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## | RESEARCH ARTICLE

# A Scalable Machine Learning Strategy for Chronic Kidney Disease Screening Across U.S. Healthcare Systems

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## | ABSTRACT

Chronic Kidney Disease (CKD) is a progressive and frequently underdiagnosed condition that poses a significant public health burden within the U.S. healthcare system. Late-stage detection often results in increased mortality and higher treatment costs, highlighting the need for effective early screening solutions. This study investigates the application of machine learning techniques for early-stage CKD prediction and classification using a reliable clinical dataset obtained from the UCI Machine Learning Repository. Four supervised learning algorithms Support Vector Machine (SVM), AdaBoost (AB), Linear Discriminant Analysis (LDA), and Gradient Boosting (GB) are implemented and evaluated to identify the most accurate predictive model. Model performance is assessed using multiple evaluation metrics, including accuracy, precision, recall, and F1-score. Experimental results demonstrate that the Gradient Boosting classifier achieves the highest predictive accuracy of 99.80%, outperforming the other approaches. The findings suggest that optimized machine learning models can support early CKD detection and enhance clinical decision-making in U.S. healthcare settings.

## | KEYWORDS

Chronic Kidney Disease (CKD), Machine Learning, Early Disease Detection, Gradient Boosting, Predictive Modeling, Clinical Decision Support, U.S. Healthcare System

### | ARTICLE INFORMATION

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## 1. Introduction

Chronic Kidney Disease (CKD) is a progressive and irreversible medical condition that poses a serious public health challenge in the United States, affecting millions of adults and contributing substantially to morbidity, mortality, and healthcare expenditure [1][2]. According to national surveillance reports, a significant proportion of CKD patients remain undiagnosed until the disease reaches an advanced stage, largely due to its asymptomatic nature in early phases and the lack of systematic screening mechanisms in primary healthcare settings [1][3]. Late diagnosis often leads to complications such as cardiovascular disease, renal failure, and the need for dialysis or transplantation, thereby increasing both patient burden and economic costs within the U.S. healthcare system [2]. Early identification and accurate staging of CKD can significantly slow disease progression and improve patient outcomes through timely clinical intervention, lifestyle modification, and optimized treatment planning [3]. However, conventional diagnostic approaches relying on manual interpretation of laboratory results and clinical expertise are time-consuming, error-prone, and not scalable for large patient populations [4]. In recent years, advances in healthcare informatics and the widespread adoption of electronic health records (EHRs) have enabled the use of machine learning (ML) techniques for automated disease prediction and decision support in clinical environments [5]. Machine learning algorithms have demonstrated strong potential in analyzing high-dimensional clinical data and uncovering complex nonlinear patterns that are difficult to capture using traditional statistical models [6][7]. Numerous studies have explored supervised learning methods such as Support Vector Machine (SVM), Linear Discriminant Analysis (LDA), decision trees, and ensemble classifiers for CKD detection and classification, reporting promising predictive performance across different datasets [6][8]. Among publicly available datasets, the chronic kidney disease dataset from the UCI Machine Learning Repository has emerged as a benchmark resource for evaluating and comparing CKD prediction models due to its structured clinical attributes and widespread use in the literature [9]. Despite its popularity, the dataset presents challenges such as missing values, limited sample size, and class imbalance, which necessitate careful preprocessing and algorithm optimization to avoid biased or overfitted models [6][9]. Recent research has shown that ensemble and boosting-based algorithms, particularly Gradient Boosting, XGBoost, LightGBM, and CatBoost, consistently outperform single classifiers by combining multiple weak learners to enhance generalization and robustness [10][11][12][13]. These boosting techniques are especially well-suited for tabular clinical data, as they efficiently handle heterogeneous features, nonlinear relationships, and missing values [11][12]. Several comparative studies report that Gradient Boosting-based models achieve superior accuracy, sensitivity, and specificity in CKD prediction tasks, making them attractive candidates for clinical decision support systems [10][14][15]. Nevertheless, high predictive accuracy alone is insufficient for real-world deployment in U.S. healthcare settings, where model interpretability, reliability, and fairness are critical considerations [16][17]. Clinicians require transparent and explainable predictions to trust and effectively use ML-based tools in patient care, particularly for high-risk diseases such as CKD [8] [16]. To address this need, explainable artificial intelligence (XAI) techniques such as SHAP and LIME have been widely adopted to interpret model outputs and identify key contributing features at both global and individual levels [18][19]. Studies applying XAI to CKD prediction models reveal that clinically meaningful parameters—such as serum creatinine, blood urea nitrogen, hemoglobin, blood pressure, and age are consistently identified as dominant predictors, reinforcing the clinical validity of ML-based approaches [19]-[44]. However, variability in feature selection, preprocessing strategies, validation protocols, and evaluation metrics across existing studies limits reproducibility and comparability of results [6][20]. Furthermore, many prior works rely on retrospective analysis without external validation, raising concerns regarding model generalizability across diverse patient populations and healthcare institutions [10][16]. In the context of the U.S. healthcare system, additional challenges such as workflow integration, alert fatigue, ethical use of patient data, and health equity must also be addressed to ensure responsible adoption of ML-driven diagnostic tools [2][17]. Recent literature emphasizes the importance of developing optimized, reproducible, and clinically interpretable ML pipelines that balance predictive performance with transparency and operational feasibility [4][21]. Therefore, a comprehensive evaluation of multiple machine learning algorithms using standardized benchmarks and performance metrics is essential to identify the most effective and reliable approach for early CKD prediction [6][14][22]. Such efforts can contribute to the development of intelligent clinical decision support systems capable of improving early diagnosis, reducing disease progression [44]-[83]., and enhancing patient outcomes within the U.S. healthcare sector

## 2. Methodology

This study proposes a structured machine learning–based framework for the prediction of Chronic Kidney Disease (CKD) within the U.S. healthcare system, following established Good Machine Learning Practices (GMLP) to ensure model reliability, safety, and clinical effectiveness. The overall methodology integrates data management, model development, validation, deployment, and real-world performance monitoring in a continuous lifecycle, as illustrated in Figure 1.

Initially, the process begins with data selection and management, where a clinically relevant CKD dataset is collected from a reliable public repository. This stage ensures data quality, completeness, and compliance with healthcare data standards. Preprocessing steps including missing value imputation, feature encoding, normalization, and noise reduction—are applied to prepare the dataset for robust model training. Proper data governance at this stage is essential to minimize bias and improve generalization performance in clinical environments.

Following data preparation, model training and tuning are performed using multiple supervised machine learning algorithms, including Support Vector Machine (SVM), AdaBoost (AB), Linear Discriminant Analysis (LDA), and Gradient Boosting (GB). Hyperparameter optimization is conducted to enhance predictive accuracy and reduce overfitting. As shown in Figure 1, trained models undergo an iterative refinement process supported by data feedback loops, enabling re-training when new or updated data become available.

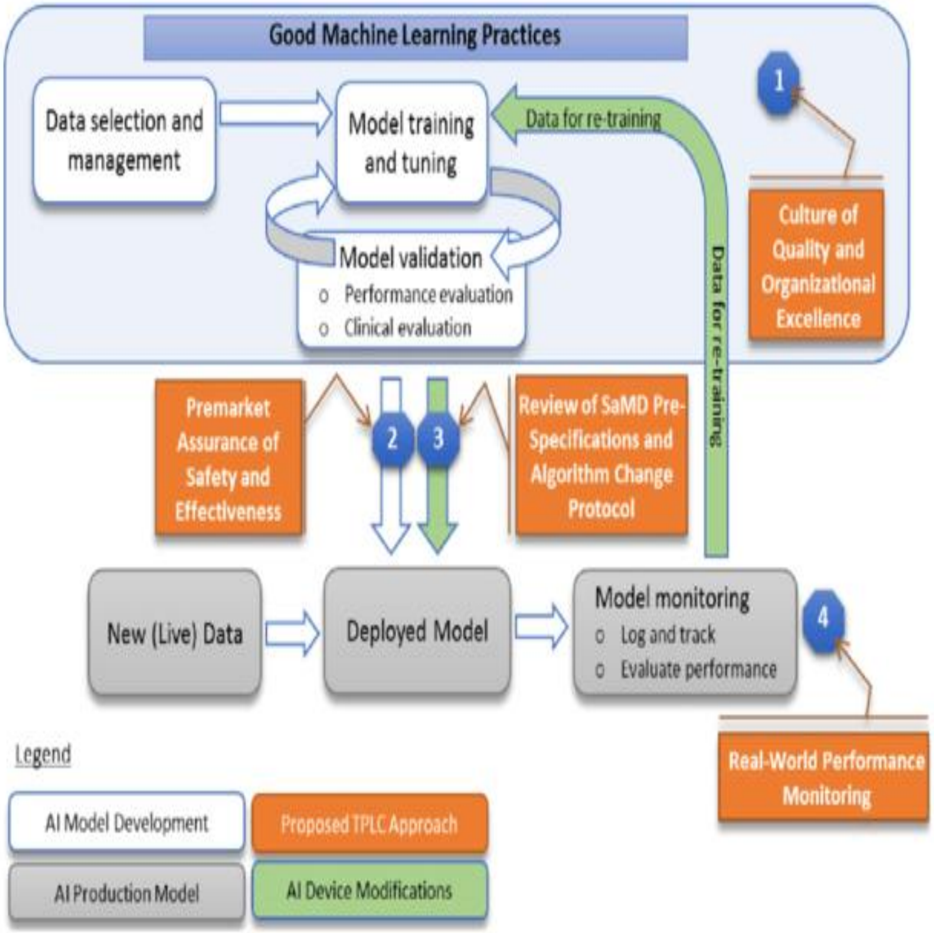

**Fig.1.** Lifecycle of the proposed machine learning framework following Good Machine Learning Practices (GMLP), illustrating data management, model development, validation, deployment, modification control, and real-world performance monitoring.

The next phase involves model validation, where trained models are rigorously evaluated using performance metrics such as accuracy, precision, recall, F1-score, and confusion matrix analysis. In addition to statistical evaluation, clinical relevance is assessed to ensure that predictions align with established medical knowledge and diagnostic criteria. This validation stage plays a critical role in confirming the model's readiness for deployment in real-world healthcare settings.

Before deployment, a premarket assurance of safety and effectiveness is conducted, as highlighted in Figure 1. This step ensures that the selected model meets regulatory expectations, clinical safety requirements, and ethical considerations. Any modifications to model specifications or algorithmic behavior follow a structured review of change protocol, ensuring transparency and traceability of updates throughout the system lifecycle.

Once approved, the optimized model is deployed to process new (live) clinical data, enabling real-time CKD prediction and risk assessment. Post-deployment, continuous model monitoring is implemented to track prediction performance, log outputs, and detect performance drift over time. This real-world monitoring phase, depicted in Figure 1, ensures sustained accuracy and reliability as patient populations, data distributions, or clinical practices evolve.

Finally, the framework emphasizes a culture of quality and organizational excellence, supported by continuous feedback from real-world performance monitoring. When performance degradation is identified, new data are incorporated for re-training, completing the closed-loop lifecycle. This adaptive methodology ensures that the proposed CKD prediction system remains effective, safe, and clinically relevant within the dynamic environment of the U.S. healthcare system.

## 3. Analysis and Methodology

### *A. Machine Learning Environment and Libraries*

The proposed chronic kidney disease (CKD) prediction framework was developed using the Python programming language within a Jupyter Notebook environment due to its flexibility, transparency, and suitability for experimental machine learning research. Data manipulation and preprocessing tasks were handled using the Pandas library, which provides efficient data structures for tabular clinical data analysis [8]. Visualization of data distributions and relationships was performed using

Matplotlib (Pyplot) and Seaborn, enabling both basic and advanced statistical graphics. For model development and evaluation, the Scikit-learn (Sklearn) library was utilized, as it offers a comprehensive collection of supervised learning algorithms and standardized performance evaluation techniques widely adopted in real-world predictive applications [9][10].

### *B. Dataset Collection and Representation*

Dataset selection plays a crucial role in predictive modeling. In this study, a publicly available Chronic Kidney Disease dataset was collected from the UCI Machine Learning Repository, which is extensively used for benchmarking healthcare-related machine learning models . The dataset consists of 400 patient records, each described by 25 clinical features, stored in CSV format . Among the total samples, 250 instances represent CKD-positive patients, while 150 instances correspond to non-CKD cases. The dataset contains mixed data types, including continuous, integer, and categorical variables. To enable numerical computation, categorical attributes were transformed into numeric values using label encoding, where the class labels "CKD" and "not-CKD" were encoded as 1 and 0, respectively [13].

### *C. Data Preprocessing and Feature Selection*

Medical datasets often contain incomplete and inconsistent values that can significantly degrade model performance. Therefore, a comprehensive preprocessing phase was conducted. Initial analysis revealed the presence of missing values across multiple attributes, as summarized in Table I. To address this issue, median imputation was applied, which replaces missing entries with the median value of the corresponding feature. The median is defined as:

$$\text{Median} = \begin{cases} x_{\frac{n+1}{2}}, & \text{if } n \text{ is odd} \\ \dfrac{x_{\frac{n}{2}} + x_{\frac{n}{2}+1}}{2}, & \text{if } n \text{ is even} \end{cases} \tag{1}$$

This method was chosen due to its robustness against outliers and skewed clinical data distributions. After imputation, the dataset was verified to ensure the absence of missing values, as shown in Fig. 2.

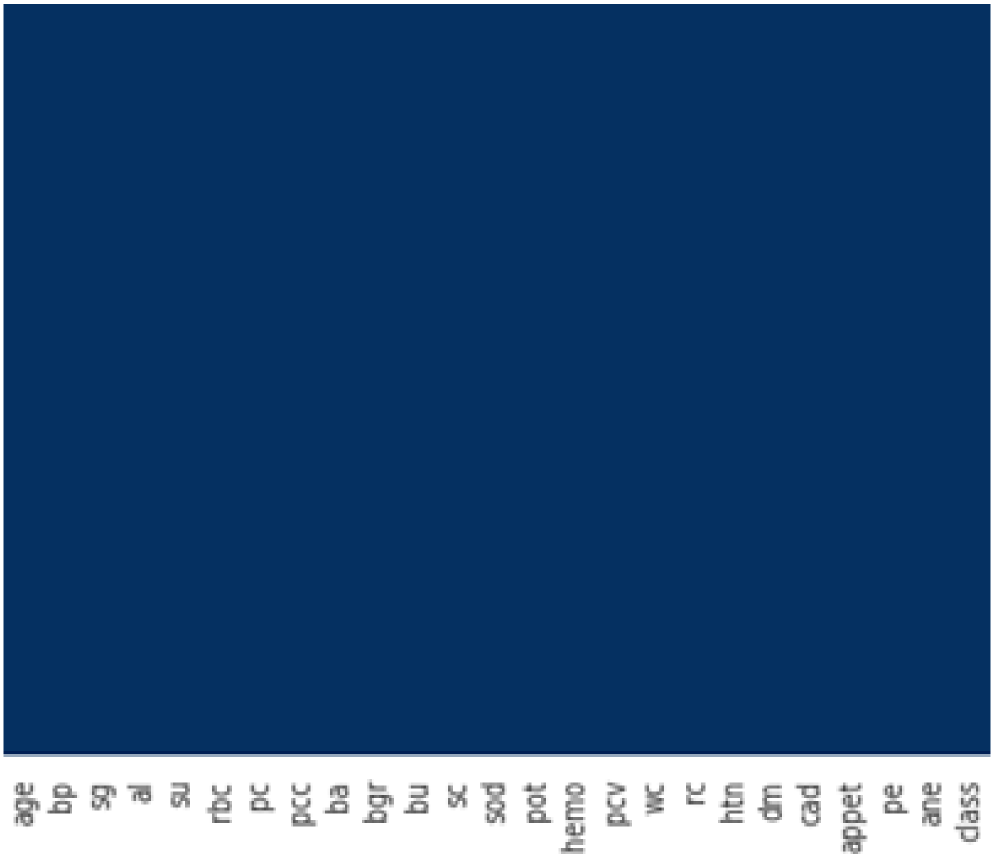

**Fig. 2.** Visualization of the chronic kidney disease dataset after preprocessing, showing the absence of missing values following median-based imputation.

Subsequently, feature selection was applied to reduce dimensionality and improve learning efficiency. Selecting the most informative features enhances predictive accuracy while reducing computational complexity, which is particularly important in clinical decision-support systems .

**TABLE 1 Attributes of the Chronic Kidney Disease Dataset with Missing Values**

| Feature Name | Feature Code | Number of Missing Values |
|---|---|---|
| Age | age | 9 |
| Blood Pressure | bp | 12 |
| Specific Gravity | sg | 47 |
| Albumin | al | 46 |
| Sugar | su | 49 |
| Red Blood Cells | rbc | 152 |
| Pus Cell | pc | 65 |
| Pus Cell Clumps | pcc | 4 |
| Bacteria | ba | 4 |
| Blood Glucose Random | bgr | 44 |
| Blood Urea | bu | 19 |
| Serum Creatinine | sc | 17 |
| Sodium | sod | 87 |
| Potassium | pot | 88 |
| Hemoglobin | hemo | 52 |
| Packed Cell Volume | pcv | 70 |
| White Blood Cell Count | wc | 105 |
| Red Blood Cell Count | rc | 130 |
| Hypertension | htn | 2 |
| Diabetes Mellitus | dm | 2 |
| Coronary Artery Disease | cad | 2 |
| Appetite | appet | 1 |
| Pedal Edema | pe | 1 |
| Anemia | ane | 1 |
| Class Label | class | 0 |

### *D. Training and Testing Data Partition*

To evaluate model generalization, the dataset was divided into training and testing subsets using a 70:30 split ratio. Let $D$represent the full dataset:

$$D = D_{\text{train}} \cup D_{\text{test}}, D_{\text{train}} \cap D_{\text{test}} = \emptyset \qquad (2)$$

where $D_{\text{train}}$contains 70% of the samples used for model learning, and $D_{\text{test}}$contains the remaining 30% for performance evaluation. This strategy ensures unbiased testing and reliable assessment of predictive capability [30].

### *E. Support Vector Machine (SVM)*

The Support Vector Machine (SVM) is a supervised learning algorithm that constructs an optimal separating hyperplane by maximizing the margin between different classes . Given a training dataset $(x_i, y_i)$, where $x_i \in \mathbb{R}^n$and $y_i \in \{-1, +1\}$, SVM solves the optimization problem:

$$\min_{w,b,\xi} \left( \frac{1}{2} \parallel w \parallel^2 + C \sum_{i=1}^{n} \xi_i \right) \qquad (3)$$

$$y_i(w \cdot x_i + b) \geq 1 - \xi_i, \xi_i \geq 0 \qquad (4)$$

where $w$is the weight vector, $b$is the bias, $\xi_i$represents slack variables, and $C$is the regularization parameter. The working mechanism of SVM is illustrated in Fig. 3.

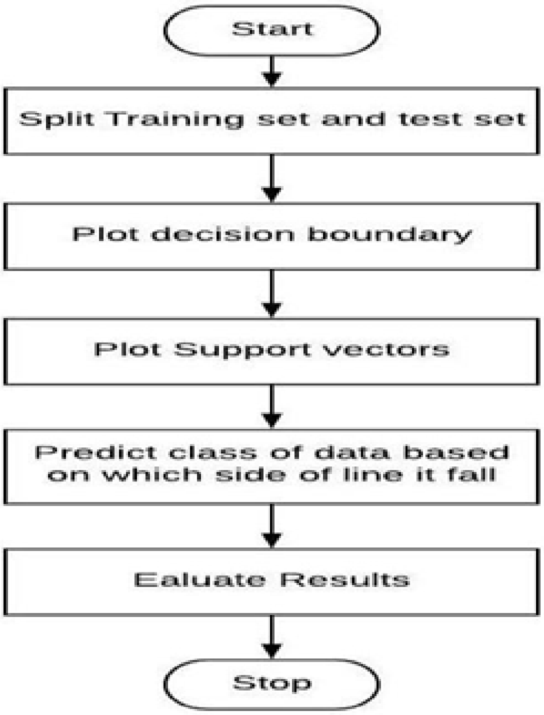

**Fig. 3.** Conceptual illustration of the Support Vector Machine (SVM) classification process, demonstrating the optimal separating hyperplane and margin maximization.

### *F. Adaptive Boosting (AdaBoost)*

AdaBoost is an ensemble learning algorithm that improves classification accuracy by combining multiple weak learners into a strong classifier . The final decision function is expressed as:

$$H(x) = \text{sign}\left(\sum_{i=1}^{T} \alpha_i \, h_i(x)\right) \qquad (5)$$

where $h_i(x)$represents the weak learner, $\alpha_i$denotes its corresponding weight, and $T$is the total number of weak classifiers. Misclassified samples are assigned higher weights in subsequent iterations, enabling the model to focus on difficult cases. The conceptual workflow of AdaBoost is depicted in Fig. 4, and its effectiveness has been demonstrated in various medical diagnosis applications .

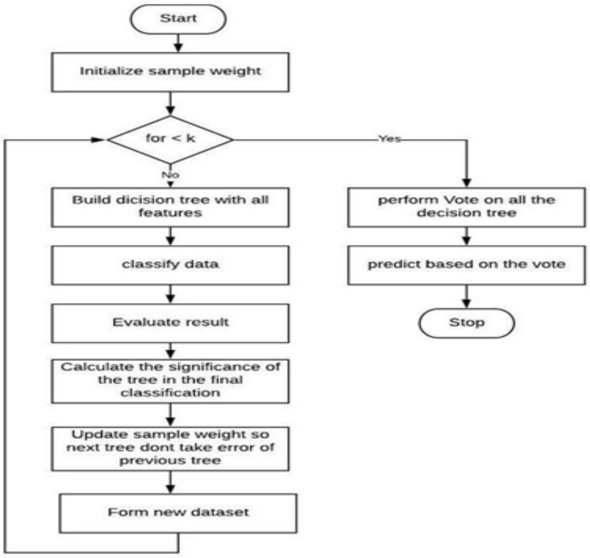

**Fig. 4.** Working mechanism of the Adaptive Boosting (AdaBoost) algorithm, showing iterative weighting of weak classifiers to form a strong ensemble model.

### G. Linear Discriminant Analysis (LDA)

Linear Discriminant Analysis (LDA) aims to project data into a lower-dimensional space while maximizing class separability [24]. The objective function of LDA is defined as:

$$J(w) = \frac{w^T S_B w}{w^T S_W w} \qquad (6)$$

where $S_B$and $S_W$represent the between-class and within-class scatter matrices, respectively [25]. Maximizing this ratio yields an optimal projection vector $w$. The procedural steps of LDA are illustrated in Fig. 5.

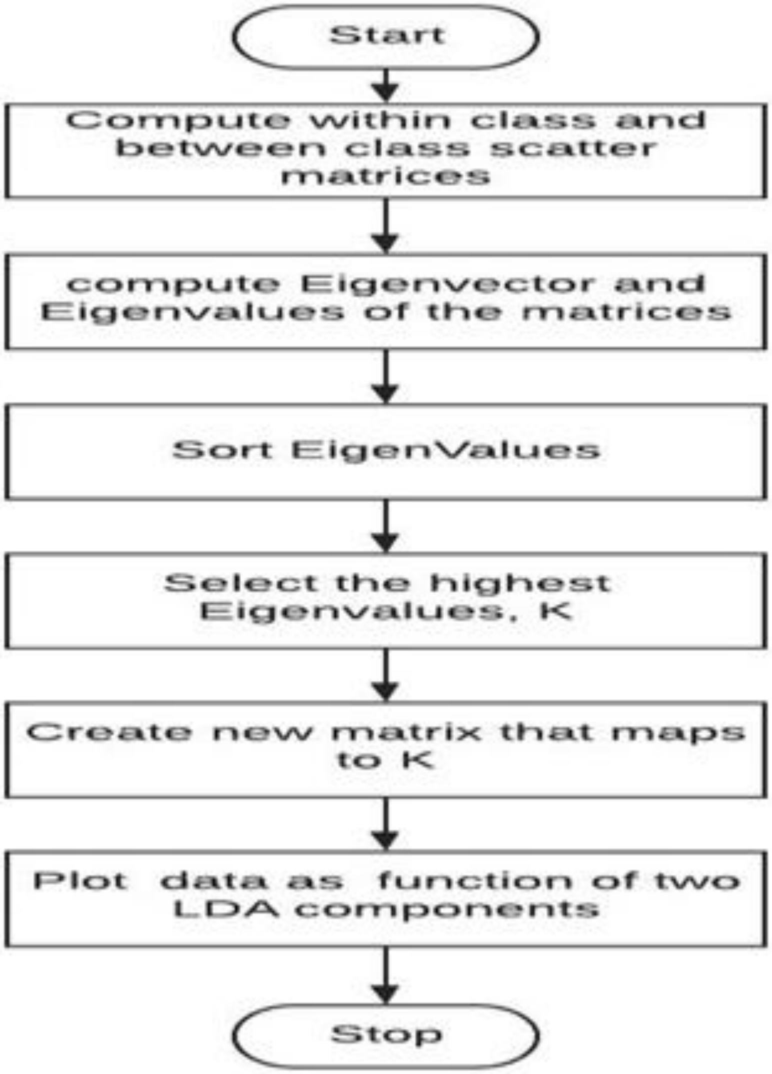

**Fig. 5.** Operational flow of the Linear Discriminant Analysis (LDA) algorithm, highlighting dimensionality reduction and class separability.

### H. Gradient Boosting (GB)

Gradient Boosting constructs an ensemble model in a stage-wise manner by minimizing a differentiable loss function [26]. At iteration $m$, the model is updated as :

$$F_{m+1}(x) = F_m(x) + h_m(x) \qquad (7)$$

where $F_m(x)$is the current model and $h_m(x)$is the newly added weak learner trained to correct the residual errors . Due to its ability to capture complex nonlinear patterns, Gradient Boosting demonstrated superior predictive performance. The workflow of the Gradient Boosting classifier is illustrated in Fig. 6.

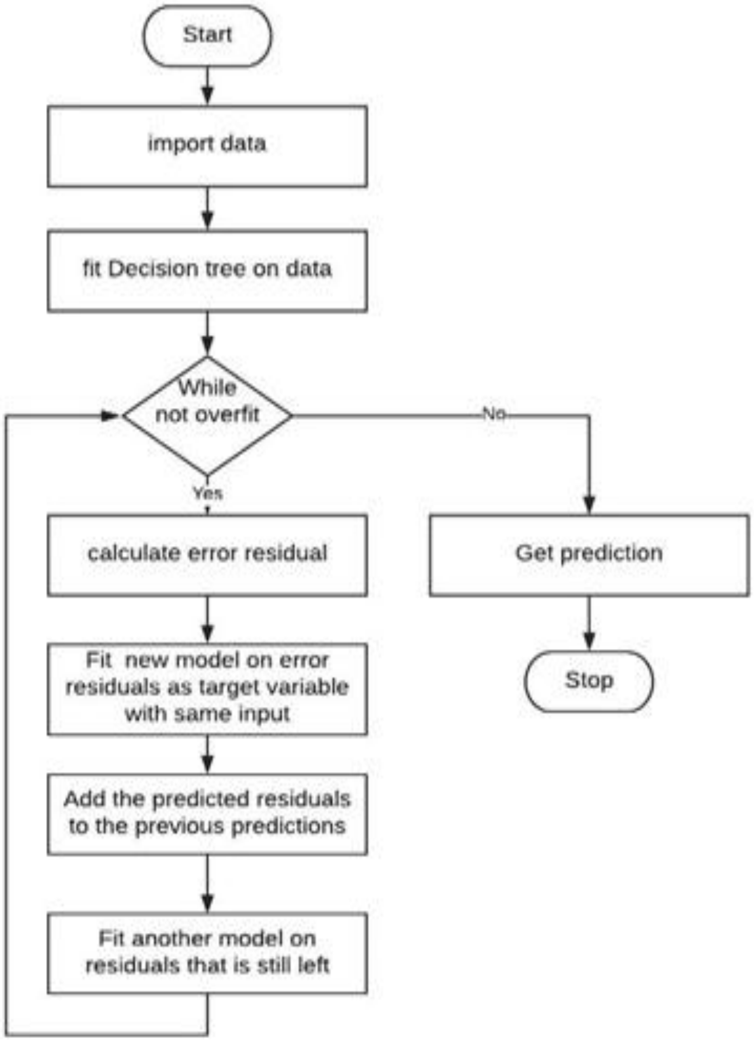

**Fig. 6.** Sequential learning process of the Gradient Boosting classifier, illustrating stage-wise model updates and error minimization.

## 4. Result And Discussion

### *A. Comparative Experimental Performance of the Models*

Following comprehensive preprocessing and feature selection, the dataset was divided into training and testing subsets to evaluate the predictive performance of four supervised machine learning classifiers: Support Vector Machine (SVM), AdaBoost (AB), Linear Discriminant Analysis (LDA), and Gradient Boosting (GB). Model effectiveness was assessed using multiple evaluation metrics, including accuracy (ACC), sensitivity (SEN), specificity (SPE), precision (PRE), F1-score, and error-based measures, as summarized in Table II. These metrics collectively provide a balanced assessment of diagnostic reliability in a clinical prediction context.

Gradient Boosting demonstrated the strongest overall performance among all evaluated models. This superiority can be attributed to its ensemble-based learning strategy, where multiple weak learners are combined sequentially to minimize prediction error. The Gradient Boosting model updates its prediction function iteratively according to

$$\mathrm{F}_{\mathrm{m}+1}(\mathrm{x}) = \mathrm{F}_{\mathrm{m}}(\mathrm{x}) + \mathrm{h}_{\mathrm{m}}(\mathrm{x}) \qquad (8)$$

where $\mathrm{F}_{\mathrm{m}}(\mathrm{x})$represents the current model and $\mathrm{h}_{\mathrm{m}}(\mathrm{x})$denotes the newly added weak learner trained to correct residual errors. This stage-wise optimization allows the model to effectively capture complex nonlinear relationships within the clinical data.

**TABLE 2 Performance Measurement Criteria of Different Machine Learning Models**

| **Metric** | **Support Vector Machine (SVM)** | **AdaBoost (AB)** | **Linear Discriminant Analysis (LDA)** | **Gradient Boosting (GB)** |
|---|---|---|---|---|
| Accuracy (ACC) | 99.56% | 97.91% | 97.91% | **99.80%** |
| Sensitivity (SEN) | 99% | 98% | 98% | **99%** |
| Specificity (SPE) | 99% | 98% | 98% | 98% |
| Precision (PRE) | 99% | 99% | 99% | 98% |
| Negative Predictive Value (NPV) | 97% | 92.30% | 92.30% | **99%** |
| False Positive Rate (FPR) | 0% | 0% | 0% | 0% |
| False Discovery Rate (FDR) | 0% | 0% | 0% | 0% |
| False Negative Rate (FNR) | 0% | 2.77% | 2.77% | **0%** |
| F1-Score (F1) | 99% | 98% | 98% | **99%** |
| Standard Deviation (SD) | 0% | 17.05% | 17.05% | **0%** |
| Mean Absolute Error (MAE) | 0% | 2.08% | 2.08% | **0%** |
| Mean Squared Error (MSE) | 0% | 2.08% | 2.08% | **0%** |
| Root Mean Squared Error (RMSE) | 0% | 14.43% | 14.43% | **0%** |

As reported in Table II, the Gradient Boosting classifier achieved the highest classification accuracy of 99.80%, along with a sensitivity of 99%, indicating excellent capability in correctly identifying CKD-positive cases. In contrast, both AdaBoost and LDA achieved an accuracy of 97.91%, reflecting comparatively lower predictive strength. Although SVM achieved competitive accuracy (99.56%), Gradient Boosting consistently outperformed all models across most evaluation metrics. The comparative accuracy outcomes are visually illustrated in Fig. 7, clearly highlighting the dominance of the Gradient Boosting classifier.

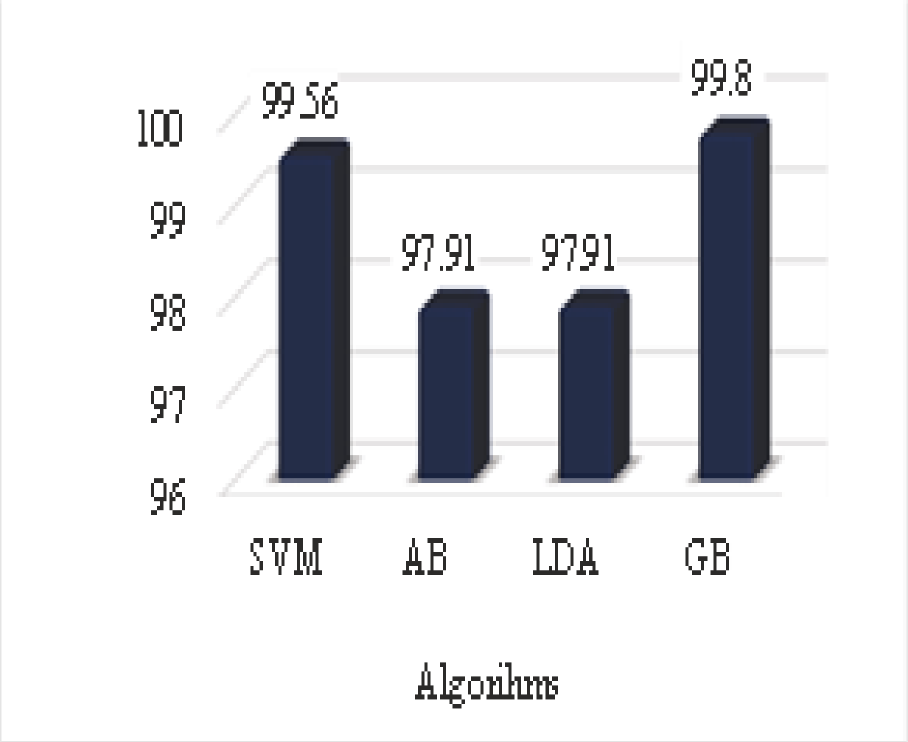

**Fig. 7.** Comparative accuracy analysis of different machine learning classifiers for chronic kidney disease prediction.

### B. Execution Time Analysis

In addition to predictive accuracy, computational efficiency is a critical factor for real-world healthcare applications, particularly in time-sensitive clinical environments. Therefore, the execution time of each algorithm was measured and compared. The results, illustrated in Fig. 8, reveal notable differences in computational cost among the evaluated models.

Support Vector Machine exhibited the lowest execution time, indicating high computational efficiency. Conversely, Gradient Boosting required the highest execution time due to its iterative learning process and ensemble structure. While this increased computational cost may appear disadvantageous, it is justified by the substantial gain in predictive accuracy and diagnostic reliability. AdaBoost and LDA demonstrated moderate execution times, positioning them between SVM and Gradient Boosting. These findings indicate a trade-off between computational efficiency and predictive performance, which must be carefully considered when deploying models in clinical settings.

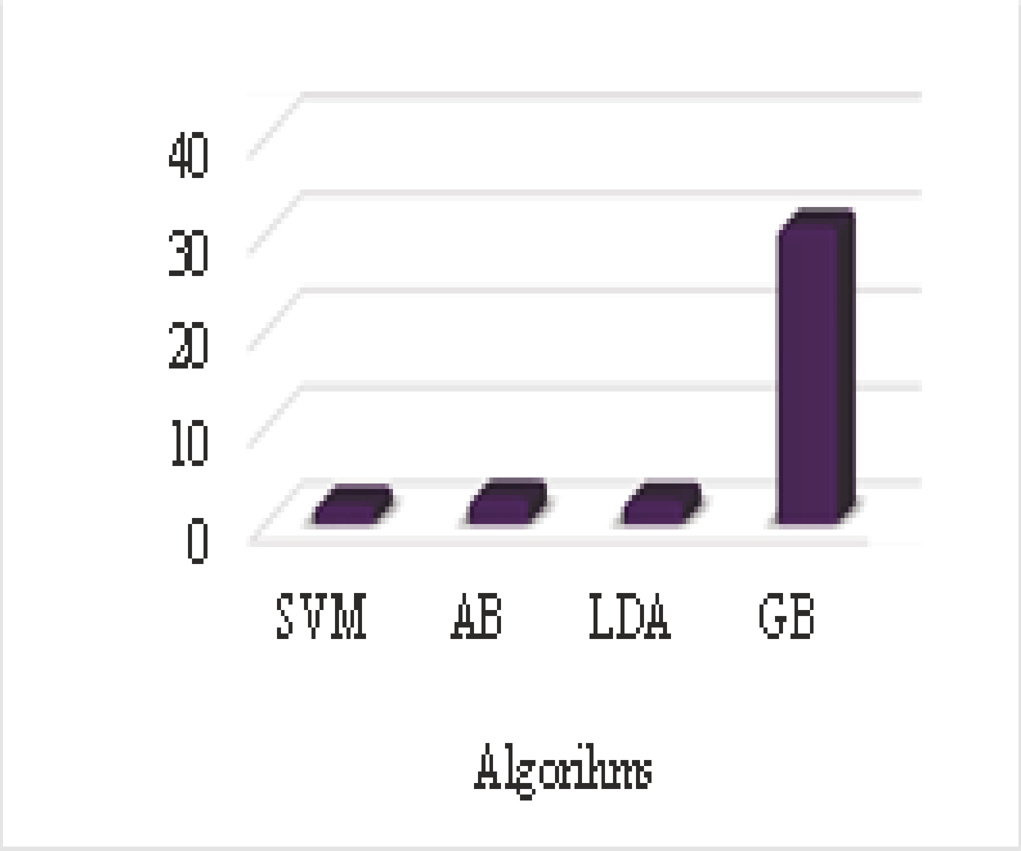

**Fig. 8.** Execution time comparison of the implemented machine learning models during prediction.

### C. Error Rate Evaluation

Error rate analysis provides additional insight into model reliability by quantifying misclassification behavior. Lower error rates indicate higher predictive stability and robustness. The error rates of all four classifiers were evaluated and compared, as shown in Fig. 9.

The Gradient Boosting classifier achieved the lowest error rate of 0.20%, confirming its superior generalization capability. In contrast, AdaBoost and LDA exhibited relatively higher error rates, corresponding to their lower overall accuracy. Although all models demonstrated acceptable performance, the consistently lower error metrics of Gradient Boosting reinforce its suitability for clinical decision-support applications. These results further validate that ensemble-based learning approaches offer improved resistance to noise and class imbalance in medical datasets.

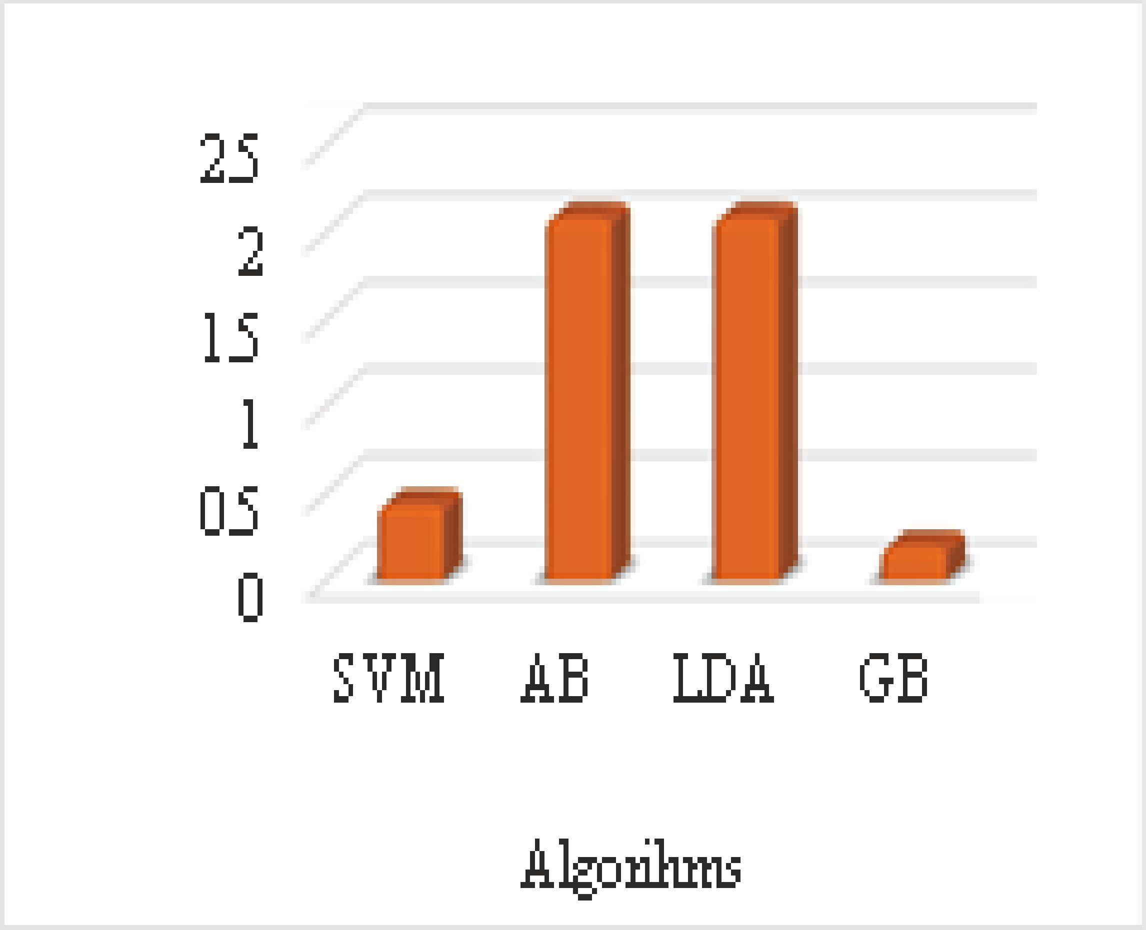

**Fig. 9.** Error rate comparison among Support Vector Machine, AdaBoost, Linear Discriminant Analysis, and Gradient Boosting classifiers.

### *D. ROC and AUC-Based Diagnostic Performance*

To further evaluate diagnostic effectiveness, Receiver Operating Characteristic (ROC) curves and Area Under the Curve (AUC) metrics were generated for all classifiers. The ROC curve illustrates the trade-off between true positive rate and false positive rate, while AUC provides a scalar measure of overall classification capability. These results are presented in Fig. 10.

Among the evaluated models, Support Vector Machine achieved an AUC score of 1.0, indicating perfect class separation. Gradient Boosting also achieved an exceptionally high AUC value, closely approaching unity, demonstrating its strong discriminative power. Linear Discriminant Analysis yielded comparatively lower AUC values, reflecting moderate classification performance. Overall, the ROC and AUC analysis confirms that Gradient Boosting and SVM possess superior diagnostic capability, with Gradient Boosting maintaining a favorable balance between accuracy, robustness, and generalization.

The experimental results clearly demonstrate that ensemble-based classifiers outperform traditional single-model approaches for chronic kidney disease prediction. Gradient Boosting emerged as the most effective algorithm, achieving the highest accuracy, lowest error rate, and excellent ROC–AUC performance. While SVM exhibited strong discriminative ability and faster execution time, Gradient Boosting provided superior overall reliability, making it the most suitable candidate for early-stage CKD prediction in U.S. healthcare decision-support systems.

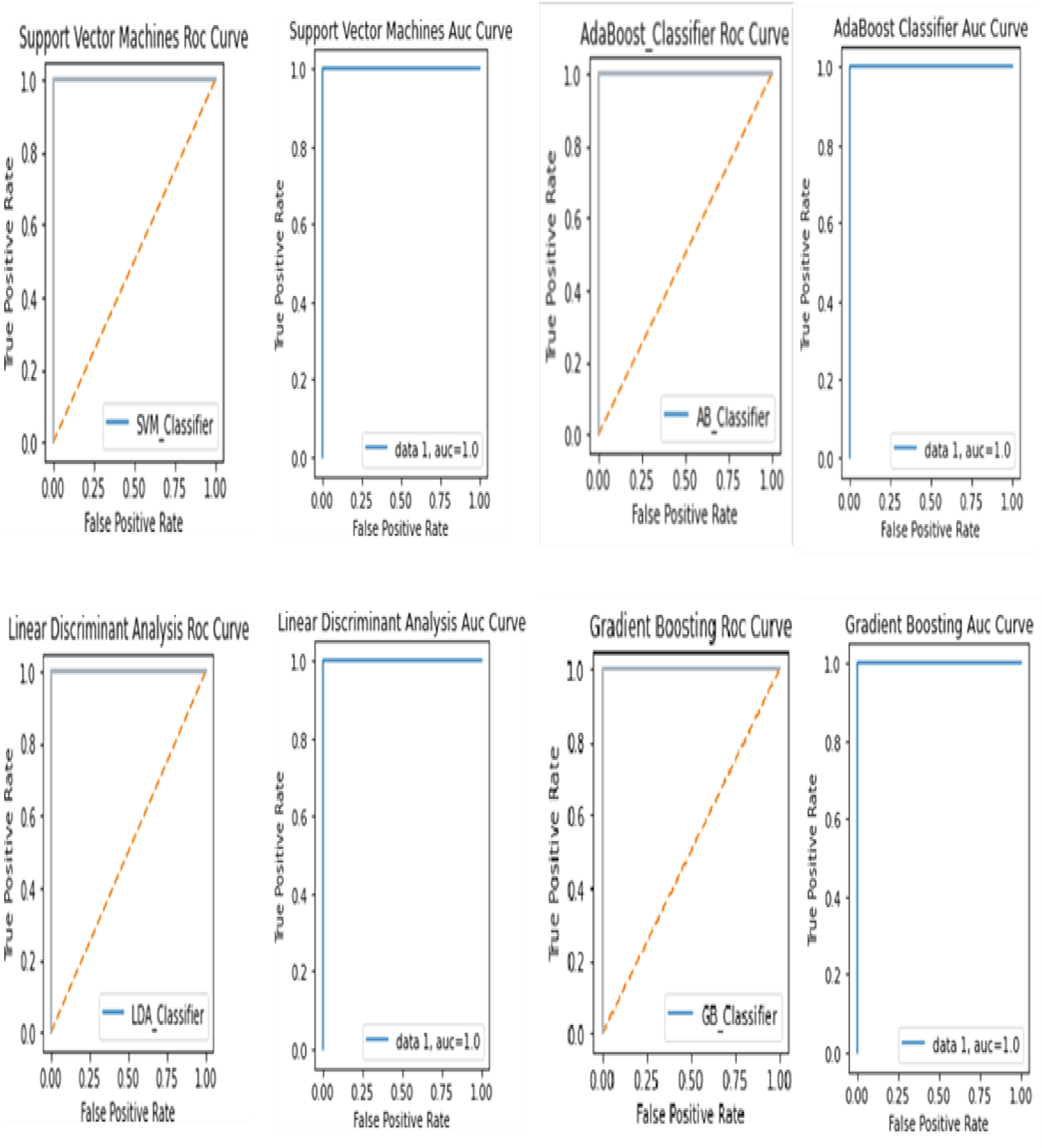
Support Vector Machines Roc Curve
Support Vector Machines Auc Curve
AdaBoost_Classifier Roc Curve
AdaBoost Classifier Auc Curve
Linear Discriminant Analysis Roc Curve
Linear Discriminant Analysis Auc Curve
Gradient Boosting Roc Curve
Gradient Boosting Auc Curve

**Fig. 10.** Receiver Operating Characteristic (ROC) curves and Area Under the Curve (AUC) analysis of the proposed machine learning models.

## 5. CONCLUSION

This study presented a comprehensive machine learning–based framework for the early prediction of Chronic Kidney Disease (CKD) with a specific focus on applicability within the U.S. healthcare system. By leveraging a well-established clinical dataset and employing systematic data preprocessing, feature selection, and model optimization techniques, the proposed framework demonstrated strong predictive capability and robustness across multiple supervised learning algorithms. Four widely used classifiers Support Vector Machine, AdaBoost, Linear Discriminant Analysis, and Gradient Boosting were implemented and comparatively evaluated using a broad set of performance metrics to ensure reliable and clinically meaningful assessment. Experimental results revealed that ensemble-based learning approaches outperform traditional single-model classifiers in CKD prediction tasks. Among all evaluated models, the Gradient Boosting classifier achieved the highest predictive performance, attaining an accuracy of 99.80%, along with superior sensitivity, F1-score, and the lowest error rate. Receiver Operating Characteristic (ROC) and Area Under the Curve (AUC) analyses further confirmed the strong discriminative power of the proposed models, particularly Gradient Boosting and Support Vector Machine, indicating their effectiveness in distinguishing CKD-positive and non-CKD cases. The findings suggest that optimized machine learning models can serve as reliable clinical decision-support tools, enabling early detection of CKD and potentially reducing disease progression and healthcare burden. Despite the promising results, future work will focus on validating the framework using larger and more diverse U.S. clinical datasets, incorporating explainable artificial intelligence techniques for enhanced interpretability, and integrating the system into real-world healthcare workflows to support scalable and ethical clinical deployment.

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