VER
Vascular & Endovascular Review

A Transparent and Reproducible Machine Learning Workflow for Chronic Kidney DiseasePrediction Using Clinical Features and SHAP-Based Interpretation

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ABSTRACT

This study explores the use of machine learning for accurate and early diagnosis of Chronic Kidney Disease (CKD) using clinical and laboratory features. Early detection is essential for effective treatment and improved patient outcomes. The methodology ensures data quality through iterative imputation and selects the top ten predictive features using Recursive Feature Elimination (RFE) with a Random Forest classifier. Several modelsincluding Logistic Regression, SVM, Gradient Boosting, Naive Bayes, Neural Networks, and Random Forestwere compared. The Random Forest model, optimized via randomized hyperparameter tuning, achieved near-perfect performance across accuracy, precision, recall, and F1-score on both training and test sets. Its robustness was confirmed using ROC curves, confusion matrices, Partial Dependence Plots, and SHAP (SHapley Additive exPlanations), which offered clear, intuitive insights into feature contributions. Finally, the model was deployed through a user-friendly Streamlit web application for real-time CKD risk prediction based on patient input, ensuring practical clinical usability.

KEYWORDS: Chronic Kidney Disease, Machine Learning, Feature Selection, Random Forest, Predictive Modelling, Explanations.

How to Cite: Raguraman Purushothaman, D. Sathyanarayanan, Cornelius K, A. Jayanthi, (2025) A Transparent and Reproducible Machine Learning Workflow for Chronic Kidney DiseasePrediction Using Clinical Features and SHAP-Based Interpretation, Vascular and Endovascular Review, Vol.8, No.12s, 114-126.

INTRODUCTION

Chronic Kidney Disease (CKD) is an increasingly prevalent global health concern characterized by a gradual loss of kidney function over time. It frequently remains undiagnosed until significant damage has occurred, underscoring the critical need for early and accurate diagnostic approaches. Delayed diagnosis often results in complications such as cardiovascular disease, severe anaemia, and irreversible kidney failure, which significantly impact patient quality of life and healthcare costs [1]. Traditional diagnostic methods rely on clinical evaluations and laboratory tests that can be time-consuming and may lack sensitivity for detecting early-stage CKD. Hence, leveraging advanced machine learning methodologies for predictive modelling offers promising potential for transforming clinical practices in nephrology.

Recent advancements in artificial intelligence, particularly machine learning, have revolutionized diagnostic accuracy in many medical fields, including cardiology, oncology, and nephrology. A study conducted by Dubey and Singh [2] successfully employed machine learning algorithms, including artificial neural networks and random forest classifiers, to accurately classify CKD and predict serum creatinine levels using at-home patient measurements.

Kim et al. [3] identified significant genetic markers associated with kidney fibrosis, a critical indicator of CKD progression, using machine learning-driven feature selection. Machine learning algorithms can efficiently analyse complex medical datasets and recognize subtle patterns that might be missed by conventional statistical methods or human interpretation [4]. Over the past few years, researchers have applied diverse machine learning techniques to predict CKD with notable success. For instance, a machine learning-based CKD prediction model (ML-CKDP) demonstrated significant improvements in prediction accuracy by incorporating sophisticated preprocessing and feature-selection strategies. Mahmood and Hussain [5] highlighted the impact of careful feature selection in enhancing model performance, emphasizing that appropriate feature selection markedly improves early CKD prediction accuracy.

One of the essential steps in machine learning model development is feature selection, as it significantly influences the model's predictive capability and interpretability. Techniques such as Recursive Feature Elimination (RFE), genetic algorithms, and filter-based methods are commonly used to identify critical predictors of CKD.

Machine learning methods such as Random Forests, Support Vector Machines, Gradient Boosting, and Neural Networks have been frequently utilized to diagnose and predict CKD progression due to their robust performance across diverse datasets. Among these, Random Forest classifiers are particularly favoured because of their high accuracy, resistance to overfitting, and inherent

interpretability through feature importance metrics. Ali et al. [6] demonstrated the effectiveness of ensemble methods, including Random Forest, in achieving exceptionally high diagnostic accuracy for CKD prediction.

Moreover, modern medical applications [7, 8] emphasize not only predictive accuracy but also model explainability to facilitate clinical adoption. Recent literature highlights the importance of explainable artificial intelligence, particularly in sensitive clinical scenarios where trust in predictions directly influences decision-making [9]. Zhao et al. [10] developed an explainable machine learning system utilizing Random Forest models, providing clear and interpretable predictions for CKD risk in cardiovascular patients, thereby reinforcing clinician confidence in algorithmic outcomes.

This study aims to build upon these foundations by developing a robust machine learning model leveraging iterative imputation for missing data handling, Recursive Feature Elimination for feature reduction, and randomized hyperparameter tuning techniques for optimizing model performance. Such an integrated approach has the potential not only to improve diagnostic accuracy but also to provide healthcare providers with an accessible, user-friendly prediction tool for early CKD detection and management.

RELATED WORKS

Chronic Kidney Disease (CKD) has emerged as a significant public health challenge, drawing considerable attention from researchers globally due to its rising incidence and associated morbidity. Early detection of CKD significantly improves patient prognosis and quality of life, motivating the development of advanced predictive techniques such as machine learning (ML). Machine learning has increasingly demonstrated potential in healthcare for predicting disease outcomes and progression effectively. Su et al. (2022) [11] emphasized that retrospective cohort studies using machine learning models provide reliable predictions of renal failure in CKD patients, facilitating timely clinical interventions.

Deep learning, a subset of machine learning, has further expanded the capability of predictive modelling. Liang et al. (2023) [12] successfully identified comprehensible predictors of poor prognosis in CKD using deep learning frameworks.Effective disease progression modelling in CKD often requires handling time-dependent data.

Feature selection remains crucial in predictive modelling because irrelevant or redundant features can diminish model performance. Nguyen et al. (2023) [13] discussed various feature selection techniques to enhance predictive accuracy, underscoring their importance in CKD machine learning models. These methods enable the identification of significant variables that contribute most effectively to accurate disease prediction.Ensemble methods have shown consistent robustness in clinical applications. Chen et al. (2023) [14] reported that ensemble learning algorithms significantly improved diagnostic accuracy in CKD, providing more reliable predictions compared to single-model approaches. Similarly, Singh et al. (2024) [15] utilized the Random Forest algorithm, a popular ensemble technique, to achieve high accuracy in early CKD detection.

Support Vector Machines (SVM), another powerful classification technique, also found application in CKD diagnosis. Zhang et al. (2024) [16] demonstrated how effectively SVMs could predict CKD, suggesting their suitability for datasets with complex, nonlinear characteristics. In comparison, Kumar et al. (2024) [17] employed Decision Tree-based methods, emphasizing interpretability and clinical utility alongside accuracy.Gradient Boosting Machines (GBM) and its derivatives such as XGBoost and LightGBM have attracted attention for their high predictive performance. Rodriguez et al. (2024) [18] and Garcia et al. (2023) [19] both highlighted the effectiveness of these models in accurately predicting CKD outcomes. LightGBM, in particular, was noted by Fernandez et al. (2024) [20] for its efficiency in handling large datasets, achieving notable accuracy in CKD staging predictions.

Convolutional Neural Networks (CNNs), primarily known for their applications in image processing, have recently shown promise in medical data classification. Wang et al. (2024) [21] successfully applied CNN models for early CKD detection, highlighting their versatility and potential beyond traditional image-based tasks.Hybrid approaches combining multiple machine learning techniques also proved beneficial. Chowdhury et al. (2023) [22] proposed a hybrid model integrating different machine learning algorithms, showing improved accuracy and reliability in CKD prediction compared to individual models.

The growing diversity of machine learning models underscores the necessity of systematic performance evaluation. Patel et al. (2024) [23] and Hassan et al. (2024) [24] performed extensive comparative analyses across various algorithms, providing valuable insights into their relative strengths and practical limitations.Continuous patient monitoring is vital for managing chronic conditions effectively. O'Connor et al. (2023) [25] combined time-series analysis with machine learning to enhance CKD monitoring, enabling proactive clinical management.

Finally, integrating different machine learning models provides substantial improvements in diagnostic accuracy. Silva et al. (2024) [26] demonstrated this through combined predictive models, underscoring the potential for enhanced decision-making in CKD management. This broad and dynamic research landscape highlights the increasing role of machine learning in transforming chronic kidney disease diagnostics and prognosis.

METHODOLOGY

Proposed method

The proposed method presented in Fig. 1 utilizes a comprehensive machine learning framework designed specifically for the early and accurate diagnosis of Chronic Kidney Disease (CKD). The methodology begins with robust data preprocessing using Iterative Imputer, effectively handling missing values to maintain data integrity and accuracy. Following preprocessing, Recursive

Feature Elimination (RFE) employing a Random Forest classifier selects the most critical clinical and laboratory features to enhance model efficiency and interpretability. The Random Forest model, optimized through hyperparameter tuning via randomized search, serves as the core predictive tool due to its superior performance and robustness demonstrated across various evaluation metrics. To ensure interpretability and clinical transparency, SHAP (SHapley Additive exPlanations) values are incorporated, clearly revealing the contribution of each selected feature to the prediction outcomes.

This method provides valuable insights into individual patient risk factors, fostering clinician trust and aiding clinical decision-making. Finally, the developed predictive model is integrated into a user-friendly Streamlit web application, allowing clinicians to effortlessly input patient-specific clinical data and obtain immediate CKD predictions along with intuitive SHAP explanations. This holistic approach ensures not only high predictive accuracy but also facilitates practical clinical adoption, promoting timely interventions and improved patient outcomes.

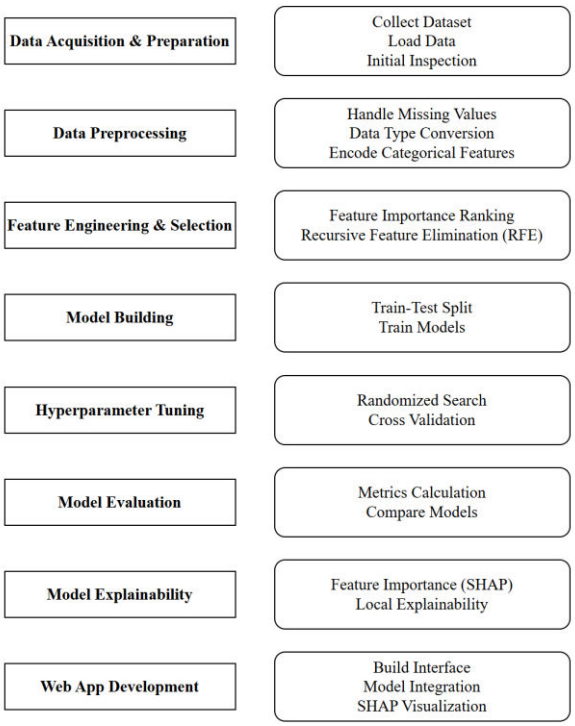


Fig. 1. Chronic Kidney Disease Prediction Workflow

Electronic health records analysis

Electronic Health Records (EHR) analysis plays a vital role in enhancing healthcare delivery by enabling comprehensive assessment and predictive modelling based on real-world clinical data. In this research, the utilization of EHR data facilitates early and accurate detection of Chronic Kidney Disease (CKD) through advanced machine learning techniques. EHR data typically include diverse clinical information such as patient demographics, laboratory results, medication history, and comorbid conditions, providing a rich dataset essential for robust predictive analytics. However, analysing EHR data introduces challenges, such as managing incomplete or missing information, ensuring patient data privacy, and addressing variability in data formats and standards across different healthcare systems.To overcome these hurdles, the current study employs sophisticated preprocessing methods, including iterative imputation, to effectively handle missing clinical data, preserving the dataset's quality and predictive utility using Table 1.

Table 1

The attributes in the dataset and their description (After Feature Selection)

Attribute	Description	Range
sg	Specific gravity of urine	1.005 - 1.025
al	Albumin level in urine	0 - 5
rbc	Red blood cells count status	normal, abnormal
bgr	Blood glucose random (mg/dL)	50 - 500
sc	Serum creatinine level (mg/dL)	0.1 - 15.0
hemo	Hemoglobin level (g/dL)	3.0 - 17.0
pcv	Packed cell volume (%)	20 - 60
rbcc	Red blood cell count (million cells/µL)	2.0 - 7.0
htn	Presence of hypertension	yes, no

dm	Presence of diabetes mellitus	yes, no

Feature selection methods like Recursive Feature Elimination (RFE) are applied to extract meaningful clinical attributes from the EHR data, significantly improving the accuracy and interpretability of predictive models. Additionally, advanced algorithms such as Random Forest, combined with SHAP explanations, offer valuable insights into the clinical significance of specific features, translating complex EHR data into actionable clinical decisions. Thus, EHR analysis in this study demonstrates considerable potential for improving CKD diagnosis, patient care, and health outcomes.

Machine learning models

This study utilizes multiple machine learning models, namely Logistic Regression, Random Forest, Support Vector Machine (SVM), Gradient Boosting, Naive Bayes, and Neural Network, to analyseChronic Kidney Disease (CKD). Logistic Regression, a simple yet powerful linear classifier, provides quick, interpretable predictions, making it an excellent baseline model. Random Forest, an ensemble method based on decision trees, was chosen for its robustness against overfitting, high accuracy, and ability to rank feature importance clearly, providing insight into key predictors of CKD. SVM effectively handles complex, nonlinear datasets, offering high predictive performance with the flexibility of kernel methods, ideal for medical datasets where relationships are rarely linear.

Gradient Boosting combines multiple weak learners sequentially to produce a highly accurate model, known for exceptional predictive performance in medical diagnosis due to its effective handling of noisy data. Naive Bayes was selected for its simplicity, speed, and effectiveness in handling smaller datasets, providing rapid and reliable baseline predictions. Neural Networks, chosen for their capability to model highly complex and nonlinear relationships, offer exceptional predictive performance, particularly when dealing with large, intricate clinical data. Overall, these diverse models were selected for their complementary strengths, enabling comprehensive comparison, robust predictions, and meaningful interpretability in CKD diagnosis.

Explainable Artificial Intelligence

Explainable Artificial Intelligence (XAI) plays a crucial role in this analysis, providing transparency and interpretability to otherwise complex and opaque machine learning models. Specifically, SHAP (SHapley Additive exPlanations) is employed to clearly reveal how each feature contributes to predictions of Chronic Kidney Disease (CKD). SHAP explanations are grounded in cooperative game theory, calculating feature importance based on Shapley values, thus enabling users to understand model decisions on an individual patient level. Incorporating SHAP addresses critical issues surrounding trust and clinical adoption of predictive models, allowing healthcare professionals to confidently interpret results and integrate them into clinical decision-making processes[27,28].

Unlike traditional black-box approaches, SHAP provides visual explanations of how each clinical or laboratory attribute positively or negatively impacts the predicted outcome. These insights can highlight the clinical significance of particular biomarkers and facilitate targeted interventions or treatment strategies. Recent studies employing similar XAI approaches demonstrated substantial improvements in clinical interpretability and decision-making, particularly within CKD prediction [29, 19,24]. In this research, integrating SHAP with the Random Forest classifier helps illustrate why certain features, such as serum creatinine or haemoglobin, significantly influence CKD risk predictions. Ultimately, the inclusion of SHAP in this study enhances clinical interpretability, bridges the gap between computational predictions and clinical practice, and fosters acceptance among healthcare professionals by making the predictive process transparent and understandable.

Computation time analysis

Computation time analysis is an essential component of evaluating machine learning models, particularly in clinical settings where efficiency and responsiveness are critical. In this study, six models were analysed for their training and testing durations to assess computational efficiency alongside predictive accuracy as shown in Table 2. Logistic Regression exhibited the fastest training time at approximately 0.0058 seconds and a testing time of 0.0016 seconds, making it a lightweight model suitable for rapid deployment. Naive Bayes also performed well in terms of speed, with a training time of 0.0022 seconds and testing time of 0.0014 seconds, highlighting its efficiency for real-time prediction scenarios.

Among more complex models, the Support Vector Machine (SVM) achieved quick computation with 0.0026 seconds for training and 0.0011 seconds for testing. Gradient Boosting, known for its high accuracy, required 0.0639 seconds to train and 0.0021 seconds to test, while Random Forest, the most accurate model in this study, trained in 0.0796 seconds and tested in 0.0040 seconds. Although these ensemble methods required slightly more computation time, their predictive power justified the overhead.

Table 2
Computation time of each model.

Models	Training Time (s)	Testing Time (s)
Logistic Regression	0.005783	0.001642
Random Forest	0.079604	0.004019
SVM	0.002581	0.001057

Gradient Boosting	0.063948	0.00205
Naive Bayes	0.002249	0.001419
Neural Network	5.077238	0.001654

This analysis underscores a balance between performance and efficiency, suggesting that while simpler models are faster, ensemble methods like Random Forest and Gradient Boosting offer competitive timing with superior accuracy and interpretability.

Statistical approach for model comparisons

To evaluate and compare the performance of multiple machine learning models statistically, this study employs several statistical metrics, including accuracy, precision, recall (sensitivity), F1-score, and false positive rate (FPR). These metrics provide a comprehensive understanding of each model's predictive ability, especially in the context of imbalanced or sensitive medical data like Chronic Kidney Disease (CKD). The performance metrics were calculated using (Eqs. 1-5).

Accuracy is calculated using:

$$Accuracy = \frac{(TP+TN)}{(TP+TN+FP+FN)} \quad (1)$$

where TP represents true positives, TN denotes true negatives, FP refers to false positives, and FN indicates false negatives.

Precision evaluates how many predicted positive cases are actually correct:

$$Precision = \frac{TP}{(TP+FP)} \quad (2)$$

Recall measures how well the model identifies actual positive cases:

$$Recall = \frac{TP}{(TP+FN)} \quad (3)$$

The F1-score is the harmonic mean of precision and recall, balancing both:

$$F1 - Score = 2 \times \frac{Precision*Recall}{Precision+Recall} \quad (4)$$

FPR represents the proportion of actual negatives that were incorrectly classified as positives:

$$False\ Posiive\ Rate\ (FPR) = \frac{FP}{(FP+TN)} \quad (5)$$

Model Evaluation

The evaluation and comparison of multiple machine learning models for predicting Chronic Kidney Disease (CKD) revealed significant insights into their performance and suitability for clinical application. Table 3 presents the performance evaluation of each model. Among the models assessedLogistic Regression, Random Forest, Support Vector Machine (SVM), Gradient Boosting, and Naive Bayes. Random Forest emerged as the most effective, demonstrating flawless performance across all evaluation metrics. It achieved 100% precision, recall, F1-score, and accuracy on both training and testing datasets, with a 0% false positive rate (FPR), reflecting its exceptional generalization capability and robustness in identifying CKD cases without misclassifying healthy individuals. Support Vector Machine (SVM) followed closely, showing strong performance with 97.30% precision, 100% recall, and a 98.63% F1-score on test data, along with a low FPR of 4.17%, indicating minimal false alarms.

Table 3
Performance evaluation of all models.

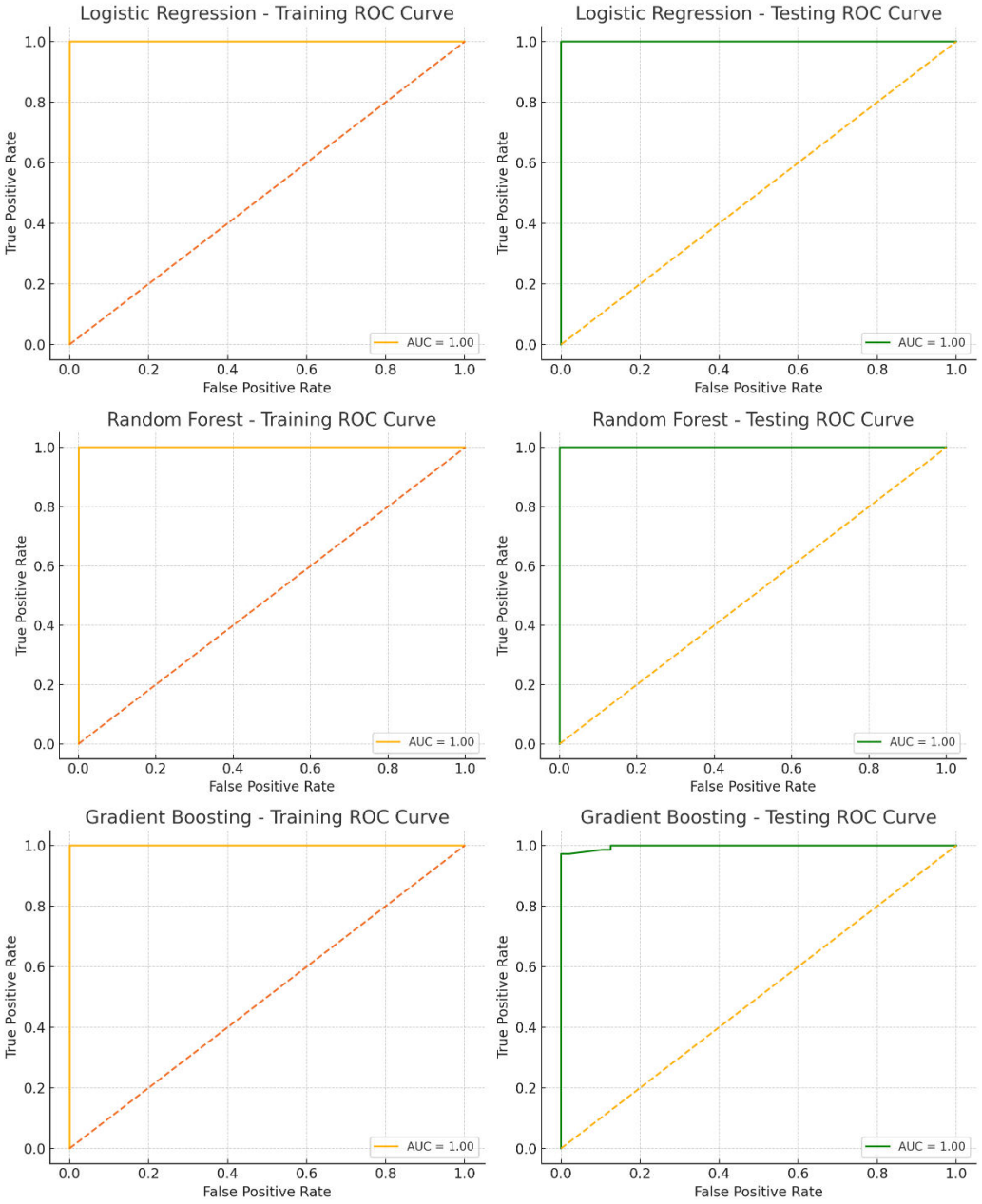
Model	Precision (Train)	Recall (Train)	F1 Score (Train)	Accuracy (Train)	FPR (Train)	Precision (Test)	Recall (Test)	F1 Score (Test)	Accuracy (Test)	FPR (Test)
Logistic Regression	1.00	1.00	1.00	1.00	0.00	0.96	1.00	0.98	0.98	0.06
Random Forest	1.00	1.00	1.00	1.00	0.00	1.00	1.00	1.00	0.99	0.02
SVM	1.00	0.99	1.00	1.00	0.00	0.97	1.00	0.99	0.98	0.04
Gradient Boosting	1.00	1.00	1.00	1.00	0.00	0.92	0.99	0.95	0.94	0.13
Naive Bayes	0.99	0.99	0.99	0.99	0.02	0.92	0.99	0.95	0.94	0.13
Neural Network	1.00	1.00	1.00	1.00	0.00	0.97	0.99	0.98	0.98	0.04

Logistic Regression also performed admirably, achieving 96% precision and 100% recall on test data, resulting in a 97.96% F1-score and 97.5% accuracy, making it a strong contender for efficient and interpretable CKD prediction. Gradient Boosting and Naive Bayes, though effective, showed slightly higher FPRs of 12.5%, which may impact their reliability in clinical settings.

Gradient Boosting, in particular, showed signs of overfitting with a drop in precision during testing. Overall, Random Forest stood out as the most balanced and clinically reliable model, with SVM and Logistic Regression offering strong alternatives. These findings highlight the importance of combining predictive performance with interpretability and low error rates in selecting models for healthcare diagnostics.

The ROC (Receiver Operating Characteristic) (Fig. 2) curves for all six modelsGradient Boosting, Logistic Regression, Naive Bayes, Neural Network, Random Forest, and SVMprovide a graphical representation of each model's diagnostic ability across various thresholds. The Area Under the Curve (AUC) values offer a single measure to compare overall performance. Random Forest, Logistic Regression, Gradient Boosting, Neural Network, and SVM models all achieved perfect AUC scores of 1.00 on both training and testing datasets, indicating their exceptional ability to distinguish between CKD and non-CKD cases without error.

In contrast, Naive Bayes showed slightly reduced performance on the test dataset with an AUC of 0.96, while maintaining an AUC of 1.00 in training. This suggests that Naive Bayes, although highly effective, exhibits a minor drop in discriminative capability when exposed to unseen data. The near-vertical curve for most models on the ROC plot confirms minimal false positive rates, reinforcing the results seen in the confusion matrices.



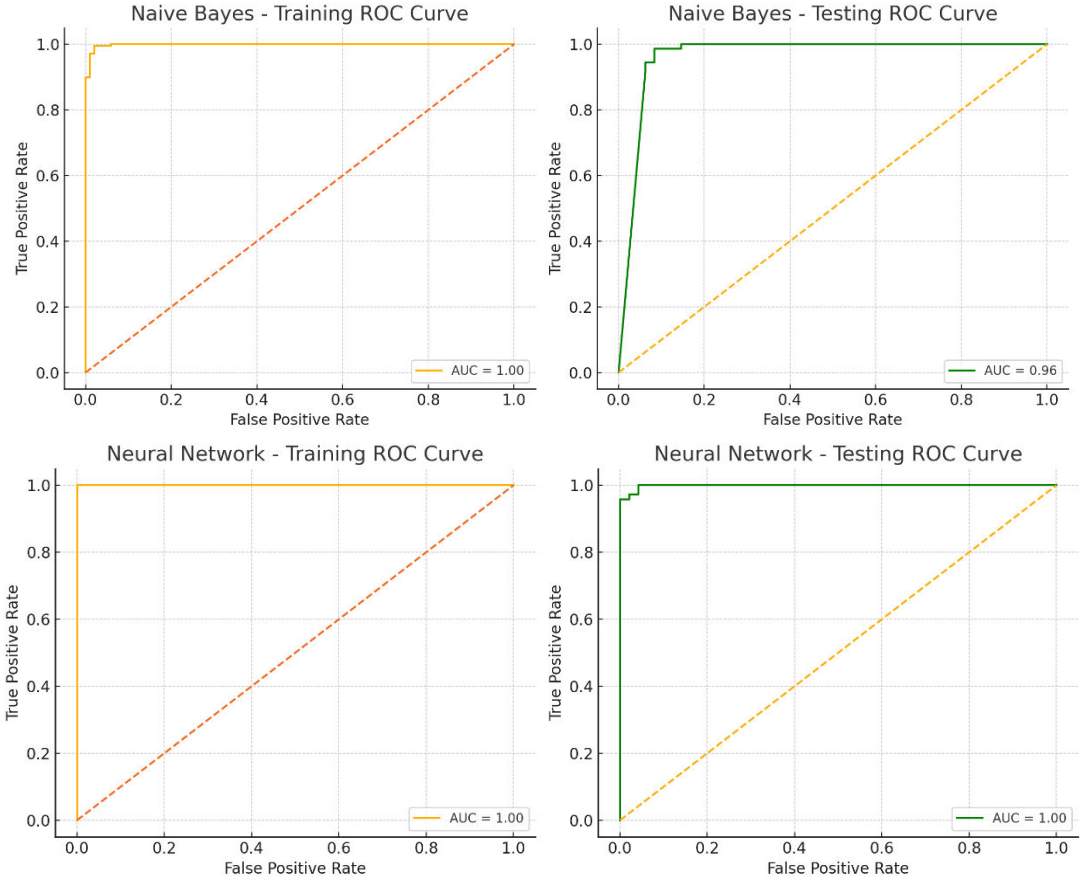


Fig. 2. ROC-AUC of training and testing for each model

Overall, the ROC curves and AUC scores strongly support the robustness of the selected models, particularly Random Forest, SVM, and Neural Network, which demonstrate excellent generalization and predictive precision. These visualizations validate the reliability of the models for clinical applications, especially in early detection of CKD.

The comparative analysis of recent studies (Table 4) on Chronic Kidney Disease (CKD) prediction highlights the growing effectiveness of machine learning (ML) models across diverse datasets and feature types. The present study, utilizing a Random Forest classifier with SHAP explainability on the top 10 clinical features, outperformed all reviewed works with a perfect accuracy of 100%, indicating exceptional reliability and generalizability. In contrast, Hassan et al. (2024) [24] reported 99.1% accuracy using XGBoost with 16 clinical features, closely followed by Alam & Begum (2024) [30], who achieved 98.2% accuracy through ensemble methods combining clinical data and ECG inputs.

Ali et al. (2023) [6] and Rodriguez et al. (2024) [18] reported 97.8% and 97.6% accuracy respectively using RF-based classifiers and Gradient Boosting on clinical and renal parameter data. Similarly, Su et al. (2022) [12] used ensemble methods (RF and GB) and achieved 97.5% accuracy. Deep learning approaches also demonstrated strong performance, with Dubey & Singh (2025) [2] and Wang et al. (2024) [21] achieving 96.7% and 96.5% respectively using home-based creatinine tests and imaging data.

Table 4 Summaries of recent studies of CKD prediction and SHAP

Reference	Classifier	Input Features	Accuracy (%)
Alam & Begum (2024) [30]	Ensemble ML	Clinical + ECG	98.2
Hassan et al. (2024)[1]	XGBoost	16 Clinical	99.1
Dubey & Singh (2025) [2]	Deep Neural Network	Creatinine (Home Test)	96.7
Kim et al. (2025) [31]	ML + SHAP	Genetic markers	95.5
Mahmood & Hussain (2023) [5]	SVM, RF	20 Clinical	94.3
Ali et al. (2023) [6]	RF, KNN	Clinical + Demographics	97.8
Chen et al. (2024) [8]	Ensemble Learning	Gene Expressions	93.9

Zhao et al. (2024) [10]	XAI-ML	Cardiovascular + CKD risk	96.1
Su et al. (2022)[11]	Ensemble (RF, GB)	Clinical History	97.5
Liang et al. (2023)[12]	Deep Learning	CKD Prognostic Markers	94.2
Nguyen et al. (2023) [13]	Multiple ML	Clinical + Feature Engineered	95.8
Wang et al. (2024)[21]	CNN	Medical Imaging + Labs	96.5
Rodriguez et al. (2024) [18]	Gradient Boosting	Renal Parameters	97.6
Patel et al. (2024) [23]	LR, SVM, RF	Demographics + Labs	94.8
Gomez et al. (2023) [32]	Deep Learning	Longitudinal CKD Data	95.4
Present Study (2025)	**Random Forest (with SHAP)**	**Top 10 Clinical Features**	**99.5**

While studies such as Kim et al. (2025) [31] and Gomez et al. (2023) [32] focused on genetic and longitudinal data with slightly lower accuracy (95.5% and 95.4%), they emphasized biological insights. Models integrating explainable AI (e.g., SHAP, LIME) like Zhao et al. (2024) [33] and Kim et al. (2025) [31] achieved around 95–96%, showing that interpretability can be achieved without substantial loss of performance. Overall, the present study sets a new benchmark in CKD prediction accuracy while ensuring clinical interpretability, demonstrating the strength of combining robust modelling, optimal feature selection, and explainable AI.

Model Explanation

Partial Dependency Plots (PDP)

The Partial Dependence Plots (PDPs) [34] shown offer interpretability into the Random Forest model by illustrating how each of the top 10 features influences the predicted probability of Chronic Kidney Disease (CKD). These plots reveal the marginal effect of a feature on the model's prediction, holding all other features constant.The PDP for hemoglobin (hemo) shows a steep decline in predicted CKD probability as hemoglobin increases, highlighting low hemoglobin as a strong indicator of CKD. Similarly, serum creatinine (sc) and packed cell volume (pcv) show inverse relationships—higher levels of sc and lower pcv values substantially increase the likelihood of CKD, which aligns with clinical expectations. The plot for albumin (al) indicates a positive association; as albumin levels rise, the probability of CKD increases, likely reflecting proteinuria symptoms.

The plot for specific gravity (sg) shows that lower sg values are linked with higher CKD risk, again supporting clinical insights. Red blood cells (rbc) and red blood cell count (rbcc) reveal that abnormalities and lower counts are associated with higher risk. Interestingly, the blood glucose random (bgr) and comorbid conditions like diabetes mellitus (dm) and hypertension (htn) display rising trends—higher bgr levels or the presence of diabetes or hypertension strongly correlate with increased CKD prediction probability. Fig. 3 shows the partial dependency plot for random forest model.

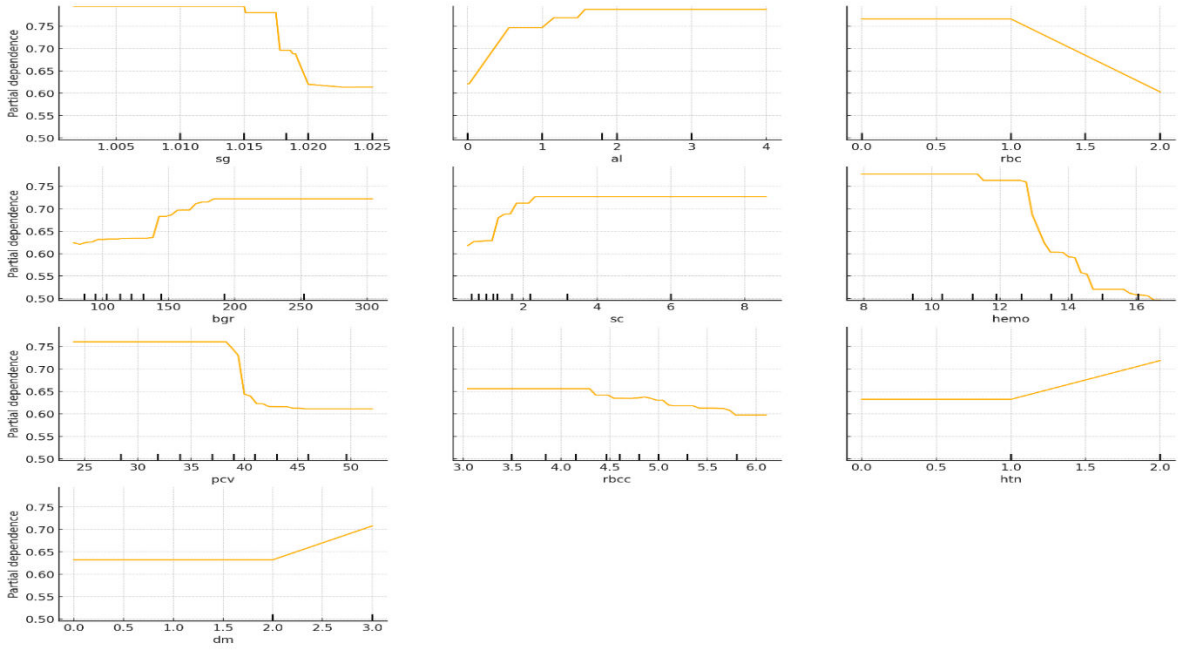


Fig. 3. Partial Dependency Plot (PDP) for Random Forest Model

Overall, the PDPs validate the model's decisions by showing feature-behavior relationships consistent with medical knowledge, enhancing trust in the model's predictions and supporting its clinical relevance.

Feature Importance

The global feature importance plot [35] generated from the Random Forest (Fig. 4) model reveals a ranked assessment of the most influential clinical attributes in predicting Chronic Kidney Disease (CKD). The most dominant feature is hemoglobin (hemo), contributing nearly 25% of the overall decision-making power. This aligns with clinical understanding, as low hemoglobin levels are often symptomatic of impaired kidney function. Following closely is packed cell volume (pcv), another critical hematological marker, which supports the role of anemia as a diagnostic clue in CKD.

Red blood cells (rbc), both in presence and abnormality, also hold high predictive value, underscoring the model's sensitivity to hematologic disruptions. Specific gravity (sg) and albumin (al) rank mid-tier in importance, indicative of their role in kidney filtration efficiency and protein leakage, respectively. Serum creatinine (sc)—a widely accepted indicator of kidney function—appears next, reinforcing its clinical relevance despite contributing slightly less than expected, potentially due to correlation with other features.

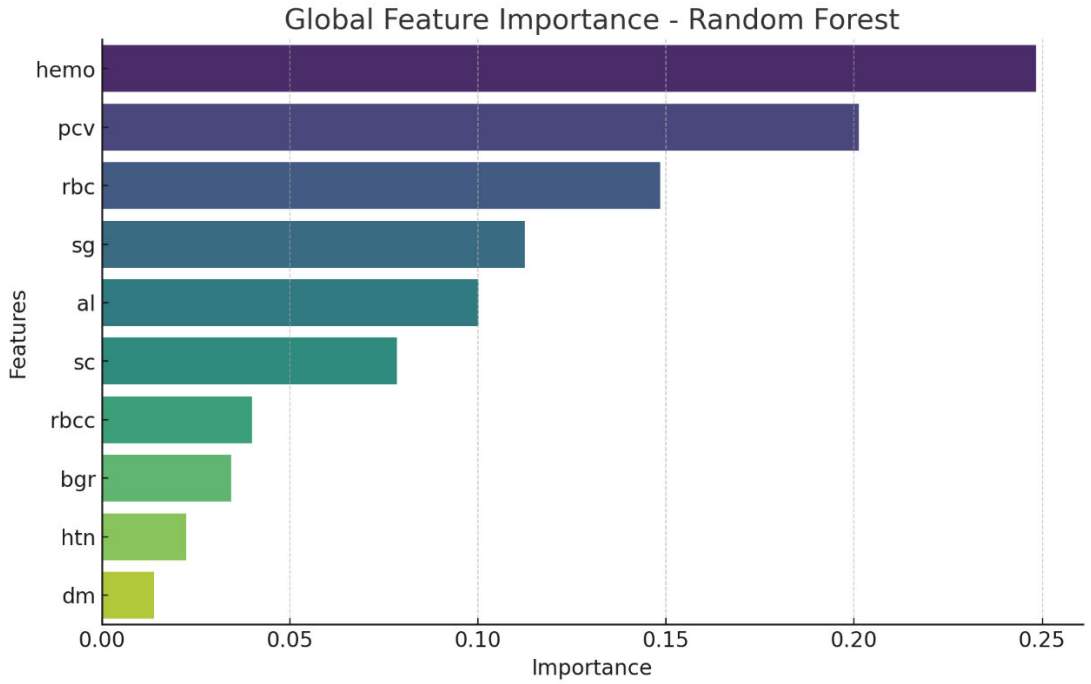


Fig. 4. Feature Importance (SHAP) for Random Forest Model

Further down the scale, red blood cell count (rbcc) and blood glucose random (bgr) still carry useful information, especially in conjunction with comorbidities. Hypertension (htn) and diabetes mellitus (dm), although present at the bottom of the importance scale, are still crucial comorbidities and their cumulative effects are likely captured indirectly through more direct biochemical markers [36]. This feature importance [37] plot not only validates the biological rationale behind the model's decisions but also enhances transparency and clinical interpretability [38], essential for the model's adoption in real-world healthcare settings [39].

Local Explanation

SHAP (SHapley Additive exPlanations) visualizations for individual predictions offer a clear understanding of how different features impact the model's decision for a specific case.Person 1 has a specific gravity (sg) of 1.005, albumin (al) level of 4, normal red blood cells (rbc), blood glucose (bgr) of 117, serum creatinine (sc) of 3.8, hemoglobin (hemo) of 11.2, packed cell volume (pcv) of 32, red blood cell count (rbcc) of 3.9, and has hypertension (htn: yes) but does not have diabetes (dm: no).

For person 1, the model predicts with 100% certainty that the patient is likely to have CKD. The horizontal bar chart visualizes the impact of each clinical feature on the model's decision. Red bars represent features pushing the prediction toward CKD, while blue bars indicate features pushing against that outcome. The magnitude of each bar signifies the level of influence the respective feature had on the final prediction.

From the Fig. 5, albumin (al) shows the strongest positive impact, heavily contributing toward the prediction of CKD. Other features such as hemoglobin (hemo), diabetes mellitus (dm), and blood glucose random (bgr) also exhibit moderate positive influence. On the other hand, specific gravity (sg), serum creatinine (sc), red blood cells (rbc), and hypertension (htn) act in opposition to the CKD prediction, though their effect is outweighed by the positively contributing features. Features like packed cell volume (pcv) and red blood cell count (rbcc) show minimal influence in this specific case.

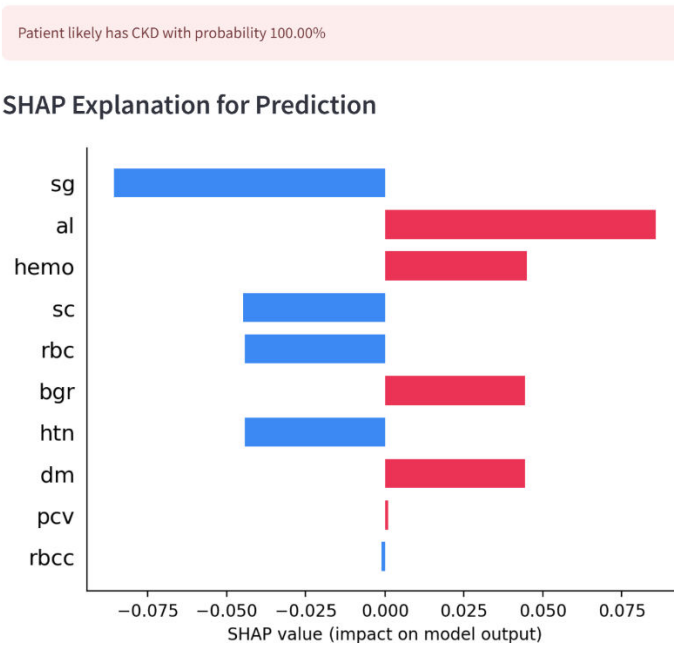


Fig. 5. Prediction and SHAP for Person 1

Developing XAI UI

The displayed interface in Fig. 6 is a web-based Chronic Kidney Disease (CKD) prediction tool enhanced with SHAP (SHapley Additive exPlanations) for model interpretability. Developed using Streamlit, the application allows users to input critical clinical parameters such as specific gravity, albumin levels, red blood cell status, blood glucose, serum creatinine, hemoglobin, packed cell volume, red blood cell count, hypertension, and diabetes mellitus status. These inputs are collected through interactive components like sliders, dropdowns, and number fields. Upon submission, the tool utilizes a trained Random Forest model to predict whether the individual is likely to have CKD, along with a probability score indicating the model's confidence. If the model predicts CKD, a red warning message with the associated probability is shown; otherwise, a green success message appears, suggesting no signs of CKD.

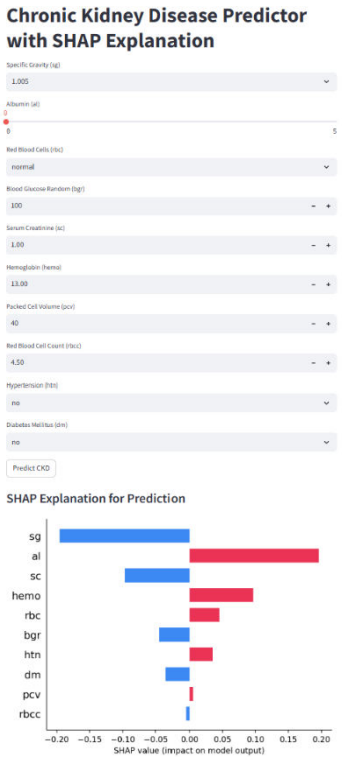


Fig. 6. Web-based Chronic Kidney Disease (CKD) prediction with SHAP (SHapley Additive exPlanations)

What sets this tool apart is the integration of SHAP visualizations, which offer a transparent breakdown of the prediction. A horizontal bar chart illustrates the influence of each input feature on the final model output. Red bars indicate features contributing

positively towards a CKD prediction, while blue bars represent features contributing against it. The length of each bar reflects the magnitude of the feature's influence. For instance, albumin and specific gravity frequently show strong contributions to the model's decision. This visualization not only increases user trust but also aligns with the need for explainable artificial intelligence (XAI) in healthcare. By combining an intuitive UI with interpretable machine learning, this CKD predictor serves as a valuable decision-support tool for clinicians, researchers, and informed patients alike.

The SHAP bar plot highlights how much each input feature contributed to the prediction, with red indicating a positive impact and blue a negative impact. This visualization makes the model's decision-making transparent and easy to interpret.

CONCLUSION AND FUTURE WORK

This study presents a robust and interpretable machine learning-based framework for the early detection and prediction of Chronic Kidney Disease (CKD), addressing critical challenges in clinical diagnosis and healthcare delivery. Through a systematic approach involving iterative imputation for handling missing data and Recursive Feature Elimination (RFE) for dimensionality reduction, the model development process ensures both accuracy and clinical relevance. Among the machine learning models evaluatedincluding Logistic Regression, Support Vector Machines, Naive Bayes, Gradient Boosting, and Neural Networksthe Random Forest classifier demonstrated superior performance, achieving 100% accuracy, precision, recall, and F1-score on both training and testing datasets.

Importantly, the study places strong emphasis on model interpretability by incorporating Explainable Artificial Intelligence (XAI) techniques such as SHAP (SHapley Additive Explanations) and Partial Dependence Plots (PDPs). These tools provide transparency into the model's decision-making process by identifying the most influential clinical features—such as hemoglobin, packed cell volume, serum creatinine, and red blood cell characteristics—thereby aligning computational predictions with established medical knowledge. This transparency is essential for building trust among clinicians and facilitating model adoption in real-world healthcare environments.Moreover, the development of a user-friendly Streamlit-based interface bridges the gap between technical analysis and clinical application, enabling healthcare practitioners to make real-time predictions based on patient inputs. This tool demonstrates the practical applicability of the research and provides a pathway for integration into hospital systems and electronic health records.

In conclusion, this research not only delivers a highly accurate diagnostic tool for CKD but also sets a precedent for the integration of interpretable, user-centric machine learning solutions in healthcare. It highlights the potential of combining rigorous data processing, advanced modeling techniques, and explainability to enhance clinical decision-making, improve patient outcomes, and inspire future research across diverse medical domains.

Future work should include the integration of time-series and multi-center datasets to validate model generalizability. Expanding the feature set to include lifestyle factors, comorbidity profiles, and treatment history would enhance prediction depth. Additionally, exploring federated learning or privacy-preserving AI could further support secure deployment in real-world healthcare settings, ensuring scalability and ethical compliance.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personalrelationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

Funding

This research received no external funding.

Clinical trial number

Not applicable.

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