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Predicting Chronic Kidney Disease using ML algorithms and LIME

Tara Bahadur Thapa [1]*, Mohan Bhandari [2]

[1]Gandaki College of Engineering and Science, Pokhara

[2]Samriddhi College, Bhaktapur

*tara@gces.edu.np

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Abstract: Numerous researchers have implemented machine learning (ML), and deep learning (DL) to predict chronic kidney diseases (CKD). But these studies have succeeded in early diagnosis, they lack transparency. Such ambiguity has raised red flags in adopting AI in the critical domain of healthcare and medical analyses. This paper aims at interpreting the outcome of predictive models by proposing an explainable AI (XAI) interface using local interpretable model-agnostic explanation (LIME). The intended model aims to hold the system accountable for its projections, which will assist efficient decision-making in the field of clinical research and therapeutic practice.

Keywords: Machine Learning, Deep Learning, Explainable AI, LIME, Chronic Kidney Disease

1 Introduction

Chronic kidney disease (CKD) is the impairment of kidneys, leading to a gradual decrease in kidney functions [1]. Kidney disease has been one of the major causes of global mortality and morbidity, along with a fair share of contributions towards cardiovascular diseases and renal failure [2]. In most developing countries, like India, the pervasiveness of this disease is 800 per million population [3] or 17.2 percent, with 6 percent at CKD stage 3 and above [4]. Diabetes mellitus and high blood pressure form the common ground of CKD, accounting for two-thirds of the cases [5].

The distribution of kidney malfunction is highest among people aged 65 and above (38%), followed by the 45-64 age group (12%). A disturbed lifestyle and unhealthy eating habits have brought young adults under the radar [6]. The Global Burden of Disease (GBD) study has categorized CKD into five stages, starting from early to end-stage kidney disease, which usually requires organ transplant [7]. Simple laboratory tests primarily check eGFR (estimated Globular Filtration Rate) level on serum creatinine for examining the functionality of kidneys. The variable discussion is detailed in later sections.

Progression in artificial intelligence and machine learning has allowed for determining the early onset of the disease, disabling further deterioration in the condition of the organs. Previous implementations of ML models have approached the issue with a high success rate and novel methods to address the infection. AI has enabled professionals to either detect, diagnose, or extract information, moving the avenue towards a more data-driven approach in healthcare analysis.

Explainable AI has further paved the way to decipher the results delivered by these medical systems, opening doors for interpreting, and comprehending the decisions of the predictive models, simultaneously identifying the errors and miscalculations in the analysis.

The aim of Explainable Artificial Intelligent systems, also referred to as XAI, is to create such techniques that:

- Create more transparency in the model while keeping intact a high rate of performance.
- Allow and help the users (medical professionals, clinicians, etc.) in efficiently managing the ever-increasing number of trustable and reliable AI partners.

Clarity within the ML system reduces the chances of erroneous decisions, which are quite common in the clinical recommendation system [8]. Healthcare practitioners' acceptance of any recommendation is dubious without much evidence [9-14].

For this research, XAI techniques using LIME is utilized in collaboration, to measure the extent of patients suffering from chronic kidney disease by highlighting the local and global determinants of the illness. By holding the system accountable for its predictions, this study aims to explore the potential of XAI in the ethical evaluation of kidney disease infections.

2 Related Work

Ample research papers and medical studies have been referred for this paper. Literature review of previous analysis catered for a deeper understanding of ML and DL models, along with Explainable AI.

2.1 Machine Learning and Deep Learning

Machine Learning (ML) has come a long way in healthcare analysis. The techniques developed and the models deployed have not only achieved high accuracy but have also paved the way for advanced models to be built. For this research, several papers utilizing such models for detecting and classifying diseases have been referred.

Thiyaagraj and Suseendran [15] have detailed out various ML techniques used for disease classification. Their thorough analysis allows for clarity in conceptual understanding. From a practical perspective, Polat, Mehr, and Cetin [16] applied two feature selection approaches, wrapper, and filter, followed by the Support Vector Machine (SVM) classifier. The resultant comparison between SVM on training data and SVM on filtered data favored the latter, with an accuracy rate of 98.5%. Numerous researchers employed the CKD dataset available on the UC Irvine repository for their diverse analysis. Koklu and Tutuncu [17] assessed the kidney disease classification using SVM, Naive Bayes (NB), C4.5, and Multilayer Perceptron, where the last approach outperformed the others with 99.75% accuracy. Multiple ML models with feature selection have been executed by Saurabh and Nargis [18]. Out of the 24 features used in the study, 16 advanced the prediction, and Random Forest (RF) gave the highest classification rate of 99.75% among its peers SVM, NB, K Nearest Neighbour (KNN), and J48.

Methods consisting of deep learning approaches leveled up the predictive detection of kidney disease. A team of researchers consisting of Azimi, Hathikal, H.Won, and Gharibdousti [19] presented their work on the application of five ML models, NB, SVM, Decision Trees (DT), Logistic Regression (LR), and ANN on normalized features. While the first four showed high performance, the same was not with ANN. Salekin and Stankovic [20] used KNN, RF, and ANN to predict, and identify a cost-effective classifier using five features for improving precision. Aqlan and Markle [21] utilized six analytics methods, namely NN, LR, SVM, RF, Bayes Net (BN), and Discriminant Analysis (DA). They implemented K-Means clustering to further divide the cases into five groups, with varying percentages. ANN acted as a better classifier in the analysis done by Chakrapani, Kalita [22], where it achieved a higher detection rate in comparison to other classifiers. Kriplani, Patel, and Roy [23] advanced their calculations with the inclusion of Deep Neural Networks (DNN) and Adaboost optimization to accomplish improved predictability. Another variation is visible in the research work by Tabassum and Majumdar [24], where the authors have included the Expectation-Maximization (EM) algorithm to create five clusters of infected and healthy patients, followed by classification using C4.5 and ANN, with the former performing better. The team of researchers in Taiwan [25] developed a deep learning model on Taiwan's National Health Insurance claims, to forecast a patient's risk of developing kidney disease infections.

2.2 Explainable AI

A lot of previous works have been done to rationalize and deduce models to make the entire process as transparent as possible. For this research, papers irrespective of health issues have been included for clarity. To give a clear idea of what exactly entails an XAI model, Arrieta, Rodriguez, and Ser [26] described various notions and concepts to help understand and stimulate advanced methods for individual research. Along similar lines, Samek, Wiegand, and Muller [27] summarized visualization techniques in their research, to defend deep learning models, followed by Linardatos and team [28], who tabulated several methods and resources XAI for others to refer to. Authors in [29] described the application of XAI models for interpreting medical images. Amann, Blassime, and their team [30] explored XAI in clinical decisions from a technological, legal, and patient perspective to address societal and ethical questions for the same.

Apart from subjective papers, technological advancement has paved way for achieving XAI in a practical aspect. Montavon and Samek [31] proposed techniques for clarifying predictions calculated by deep neural networks. They provided a detailed tutorial for supporting the outcome of their predictive model and on the individual parameters. Kindermans and his fellow researchers in [32] applied PatternNet and PatternAttribution to expand the projections of neural networks. Researchers [33] calculated input based on the attribution method to clarify convolutional neural network (CNN) models.

Lauritsen, Kristensen, and Olsen [34] potentiated electronic health records (EHR) data into an early warning score, backed by an explanation of its results, to predict acute critical illness. Ibrahim, Mesinovic, Yang, and Eid [35] demonstrated the application of XAI in predicting cardiovascular diseases. Using visualization as an effective technique, the research work

Samala and Chan in [36] made the learning by deep convolutional neural networks (DCNN) comprehensible to the readers.

Shapely values were estimated by Bloch and Friedrich [37] in their work to improve the classification of my existing ML models by analyzing automatic subject selection in Alzheimer's disease. Park, Lee, and Kim [38] investigated specific diseases to develop a classification model for prediction and diagnosis using SHAP. In the study performed by Tang, Ghorbani, and Yamashita [39], SHAP values were utilized to perform data valuation by denoising the data and identifying mislabeled or low-quality images. Shapley values provide both local and global explanations of data, which Lundberg, Erion, and Chen [40] projected for better understanding. Khanal and Khadka [41] explain the major contributing factors are explained with local interpretable model-agnostic explanation (LIME).

3 Methodology

3.1 Proposed Architecture

Figure 1 describes the framework used in this study. The archetype comprises the input unit, preprocessing section, ML models implementation, performance metric calculations, and an explanation extraction component.

The Input unit consists of the dataset, followed by data cleaning and data transformation. The next step dealt with classification using individual algorithms, tailed with statistical calculations for performance evaluations. The concluding stage involves interpretation by means of LIME explanations.

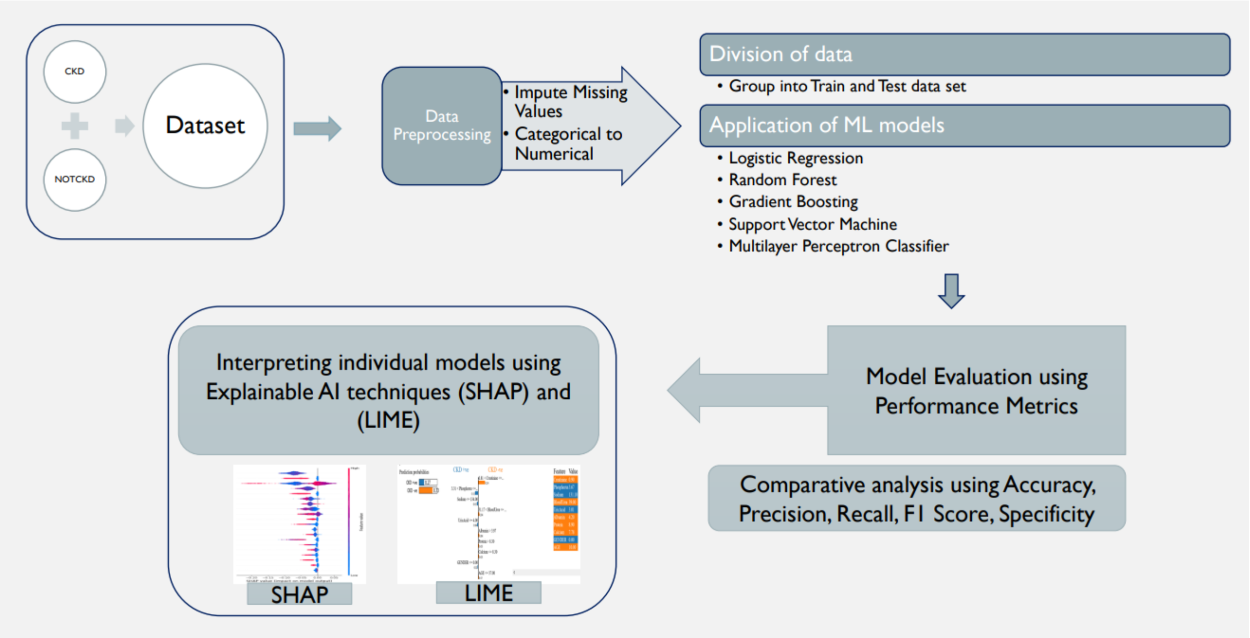


Fig. 1: Process Methodology

3.2 Dataset

3.2.1 Description: For this paper, laboratory reports about kidney disease patients were collected, and compiled. The dataset generated contained records of 417 patients, aged between 3 years to 86 years. Out of these 417 records, 161 belong to healthy or Not CKD, while the remaining 256 fit as CKD-infected patients. 206 categorizes as male patients while females make for 211 cases. The data consist of the following parameters:

Table 1: List of features in the data

Feature 0	Age
Feature 1	Gender
Feature 2	Sodium
Feature 3	Blood Urea
Feature 4	Creatinine
Feature 5	Potassium
Feature 6	Uric Acid
Feature 7	Calcium
Feature 8	Phosphorus
Feature 9	Protein
Feature 10	Albumin
Predictor Variable	Classification (CKD/ Not CKD)

3.2.2 Variable Definition: The attributes in the data play an important role in determining the status of a person as CKD positive or negative. Henceforth, it becomes equally important to consider their role and importance in contributing towards the outcome. This section defines these variables from a medical point of view.

- Sodium: Important for nerve and muscle function, it is both an electrolyte and a mineral. High levels indicate high blood pressure. The normal range varies between 135-145 mEq/L (milliequivalents per liter)
- Blood Urea: Measures the nitrogen levels in the body, which is one of the waste products in blood. Normally ranging between 5 to 26 mg/dl, higher values indicate poor functioning of the kidneys. Though urea nitrogen levels tend to increase with age.
- Creatinine: A waste product left out after muscle energy production; it determines the overall functioning of the kidney with eGFR level. Typical levels of serum creatinine are 60-110 µmol/L (micromoles per liter) for men and 45-90 µmol/L for women.
- Potassium: One of the seven macro minerals, potassium affects overall cell and muscle health. Blood potassium levels fall between 3.6 - 5.2 mmol/L (millimoles per liter). Higher levels can result in buildup, tampering with the kidney filtration process.
- Uric Acid: It is a waste product that initiates the inflammatory process necessary in tissue healing. Higher levels can lead to kidney stones. Standard levels are 2.4-6.0 mg/dL (female) and 3.4-7.0 mg/dL (male).
- Calcium: Healthy kidneys convert Vitamin D to calcitriol for calcium absorption from the intestines into the blood. The body has somewhere around 8.6-10.3 mg/dL levels of calcium in the safe range.
- Phosphorus: Important for bone and teeth formation, high phosphorus levels can disrupt cardiovascular activities. The regular range varies between 2.5-4.5 mg/dL.
- Protein: Essential for muscle buildup, tissue repair, and evading infections in the body, excess protein waste in the blood can hinder kidney function, and cause damage. The typical levels of protein in the blood fluctuate between 6.0-8.3 g/dL (grams per deciliter).
- Albumin: A type of protein created by the liver; it helps maintain the fluid within blood vessels to avoid leakage into other tissues. The normal range of albumin in the blood varies between 3.4-5.4 g/dL.

3.2.3 Data Preprocessing: The entire process of analysis becomes clear and comprehensible if the data is free of any inconsistencies. To achieve the same for this research, missing data were imputed. Categorical data points like age, gender, and classification were encoded into numerical values. The last phase concluded with dividing the data into training and testing divisions.

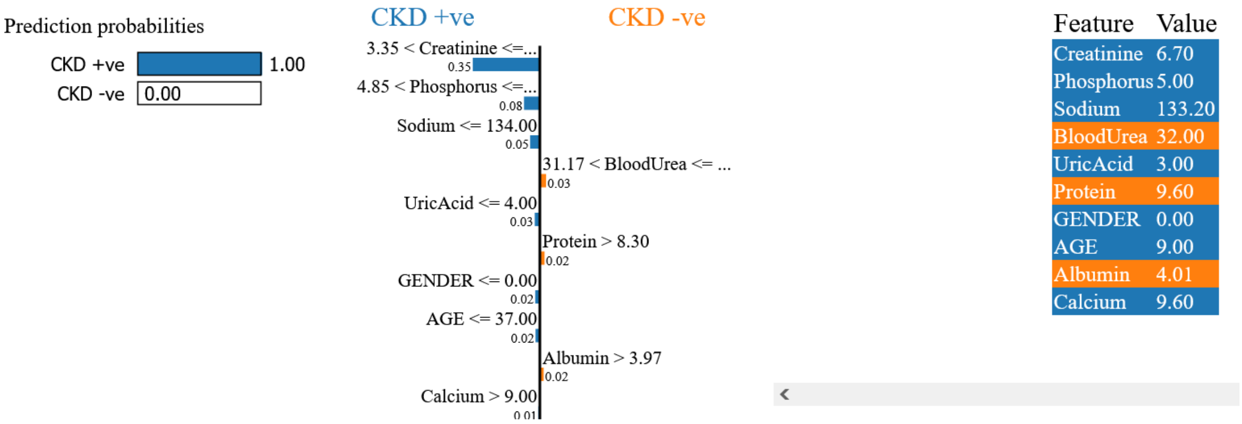
4 Results and Discussion

After the dataset is processed, it is fed into the machine learning models consumed in this study. The ML algorithms are considered from the inbuilt python sklearn library and classify data cases into CKD or NOTCKD. The results are interpreted individually using LIME. The table below depicts the performance of the ML models used.

Table 2: Performance comparison of the ML models

	F1 Score	Precision	Recall/ Sensitivity	Specificity	ROC AUC
Logistic Regression	97.19	98.21	96.49	97.91	97.20 %
Random Forest	98.08	98.24	98.24	97.91	98.08 %

4.1 Logistic Regression*:* Achieving an accuracy of 97.20 %, an explanation model is developed for LR. Figure 2 depicts cases for both, CKD +ve and CKD -ve (NOTCKD) patients, and the respective attributes promoting towards specific category. In (a), it is visible that Creatinine (35%), Phosphorus (8%), and Sodium (5%) contribute highly in favor of a kidney disease infection, while in (b), Creatinine (24%), Blood Urea (4%) and Albumin (4%) promote a healthy case.



Feature	Value
Creatinine	6.70
Phosphorus	5.00
Sodium	133.20
BloodUrea	32.00
UricAcid	3.00
Protein	9.60
GENDER	0.00
AGE	9.00
Albumin	4.01
Calcium	9.60

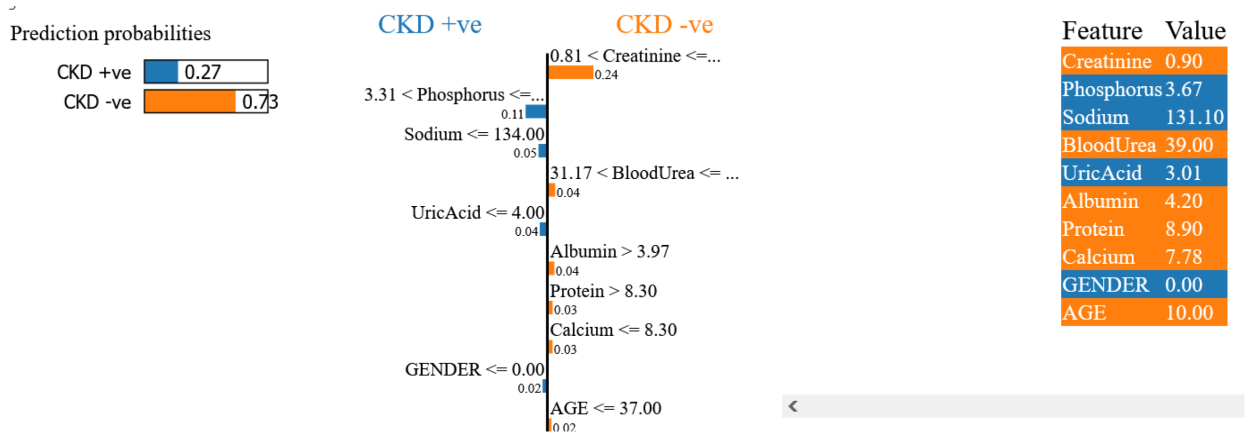


Fig. 2: Logistic Regression model explanation for (a) CKD +ve (b) CKD -ve

4.2 Random Forest: The model with an RF classifier gave the highest accuracy of 98.08 %, and when interpreted using LIME and SHAP, displays the results as in figure 3. Creatinine (28%) and age (3%) act as major determinants towards a CKD +ve case, while Blood Urea (5%) and Protein (2%) occupy higher shares of contribution for a CKD -ve case.

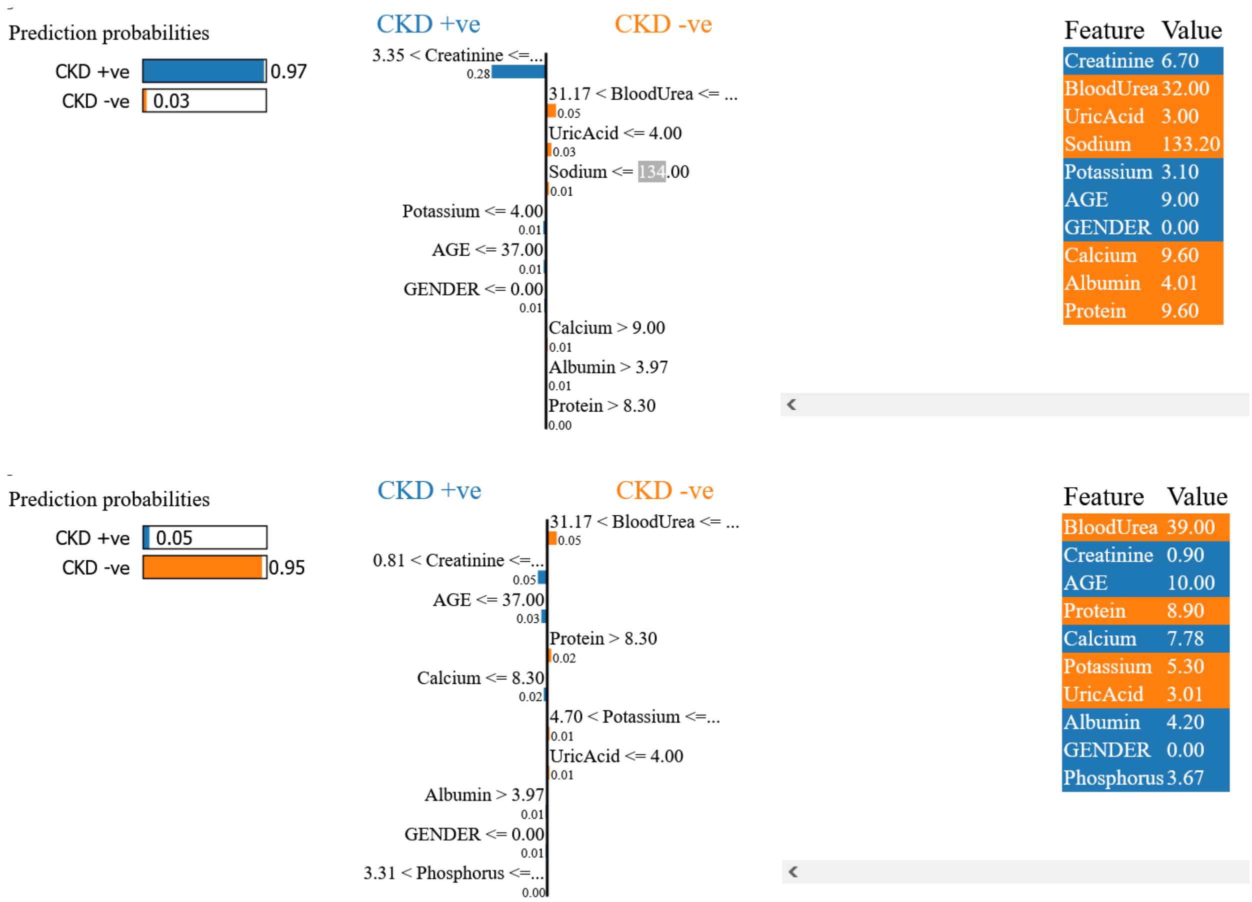


Fig. 3: LIME explanation for Random Forest for (a) CKD +ve and (b) CKD -ve

5 Conclusion and Future Work

Implementation of LIME permits clarification in terms of recognizing the impact of each variable on the final decision. LIME expounds each record in detail and shows the extent to which it believes a certain case belongs in either category. Where Creatinine remained a dominant feature in every result, several other elements like Blood Urea, Protein, Albumin, Sodium, and Potassium also bore an effect. Among all the ML models employed, Random Forest achieved the highest accuracy. LIME gave rational explanations, paving way for a transparent model. The present system can be improved in the future by accumulating more data from the healthcare industry, along with the integration of deep learning algorithms.

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