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Research Article

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Leveraging Machine Learning Algorithms for Prediction Chronic Kidney Disease: A Comparative Analysis

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ABSTRACT
Chronic kidney disease (CKD) is a progressive condition characterized by the gradual decline of kidney function, often caused by diabetes, hypertension, or cardiovascular issues. It develops silently, with symptoms emerging slowly, leading to significant health complications. The increasing global prevalence of CKD highlights the urgent need for early detection and effective treatment strategies. In this study, we leverage machine learning techniques to improve the identification and prediction of CKD. Four models. AdaBoostClassifier, XGBClassifier, LGBMClassifier, and RandomForestClassifie. were evaluated for their performance. Among these, the XGBClassifier achieved the highest average training accuracy of 95.78%. Evaluation metrics such as the confusion matrix, ROC curve, and classification report (including F1-score, precision, and recall) were employed to assess the models comprehensively. The study demonstrates the potential of machine learning in enhancing CKD diagnosis by leveraging advanced algorithms to analyze patient data effectively.

Keywords: Parkinson's Disease, Machine Learning, Classification Algorithms, Predictive Modeling

Introduction

Chronic Kidney Disease (CKD), also commonly referred to as chronic renal disease or chronic kidney failure, is a progressive and life-threatening condition that occurs when the kidneys are unable to perform their normal functions, such as filtering waste products and maintaining fluid balance in the body [1,2]. CKD is often caused by underlying conditions such as diabetes, hypertension, or cardiovascular diseases, which damage the kidneys over time. Early detection of CKD is critical, as the disease progresses silently with subtle symptoms until significant damage has occurred. Despite advancements in healthcare, CKD remains a significant global health challenge. Routine laboratory tests can help in identifying the disease at an early stage, and timely interventions can slow its progression, reduce complications associated with decreased glomerular filtration rate (GFR), and improve the quality of life for affected individuals [3]. Treatments that address these aspects can significantly enhance survival rates and minimize cardiovascular risks associated with CKD [4].

The global burden of chronic kidney disease is immense and continues to grow at an alarming rate. Approximately 10% of adults worldwide are affected by some form of CKD, resulting in 1.2 million deaths annually and contributing to a loss of 28 million years of life each year. It is projected that by 2040, CKD will become the fifth leading cause of death globally, marking one of the largest anticipated increases among all major causes of mortality [5]. Such a staggering rise in CKD cases underscores the urgent need for effective prevention, early detection, and efficient treatment strategies to mitigate its impact on public health systems and individuals worldwide.

In recent years, modern technologies like machine learning (ML) and artificial intelligence (AI) have revolutionized personalized clinical support and healthcare practices [6,7]. Machine learning algorithms provide powerful tools for analyzing complex medical data, enabling the development of predictive models

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with high accuracy. CKD, recognized as a pressing public health concern, disproportionately affects individuals in low-resource settings where access to healthcare and preventive education is limited. Millions of lives are lost each year due to insufficient healthcare provisions and a lack of awareness regarding early detection and prevention of CKD [8].

Machine learning offers a transformative approach for identifying CKD and other diseases by leveraging diverse datasets, including patient demographics, laboratory test results, and medical histories. ML models can uncover hidden patterns in these datasets to make predictions with improved precision and speed compared to traditional diagnostic methods. In this study, several machine learning algorithms, such as AdaBoost, XGBoost, LightGBM, and Random Forest, have been employed to predict the likelihood of CKD. Each algorithm presents unique advantages in terms of handling large datasets, feature importance, and prediction accuracy, making them suitable candidates for comprehensive evaluation [9].

The objectives of the proposed study are:

1. To evaluate and compare the accuracy of various machine learning models in predicting chronic kidney disease.
2. To explore feature importance and selection techniques to improve model interpretability and prediction accuracy for chronic kidney disease.
3. To assess the robustness of selected models using crossvalidation and different performance metrics.

Related Works

Ilyas et al. Implemented the J48 and Random Forest algorithms, achieving an accuracy of 96% [2]. The Random Forest algorithm recorded a sensitivity of 43%, while J48 outperformed it by 13%. Using the J48 algorithm, the precision, recall, F-measure, and ROC area were measured at 0.56, 0.52, 0.55, and 0.86, respectively. In contrast, the Random Forest algorithm produced precision, recall, F-measure, and ROC area values of 0.429, 0.176, 0.250, and 0.947, respectively. These results suggest that the J48 algorithm outperformed the Random Forest algorithm in predicting normal kidney function.

Padmanaban et al. Applied the Decision Tree algorithm on a diabetes dataset, achieving 91% accuracy, surpassing the performance of the Naive Bayes method [10]. The model demonstrated strong classification performance with 94% specificity and 95% sensitivity, indicating its high ability to accurately classify cases. Additionally, data mining techniques revealed hidden correlations between attributes that were not direct predictors of diabetes but still contributed to classification. This insight is crucial for improving model performance. Further research focuses on enhancing prediction accuracy through the use of neural networks and clustering algorithms, which are expected to uncover deeper patterns and enhance the overall effectiveness of models in healthcare data analysis.

Pal et al. Assessed the Random Forest classifier and found it to be highly effective for chronic kidney disease (CKD) classification, achieving an accuracy of 92% [11]. The model's precision was 0.63, recall was 0.55, F-score was 0.60, and ROC-AUC was 0.76. These results indicate that Random Forest outperformed other classifiers, such as Support Vector Machine (SVM) and Artificial Neural Networks (ANN), for CKD prediction. The findings underscore the potential of Random Forest in predictive healthcare applications, highlighting its ability to reliably identify CKD cases from complex datasets.

Islam et al. Implemented 12 different machine learning classifiers to evaluate their effectiveness in predicting outcomes [12]. Among these, the XGBoost classifier achieved the highest performance, with an impressive accuracy of 98.3%. It also demonstrated precision and recall values of 0.98, as well as an F1-score of 0.98. These results highlight the robustness and reliability of XGBoost in handling complex datasets, making it an excellent choice for predictive modeling tasks. The study emphasizes the importance of selecting the right classifier based on performance indicators to improve predictive accuracy in machine learning applications.

Wang et al. Employed the R-Squared (R2) metric to determine the optimal undersampling strategy and regression model for predicting creatinine levels [13]. The ensemble model showed the best performance, achieving an R2 value of 0.5590. Out of 23 variables, six factors sex, age, hemoglobin levels, urine protein levels, waist circumference, and smoking habits were identified as having the strongest influence on creatinine levels. Additionally, the predicted creatinine values were used to classify chronic kidney disease (CKD) samples, resulting in an AUC of 0.76, demonstrating the model's effectiveness in CKD classification.

Fauzan et al. Implemented Decision Tree, XGBoost, and Extra Trees algorithms to predict chronic kidney disease [14]. During the preprocessing phase, missing values were addressed through random sampling. The study found that the Extra Trees algorithm provided the best accuracy at 96%, followed by XGBoost at 95% and Decision Tree at 94%. These results suggest that pathologists can utilize these methods, particularly Extra Trees, to create more accurate prediction models for chronic kidney disease.

Tekale et al. Examined 14 attributes associated with chronic kidney disease (CKD) patients to predict outcomes using various machine learning algorithms, including Decision Tree and Support Vector Machine (SVM) [8]. Their analysis revealed that the Decision Tree algorithm achieved an accuracy of 91.75%, while SVM outperformed it with an accuracy of 96.75%. The study highlighted that the Decision Tree algorithm constructs its tree by considering the entire dataset and all available features. These findings demonstrate the strong performance of SVM in CKD prediction tasks, while also recognizing the solid accuracy of the Decision Tree algorithm. By leveraging the specific characteristics of CKDrelated attributes, these algorithms can be used to create more effective predictive models, providing valuable insights for medical professionals in diagnosing and managing CKD.

Abuomar et al. Implemented the Decision Tree (DT) algorithm, achieving a classification accuracy of 98.8% and a 10-fold cross-validation accuracy of 95.75% [15]. The study also evaluated clustering methods, with Self-Organizing Maps (SOMs) outperforming K-means and Fuzzy C-means (FCM) in clustering performance. SOMs achieved an accuracy of 85.0%

and an F1-score of 84.2%. The study also established minimum threshold values that could indicate the onset of CKD in patients. A neural network model predicted CKD with an accuracy of 85.0%, precision of 83.0%, recall of 84.3%, and an F1-score of 83.8%, with a 10-fold validation accuracy of 84.5%. Lastly, SOMs identified four distinct CKD clusters, revealing common characteristics leading to chronic kidney disease.

Methodology

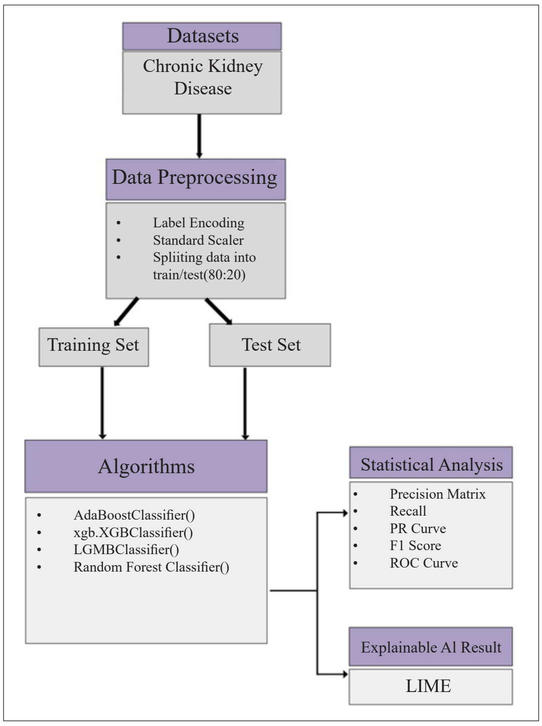

Figure 1: Methodology

The abstract architecture of the workflow, which comprises data preprocessing, the application of different algorithms, and the assessment of statistical performance metrics derived from the models and explanation frameworks, is depicted in Figure 1 To improve accuracy, samples are encoded as 1 for chronic kidney disease (CKD) and 0 for Not Chronic Kidney Disease NCKD). After labeling, a standard scaler is applied to standardize each data sample. The standardized samples are then processed through several algorithms, including AdaBoost, XGBoost (XGB), LightGBM Classifier (LGBMC), and Random Forest.

Following the calculation of statistical performance metrics for these models, they are further analyzed using an Explainable AI (XAI) technique specifically LIME. LIME's tabular explanations are utilized to identify the key features that contribute to predicting whether an instance corresponds to CKD or NCKD, represented by 0 or 1 [16].

Dataset Details

This study employs a publicly available Heart Attack Dataset [4] containing 52 distinct features, including 'Age', 'Gender', 'Ethnicity', 'Socioeconomic Status', 'Education Level', 'BMI', 'Smoking', 'Alcohol Consumption', 'Physical Activity', 'Diet Quality', 'Sleep Quality', 'Family History of Kidney Disease', 'Family History of Hypertension', 'Family History of Diabetes', 'Previous Acute Kidney Injury', 'Urinary Tract Infections', 'Systolic BP', 'Diastolic BP', 'Fasting Blood Sugar', 'HbA1c', 'Serum Creatinine', 'BUN Levels', 'GFR', 'Protein in Urine', 'ACR', 'Serum Electrolytes Sodium', 'Serum Electrolytes Potassium', 'Serum Electrolytes Calcium', 'Serum Electrolytes Phosphorus', 'Hemoglobin Levels', 'Total Cholesterol', 'LDL Cholesterol', 'HDL Cholesterol', 'Triglycerides', 'ACE Inhibitors', 'Diuretics', 'NSAID Use', 'Statins', 'Antidiabetic Medications', 'Edema', 'Fatigue Levels', 'Nausea/Vomiting', 'Muscle Cramps', 'Itching', 'Quality of Life Score', 'Exposure to Heavy Metals', 'Occupational Exposure to Chemicals', 'Water Quality', 'Frequency of Medical Checkups', 'Medication Adherence', and 'Health Literacy'. The objective of this research is to identify the key predictors for diagnosing chronic kidney disease (CKD) by applying machine learning techniques and explainable AI (XAI) methods, particularly utilizing LIME to interpret and clarify the model's predictions.

Algorithm 1 chronic kidney disease using Machine Learning and Explainable AI Technique using LIME

1. Require: Categorical Data (Split in ratio 80:20) with size 1319 × 9
2. Algorithms Used: ABC, RF, XGB, and LGBM
3. for each sample in individual algorithm do
4. Calculate LIME values
5. end for
6. Calculate: Confusion Matrix, Recall, Precision, F1 Score, and PR Curve
7. Implement XAI: Apply ABC, RF, XGB, and LGBM to LIME to generate explainable results

Lime

LIME operates by selecting a target instance x and model f, then generating perturbed instances around x. The predictions f(x) and are obtained, and interpretable features zi are derived from these perturbed instances. An interpretable model g(z) is then trained on pairs (zi,f(x′i)) to approximate the behavior of f in the local vicinity of x. Analyzing g(z) involves examining the coefficients βi, which indicate the impact of features zi on predictions. The higher absolute value (βi) suggests a stronger influence of the respective features [17-19].

Evaluation Metrics and Experimental Setup

1. **Evaluation Metrics:** The performance of all implemented algorithms is measured using the following metrics: confusion matrix, precision, recall, F1-score, and PR curve.
2. **System Environment:** The machine learning models and XAI algorithms were developed in Python. Experiments were conducted on Google Colab, using an NVIDIA K80 GPU and 12 GB of RAM provided by Google. The Google Colab environment was configured with Python version 3.7, Keras version 2.5.0, and TensorFlow version 2.5.0.

Result Analysis

A. AdaBoost Classifier

1. **Confusion Matrix:** Figure 2 shows that 9 normal samples were misclassified as CKD, whereas 6 CKD samples were misclassified as normal. Additionally, 5 normal samples were correctly classified as not CKD, and 312 CKD samples were correctly classified as CKD.

2. **Classsification Report:** Table 1 provides the classification report for the AdaBoost model, showing an overall accuracy of 95.48%. The macro-average metrics, which treat all classes equally, indicate a balanced performance with a precision of 0.71, recall of 0.67, and F1-score of 0.69. The weighted-average metrics, taking class distribution into account, report a precision, recall, and F1-score of 0.95, reflecting the strong performance of the model, particularly in the majority class.

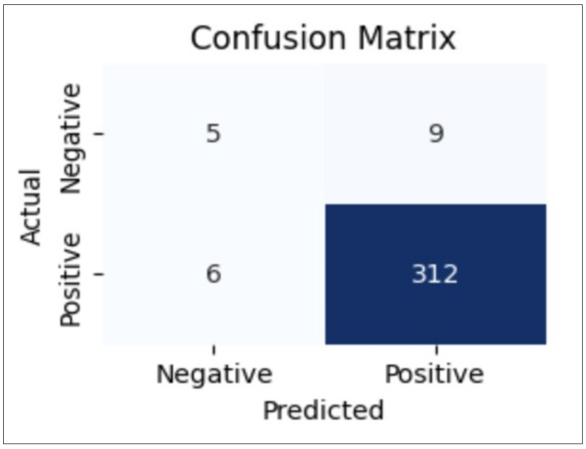

Figure 2: Confusion Matrix for AdaBoost

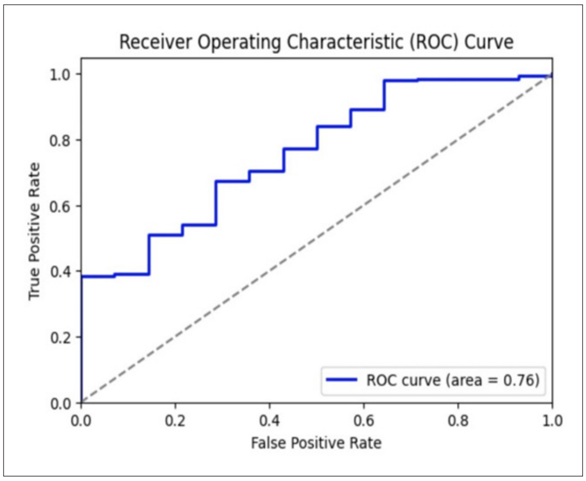

Figure 3: PR Curve for AdaBoost

Table 1: Classification Report for AdaBoost

Category / Metrics	Precision	Recall	F1-score	Support
0	0.45	0.36	0.40	14
1	0.97	0.98	0.98	318
Accuracy			0.95	332
Macro Avg	0.71	0.67	0.69	332
Weighted Avg	0.95	0.95	0.95	332

PR Curve: Figure 3 shows the precision-recall relation with an AUC value of 76%. This indicates that the model performs exceptionally well in distinguishing between CKD and non-CKD cases.

LIME: Figure 4 Using LIME with the AdaBoost classifier, the model predicted CKD with a 49% probability.The key positive features include SerumCreatinine > 0.87 and MuscleCramps > 0.84, each contributing 0.01. On the negative side, ProteinInUrine < -0.87 also influenced the prediction, pushing towards non-CKD. Other features like SystolicBP and MedicalCheckup had minimal impact.

XGB Classifier

Confusion Matrix: Figure 5 shows that 12 normal samples were misclassified as CKD, whereas 2 CKD samples were misclassified as normal. Additionally, 2 normal samples

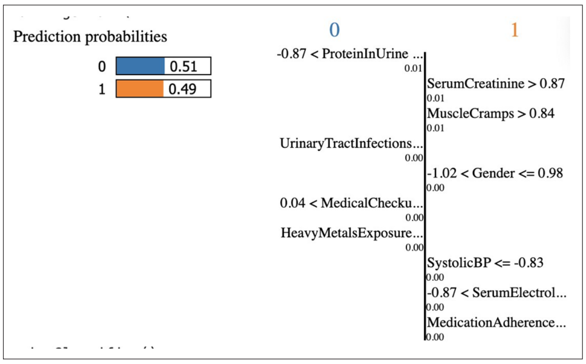

Figure 4: AdaBoost LIME Tabular Plots

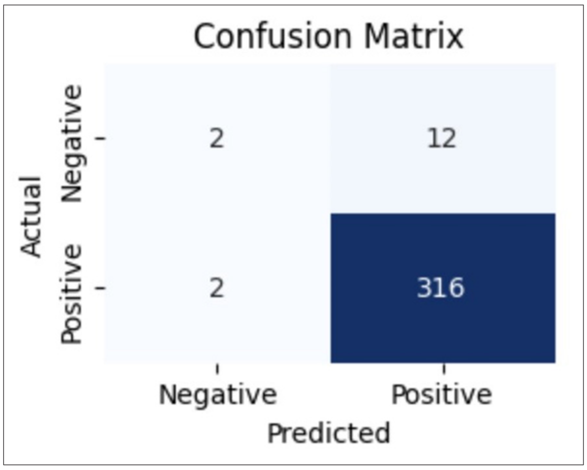

Figure 5: Confusion Matrix for XGB

Classsification Report: Table 2 presents the classification metrics for the XGBoost (XGB) model for two classes (0 and 1). Class 1 exhibits strong performance with a precision of 0.96, recall of 0.99, and F1-score of 0.98, indicating excellent prediction. However, Class 0 shows lower performance with a precision of 0.50, recall of 0.14, and F1-score of 0.22, indicating poor prediction for this class. The model achieves an overall accuracy of 95.78%, with a higher weighted average due to the class imbalance.

Table 2: Classification Report for XGB

Category / Metrics	Precision	Recall	F1-Score	Support
0	0.50	0.14	0.22	14
1	0.96	0.99	0.98	318
Accuracy			0.96	332
Macro Avg	0.73	0.57	0.60	332
Weighted Avg	0.94	0.96	0.95	332

PR Curve: Figure 6 shows the precision-recall relation with an AUC value of 85%. This indicates that the model performs exceptionally well in distinguishing between CKD and non-CKD cases.

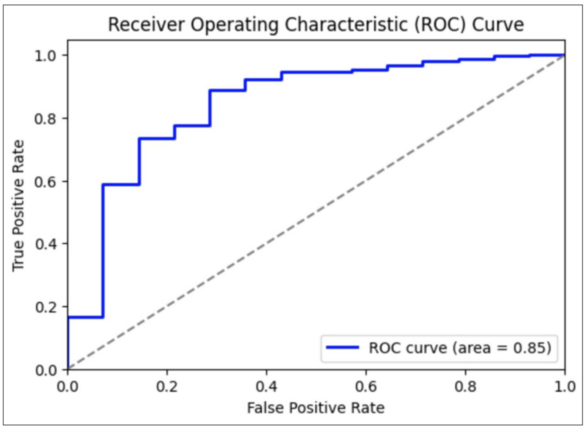

Figure 6: PR Curve for XGB

LIME: Figure 7 Using LIME with the XGB classifier, the model predicted non-CKD with 72% confidence. The key factors supporting this prediction include ProteinInUrine <-0.87 with 0.18 impact, MedicalCheckups > 0.04 with 0.08 impact, and absence of NauseaVomiting with 0.04 impact. Minor factors contributing to the CKD outcome (class 1) include HeavyMetalsExposure (0.03) and Itching > 0.88 with 0.02 impact. UrinaryTractInfections, FamilyHistoryHypertension, and Edema had minimal influence on the prediction.

LGBM Classifier

Confusion Matrix: Figure 8 shows that 12 normal samples were misclassified as CKD, whereas 2 CKD samples were misclassified as normal. Additionally, 2 normal samples were correctly classified as not CKD, and 316 CKD samples were correctly classified as CKD.

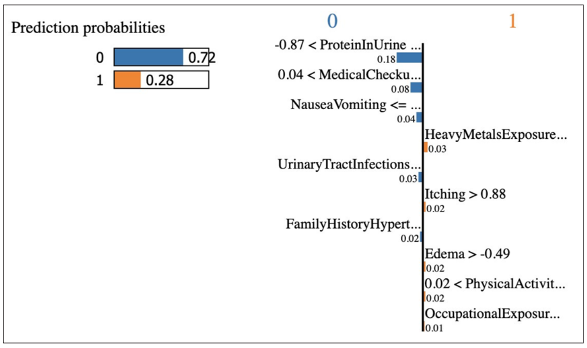

Figure 7: XGB LIME Tabular Plots

Classsification Report: Table 3 presents the classification metrics for the LightGBM (LGBM) model for two classes (0 and 1). Class 1 demonstrates strong performance with a precision of 0.96, recall of 0.99, and F1-score of 0.98, reflecting accurate predictions. In contrast, Class 0 has lower performance with a precision of 0.50, recall of 0.14, and F1score of 0.22, indicating poor prediction. The model achieves an overall accuracy of 96.78%, with a higher weighted average due to the class imbalance.

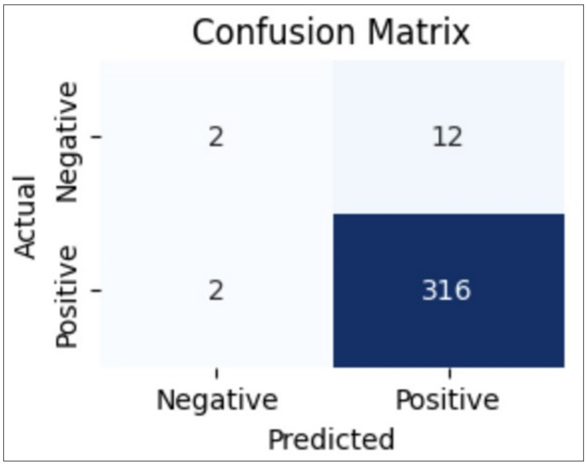

Figure 8: Confusion Matrix for LGBMC

Table 3: Classification Report for LGBM

Category / Metrics	Precision	Recall	F1-Score	Support
0	0.50	0.14	0.22	14
1	0.96	0.99	0.98	318
Accuracy			0.96	332
Macro Avg	0.73	0.57	0.60	332
Weighted Avg	0.94	0.96	0.95	332

PR Curve: Figure 8 shows the precision-recall relation with an AUC value of 81%. This indicates that the model performs exceptionally well in distinguishing between CKD and non-CKD cases.

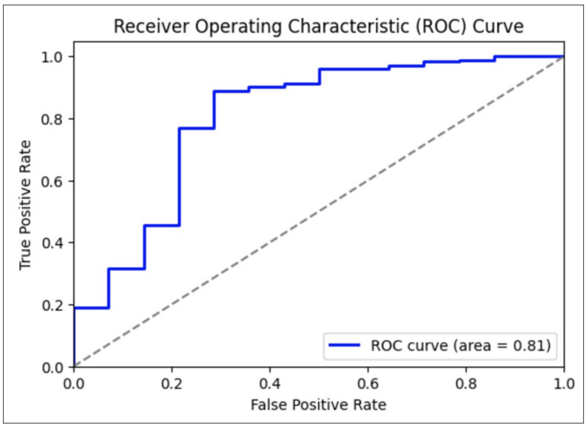

Figure 9: PR Curve for LGBM

LIME: Figure 10 Using LIME with the LGBM classifier, the model predicted non-CKD with 65% confidence. The key factors supporting this prediction include ProteinInUrine< -0.87 with 0.25 impact, MedicalCheckups > 0.04 with 0.05 impact, and UrinaryTractInfections with 0.04 impact. Primary contributors to the CKD outcome (class 1) include Itching > 0.88 with 0.05 impact and MuscleCramps > 0.84 with 0.04 impact. FamilyHistoryHypertension, Gender, Ethnicity, and PhysicalActivity had minor influences on the prediction. FamilyHistoryDiabetes showed minimal impact on the CKD outcome.

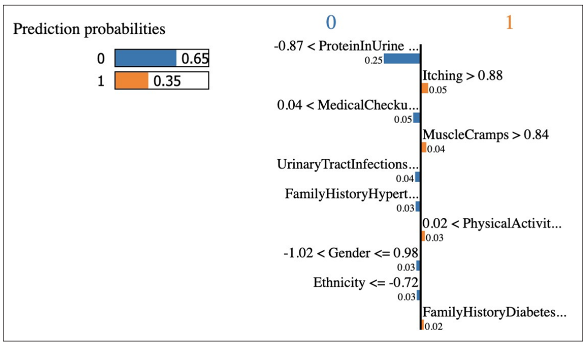

Figure 10: LGBMC LIME Tabular Plots

Random Forest Classifier

Confusion Matrix: Figure 11 shows that 14 normal samples were misclassified as CKD, whereas 0 CKD samples were misclassified as normal. Additionally, 0 normal samples were correctly classified as not CKD, and 318 CKD samples were correctly classified as CKD.

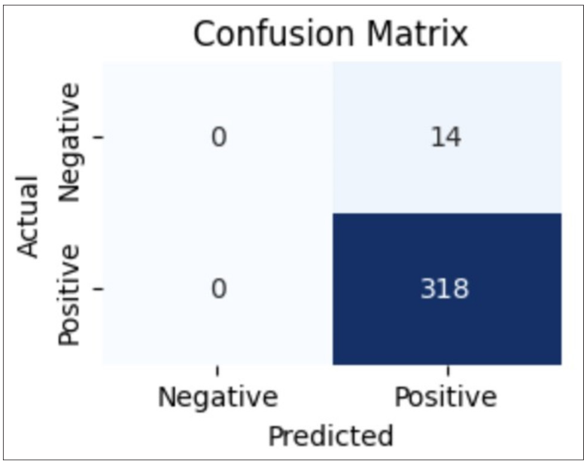

Figure 11: Confusion Matrix for RandomForest

Classsification Report: Table 4 displays the classification metrics for the Random Forest model across two classes (0 and 1). Class 1 achieves strong results with a precision of 0.96, recall of 1.00, and an F1-score of 0.98, demonstrating nearly flawless prediction. Conversely, Class 0 has all metrics at 0.00, indicating very poor performance. The model maintains an overall accuracy of 95.78%, with a higher weighted average due to class imbalance.

Table 4: Classification Report for Random Forest

Category / Metrics	Precision	Recall	F1-Score	Support
0	0.00	0.00	0.00	14
1	0.96	1.00	0.98	318
Accuracy			0.96	332
Macro Avg	0.48	0.50	0.49	332
Weighted Avg	0.92	0.96	0.94	332

PR Curve: Figure 12 shows the precision-recall relation with an AUC value of 78%. This indicates that the model performs exceptionally well in distinguishing between CKD and non-CKD cases.

LIME: Figure 13 Using LIME with the RandomForest classifier, the model predicted non-CKD with 54% confidence, a relatively close prediction. The primary factor supporting this prediction is ProteinInUrine < -0.87 with 0.03 impact. Contributing to the CKD outcome (class 1) are Itching > 0.88 with 0.02 impact, and ACEInhibitors <= -0.65 with 0.01 impact. Gender, SerumCreatinine, NauseaVomiting, Statins use, and AlcoholConsumption had minor influences on the prediction, each with 0.01 impact. FatigueLevels and Edema showed minimal impact on the outcome.

In the comparative analysis of machine learning algorithms applied to classify samples as ”CKD” or ”NotCKD”. In this study, four machine learning algorithms XGBoost (XGB).

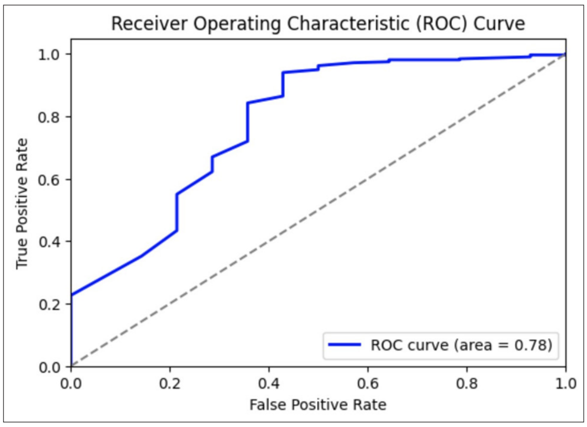

Figure 12: PR Curve for Random Forest

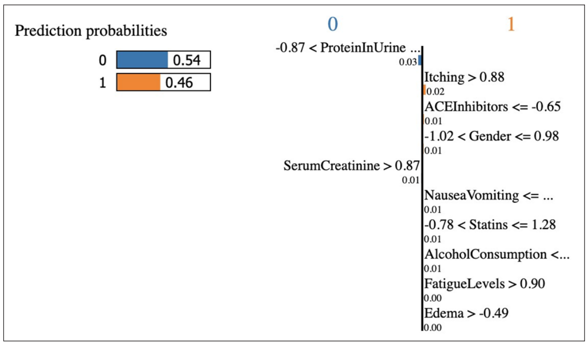

Figure 13: Random Forest LIME Tabular Plots

LightGBM (LGBM), Random Forest (RF), and AdaBoost (SVM) were implemented to predict whether a sample was affected by chronic kidney disease (CKD) or not (non-CKD). The results of K-fold cross-validation were analyzed, with a particular focus on their accuracy, precision, recall, and F1scores across two categories:” CKD” and” non-CKD.” Upon comparison of these algorithms (Table 5), XGB achieved an overall accuracy of 95.78%, slightly outperforming LGBM at 95.53%, followed by RF at 95.23%, and AdaBoost at 95.48%. These minor differences suggest that the algorithms perform similarly in terms of accuracy, with XGB and LGBM showing a marginal edge over the others.

The classification report illustrates that XGBoost (XGB) and LightGBM (LGBM) exhibited strong performance across most metrics, with XGB achieving a weighted average precision of 0.94, a recall of 0.96, and an F1-score of 0.95. LGBM showed comparable performance, boasting a weighted average F1score of 0.94. Both models achieved an impressive accuracy of 96%, highlighting their effectiveness in accurately classifying chronic kidney disease (CKD) and non-CKD instances. In addition to XGB and LGBM, AdaBoost also performed admirably, with the classification report indicating a precision of 0.45 for class 0 and 0.97 for class 1, leading to an F1-score of 0.40 for class 0 and 0.98 for class 1. The overall accuracy for AdaBoost was recorded at 95%, while the macro average F1-score stood at 0.69, reflecting some challenges in balancing performance across classes. The weighted average F1-score of 0.95 indicates that AdaBoost performed well in classifying the majority class but struggled more with the minority class. When considering the macro average F1-scores, which provide a balanced view across both categories, it is clear that XGB and LGBM handle both CKD and non-CKD instances similarly, achieving high scores. Additionally, Random Forest (RF) demonstrated slight variations in precision and recall but still maintained strong overall performance, with average F1scores near 95.80.

Table 5: Comparison of Training Accuracy with K-fold Cross Validation

Training Accuracy	XGB	LGBM	Random Forest	Adaboost
K1	95.73	94.71	95.25	94.90
K2	95.75	95.57	95.11	94.96
K3	95.85	95.73	95.48	95.32
K4	95.80	95.80	95.02	95.58
K5	95.78	95.85	95.30	95.64
K6	95.78	95.60	95.23	96.50
K7	95.78	95.50	95.23	95.48
K8	95.78	95.53	95.23	95.48
K9	95.78	95.53	95.23	95.48
K10	95.78	95.53	95.23	95.48
Average	95.78	95.53	95.23	95.48

The results underscore that all four algorithms XGB, LGBM, AdaBoost, and RF performed well in classifying CKD, with XGBoost and LightGBM demonstrating a slight edge in terms of accuracy and consistency across various metrics. This highlights the importance of careful model selection based on the specific application requirements and the characteristics of the dataset, particularly when diagnosing chronic kidney disease [20,21].

Conclusion and Implications

In analyzing machine learning models for classifying" CKD" and" NotCKD," the LGBMClassifier stood out as the most accurate and reliable model, achieving an impressive accuracy of 95.78%. It demonstrated high precision (0.96), recall (0.99), and an F1 score of 0.98 for the" CKD" class. This balanced performance across both classes highlights its potential for real-world application in medical diagnosis. Accurately identifying" CKD" cases while minimizing the misclassification of" NotCKD" patients is critical for ensuring timely intervention and treatment. These findings suggest that LGBM could play a significant role in enhancing diagnostic tools for early CKD detection. Additionally, further improvements could be achieved by applying optimization techniques [22,23] and implementing strategies to address adversarial challenges in neural networks [24,25].

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