation (3).

$$\frac{1}{2}||w||^2 \text{ with conditions } y_i\left(w^T x_i + b\right) \geq 1,\ \forall_i \qquad (3)$$

To account for non-linearly separable data, slack variables and a penalty parameter *C* were introduced. These allow the model to tolerate some misclassifications while maintaining a wide margin. While SVM is known for its generalization ability, it is also sensitive to noisy data and outliers [20]. Therefore, applying IQR-based outlier removal before model training is expected to enhance classification stability and accuracy.

The RBF kernel was chosen over linear kernels because it provides greater flexibility in capturing complex, nonlinear interactions among clinical features commonly found in medical datasets [21]. Unlike linear kernels that assume a straight-line separation, the RBF kernel maps input features into a higher-dimensional space where class boundaries can be more effectively defined [22]. This makes it especially suitable for handling the subtle patterns and overlapping characteristics present in liver disease data.

2.5. Model Evaluation

Model evaluation was conducted by assessing the SVM's performance on the test set using various classification metrics. The evaluation included the construction of a confusion matrix and Receiver Operating Characteristic (ROC) curve. From the confusion matrix, several key metrics were calculated to assess the model's predictive quality and class-wise performance. These included accuracy, which measures the proportion of correct predictions over the total number of cases [23]; precision, which indicates the proportion of correctly predicted positive instances among all predicted positives [24]; recall, which quantifies the proportion of actual positive instances correctly identified by the model [24]; and F1-score, which provides a harmonic mean of precision and recall, balancing both false positives and false negatives [25]. The ROC curve was used to calculate the Area Under the Curve (AUC), which reflects the model's ability to distinguish between positive and negative cases [26]. Finally, the performance of the SVM model with and without IQR-based outlier removal was compared to evaluate the impact of the preprocessing technique on classification outcomes.

3. RESULTS AND DISCUSSION

The development of a liver disease classification model using the Support Vector Machine (SVM) approach began with the preparation and selection of a suitable dataset. The dataset used in this study was obtained from a publicly available source and contains medical records of 1,700 individuals, each represented by several clinical and behavioral attributes [16]. These features include Age, Body Mass Index (BMI), Alcohol Consumption, Smoking, Genetic Risk, and Liver Function Test results. The target variable is labeled as *Diagnosis*, indicating whether a patient has been diagnosed with liver disease (1) or not (0). Prior to the modeling phase, the dataset was subjected to a data cleaning process that involved the removal of missing or inconsistent values, conversion of all features into appropriate numerical formats, and verification of class label integrity. These preprocessing steps were carried out to ensure that the dataset was of high quality and suitable for reliable model training and evaluation in subsequent stages.

The next step is exploratory data analysis involving several visual techniques to better understand the underlying structure and characteristics of the liver disease dataset. The data exploration process begins by visualizing the distribution of each numeric feature using histograms. This approach is particularly useful for identifying non-normal distributions, detecting skewness, and assessing class imbalance, all of which may influence the learning behavior of classification algorithms. A histogram showing the numeric features is presented in Figure 2.

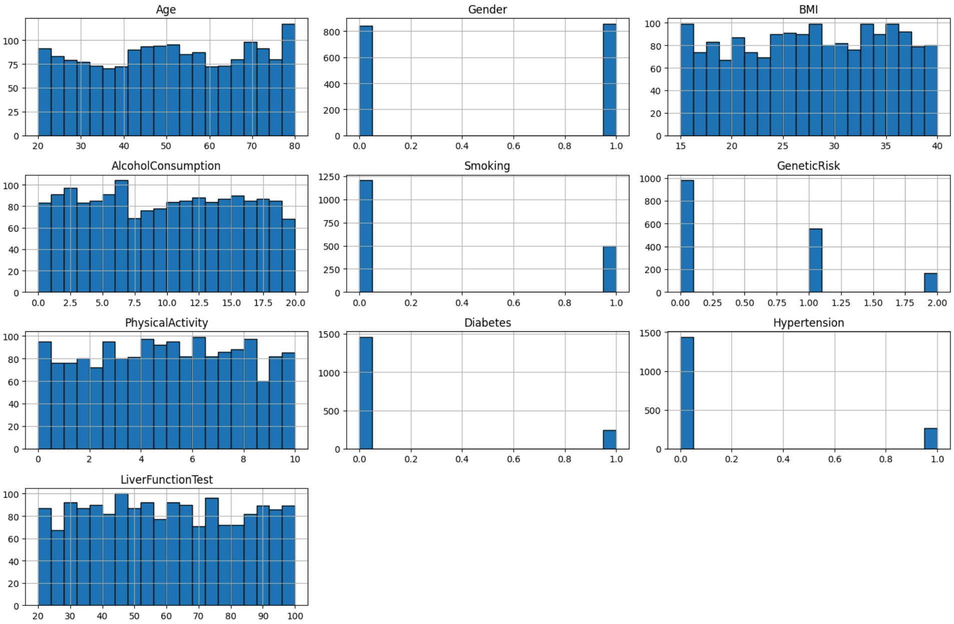
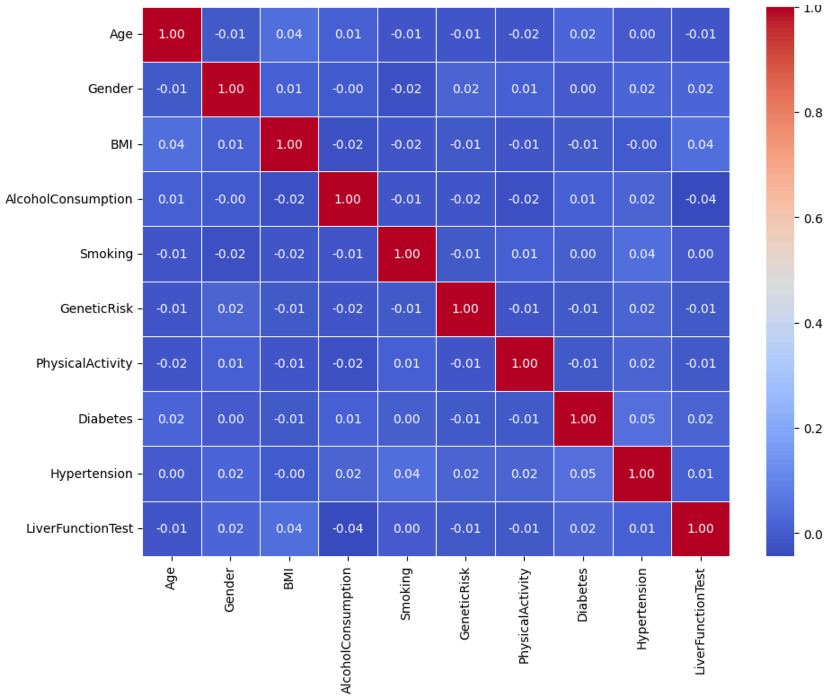


Figure 2. Histogram of Numeric Features in the Liver Disease Dataset

Figure 2 shows that features such as Age, BMI, AlcoholConsumption, PhysicalActivity, and LiverFunctionTest exhibit near-uniform or multimodal distributions. Among the binary variables, Gender appears relatively balanced, whereas Smoking, Diabetes, and Hypertension show noticeable class imbalance. While this imbalance is typical in clinical data, it does not substantially impact the exploratory objective of visualizing overall feature distributions.

The next step in data exploration is correlation analysis, which reveals pairwise relationships between features through a heatmap. This visualization helps identify strong or redundant correlations that may lead to multicollinearity, which can negatively affect some machine learning models. A heatmap illustrating the correlation matrix of the numeric features is provided in Figure 3.



	Age	Gender	BMI	AlcoholConsumption	Smoking	GeneticRisk	PhysicalActivity	Diabetes	Hypertension	LiverFunctionTest
Age	1.00	-0.01	0.04	0.01	-0.01	-0.01	-0.02	0.02	0.00	-0.01
Gender	-0.01	1.00	0.01	-0.00	-0.02	0.02	0.01	0.00	0.02	0.02
BMI	0.04	0.01	1.00	-0.02	-0.02	-0.01	-0.01	-0.01	-0.00	0.04
AlcoholConsumption	0.01	-0.00	-0.02	1.00	-0.01	-0.02	-0.02	0.01	0.02	-0.04
Smoking	-0.01	-0.02	-0.02	-0.01	1.00	-0.01	0.01	0.00	0.04	0.00
GeneticRisk	-0.01	0.02	-0.01	-0.02	-0.01	1.00	-0.01	-0.01	0.02	-0.01
PhysicalActivity	-0.02	0.01	-0.01	-0.02	0.01	-0.01	1.00	-0.01	0.02	-0.01
Diabetes	0.02	0.00	-0.01	0.01	0.00	-0.01	-0.01	1.00	0.05	0.02
Hypertension	0.00	0.02	-0.00	0.02	0.04	0.02	0.02	0.05	1.00	0.01
LiverFunctionTest	-0.01	0.02	0.04	-0.04	0.00	-0.01	-0.01	0.02	0.01	1.00

Figure 3. Correlation Heatmap of Numeric Features

Figure 3 shows that most features have very low correlation coefficients, with values close to zero. This indicates minimal linear relationships among the variables, suggesting that no significant multicollinearity is present in the dataset. As a result, all features were retained for the modeling stage without the need for dimensionality reduction or feature elimination due to redundancy.

Next, data exploration was conducted to identify potential outliers using boxplots. This visualization provides a clear representation of which features contain values that significantly deviate from the majority of the data, thereby justifying the need for outlier filtering. The boxplot illustrates the interquartile range and highlights extreme values that fall outside the whiskers, as shown in Figure 4.

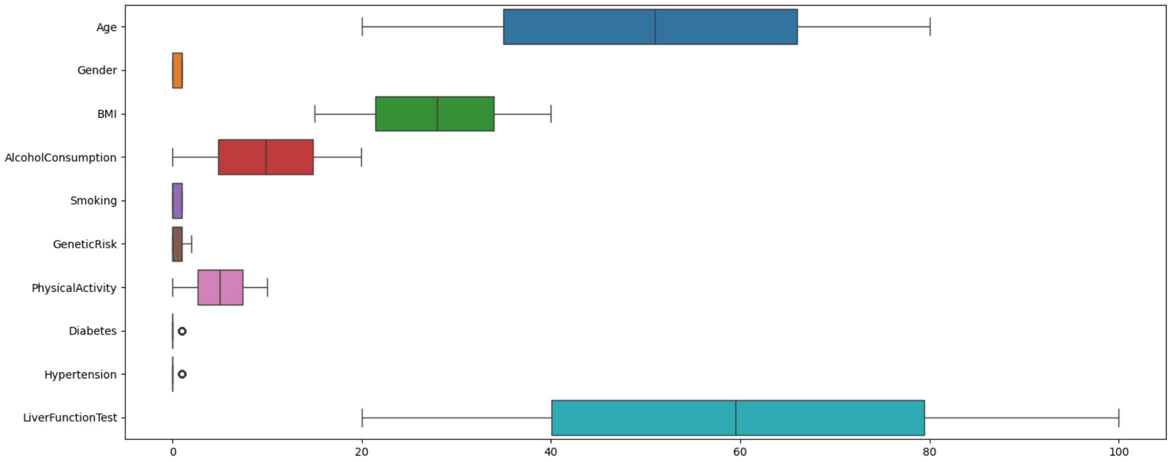


Figure 4. Boxplot of Numeric Features for Outlier Detection

Figure 4 shows that outliers are present in several features, most notably *Diabetes*, *Hypertension*, and *LiverFunctionTest*, where points lie well beyond the upper and lower whiskers. These extreme values may distort the model's decision boundaries and reduce overall accuracy. Therefore, an outlier handling step using the Interquartile Range (IQR) method was considered as part of the data preprocessing strategy. To illustrate how outlier detection and removal using the Interquartile Range (IQR) works, a manual example is presented using a sample of five *LiverFunctionTest* values: [30, 40, 50, 100, 45]. The first step is to calculate the median (Q2):

Sorted values: [30, 40, 45, 50, 100]

Q_2 (Median) = 45

Next, the lower quartile (Q1) and upper quartile (Q3) are determined as follows:

$Q_1 = (30 + 40) / 2 = 35$

$Q_3 = (50 + 100) / 2 = 75$

The Interquartile Range (IQR), which represents the central spread of the dataset, is then computed:

$IQR = Q_3 - Q_1 = 75 - 35 = 40$

Using the IQR, the lower and upper bounds for acceptable data values are established:

Lower bound $= Q_1 - 1.5 \times IQR = 35 - 60 = -25$

Upper bound $= Q_3 + 1.5 \times IQR = 75 + 60 = 135$

Any value outside this range is considered an outlier. In this case, all values fall within the threshold, so no outliers are removed. However, if a value such as 200 were present, it would be excluded during preprocessing. A summary of the outlier filtering process is shown in Table 1.

Table 1. Example of IQR-Based Outlier Filtering

Original Value	Status
30	Retained

40	Retained
45	Retained
50	Retained
100	Retained
200 (example)	Removed (Outlier)

Unlike scaling techniques such as RobustScaler, which preserve extreme values by reducing their influence through normalization, the IQR method actively removes outliers from the dataset before training. This approach is particularly effective for sensitive models like Support Vector Machine (SVM), which are prone to distortion when trained on skewed or noisy data. The result of applying IQR-based outlier removal in this study contributed to more stable and accurate classification performance. The results of applying IQR to the dataset are visualized in Figure 5.

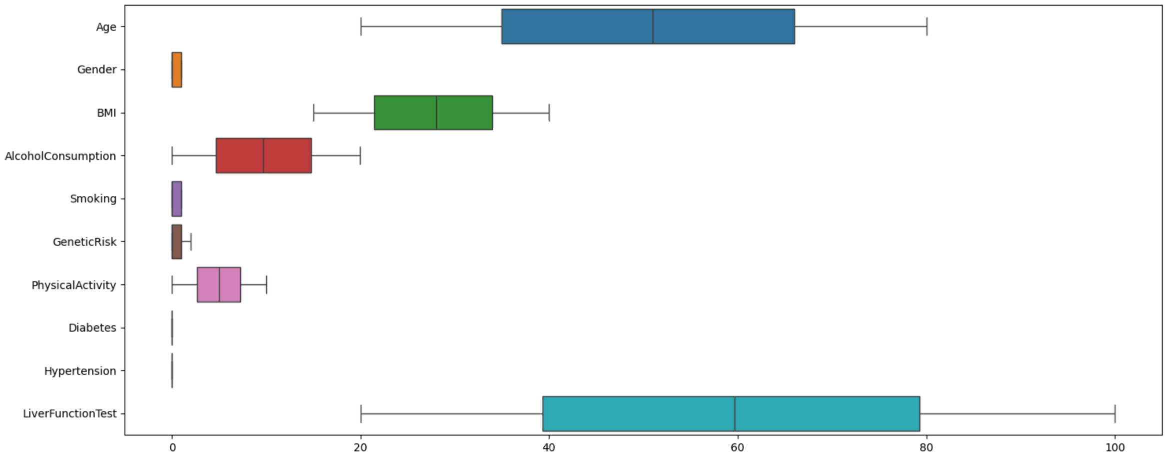
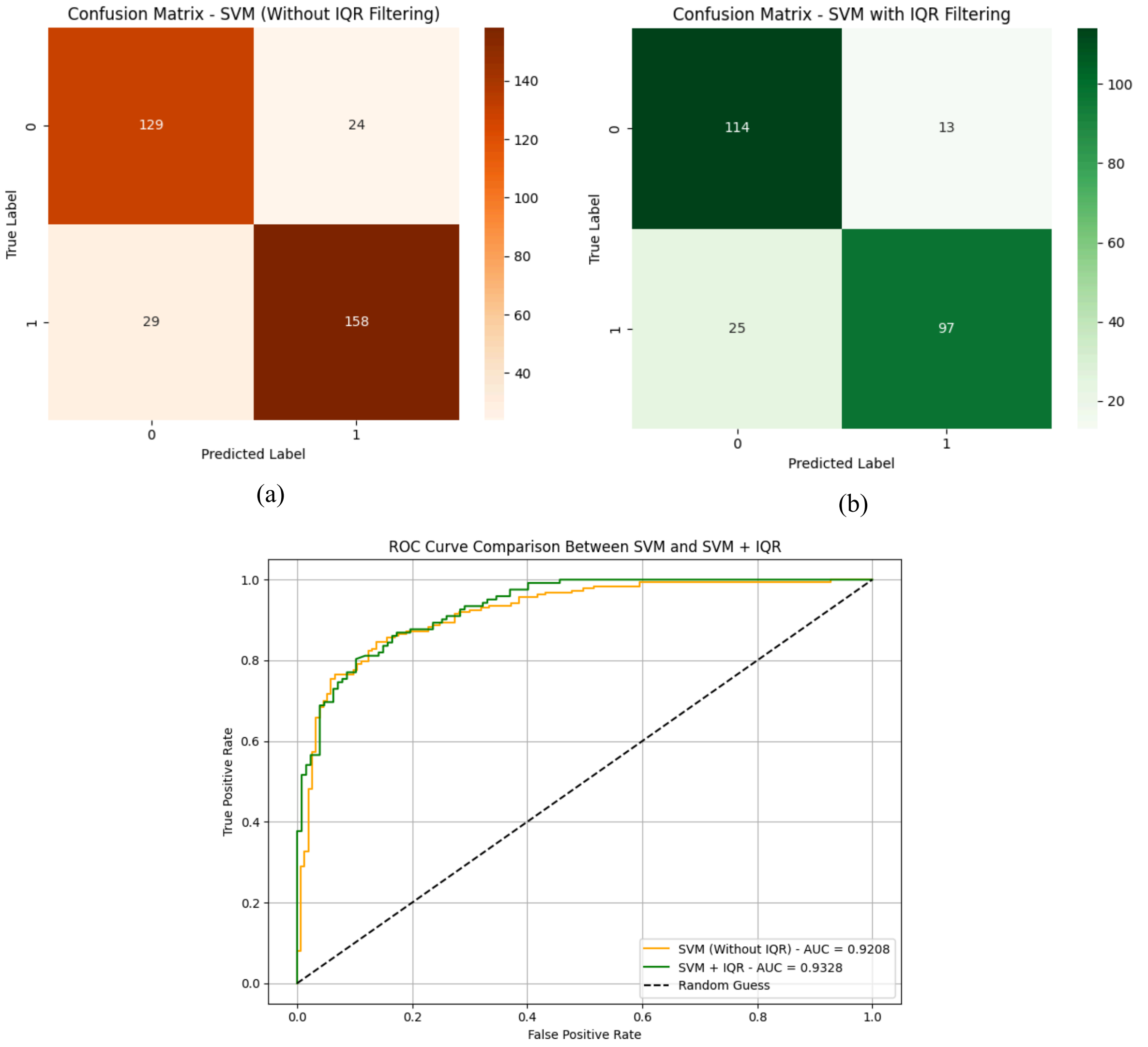


Figure 5. Boxplot of Numeric Features After IQR-Based Outlier Removal

Figure 5 shows boxplots of numeric features before and after applying IQR-based outlier removal. The upper plot illustrates the presence of extreme values in features such as *Diabetes*, *Hypertension*, and *LiverFunctionTest*. After filtering, as shown in the lower plot, these outliers are no longer present, resulting in cleaner and more consistent data distributions. This confirms the usefulness of IQR in preparing the dataset for reliable model training.

The next step involved building the classification model using the Support Vector Machine (SVM) algorithm, which was applied to both training and testing phases. The dataset was divided into 80% training data and 20% testing data using stratified sampling to preserve the proportion of target classes across both subsets. In this study, the SVM algorithm was implemented using the scikit-learn (sklearn) library, a popular machine learning framework in Python. The model was constructed using the SVC (Support Vector Classifier) class from the sklearn.svm module, with the kernel='*rbf*' parameter specified to utilize the Radial Basis Function (RBF). This kernel was selected due to its ability to effectively capture complex and nonlinear relationships in high-dimensional data.

Model evaluation was performed using several metrics, including the confusion matrix, precision, recall, F1-score, accuracy, and ROC-AUC score. These evaluation metrics collectively offer a comprehensive view of the model's predictive performance, especially in binary classification settings. Precision and recall were reported separately for each class to assess the model's behavior in detecting both positive and negative cases. The ROC-AUC score was used to quantify the model's ability to distinguish between the two classes across various decision thresholds. The confusion matrices and ROC curve comparisons for the SVM model without outlier removal and the SVM model with IQR-based outlier filtering are shown in Figure 6.



(a)

(b)

(c)

Figure 6. (a) Confusion Matrix of SVM Without IQR Filtering, (b) Confusion Matrix of SVM With IQR Filtering, and (c) ROC Curve Comparison Between SVM and SVM With IQR

Figure 6 provides a visual comparison of the classification performance between the baseline SVM model and the SVM model with IQR-based outlier filtering. Figure 6(a) shows the confusion matrix for the baseline SVM, where misclassifications are relatively higher for class 0 (negative). Figure 6(b) displays the confusion matrix after applying IQR, showing a more balanced prediction with improved precision for both classes. Figure 6(c) presents the ROC curves for both models, where the SVM with IQR achieves a higher AUC (0.9328) compared to the baseline (0.9208), indicating improved discriminative ability after outlier removal.

Further evaluation was conducted by comparing the classification metrics of several models, including SVM, KNN, and Naïve Bayes. This internal comparison was conducted to ensure fairness and consistency in evaluating the impact of IQR-based outlier removal. Rather than relying on previous studies that may use different datasets, class distributions, or preprocessing pipelines, this study applies identical experimental conditions across all models to directly observe how each algorithm responds to noise reduction. The complete comparison of accuracy, precision, recall, F1-score, and ROC-AUC for all models, both with and without IQR filtering, is presented in Table 2.

Table 2. Performance Comparison of Classical Machine Learning Models With and Without IQR-Based Outlier Removal for Liver Disease Classification

Method	Class	Precision	Recall	F1-Score	Accuracy	ROC-AUC Score
KNN	Negative	77.99%	81.05%	79.49%	81.18%	88.77%
	Positive	83.98%	81.28%	82.61%		
KNN + IQR	Negative	79.26%	84.25%	81.68%	80.72%	89.16%
	Positive	82.46%	77.05%	79.66%		
Naïve Bayes	Negative	74.07%	78.43%	76.19%	77.94%	86.52%
	Positive	81.46%	77.54%	79.45%		
Naïve Bayes + IQR	Negative	77.70%	85.04%	81.20%	79.92%	91.03%
	Positive	82.73%	74.59%	78.45%		
SVM	Negative	81.65%	84.31%	82.96%	84.41%	92.08%
	Positive	86.81%	84.49%	85.64%		
SVM + IQR	Negative	82.01%	89.76%	85.71%	84.74%	93.28%
	Positive	88.18%	79.51%	83.62%		

The evaluation results presented in Table 2 indicate that applying IQR-based outlier removal improved the overall performance of the SVM model. The accuracy increased from 84.41 percent to 84.74 percent, reflecting a modest improvement of 0.33 percentage points. While this increase may appear minor, it highlights the benefit of preprocessing in refining the decision boundary for classification tasks. Although the accuracy gain was only 0.33 percentage points, such an increase is clinically meaningful, as even small improvements can reduce misdiagnosis rates in real-world healthcare settings.

In terms of precision, both classes exhibited better values after outlier removal. For the negative class, precision increased from 81.65 percent to 82.01 percent, and for the positive class, it rose from 86.81 percent to 88.18 percent. These improvements suggest that the model became more confident in its predictions for both classes after extreme values were filtered out.

Looking at the recall scores, the effect of IQR filtering was more nuanced. The recall for the negative class increased significantly from 84.31 percent to 89.76 percent, indicating that the model was better able to identify true negative cases after removing outliers. However, the positive class recall slightly decreased from 84.49 percent to 79.51 percent, showing a trade-off where some positive cases were no longer correctly detected. Despite this, the average recall across classes still showed improvement.

The F1-score, which balances precision and recall, also improved for the negative class (from 82.96 percent to 85.71 percent) and slightly decreased for the positive class (from 85.64 percent to 83.62 percent), consistent with the recall behavior. Additionally, the ROC-AUC score rose from 92.08 percent to 93.28 percent, confirming an overall enhancement in the model's discriminative ability.

The same evaluation approach was extended to classical classifiers such as KNN and Naïve Bayes. Both models also demonstrated slight improvements in ROC-AUC after the application of IQR filtering, though not all metrics consistently increased. For instance, KNN saw a small gain in ROC-AUC (from 88.77 percent to 89.16 percent), while Naïve Bayes exhibited a more notable improvement (from 86.52 percent to 91.03 percent). These results further support the relevance of IQR-based preprocessing in handling data irregularities that may affect classifier performance.

In summary, the findings confirm that IQR-based outlier removal contributes positively to the performance of machine learning models in liver disease classification. While the trade-off in recall for the positive class is a known limitation, especially for SVM, the overall improvements in precision, F1-score, and ROC-AUC suggest enhanced classification reliability. Further enhancements may include SVM kernel tuning, cross-validation, and integration with additional preprocessing strategies such as feature selection or SMOTE to handle potential class imbalance.

4. CONCLUSIONS

This study demonstrated that applying Interquartile Range (IQR) filtering as a preprocessing technique can improve the performance of the Support Vector Machine (SVM) algorithm in classifying liver disease. Without outlier removal, the baseline SVM model achieved an accuracy of 84.41% and a ROC AUC score of 92.08%. After applying IQR-based filtering, the accuracy increased to 84.74%, and the ROC AUC score rose to 93.28%, indicating an improvement of 1.20% points in the model's ability to distinguish between classes. The enhancement was especially noticeable in the negative class, where the recall increased from 84.31% to 89.76%, showing better identification of patients without liver disease. However, the positive class recall slightly decreased from 84.49% to 79.51%, suggesting that some liver disease cases were still misclassified. This outcome illustrates the trade-off that can occur when filtering outliers, as certain borderline samples that might carry clinical relevance may also be removed. Although the gain in accuracy was relatively small, the improvement across other evaluation metrics such as precision, F1-score, and AUC highlights the value of choosing an appropriate preprocessing strategy, especially when dealing with medical datasets that often contain noisy or extreme values. This research contributes to the field by empirically validating that IQR-based outlier removal can enhance the robustness of SVM classification in medical diagnostics, offering a low-complexity yet effective solution for improving data quality. Nonetheless, this research has limitations. The dataset used was limited in size, and no external validation was performed. Additionally, the study focused only on IQR filtering and did not compare other outlier handling methods. Future research is encouraged to evaluate alternative preprocessing approaches, such as Local Outlier Factor or Z-score methods, as well as to incorporate hyperparameter tuning, larger datasets, and broader testing in different clinical contexts to improve model robustness and generalizability.

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