

# A Study of LIME and SHAP Model Explainers for Autonomous Disease Predictions.

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**Abstract**— *Autonomous disease prediction systems are the new normal in the health industry today. These systems are used for decision support for medical practitioners and work based on users' health details input. These systems are based on Machine Learning models for generating predictions but at the same time are not capable to explain the rationale behind their prediction as the data size grows exponentially, resulting in the lack of user trust and transparency in the decision-making abilities of these systems.*

*Explainable AI (XAI) can help users understand and interpret such autonomous predictions helping to restore the users' trust as well as making the decision-making process of such systems transparent. The addition of the XAI layer on top of the Machine Learning models in an autonomous system can also work as a decision support system for medical practitioners to aid the diagnosis process. In this research paper, we have analyzed the two most popular model explainers Local Interpretable Model-agnostic Explanations (LIME) and SHapley Additive exPlanations (SHAP) for their applicability in autonomous disease prediction.*

**Keywords**— *DSS, XAI, Interpretability, LIME, SHAP.*

## I. INTRODUCTION

With the help of numerous sensors equipped in healthcare devices today, enormous medical data is readily available for detailed analysis. Various Machine Learning (ML), Artificial Intelligence (AI), and Deep Learning (DL) approaches, are being used to help healthcare businesses to process this enormous data. There are various challenges possible in the traditional diagnosis process viz. any misdiagnoses which may lead to unnecessary additional tests for diagnosis confirmation or delay in obtaining test results from labs/machines resulting in the delay for appropriate treatment. The AI-ML models can scrub through the huge volumes of data collected, detect patterns, and make predictions faster and more efficiently than human diagnosis and analysis. This would benefit the healthcare business by improving diagnostic and treatment planning far earlier, resulting in improved public health infrastructure. Artificial intelligence and machine learning algorithms are being trained on the digital data created by hospitals, labs, and government agencies, the volume of which is growing exponentially. Because these enhancements to the existing healthcare system have the potential to save lives and money, healthcare has emerged as a crucial domain for AI and machine learning research and development.

In today's era of Artificial Intelligence, most artificial intelligence-based systems are observed to be very complex to be comprehended by their users [1]. The results obtained or the predictions made by underlying machine learning models are often found difficult to be interpreted by the developers and the users have a difficult time understanding how and why a particular prediction was made. Hence extensive use of such autonomous disease prediction models is not yet adapted to the significant level as normal users do not completely trust these systems since they could not properly understand the rationale (i.e. which factors were taken into consideration) behind the decision.

### A. Need for Explainability AI in the Healthcare Industry

The inclusion of Artificial Intelligence capabilities in healthcare equipment has provided some hope for a more sustainable healthcare system and cost-effective alternatives. However, AI cannot be considered a universal solution despite its apparent potential because all these technological developments are accompanied by unique questions and major challenges [2]. Some of the difficulties are related to the technical aspects of AI, which leads to the problem of ethics of AI models employed in medical sciences in the form of CDSS (clinical decision support system). A previously established knowledge base is used to train AI models to match them with the use case at hand in AI-based CDSS. As previously said, AI models outperform human analytical thinking and the ability to comprehend why a choice was made; nevertheless, this is where the critique of lack of explainability and transparency comes into play.

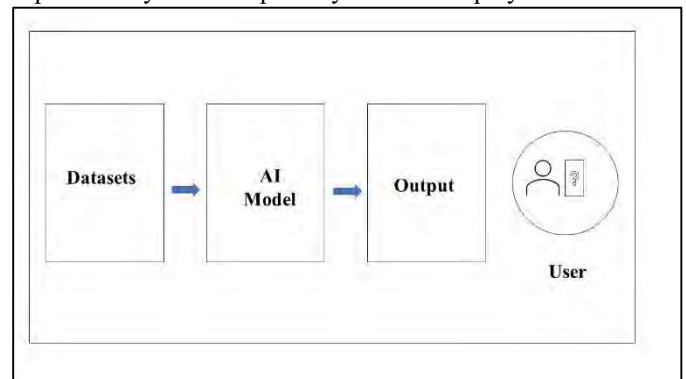


Figure 1: A Typical AI Model.

A typical AI model, as shown in Figure 1, provides output in the form of prediction/choice based on the dataset inputted.

But it does not provide any additional information as an explanation for predictions made; hence, it is referred to as a black-box model. In the context of AI, a black-box model is one whose underlying workings are hidden and unknown [1]. In the medical realm, this black-box model cannot be trusted since the cost of an output that cannot be explained or understood could result in erroneous treatment or even the loss of a person's life, which would adversely affect the overall performance of utilizing AI/ML in healthcare.

The prediction of disease occurs when symptoms begin to appear in the patient's body; depending on the severity of the ailment, the diagnosis of these symptoms might take minutes or even days to confirm. Few diseases share common symptoms, so a clinician could mistakenly diagnose a critical problem as a minor one, but if the symptoms or test data are fed into the AI model with high accuracy, the prognosis will be accurate. Even if the AI model offered accurate diagnoses, clinicians and users are hesitant to completely rely on it as there is no justification obtained for the prediction. As a result, including XAI becomes even more critical, as it has the potential to elaborate autonomous decision-making.

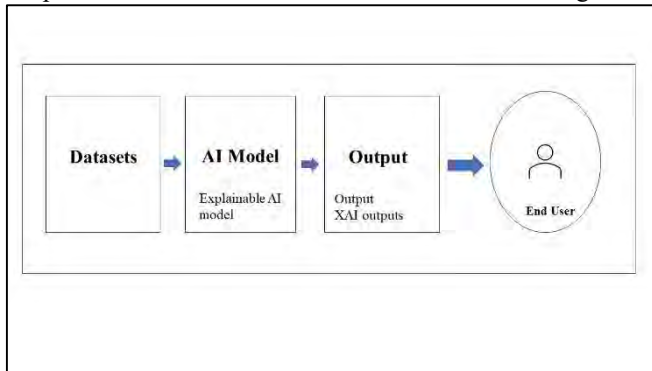


Figure 2: Artificial Intelligence with XAI.

Figure 2 shows how an AI model and XAI capabilities can work together to assist users to understand how the black-box model works, which helps in developing trust among its users. The explanation provided enables both the developer and the user to better grasp the predictions produced. The user would have faith in the algorithm since he would know how the result was obtained and whether the output was correct. XAI promises to provide openness, rationale, and traceability of machine learning, artificial intelligence, and deep learning models, which otherwise seem to be black boxes [3].

## II. LITERATURE REVIEW

The black-box models utilized for predictions in the study [4] mostly include neural network models and ensemble models, which include Artificial Neural Networks (ANN), LightGBM, and random forest. These black-box models are explained using LIME, and SHAP XAI approaches to derive explainability and visually demonstrate the framework.

LIME stands for Local Interpretable Model-Agnostic Explanations and is one of the prominent XAI frameworks provided for interpreting ML predictions [5]. It is a visualization approach that aids in the comprehension of every individual prediction made with any Machine Learning model. LIME is based on the notion that all models are linear on a local scale, which means it tries to fit the model around a single observation to replicate how the global model behaves at the locality. LIME uses this simple model to

explain the predictions of the more complicated models on a local level. The LIME framework was proposed in the research work [6] to help establish knowledge and explain the predictions provided by any machine learning model. The LIME framework was applied to multiple ML models in the research to demonstrate the method's versatility and to help users grasp the utility of these unique explanations in various contexts to empower users to establish trust and pick between different models.

SHAP stands for SHapley Additive exPlanations, and it seeks to provide explanations for an instance's/predictions observation by computing each feature's contribution to the prediction [7]. SHAP was introduced as a uniform measure of feature importance in the study work [8]. For each prediction, SHAP assigns an importance rating to each feature. It has two novel elements: (1) the discovery of a new class of additive feature significance measures, and (2) theoretical results demonstrating that this class has a unique solution with a set of desired qualities. SHAP integrates game theory into local explanations by combining all previous methods and offering new methods that outperform earlier approaches in terms of computer performance and/or coherence with human intuition.

One of these frameworks is ELI5. It is a Python library for debugging and explaining machine learning classifiers [9]. It works with a variety of machine learning frameworks, including scikit-learn, Keras, XGBoost, LightGBM, and CatBoost. Other tools include Google's 'What If Tool,' which may be used to study or evaluate the performance of hypothetical situations, analyze the value of various data attributes, and show model behaviour across many models and subsets of input data, as well as for several ML fairness criteria [10].

Only LIME and SHAP are model-agnostic techniques, as they may be used with a wide range of machine learning algorithms, from simple to large deep learning models [11]. Support vector machines (SVM) and complicated neural networks can both benefit from them.

The need for explainability has been discovered in every sector where AI and ML are being used. For example, in [12], the researchers used LIME to explain the prediction of heart failure using RNN (Recurrent Neural Network), which helped them identify the most common health conditions such as kidney failure, anaemia, and diabetes that increased individual risk of heart failure. Many other solutions have been created to provide the explainability feature to enterprises and sectors that use machine learning and artificial intelligence. The need for and use of XAI is growing all the time, and research is underway to create better frameworks that will aid in better understanding black-box models and, as a result, better prediction models.

The importance of early diagnosis of the disease Glaucoma is critical as it leads to early blindness, but the current predictions model is considered not to be trustworthy as medical professionals are unaware of how the decision-making is taking place, to overcome this challenge the research work [13] proposed the use of XAI and Interpretable Machine Learning (IML) for analyzing the glaucoma predictions/ results. Adaptive neuro-fuzzy inference system (ANFIS) and pixel density analysis (PDA) are the two main techniques that XAI has principally used to offer reliable justifications for glaucoma predictions from infected and

healthy images. To explain outcomes coherently, IML employs sub-modular pick local interpretable model-agnostic explanation (SP-LIME). Spike neural network (SNN) findings are interpreted using SP-LIME.

### III. METHODOLOGY AND APPROACH

#### A. System Architecture

The system architecture of the system is shown in Figure 3 below. When a user or medical practitioners have received the test results and preliminary diagnosis, the user may choose to further interpret these results. Once the user logs in, the user needs to select a disease for which the user wants to interpret the predictions. When a particular disease is selected, the user needs to fill in the details of test results obtained, and other information asked as per the requirement of the system by referring to his/her medical reports. Then using the Naive Bayes Prediction Model, the prediction is made. To understand the predictions made by the model the feature values are passed on to the LIME framework of XAI which would give a visual presentation of the contribution of different attributes.

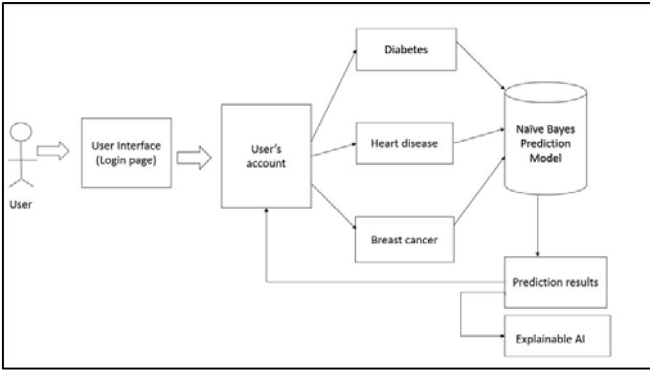


Figure 3: System Architecture of Disease Prediction System with XAI.

#### B. LIME and SHAP implemented in the Disease Prediction System

For the three chronic diseases of diabetes, heart disease, and breast cancer, a disease prediction system was created. The datasets for the various diseases were trained using the Naive Bayes Classifier, which is a fast-learning classifier that may be used to make real-time predictions [14]. However, to develop trust among system users, it was required to explain the predictions made, hence LIME and SHAP were utilized because of their model-agnostic nature.

The diabetes prediction model was trained on the Pima Indians Diabetes Dataset [15], which contains data from a variety of female patients over the age of 21 who are all of Pima Indian ancestry. The database contains several medical parameters as well as one outcome variable. Among the medical factors, are pregnancy, glucose levels, blood pressure, BMI (body mass index), skin thickness, insulin levels, age, and diabetes pedigree function. Age, sex, type of chest pain, resting blood pressure, serum cholesterol in mg/dl, fasting blood sugar level, resting electrocardiographic results (values 0,1,2), maximum heart rate achieved, exercise-induced angina, and a few other attributes were used in the heart disease prediction model for predicting the risk of heart disease by using the dataset [16]. Since breast cancer is the most frequent cancer in women and has the second-highest

fatality rate, early detection is critical. As a result, the prediction model was trained using the dataset [17], which includes real-valued features generated for each cell nucleus. The database comprises different attributes computed for each cell nucleus, as well as one target variable Diagnosis, which might be benign (not cancerous) or malignant (cancerous) (considered cancerous).

There are three values directly above the visualizations given below in Figures 4, 5, 6, 7, 8 and 9: Intercept, Prediction local, and Right. Right denotes the Naive Bayes prediction model's prediction for the given test vector, prediction local denotes the value outputted by a linear model trained on perturbed samples (obtained by sampling around the test vector following a normal distribution) and using only the top k features outputted by LIME, and the intercept denotes the constant part of prediction given by the linear model prediction for the given test vector.

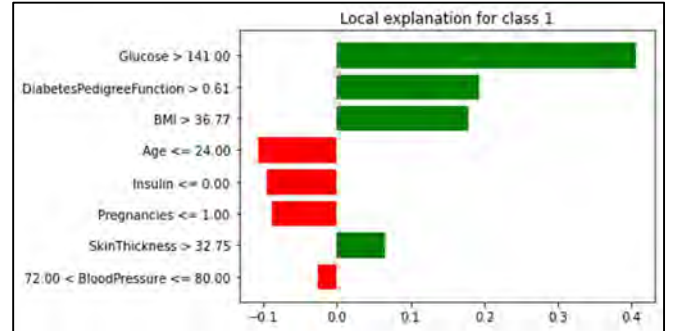


Figure 4: LIME visualization for a given diabetes test vector.

Figure 4 shown above depicts the result obtained after applying the LIME framework to observation for the diabetes prediction model, the attributes on which the prediction depends are glucose, Diabetes pedigree function, BMI (body mass index), age, insulin level, no. of pregnancies, skin thickness, and blood pressure. Using the LIME framework, one can identify the features that positively contribute to the prediction being made. From the above output, it can be observed that there is a positive prediction (a person has a high risk of diabetes), and the factors which contribute are marked in green on the positive side, and the features that have no contribution to a particular suggestion are marked in red on the negative side. Since the glucose level (199) is more than 144, it becomes the highest contributing factor, next, there is the diabetes pedigree function (1.39) > 0.61, similarly, all features contribution is measured and depicted has led to the prediction made by the Naïve Bayes Classifier. As age (22) less than 24 has no contribution to the prediction, the same for insulin and the count of pregnancy.

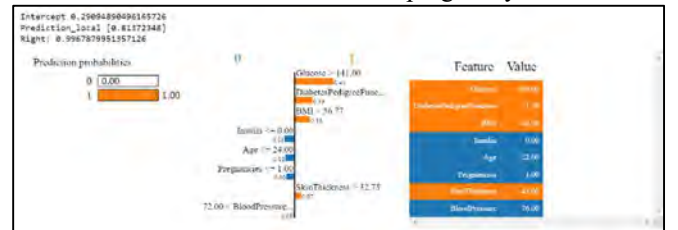


Figure 5: A detailed explanation obtained using LIME for Diabetes prediction.

In Figure 5 as well, the output for the LIME framework is depicted. Here, the orange colour shows a positive prediction and the blue colour shows a negative prediction. The model



predicts a high risk of diabetes, as the glucose level is higher than 144, and BMI is more than 36.77, on the right, there are the actual feature values of the patient.

Figures 6 and 7 given below show that the model predicts a risk of heart disease, based on the explanation that exercise-induced angina (exang) has a value of 0 which has a contribution of 0.36, next the chest pain type (cp) is 2 and as it lies between the range it contributes to the risk of having heart disease. Similarly, all the feature values are shown on the right in figure 6, where the slope (the slope of the peak exercise ST segment) is shown in red (in figure 5) and blue (figure 6) as the value is less than or equal to 1.

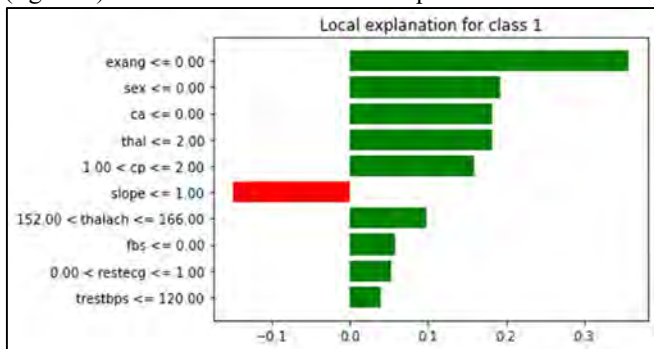


Figure 6: LIME visualization for a prediction of heart disease.

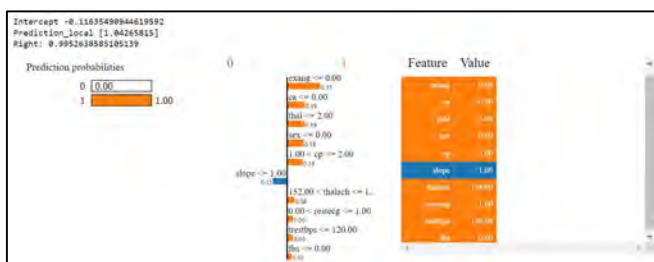


Figure 7: A detailed explanation obtained using LIME for Heart Disease Prediction.

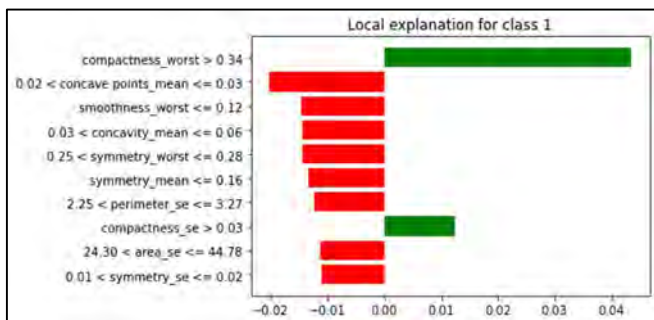


Figure 8: LIME Visualization for Breast Cancer Prediction.

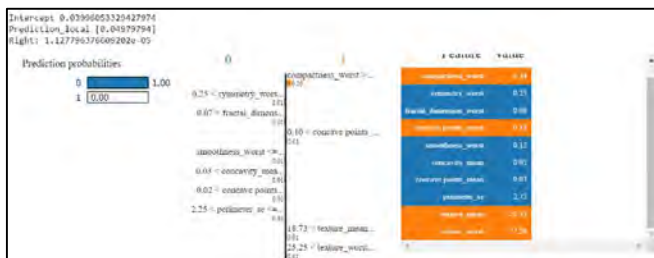


Figure 9: A detailed explanation obtained using LIME for Breast Cancer Prediction.

Figures 8 and 9 shown above predict that the person does have a risk of Breast Cancer and the explanations are visually

represented in both the above figures. From figure 7, all the features except for compactness and the concave point (worst) values majorly contribute to the positive side but all the other features show a negative outcome. As concave\_point\_mean (0.03) lies between 0.02 and 0.03 it is contributing to a benign outcome, similarly, the explanation can be given why the Naïve Bayes Model gives a negative prediction for this patient.

Figures 10, 11, and 12 given below show the results of feeding the trained models into the SHAP XAI framework. The SHAP summary plot is a simple visualization that combines all the elements into a single plot. The characteristics are ranked on the y-axis, with the highest contributor being first and the lowest contributor being last. The SHAP values are represented on the x-axis, with a value of zero representing no contribution and increasing contributions as the SHAP value travels away from zero.

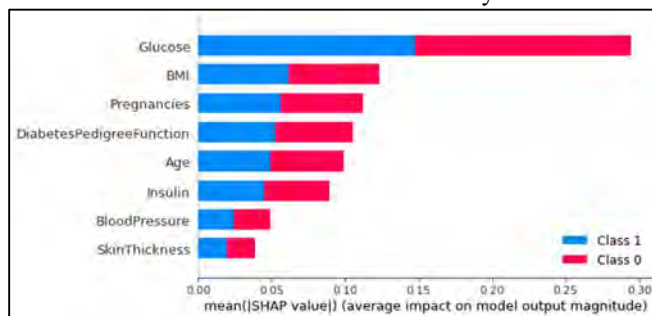


Figure 10: Visualization using SHAP for the dataset used for Diabetes Prediction.

Figure 10 represents the Variable Importance plot for Diabetes, considering all the attributes glucose is the highest contributing factor to the presence of diabetes. Next comes the Body Mass Index, then pregnancies, and so on. It is observed that skin thickness has the least contribution and hence is at the bottom of the ranking.

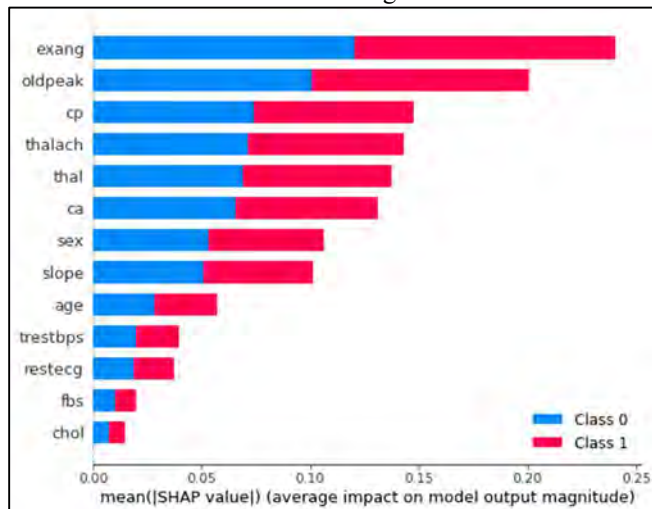


Figure 11: Visualization using SHAP for the dataset used for Heart Disease Prediction.

Figure 11 depicts the variable importance for heart disease, exercised induced angina is the highest contributing factor, followed by ST depression induced by exercise relative to rest, then chest pain type, and lastly cholesterol levels contributing the least.

Figure 12 given below shows that the attribute's largest mean (mean of the three largest values) or 'worst' of concave points (number of concave portions of the contour) gives the highest contribution followed by 'worst' perimeter, then 'worst' radius.

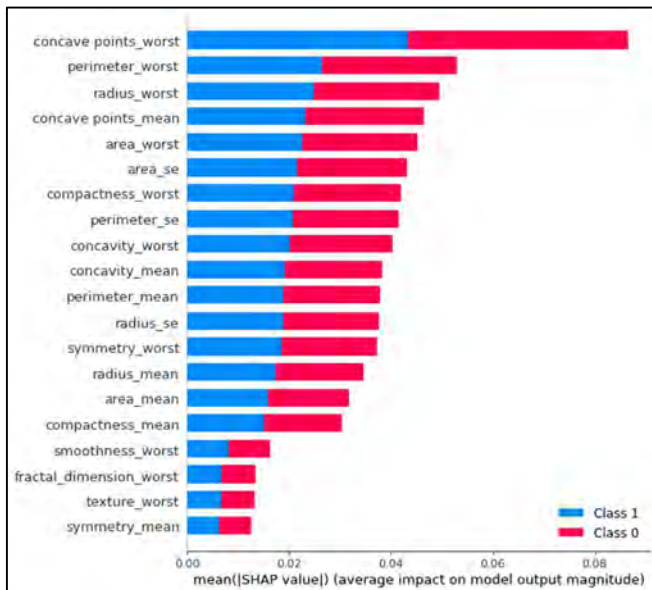


Figure 12: Visualization using SHAP for the dataset used for Breast Cancer Prediction.

The mean symmetry is the least contributing factor. Here, the Kernel Explainer has been used to get the SHAP outcome as the training model used was Naïve Bayes Classifier.

#### IV. RESULTS AND DISCUSSIONS

To obtain the most precise prediction result, the datasets were split into training and testing sets in the ratio of 80:20 and the Naive Bayes (NB) model was used. In multi-class prediction, NB does well and outperforms competing models, especially when the independence condition is true and little training data is needed. Since most disease datasets contain sequential information, using the NB algorithm is a useful way of classifying sick sequences with improved accuracy.

Figures 13 and 14 depict the prediction of Breast Cancer corresponding to the attributes entered by the user which are ten real-valued features calculated for every cell nucleus they include radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimensions. Figure 14 explains the Naïve Bayes Classifier using the LIME Model.

```
input_data=(8.822402,0.929,17.18,68.79,259.5,0.1866,0.1418,0.211,0.08379,0.211,0.08849,0.3274,1.194,1.885,17.47,0.009549,0.08606,0.3838,0.03322,0.04197,0.009559,10.31,22.45,45.5,324.7,0.1482,0.4365,1.252,0.175,0.4228,0.1375)

#changing input data to numpy
input_data_numpy=np.asarray(input_data)
#reshape the array
input_data_reshape=input_data_numpy.reshape(1,-1)
#standard input data
std_data=scaler.transform(input_data_reshape)
#print(std_data)
prediction=classifier.predict(std_data)
#print(prediction)

if prediction[0]==0:
    print("You don't have breast cancer")
else:
    print("Person have breast cancer")
Person have breast cancer
```

Figure 13: Prediction using Naive Bayes Classifier for a given patient data for Breast cancer.

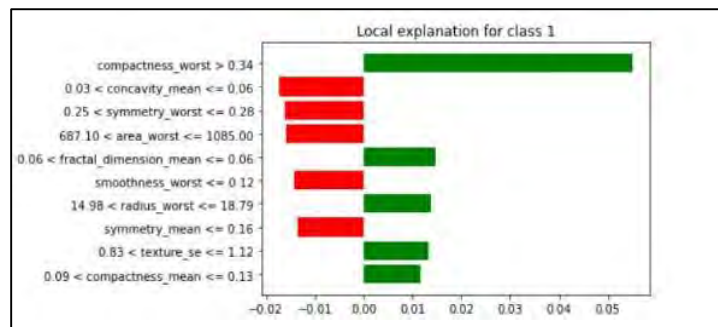


Figure 14: LIME Explanation via visualization for the entered patient data (breast cancer).

```
input_data=(9,170,74,31,0,44,0.403,43)
#changing input data to numpy
input_data_numpy=np.asarray(input_data)
#reshape the array
input_data_reshape=input_data_numpy.reshape(1,-1)
#standard input data
std_data=scaler.transform(input_data_reshape)
#print(std_data)
prediction=classifier.predict(std_data)
#print(prediction)

if prediction[0]==0:
    print("The person is non-diabetic")
else:
    print("Person is diabetic")

[1]
Person is diabetic
```

Figure 15: Prediction using Naive Bayes Classifier for a given patient data for Diabetes.

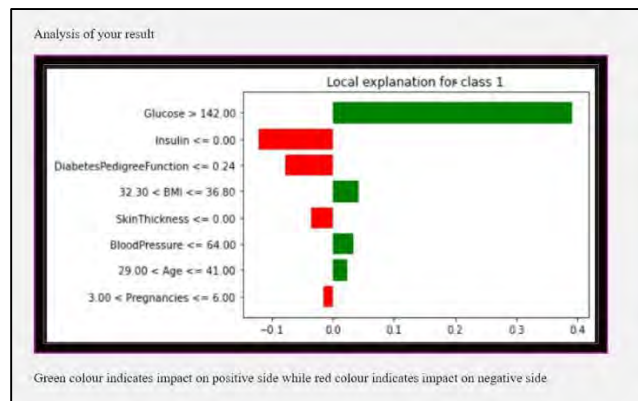


Figure 16: LIME Explanation via visualization for the entered patient data (diabetes).

Figures 15 and 16 shown above depict the prediction by the Naive Bayes Classifier for diabetes, with the input to the system where the number of pregnancies is 9, the glucose level is 170, the blood pressure level is 74, insulin can be 0, the body mass index is 44kg/m2, the skin thickness is 31mm, the diabetes pedigree function value is 0.403 and age is 43. Based on the inputs the system predicts that the 'Person is Diabetic.' Figure 16 depicts the LIME model explainer for the test result, and it can be observed that the two attributes that contribute positively to the prediction are insulin and blood pressure



```

input_data=(54,1,0,120,188,0,1,113,0,1.4,1,1,3)
#changing input data to numpy
input_data_numpy=np.asarray(input_data)
#reshape the array
input_data_reshape=input_data_numpy.reshape(1,-1)
#standar input data
std_data=scaler.transform(input_data_reshape)
#print(std_data)
prediction=classifier.predict(std_data)
#print(prediction)

if prediction[0]==0:
    print("The person don't have heart disease")
else:
    print("Person have heart disease")

The person don't have heart disease

```

Figure 17: Prediction using Naive Bayes Classifier for a given patient data for heart disease.

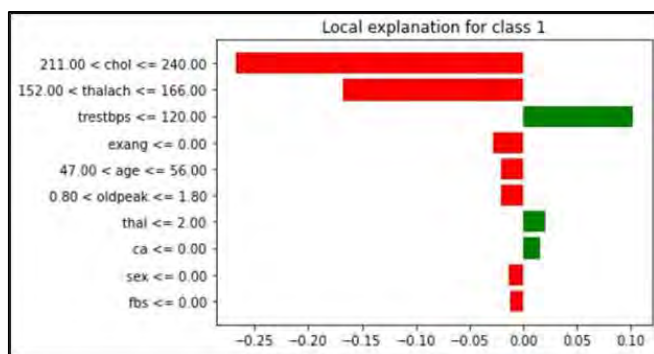


Figure 18: LIME Explanation via visualization for the entered patient data (heart disease).

Figures 17 and 18 shown above depict the prediction by the Naive Bayes Classifier for heart disease, with the input to the system where the age of the user is 54, sex is 1 depicts male, chest pain type is 0, resting blood pressure is 120 mm Hg, serum cholesterol level is 188mg/dl, fasting blood sugar is less than 120mg/dl hence value is 0, resting electrocardiographic result is 1, maximum heart rate achieved is 113, exercise-induced angina is negative, ST depression induced by exercise relative to rest is 1.4, the slope of the peak exercise ST segment is 1, number of major vessels (0-3) coloured by fluoroscopy is 1, the value of thal is 3 i.e. reversible defect. Based on the inputs the system predicts that the 'Person does not have heart disease.' Figure 18 depicts the LIME model explainer for the test result, and it can be observed that the two attributes that contribute negatively to the prediction are serum cholesterol level and maximum heart rate achieved.

## V. CONCLUSION

The importance of Explainable AI (XAI) in the disease prediction system was highlighted in this research. Also, how the XAI can help strengthen the user's trust in autonomous systems is elaborated in this research work. Because of the model-agnostic nature, LIME and SHAP were identified as the best XAI models to represent the disease datasets. It not only helps in the comprehension of a machine learning model outcomes but also makes predictions visible. The moral principles in healthcare are jeopardized without explainability in clinical decision support systems, posing a hazard to individual and public health. Although it is still in the preliminary stages of research, it shows promise for the future.

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