TARC
TUNKU ABDUL RAHMAN UNIVERSITY COLLEGE
BEYOND EDUCATION

BACS2003 ARTIFICIAL INTELLIGENCE

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Assignment Documentation

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Programme: RSW2
Tutorial Class: G4
Project Title: MACHINE LEARNING(SUPERVISED): Heart Disease Prediction
Module In-Charged: RANDOM FOREST CLASSIFIER

Other team members' data

No	Student Name	Module In Charge
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3		

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1. Introduction

1.1. Problem Background

Artificial intelligence adoption has been accelerating over the past few years, and there is no doubt that AI offers a large number of benefits and prospects. Providing relevant or useful information, knowledge, research, and prediction are a few examples. Artificial intelligence and the machine learning algorithms enable prediction tasks such as the prediction of heart disease, which is the subject of our assignment. Our team created a heart disease prediction software primarily because we firmly believe that excellent health is the best investment because it allows you to do anything.

However, Malaysians have a poor level of awareness of heart illnesses. Malaysians don't seem to care about their own health, which may be because they aren't exposed to enough health information. About 80% of Malaysia's elderly may experience chronic health issues like heart attacks, which may cause premature mortality, according to research by Murat N. Through regular medical examinations that help to identify any early indications, one of the greatest methods to prevent heart disease is to do so. However, CodeBlue has conducted research on this issue and from their findings it showed that nearly half of Malaysians are lacking health coverage beyond public care. It is very clear that the number of Malaysians who undergo monthly or yearly medical checkups are significantly lower than our neighboring countries. Our chief statistician Mohd Uzir Mahidin has stated that heart diseases have remained the principal cause of death in Malaysia with an increase of 5.4% from 11.6% in 2000 to 17% in 2020. Therefore, in Malaysia it is now more important than ever to prevent heart diseases.

The high cost of medical care is one of the main reasons Malaysians do not visit the doctor. Since, there are no obvious indicators of a significant health issue, they felt they are in good condition but it's vital to remember that not all medical issues will have readily observable early signs. Our team has developed a heart disease prediction tool that helps users determine whether they are susceptible to heart illnesses or not in the spirit of the adage "prevention is better than cure". Our team has employed a supervised machine learning algorithm in our heart disease prediction programme to determine whether a user was likely to develop heart disease. In order to ensure that people are more aware of this fatal disease, a good data driven approach helps to improve the entire research and prevention process.

A prediction system can be created by analyzing large and complex amounts of data with the aid of machine learning. Age, Sex, Type of chest discomfort, Resting Blood Pressure, Cholesterol, Fasting Blood Sugar, Result of a Resting ECG, Highest Heath Rate attained during exercise, and an older peak heart rate are the factors that be used to classify people who is being at risk for getting heart disease. The 3 different algorithms included Random Forest, K-nearest neighbor and Support Vector Machine(SVM).

1.2. Objectives/Aims

The main objective of this project is to increase the awareness of heart disease among Malaysians because heart disease is one of the principal causes of death in Malaysia. The project allows the users to check if they are suffering from the risk of getting heart disease or not. The notice message will be prompt on showing whether the users are prone to heart disease or not. There is a far greater possibility that they will either be able to reverse their heart condition or take the steps to stop it from worsening.

The heart disease prediction application helps to reduce the amount of cost used by the people to undergo monthly or yearly medical checkups as the users can get a grasp on how healthy their heart is. Although the application can only be taken with a grain of salt, it still lets users get an idea on the condition of their heart. Therefore, it helps the users to plan for their medical checkup to save costs by preventing excessive medical checkups.

The adoption of machine learning for heart disease prediction helps users to save their time by knowing their heart condition without reading any relevant books, browse the internet to further find the symptoms of heart disease. The users can know whether they are prone to have heart disease or not by just need enter relevant details that are necessary into the system

1.3. Motivation

There is a saying that goes, “no human being is perfect”. Doctors might make the mistakes when they are curing a patient but the mistakes they made may lead to a worse case which is a life lost. For instance, if a person who is healthy was said to have heart disease which was diagnosed wrongly by a doctor, this human error could cause serious complications to a person’s health. With the wrong prescription of medicines, it could take a major toll on the person’s health and might lead to other complications of diseases. The easiest and cheaper solution for this problem is to create a program for avoiding the problem. Therefore, our team has created this application that uses machine learning and natural language as the algorithm to make the tasks automated and provide a highly accurate and time efficient result.

1.4. Timeline/Milestone

Task\Week	1	2	3	4	5	6	7	8	9	10	11	12
Research and choose the suitable topic												
Searching datasets												
Study the implementation of model to Machine Learning System												
Draw Flowchart												
Code implantation of Machine Learning System												
Code testing												
Report Documentation												
Submission												

2. Research Background

2.1. Background of the applications

In recent years, the world has started changing, everythings is connected to a data source and it is digitally recorded. Most of the tasks are being done automatically with the help of machine learning such as health prediction systems, stock price prediction systems and even financial prediction systems. With these prediction systems around the world, it cannot be denied that machine learning has given humans a lot of convenience in life. Machine learning is an algorithm that can automatically improve itself over time without requiring human programmers to feed in additional information. This is because after analyzing large amounts of data, Machine learning will start to modify itself in response to the data's quality and this helps to increase the precision and accuracy of the entire system overtime.

By adding and feeding Machine Learning with large amounts of medical history data, it will help to predict whether the person is prone to heart disease or not. This is because it will recognize whether the individual is having any symptoms of heart disease such as high blood pressure, old age or different levels of chest pain. Before planning for a medical checkup, users can use our application to get a grasp on what is the condition of their heart. This helps the users to save money and time.

The application utilizes the machine learning algorithms to predict whether a user is prone to heart disease. Our team has chosen 3 types of algorithms and 1 technique by combining 2 of the algorithms which are Random Forest, K-Nearest Neighbor(KNN), Support Vector Machine(SVM) and Stacking CV technique as the basis of models for improving the performance of models. The reason for implementing multiple algorithms to use is because it helps to increase the accuracy and precision of the data being fed. Before any data is being sent to the models, we will be converting all the raw data into an intelligible format which is during the data preprocessing stage. During the data preprocessing stage, missing values, cleaning of data and also normalization will be done. Therefore, the accuracy and performance of our models can be easily evaluated through a variety of performance metrics.

2.2. Analysis of selected tool with any other relevant tools

Tools comparison	**Remark**	**Jupyter notebook**	**Excel**
Type of license and open source license	State all types of license	Release under the modifier DSB 3-Clause "New" or "Revised" License	Microsoft Office License Required
Year founded	When is this tool being introduced?	First Release in 2014	1985
Founding company	Owner	Created by a team of developers and researchers from a variety of academic and industry institutions, including the University of California, Berkeley, Cal Poly San Luis Obispo, and Continuum Analytics	Microsoft Corporation
License Pricing	Compare the prices if the license is used for development and business/commercialization	Free	Office Home & Business 2021 $249.99 365 Personal Plan $69.99/year 365 Family Plan $99.99/year
Supported features	What features that it offers?	Support a variety of programming languages,	• Inserting pivot table • Sorting of tabulated

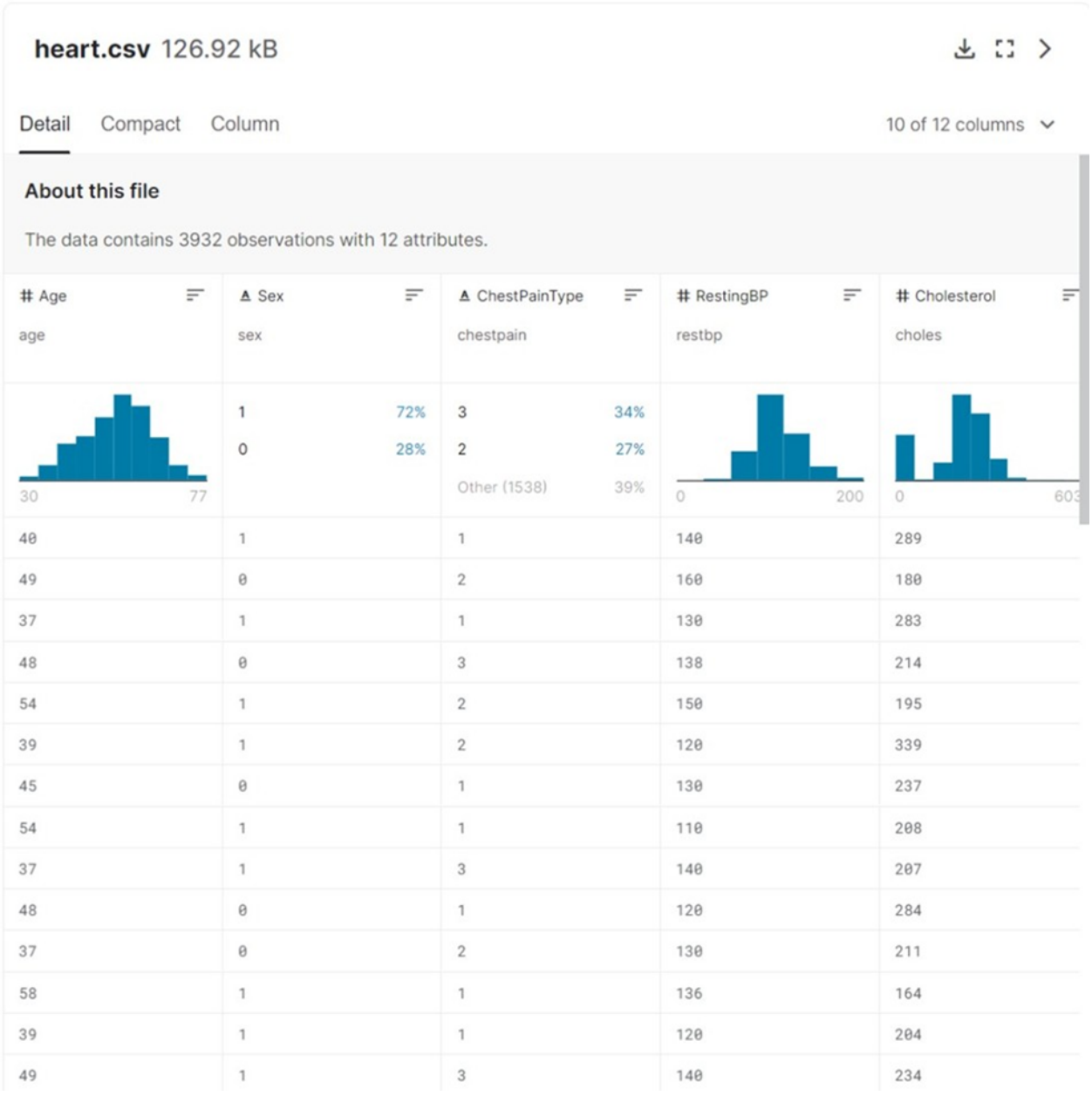
		including Python, R, Julia etc. Inline plotting, markdown cells for rich text formatting and support for interactive widgets.	data ● Visualize the data
Common applications	In what areas this tool is usually used?	Data analysis, scientific computing, and machine learning as well as for educational purposes.	Perform data analysis
Customer support	How the customer support is given, e.g. proprietary, online community, etc.	A large and active community of developers and users with online documentation, forums and resources available for troubleshooting and assistance	Microsoft support
Limitations	The drawbacks of the software	Not be well suited for large scale production deployments or highly specialized use cases. Requires some technical expertise to set up and configure for certain applications.	Hard to detect fraud / corruption

2.3. Justify why the selected tool is suitable

Tools	Reason
Jupyter notebook	● Support Python Programming Language which is used by our team to develop this machine learning project ● Allows for interactive development and testing of code, making it easy to experiment with different models and techniques ● Support inline plotting which allows for visualization of data and model performance ● Support the use of markdown cells, which allow for the inclusion of rich text and documentation within the project ● Allows the use of interactive widgets, which can provide an intuitive and user-friendly interface for inputting data and exploring model results ● Open Source and has large and active community providing access to resources and support for the project
Excel	● Preparing and cleaning data ● Used in ML by importing data from CSV(comma-separated values) files which are a common format for storing structured data.

3. Methodology

3.1. Description of dataset



heart.csv 126.92 kB

Detail Compact Column 10 of 12 columns

About this file

The data contains 3932 observations with 12 attributes.

# Age age	▲ Sex sex	▲ ChestPainType chestpain	# RestingBP restbp	# Cholesterol choles
30 77	1 72% 0 28%	3 34% 2 27% Other (1538) 39%	0 200	0 603
40	1	1	140	289
49	0	2	160	180
37	1	1	130	283
48	0	3	138	214
54	1	2	150	195
39	1	2	120	339
45	0	1	130	237
54	1	1	110	208
37	1	3	140	207
48	0	1	120	284
37	0	2	130	211
58	1	1	136	164
39	1	1	120	204
49	1	3	140	234

The heart.csv dataset was obtained through kaggle, This data is being used to build a heart disease prediction system. There are a total of 3932 rows and 12 columns in this dataset. The 12 columns are age, sex, chest pain, restbp, choles, fastbs, restecg, maxhr, exagina, oldpeak, stslope and target respectively.

Column's Name	Description
Age	Data under 28 to 77 years old
Sex	1: Male 0: Female
Chestpain	0: Typical Angina 1: Atypical Angina 2: Non-Aginal Pain 3: Asymptomatic
restbp	A range of up to 200
choles	A range of up to 600
fastbs	0: No 1: Yes
maxhr	A range from 60 to 200.
exagina	0: No 1: Yes
oldpeak	A range from 2.6 to 6.2
stslope	0: Upsloping = better heart rate with exercise(uncommon) 1: Flatsloping = minimal change(typical healthy heart) 2: Downsloping = signs of unhealthy heart
target	0:No Heart Disease 1: Heart Disease

3.2. Applications of the algorithm(s)

3.2.1 Data Representation

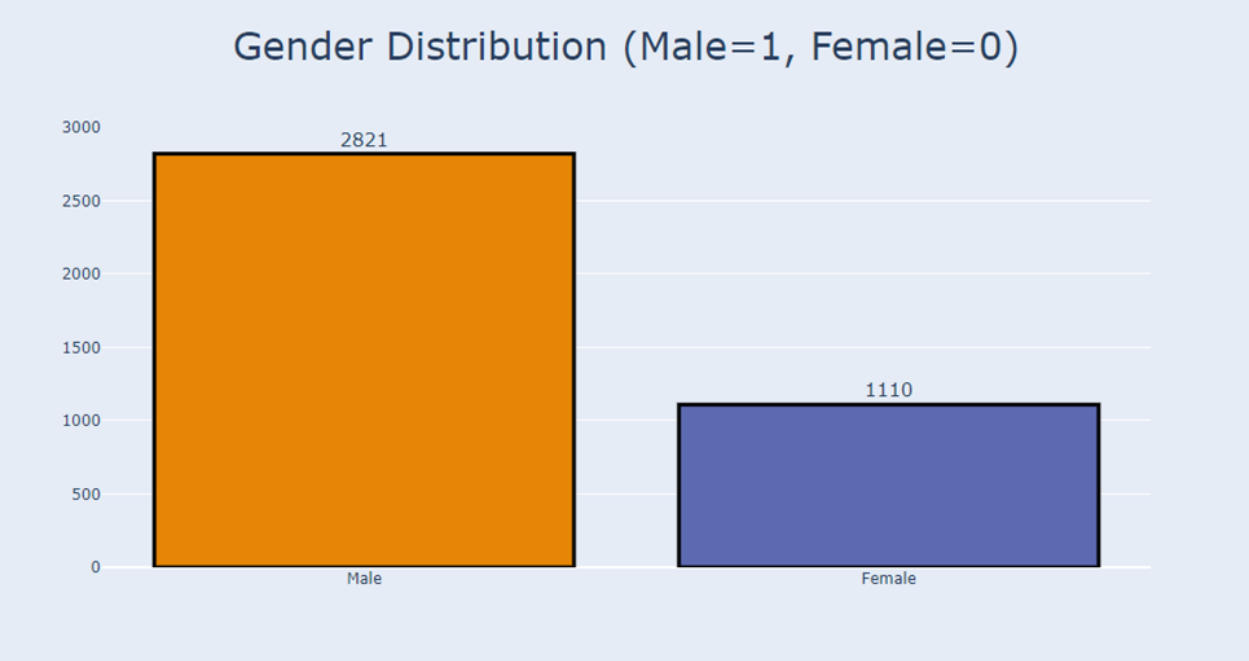


Figure 1: Bar Chart of the Gender Distribution

Figure above shows the bar chart of the gender distribution inside the dataset. The orange bar represents the number of males and the purple bar represents the number of females in the dataset. The total number of males is 2821 and the total number of females is 1110.

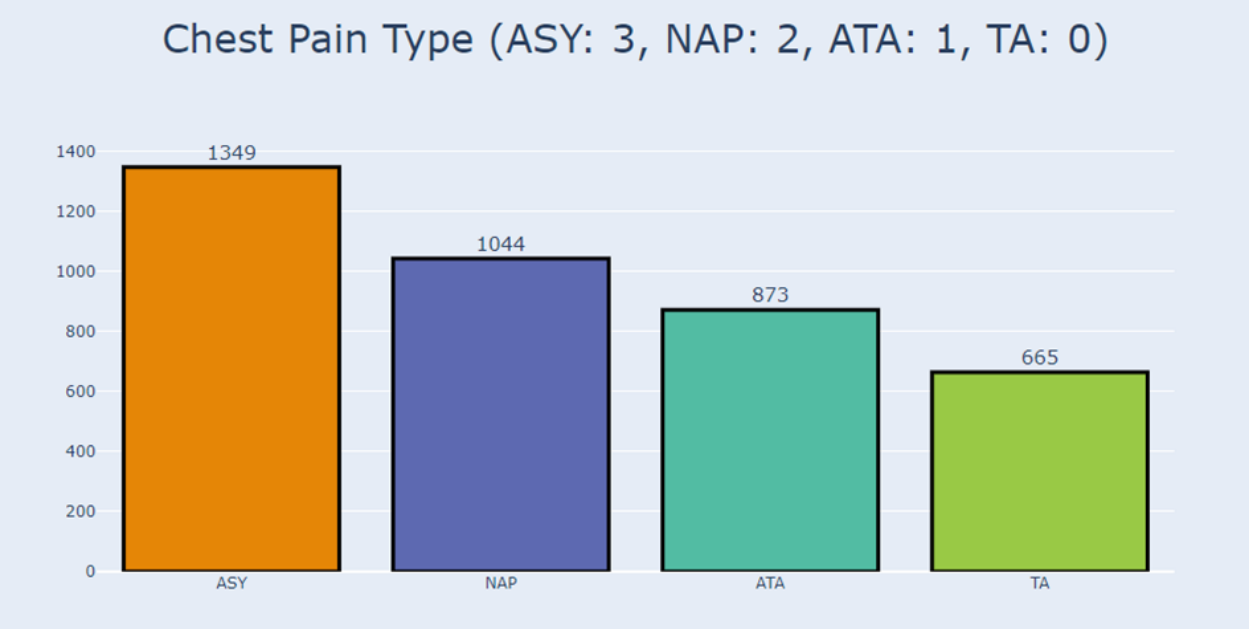


Figure 2: Bar Chart of the Chest Pain on different types

Above figure shows the bar chart of Chest Pain different types.

Orange Bar: Asymptomatic(ASY). Total = 1349

Purple Bar: Non-Anginal Pain(NAP). Total = 1044

Green Bar: Atypical Angina(ATA). Total = 873

LIght Green Bar: Typical Angina (TA). Total = 665

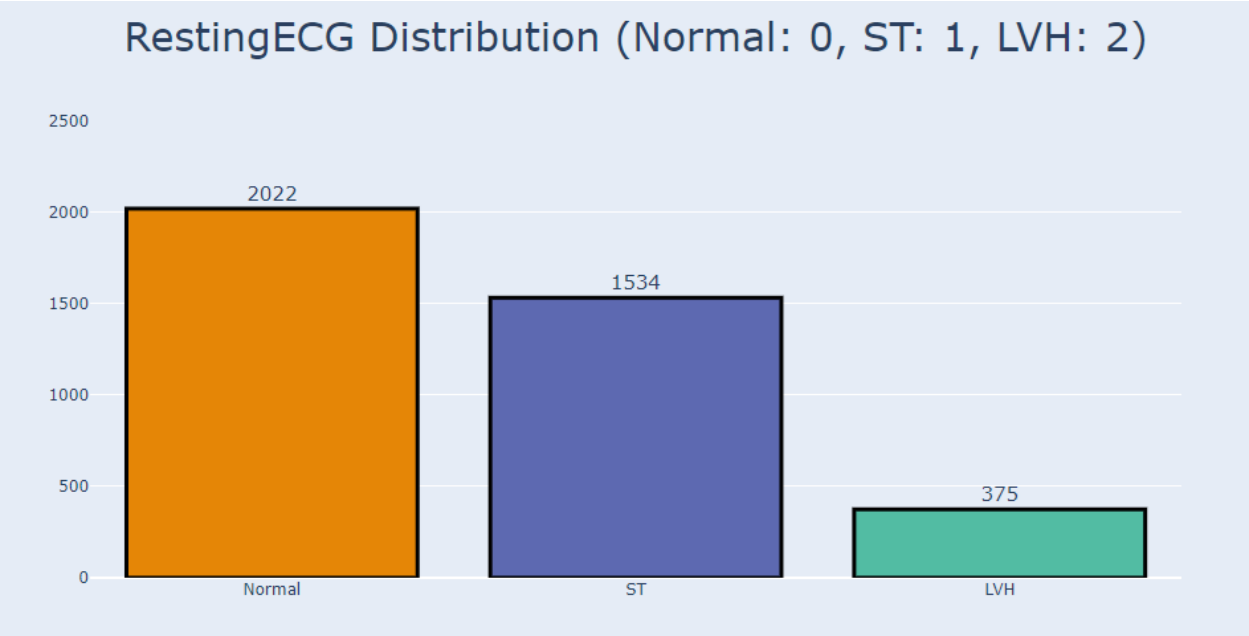


Figure 3: Bar Chart of the Resting ECG Distribution

Above figure shows the bar chart of the number of people who have the different types of resting electrocardiograms.

Orange Bar: Normal of resting electrocardiograms(Normal). Total = 2022

Purple Bar: ST-T Wave Abnormality(ST). Total = 1534

Green Bar: Left Ventricular Hypertrophy(LVH). Total = 375

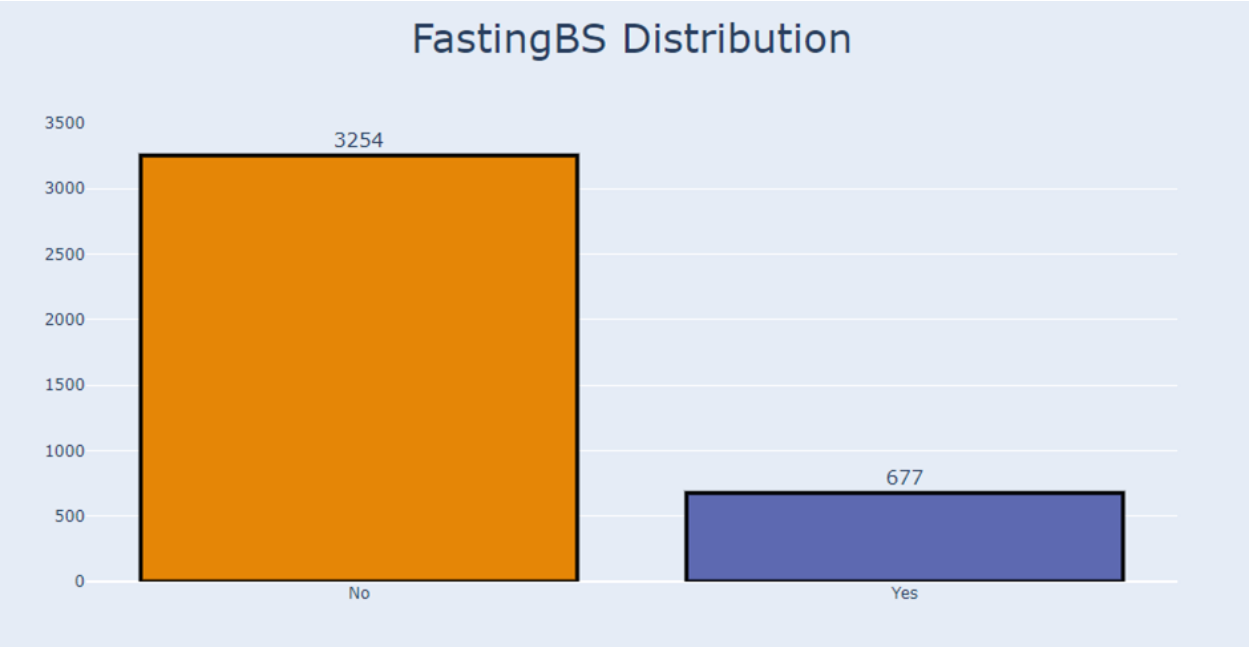


Figure 4: Bar Chart of the FastingBS Distribution

Above figure shows the bar chart of the fasting blood sugar distribution in the dataset.

Orange Bar: who have a blood sugar of less than 120 mg/dl. Total = 3254

Purple Bar: who have a blood sugar of more than 120 mg/dl. Total = 677

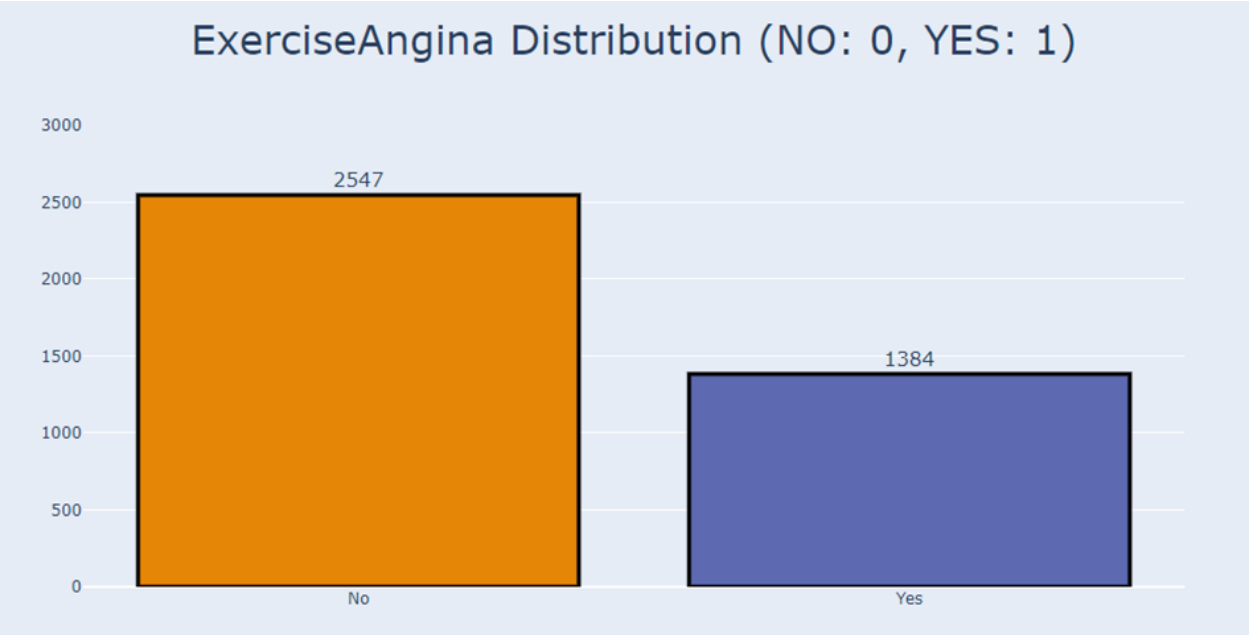


Figure 5: Bar Chart of the ExerciseAngina Distribution

Above figure shows the exercise induced angina distribution in the dataset.

Orange Bar: who do not have exercise induced angina. Total = 2574

Purple Bar: who have exercise induced angina. Total =1384

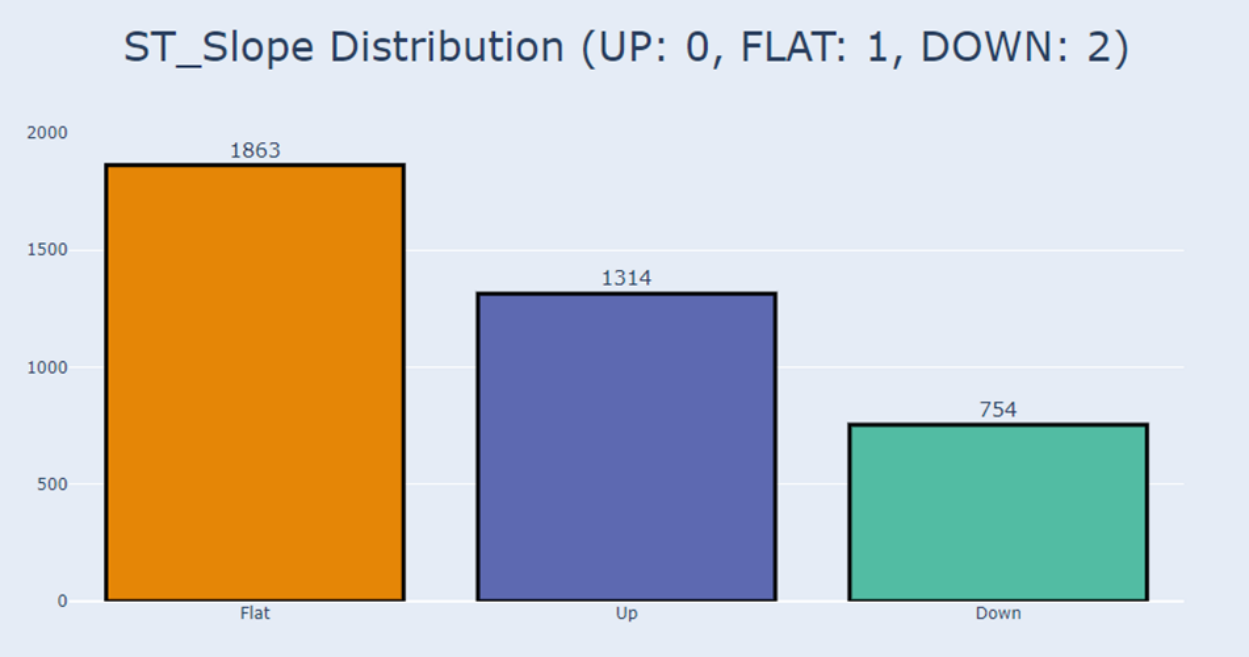


Figure 6: Bar Chart of the ST_Slop Distribution

Above figure shows the number of individuals who have different types of ST Slope in the dataset.

Orange Bar: who have a flat slope. Total = 1863

Purple Bar: who have an up slope. Total = 1314

Green Bar: who have a down slope. Total = 754

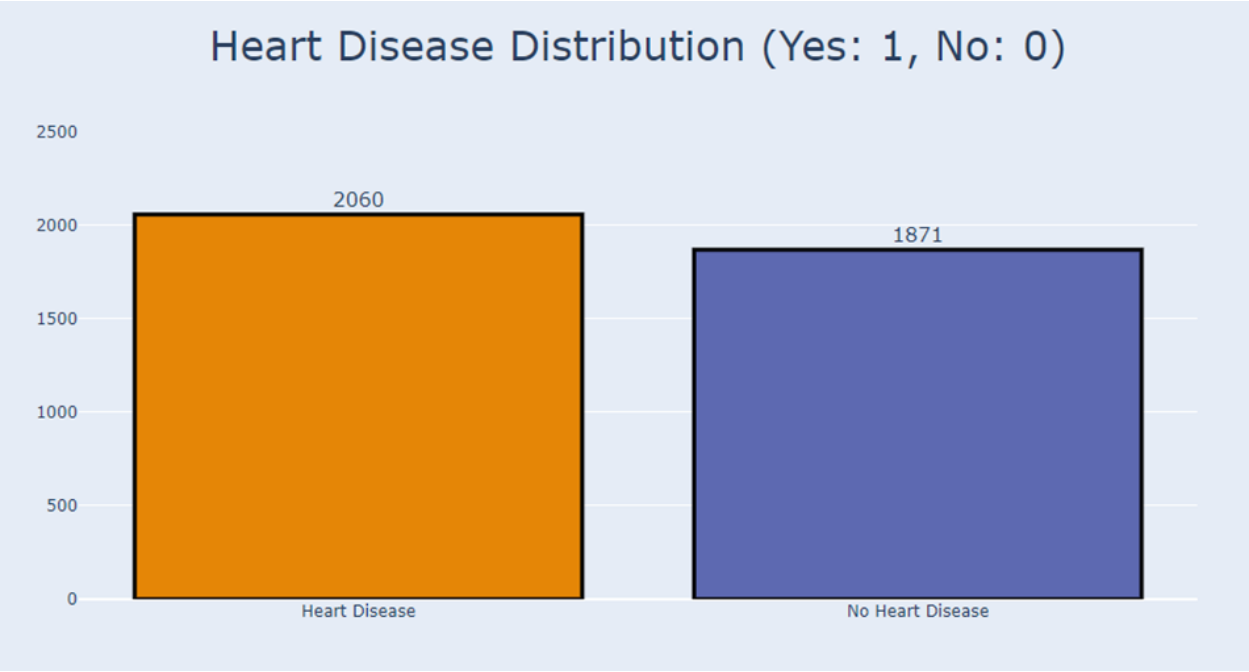


Figure 7: Bar Chart of the Heart Disease Distribution

Above figure shows the number of individuals who have different types of ST Slope in the dataset.

Orange Bar: who has heart disease. Total = 2060

Purple Bar: who does not have heart disease. Total = 1871

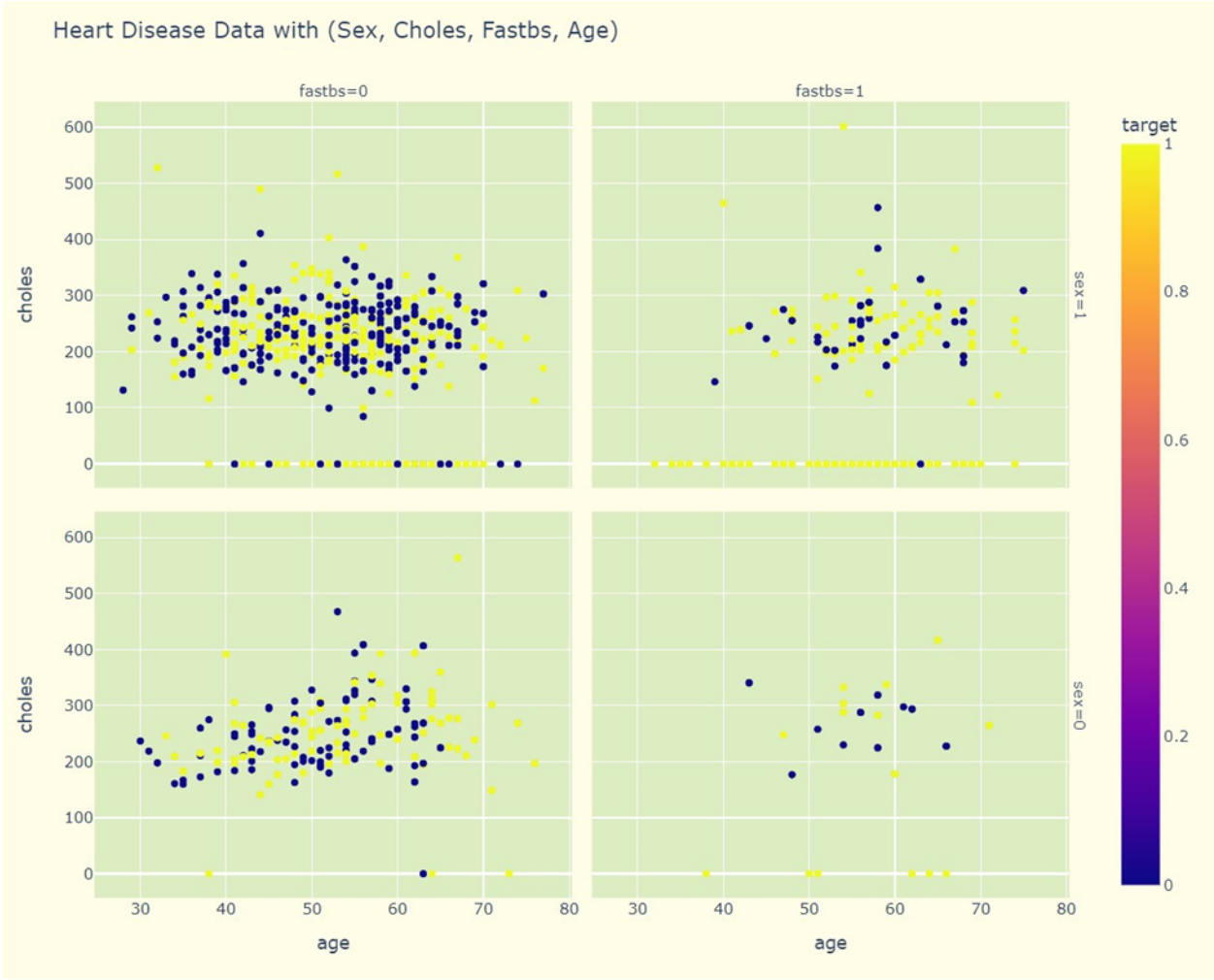


Figure 8: Scatter Plot Correlation Graph

Above figure shows the scatter plot graph which indicates the correlation between sex, choles, fastbs and age.

Blue Color Dots: who do not have heart disease

Yellow Color Dots: who have the heart disease

Top Left of the graph: who have a fasting blood sugar of less than or equal to 120 mg/dl.

Top Right and Bottom Right of the graph: shows both sex with fasting blood sugar of more than 120 mg/dl.

Above graph shows that male who are in the age of 40 to 70 and have a cholesterol level between 150 to 300 mg/dl are more prone to heart disease.

The females who are in the age of 45 to 60 and cholesterol level between 150 to 300 mg/dl are more prone to heart disease.

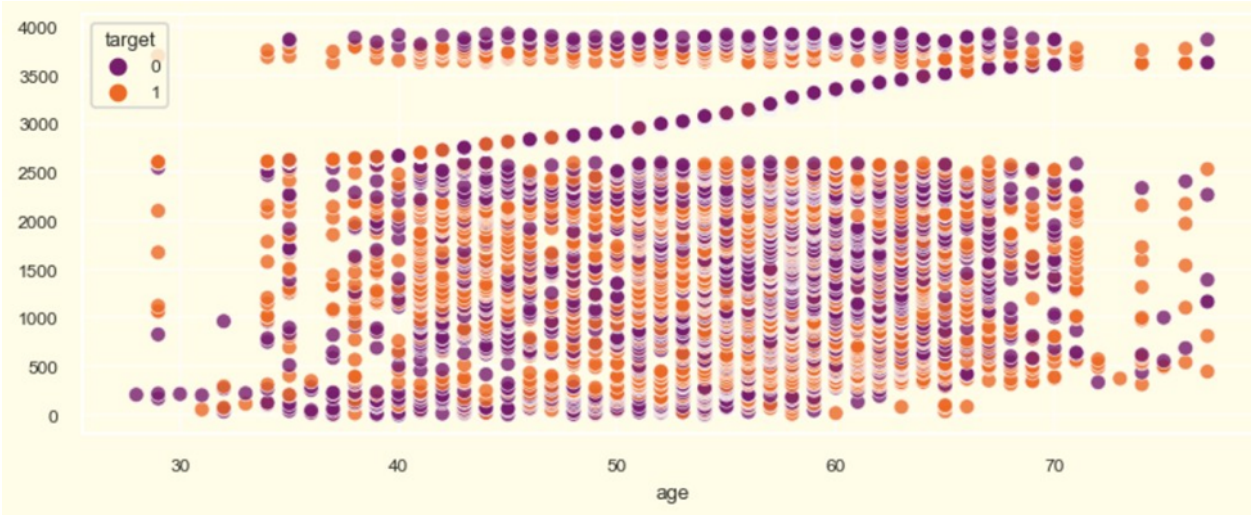


Figure 9: Scatter Plot of Age with target (heart disease)

Above figure shows the scatter plot of individuals whose age is between 28 to 77 and it shows which individual is more likely to have heart disease.

Those aged 30 to 70 are more prone to heart disease because the orange dots (1)representing those who have heart disease are frequently shown between age 30 to 70.

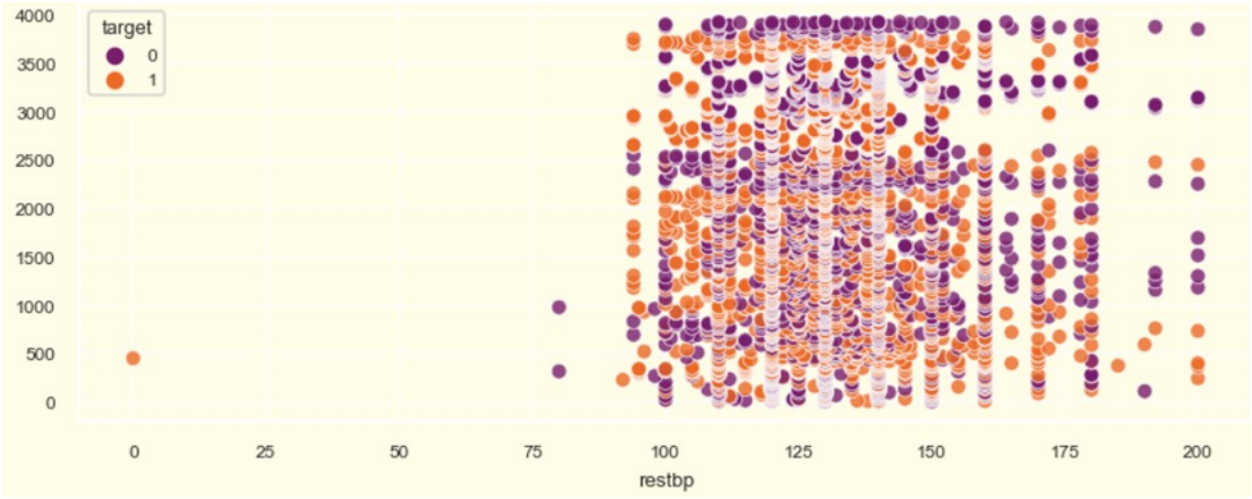


Figure 10: Scatter Plot of Resting Blood Pressure with target(heart disease)

Above figure shows the scatter plot of the resting blood pressure that determines whether an individual is prone to heart disease or not.

From the above figure, most of the individuals have a resting blood pressure between 100 to 180.

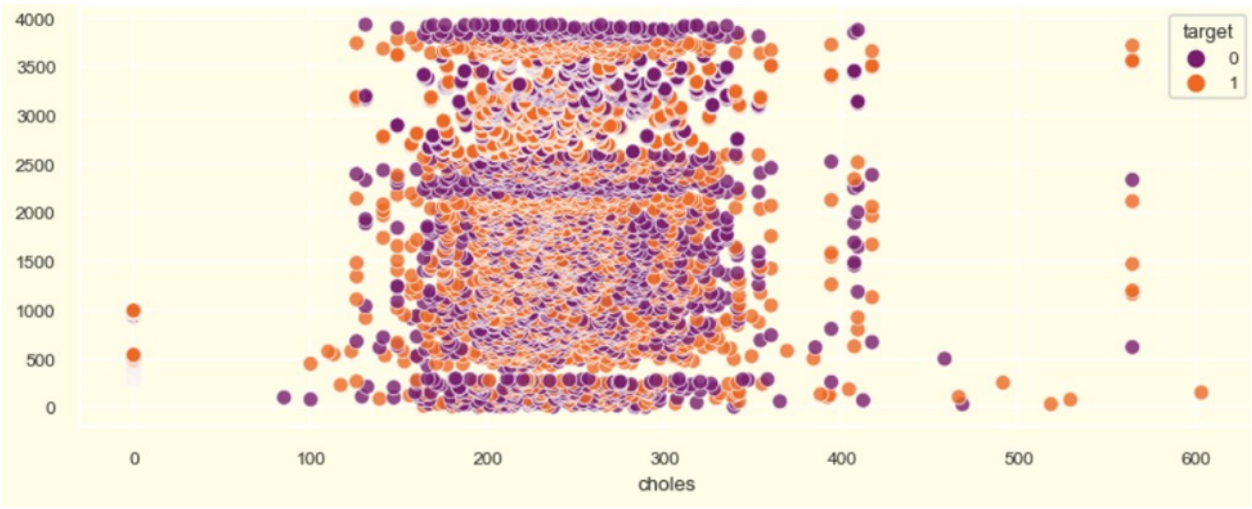


Figure 11: Scatter Plot of Cholesterol with target(heart disease)

Above figure shows the scatter plot of the cholesterol that determines whether an individual is prone to heart disease or not.

From the above figure, most of the individuals have a cholesterol between 150 to 350.

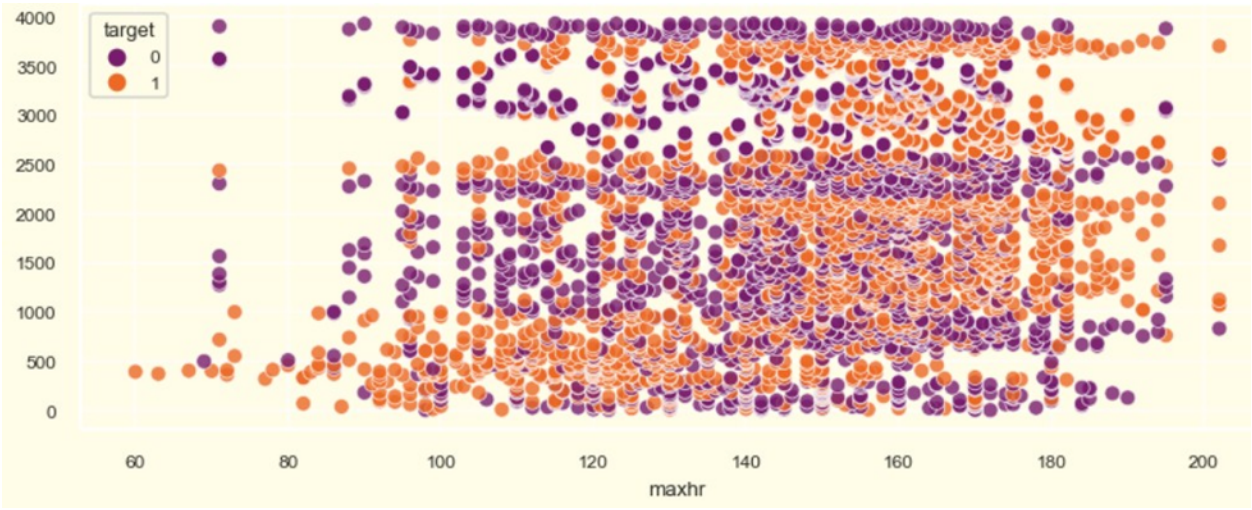


Figure 12: Scatter Plot of Maximum Heart Rate achieved with target(heart disease)

Above figure shows the scatter plot of the maximum heart rate achieved that determines whether an individual is prone to heart disease or not.

From the above figure, most of the individuals have a heart rate more than 80

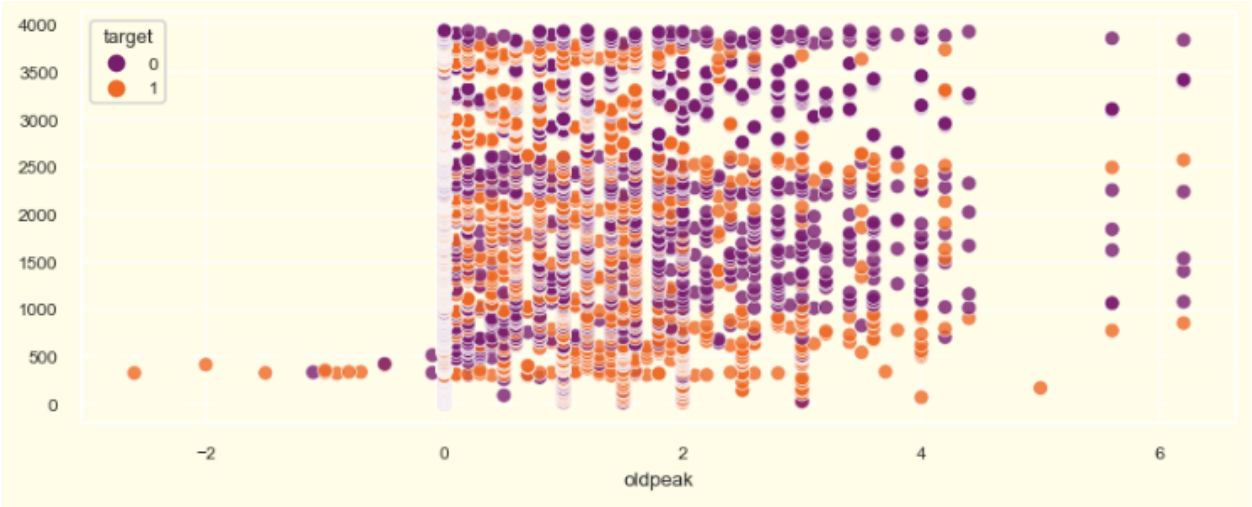


Figure 13: Scatter Plot of old peak with target(heart disease)

Above figure shows the scatter plot of the old peak with a target that determines whether an individual is prone to heart disease or not.

From the above figure, most of the old peaks are between 0 and 4.

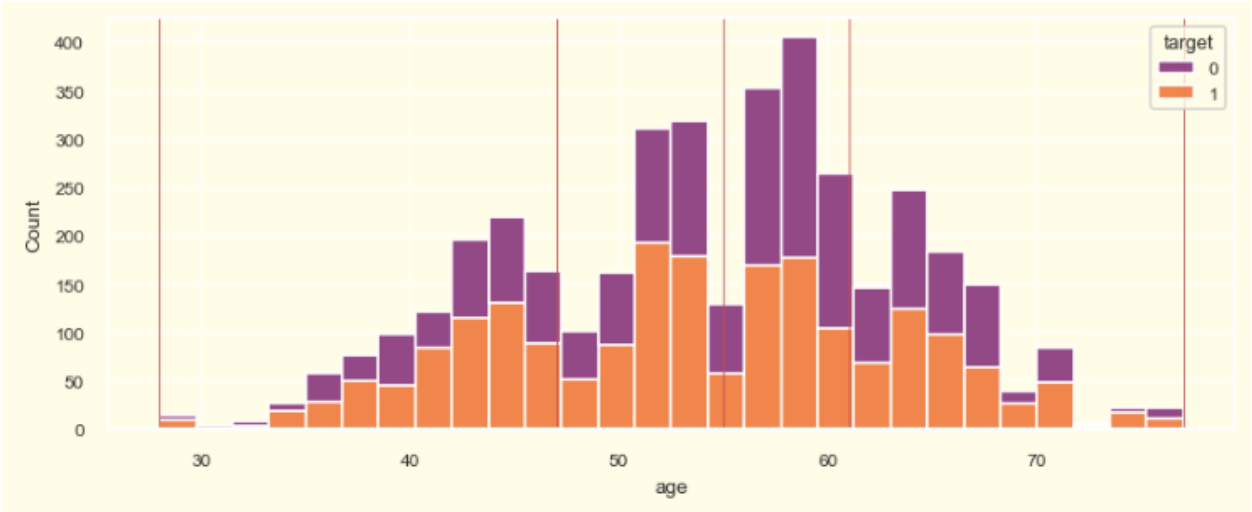


Figure 14: Histogram Plot of age with target(heart disease)

Above figure shows the histogram plot of the age with a target that determines whether an individual is prone to heart disease or not.

From the above figure, those who are aged 40 till aged 77 are at the risk of getting heart disease.

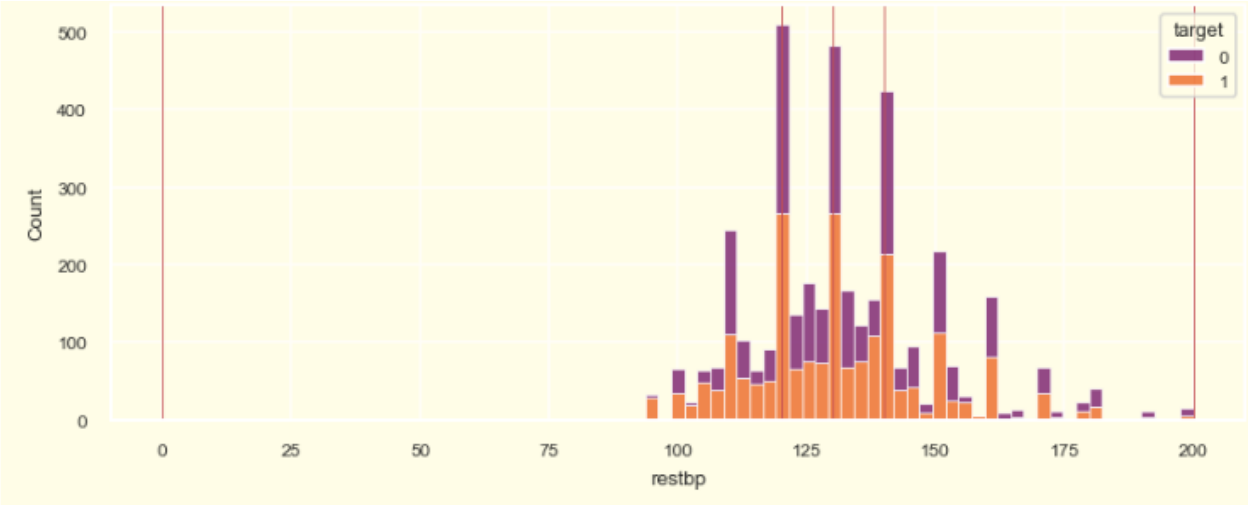


Figure 15: Histogram Plot of restbp with target(heart disease)

Above figure shows the histogram plot of the restbp with a target that determines whether an individual is prone to heart disease or not.

From the above figure, those who are have the resting blood pressure between 100 to 180 are at the risk of getting heart disease.

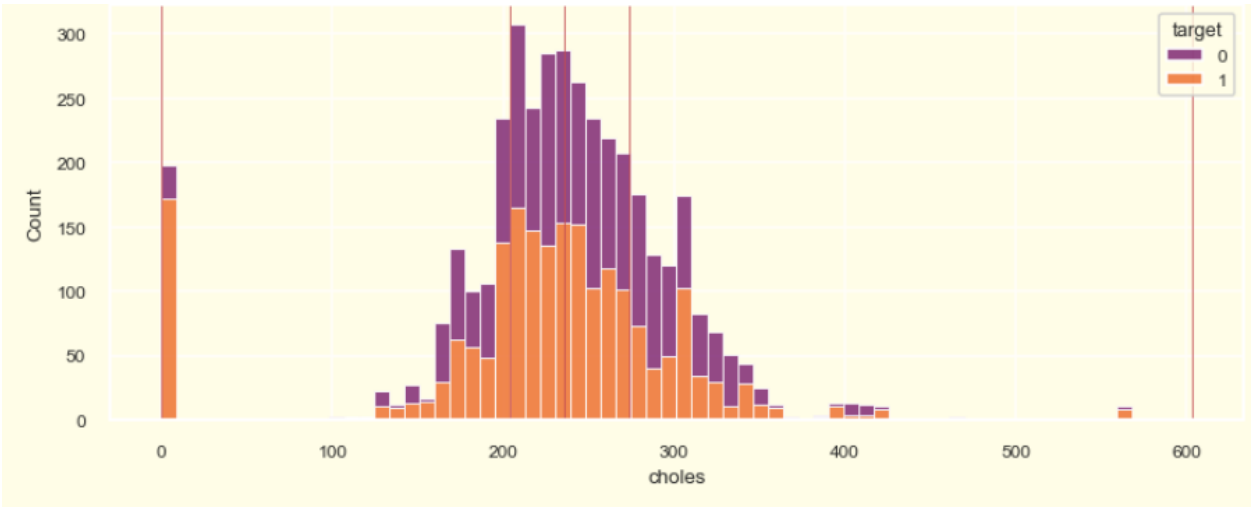


Figure 16: Histogram Plot of Cholesterol with target(heart disease)

Above figure shows the histogram plot of the cholesterol that determines whether an individual is prone to heart disease or not.

From the above figure, most of the individuals have a cholesterol between 150 to 350 s prone to heart disease.

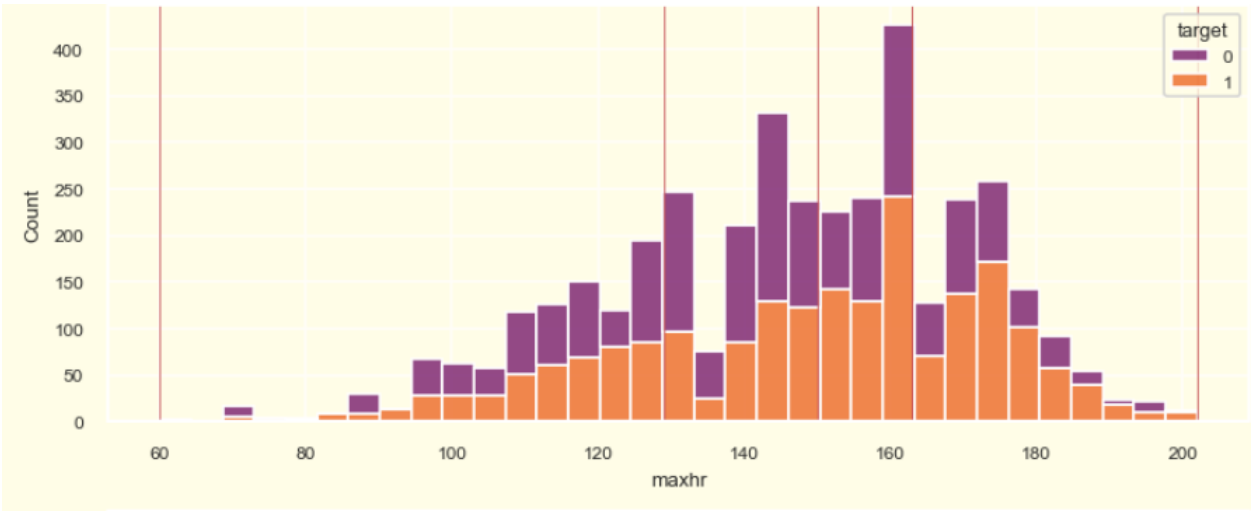


Figure 17: Histogram Plot of Maximum Heart Rate with target(heart disease)

Above figure shows the scatter plot of the maximum heart rate achieved that determines whether an individual is prone to heart disease or not.

From the above figure, most of the individuals have a heart rate more than 100 till 135 is prone to heart disease and start with 145 till 200 is prone to the heart disease.

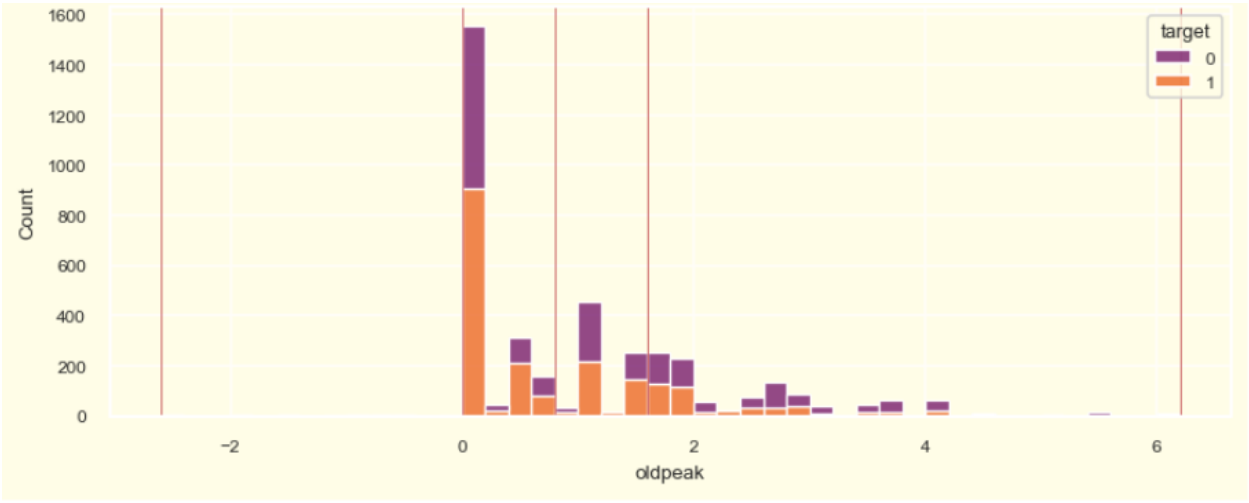


Figure 18: Histogram Plot of old peak with target(heart disease)

Above figure shows the scatter plot of the old peak with a target that determines whether an individual is prone to heart disease or not.

From the above figure, most of the old peaks are between 0 and 4 and the old peak at the 0 till 1 is prone to heart disease and starts with 1.7 to 2 also prone to heart disease.

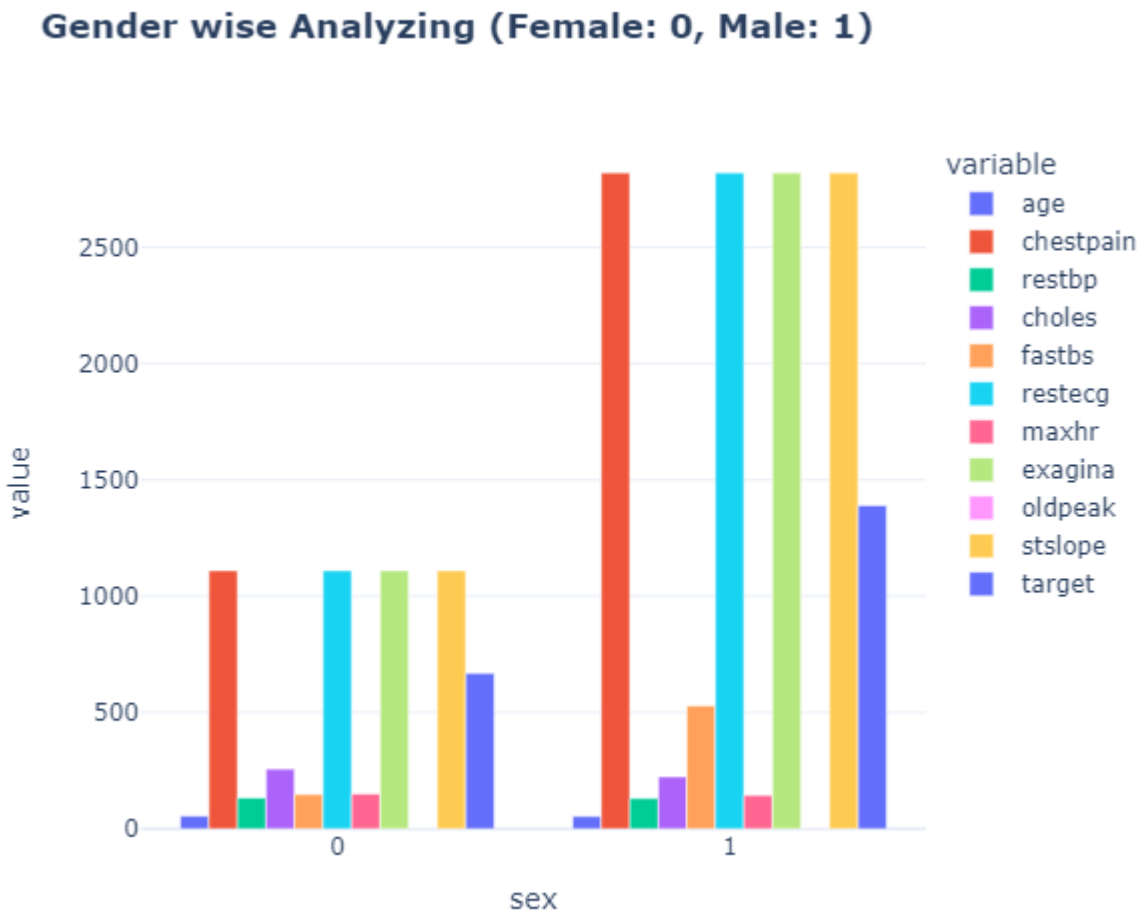


Figure 19: Bar Chart of showing the average gender wise analyzing with different variables

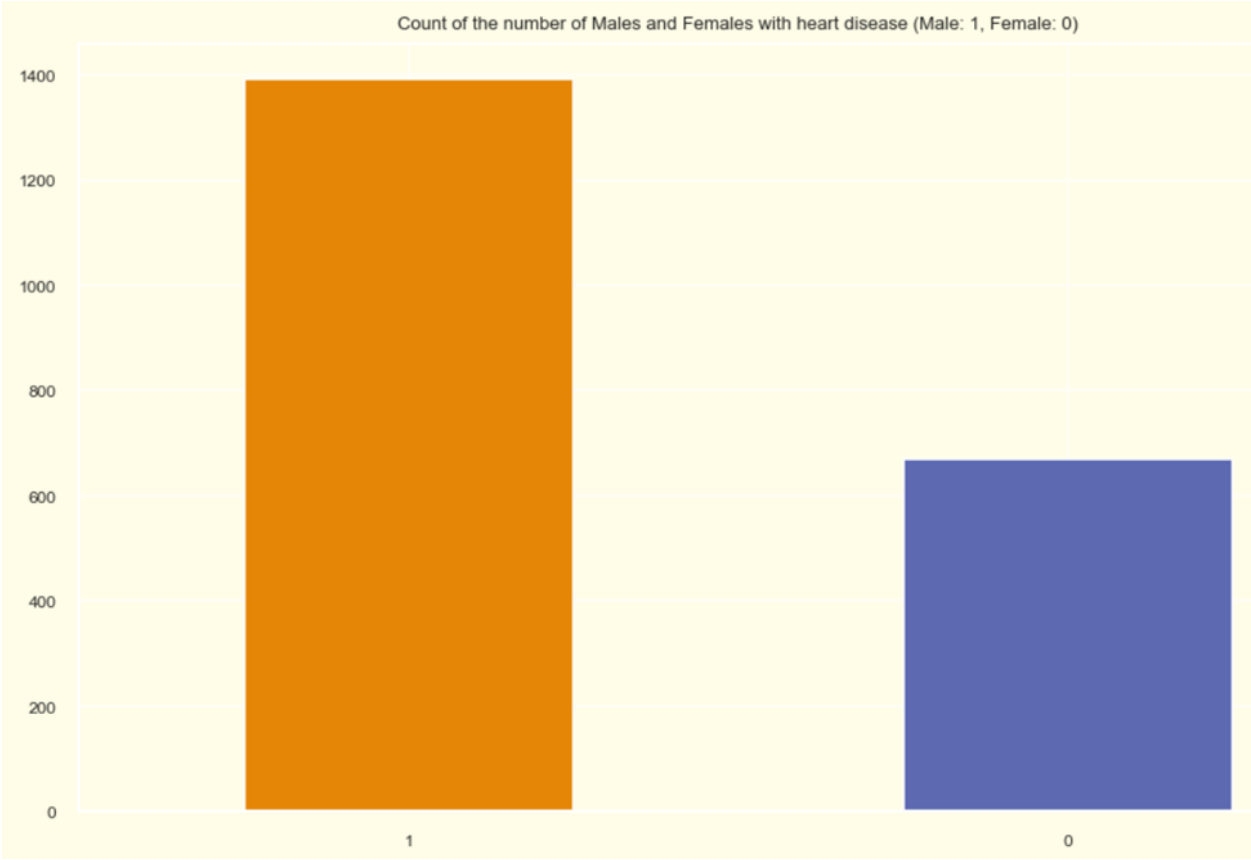


Figure 20: Bar Chart of Males and Females with Heart Disease

Above figure shows the bar chart of the genders who are prone to heart disease or not.

Orange Bar: Males who are prone to heart disease. Total = 1391

Purple Bar: Females who are prone to heart disease. Total = 669

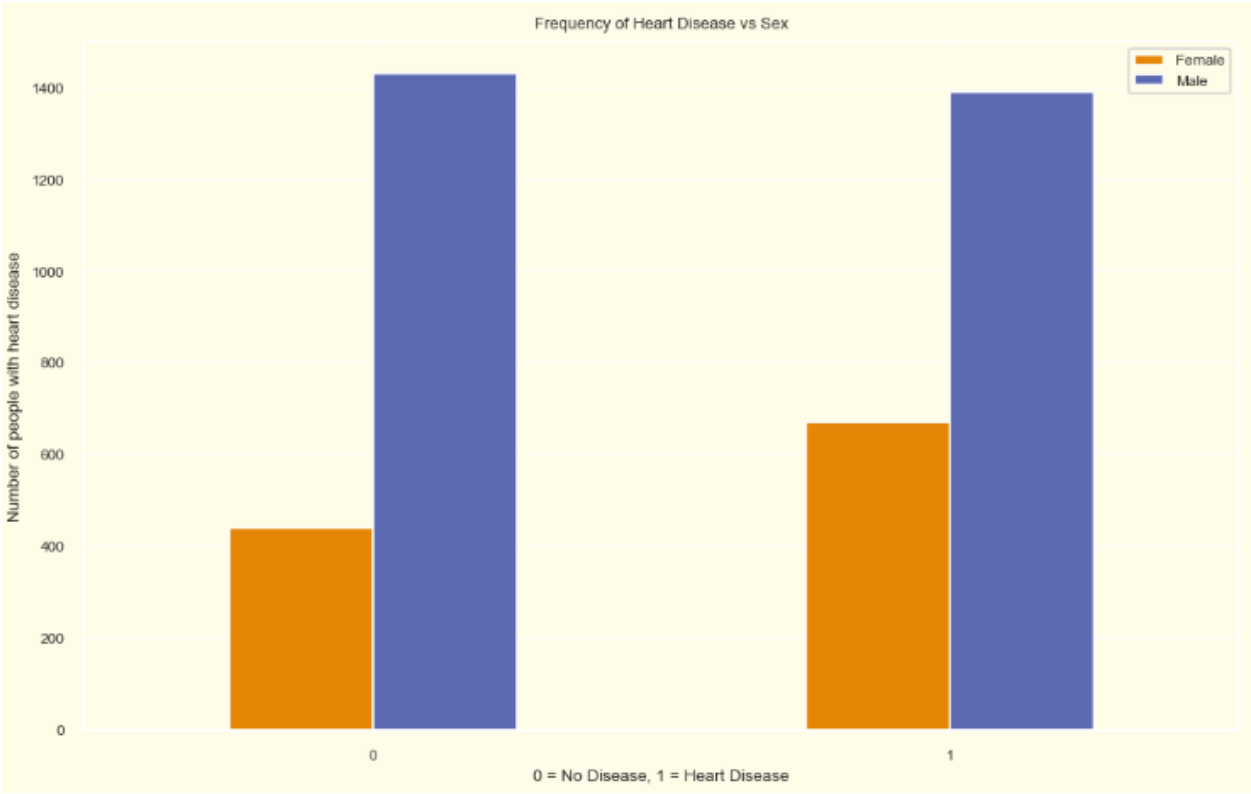


Figure 20: Bar Chart of Frequency of Heart Disease vs Sex

Above figure shows the bar chart of the Frequency of Heart Disease vs Sex.

Males have a higher risk of being prone to heart disease than Females.

3.2.2 Data Preprocessing

```
from sklearn.preprocessing import MinMaxScaler
scal=MinMaxScaler()
feat=['age', 'sex', 'chestpain', 'restbp', 'choles', 'fastbs', 'restecg', 'maxhr', 'exagina', 'oldpeak', 'stslope']
df[feat] = scal.fit_transform(df[feat])
df.head()
```

Code for performing the MinMaxScaler.

	age	sex	chestpain	restbp	choles	fastbs	restecg	maxhr	exagina	oldpeak	stslope	target
0	0.244898	1.0	0.333333	0.70	0.479270	0.0	0.0	0.788732	0.0	0.295455	0.0	0
1	0.183673	1.0	0.333333	0.65	0.469320	0.0	0.5	0.267606	0.0	0.295455	0.0	0
2	0.530612	1.0	0.666667	0.75	0.323383	0.0	0.0	0.436620	0.0	0.295455	0.0	0
3	0.224490	1.0	0.666667	0.60	0.562189	0.0	0.0	0.774648	0.0	0.295455	0.0	0
4	0.346939	0.0	0.333333	0.65	0.393035	0.0	0.0	0.774648	0.0	0.295455	0.0	0

Display the output after performing MinMaxScaler.

Transforming all our features by scaling each of the features to a given range using the MInMaxScaler. For instance, chestpain can be categorized into 4 different scales which range from 0 1 2 3. In the first row 0, 0.33333 can be seen outputted after it is being processed through the minmaxscaler, this is calculated through the formula X-X(min) / X(max) – X(min). This formula is used throughout the whole dataset as shown in the picture above.

```
X=df.drop("target",axis=1).values
Y=df.target.values
```

Code to perform drop target column

Target column is being dropped before the dataset is written into the model.
Column from age to stslope is being written into variable X
Column target is being written into variable Y

```
from sklearn.model_selection import train_test_split
X_train,X_test,Y_train,Y_test=train_test_split(X,Y,test_size=0.2,random_state=42)
```

Code to split data into train and test data

The data is split into train and test data and used 80/20 train/test split.
Train size is 80%
Test size is 20%

3.2.3 Classification Methods/Algorithms/Techniques

Our team has a total of 3 different types of algorithms which are Random Forest, K-Nearest Neighbor(KNN) and Support Vector Machine(SVM) as well as 1 technique combining 2 of the algorithms which is Stacking CV. After we have identified all the accuracy scores of all the algorithms, our team will try to stack up 2 algorithms together to increase the accuracy of the algorithms.

Random Forest Classifier Model

After preprocessing and splitting the data into training and testing sets, the training set of data is being fit to process the machining learning model. Then, the testing set of data will be used to estimate the model in order to get the accuracy of the result, The result of the testing set will be used for comparison. The random forest classifier was used to test the accuracy of the testing set of data.

Reason of using random forests is because this algorithm uses a low correlation between the models. Having uncorrelated models come together to produce ensemble predictions will help to increase the accuracy of the heart disease prediction application when comparing with other individual errors. The trees protect each other from their individual errors even in some cases where some of the trees might be wrong, but other trees will still be right so the result is the group of trees being able to move in the correct direction.

2 of the steps are being taken to ensure that the trees inside the forest are uncorrelatedness.

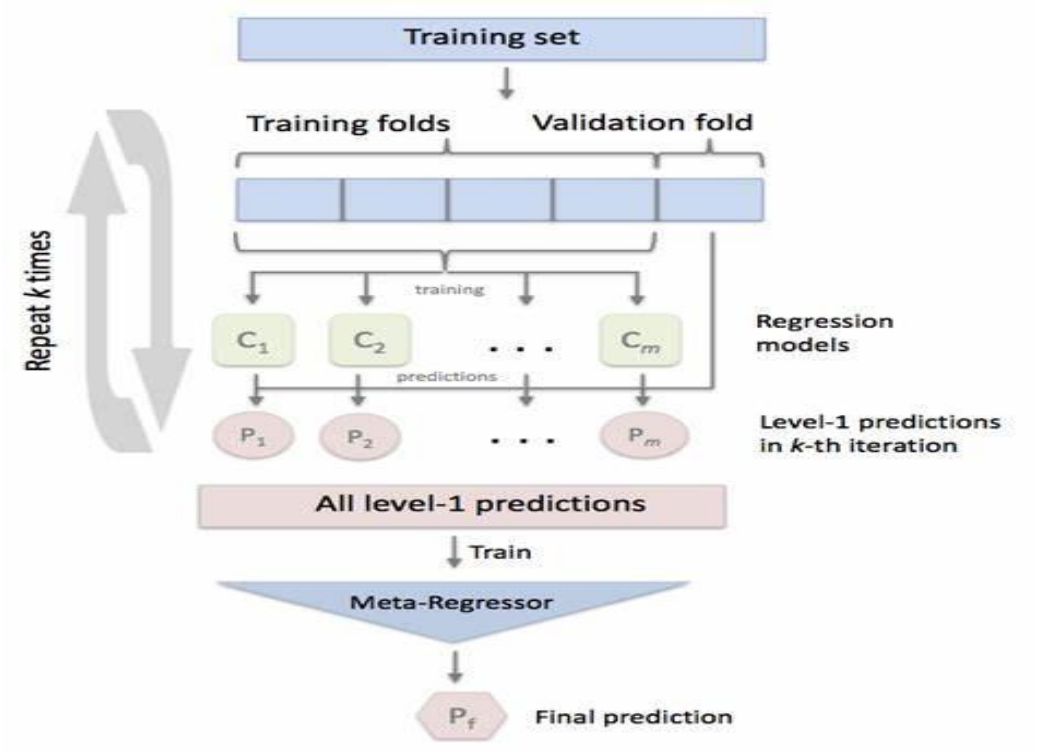
- Bagging(Bootstrap Aggregation): Decision trees are sensitive to the testing data. Any small changes that are being made to the training set will greatly affect the tree's structures. However Random Forest creates subsets from the datasets which is known as bootstrapping. Random Forest allows these subset of trees to randomly sample the dataset with replacement which result in different trees. With replacement, there might be duplicates of data inside the dataset. This whole process is known as bagging.

- Feature randomness. With decision trees, random forest will take every possible feature to be split into nodes. However, it actually limits the amount of features that each tree can split on. This means that each of the trees in the random forest can pick only a curtain random subset of features to be further split on. In the application, the forest will limit the features to

be selected. The features for the first tree might be restbp, choles and age whereas the second tree has a feature of choles, oldpeak, stslope and this randomized feature for the trees will keep going until all the subset trees have been created. Feature randomness encourages diverse trees where every tree will have a different set of features. It will take a vote after all the trees have been created and the classification with the most votes will become the output of the forest

Stacking Cross Validation (SCV) Classifier Model

After our team identified all the accuracy of the 3 algorithms which are Random Forest, K-Nearest Neighbors and Support Vector Machine (SVM). Our team decided to use a stacking cross validation(SCV) classifier model to stack 2 of the algorithms together to produce a higher accuracy model for better prediction accuracy. SCV uses the ensemble learning technique in order to combine multiple classification models together. This SCV is an extension of the usual stacking algorithm and by using cross validation to prepare input data at the level 2 classifier. This might cause overfitting as the dataset to fit into the level 1 classifier will be used as the inputs for the level 2 classifier. However, through the concept of cross validation, it allows the dataset to be split up into k folds and in k successive rounds. The k-1 folds will be used to fit the level 1 classifier and after that in each round, the remaining 1 subset that was applied to the level 1 classifier will be added in each iteration. Next, the level 2 classifier will be used to predict the results that were stacked as the input data. After the SCV has finished training, the level 1 classifier will be fitted entirely into the dataset as the figure shown below



Source Code of Random Forest

```
np.random.seed(42)
from sklearn.ensemble import RandomForestClassifier
#Define Model
RF_clf=RandomForestClassifier(n_estimators=40)
#Fit the model
RF_clf.fit(X_train,Y_train)
RF_score=RF_clf.score(X_test,Y_test)
#Make Predictions
RF_Y_pred=RF_clf.predict(X_test)
#print(RF_score)
evaluation(Y_test,RF_Y_pred)
```

```
{'accuracy': 0.973, 'recall': 0.974, 'F1 score': 0.975}
```

Above shows the source code of random forest. I have imported the Random Forest Classifier from the Scikit learn library. Then, define the name of the model known as RF_clf. After the defining, the model will be trained by fitting the training set of X_train and Y_train. The test data(X_test, Y_test) wil be used to predict the score of the model. The accuracy is 0.973.

Source Code of Stacking CV Model (SCV)

```
from mlxtend.classifier import StackingCVClassifier
#Stack the the model
scv=StackingCVClassifier(classifiers=[Knn_clf,RF_clf],meta_classifier= Knn_clf)
scv.fit(X_train,Y_train)
scv_score=scv.score(X_test,Y_test)
scv_Y_pred=scv.predict(X_test)
evaluation(Y_test,scv_Y_pred)
```

```
{'accuracy': 0.978, 'recall': 0.983, 'F1 score': 0.98}
```

Above shows the source code of random forest. I have imported the SCV from mlxtend library. Then, define the name of the model known as scv. In order to stack the 2 algorithms together, we would have to include the two models that we have identified which are K-Nearest Neighbor (KNN) and Random Forest (RF). After stacking the models together, the model will be trained by

fitting the training set of X_train and Y_train. The test data (X_test, Y_test) will be used to predict the score of the model. The accuracy score of the SCV model is 0.978.

3.2.4 Comparing the result of different classification models

	Model	Accuracy
0	SCV	97.839898
1	Random Forest	97.331639
2	SVM	81.194409
3	KNN	93.646760

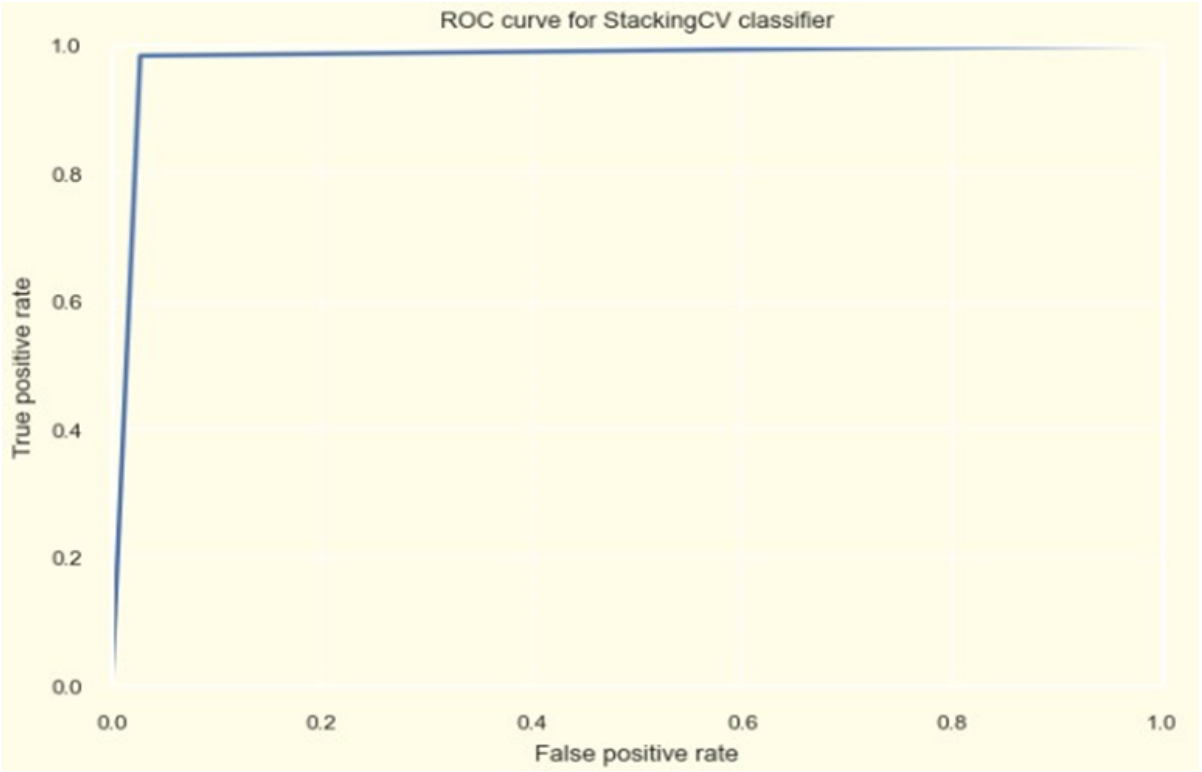
Accuracy result of different algorithms and Stacking CV(SCV) Model

The result of stacking up 2 algorithms is 97.83% which is higher than the Random Forest (RF), K-Nearest-Neighbours (KNN) and (Support Vector Machine (SVM) algorithms. The ranking of the accuracy of the model will be Stacking CV Classification which is 97.83%, followed by Random Forest which is 97.33% and the K-Nearest Neighbor will be the last which is 93.64%.then SVM which is 81.19%. In short, the SCV is the most accurate model to be used for the heart disease prediction application and the Random Forest can be said is the most accurate algorithm compared to other algorithms such as SVM and KNN that are being used in the application.

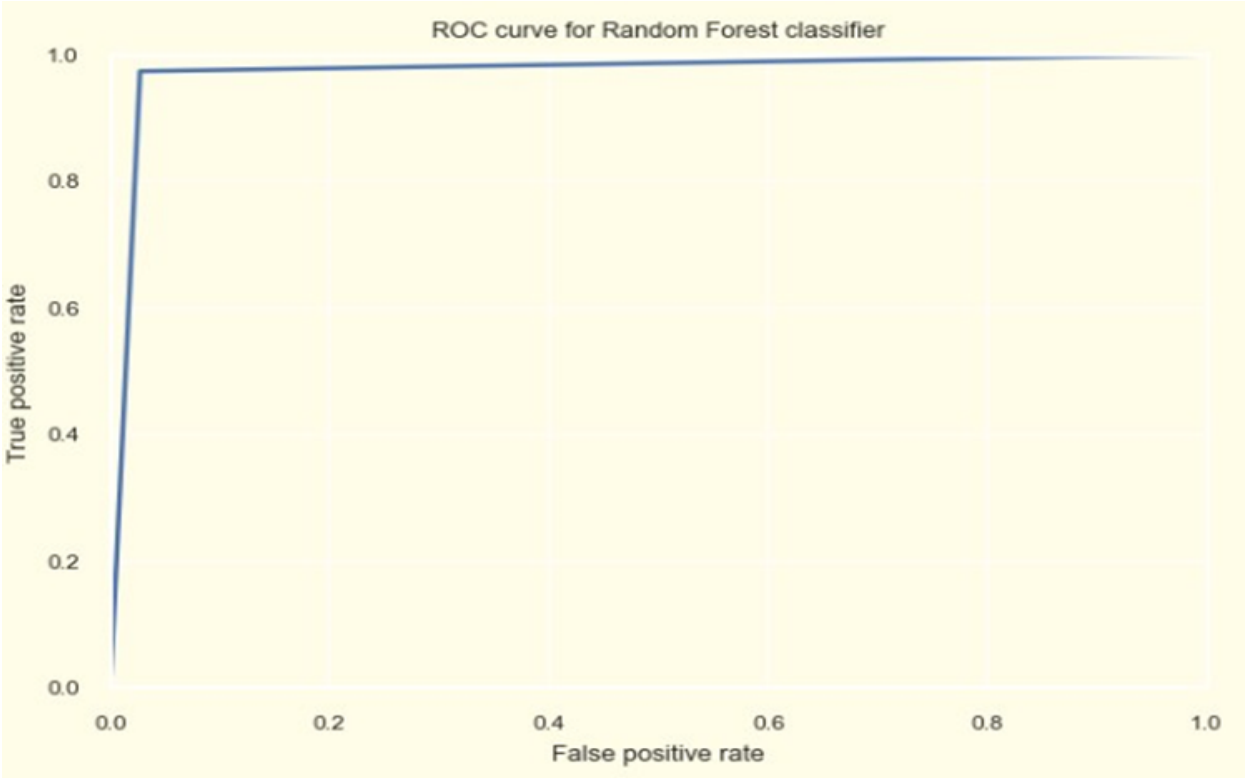
Roc Curve

Roc Curve is used to summarize the trade off between the true positive rate and false positive rate for the predictive model using different probability thresholds. All the roc curve shows below can be seen that all the models are slanting towards the y-axis. The accuracy for the Roc Curve of all the models are followed by 97.81% and 97.33%, 93.59%, 81.19%. Hence, stacking cv will be the highest accuracy score and if compared to algorithms Random Forest will be the highest compared to KNN and SVM.

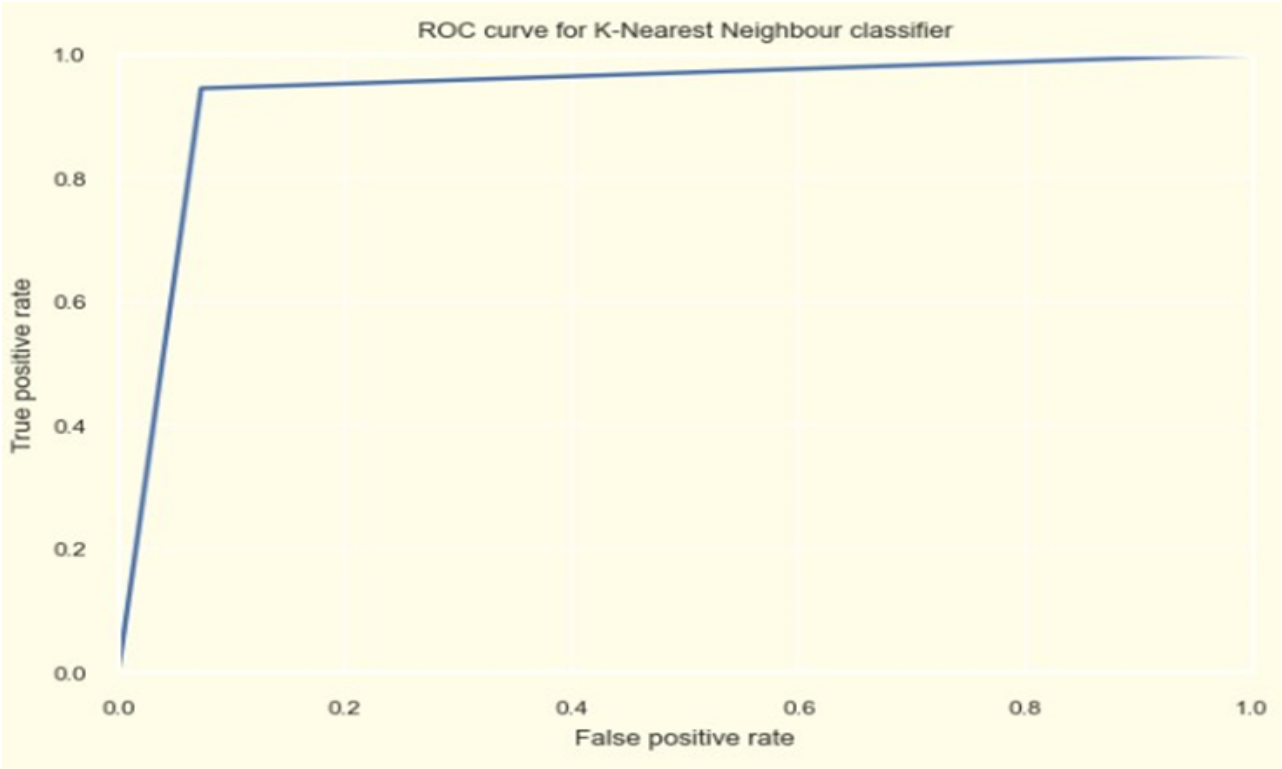
Stacking CV(SCV)



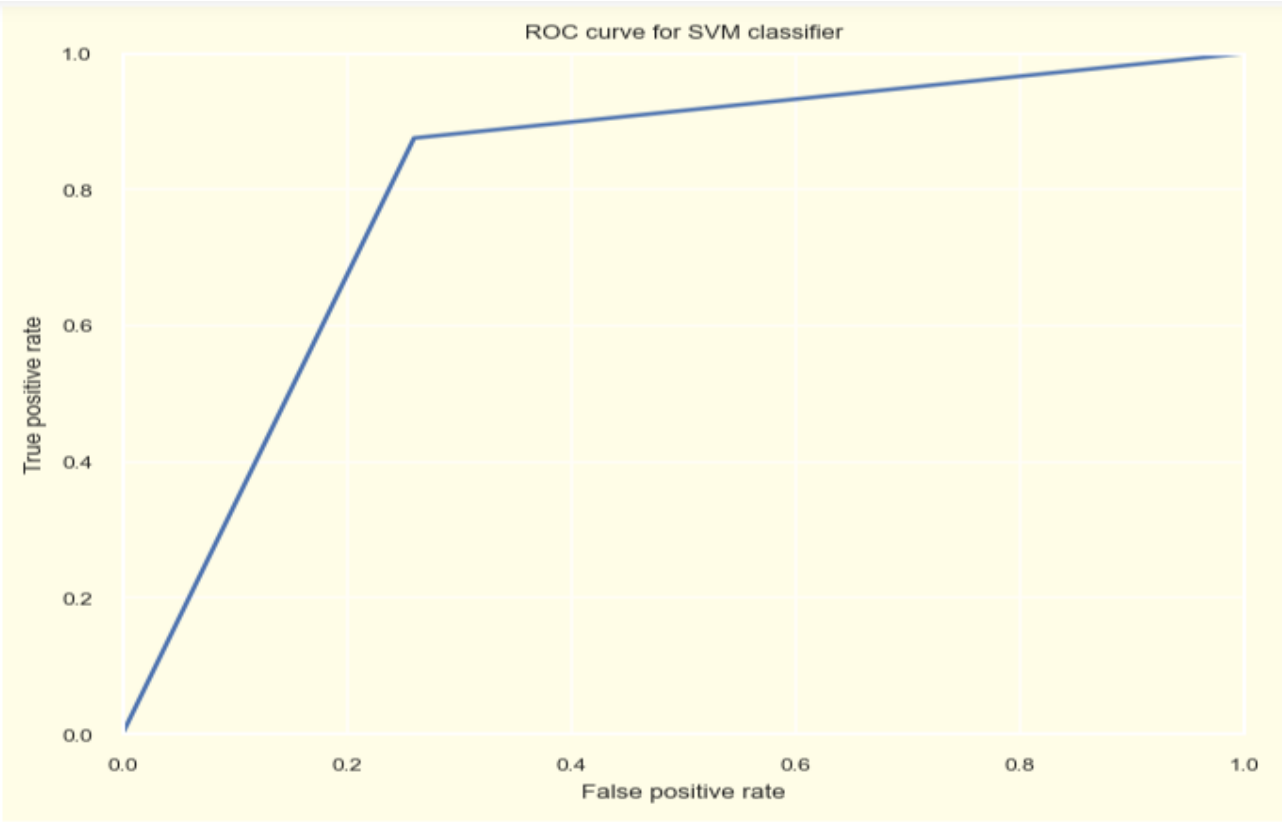
Random Forest



K-Nearest Neighbors(KNN)

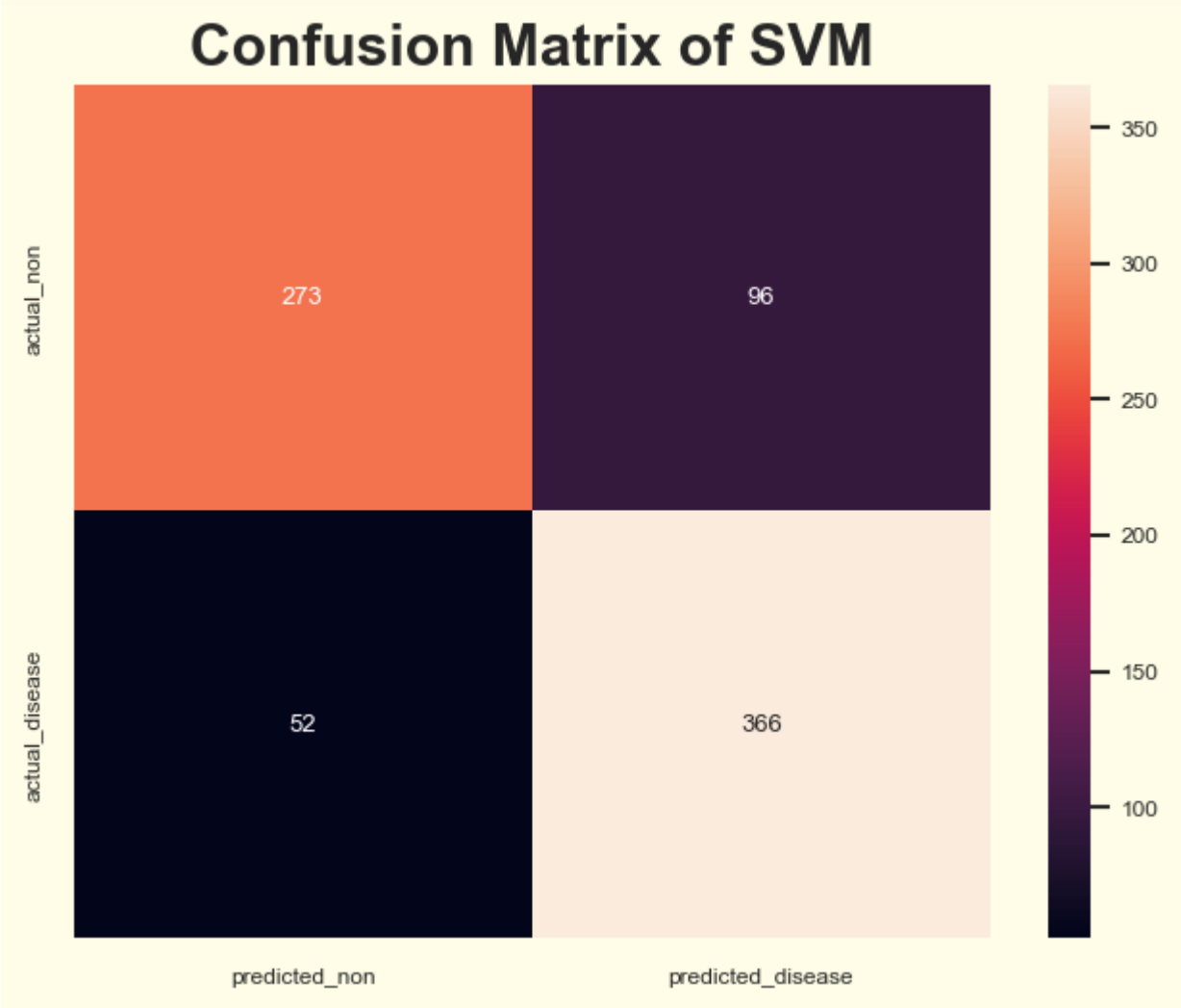


Support Vector Machine(SVM)

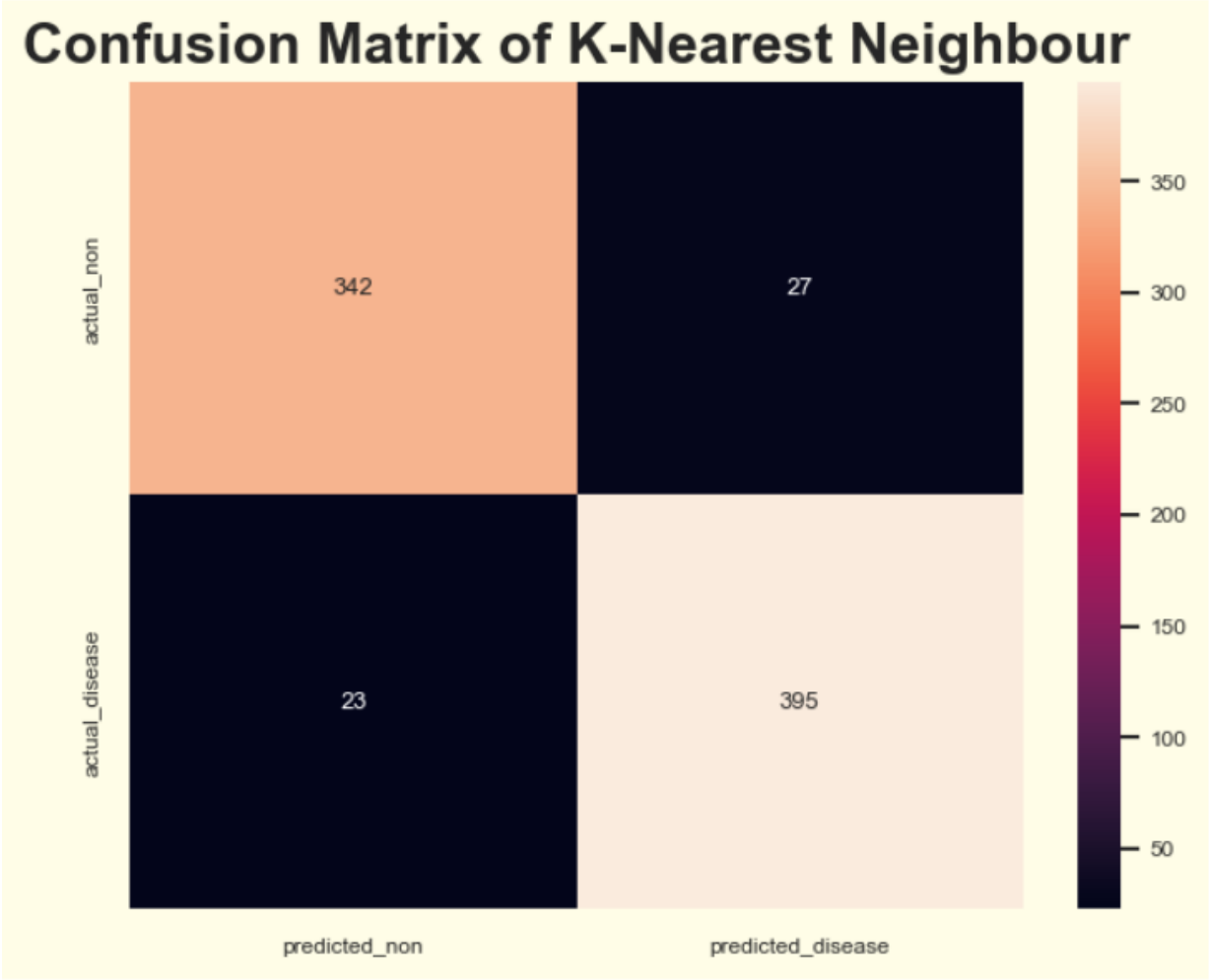


Confusion Matrix

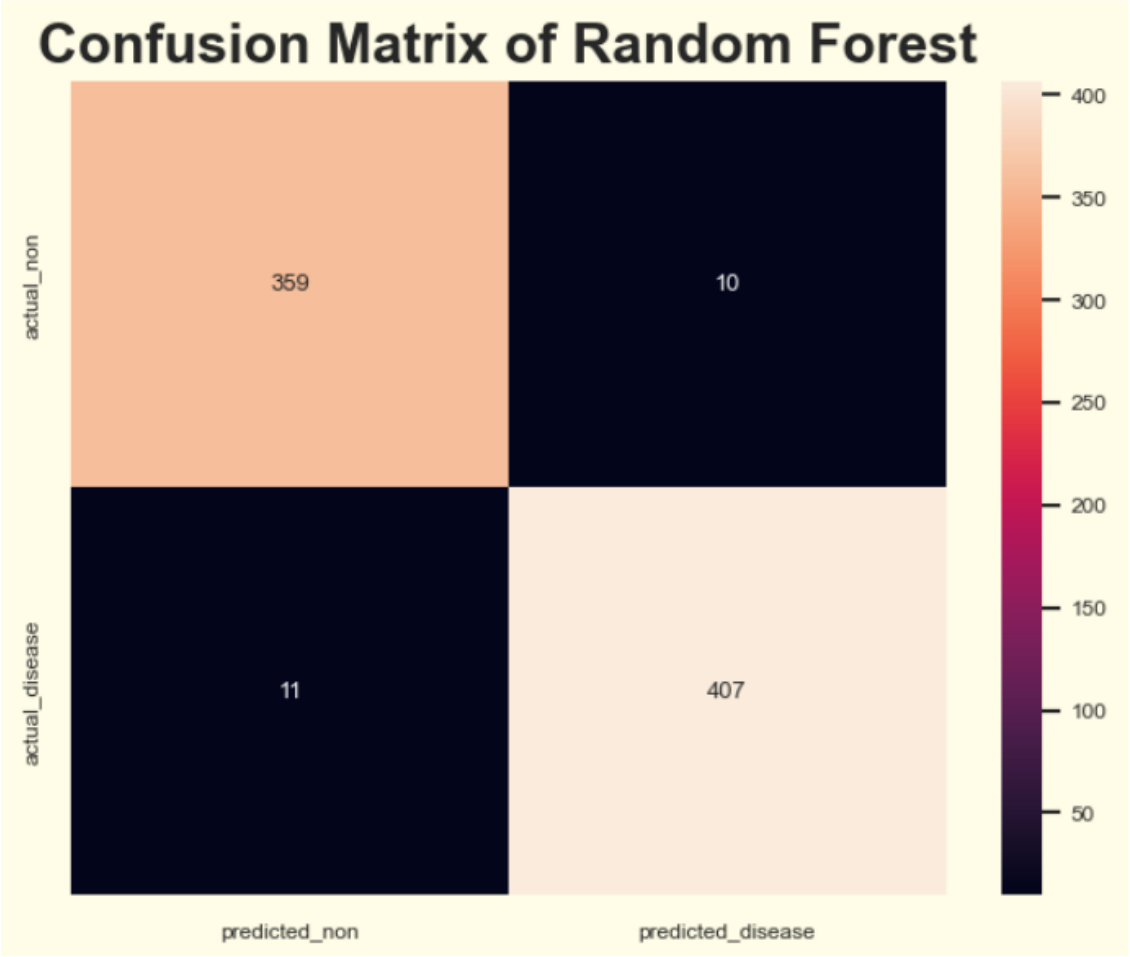
Support Vector Machine (SVM)



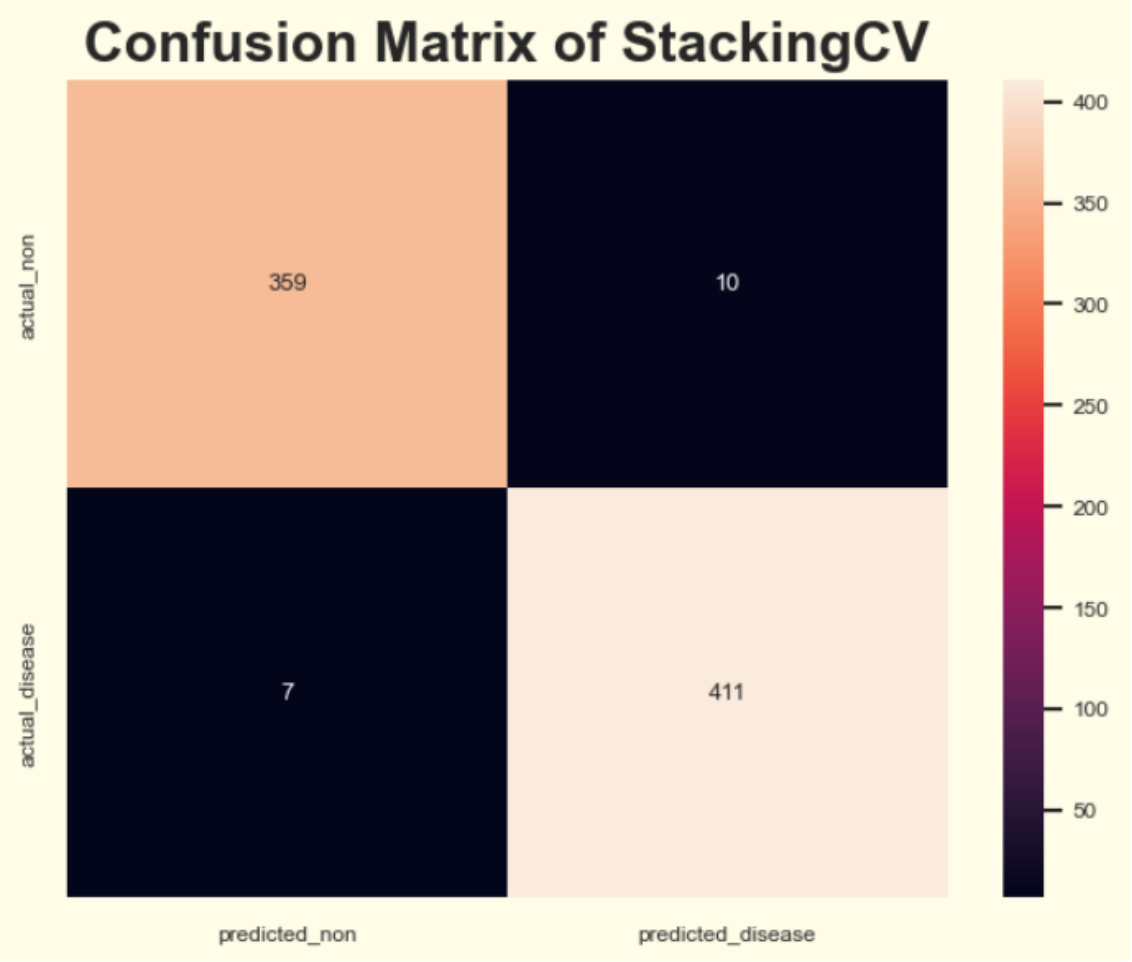
K-Nearest Neighbors (KNN)



Random Forest (RF)



Stacking SV (SVC)



Confusion matrix is used to help the summarization on how each model performed based on the testing data. Below are the descriptions of the confusion matrix.

	TP = True Positive TN = True Negative		
	FP = False Positive FN = False Negative		
Actual	**actual_non**	TP: An individual that is not having heart disease and correctly identified by the algorithm.	FN: An individual that is not having heart disease but the algorithm said is diagnosed with heart disease.
	actual_disease	FP: An individual that is diagnosed heart disease but the algorithm said not having heart disease.	TN: An individual that is diagnosed with heart disease and correctly identified by the algorithm.
		predicted_non	**predicted_disease**
	Predicted		

The TP and TN indicate how many times the algorithm has been correctly classified. According to the confusion matrix above, we can see that the number of correctly classified by Support Vector Machine(SVM) is 273+366= 642, K-Nearest Neighbor(KNN) is 342+395=737, Random Forest(RF) is 359+407=766 and Stacking CV (SCV) is 359+411=770. With these numbers, we can conclude that the StackingCV classifier is the most suitable classification model to be used for our heart disease prediction application and Random Forest will be the second choice.

Classification Report:

Support Vector Machine(SVM), K-Nearest Neighbor(KNN), Random Forest(RF) and Stacking CV (SCV)

Suppot Vector Machine Classification Report

	precision	recall	f1-score	support
0	0.84	0.74	0.79	369
1	0.79	0.88	0.83	418
accuracy			0.81	787
macro avg	0.82	0.81	0.81	787
weighted avg	0.81	0.81	0.81	787

K-Nearest Neighbour Classification Report

	precision	recall	f1-score	support
0	0.94	0.93	0.93	369
1	0.94	0.94	0.94	418
accuracy			0.94	787
macro avg	0.94	0.94	0.94	787
weighted avg	0.94	0.94	0.94	787

Random Forest Classification Report

	precision	recall	f1-score	support
0	0.97	0.97	0.97	369
1	0.98	0.97	0.97	418
accuracy			0.97	787
macro avg	0.97	0.97	0.97	787
weighted avg	0.97	0.97	0.97	787

Stacking CV Classification Report

	precision	recall	f1-score	support
0	0.98	0.97	0.98	369
1	0.98	0.98	0.98	418
accuracy			0.98	787
macro avg	0.98	0.98	0.98	787
weighted avg	0.98	0.98	0.98	787

Precision

The proportion of properly predicted positive observations to the total anticipated positive observations.

Recall

The ratio of properly predicted observations to the total number of observations in the actual class.

F1 Score

Showing us the weighted average of Precision and Recall.

The formula for precision, recall and F1 score is shown below:

$$\text{Precision} = \frac{True\ Positive}{True\ Positive + False\ Positive}$$

$$\text{Recall} = \frac{True\ Positive}{True\ Positive + False\ Negative}$$

$$\text{F1} = 2 \times \frac{Precision * Recall}{Precision + Recall}$$

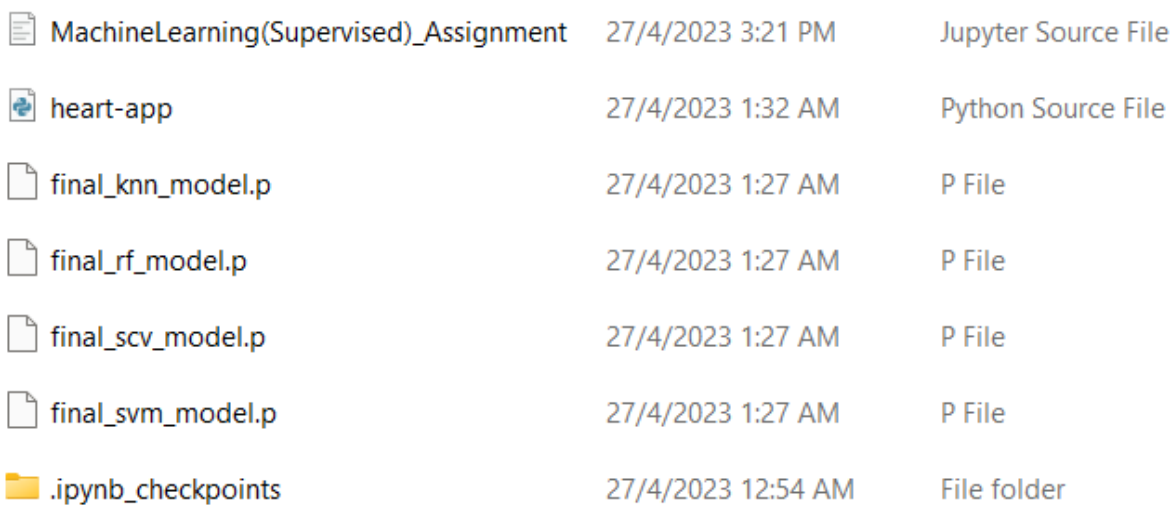
Support Machine Vector(SVM) has the worst precision, recall and F1 score and K-Nearest Neighbor (KNN) will be the second last even though it is higher than the SVM. Therefore, SVM and KNN will be excluded from being used in our heart disease prediction application . In contrast, both models of Random Forest (RF) and Stacking CV (SCV) have a high value when it comes to the precision, recall and F1 value. The SCV model has a slight advantage when compared to RF with a slight increase by 0.01 in terms of precision, recall and F1 value. With this, it is able to conclude that the SCV model has the highest accuracy out of all the models therefore it is the most suitable model to be used for our heart disease prediction application and Random Forest will be the second choice.

3.2.5 User Interface of Heart Disease Prediction System

Source Code of Writing pkl file:

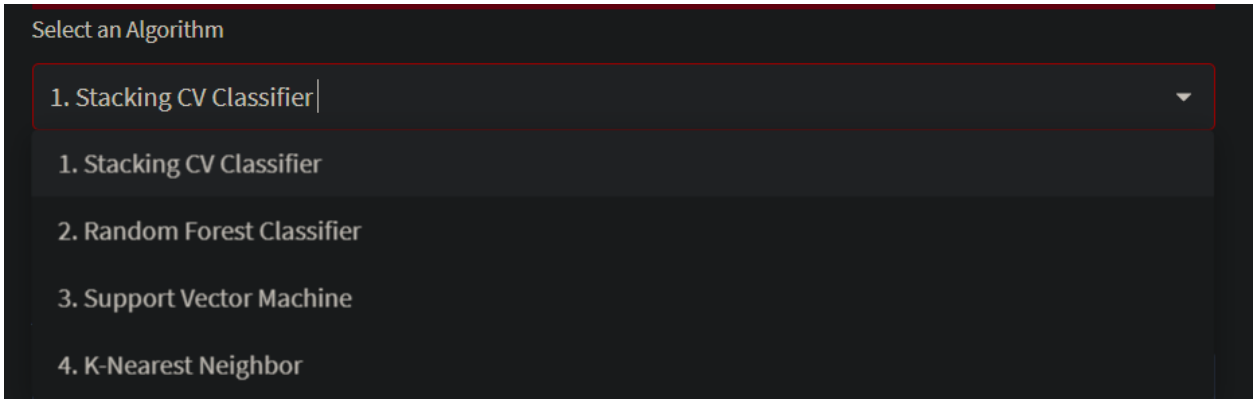
```
import pickle as pkl

#Save Model

# StackingCV
pkl.dump(scv,open("final_scv_model.p","wb"))

#Random Forest
pkl.dump(RF_clf, open("final_rf_model.p","wb"))

#SVM
pkl.dump(Knn_clf,open("final_knn_model.p","wb"))

#KNN
pkl.dump(svm_model,open("final_svm_model.p","wb"))
```

In this step we will store all the models that will be displayed in the User Interface (UI). All the models will be included which are the StackingCV classifier model, the Random Forest classifier model Support Vector Machine Model(SVM) and K-Nearest-Neighbor (KNN) to make the comparison easily. The models are being stored in a pkl format which enables us to load the model into the heart-app.py. After storing the model into pkl file:



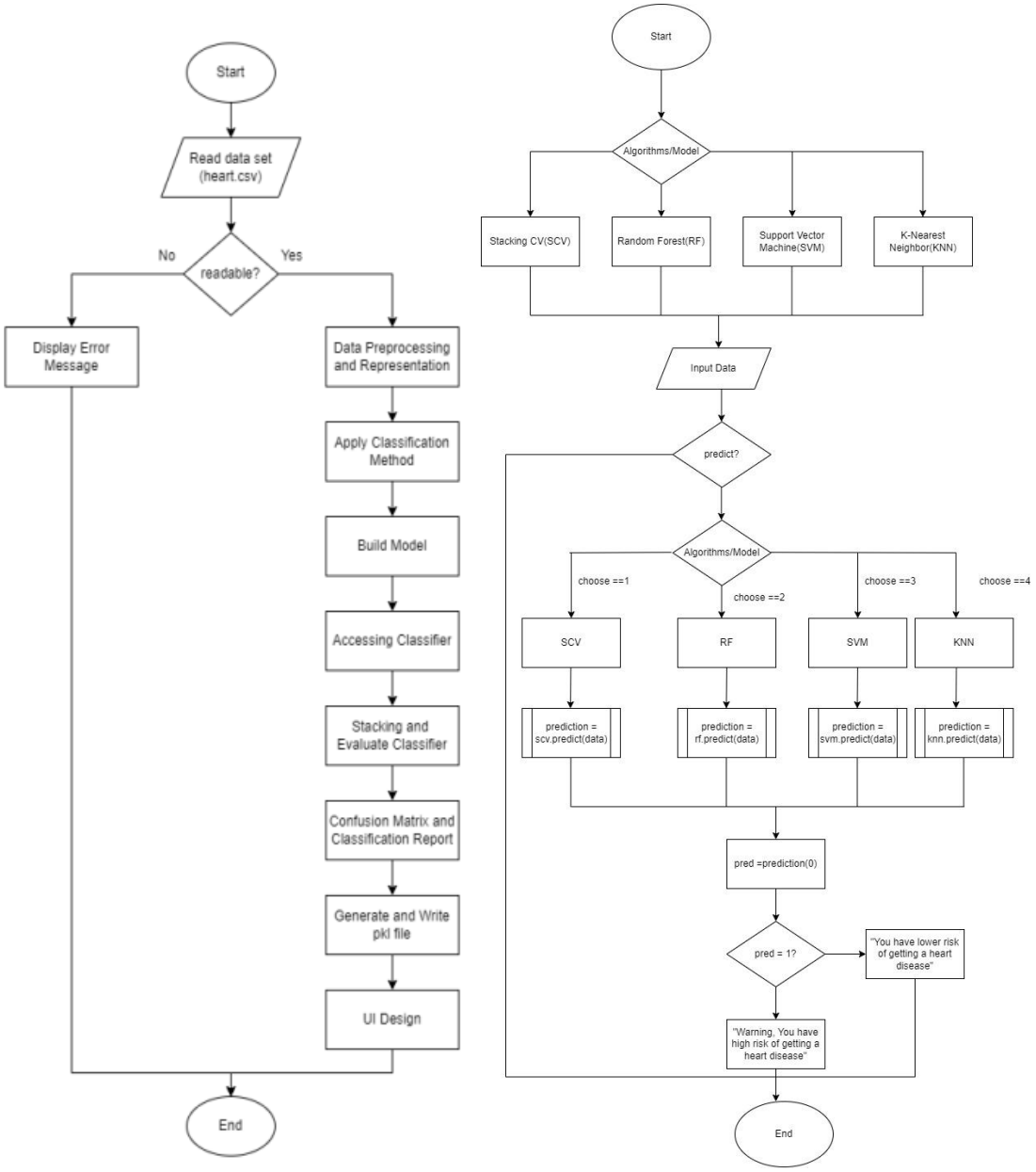
The Random Forest Classifier Model pkl file named as final_rf_model.p ,StackingCV Classifier Model pkl file named as final_scv_model.p, K-Nearest Neighbor (KNN) pkl file named as final_knn_model.p and Support Vector Machine (SVM) pkl file names as final_svm_model.p.

User Interface of Heart Disease Prediction Application:



In the heart disease prediction application, it allows users to choose which algorithm to use for predicting whether they are prone to heart diseases or not.

3.3. System flowchart/activity diagram



3.4. Proposed test plan/hypothesis

Step 1: Select the data from the dataset heart.csv that I chose to input and test in the project.

	Data										
S	Age	Sex	Chest Pain	RestBp	Choles	FastBs	RestEeg	MaxHr	Exagina	Oldpeak	Stslope
S1	58	Male	Atypical Angina	136	164	No	ST-T Wave abnormality	99	Yes	2.00	Flatsloping
S2	70	Male	Asymptomatic	170	192	No	ST-T Wave abnormality	129	Yes	3.00	Downsloping
S3	52	Male	Atypical Angina	140	100	No	Nothing to note	138	Yes	0.00	Upsloping
S4	42	Male	Non-Anginal Pain	160	147	No	Nothing to note	146	No	0.00	Upsloping
S5	48	Female	Asymptomatic	138	214	No	Nothing to note	108	Yes	1.50	Flatsloping
S6	59	Female	Asymptomatic	130	338	Yes	ST-T Wave abnormality	130	Yes	1.50	Flatsloping

S7	45	Female	Atypical Angina	130	237	No	Nothing to note	170	No	0.00	Upsloping
S8	48	Female	Atypical Angina	120	284	No	Nothing to note	120	No	0.00	Upsloping

Step 2: State the hypothesis for these selected input data

Predicting based on the Random Forest Model

H1)	S1 will be diagnosed as a heart disease patient
H2)	S2 will be diagnosed as a heart disease patient
H3)	S3 will be diagnosed as a non-heart disease patient
H4)	S4 will be diagnosed as a non-heart disease patient
H5)	S5 will be diagnosed as a heart disease patient
H6)	S6 will be diagnosed as a heart disease patient
H7)	S7 will be diagnosed as a non-heart disease patient
H8)	S8 will be diagnosed as a non-heart disease patient

4. Result

4.1. Results

Figure 1: Predict S1

Figure 2: Predict S2

Figure 3: Predict S3

Figure 4: Predict S4

Figure 5: Predict S5

Figure 6: Predict S6

Figure 7: Predict S7

Figure 8: Predict S8

4.2. Discussion/Interpretation

Predicting results based on the Random Forest Model.

Hypothesis	Prediction Result based on Random Forest
H1	S1 will be diagnosed as a heart disease patient
H2	S2 will be diagnosed as a heart disease patient
H3	S3 will be diagnosed as non-heart disease patient
H4	S4 will be diagnosed as non-heart disease patient
H5	S5 will be diagnosed as a heart disease patient
H6	S6 will be diagnosed as a heart disease patient
H7	S7 will be diagnosed as non-heart disease patient
H8	S8 will be diagnosed as non-heart disease patient

Input Data:

S1	58	Male	Atypical Angina	136	164	No	ST-T Wave abnormality	99	Yes	2.00	Flatsloping

“Warning! You have a high risk of getting a heart attack!”

H1 is not rejecting and concludes that S1 Is prone to heart disease after predicting using Random Forest

S2	70	Male	Asymptomatic	170	192	No	ST-T Wave	129	Yes	3.00	Downsloping

							abnormality				

“Warning! You have a high risk of getting a heart attack!”

H2 is not rejecting and concludes that S2 Is prone to heart disease after predicting using Random Forest

S3	52	Male	Atypical Angina	140	100	No	Nothing to note	138	Yes	0.00	Upsloping

“You have lower risk of getting a heart disease!”

H3 is not rejecting and concludes that S3 is not prone to heart disease after predicting using Random Forest

S4	42	Male	Non-Anginal Pain	160	147	No	Nothing to note	146	No	0.00	Upsloping

“You have lower risk of getting a heart disease!”

H4 is not rejecting and concludes that S4 is not prone to heart disease after predicting using Random Forest

S5	48	Female	Asymptomatic	138	214	No	Nothing to note	108	Yes	1.50	Flatsloping

“You have lower risk of getting a heart disease!”.

H5 is rejecting and concludes that the output for S5 was wrong by using the Random Forest to make the prediction. The accuracy score was slightly lower than the StackCV model.

S6	59	Femal	Asymptomatic	130	338	Yes	ST-T	130	Yes	1.50	Flatslopin

		e					Wave abnormality				g

“Warning! You have a high risk of getting a heart attack!”

H6 is not rejecting and concludes that S6 Is prone to heart disease after predicting using Random Forest

S7	45	Female	Atypical Angina	130	237	No	Nothing to note	170	No	0.00	Upsloping

“You have lower risk of getting a heart disease!”

H7 is not rejecting and concludes that S7 is not prone to heart disease after predicting using Random Forest

S8	48	Female	Atypical Angina	120	284	No	Nothing to note	120	No	0.00	Upsloping

“You have lower risk of getting a heart disease!”

H8 is not rejecting and concludes that S8 is not prone to heart disease after predicting using Random Forest

In the nutshell, not all the prediction outcomes of the Random Forest are accurate because some output is different from the hypothesis that have been stated early. However, Random Forest also can be concluded as a reliable algorithm that can be used to predict heart disease because it has higher accuracy.

5. Discussion and Conclusion

5.1. Achievements

In this project I have learned how to use the different algorithms and how to apply them into the heart disease prediction project. In the process of developing the prototype I can define the benefits and disadvantages of each of the algorithms and differentiate between the algorithms. Besides learning algorithms such as Random Forest, Support Vector Machine and K-nearest neighbor, I also have tried using Stacking cross-validation in the project. Stacking CV is an ensemble learning technique by combining multiple models to improve the overall performance. It helps to reduce the overfitting and improve the generalization performance of the models. In the nutshell, I have learned evaluation of these algorithms and the technique based on their precision and accuracy based on the extraction dataset consisting of 3932 data from kaggle. All the algorithms and techniques have been evaluated and the most reliable algorithm is Random Forest but it is also lower than using the Stacking CV and the most unreliable is Support Vector Machine.

The project has fulfilled the objectives by providing the high prediction and accuracy result. The users have a simple prediction machine and can use the proposed prediction machine to predict the risk of getting heart disease. Therefore, they can save their money, time and the most important is increase their awareness about getting heart disease as they can easily and simply use the proposed machine to predict risk of getting heart disease. In conclusion, we can say that we have achieved the objectives.

5.2. Limitations and Future Works

The first limitation of the project is that the system only helps to predict the risk of getting heart disease but does not provide what type of heart disease might be prone to the users. For instance, the system only predicts based on the user's input and the output message only shows you have a high risk of getting heart disease and you have a low risk of getting heart disease does not contain the type of heart disease. Therefore, the solution can incorporate additional features into the model that can help to distinguish between the types of heart disease such as information about the user's medical history, family history disease and so on.

The second limitation is that the project does not provide any medical knowledge. For instance, if the user has a high risk of getting heart disease but it can be solved by changing the lifestyle without going to visit the doctor, it might help the user to save a lot of time and money and also take care of their body. The solution can be when in the designed process we can include the information of how to reduce the risk of heart disease through lifestyle change. The information includes the recommendations on diets, exercise, stress reduction and so on. Then after the prediction the system can provide this kind of message or suggestion to the user, if it is very serious it will also include the message of visit to the doctor the message will be priority on all the suggestions.

The third limitation is the application is language constraints This is because the application only supports a language which is English; this might not help the users who are without English knowledge. To address the limitation of this lack of scalability due to language constraints, the application can be designed to support multiple languages by involving incorporating machine translation capabilities which allows the users to input the information by using the native language if hope to have a higher accuracy, we can work with the medical experts in different regions to validate the risk assessment models and recommendations.

The last limitation is data update of supervised machine learning. The supervised machine learning relies on the train data to learn and make the predictions, if the data is outdated it may affect the accuracy of the prediction result. The solutions can be updated train data regularly. For example, regularly updating the training data with the new examples and data points of the application can help the model to adapt to changing trends and patterns in the data and improve the accuracy and performance over time.

Reference & Source

1. Brownlee, J. (2014). *A Gentle Introduction to Scikit-Learn*. [online] Machine Learning Mastery. Available at: https://machinelearningmastery.com/a-gentle-introduction-to-scikit-learn-a-python-machine-learning-library/#:~:text=Scikit%2Dlearn%20was%20initially%20developed.

2. Kaggle (2022). *Kaggle: Your Home for Data Science*. [online] Kaggle.com. Available at: https://www.kaggle.com/.

3. Donges, N. (2021). *A Complete Guide to the Random Forest Algorithm*. [online] Built in. Available at: https://builtin.com/data-science/random-forest-algorithm.

4. JavaTpoint (2021). K-Nearest Neighbor(KNN) Algorithm for Machine Learning - Javatpoint. [online] www.javatpoint.com. Available at: https://www.javatpoint.com/k-nearest-neighbor-algorithm-for-machine-learning.

5. Khan Academy. (n.d.). Machine learning algorithms (article). [online] Available at: https://www.khanacademy.org/computing/ap-computer-science-principles/data-analysis-101/x2d2f703b37b450a3:machine-learning-and-bias/a/machine-learning-algorithms#:~:te [Accessed 27 Apr. 2023].

6. Sunil, R. (2019). *Understanding Support Vector Machine algorithm from examples (along with code)*. [online] Analytics Vidhya. Available at: https://www.analyticsvidhya.com/blog/2017/09/understaing-support-vector-machine-example-code/.

7. Jindal, H. et al. (2021) “Heart disease prediction using machine learning algorithms,” in IOP Conference Series: Materials Science and Engineering. IOP Publishing Ltd. doi:10.1088/1757-899X/1022/1/012072.

8. FTM. 2021. [online] Available at: <https://www.freemalaysiatoday.com/category/nation/2021/11/16/heart-diseases-remain-the-top-killer-in-malaysia/>

9. CodeBlue (2020). *Nearly Half Of Malaysians Lack Health Coverage Beyond Public Care*. [online] CodeBlue. Available at: https://codeblue.galencentre.org/2020/06/02/nearly-half-of-malaysians-lack-health-coverag

-beyond-public-care/.