Cardiovascular Disease Prediction Using Machine Learning and XAI

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Abstract: Advances in supporting technology, particularly in big data and machine learning, have given predictive analytics a lot of attention in recent years. The healthcare sector has recently seen the application of disease prediction. This project has been demonstrated the prediction of a heart attack among many others. Heart disease, more commonly referred to as cardiovascular disease, is a group of conditions that affect the heart and has emerged as the world's leading cause of death in recent decades. It connects a slew of heart disease risk factors to the urgent need for precise, dependable, and practical methods for early diagnosis and management. Data mining is a common method for analyzing a lot of data in the healthcare industry because it is difficult to predict cardiac disease. To avoid the risks associated with it and to inform the patient well in advance, the procedure must be automated. Data mining methods like XG-Boost , Logistic Regression, Decision tree, Support Vector Classifier, Random Forest, K-neighbors classifier, and Naive Bayes can be used to identify heart diseases. We have demonstrated through this project that, when it comes to predicting heart attacks, XG-BOOST and KNN performs better than the other machine learning models mentioned above. Consequently, the performance of several machine learning algorithms is compared in this paper. The dataset's features play a crucial role in any kind of prediction. The final prediction can be influenced positively or negatively by features. We have got a 95.60% accuracy rate by using KNN algorithm and used explainable AI technique to explain the reason of heart disease. The XAI methods can be used to show how important features are. The predictability of the model is also interpreted using a new method in this paper. By utilizing the XAI technique LIME with the assistance of the idea of a black box, this exploration leads the KNN calculations expectation

Keywords :Heart Disease; Prediction; Machine learning; Random Forest; KNN algorithm; Support Vector Machine; Decision Tree; Logistic Regression; Naive Bayes, XG Boost,XAI.

1 Introduction

Everyone is concerned about their health. However, due to a variety of external factors such as unhealthy lifestyles, work stress, psychological strain, and pollution, millions of people worldwide are at risk for chronic illnesses such as cardiovascular diseases (CVD), which affect both the heart and blood vessels and result in death or disability. Cardiovascular disease (CVD) causes our hearts and blood vessels to malfunction, which frequently results in death or paralysis. As a result, early and automatic CVD detection has the potential to save many lives. According to estimates, 17.9 million people die each year from cardiovascular diseases (CVDs), accounting for 31% of all deaths worldwide. One-third of all CVD deaths occur in people under the age of 70, with heart attacks and strokes accounting for four out of every five deaths. This dataset contains 11 variables that can be used to predict a possible heart condition. Heart failure is frequently caused by CVDs. [1] In this regard, a machine learning model can be very useful in terms of early detection and management of people who have cardiovascular disease or are at high cardiovascular risk due to the presence of one or more risk factors such as hypertension, diabetes, hyperlipidemia, or pre-existing disease. This project analyzes various information mining techniques, particularly Support Vector Machine, Naive Bayes, Random Forest, and Decision Tree, using a validated dataset for coronary illness prediction that includes a variety of characteristics such as gender, age, chest pain type, pulse, and glucose. Heart disorders are identified in this study using machine learning features such as the K closest neighbor (KNN), Random Forest, and Decision tree algorithms, as well as the algorithm described in the preceding text. Furthermore, the use of such algorithms can improve the accuracy of heart disease prediction. The aforementioned algorithm was 97.65% accurate in predicting the disease, with a sensitivity of 75% and a specificity of 98.44%. If you provide every detail, you will get a precise result.

Description of the issue The most difficult challenge is identifying heart disease. Some technologies can predict heart disease, but they are either too expensive or do not perform well enough to determine how likely humans are to develop heart disease. It has been demonstrated that early detection of cardiac problems reduces mortality and overall consequences. Some tools can predict heart disease, but they are either too expensive or do not work well enough to determine how likely humans are to develop heart disease. However, it is impossible to effectively monitor patients at all times and days, and it is also impossible to consult with a doctor for 24 hours due to the increased intelligence, time, and skill required. We can now search for hidden patterns in data using a variety of machine-learning algorithms. To continue the research, we may employ a variety of different algorithms and techniques. To improve accuracy, this paper employs machine learning techniques.

Machine learning (ML), according to Senthil Kumar et al. [2], is effective in assisting in making decisions and predictions from the large amount of data produced by the healthcare industry. In machine learning, we could employ the following algorithm: Decision tree based on KNN Bayesian Inference SVM based on random forest Logistic regressive analysis XG enhancement Existing System Evaluation Machine learning (ML) methods have recently been used in a variety of IoT domains. Only a few studies have looked into the use of machine learning techniques to predict heart disease. The authors devised a novel strategy for detecting important features and improving the accuracy of cardiovascular disease predictions using machine learning. The prediction model is shown with different feature combinations and well-known classification methods. They achieve an improved performance level and an accuracy level of 88.7% using the hybrid random forest with a linear model (HRFM) prediction model for heart disease.

According to C. Sowmiya and P. Sumitra[3,] it is critical to have a framework that can identify the prevalence of heart disease in thousands of samples quickly and accurately. The researchers investigated how well nine classification methods predicted heart disease SVM. Some examples include ANN, KNN, and the naive Bayesian neural network. Prediction of heart disease using my proposed A prior algorithm and SVM (support vector machine) algorithm. Using clinical profiles such as age, gender, circulatory strain, chest pain type, and fasting glucose. It can forecast whether or not a patient will develop heart disease. Based on this, the medical community takes part in the detection and prevention of heart disease. The results show that classification-based techniques outperform previous approaches in terms of both effectiveness and accuracy.

Anjan Nikhil Repaka, Sai Deepak Ravikanti, and Ramya G Franklin[4] used the Naive Bayesian approach in the design and implementation of heart disease prediction. SHDP, or Smart Heart Disease Prediction, is a program that predicts heart disease risk factors using Navies Bayesian methods. As a result of the rapid advancement of technology, one of the web applications, mobile health technology, has seen a remarkable rise. The required information is compiled in a standardized format. To predict a patient's risk of heart disease, the following characteristics are extracted from medical profiles: The Navies Bayesian classification, which is used to predict heart disease, uses age, blood pressure, cholesterol, sex, blood sugar, and other variables as input. The dataset used is divided into two sections: 20% for testing and 80% for training. The proposed method has the following stages: For data collection, user registration and login, classification using Navies Bayesian, prediction, and secure data transfer, Advanced Encryption Standard is used. The result is then produced. The study develops and presents a variety of knowledge abstraction techniques using data mining techniques used to predict heart disease.

The output demonstrates that the established diagnostic system effectively assists in predicting heart disease risk factors based on the patient's medical characteristics such as gender, age, chest pain, fasting sugar level, and so on. The primary goal of this study is to determine whether or not the patient is likely to be diagnosed with any cardiovascular heart conditions. The primary goal of the project is to forecast the input datasets as accurately as possible. This ensures the credibility and dependability of the results. The accuracy rate is the primary goal when using the dataset. A variety of methods have been used to improve accuracy, which will be discussed further in this project.
There is no need for human intervention: To detect heart disease, one must provide medical information such as age, cholesterol, and other factors. Following that, the algorithm will return results based on the extracted features. There is very little chance of making a mistake because no one is involved. It also saves patients and doctors a significant amount of time, allowing them to complete treatments and other procedures more quickly. In this case, they get the results faster. As a result, the precaution/prevention phase of heart disease will be accelerated, as doctors and patients will have more time to focus on other treatments and preventative measures to mitigate its effects.
It not only identifies the type of heart disease but also makes safety recommendations: This project's goal is to not only identify and predict the type of heart disease, but also to emphasize the measures that must be taken to mitigate its effects. Receiving suggestions for activities to engage in can make it easier for patients and clinicians to continue with treatment.
To predict and classify the patient with heart disease, we used 7 different machine learning algorithms, including logistic regression, KNN, SVM, Decision tree, Nave Bayes, Random forest, and others. To

regulate how the model can be used to improve the accuracy of prediction of Heart Attacks in any individual, a very helpful approach was used.

2 Method and Materials

These will be the main lessons learned from the predictions for cardiovascular disease. As previously announced, we will be using the heart disease detection dataset and releasing intriguing inferences from the data to produce some significant findings. For accurate results, exploratory data analysis is the essential first step. After gaining insights from the data, we must modify the features before moving on to the model-building stage. [5]. We will construct our machine learning model for heart disease diagnosis during this phase.

2.1 DATASETS

These will be the main lessons learned from the predictions for cardiovascular disease. As previously announced, we will be using the heart disease detection dataset and releasing intriguing inferences from the data to produce some significant findings. For accurate results, exploratory data analysis is the essential first step. After gaining insights from the data, we must modify the features before moving on to the model-building stage. [5]. We will construct our machine learning model for heart disease diagnosis during this phase.

Table 1: Original Dataset Snapshot

Out[5]:

age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
52	1	0	125	212	0	1	168	0	1.000000	2	2	3	0
53	1	0	140	203	1	0	155	1	3.100000	0	0	3	0
70	1	0	145	174	0	1	125	1	2.600000	0	0	3	0
61	1	0	148	203	0	1	161	0	0.000000	2	1	3	0
62	0	0	138	294	1	1	106	0	1.900000	1	3	2	0

The education data is unrelated to an individual's heart illness, thus it is removed. Pre-processing and experiments are then carried out on this dataset.

Training Models

Machine learning approaches include K closest neighbors (KNN), Decision Tree, Logistic Regression, Naive Bayes, XG Boost, Support Vector Machine, and Random Forest. Random Forest is used to classify heart disease.

2.2 Block Diagram

Figure 1 illustrates the machine learning system's block diagram. This dataset, which comprised all of the attributes and values, was used by the system. To begin, we searched the dataset for any category values, which include numerous categorical values. The gender attribute is one of the columns that is transformed into 0 and 1 integer values.

We used the correlation matrix, a function based on group features, to assess the link and plot the results to better comprehend them. The dataset is next examined for null or missing values.

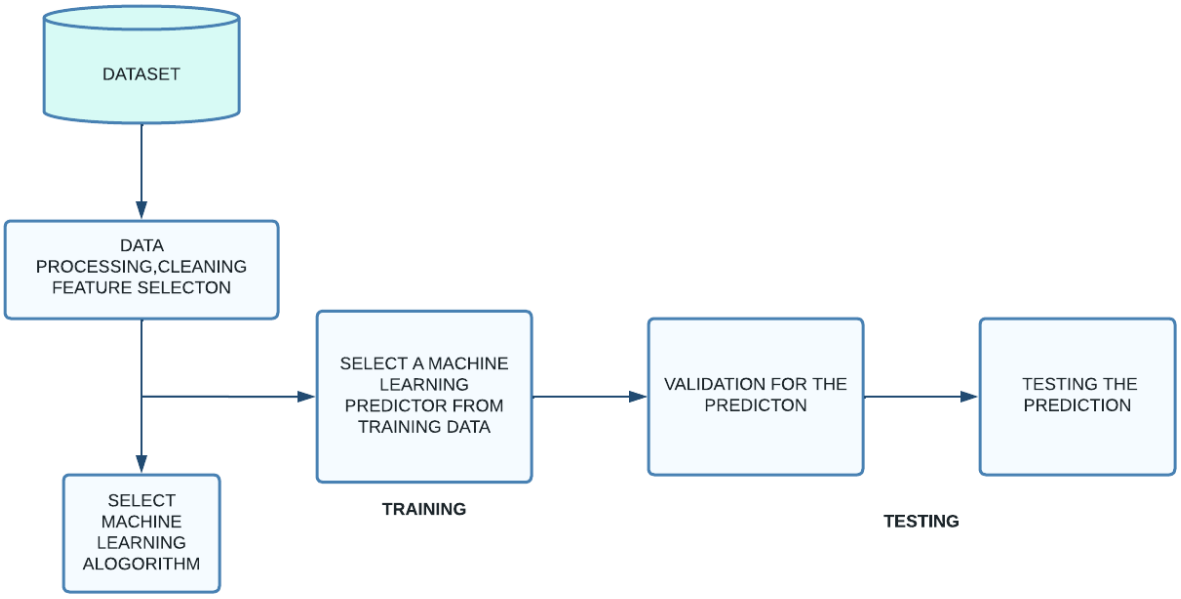

Figure 1(a): Full system block diagram .

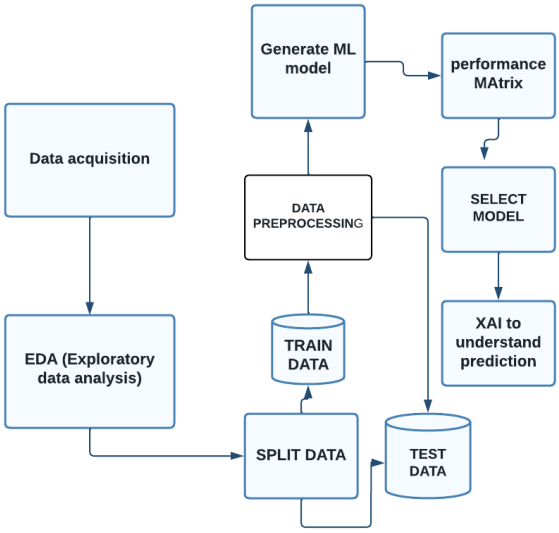

Figure 1(b): Full system block diagram

The characteristics for making the prediction were then allocated, and the goal value for the model to forecast was specified. The dataset was then divided into two parts: training validation and testing. The group was divided via random sampling, which resulted in an imbalance between the training and testing halves. As a consequence, stratified sampling with an 80 percent training-validation size and a 20% testing size was used. The features were then resized according to industry norms. To better comprehend the scenario, various histograms and scatter plot visualizations were produced on the training split. After that, the system's training began.

2.3 Flow Chart Diagram

2.3.1 Random Forest

Figure 2 depicts the stream outline for the entire arbitrary woodland model. It is made up of a variety of trees. The system is indistinguishable from the choice tree system. It pre-processes the data and selects a few irregular examples from the dataset for preparation. It generates a choice tree for each example. The arbitrary timberland model was created without any modifications. [6] Lepetit was the first to propose Arbitrary Timberlands. His dedication to this field prepared him for tasks such as class recognition. [8] [9], bi-layer video division [10], picture characterization [11], and individual ID [12] are all applications that make use of his work. Timberlands that are arbitrary. The Irregular Woods enable a wide range of obvious signals, including variety, shape, surface, and profundity. Arbitrary Backwoods are regarded as competent and universally useful vision instruments.

Organized irregular woodland is a type of coordinated revelation that can be used for gathering purposes, such as backsliding. Nonetheless, it is commonly used for request fulfillment. We realize that the woods are made up of trees, and that as the number of trees grows, the land becomes more densely forested. As a result, self-emphatic inconsistent forest area computation selects trees based on data testing and employs dynamic techniques to select the best game plan after gathering gauges from all of them. It's a better clothing technique than a single choice tree because it balances the results and prevents over-fitting.

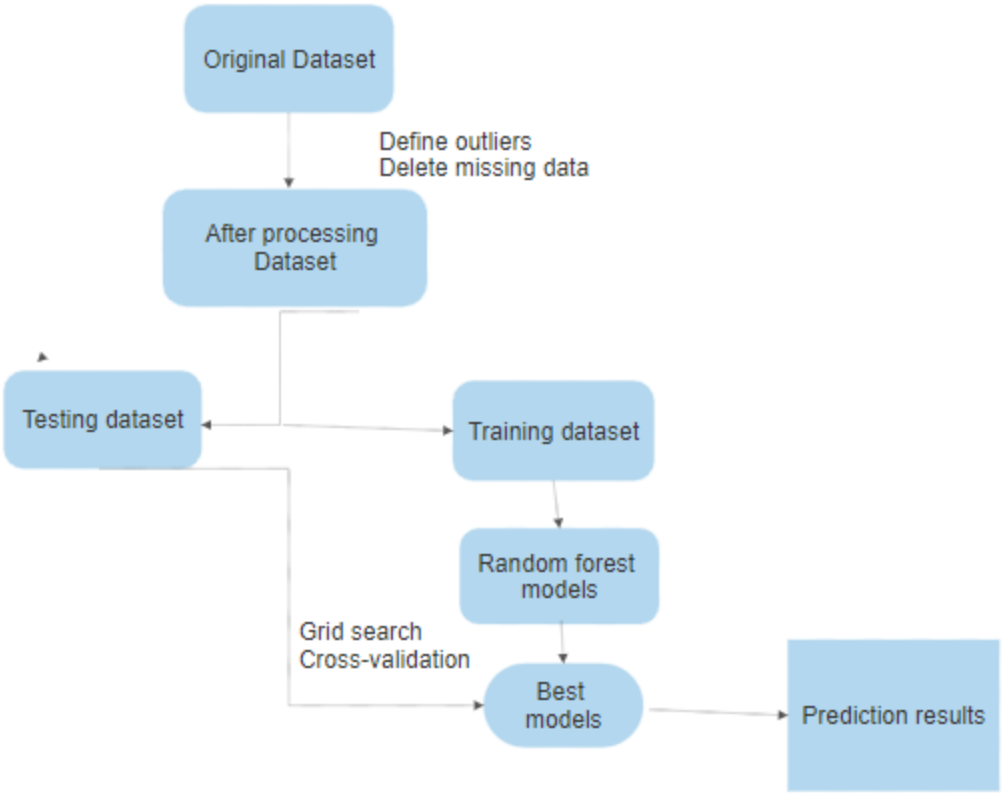

Figure 2: Random Forest Flowchart

2.3.2 K-Nearest Neighbor Algorithm

In many situations, the k-Closest Neighbors (KNN) grouping strategy is a simple yet effective non-parametric order approach. [12]In order to order an information record t, the k nearest neighbors are obtained, resulting in a t area. Ordinarily, a larger part vote among nearby information records, regardless of distance-based weighting, is used to order it.

Wang [13] suggested looking at various arrangements of nearest neighbors rather than only one bunch of k-closest neighbors to make KNN less dependent on the choice of k. The K-nearest neighbors (KNN) method is a directed AI calculation for predicting order and relapse problems. KNN is a slow learning calculation because it does not have a separate preparation stage and, on second thought, involves all of the information for preparation and characterization. K-nearest neighbors (KNN) is a controlled AI strategy capable of anticipating both order and relapse issues. KNN is a languid learning calculation because it does not have a separate preparation stage and uses the information on second thought.

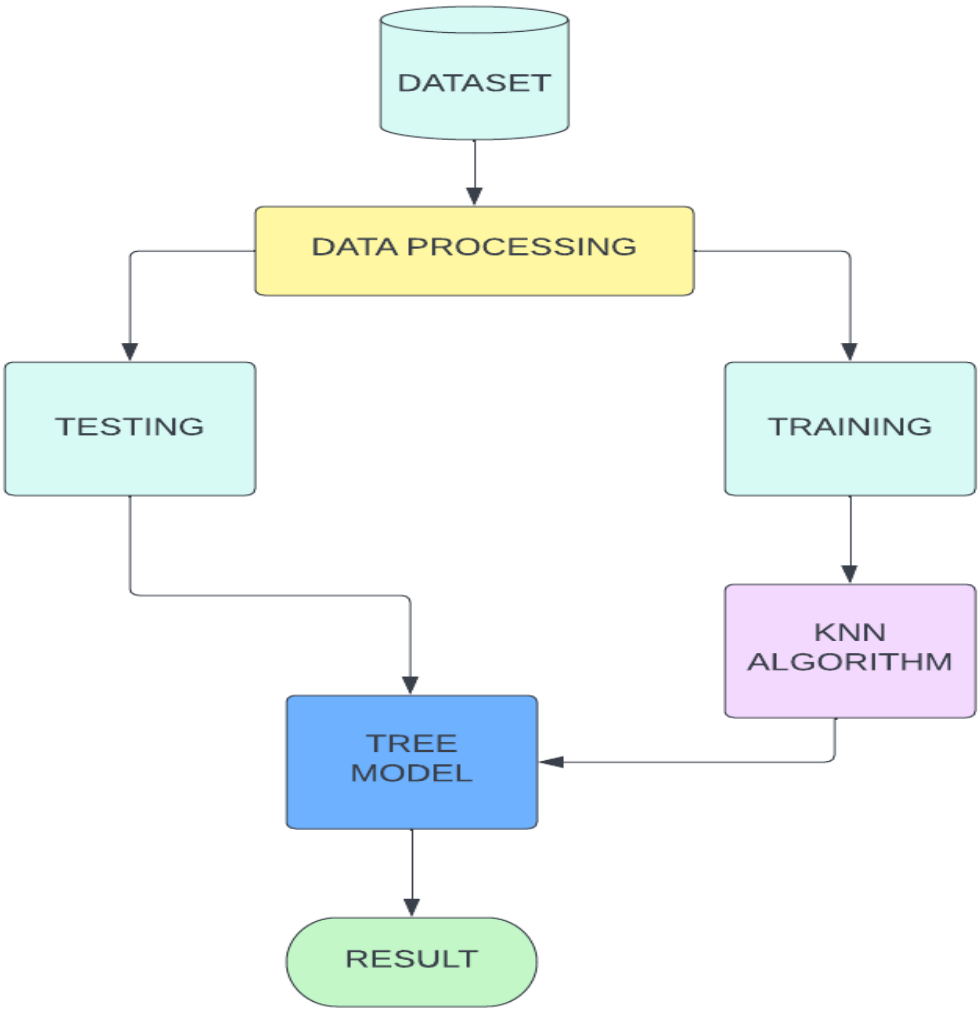

Figure 3: KNN Flowchart

2.3.3 DECISION TREE

The Choice Tree calculation [14] has been used to solve a wide range of problems. They are used in text classification and extraction, measurable information correlation, and a variety of other areas. Furthermore, using the Choice Tree strategy, books in libraries can be classified into discrete groups based on their features. It is used in clinics to distinguish things like brain tumors, disease, heart problems, and hepatitis, among other things. It is used to track records by organizations, clinics, schools, colleges, and associations. It is also possible to use it to gain financial exchange insights. Calculations for Choice Trees [15] are useful because they produce people-friendly arrangements. Aside from that, there are a few flaws, one of which is the tree's proclivity to rank all mathematical properties while splitting a hub. When using Choice Trees on data with numerous examples, such a split on organizing all mathematical qualities is inefficient in terms of effectiveness, running time, and memory limit. Breiman [16] introduced Irregular Woodlands as a classifier that outperforms regular classifiers such as Help Vector Machines, Brain Organizations, and Discriminant Examination while avoiding overfitting.

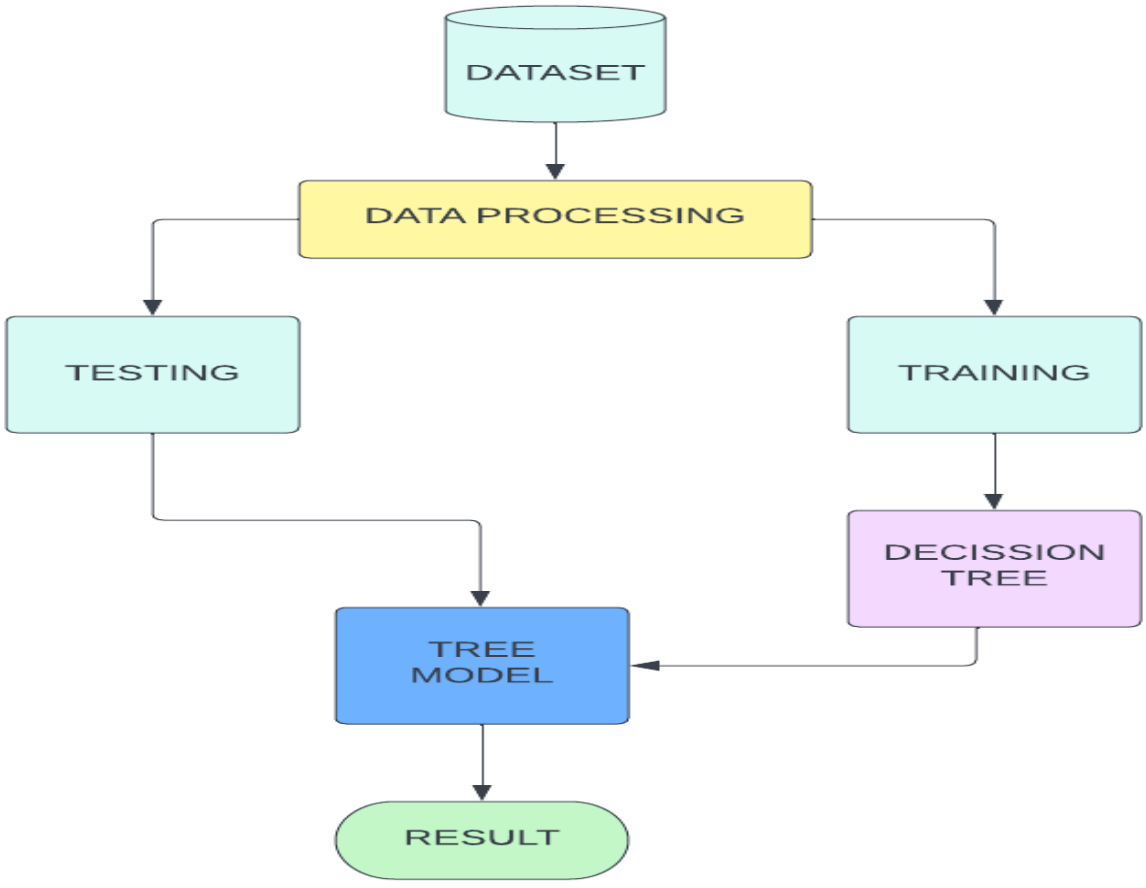

Figure 4: Decision Tree Flowchart

The type of decision tree employed in this study was the advantage proportion decision tree. The addition proportion choice tree is generated using the entropy (data acquire) strategy, which picks the splitting characteristic that limits entropy and hence amplifies data acquisition

2.3.4 Support Vector Machine

Figure 5 depicts the general stream outline of the SVM model. At first, the support vector machine required almost no tweaking. In this case, the spiral premise capability is used (RBF). A matrix search was then used to fine-tune the model. The boundary blends were then subjected to a variety of regularization boundaries, including C qualities, gamma values, and four distinct part types: RBF, straight, poly, and sigmoid. Furthermore, a 5-overlay cross-approval was used to investigate every possible combination. The model was then retrained, and the results were significantly improved. The disarray framework was determined using this form. SVM is a two-grouping model that finds a reasonable hyperplane to divide the information.

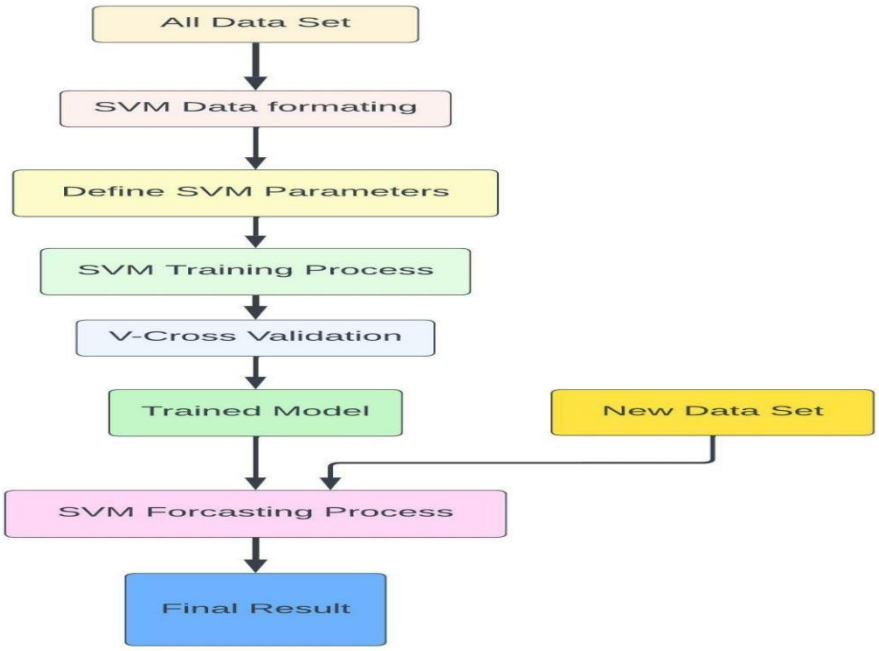

Figure 5: SVM Flowchart

The idea behind segmentation is to maximize the interval (including hard and soft intervals) and convert it into a one-of-a-kind quadratic programming problem to solve. If the training sample is linearly time-sharing, maximize the hard interval; if the training sample is approximately linearly time-sharing, maximize the soft interval and select the appropriate kernel function; if the training sample is linearly non-time-sharing, maximize the soft interval and select the appropriate kernel function. The Support Vector Machine is a fundamental model for relapse and arrangement issues. It can deal with both direct and indirect problems and excels in a variety of real-world situations. SVM is a straightforward method for dividing data into classes by drawing a line or hyperplane.

2.3.5 Naive Bayes

Naive Bayes is one of the data categorization techniques. This algorithm ranks among the top ten data mining algorithms. [17]. The Naive Bayes method is a simple probabilistic classification method. This algorithm computes a set of probabilities by analyzing the frequency and combination of values in a specific data set. [18]. The frequency of each feature value in the class from the training data set is used to

calculate the probability of specific data features appearing as members in a probability sequence. Classification algorithms are trained using a subset of the training data set. The training data set is a subset of the entire data set that is used to train classification algorithms. The training procedure employs known values to forecast unknown values. [19].

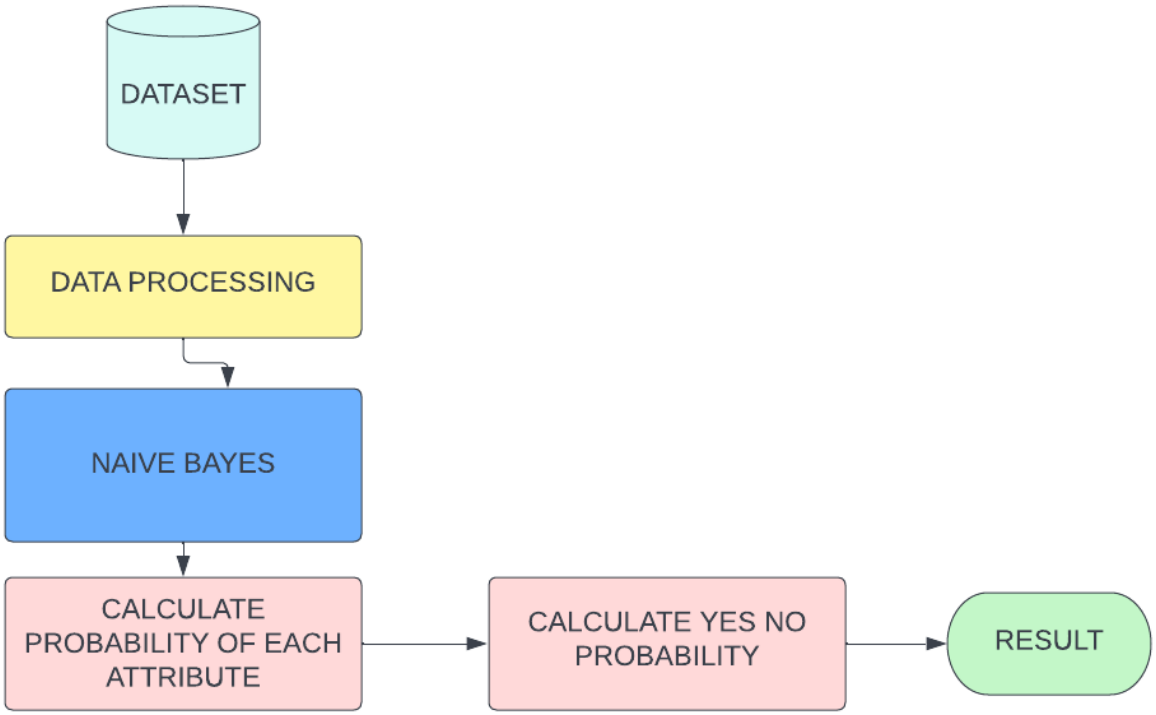

Figure 5: SVM Flowchart

Naive Bayes is a classifier that makes use of the Bayes Theorem. Each class's enrollment probabilities, such as the likelihood that a given record or information point belongs to that class, are predicted by it. The class with the greatest apparent likelihood is the most probable one.[19]

2.3.6 Logistic Regression

Figure 6 depicts the logistic regression model's comprehensive flowchart. It differentiates between variables that are independent and dependent. The sigmoid function is used to predict probabilities and set decision limits. Although calculated relapse is particularly useful for joining the best indicator factors for a minimal price, it has a penchant to exploit irregular example highlights. [20].

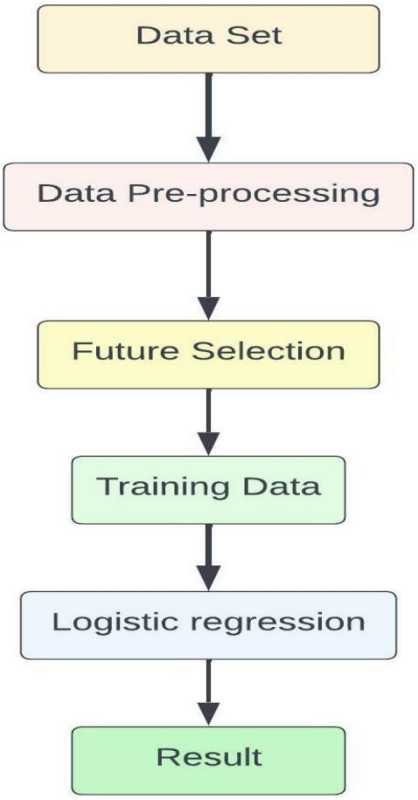

Figure 6: Logistic Regression Flowchart

The logistic regression method [21] automatically generates new variables for categorical variables. As opposed to multiple linear regression's "dummy variables," this eliminates the need for them [22]. A method for machine learning that is based on supervised learning is logistic regression. Regression analysis is done by it. Regression models the desired prediction value based on independent variables. The value of a dependent variable (y) based on an independent variable is predicted using linear regression.

2.3.7 XG BOOST

Extreme Gradient Boosting (XGBoost) is a gradient-boosted decision tree (GBDT) machine learning framework that is distributed and scalable. It is the best machine learning library for regression, classification, and ranking problems, and it includes parallel tree boosting.

In GRADIENT BOOSTING[23], regression trees serve as the weak learners, with each tree transferring an input data point to a leaf containing a continuous score. XG Boost minimizes a regularized (L1 and L2) objective function using a convex loss function (based on the difference between predicted and target outputs) and a penalty term for model complexity (in other words, the regression tree functions).

Iterative training is used to add new trees that predict the residuals or errors of previous trees, which are then combined with previous trees to make the final prediction. Gradient boosting is so named because it employs a gradient descent algorithm to minimize loss when adding new models. [24]

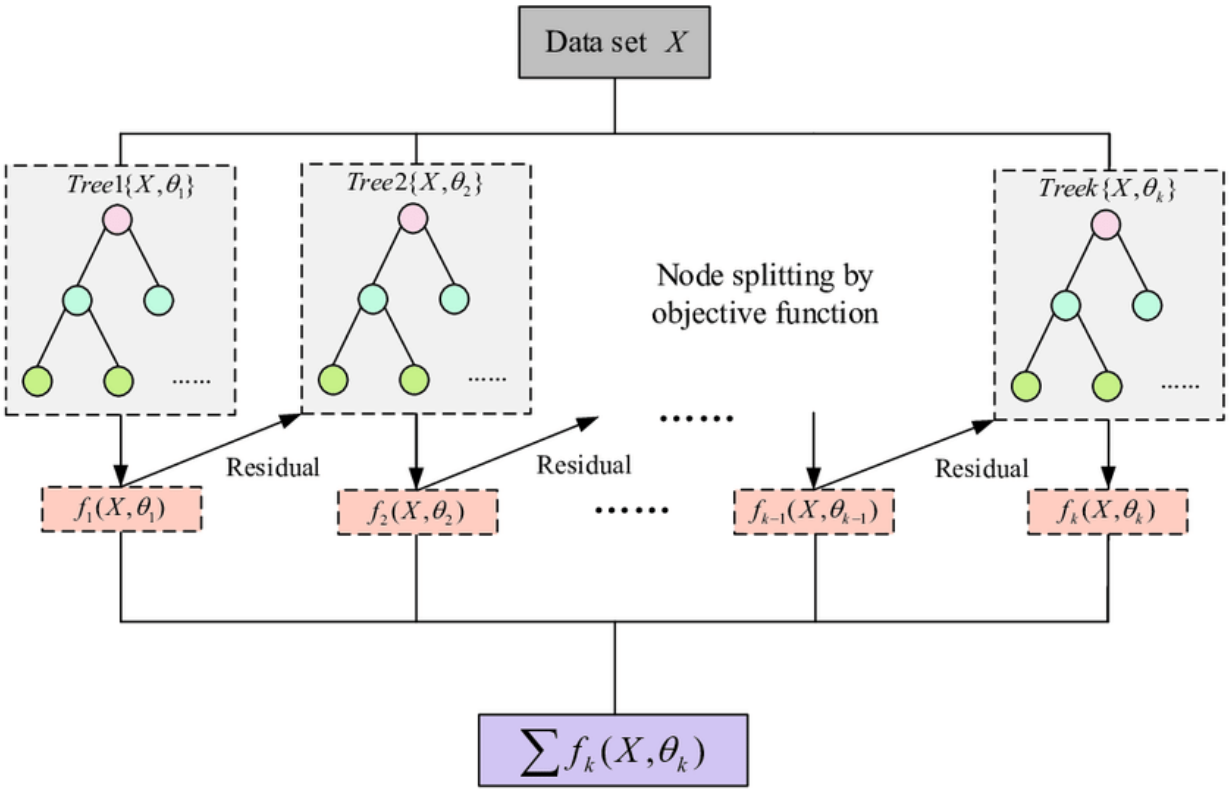

Figure 7: XG Boost Block Diagram

2.3.8 XAI Method

Explainable AI, also known as XAI, aids in defending a model's decision-making. By offering reasons that laypeople can understand, it makes the choice clear. There are several XAI frameworks on the market. This thesis chose to employ LIME as one of them for the project.

2.3.9 Working Process for Explaining Prediction of Heart Attack by using LIME

The working process to use the LIME method of this thesis will address the explanation of the prediction of a heart attack. LIME is a kind of method that not only visualize the prediction but also gives an explanation of the individual prediction.

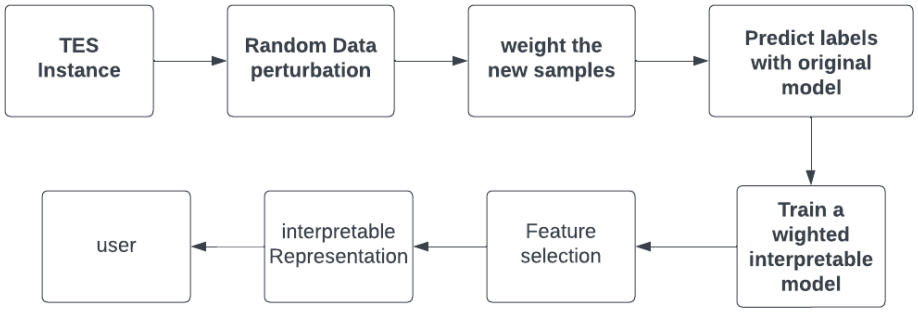

Figure 8: Process Flow of LIME

2.3.10 LIME Framework:

The ability of XAI is crucial in the healthcare industry. Machine learning and deep learning models were formerly thought of as "black boxes" that accepted some input 15 and made a decision to produce an output, but it was unclear from which parameters these judgments were made. The necessity for Explainability in AI has increased, as a result of the growing use of AI in our daily lives. And also the decision-making capabilities of AI in situations like autonomous vehicles and cancer prediction software. To deal with this issue the concept of black-box is very prominent. The usage of black-box in machine learning makes the machine learning models more transparent. LIME is one of the promising frameworks of the XAI method which explains how any machine learning model works. LIME stands for Local Interpretable Model-agnostic Explanations. The basic idea of the LIME is that we just have to zoom into the local area of the individual prediction. LIME can easily create a simple explanation that makes sense in that local region. This way we do not have to worry about the rest of the model, and still get a valid explanation of why the prediction was made for an instance. Any black box model can be explained by creating such a local approximation. The complex models are complete black boxes and the internals are hidden for LIME. So, it's just based on the inputs and outputs of the model. To explain individual predictions LIME focuses on training local surrogate models Instead of training a global surrogate model [39].

Mathematically, local surrogate models with interpretability constraints can be expressed as follows [40]:

$$\text{explanation}(x) = \arg\min_{g \in G} L(f, g, \pi_x) + \Omega(g)$$

The explanation model for instance x is the model g (e.g. linear regression model) that minimizes loss L (e.g. mean squared error), which measures how close the explanation is to the prediction of the original model f (e.g. an xgboost model), while the model complexity Ω(g) is kept low (e.g. prefer fewer features). G is the family of possible explanations, for example, all possible linear regression models. The proximity measure x defines how large the neighborhood around instance x is that we consider for the explanation. In practice, LIME only optimizes the loss part. The user has to determine the complexity, e.g. by selecting the maximum number of features that the linear regression model may use. Reference. This paper conducts the LIME method on the KNN ML algorithm

3 Investigation/Experiment, Result, Analysis, and Discussion

This section of the thesis will describe the findings and analyze the results of the research. 4.1 Result Analysis of Heart Attack Prediction Using Multiple ML Algorithms In this paper, the chance of a heart attack is predicted using different models. On Jupyter Notebook which operates under Ubuntu 64 bits and is composed of a single core hyper threaded Intel Xeon processor@2.3 GHz and 8 GB of RAM, I performed all the computations. As Python programming has open-source packages, I used those to simulate our code and experiments. This work has used confusion matrices such as accuracy, sensitivity, specificity, and F1-score for the XG-Boost Classifier and KNN algorithm. Accuracy is the percentage of total subjects classified correctly. Sensitivity is the proportion of those who do have the disease who test positive. Specificity is the proportion of those who do not have the disease who test negative. Sensitivity can also be identified as Recall. Precision is the number of subjects correctly identified as positive out of the total subjects identified as positive. F1-Score is a harmonic mean of precision and recall [41].

$$Accuracy = \frac{TP + TN}{Data\ Size} \quad (7)$$

$$Precision = \frac{TP}{TP+FP} \quad (8)$$

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

$$f1 - score = 2 * \frac{precision * Recall}{precision + Recall} \quad (10)$$

Here, TP and FP denote the number of correctly and wrongly classified subjects having heart disease, respectively. Similarly, TN and FN denote the number of correctly and wrongly classified subjects not having heart disease, respectively [41]. The paper is shown the confusion matrix which is contained the summary of prediction results of all instances for the XG-Boost and KNN Classifier of the dataset used for both testing in Fig 4.1 and 4.2 respectively. The paper is also shown the performance of the XG-Boost Classifier algorithm in Fig 4.3 and Fig 4.4 respectively.

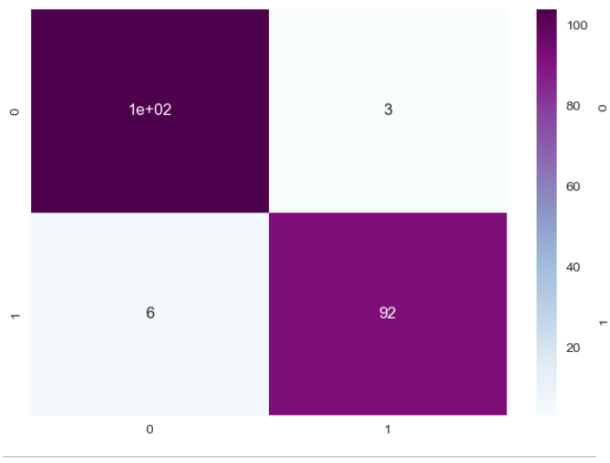

Figure 9: Confusion Matrix of KNN

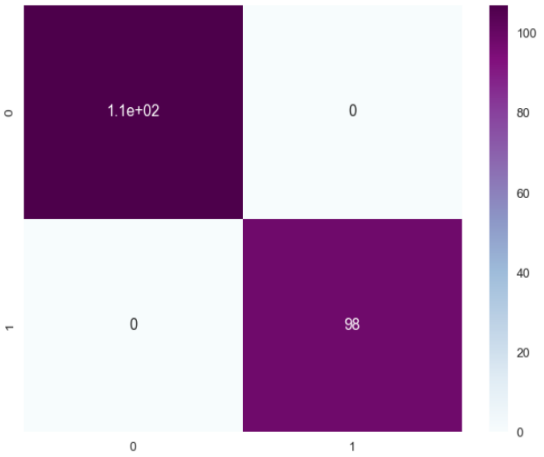

Figure 10: Confusion Matrix of XGB

With an accuracy of 95.60 percent, the KNN model makes 100 right predictions and 92 incorrect predictions. By using this model, we have got a precision of 0.95, recall of 0.97, and f-score of 0.96 for negative results. But for positive results, we have got 0.97 precision,0.94 recall and 0.95 f-1 score. At last, we have got a 95.60% accuracy rate which we can show in Figure 4.3 and Figure 4.4.

	precision	recall	f1-score	support
0	1.00	1.00	1.00	107
1	1.00	1.00	1.00	98
accuracy			1.00	205
macro avg	1.00	1.00	1.00	205
weighted avg	1.00	1.00	1.00	205

Figure 11: Performance Matrix of XGB

	precision	recall	f1-score	support
0	0.95	0.97	0.96	107
1	0.97	0.94	0.95	98
accuracy			0.96	205
macro avg	0.96	0.96	0.96	205
weighted avg	0.96	0.96	0.96	205

Figure 12: Performance Matrix of KNN

With an accuracy of 100 percent, the KNN model makes 100 right predictions and 98 incorrect predictions. By using this model, we have got a precision of 1.00, recall of 1.00, and f-score of 1.00 for negative results. But for a positive result, we have got 1.00 precision,1.00 recall, and 1.00 f-1 score. At last, we have got a 100% accuracy rate which we can show in Figure 4-2 and Figure 4.3.

3.1 Accuracy Comparison of All Models

In the paper, the heart attack rate is predicted for some different models. We have used Logistic Regression, Decision Tree, Random Forest, Support Vector Classifier, Naive Bayes Classifier, XG-Boost Classifier, and K-Neighbors Classifier algorithms to find the accuracy of a heart attack. We have shown the accuracy percentage of different algorithms in Fig 4.4.

Model	Accuracy
XGBoost	100.000000
K-Nearest Neighbour	95.609756
Random Forest	88.780488
Logistic Regression	83.902439
Support Vector Machine	83.902439
Decision Tree	83.902439
Gaussian Naive Bayes	82.439024

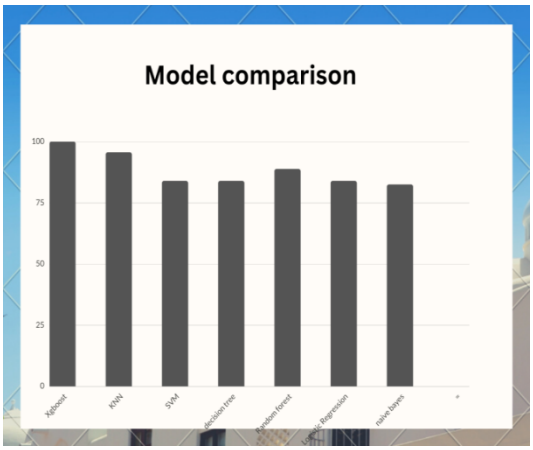

Figure 13: Accuracy Comparison

Here, XG-Boost and KNN Classifier give the best performance with 100% and 96% accuracy among all other algorithms.

3.2 Feature Importance

A heart attack may vary depending on various circumstances. In machine learning, these circumstances are defined as features. The features that have the biggest impact on predictions are called feature importance. In some cases, a few attributes may decrease the accuracy level of a model. So, it is important to work with the correct attributes. Though we have used all the features, feature importance from the dataset is shown in Fig 4.6.

Weight	Feature
0.1732 ± 0.0186	thal_2
0.1488 ± 0.0276	ca
0.1134 ± 0.0121	cp_0
0.1102 ± 0.0168	oldpeak
0.0905 ± 0.0219	age
0.0685 ± 0.0071	chol
0.0600 ± 0.0195	thalach
0.0220 ± 0.0041	restecg
0.0185 ± 0.0066	slope_1
0.0180 ± 0.0061	cp_2
0.0124 ± 0.0039	exang
0.0107 ± 0.0047	sex
0.0076 ± 0.0018	trestbps
0.0061 ± 0.0034	thal_1
0.0056 ± 0.0033	cp_1
0.0015 ± 0.0018	slope_2
0 ± 0.0000	thal_0
0 ± 0.0000	cp_3
0 ± 0.0000	thal_3
0 ± 0.0000	slope_0
0 ± 0.0000	fbs

Figure14: Important Features of The Dataset

As shown in Fig 4.6, the feature cp which is chest pain has the most impact on the chances of having a heart attack.

We have taken a local example here. We can see that the top 4 features contributing to the prediction of the feature are old peak, ca, cp, and that.

Old-peak, which is the most important feature in this prediction is related to the electrocardiograph results of the patient. If the electrocardiograph shows an ST Depression (indicating that the patient is suffering from myocardial ischemia), the value of the old peak shows us the level of the ST Depression. The more the depression, the likelier it is that the patient is suffering from heart disease.

3.3 Feature Analysis

All the features have value to count. By analyzing all the value counts we predict the rate of a heart attack. All the features have value to count. By analyzing all the value counts we predict the rate of a heart attack.

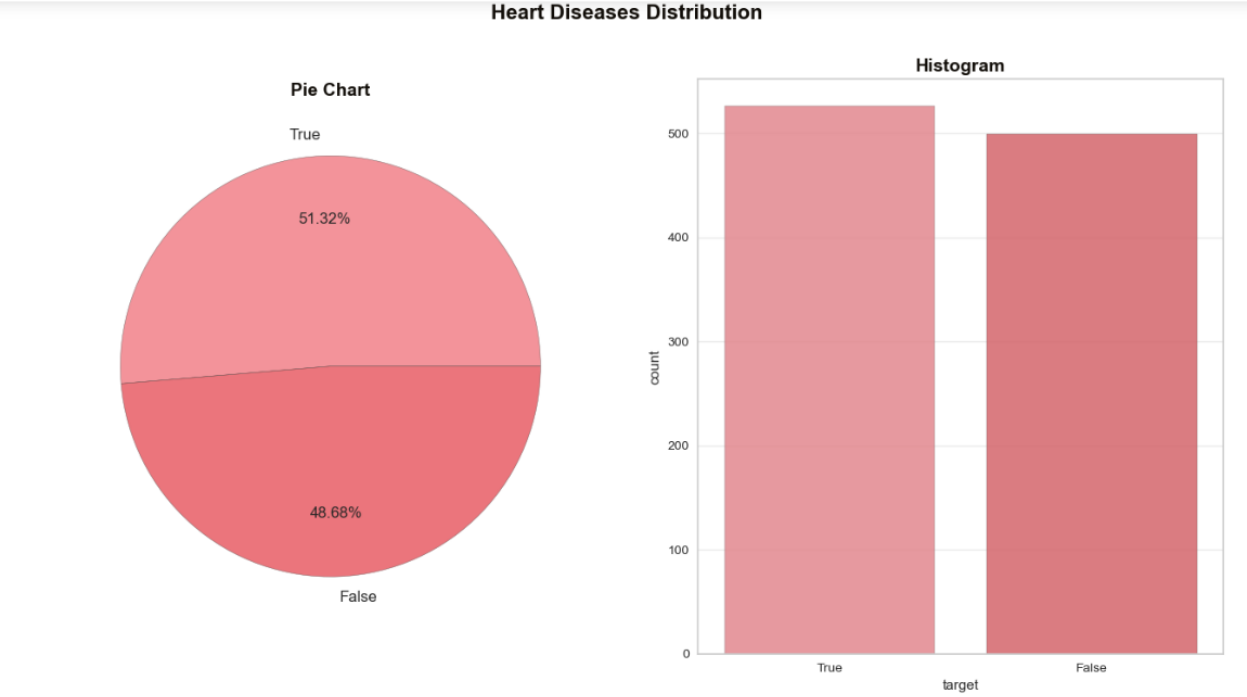

Figure 16: Value Counts of The Feature

In the paper, Fig 4.7 represents the more and fewer chances of heart attack from value counts. It means the dataset has 51.32% of '1' which predicts more chances of heart attack and 48.68% of '0' which predicts fewer chances of a heart attack.

3.4 Result Analysis of the Heart Attack Prediction Using LIME

This section of the paper will explain heart attack prediction through the KNN Machine Learning algorithm using LIME.

3.4.1 Feature Importance Result

The LIME method can give a visual representation of it which features give more contribution to the prediction. Using LIME is so beneficial because it can provide the feature importance by using 2 different methods. By using the show in the notebook() method Fig 4.8 and 4.9 shows the volume of the impact of the feature.

The figure consists of 3 types of representation- progress bar, bar chart, and table. In the figure, the progress bar indicates the range of which value varies and the actual prediction; the bar chart shows the features of their weights positive and negative to prediction; and the table represents the features' importance by showing the actual feature values. Here, the orange color indicates the positive contribution and the blue color indicates the negative contribution toward the prediction [42].

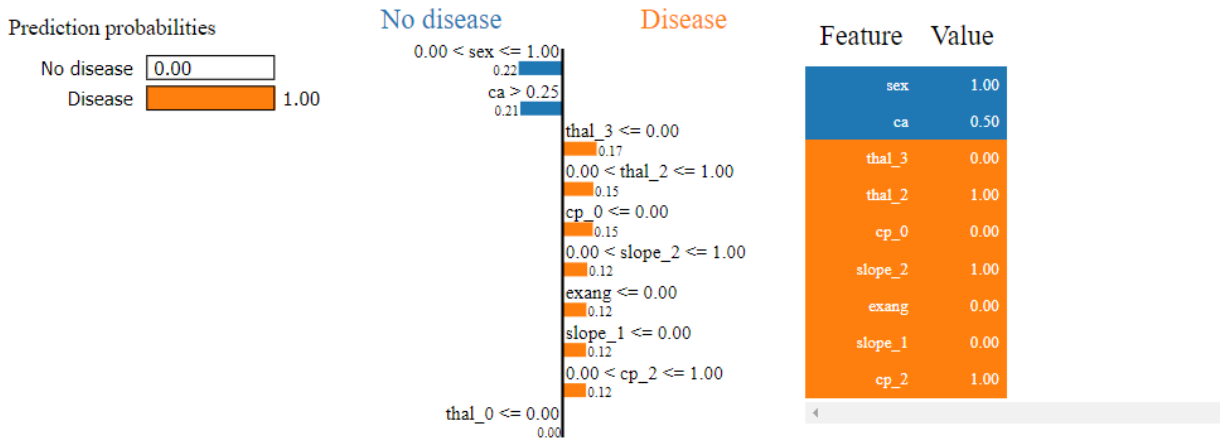

Figure 17: Feature Importance Using LIME

In fig-4.8, for this patient, heart disease is predicted for orange features which are important features for heart disease whereas blue features are less important. Orange features are a more important feature for heart disease. These volumes are high for predicting heart disease.

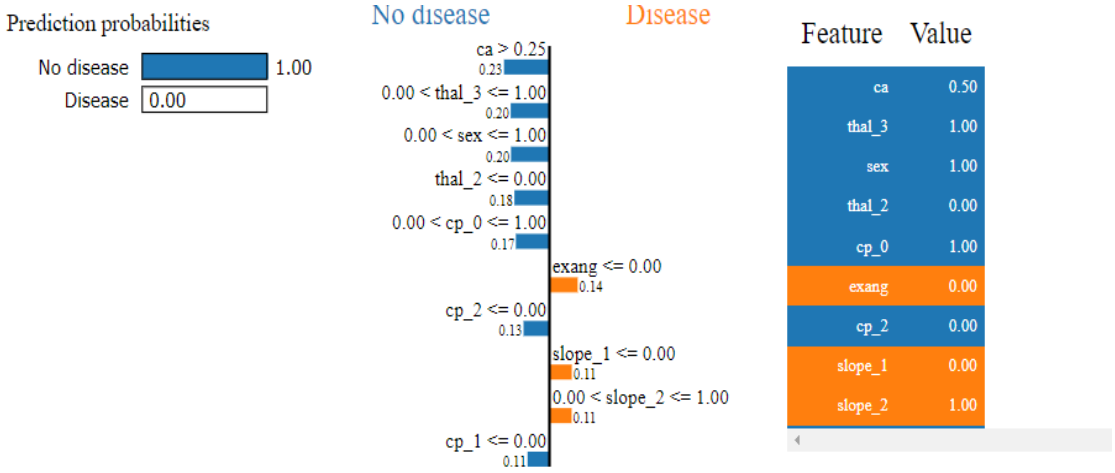

Figure 18: Feature Importance Using LIME

In fig-4.9, for this patient, heart disease is not predicted for blue features which are not important features for heart disease whereas orange features are more important. Here, the volume of blue features is higher than the orange volume. For that reason, our model is predicting "No Disease" for this particular patient.

3.4.2 Retrieve Features Importance

LIME XAI method has the advantage of retrieving the feature's importance shown in Fig 4.10. Here the first value of the tuple is condition and the second value is the feature value based on condition.

Weight	Feature
0.1732 ± 0.0186	thal_2
0.1488 ± 0.0276	ca
0.1134 ± 0.0121	cp_0
0.1102 ± 0.0168	oldpeak
0.0905 ± 0.0219	age
0.0685 ± 0.0071	chol
0.0600 ± 0.0195	thalach
0.0220 ± 0.0041	restecg
0.0185 ± 0.0066	slope_1
0.0180 ± 0.0061	cp_2
0.0124 ± 0.0039	exang
0.0107 ± 0.0047	sex
0.0076 ± 0.0018	trestbps
0.0061 ± 0.0034	thal_1
0.0056 ± 0.0033	cp_1
0.0015 ± 0.0018	slope_2
0 ± 0.0000	thal_0
0 ± 0.0000	cp_3
0 ± 0.0000	thal_3
0 ± 0.0000	slope_0
0 ± 0.0000	fbs

Figure 19: Retrieving Features Using LIME

As we know, the KNN algorithm is a regression model. But this algorithm is also defined as a classifier. So if we want to retrieve the feature's importance for classifier task LIME will allow us to do so. Fig 4.10 shows that it returns a dictionary where the key is each class of task and the value is a list of feature indexes and their contribution in predicting that class.

4 CONCLUSION AND FUTURE WORK

It is very challenging to implement the ML algorithms in healthcare field for it's limited availability of dataset. The paper proved that the XGBoost algorithm gives the best accuracy. So the LIME method should be implemented on the XGBoost algorithm. To do so, a huge and populated dataset must be needed. Furthere more, the dataset needed to be preprocessed. All of these above reasons limited the papers significance. In recent years, the ML algorithms along with AI has been shown great impact on healthcare area. This thesis is a little approach to it. As the paper requires some limitations, we want to move forward the implementation as future approach. Implementation of LIME on XGBoost algorithm can be targeted as future work. Moreover, in future we would like to work on a huge dataset to see how accurately the model predicts. We will extend this work and try to get SHAP values for the whole dataset. Despite having some limitations this thesis performed all the predictions and provides prominent future works. So, we dream to take the work forward and enrich further

Data Availability

The data used to support the findings of this study are freely available at ***https://www.kaggle.com/ronitf/heart-disease-uci***

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Conflicts of Interest: The authors would like to confirm there are no conflicts of interest regarding the study.

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