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PREDICTIVE MODELING OF CARDIOVASCULAR DISEASE USING MACHINE LEARNING APPROACH

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Article Info

Abstract

The primary causes of death worldwide are Chronic Cardiac diseases. Accurately diagnose and predicting chronic cardiac disease is important to the proper treatment of cardiac patients before a heart attack occurs. The goal of accurate disease prediction will be achieved using a ML algorithm with health examination data. Early prediction of the risk factors of cardiac disease is critical for preventing heart disease. In our research, this is a follow-up study the statistical analysis will be used to assess the prediction of CCD as many high-risk factors (hypertension, smoking, high blood cholesterol, increasing age, male gender, being overweight) are involved. The heat-map cluster and machine learning algorithm provide interactive visualization for the classification of patients with different CCD stages. Early stages of cardiac patients are grouped into one cluster and advanced staged cardiac patients could be at high risk for the expeditious decline of heart function and should be closely monitored. The clustering heatmap provided a new predictive model for health care management for patients at high risk of rapid CCD progression. This model could help physicians make an accurate diagnosis of this progressive and complex disease.

Keywords:
Chronic Cardiac, Heart Attach, Machine Learning, Classifier

Introduction

The heart is the second largest organ in comparison to the brain, which is of higher priority in the Human body. Heart disease accounts for 16% of the world's total deaths. An estimated 30 to 40 percent of deaths in Pakistan are due to heart diseases. In living creatures, the heart plays a very significant role. (Marimuthu et al., 2018). The identification of the heat disease is problem due to unavailability of machine, limited medical staff and other valuable resources to verify the presence of this disease in developing countries. (Yahaya et al., 2020) By use of supervise learning, we can able to create agent base machine, which able to identify the behavior of certain problem independently. In supervised learning, the first step is to make learning about attributes of some problem with the specific output label. Following this, this train algorithm has been used for the identification of a class label of the test dataset.

The algorithm creates a mathematical model from a set of data that includes both the inputs and the desired outputs. Different machine learning approaches were applied to classify a new data set of cardiac disease. Different findings from experiments the best results from the SVM classifier when used the entire dataset (14 characteristics, 303 instances): only 48 examples were erroneously categorized. The naive Bayes and C4.5 algorithms produced comparable findings. However, they were inferior to the SVM. Based on the results, it can conclude that all classifiers performed admirably. On the data set, however, discovered that SVM outperformed both C4.5 and the naive Bayes classifier. (Chaki et al., 2015). This system employs the Naive Bayesian and K-Nearest Neighbor algorithms, which are both data mining approaches. From the historical database, the system extracts patterns and relationships. This technique is helpful in hospitals for disease prediction. After testing, I discovered that the Naive Bayesian algorithm outperforms the KNN algorithm. To improve and expand the system, add other attributes. Other techniques, such as clustering, time series, and association rules used. Text mining can also use to mine data that isn't structured. Data mining and text mining can also combine. (B. and Priyadarshi, 2015)

There is a need for a practical feature selection method that identifies the significant traits contributing more to disease diagnosis. Particle Swarm Optimization (PSO) is one of the met heuristic algorithms used to discover the optimal solution in the shortest amount of time. The PSO algorithm identifies the more significant characteristics in a dataset and removes the irrelevant and redundant features. On the other hand, the standard PSO method has a problem picking the ideal weight to update the velocity and position of the particles. They also presented a new fitness function for PSO using the Support Vector Machine (SVM). (Vijayashree and Sultana, 2018). Data mining and machine learning are used to forecast the occurrence of cardiac disease. Analyze the performance of each algorithm's forecast and apply the system to the required area. Improve the accuracy of the algorithm by selecting more relevant features. Conclusion: From the literature review, they believe that creating a predictive model for heart disease patients is only marginally suc cessful. That complicated models are required to boost the accuracy of early detection. The database gets more intelligent as more data is fed into it. (Marimuthu et al., 2018).

Data mining is used in hospitals to extract secret information that indicates the presence of some diseases. Various types of algorithms used that predict the heart diseases are playing crucial roles in the automatic detection of disease in hospitals. Support Vector Machine, Decision Tree, Nave Bayes, K-Nearest Neighbor, and Artificial Neural Network are some machine methods used for cardiac disorders. (Chala Beyene, 2018).

A survey, begin by providing an overview of machine learning and providing brief explanations of the most often utilized classification approaches to diagnose heart disease. Then, in this subject, the review represents research papers on machine learning classification approaches. A complete tabular comparison of the surveyed papers is also offered. (Al-Janabi et al., 2018). The proposed model proves to be an efficient and effective one for accuracy improvement of the Naive Bayes classifier in which particle swarm optimization is implemented for feature subset selection, therefore providing comparable and even better performance in classification. They achieved that by developing an innovative algorithm to maximize the classification performance while decreasing features. The simulation results indicated that this method can automatically evolve a feature subset selection with fewer features and improve classification performance over the use of all of the elements in a dataset. (Dulhare, 2018).

This article covers data mining approaches in the prediction of heart disease. Heart disease is, by definition, a fatal disease. Several steps are taken to apply relevant methodologies in disease prediction. This report looked at research projects that used effective methods and were carried out by various researchers. Based on the comparison analysis, we can conclude that the SVM technology effectively predicts heart disease. It provides good accuracy by viewing various study articles. (Raju et al., 2018).

MAPO is a modified APO that tested on the heart disease real-world issue domain and predicts heart disease. Relational MAPO identifies optimal features from any relational dataset with great accuracy when the evaluation is on datasets like heart disease, MNIST, and Framingham. This method eliminates collinearity and dependency among related variables, which further enables the extraction of optimal non-collinear attributes from a relational dataset. The experiments indicate that video MAPO may be used for heart rate calculation from fingertip video. Hence, it may be used for accurate computation of heart rate in a person through fingertip video. (Sharma et al., 2020).

Literature Review

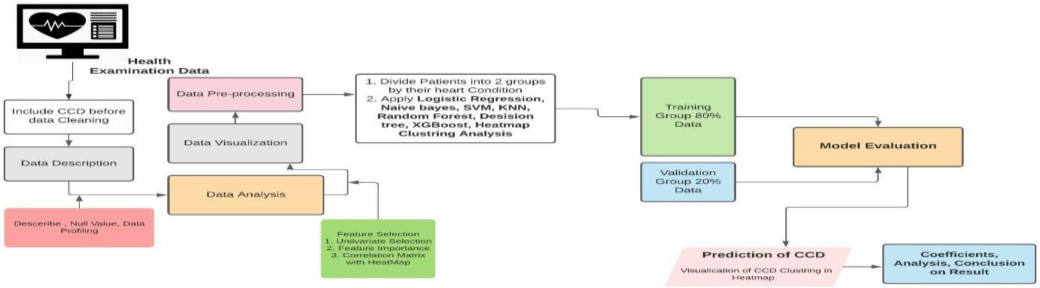
Clinical diagnosis highly depends on a doctor's skills. However, there are misdiagnosis and mistreatment cases. The patients are requested to participate in several tests of diagnosis. In most instances, not all the tests diagnose an illness. It is about forecasting heart disease using fewer parameters. Initially, it used 13 characteristics for heart disease prediction. A genetic algorithm discovered the most frequent heart problems, which reduced the number of tests needed by patients. 13 attributes were reduced to 6 Genetic searches. Subsequently, three classifiers are used to predict the diagnoses of patients with the same accuracy as above: Naive Bayes, Classification by Clustering, and Decision Tree. The decision tree outperforms the other two data mining algorithms combined with feature subset selection and model building time. After attribute reduction, Nave Bayes performs well as before. Clustering performs better than the other two methods. (M Anbarasi, E Anupriya, 2010).

The ensemble techniques used to boost classifiers using three powerful and leading methods such as bagging, boosting, and random subspace for the diagnosis of heart diseases. Compare and evaluate the performances of three prominent ensemble techniques designed for diagnosing valvular heart illnesses, thereby diagnosing valvular heart disease. In the study, a set of 215 samples were employed for validating the performance of the developed ensemble technique in the comparative research. The tests indicate that ensemble classification methods are feasible and draw important conclusions about the efficacy of ensemble approaches in identifying valvular heart disease. (M Anbarasi, E Anupriya, 2010). An expert system was designed to identify heart illness using a (SVM) and the feedforward back propagation technique. This paper includes the detailed medical data along with preprocessing. The expert system used the (SVM) and feedforward Backpropagation techniques. 300 patients, 250 were employed to use as the training set and 50 use the evaluation process to make the system more authentic and dependable. Finally, they employed two neural network methodologies. However, the output was only 50% to 60%, indicating unreliable for the patient. Using other neural network approaches, this can use this expert system data to improve the accuracy of medicine. (Hannan et al., 2010).

Coronary artery calcium score improves risk classification in a typical risk factor-based prediction model. A total of 209 CHD events occurred during a median of 5.8 years of follow-up among a final cohort of 5878, with 122 of them being myocardial infarction, death from CHD, or resuscitated cardiac arrest. Model 2 compared with model 1 resulted in considerable improvement in risk prediction (net reclassification improvement=0.25; 95 percent confidence interval, 0.16-0.34; P.001). In model 1, 69 percent of the cohort was assigned to the highest or lowest risk categories, but in model 2, 77 % were highest or lowest risk categories. Using model 2, another 23% of those who experienced events was reclassified as high risk and another 13% who did not experience an incident was also reclassified as low risk. (Polonsky et al., 2010). An example of the neuro-fuzzy integrated system is shown below. From this study, it is clear that it is possible to identify risk based on the inputs from physicians. By using neuro-fuzzy integrated systems, in the process of getting an agreement with doctors' opinions, in NFIS training, the maximum classification accuracy in these systems has been achieved. Noisy voice recognition, noisy image filtering, nonlinear adaptive control, intelligent agents, and dynamical system performance analysis all gain advantages from the proposed research. The initial diagnosis of CHD by considering this proposed research activity through mobile SMS in remote locations, where doctors are not easily accessible. (Ansari and Gupta, 2011). The classification approach adopted a Multi-Layer Perceptron (MLP) using a Back Propagation learning algorithm along with a feature selection algorithm and biological test values. It used Thirteen characteristics to classify heart disease. Employ Information Gain to determine attributes, reducing the number of features collected from patients. Artificial neural networks are used to classify patient diagnoses. The number of qualities is reduced from thirteen to eight. For example, the percentage accuracy difference between 13 and 8 attributes in the training data set is 1.1 percent and in the validation data set is 0.82 percent. Khemphila and Boonjing, 2011). Rotation forest (RF) ensemble classifiers were built using 30 machine learning algorithms to examine their classification performance using Parkinson's, diabetes and heart disorders as illustrations from the literature. The datasets with three-dimension are first reduced using a correlation-based feature selection approach while testing. Second, the classification performance of 30 machine learning algorithms is computed for three datasets. Third, using the RF technique, 30 classifier ensembles are constructed to compare the performance of different classifiers using the same illness data. All of the tests are conducted using a leave-one-out cross-validation approach, along with the performance of 60 algorithms. In the case of the diabetes, heart, and Parkinson's datasets, base classifiers led to 72.15 %, 77.52%, and 84.43% avg accuracy. (Ozcift ,Gulten, 2011).

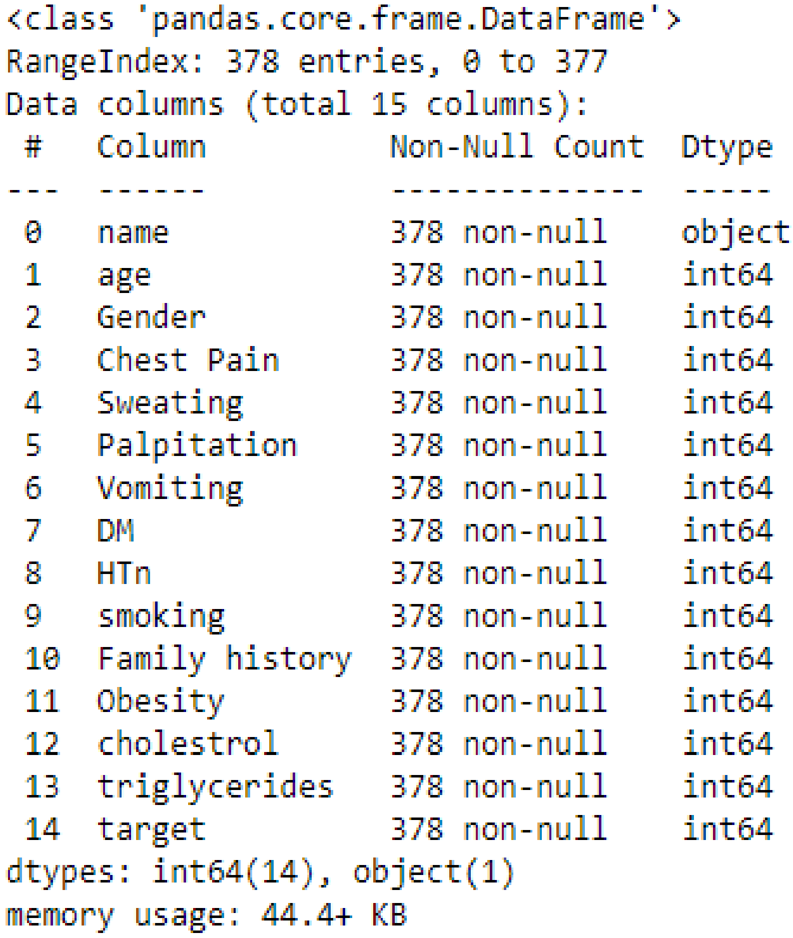
Methodology

A prediction technique of cardiac diseases diagnosis is an important part of this chapter. To put a stop to Cardiac Disease has nowadays more than required. Quality of data-driven of health management for predict Cardiac Disease can uplift the entire research and safe process, so these health systems make sure that a large number of people can live good lives. So here Machine Learning (ML) comes into play. We will use the ML algorithms in the prediction of Cardiac Disease, and ML makes predictions quite accurate as well as easy. For feature selection, we have used the univariate selection and find out the best three features (Sweating, Vomiting, cholesterol) of our dataset. After that, we have used the Classifier property model (Extra Tree Classifier) for feature improvement. Then we have drawn a correlation matric heatmap to investigate our univariate selected feature with Extra Tree Classifier. In the subsequent step which is Data visualization, we have carried out some statistical analysis on our dataset like Gender V/s Target, Cholesterol V/s Target, Chest Pain V/s Target, ClusterMap, etc. We have performed the analysis of the Cardiac Disease patient dataset with proper data pre-processing. In pre-processing, we have checked the missing values, noisy data. Then, use different ML models were trained. The predictions are performed with Logical Regression, K-Nearest Neighbor, Decision Tree, Random Forest, Support Vector Machine, etc. A detailed description of each step is given below. The proposed methodology has nine main steps and nineteenth sub-steps to predict Cardiac Disease. Figure 01 has shown the flow chart of our methodology.


Health
Examination Data
Include CCD before data Cleaning
Data Description
Describe , Null Value, Data Profiling
Data Pre-processing
Data Visualization
Data Analysis
Feature Selection
1. Univariate Selection
2. Feature Importance
3. Correlation Matrix with HeatMap
1. Divide Patients into 2 groups by their heart Condition
2. Apply Logistic Regression, Naive bayes, SVM, KNN, Random Forest, Desision tree, XGBoost, Heatmap Clustring Analysis
Training Group 80% Data
Validation Group 20% Data
Model Evaluation
Prediction of CCD
Visualication of CCD Clustring in Heatmap
Coefficients, Analysis, Conclusion on Result

Data collection

We have collected the dataset from the city hospital; the name of the Dataset is Heart Disease Data (Comprehensive). The heart disease dataset consists of 15 heart features (name, age, gender, chest pain, sweating, palpitation, dm, htn, smoking, family history, cholesterol, triglycerides, and one target class. Our dataset has a total of 379 samples of Cardiac Disease patients. Below Figure 02 shows the details of a dataset.



```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 378 entries, 0 to 377
Data columns (total 15 columns):
 #   Column          Non-Null Count  Dtype 
---  ------          --------------  ----- 
 0   name            378 non-null    object
 1   age             378 non-null    int64 
 2   Gender          378 non-null    int64 
 3   Chest Pain      378 non-null    int64 
 4   Sweating        378 non-null    int64 
 5   Palpitation     378 non-null    int64 
 6   Vomiting        378 non-null    int64 
 7   DM              378 non-null    int64 
 8   HTn             378 non-null    int64 
 9   smoking         378 non-null    int64 
 10  Family history  378 non-null    int64 
 11  Obesity         378 non-null    int64 
 12  cholestrol      378 non-null    int64 
 13  triglycerides   378 non-null    int64 
 14  target          378 non-null    int64 
dtypes: int64(14), object(1)
memory usage: 44.4+ KB
```

Figure 2 Dataset Detail

Dataset Description;

In previous research, there have been many conflicts regarding the description of the metadata related to Cardiac Disease. As we know, there are various categories of metadata utilized in earlier studies. We have employed the two common metadata types shown below.

Description – Meta Data - 01

This type of Meta Data Description is a clean, well understand set of records. Anyhow the significance of some of the attributes is not much clear. Let’s see the meaning of;

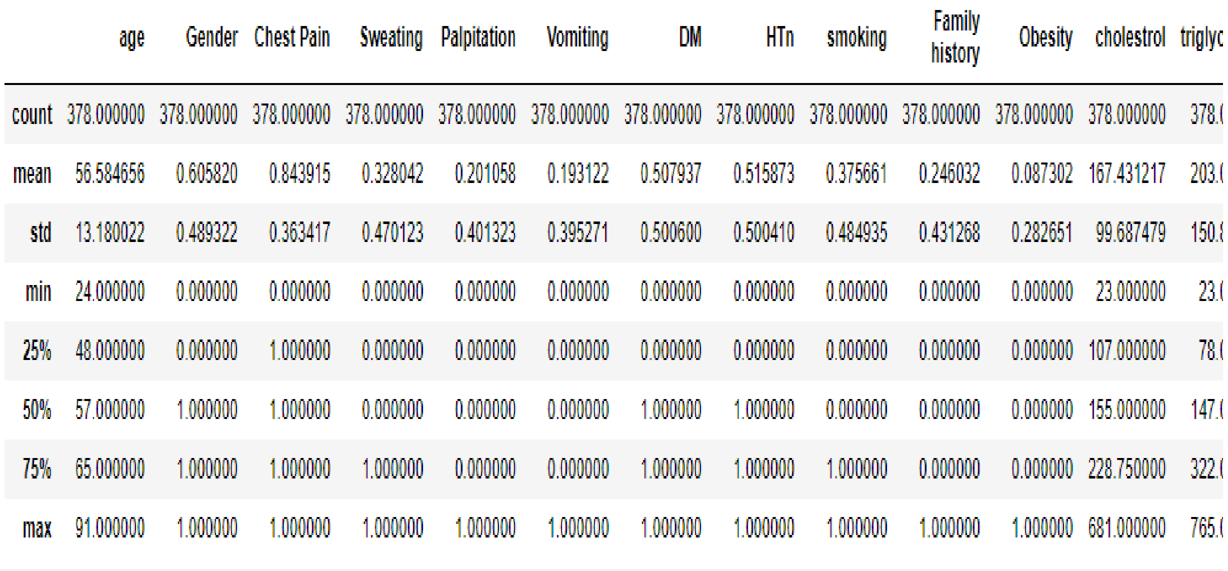
- Age: How much person’s old now in terms of years
- Gender: Differentiate between Male and Female in term of (1 = Male, 0 = Female)
- cp: The experience of Chest Pain (typical angina is related to Value 01, atypical angina is related to Value 02, non-anginal pain is related to Value 03, asymptomatic is related to Value 04)
- chol: The Cholesterol amount in a person's body in terms of MG/DL

- restecg: This is the measurement of resting electrocardiographic in-person body (1 = normal, 2 = ST – T wave abnormality, 3 = probable)
- smoking: The smoking-related values are (Yes is 1, No is 0)
- target: This is the attribute, which classifies Cardiac Disease (Yes is 1, No is 0)

Our research use Description – Meta Data 01 with the complete details of this attribute to understand it.

Description – Meta Data -02

- target: This is the identification of Cardiac Disease
    - Val 0: No
    - Val 1: Yes
- smoking: This is the smoking value
    - Val 0: No
    - Val 1: Yes
- cp: This is chest pain type
    - Val 1: Asymptomatic
    - Val 2: Atypical Angina
    - Val 3: Non-anginal Pain
    - Val 4: Typical Angina



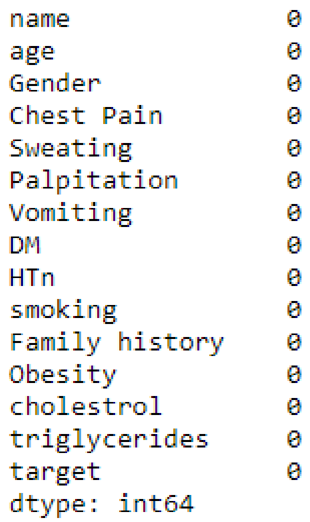
	age	Gender	Chest Pain	Sweating	Palpitation	Vomiting	DM	HTn	smoking	Family history	Obesity	cholestrol	triglyc
count	378.000000	378.000000	378.000000	378.000000	378.000000	378.000000	378.000000	378.000000	378.000000	378.000000	378.000000	378.000000	378.
mean	56.584656	0.605820	0.843915	0.328042	0.201058	0.193122	0.507937	0.515873	0.375661	0.246032	0.087302	167.431217	203.
std	13.180022	0.489322	0.363417	0.470123	0.401323	0.395271	0.500600	0.500410	0.484935	0.431268	0.282651	99.687479	150.
min	24.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	23.000000	23.
25%	48.000000	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	107.000000	78.
50%	57.000000	1.000000	1.000000	0.000000	0.000000	0.000000	1.000000	1.000000	0.000000	0.000000	0.000000	155.000000	147.
75%	65.000000	1.000000	1.000000	1.000000	0.000000	0.000000	1.000000	1.000000	1.000000	0.000000	0.000000	228.750000	322.
max	91.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	681.000000	765.

Figure 3 Describe Dataset Attributes

Figure 03 is showing the details of our Dataset in terms of the total number of records (379), Find out the mean, Standard deviation, Min value, Max value, 25%, 50%, 75% Percentage of the Dataset.

Null Value

In this step, we need to identify the missing values in each attribute of the dataset. Figure 4 below illustrates that there are no null values present in any of the attributes.



```
name              0
age               0
Gender            0
Chest Pain        0
Sweating          0
Palpitation       0
Vomiting          0
DM                0
HTn               0
smoking           0
Family history    0
Obesity           0
cholestrol        0
triglycerides     0
target            0
dtype: int64
```

Figure 4 Null values in Dataset

We utilized a widely-used Heat Map tool to identify any null values in the dataset's attributes. To achieve this, we employed the Seaborn library to create a bar graph representing the null values. Figure 5 illustrates the results of the Heat Map, which indicates that there are no null values present in any of the dataset's attributes.

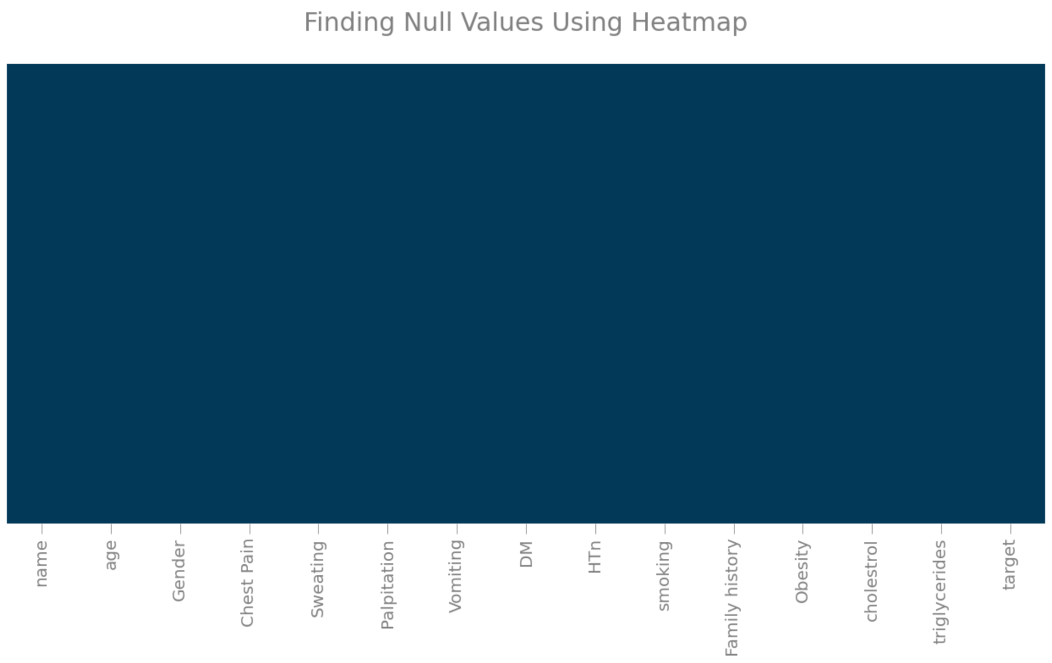


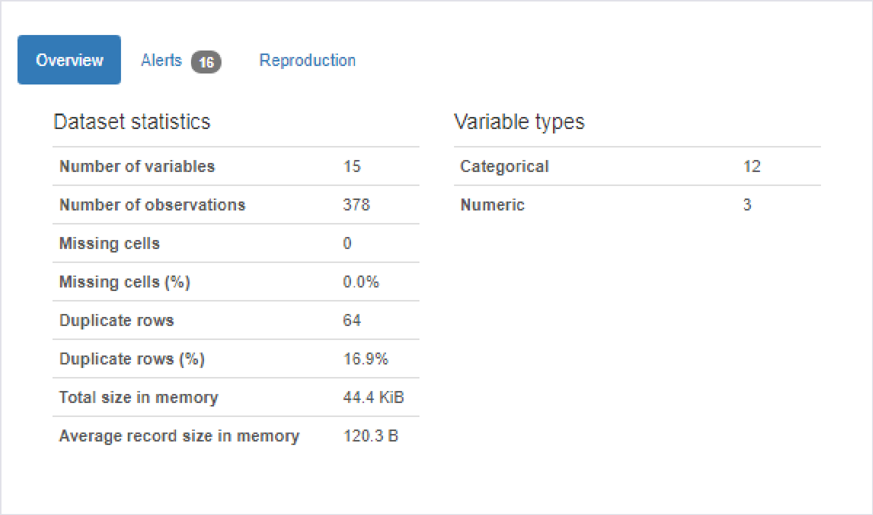
Figure 5 Heat Map Result for Null Values

Data Profiling

We have used the Pandas Profiling Library to further description of our dataset in terms of Overview, Variables, Missing Value, Correlations.

Overview

The dataset statistics indicate that there are no missing values in any of the attributes, resulting in a 0.0% missing value percentage. There are a total of 15 attributes, with 13 serving as input variables and 1 designated for classification or results. The ratio of duplicate rows stands at 5.5% of the total. Our dataset comprises two types of attributes: 14 with a numeric data type and 1 with a categorical data type.



Dataset statistics

Number of variables	15
Number of observations	378
Missing cells	0
Missing cells (%)	0.0%
Duplicate rows	64
Duplicate rows (%)	16.9%
Total size in memory	44.4 KiB
Average record size in memory	120.3 B

Variable types

Categorical	12
Numeric	3

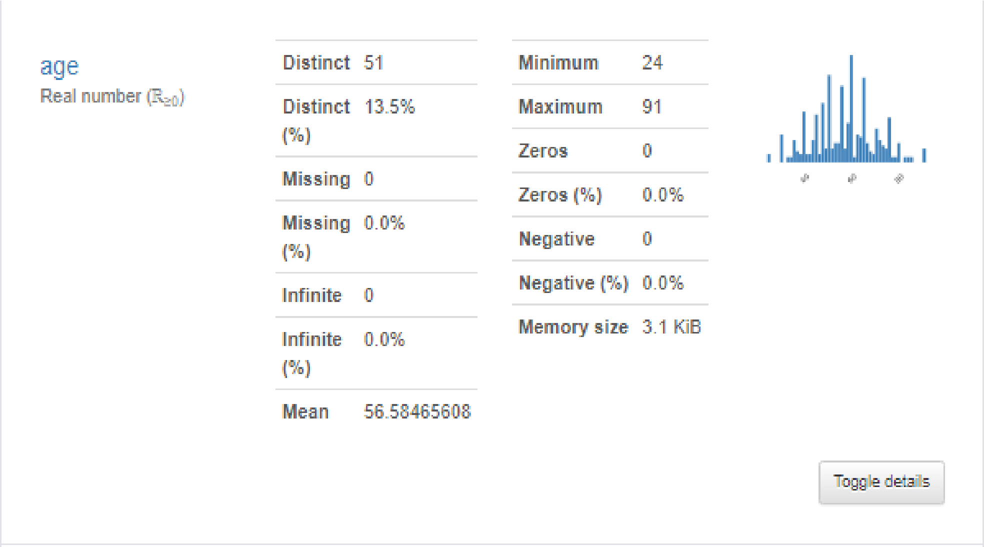
Figure 6 Overview of Dataset

Variables

In this section, we have a detailed view of each attribute of the dataset.

Age Attribute

The data profiling indicates that the age attribute contains 56 unique records. The ratio of distinct ages is 13.5% of the total. There are no missing values in the age attribute, which stands at 0.0%. The average value for this variable is approximately 56.58465608.



age

Real number ($\mathbb{R}_{\geq 0}$)

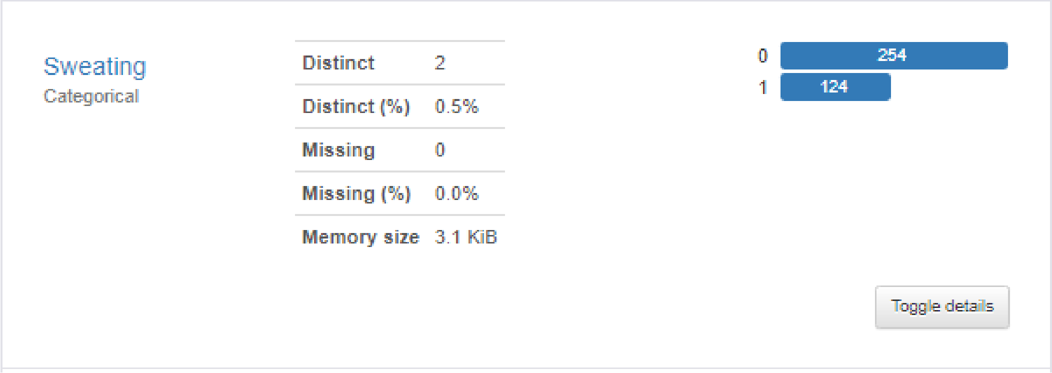
Distinct	51
Distinct (%)	13.5%
Missing	0
Missing (%)	0.0%
Infinite	0
Infinite (%)	0.0%
Mean	56.58465608

Minimum	24
Maximum	91
Zeros	0
Zeros (%)	0.0%
Negative	0
Negative (%)	0.0%
Memory size	3.1 KiB

Figure 7 Age Variable Details

Sweating

The data profiling indicates that the Sweating attribute contains 2 unique records. The ratio of distinct sweating is 0.5% to 100%. There are no missing values in the sweating attribute.



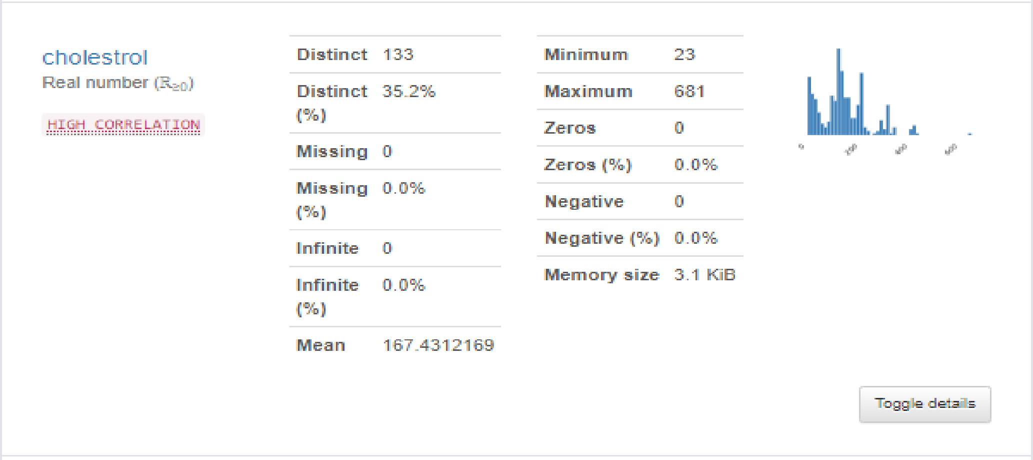
Sweating
Categorical

Distinct	2
Distinct (%)	0.5%
Missing	0
Missing (%)	0.0%
Memory size	3.1 KiB

Figure 8 Sweating Variable Details

Cholesterol

The Data Profiling indicates that the cholesterol attribute contains 133 distinct records. The ratio of distinct cholesterol values is 35.2% to 100%. This cholesterol type is a numeric attribute, with values ranging from 681 to 23. There are no missing values in the cholesterol attribute, which stands at 0.0%. The mean value for this variable is 167.4312169.



cholestrol
Real number ($\mathbb{R}_{\geq 0}$)

HIGH CORRELATION

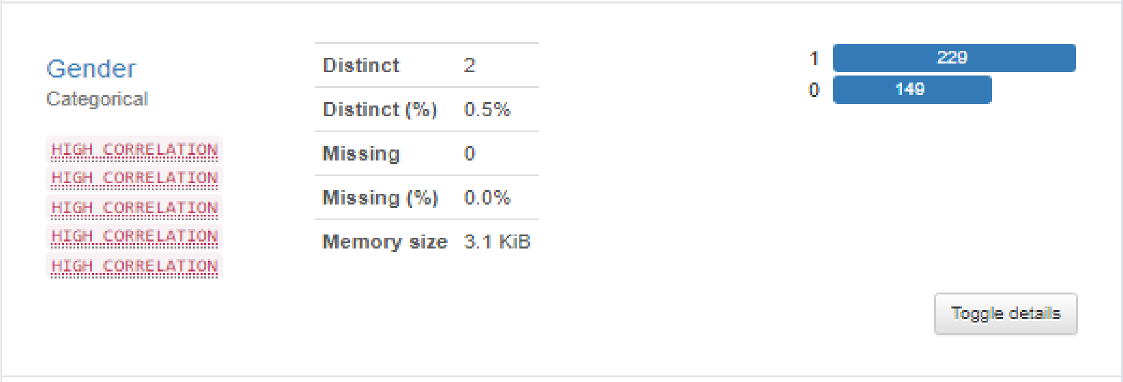
Distinct	133
Distinct (%)	35.2%
Missing	0
Missing (%)	0.0%
Infinite	0
Infinite (%)	0.0%
Mean	167.4312169

Minimum	23
Maximum	681
Zeros	0
Zeros (%)	0.0%
Negative	0
Negative (%)	0.0%
Memory size	3.1 KiB

Figure 9 cholesterol type variable Details

Sex (Gender)

The Data Profiling indicates that the Sex attribute contains 2 distinct records. The ratio of distinct Sex is 0.5% for females and 100% for males. This attribute is categorical, with 0 representing females and 1 representing males. Out of the 379 records, 229 are classified as type 0 (females) and 149 as type 1 (males).



Gender
Categorical

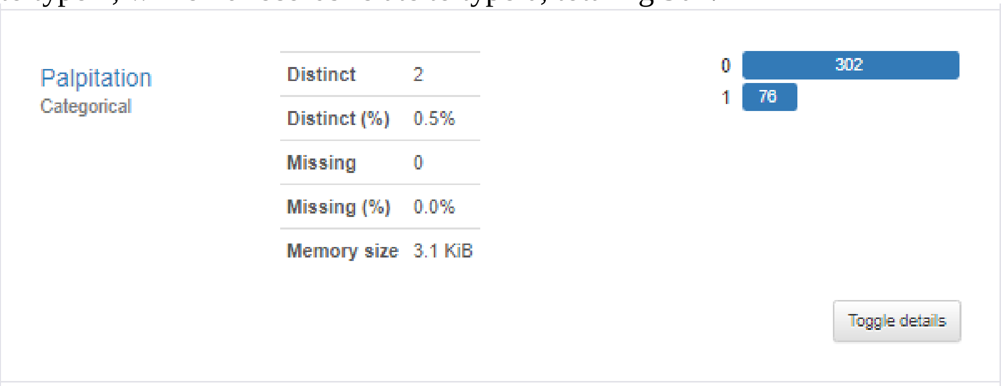
HIGH CORRELATION
HIGH CORRELATION
HIGH CORRELATION
HIGH CORRELATION
HIGH CORRELATION

Distinct	2
Distinct (%)	0.5%
Missing	0
Missing (%)	0.0%
Memory size	3.1 KiB

Figure 10 Gender variable Details

Palpitation

The Data Profiling indicates that the Palpitation attribute contains 2 distinct records. The ratio of distinct Sex is 0.5% to 100%. Palpitation is a categorical attribute with two values: 0 and 1. The record 379 corresponds to type 1, while 76 records relate to type 0, totaling 302.



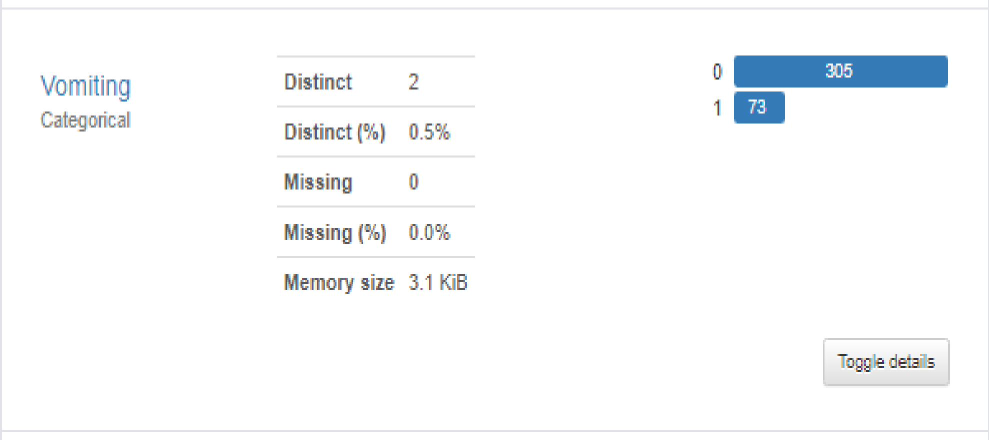
Palpitation
Categorical

Distinct	2
Distinct (%)	0.5%
Missing	0
Missing (%)	0.0%
Memory size	3.1 KiB

Figure 11 Palpitation variable Details

Vomiting

The Data Profiling is showing that the vomiting attribute has a 02 distinct record in it. The ratio of distinct vomiting is 0.5%:100%. The vomiting is a Categorical attribute. The 379 record is presenting type 1: 305 records is relating to type 0:73.



Vomiting
Categorical

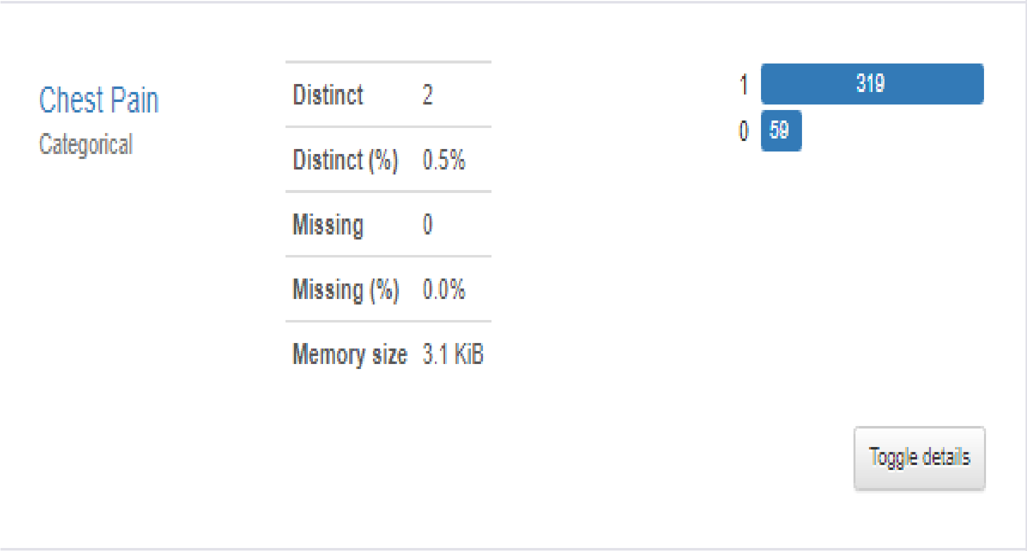
Distinct	2
Distinct (%)	0.5%
Missing	0
Missing (%)	0.0%
Memory size	3.1 KiB

Figure 12 Vomiting Attribute Details

Chest Pain (chest_pain)

The Data Profiling is showing that the chest_pain attribute has a 02 distinct record in it. The ratio of distinct chest_pain_type is 0.5%:100%. The chest_pain_type is a Categorical attribute. The 379 record is presenting type 1: 319 records is relating to type 0:59.

Figure 13 chest_pain Variable Details



Chest Pain
Categorical

Distinct	2
Distinct (%)	0.5%
Missing	0
Missing (%)	0.0%
Memory size	3.1 KiB

Missing Values

Mathematics and statistics define missing data as the absence of stored records in any attribute of a dataset during observation. Figure 15 illustrates that when 20% of the records are read from the dataset, which amounts to 75 out of 378, there are no missing values in any attribute. Similarly, when 40% of the records are read, totaling 151 out of 378, again, there are no missing values in any attribute. This pattern holds true for other percentages as well. Therefore, the data profiling of our dataset indicates that there are no missing data or values present.

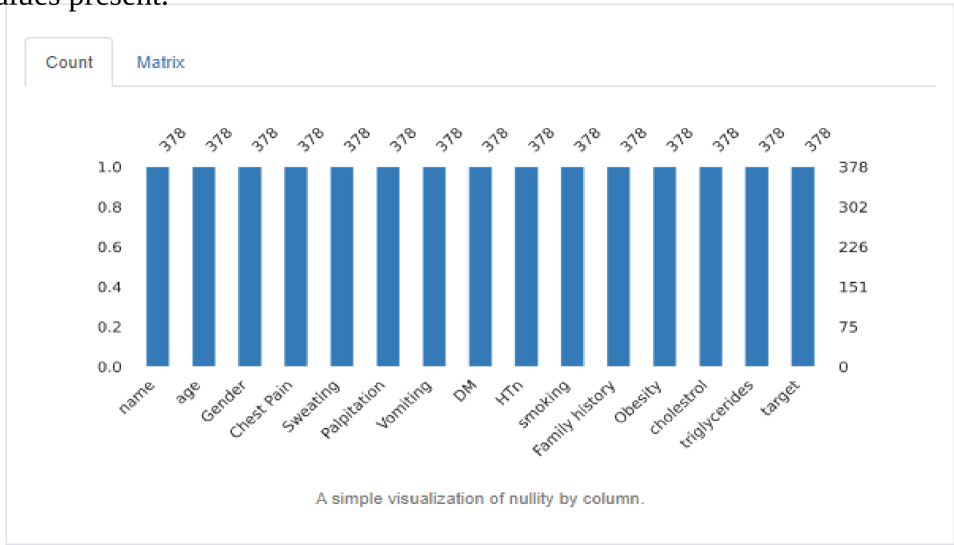


Figure 15 Missing Values

Correlation

We utilized the Phik (k) correlation coefficient to assess the relationship with the property of Cardiac Disease. Phik (k) serves as a tool for calculating correlation coefficients. In our analysis, we found that smoking has a nonlinear relationship with the target attribute. Conversely, factors such as chest pain, vomiting, perspiration, sex, age, palpitations, and obesity show a linear dependence in identifying Cardiac Disease. Phik (k) effectively measures the nonlinear dependencies among ordinal, numeric, interval, and categorical variables.

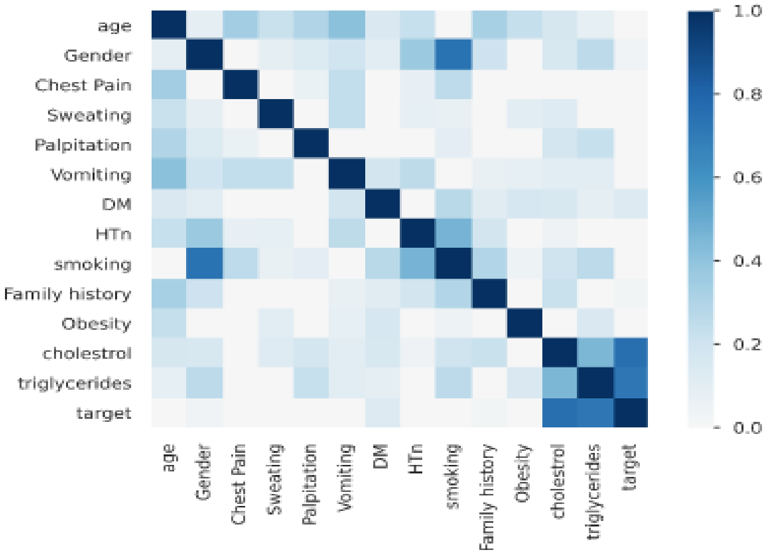


Figure 16 Correlation between Data By using Heat Map Tool

Data Analysis

This is our next step; we have employed a systematic approach and utilized statistical and conceptual techniques to illustrate, prove, describe, and condense our dataset, as well as to identify.

Feature Selection

To effectively build a successful model for Cardiac Disease, we need to apply machine learning techniques to reduce the number of input variables. This reduction is essential for lowering the computational cost and enhancing the model's performance. We can utilize methods such as univariate feature selection, feature enhancement, and a correlation matrix displayed as a heat map to illustrate our improvements.

Univariate Selection

This is a statistical test designed to identify key features that effectively correlate with performance variables. We utilized the SelectKBest class from the Scikit-learn library, which selects a specified number of the best features from a dataset. SelectKBest employs various statistical tests. Figure 21 illustrates a flowchart of our univariate selection methodology.

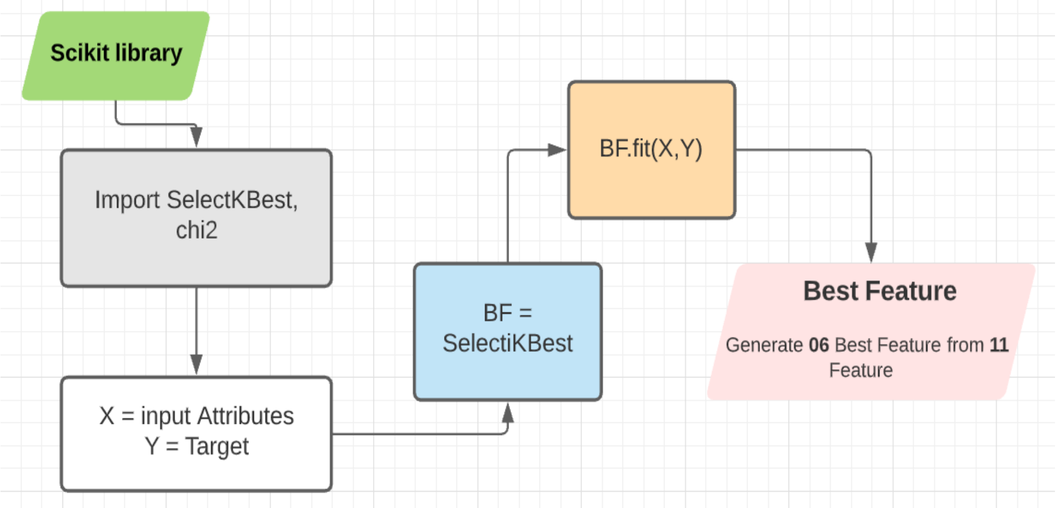
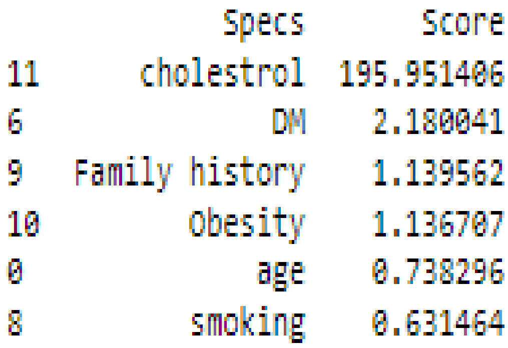


Figure 17 Univariate Feature Selection Methodology

After applying the above purpose univariate selection methodology, we have seen in Figure 16 that DM, Obesity, Smoking, Family History, age, cholesterol play an important role in reducing the model computational cost and also play role in improving model performance.



```
             Specs       Score
11      cholestrol  195.951406
6               DM    2.180041
9   Family history    1.139562
10         Obesity    1.136707
0              age    0.738296
8          smoking    0.631464
```

Figure 18 Univariate Features

Feature Improvement

To enhance our dataset, we utilized the model characteristics property. This allows us to significantly improve each feature within the dataset. The attribute value indicates the outcome for each attribute, meaning that a higher outcome signifies greater importance or usefulness in relation to the performance variable. We implemented the Extra Tree Classifier, which is a built-in class, to identify the top six features of our dataset.

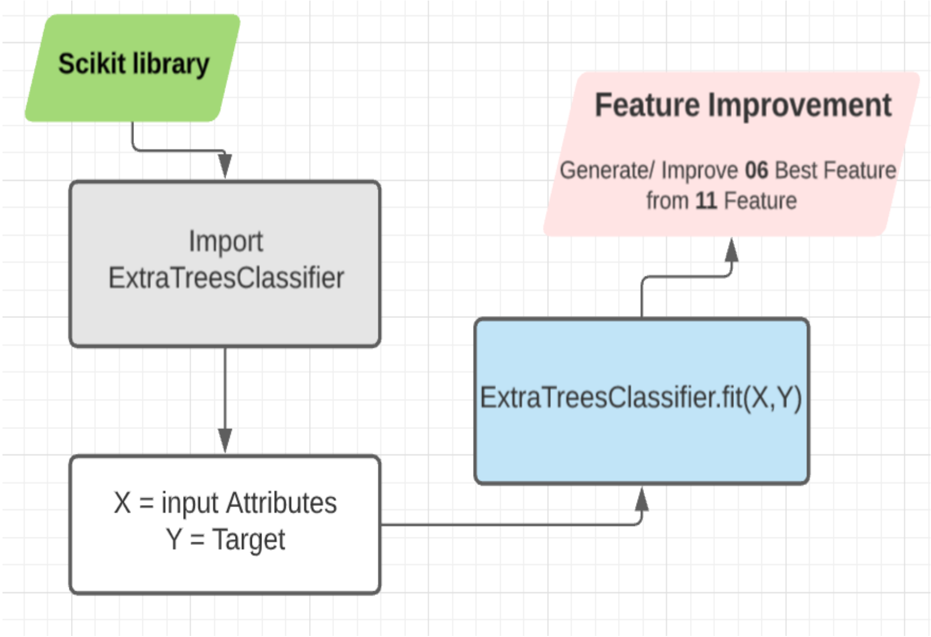
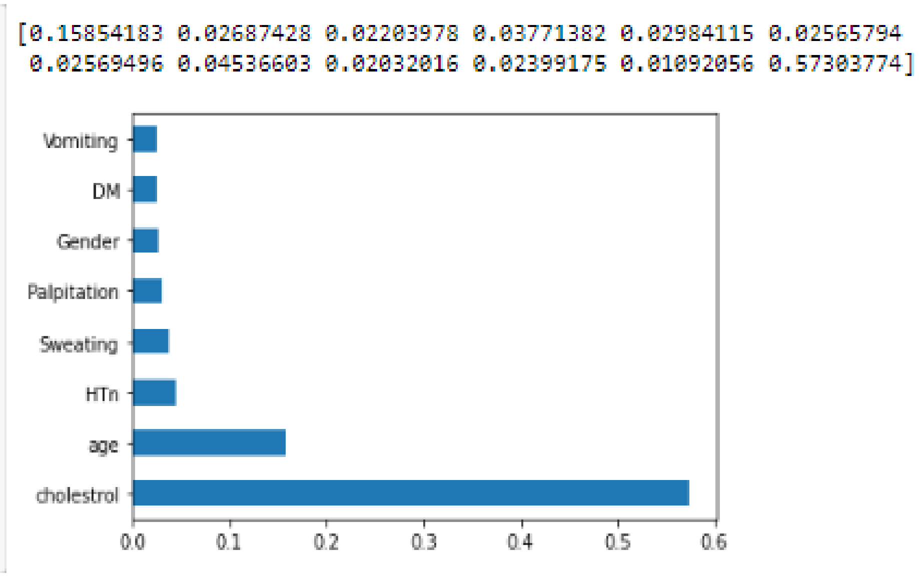

Scikit library
Import ExtraTreesClassifier
X = input Attributes
Y = Target
ExtraTreesClassifier.fit(X,Y)
Feature Improvement
Generate/ Improve 06 Best Feature from 11 Feature

Figure 19 Feature

Improvement

The below diagram shows that cholesterol, age, HTn, Sweating, Palpitation, gender, DM, Vomiting is improved as compared to early values.



```
[0.15854183 0.02687428 0.02203978 0.03771382 0.02984115 0.02565794
 0.02569496 0.04536603 0.02032016 0.02399175 0.01092056 0.57303774]
```

Figure 20 Improve Features

Correlation Matrix with Heatmap

Correlation shows how the attributes relate to the target attribute and to each other. A positive correlation means that as the value of the target variable goes up, so do the values of the features. Conversely, a negative correlation indicates that the target variable's value decreases when any of the feature values decrease. A heatmap effectively highlights which dataset attributes are most closely linked to the target attribute. We utilized the seaborn library to create the heatmap and visualize these relationships.

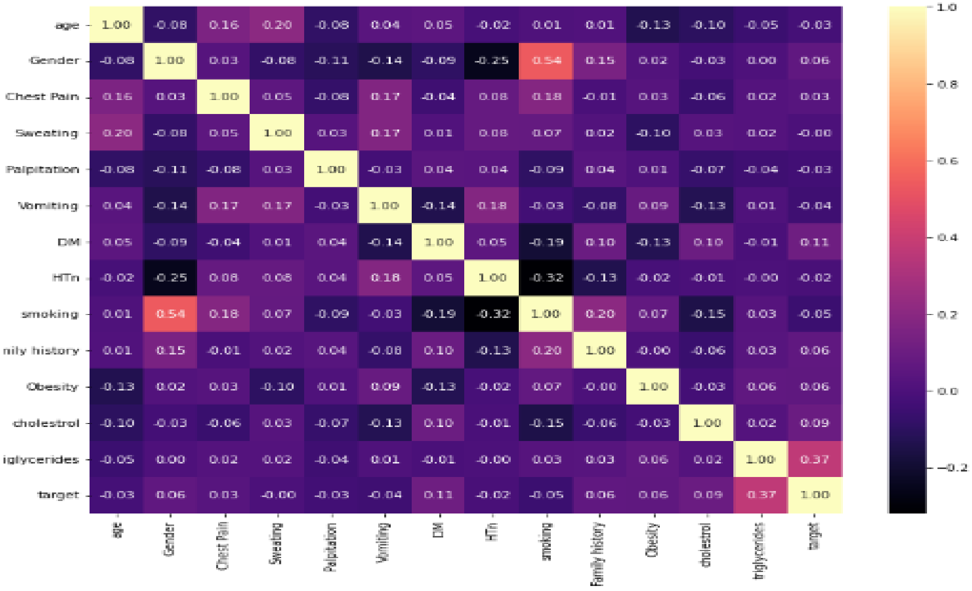


Figure 21 Correlative Matrix with heatmap

Figure 21 show that chest_pain_type, sex have a positive correlation toward the target attribute.

Data Visualization

In this step, we have illustrated various types of data visualization concerning the attributes of our dataset. We have depicted the relationships between cholesterol and resting blood pressure, chest pain and target outcomes, cholesterol and target outcomes, as well as a ClusterMap.

Chest Pain Vs Target

Figure 26 shows that most people with cardiac disease experience atypical angina chest pain. Another common type of chest pain found in patients is typical angina. Asymptomatic chest pain is a less common type of chest pain.

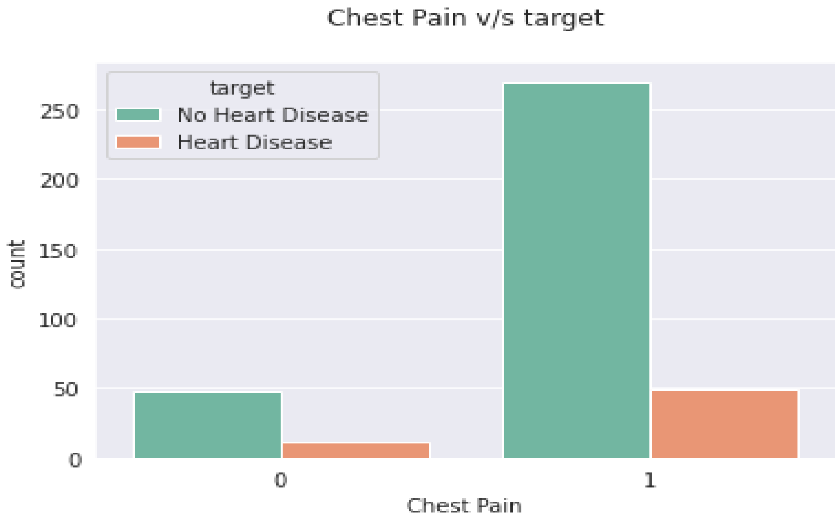


Figure 22 Chest Pain Vs Target

Gender Vs Target

Figure 23 shows that the high ratio of Cardiac Disease found in males as compared to females.

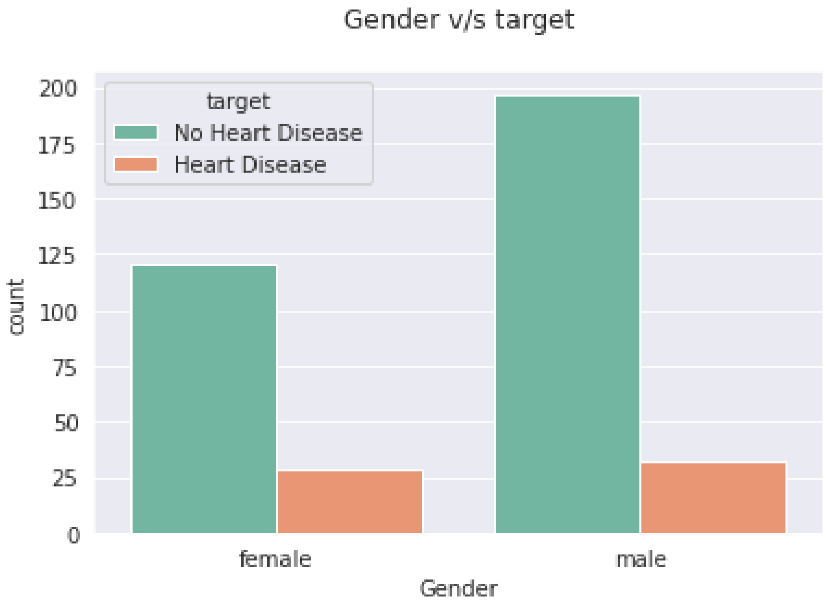


Figure 23 Gender Vs Target

Sweating Vs Target

Figure 24 shows that the high ratio of Cardiac Disease found in sweating.

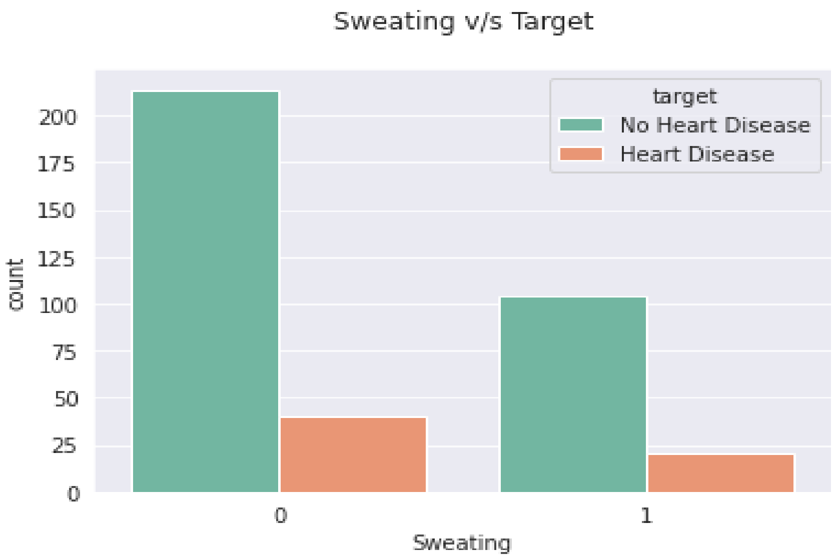


Figure 24 Sweating Vs Target

Cholesterol Vs Target

Figure 25 shows that most of the people, who have Cardiac Disease suffering from 120 mg/dl to 140 mg/dl. People, who have cholesterol levels below 90 mg/dl are suffering from some

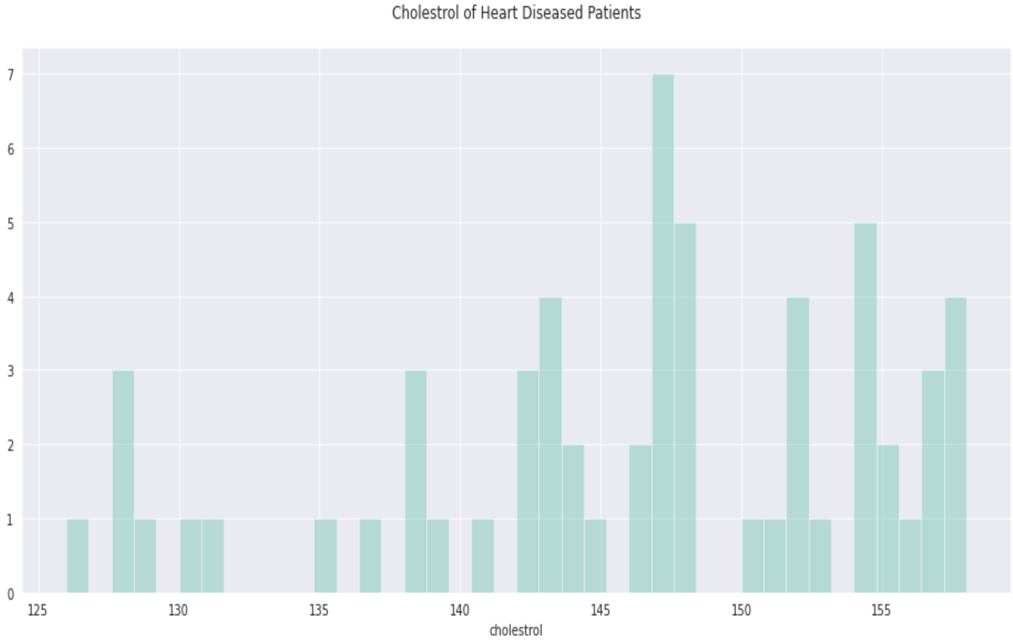


Figure 25 Cholesterol Heart Disease Patients

Cholesterol Vs Age

Medical scientists have evidence that when a person is dealing with multiple health issues, such as high cholesterol levels and age, these conditions can collectively heighten the risk of cardiac disease. Figure

26 below illustrates that if cholesterol levels fall between 120 mg/dl and 140 mg/dl, there is a significant likelihood that the individual may experience cardiac disease.

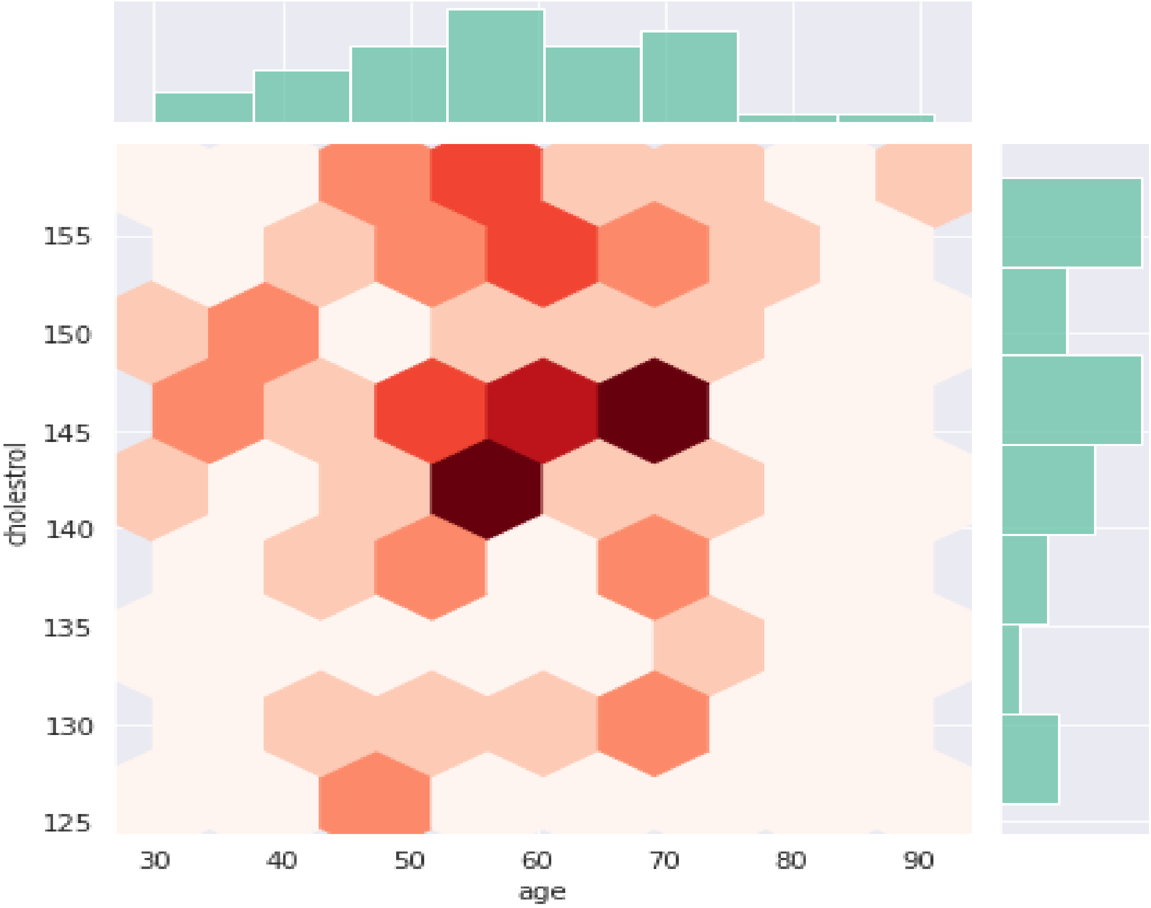


Figure 26 Cholesterol Vs Age

Cluster Map

The cluster map related to the target is illustrated in Figure 31. The cluster heatmap effectively highlights the dataset's attributes that are most closely linked to the target attribute. We utilized the seaborn library to create the heatmap showcasing these associated attributes. As shown in Figure 31, HTn, smoking, obesity, chest pain, and sex all exhibit a positive correlation with the target attribute.

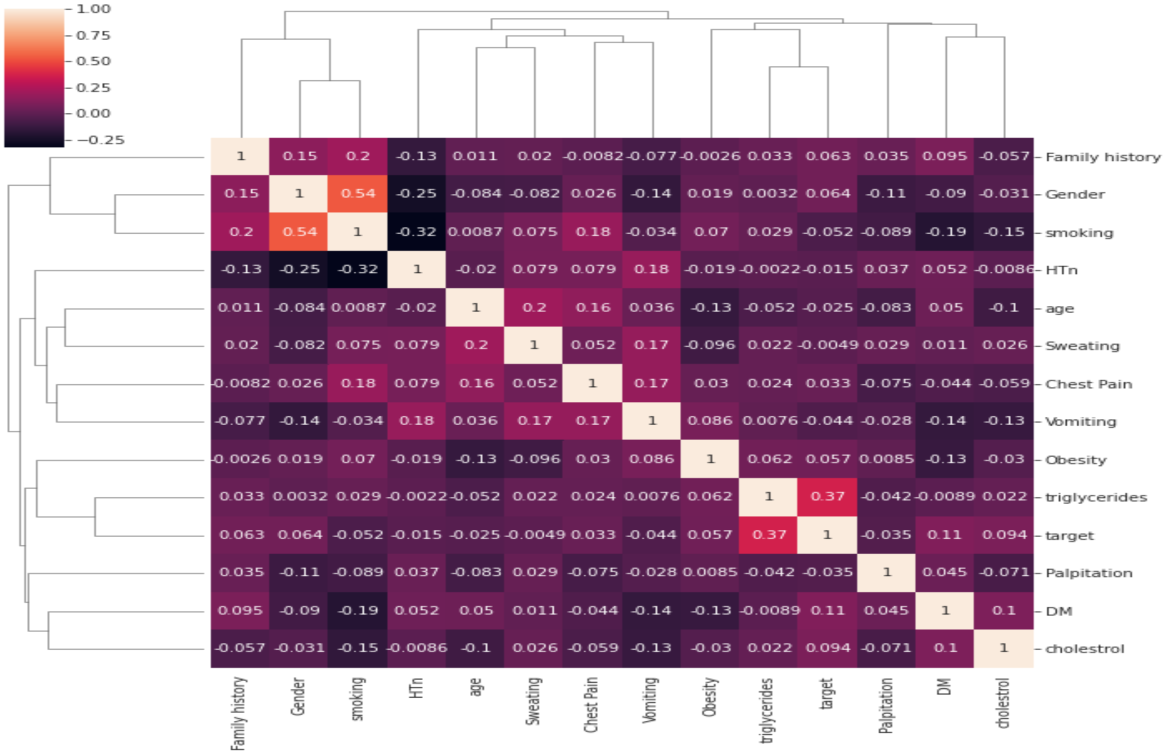


Figure 27 Cluster Map

A heatmap will be utilized to visualize the stages of patients identified through classification. This heatmap provides an interactive way to display individual values in a matrix, featuring color-coded grids and clustering for both columns and rows. Clustering will be employed to categorize a group of patients based on their health status. Patients will be sorted into various clusters using the hierarchical clustering method. (Wilkinson and Friendly, 2009)

Pre-Processing:

Preprocessing is a crucial step where we will exclude normal patients from the health examination data and focus on CCD patients using a specific algorithm. We will eliminate variables that have missing values and address any missing data using an algorithm if necessary. We will utilize various machine learning algorithms and compare their accuracy rates.

Train & Test Data Split

For data splitting, we have used the Scikit library and with the help of the train_test_split header file, we have divided the dataset into 80:20 ratios.

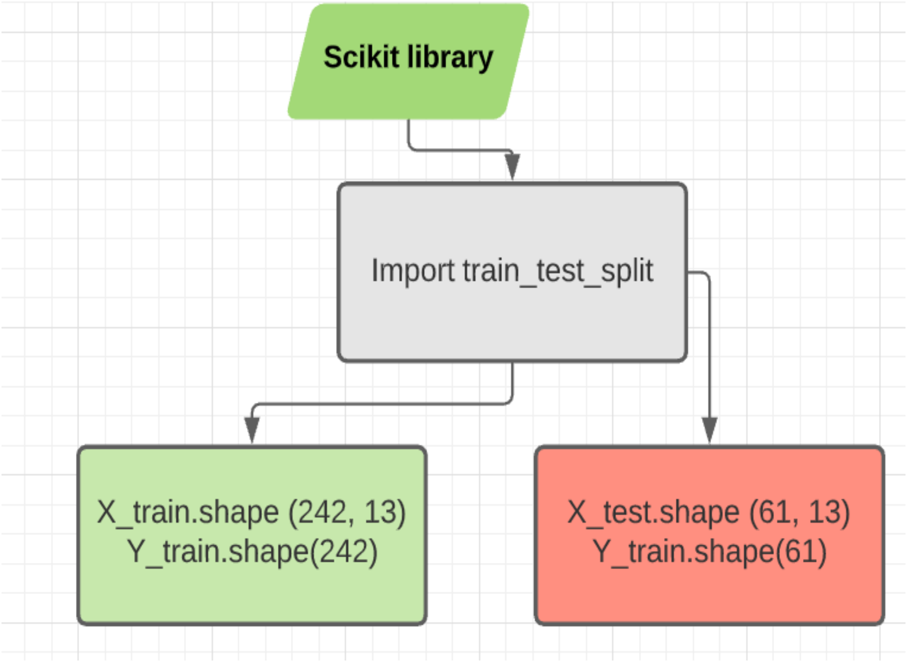


Figure 28 Train & Test Data Split

Logistic Regression

For Logistic Regression, we utilized the Scikit-learn library and, with the LogisticRegression module, we achieved an accuracy score of 81.58%.

Naïve Bayes

For Naïve Bayes, we utilized the Scikit library and, with the assistance of the GaussianNB header file, we achieved an accuracy score of 97.37% using Naïve Bayes.

Support Vector Machine

For our Support Vector Machine implementation, we utilized the Scikit-learn library and, with the SVM module, we achieved an accuracy score of 86.84%. In this experiment, we employed a linear kernel.

K Nearest Neighbors

For K Nearest Neighbors, we utilized the Scikit library and, with the assistance of the KneighborsClassifier header file, we achieved an accuracy score of 93.42% using Support Vector Machine.

Decision Tree

For our Decision Tree analysis, we utilized the Scikit library and employed the DecisionTreeClassifier. As a result, we achieved an impressive accuracy score of 97.37%.

Random Forest

For Random Forest, we utilized the Scikit library and, with the RandomForestClassifier module, we achieved an accuracy score of 100% using the Decision Tree method.

XGBoost

For XGBoost, we utilized the Scikit library and, with the assistance of the XGBClassifier header file, achieved an accuracy score of 96.05%. Figure 29 displays the graphical representation of the algorithms.

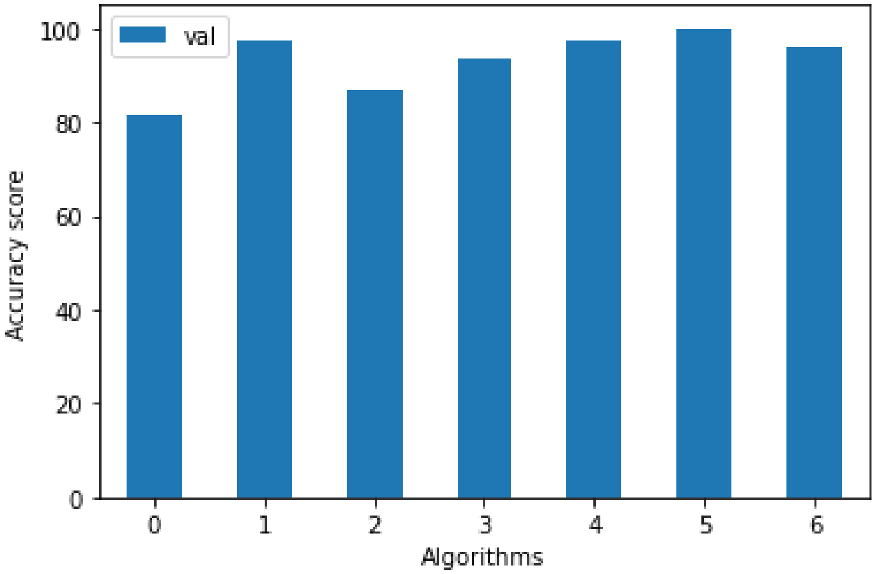


Figure 29 Machine Learning Algorithm Comparison

Discussion:

Our analysis highlights the effectiveness of predictive Machine Learning algorithms in developing health management systems and facilitating quick predictions of Cardiac Disease through component studies of a dataset. This study summarizes the results of various data visualizations, particularly focusing on cholesterol levels, maximum heart rate, chest pain types, resting blood pressure, and fasting blood sugar in relation to the target. We applied different Machine Learning algorithms to the dataset to identify the most effective predictive model. Our findings indicate that we need to assess the impact of specific publications that are statistically significant. The results illustrate the relationships between cholesterol levels and chest pain types, resting blood pressure and fasting blood sugar, among others, in the context of Cardiac Disease. The Random Forest algorithm has demonstrated superior performance in predicting Cardiac Disease compared to other Machine Learning methods. However, there is still room for improvement within the Random Forest algorithm. This issue is often referred to as publication bias, and it remains challenging to eliminate any research bias in today's landscape, as many factors contribute to the seriousness of this bias.

Conclusion and Future Work

We have utilized a range of statistical methodologies on our dataset, including Logistical Regression, Naive Bayes, Support Vector Machine, K-Nearest Neighbor, Decision Tree, Random Forest, and XGBoost machine learning techniques. Among these, only the Random Forest model yielded satisfactory results. Our goal was to create an automated health care management model for predicting Cardiac Disease in patients, which we believe will effectively help in preventing such diseases. We performed various statistical analyses, such as Heatmap Clustering and Cholesterol vs. Target assessments, to pinpoint the most significant features associated with Cardiac Disease in patients. Our predictive model aims to support doctors and physicians in making accurate diagnoses of Cardiac Disease.

Looking ahead, we intend to explore which types of chest pain have a more pronounced effect on human health and what factors contribute to this. Besides the Cluster Heat Map model, we have also examined other models, though their effectiveness still needs to be confirmed. Additionally, future research will focus on determining the appropriate levels of cholesterol, maximum heart rate, and Old Peak to mitigate the risk of Cardiac Disease.

Bench Mark Comparison

Table 03 presents a comparison of the proposed model's performance against earlier research in terms of Precision, Recall, F1-Measure, and Accuracy scores on the dataset. The findings reveal that our proposed model achieves an impressive accuracy ranging from 99.93% to 99.99%. In the study by Hannan et al. (2010), the authors utilized SVM, which resulted in 50% to 60% unreliable patient outcomes, thereby reducing the model's accuracy. K et al. (2018) employed various classification algorithms, including KNN, SVM, and ANN with modifications, leading to improved results compared to previous studies. Taylor et al. (2019) achieved an accuracy of 98.83% using Decision Tree, Random Forest, and Support Vector Machine algorithms. Mohan et al. (2019) introduced a hybrid HRFLM approach that merges the advantages of Random Forest and Linear

Table 3 Performance Metrics of Proposed Model

Data Set Name	Accuracy	Recall	F-Measure	Precision
Singh and Samagh, 2020	98.96	1.00	98.90	98.90
Meng *et al.*, 2020	93.97	0.92	93.91	94.97
Mohan *et al.*, 2019	94.96	0.93	96.50	96.42
Proposed Model	99.99	1.00	99.97	99.99

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