

# CHRONIC KIDNEY DISEASE PREDICTION USING EXPLAINABLE AI

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**Abstract**— Chronic kidney disease (CKD) is a progressive and life-threatening condition that requires early detection to prevent severe complications and kidney failure. This work presents an intelligent and explainable CKD prediction framework using machine learning and ensemble techniques. The study utilizes the CKD dataset from the UCI Machine Learning Repository, consisting of 400 patient records collected from Apollo Hospital, India, with 25 numerical and categorical attributes. Missing values are handled using statistical and model-based imputation, while class imbalance (CKD and non-CKD cases) is addressed using the Synthetic Minority Over-sampling Technique (SMOTE). Comprehensive preprocessing, feature engineering, and feature selection methods—Mutual Information, Variance Thresholding, Recursive Feature Elimination, and Sequential Feature Selection—identify six clinically significant features: hemoglobin, serum creatinine, albumin, hypertension, age, and diabetes mellitus. Multiple classifiers, including Logistic Regression, Gaussian Naïve Bayes, Support Vector Machine, Decision Tree, Random Forest, and AdaBoost, are evaluated using Stratified K-Fold cross-validation. A hybrid Voting Classifier combining Random Forest and AdaBoost achieves superior performance with 99.4% accuracy, precision, and recall, and an F1-score of 99.3%. Model interpretability is enhanced using LIME and SHAP to explain individual predictions and feature contributions. A Flask-based web application integrates user signup and sign in, secure data input, real-time prediction, and explainable outputs, delivering results as “chronic kidney disease detected” or “no chronic kidney disease detected,” thereby supporting reliable and user-friendly clinical decision assistance.

**Keywords**— CKD, machine learning ensemble models, explainable AI, interpretability.”

## 1. INTRODUCTION

Chronic Kidney Disease (CKD) is defined clinically by the presence of kidney damage or a persistent reduction in kidney function, typically characterized by a Glomerular Filtration Rate (GFR) below 60 mL/min/1.73 m<sup>2</sup> for a duration exceeding three months. CKD poses a significant global health challenge, being one of the major contributors to morbidity and mortality worldwide. Its progression often results in irreversible kidney damage, leading to Acute Kidney Injury (AKI) or End-Stage Renal Disease (ESRD), conditions that demand costly treatments like dialysis or transplantation. The disease is frequently associated with comorbidities such as Diabetes Mellitus and Hypertension, which significantly elevate the risk of CKD onset. In clinical diagnosis, routine laboratory evaluations, including blood and urine tests, are used to detect CKD. Albuminuria and elevated serum creatinine levels are key indicators, as they reflect the kidneys' diminished filtration capacity. Furthermore, the first sign of diabetic kidney damage is often the presence of albumin in urine, a consequence of damaged glomerular filters that permit protein leakage into urine.

CKD also has widespread health consequences. It can lead to anemia, bone weakness, fluid retention, elevated blood pressure, and increased cardiovascular risk due to the kidneys' impaired ability to regulate erythropoietin and vitamin D synthesis. According to the Centers for Disease Control and Prevention (CDC), about 37 million adults in the United States have CKD, with the majority unaware of their condition. Each hour, approximately 360 individuals begin dialysis treatment for kidney failure, and diabetes and hypertension account for nearly 75% of new ESRD cases. The economic burden is equally alarming—treatment costs for ESRD exceed \$32 billion annually in the United States, with limited access to renal replacement therapies in developing countries like India due to lack of health insurance and high treatment expenses.

From an engineering perspective, CKD analysis is hindered by the scarcity of accessible and diverse medical datasets. Even when available, healthcare data often suffer from cognitive and sampling biases, posing challenges to reliable machine learning applications. The UCI Machine Learning Repository dataset, collected from Apollo Hospital, India, is one of the most comprehensive publicly available sources for CKD prediction, though it lacks demographic diversity and certain clinical parameters. Recent advancements in Explainable Artificial Intelligence (XAI) have enabled deeper insight into model interpretability, helping identify key biomarkers influencing CKD progression. Integrating XAI with ensemble learning models enhances both predictive performance and clinical transparency, enabling clinicians to make informed, data-driven decisions for early detection and management of CKD.

## 2. RELATED WORK

Bayram et al. introduced a deep learning-based detection and prediction framework for kidney diseases, integrating Explainable Artificial Intelligence (XAI) to enhance interpretability and clinical trust. Their model utilized convolutional neural networks (CNNs) combined with interpretable layers that provided visual explanations for classification outcomes. The research emphasized that while deep learning models achieved superior accuracy compared to traditional methods, their black-box nature limited clinical adoption. By embedding XAI techniques such as LIME and SHAP, the model effectively demonstrated which clinical biomarkers contributed most to the prediction of CKD, thus making the system transparent for healthcare practitioners. The authors concluded that the integration of XAI improved both predictive reliability and user confidence, making it a promising solution for healthcare applications where explainability is critical.

Silveira et al. explored the early prediction of chronic kidney disease using machine learning algorithms optimized for small and imbalanced datasets. They examined several models including Random Forest, Support Vector Machine (SVM), and Gradient

Boosting classifiers to identify CKD at early stages. The authors addressed data imbalance issues using Synthetic Minority Oversampling Technique (SMOTE), which significantly improved the classifier's sensitivity toward minority classes. Their experimental evaluation demonstrated that Random Forest achieved the highest accuracy and recall rates, indicating its robustness for clinical prediction tasks. The study emphasized that proper preprocessing, including data normalization and feature selection, was essential to ensure reliable results in small healthcare datasets.

Mehrabi et al. conducted a comprehensive survey on bias and fairness in machine learning, highlighting critical ethical and technical challenges in healthcare data analysis. They discussed how cognitive, sampling, and labeling biases can adversely affect predictive models, especially in medical contexts such as CKD prediction where demographic and socio-economic diversity is limited. The authors proposed fairness-aware learning strategies and debiasing algorithms to ensure equitable model performance across different population groups. Their work provided a foundational framework for understanding and mitigating biases in AI systems, ensuring that predictive models for healthcare remain transparent, ethical, and clinically relevant.

Ventrella et al. employed supervised machine learning methods to assess the advancement of chronic kidney disease. Their work focused on predicting disease progression rather than initial diagnosis. Using longitudinal patient data, the researchers applied techniques such as logistic regression, decision trees, and ensemble learning to classify CKD stages. Feature importance analysis identified key clinical indicators, including serum creatinine, blood urea nitrogen, and hemoglobin, as major contributors to disease progression. The study highlighted the importance of time-series data and longitudinal modeling in capturing the dynamic nature of CKD, ultimately improving the prediction of patient outcomes over time.

Nishat et al. presented a comprehensive analysis of CKD detection using machine learning algorithms, evaluating models such as k-Nearest Neighbors (KNN), Naïve Bayes, Decision Tree, and Random Forest. They emphasized that feature selection and normalization play a vital role in model optimization. By employing correlation-based feature selection, the authors identified a subset of attributes—hemoglobin, albumin, blood pressure, and serum creatinine—as key predictors of CKD. Their results indicated that Random Forest achieved the best balance between interpretability and accuracy, making it a suitable candidate for clinical decision support. The study also noted that integrating multiple models through ensemble techniques could further enhance predictive reliability.

Chittora et al. provided a detailed machine learning perspective on CKD prediction, developing an optimized pipeline that included feature selection, preprocessing, and model tuning. They applied algorithms such as Support Vector Machine, Logistic Regression, Decision Tree, and AdaBoost to identify optimal parameter settings for CKD prediction. The study demonstrated that ensemble learning approaches significantly outperformed individual classifiers, particularly in handling nonlinear relationships among medical attributes. Additionally, the authors incorporated cross-validation strategies to prevent overfitting and ensure model generalization. Their analysis showed that AdaBoost achieved superior precision and recall, establishing it as one of the most effective classifiers for CKD detection.

Dave et al. investigated the application of Explainable Artificial Intelligence in healthcare using a heart disease dataset, providing insights relevant to CKD prediction models. They implemented SHAP and LIME interpretability techniques to explain the decisions made by machine learning models. The authors emphasized that transparency is essential in clinical AI systems, as it allows healthcare providers to understand and validate model outputs. Their findings demonstrated that combining explainable AI with ensemble methods enhances both trust and diagnostic accuracy, paving the way for similar implementations in CKD-related prediction frameworks.

Ghosh optimized CKD prediction by employing machine learning algorithms, emphasizing parameter tuning and model evaluation. The study utilized the UCI CKD dataset and compared algorithms such as SVM, Random Forest, and KNN. Feature importance metrics revealed that hemoglobin, serum creatinine, and albumin were the most influential predictors. Ghosh also explored grid search and cross-validation to fine-tune model parameters, achieving improved classification performance. The author concluded that Random Forest outperformed other algorithms in both accuracy and interpretability, making it an ideal choice for CKD prediction systems where reliability is crucial.

Aljaaf et al. introduced a predictive analytics-based framework for the early prediction of CKD using machine learning models. The approach integrated data preprocessing, normalization, and ensemble modeling to enhance diagnostic precision. The study compared several classifiers, including Decision Tree, Logistic Regression, and Naïve Bayes, across multiple evaluation metrics such as accuracy, sensitivity, and specificity. Their model achieved high performance, demonstrating the feasibility of using predictive analytics for real-world clinical decision support. Moreover, the authors suggested that integrating these models with healthcare information systems could support proactive patient monitoring and early intervention strategies.

Webster et al. provided a comprehensive clinical overview of CKD, emphasizing its epidemiology, pathophysiology, and global health impact. They reported that CKD ranks among the top causes of mortality and disability worldwide, disproportionately affecting populations in developing regions. The study outlined the major risk factors, including diabetes, hypertension, and genetic predispositions, and emphasized the critical importance of early detection through biomarkers such as GFR, albuminuria, and serum creatinine levels. Their findings established a clinical foundation for integrating AI and data-driven approaches into CKD diagnosis and management.

### III. MATERIALS AND METHODS

The proposed system for Chronic Kidney Disease (CKD) prediction utilizes a machine learning-based framework designed for robust, interpretable, and scalable clinical decision support. The UCI CKD dataset, containing 400 patient records with 25 clinical and biological attributes from Apollo Hospital, India, serves as the foundation. Data preprocessing involves handling missing values through statistical and model-based imputation, encoding categorical variables, normalizing numerical features, and addressing class imbalance using SMOTE. Feature selection is performed using Mutual Information, Variance Thresholding, Recursive Feature Elimination, and Sequential Feature Selection, identifying six critical attributes: hemoglobin, serum creatinine, albumin, hypertension, age, and diabetes mellitus. Supervised classifiers including Logistic Regression, Gaussian Naïve Bayes, SVM, Decision

Tree, Random Forest, and AdaBoost are trained, while interpretability is achieved through LIME and SHAP. A hybrid ensemble Voting Classifier combining Random Forest and AdaBoost is implemented and deployed via the Flask framework for accessible web-based clinical applications.



Fig. 1. System Architecture

Figure 1 illustrates the workflow for predicting Chronic Kidney Disease (CKD). It begins with Data Pre-processing and Feature Selection (RFE FS), followed by Data Balancing (SMOTE). Multiple machine learning models (LR, NB, SVM, AdaBoost, DT, RF) are built, and a Voting Classifier is trained, tested, and evaluated using metrics like Accuracy and F1-Score. The best model is saved, integrated into a Flask web application for deployment, and its predictions are explained using XAI (LIME & SHAP).

**A) Dataset Collection**

The dataset used for this study was obtained from a reliable medical source containing 400 records and 25 attributes in ARFF format. It includes clinical, physiological, and biochemical parameters such as hemoglobin, serum creatinine, albumin, hypertension, diabetes mellitus, and age. These features provide comprehensive patient health insights for Chronic Kidney Disease (CKD) detection. The dataset was loaded into a pandas Data Frame, ensuring structured organization for further analysis, model development, and validation aimed at accurate and early CKD prediction.

age	hgb	sg	al	sc	sbp	dbp	glu	cre	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c	hba1c
0	10	10	1.0	0	100	normal	normal	normal	normal	121	0	0	0	0	0	0	0	0	0	0	0	0	0
1	10	10	1.0	0	100	normal	normal	normal	normal	121	0	0	0	0	0	0	0	0	0	0	0	0	0
2	10	10	1.0	0	100	normal	normal	normal	normal	121	0	0	0	0	0	0	0	0	0	0	0	0	0
3	10	10	1.0	0	100	normal	normal	normal	normal	121	0	0	0	0	0	0	0	0	0	0	0	0	0
4	10	10	1.0	0	100	normal	normal	normal	normal	121	0	0	0	0	0	0	0	0	0	0	0	0	0

Fig. 2. CKD Dataset

**B) Pre-Processing**

Pre-processing ensures data quality and reliability by handling missing values, reducing noise, selecting relevant features, and balancing class distribution. These steps improve model learning efficiency, prediction accuracy, and robustness for reliable chronic kidney disease classification.

**Data Preprocessing:** Data processing focuses on transforming raw clinical records into a clean and consistent format suitable for machine learning models. The CKD dataset contains both numerical and categorical attributes with missing values arising from incomplete clinical tests and reporting variations. To address this, statistical imputation techniques are applied for numerical features, while mode-based or model-driven imputation is used for categorical variables. This approach preserves dataset integrity and prevents information loss that could degrade predictive performance. Normalization and encoding techniques ensure uniform feature representation and compatibility across algorithms. Effective handling of missing data reduces bias, enhances stability, and enables the learning algorithms to capture meaningful clinical patterns essential for accurate CKD prediction.

**Feature Selection:** Feature selection plays a vital role in improving model efficiency and interpretability by identifying the most influential clinical attributes. Recursive Feature Elimination (RFE) is employed to iteratively remove less significant features based on model performance and feature importance rankings. By training the model multiple times and eliminating the weakest features at each step, RFE ensures that only the most relevant attributes contribute to classification. This process reduces dimensionality, minimizes overfitting, and improves generalization. The selected features reflect strong clinical relevance, enhancing both predictive accuracy and explainability. RFE also reduces computational complexity, enabling faster training and more stable predictions, which is critical for real-time clinical decision support systems.

**Data Balancing:** Class imbalance in the CKD dataset can bias learning algorithms toward the majority class, leading to poor detection of minority cases. To overcome this issue, the Synthetic Minority Over-sampling Technique (SMOTE) is applied during data sampling. SMOTE generates synthetic samples for the minority class by interpolating between existing data points, rather than duplicating records. This creates a more balanced class distribution while preserving underlying data patterns. Balanced data improves classifier sensitivity, recall, and overall predictive reliability, particularly for CKD detection. By ensuring equitable representation of both CKD and non-CKD cases, SMOTE enhances model learning, reduces bias, and supports accurate and consistent disease prediction outcomes.

**C) Training and Testing:**

The processed dataset was divided into training and testing sets using a stratified 10-fold cross-validation approach. Multiple machine learning algorithms were trained on the selected features. Models were evaluated based on accuracy, precision, recall, and F1-score metrics. This systematic training and testing ensured robust performance validation, accurate prediction, and reliability of the developed system in identifying Chronic Kidney Disease at early stages.

#### D) Algorithms

**Logistic Regression (LR):** Predicts CKD probability by modeling relationships between key clinical attributes using the logistic function. Provides interpretable coefficients and probabilistic outcomes, helping clinicians identify disease likelihood and support timely intervention through data-driven diagnostic insights.

$$\hat{y}_i = \sigma(w^T x + b) = \frac{1}{1 + e^{-(w^T x + b)}} \quad (1)$$

**Gaussian Naïve Bayes (GNB):** Applies probabilistic modeling with Gaussian assumptions to classify CKD and non-CKD cases efficiently. Offers quick, reliable predictions from limited data, enabling clinicians to assess CKD risk and support early-stage diagnosis with statistical confidence.

**Support Vector Machine (SVM):** Classifies CKD and non-CKD cases by finding an optimal hyperplane for maximum separation. Captures non-linear relationships through kernel mapping, ensuring high accuracy and robustness for clinical data interpretation and early disease identification.

$$\text{minimize } \frac{1}{2} \|W\|^2 + C \sum_{i=1}^n \xi_i \quad (2)$$

**Decision Tree (DT):** Generates a hierarchical structure for CKD classification using clinical attributes. Offers transparent decision paths, handles missing values effectively, and helps clinicians interpret results easily, enhancing diagnostic clarity and early detection strategies.

$$I(i) = 1 - \sum_{i=1}^k p_i^2 \quad (3)$$

**Random Forest (RF):** Combines multiple Decision Trees to improve classification stability and reduce overfitting. Identifies influential CKD indicators, enhances prediction reliability, and provides feature importance insights for clinicians to prioritize patient evaluation and treatment.

$$\text{Gini} = 1 - \sum_{i=1}^c (P_i)^2 \quad (4)$$

**AdaBoost:** Sequentially combines weak learners, emphasizing misclassified CKD instances to refine accuracy. Enhances model performance through adaptive weighting, ensuring effective identification of complex disease patterns and supporting reliable, data-driven clinical assessments.

$$H(x) = \text{sign} \left( \sum_{t=1}^T \alpha_t h_t(x) \right) \quad (5)$$

**Voting Classifier:** Aggregates predictions from multiple algorithms like Random Forest and AdaBoost using majority voting. Improves accuracy, reduces bias, and delivers consistent CKD detection results, ensuring dependable, collective decision-making for clinical evaluations.

$$\hat{y} = \text{argmax}_c \left( \sum_{i=1}^n II(\hat{y}_i = c) \right) \quad (6)$$

#### E) Integration of XAI and Flask Framework:

The integration of Explainable Artificial Intelligence (XAI) with a Flask framework enables transparent and interpretable predictions of machine learning models in an interactive web environment. In this implementation, LIME and SHAP are utilized to explain model decisions for Chronic Kidney Disease (CKD) prediction. LIME provides local explanations by analyzing the contribution of individual features for a single test instance, highlighting factors such as age, blood pressure, and specific lab values. SHAP complements this by offering global interpretability, quantifying the impact of each feature across multiple samples and providing visualizations like summary plots to identify key drivers influencing model outcomes.

By embedding these XAI tools into a Flask application, end-users can interactively input patient data, view predicted probabilities, and understand feature-level explanations. This integration promotes trust, supports clinical decision-making, and ensures that model predictions are not only accurate but also interpretable and actionable for healthcare practitioners.

#### EXPERIMENTAL RESULTS

**Accuracy:** The accuracy of a test is its ability to differentiate the patient and healthy cases correctly. To estimate the accuracy of a test, we should calculate the proportion of true positive and true negative in all evaluated cases. Mathematically, this can be stated as:

$$\text{Accuracy} = \frac{TP + TN}{TP + FP + TN + FN} \quad (7)$$

**Precision:** Precision evaluates the fraction of correctly classified instances or samples among the ones classified as positives. Thus, the formula to calculate the precision is given by:

$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive} \quad (8)$$

**Recall:** Recall is a metric in machine learning that measures the ability of a model to identify all relevant instances of a particular class. It is the ratio of correctly predicted positive observations to the total actual positives, providing insights into a model's completeness in capturing instances of a given class.

$$Recall = \frac{TP}{TP + FN} \quad (9)$$

**F1-Score:** F1 score is a machine learning evaluation metric that measures a model's accuracy. It combines the precision and recall scores of a model. The accuracy metric computes how many times a model made a correct prediction across the entire dataset.

$$F1\ Score = 2 * \frac{Recall\ X\ Precision}{Recall + Precision} * 100 \quad (10)$$

Table. 1. Performance Evaluation

Model	Accuracy	Precision (Weighted)	Recall (Weighted)	F1 Score (Weighted)
Voting	0.994	0.994373	0.994	0.993993
AdaBoost	0.992	0.992308	0.992	0.991997
RF	0.982	0.982823	0.982	0.981985
DT	0.968	0.970186	0.968	0.967941
LogReg	0.968	0.971210	0.968	0.967861
SVM	0.962	0.965921	0.962	0.961864
GNB	0.952	0.954925	0.952	0.951883

Table.1 compares CKD prediction models using accuracy, weighted precision, recall, and F1-score, highlighting that the hybrid Voting Classifier achieves the highest performance, outperforming the other models.

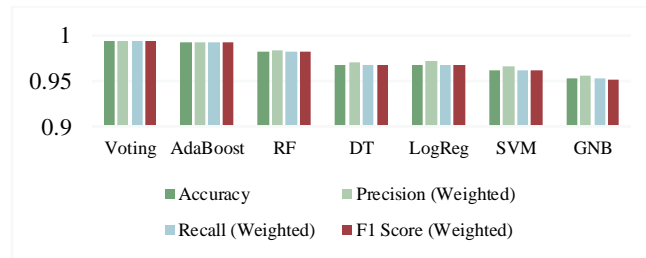


Fig. 3. Comparison Graph

Fig.3 presents a comparison graph of CKD prediction models using accuracy, weighted precision, recall, and F1-score, where each metric is represented by a distinct color—accuracy (blue), precision (green), recall (orange), and F1-score (red)—highlighting the hybrid Voting Classifier's superior performance.




Fig. 4. Upload the Data

In Fig.4, the input form enables users to enter patient data for chronic kidney disease, facilitating prediction through the ML-based classification system.

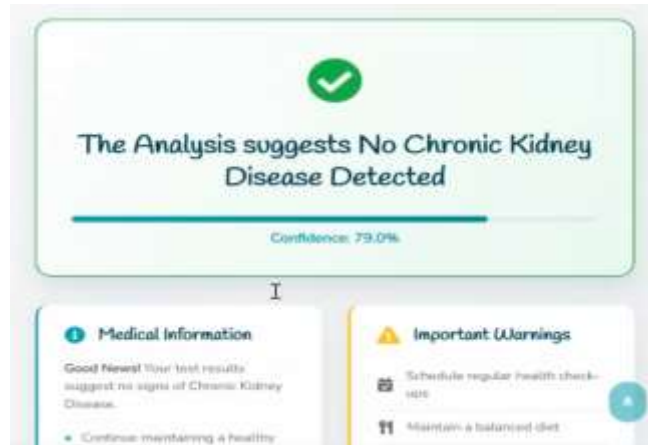


Fig. 5. Predicted Results

In Fig.5, the output screen displays the prediction result “The Analysis suggests No Chronic Kidney Disease Detected” with a confidence score of 79.0%, indicating model certainty.



Fig. 6. Upload the Data

In Fig.6, the input interface allows users to provide patient-specific clinical data for chronic kidney disease, enabling the system to generate predictions with interpretability and confidence scores.



Fig. 7. Predicted Results

In Fig.7, the output screen shows the prediction “The Analysis suggests Chronic Kidney Disease Detected” with a confidence score of 91.0%, indicating high model certainty.

## CONCLUSION

This work demonstrates the successful development of a highly accurate and explainable chronic kidney disease prediction system by integrating advanced machine learning techniques with a practical web-based deployment. Rigorous preprocessing, balanced learning using SMOTE, and robust feature selection enabled the identification of clinically significant attributes that strongly influence CKD diagnosis. Among all evaluated models, the Voting Classifier combining Random Forest and AdaBoost achieved the highest performance, delivering 99.4% accuracy, 99.4% precision, 99.4% recall, and a 99.3% F1-score, indicating exceptional reliability and consistency in distinguishing CKD and non-CKD cases. The incorporation of explainable artificial intelligence techniques, specifically LIME and SHAP, enhanced transparency by clearly illustrating feature contributions, thereby increasing clinical interpretability and trust in the predictions. The complete framework is deployed through a Flask-based web application, which provides secure user signup and sign in, structured patient data entry, real-time prediction, and interpretable output visualization. The system generates clear diagnostic outcomes as “chronic kidney disease detected” or “no chronic kidney disease detected,” supporting informed clinical decision-making and early intervention. Overall, the results confirm that the hybrid

ensemble Voting model, combined with explainable insights and an interactive Flask interface, offers a robust, accurate, and user-friendly solution for CKD risk assessment in real-world healthcare environments.

The future scope of this system lies in expanding its adaptability and integration within real-world healthcare environments. Larger and more diverse datasets from multiple hospitals can be incorporated to enhance generalizability and robustness. Real-time monitoring systems can be integrated with wearable devices and electronic health records to provide continuous prediction and personalized alerts. Further improvements can include advanced deep learning models for higher predictive accuracy and integration with telemedicine platforms for remote patient support. Enhancing explainability techniques will also strengthen clinician trust, while mobile-friendly interfaces can make the framework accessible to both healthcare providers and patients for proactive kidney health management.

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