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Predicting Chronic Kidney Disease using ML algorithms and XAI

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Abstract

Kidney disease is a significant health concern that is currently affecting individuals of all age groups. To predict the occurrence of chronic renal disease, a large number of scholars have employed machine learning and deep learning techniques. However, the efficacy of these methods is often hampered by a lack of transparency, which is a major issue in the application of artificial intelligence in healthcare and medical analysis. As such, the lack of clarity has prompted concern. To interpret the results of predictive models, the present study proposes the deployment of four machine learning algorithms, including Decision Tree, Logistic Regression, Multi-layer Perceptron Classifier, and Support Vector Machine, in combination with explainable AI (XAI) interface, leveraging the local interpretable model-agnostic explanation (LIME) and shapely additive explanation shapely additive values (SHAP). The proposed models are intended to facilitate effective decision-making in clinical research and therapeutic practices.

Keywords: Machine Learning; Decision Tree Classifier; Logistic Regression; Support Vector Machine; Explainable AI; SHAP; LIME; Chronic Kidney Disease

Introduction

The damage of the kidneys that results in a steady loss of kidney function is termedas Chronic Kidney Disease (CKD). Long-term effects of CKD include anaemia, vitamin D inadequacy, and phosphate deficit [1]. Kidney disease is the leading cause of mortality, morbidity, and plays a significant role in the development of cardiovascular diseases and kidney failure [2]. On a global scale, around 9.1% of the population, or 700 million individuals, have CKD. Women are more likely to be affected by the disease, with a prevalence of 9.5%, compared to men's 7.8%. Additionally, the death rate for CKD is 4.6% [3].

The distribution of the kidney illness is highest among individual aged 65 and older (38%), followed by those aged 45-64 (12%). Unhealthy lifestyle and poor dietary have also caused an increase in kidney malfunction among young adults [4]. Based on severity and therapy, CKD is classified into five stages, beginning with early to end stage kidney disease, which typically necessitates a transplant [5]. Basic laboratory tests primarily evaluate the function of kidneys by measuring the eGFR (estimated Globular Filtration Rate) using a serum creatinine test. eGFR is a measure of how efficiently the Glomeruli filters in our kidneys are cleaning blood every minute, determined by our body size [25]. Advances in Artificial Intelligence (AI) and Machine Learning (ML) have enabled the early detection of diseases, preventing further deterioration of organ function. Earlier implementation of ML models has shown high success rates and new ways to address the issue. AI has enabled professionals to detect, diagnose, or gather information, leading to a more data-driven approach in healthcare analysis.

Explainable AI has further facilitated understanding the outcomes produced by these medical systems enabling the interpretation and comprehension of the predictions made by the models, as well as identifying any errors or inaccuracies in the analysis. The goal of Explainable Artificial Intelligence (XAI) system is to develop methods that:

1. Achieve a high-level performance while maintaining transparency in the model.
2. Enable and assist users (such as medical professionals and clinicians) in effectively managing the growing number of trustworthy and dependable AI partners.

Transparency within the ML system lowers the risk of incorrect decisions, which are prevalent in clinical recommendation systems [6]. Healthcare providers are often hesitant to accept recommendations without substantial supporting evidence [7, 8].

In this study, XAI techniques such as SHAP and LIME are employed together to assess the severity of patients with chronic kidney disease by emphasizing the local and global factors that contribute to the illness. By holding the system accountable for its predictions, this research aims to investigate the capabilities of XAI in ethically evaluating kidney disease infections.

Related Works

In this context, many researchers and data scientists have applied various techniques to achieve satisfactory results with their ML models. In [9], authors utilized two feature selection methods, wrapper and filter followed by Support Vector Machine (SVM). The comparison between training data and filtered data using SVM favoured the latter, with an accuracy rate of 98.5%. Many researchers have used the CKD dataset available on UC Irvine repository [26] for various forms of analysis. In [10], authors have used multiple ML models with feature selection. Out of 24 features used in study, 16 improved the prediction. Random Forest (RF) gives the highest classification rate of 99.75% among the models used (SVM, Naive Bayes (NB), K Nearest Neighbour (KNN) and J48). In the same way authors in [11] used different feature selection methods and applied seven machine learning algorithms such as artificial neural network, C5.0, Chi-square Automatic interaction detector, Logistic Regression (LR), linear SVM (LSVM) with penalty L1 and L2 and random tree, LSVM with penalty L2 gives the highest accuracy of 98.86%. Methods incorporating deep learning have improved the detection of kidney disease predictions. Group of authors in [12] presented their research on using five ML models, NB, SVM, Decision Tree (DT), LR and ANN with normalized features and obtained accuracy of 99.3% using DT in taken original dataset with all features. Kriplani et. al [13] improved the probability of their calculations by incorporating deep neural network for predicting presence or absence of CKD with accuracy of 97%.

Previous research has aimed to make models more transparent. For this research, papers on various topics were included to provide a clear understanding of what constitutes an XAI model. Authors in [14] defined various concepts and notation to aid in the development of advanced method. In [15] authors discussed visualization techniques for defending deep learning models, Linardatos and team [16] provided an overview of various XAI methods and resources, and authors in [17] examined XAI in clinical decision-making from a technological, legal, and patient perspective, addressing societal and ethical concerns. With the progress of technology, it has become possible to apply XAI in a practical sense, beyond just theoretical papers. Montavon et. al [18] have presented methods for making the predictions of deep neural networks more transparent by providing explanations and insights into the specific factors that influence the predictions. Researchers [19], have used techniques like Pattern Net and Pattern Attribution to gain a greater understanding of how neural networks function. Additionally, authors in [20] have used attribution methods to uncover the inner workings of Convolutional Neural Networks (CNNs). Bloch and Friedrich [21] used Shapley values in their research to enhance the classification of machine learning models for Alzheimer's disease by examining the automatic selection of subjects. Park, Lee, and Kim [22] utilized this method to build a prediction and diagnosis model for specific diseases. Authors in [23] used Shapley values in their study to evaluate data by removing noise and identifying mislabelled or low-quality images. Shapley values offer both localized and comprehensive explanations of data, which Lundberg, Erion, and Chen [24] proposed to enhance understanding.

Materials and Methods

Data Set and pre-processing

We utilized a publicly accessible dataset of 400 patient reports on CKD, spanning ages 3 to 83, that had been pre-processed [25]. Of these 400 records, 250 were for patients diagnosed with CKD and the remaining 150 were for patients without CKD. The features that are included in the dataset are Age (yrs), Blood Pressure (mm/Hg), Specific Gravity, Albumin, Sugar, Blood Glucose Random (mgs/dL), Blood Urea (mgs/dL), Serum Creatinine (mgs/dL), Sodium (mEq/L), Potassium (mEq/L), Hemoglobin (gms), Packed Cell Volume, White Blood Cells (cells/cmm), Red Blood Cells (millions/cmm), Red Blood Cells: normal, Pus Cells: normal, Pus Cell Clumps: present, Bacteria: present, Hypertension: yes, Diabetes Mellitus: yes, Coronary Artery Disease: yes, Pedal Edema: yes, Anemia: yes, and a predictor variable Chronic Kidney Disease: yes.

The dataset was splitted into two sections: a training set and a testing set. 80% of the dataset was used to create the training set and the remaining 20% was set aside for testing. The standard scaler was applied to the training and testing sets, except for the predictor variable. The split data was then run through various ML algorithms and the results were analyzed for both with and without cross-validation [26]. A confusion matrix was used as a tool for predictive analytics to compare the actual values with the model's predicted values and evaluate the model's performance. Finally, XAI frameworks like LIME and SHAP were used to interpret the results generated by the different models.

Proposed Method

The overall architecture of the developed model shown in Figure 1 is composed of feature extraction, different machine learning algorithms, model evaluation, statistical performance measures, and explanation extraction frameworks. By importing train-test-split from sklearn. Model selection the dataset was divided into training and testing dataset. The training dataset and the testing dataset were scaled using standard scaler from sklearn. Pre-processing library followed by implementation of different ML algorithms. The overall interpreted model was evaluated using statistical approach and XAI approach.

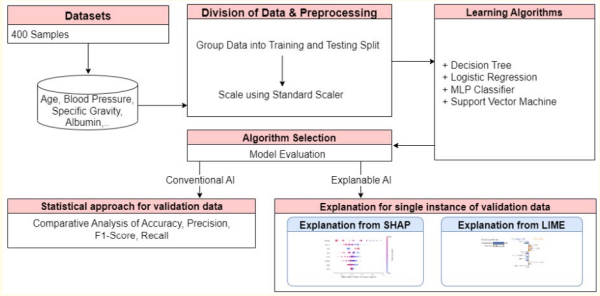

Figure 1: Proposed Methodology.

Implementational Details

The proposed model is coded in Python 3 Google Compute Engine backend. With 12.68 GB of RAM in Google Colab, 10-fold training and testing experiments were performed.

Evaluation Metrics

Confusion matrix, recall, precision, F1score, 10 fold cross validation are used as evaluation metrics.

	Accuracy	*F1 Score*	*Precision*	*Recall*
Decision Tree Classifier	99.688%	100%	100%	100%
Logistic Regression	99.688%	100%	100%	100%
MLP Classifier	100%	100%	100%	100%
SVM	100%	100%	100%	100%

Table 1: Comparative Analysis.

Following processing, the data is fitted into a variety of algorithms, DT, LR, MLP and SVM. All of these models are part of the Python's Sklearn module. The groups that make up our expected data goal are 0 or 1. If our anticipated data provide the goal value as 0, then CKD does not exist and if our predicted data supply the target value as 1, then CKD does exist. Using LIME and SHAP, each algorithm value is individually evaluated. Performance data for the applied ML models are shown in Table 1.

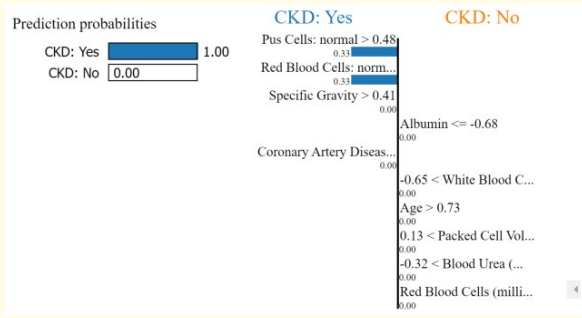

Figure 2: LIME results of DT.

Decision Tree

Using DT, we were able to achieve 99.688% accuracy in testing dataset. Results were evaluated in XAI interface using LIME and SHAP. In Figure 2, it is visible that pus cells: normal (33%), red blood cells: normal (22%) and specific gravity (19%) contribute highly in favor of chronic kidney diseases.

Figure 3 displays results with the SHAP explanatory model where hemoglobin (gms), specific gravity and albumin contribute in similar way like in LIME explanation. It demonstrates the top parameters that influence either of the results.

Logistic Regression

While implementing LR we were able to achieve an accuracy of 99.688% in testing dataset. Figure 4 revealed that the main factors that contributed to conclude that instance was CKD were the presence of red blood cells: normal (27%), pus cells: normal (27%), specific gravity (10%), and red blood cells (millions/cmm) (5%). However, it was found that an elevated level of sodium (2%) had a negative impact on the detection of chronic kidney disease. Analysis using SHAP revealed that specific gravity, hemoglobin, packed cell volume, and red blood cells (millions/cmm) were the key factors that led to the conclusion that it was a case of CKD as illustrated in Figure 5.

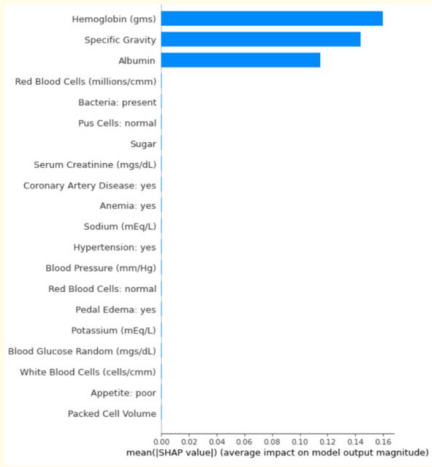

Figure 3: SHAP results of DT.

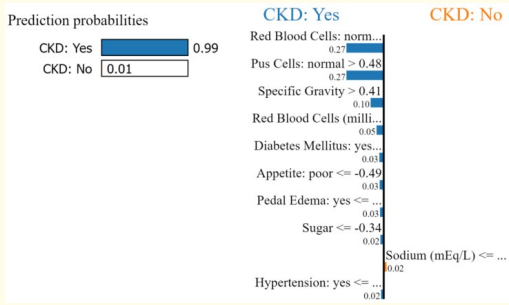

Figure 4: LIME results of LR.

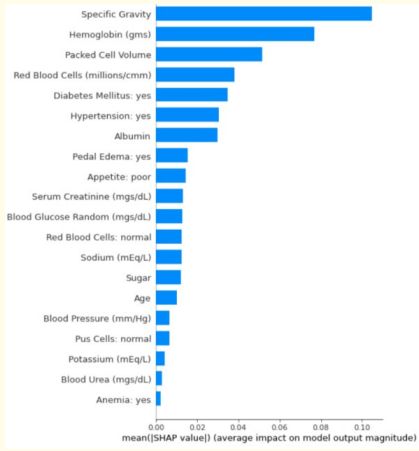

Figure 5: SHAP results of LR.

MLP Classifier

MLP Classifier was successful in reaching perfect accuracy in testing. Further analysis using LIME in Figure 6 revealed that the contributing factors in identifying CKD were red blood cells: normal (22%), pus cells: normal (22%), the specific gravity (14%), and red blood (millions/cmm) (8%). However, it was also determined that a high level of sodium (4%) had a detrimental effect on the detection of CKD. Specific gravity, hemoglobin (gms), packed cell volume and red blood cells (millions/cmm) were the main determinants that led to the conclusion that it was an instance of CKD, as depicted in Figure 7.

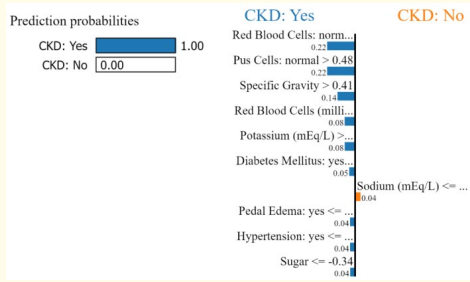

Figure 6: LIME results of MLP.

SVM

SVM distinguished between CKD and not CKD patient with accuracy of 100% while testing. Pus cells: normal (31%), red blood cells: normal (0.31) concluded instance as CKD as per LIME explanations shown in Figure 8. SHAP analysis showed that specific gravity, hemoglobin (gms), albumin, diabetes mellitus: yes, packed cell volume were the key factors that led to the diagnosis of CKD, as shown in Figure 9.

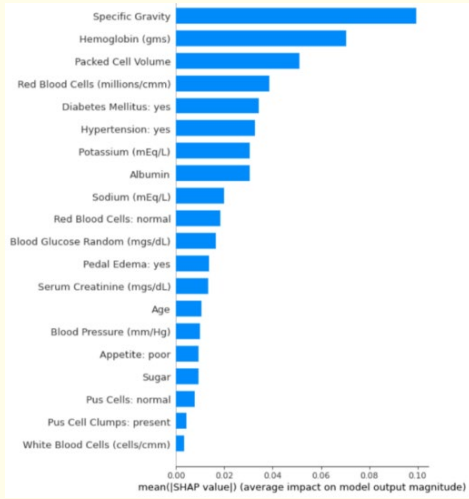

Figure 7: SHAP results of MLP.

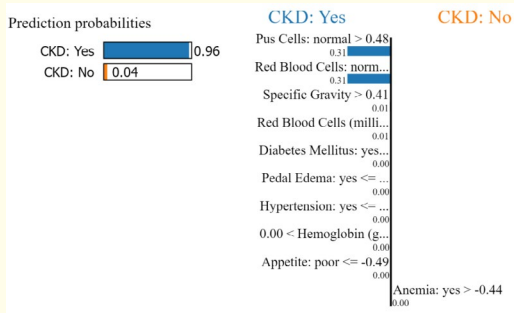

Figure 8: LIME results of SVM.

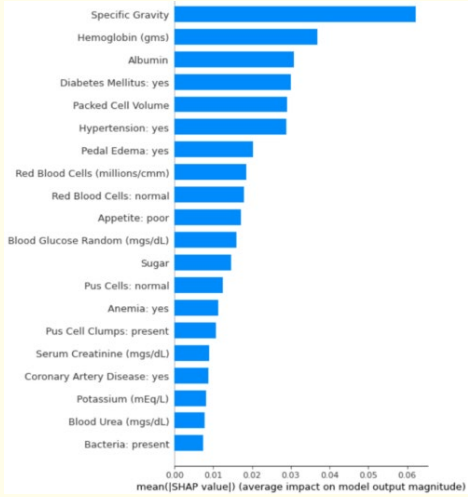

Figure 9: SHAP results of SVM.

Conclusion

The use of SHAP and LIME allowed for a better understanding of how each variable influenced the final decision. LIME provided detailed information on how much each case belonged to a certain category, while SHAP emphasized the level of impact that individual attributes had on the outcome. Red Blood Cells: normal and Pus Cells: normal were prominent feature in all results, but other factors such as Specific gravity, Red Blood Cells (millions/cmm) also had an effect. Among the machine learning models used, MLP classifier and SVM gave the highest accuracy. Both LIME and SHAP provided logical explanations, making the model more transparent. The system can be improved in the future by incorporating more data from the healthcare industry and integrating many more deep learning algorithms.

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