Project 1: Heart disease diagnosis

Machine Learning: Logistic Regression

Project build under the guidance of Professor Nitesh Karmakar

Machine Learning Mentor(KSI)

Facts

Every day, the average human heart beats around 100,000 times, pumping 2,000 gallons of blood through the body. Inside your body there are 60,000 miles of blood vessels.

The signs of a woman having a heart attack are much less noticeable than the signs of a male.

World Health Organization has estimated that four out of five cardiovascular diseases (CVD) deaths are due to heart attacks.

The prediction of heart disease is considered one of the most important topics in health domain.

Also,

The amount of data in the healthcare industry is huge.

With the machine learning algorithms and having large amounts of data, it is possible to extrapolate information that can help doctors make more accurate predictions.

Dataset

The dataset is a CSV(comma separated value) having 303 rows × 14 columns

Amongst that 14 column, there are 13 features and 1 labelled output column.

Each feature and it's significance is discussed in the next slide.

Heart disease describes a range of conditions that affect your heart.

- → Age: The person's age in years
- \rightarrow Sex: The person's sex (1 = male, 0 = female)
- → Chest Pain/Angina: The chest pain experienced
 - ♦ Value 1: typical
 - ♦ Value 2: nontypical
 - ♦ Value 3: asymptomatic
 - ♦ Value 4: nonanginal
- → **RestBP:** The person's resting blood pressure (mm Hg on admission to the hospital)
- → Chol: The person's cholesterol measurement in mg/dl
- → **Fbs:** The person's fasting blood sugar (> 120 mg/dl, 1 = true; 0 = false)
- → **RestECG:** Resting electrocardiographic measurement
 - \bullet 0 = normal
 - ◆ 1 = having ST-T wave abnormality
 - ◆ 2 = showing probable or definite left ventricular hypertrophy by Estes' criteria

- → MaxHR: The person's maximum heart rate achieved
- → ExAng: Exercise induced angina (1 = yes; 0 = no)
- → Oldpeak: ST depression induced by exercise relative to rest ('ST' relates to positions on the ECG plot.
- → Slope: the slope of the peak exercise ST segment
 - ◆ Value 1: upsloping
 - ◆ Value 2: flat
 - Value 3: downsloping
- → Ca: The number of major vessels (0-3)
- → Thal: A blood disorder called thalassemia
 - ◆ Value 1: normal
 - ◆ Value 2: fixed defect
 - ◆ Value 3: reversible defect

Understanding the code

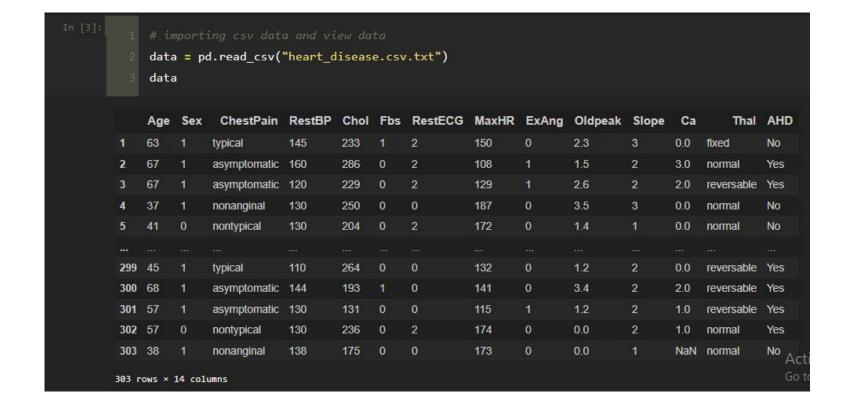
Understanding how to approach this Machine Learning Model

- 1. Importing libraries
- 2. Importing Dataset and Read the data (from csv)
- 3. Identify the dependent and independent variables.
- 4. Check if the data has missing values or the data is categorical or not.
- 5. Visualize the data.
- 6. Now split the data into the groups of training and testing for the respective purpose.
- 7. After splitting data, fit it to a most suitable model.
- 8. Prediction
- 9. Model Evaluation

1. Importing Libraries

```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

2. Importing Dataset and Reading the data



Checking rows and columns

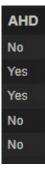
Checking first 5 values from the imported dataset

	1 da	ta.he	ead()											
	Age	Sex	ChestPain	RestBP	Chol	Fbs	RestECG	MaxHR	ExAng	Oldpeak	Slope	Ca	Thal	AHD
1	63	1	typical	145	233	1	2	150	0	2.3	3	0.0	fixed	No
2	67	1	asymptomatic	160	286	0	2	108	1	1.5	2	3.0	normal	Yes
3	67	1	asymptomatic	120	229	0	2	129	1	2.6	2	2.0	reversable	Yes
4	37	1	nonanginal	130	250	0	0	187	0	3.5	3	0.0	normal	No
5	41	0	nontypical	130	204	0	2	172	0	1.4	1	0.0	normal	No

3. Identify the dependent and independent variables.

	Age	Sex	ChestPain	RestBP	Chol	Fbs	RestECG	MaxHR	ExAng	Oldpeak	Slope	Ca	Thal
1	63	1	typical	145	233	1	2	150	0	2.3	3	0.0	fixed
2	67	1	asymptomatic	160	286	0	2	108	1	1.5	2	3.0	normal
3	67	1	asymptomatic	120	229	0	2	129	1	2.6	2	2.0	reversable
4	37	1	nonanginal	130	250	0	0	187	0	3.5	3	0.0	normal
5	41	0	nontypical	130	204	0	2	172	0	1.4	1	0.0	normal

Dependent Variable:



Dependent variable exists

- Since the AHD column exists, which depends on the independent 13 features. Hence, it is dependent variable.
- As dependent variable exists, it falls into the category of supervised learning.
- Also, the output of the model is either Yes or No. It is a binary classification.
- Hence, we will use Logistic Regression for this problem.

Why choose Logistic Regression?

Logistic Regression is a statistical and machine-learning techniques classifying records of a dataset based on the values of the input fields.

It predicts a dependent variable based on one or more set of independent variables to predict outcomes .

It can be used both for binary classification and multi-class classification

In this project, we have to predict whether the person has heart disease or not, which means, it falls into the category of binary classification(Since, we have to predict-Yes/No).

4. Check if the data has missing values or the data is categorical or not.

Changing string data type to numeric data type:

- Data generally needs to be put into numeric form for machine learning algorithms to use the data to make predictions.
- Since machine learning model completely works on mathematics and numbers, but if our dataset would have a categorical variable, then it may create trouble while building the model. So it is necessary to encode these categorical variables into numbers.

```
data["ChestPain"] = lb.fit_transform(data["ChestPain"])
```

	Age	Sex	ChestPain	RestBP	Chol	Fbs	RestECG	MaxHR	ExAng	Oldpeak	Slope	Ca	Thal
1	63	1	typical	145	233	1	2	150	0	2.3	3	0.0	fixed
2	67	1	asymptomatic	160	286	0	2	108	1	1.5	2	3.0	normal
3	67	1	asymptomatic	120	229	0	2	129	1	2.6	2	2.0	reversable
4	37	1	nonanginal	130	250	0	0	187	0	3.5	3	0.0	normal
5	41	0	nontypical	130	204	0	2	172	0	1.4	1	0.0	normal

After Label Encoding:

Age	Sex	ChestPain	RestBP	Chol	Fbs	RestECG	MaxHR	ExAng	Oldpeak	Slope	Ca	Thal	AHD
63	1	3	145	233	1	2	150	0	2.3	3	0.0	fixed	No
67	1	0	160	286	0	2	108	1	1.5	2	3.0	normal	Yes
67	1	Ö	120	229	0	2	129	1	2.6	2	2.0	reversable	Yes
37	1	1	130	250	0	0	187	0	3.5	3	0.0	normal	No
41	0	2	130	204	0	2	172	0	1.4	1	0.0	normal	No
	63 67 67 37	63 1 67 1 67 1 37 1	63 1 3 67 1 0 67 1 0 37 1 1	63 1 3 145 67 1 0 160 67 1 0 120 37 1 1 130	63 1 3 145 233 67 1 0 160 286 67 1 0 120 229 37 1 1 130 250	63 1 3 145 233 1 67 1 0 160 286 0 67 1 0 120 229 0 37 1 1 130 250 0	63 1 3 145 233 1 2 67 1 0 160 286 0 2 67 1 0 120 229 0 2 37 1 1 130 250 0 0	63 1 3 145 233 1 2 150 67 1 0 160 286 0 2 108 67 1 0 120 229 0 2 129 37 1 1 130 250 0 0 187	63 1 3 145 233 1 2 150 0 67 1 0 160 286 0 2 108 1 67 1 0 120 229 0 2 129 1 37 1 1 130 250 0 0 187 0	63 1 3 145 233 1 2 150 0 2.3 67 1 0 160 286 0 2 108 1 1.5 67 1 0 120 229 0 2 129 1 2.6 37 1 1 130 250 0 0 187 0 3.5	63 1 3 145 233 1 2 150 0 2.3 3 67 1 0 160 286 0 2 108 1 1.5 2 67 1 0 120 229 0 2 129 1 2.6 2 37 1 1 130 250 0 0 187 0 3.5 3	67 1 0 160 286 0 2 108 1 1.5 2 3.0 67 1 0 120 229 0 2 129 1 2.6 2 2.0 37 1 1 130 250 0 0 187 0 3.5 3 0.0	63 1 3 145 233 1 2 150 0 2.3 3 0.0 fixed 67 1 0 160 286 0 2 108 1 1.5 2 3.0 normal 67 1 0 120 229 0 2 129 1 2.6 2 2.0 reversable 37 1 1 130 250 0 0 187 0 3.5 3 0.0 normal

	Age	Sex	ChestPain	RestBP	Chol	Fbs	RestECG	MaxHR	ExAng	Oldpeak	Slope	Ca	Thal
1	63	1	typical	145	233	1	2	150	0	2.3	3	0.0	fixed
2	67	1	asymptomatic	160	286	0	2	108	1	1.5	2	3.0	normal
3	67	1	asymptomatic	120	229	0	2	129	1	2.6	2	2.0	reversable
4	37	1	nonanginal	130	250	0	0	187	0	3.5	3	0.0	normal
5	41	0	nontypical	130	204	0	2	172	0	1.4	1	0.0	normal

After Label Encoding:

n [11]:		1 da	ta.he	ead()											
		Age	Sex	ChestPain	RestBP	Chol	Fbs	RestECG	MaxHR	ExAng	Oldpeak	Slope	Ca	Thal	AHD
	1	63	1	3	145	233	1	2	150	0	2.3	3	0.0	0	No
	2	67	1	0	160	286	0	2	108	1	1.5	2	3.0	1	Yes
	3	67	1	0	120	229	0	2	129	1	2.6	2	2.0	2	Yes
	4	37	1	1	130	250	0	0	187	0	3.5	3	0.0	1	No
	5	41	0	2	130	204	0	2	172	0	1.4	1	0.0	1	No

Dropping NaN/Null Values:

```
data = data.dropna()
    data.isna().sum()
Age
Sex
            0
ChestPain
RestBP
Cho1
            0
Fbs
            0
RestECG
            0
MaxHR
ExAng
            0
Oldpeak
            0
Slope
            0
Ca
            0
Thal
            0
AHD
dtype: int64
```

Unique values for each variable:

```
data.nunique(axis=0)
Age
             41
Sex
ChestPain
RestBP
             50
Chol
            152
Fbs
RestECG
MaxHR
             91
ExAng
Oldpeak
             40
Slope
Ca
Thal
AHD
dtype: int64
```

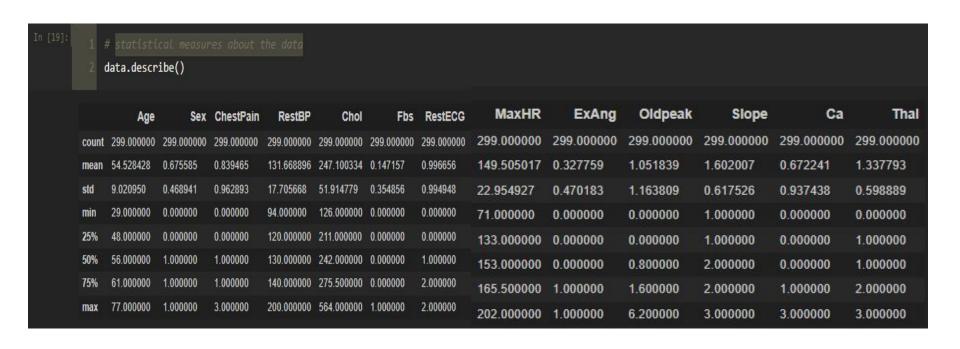
Concise summary of data:

```
data.info()
<class 'pandas.core.frame.DataFrame'>
Int64Index: 299 entries, 1 to 302
Data columns (total 14 columns):
               Non-Null Count Dtype
    Column
    Age
               299 non-null
                               int64
    Sex
               299 non-null
                                int64
    ChestPain
               299 non-null
                               int32
    RestBP
               299 non-null
                               int64
    Chol
                299 non-null
                               int64
    Fbs
                299 non-null
                               int64
    RestECG
                299 non-null
                               int64
    MaxHR
               299 non-null
                               int64
    ExAng
               299 non-null
                               int64
    01dpeak
               299 non-null
                               float64
    Slope
               299 non-null
                               int64
11
    Ca
               299 non-null
                               float64
    Thal
               299 non-null
                               int32
12
13
    AHD
               299 non-null
                               object
dtypes: float64(2), int32(2), int64(9), object(1)
memory usage: 32.7+ KB
```

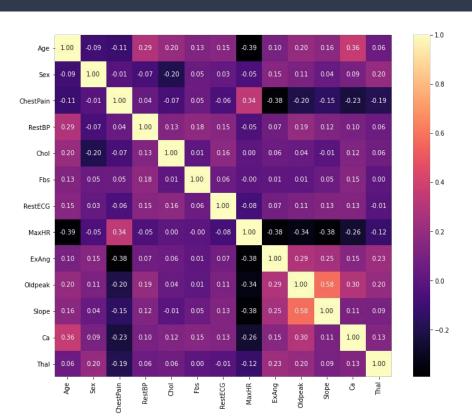
Rows and columns in the dataset after dropping NaN values:

```
In [16]: 1 # number of rows and columns in the dataset
2 data.shape
(299, 14)
```

Statistical measures about the data:



Correlation matrix: Correlation indicates how the features are related to each other or to the target variable.



5. Visualizing the data

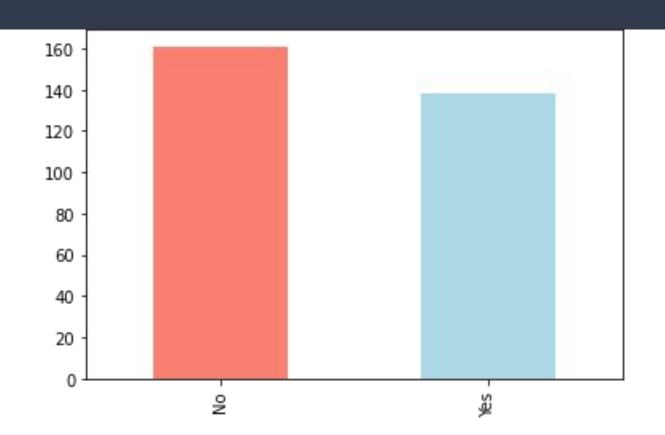
```
1. Counting the AHD value and plotting the graph for number of pateints having heart disease

In [21]:

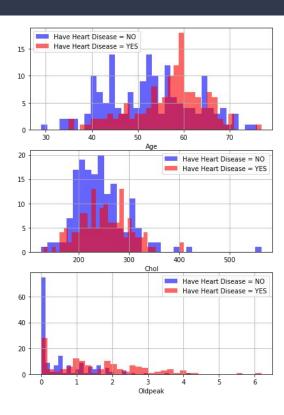
# checking the distribution of AHD Variable
data['AHD'].value_counts()

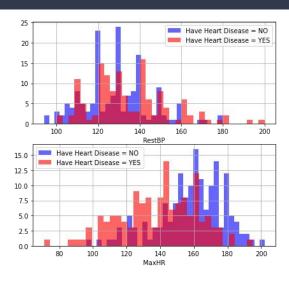
No 161
Yes 138
Name: AHD, dtype: int64
```

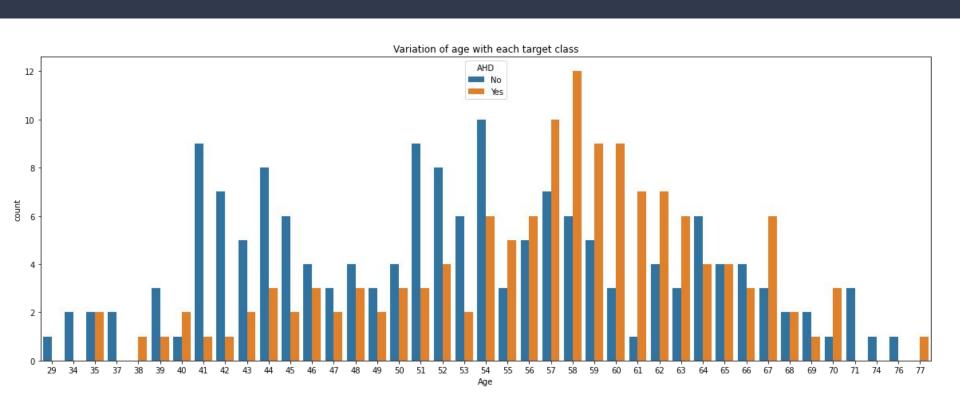
Graph for number of patients having heart disease:



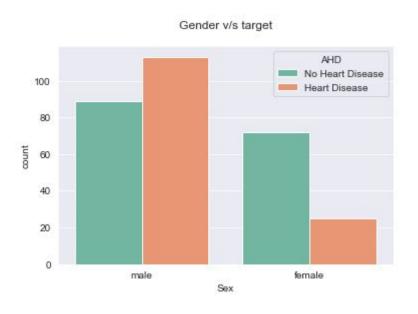
Relation of various attributes with the target:



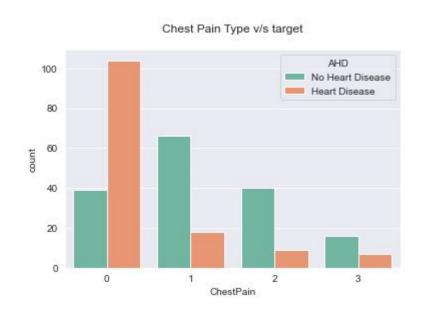




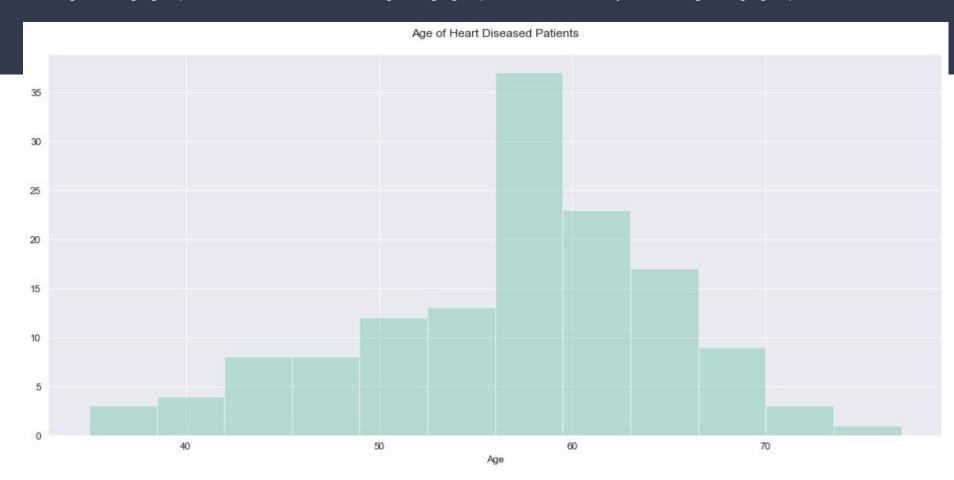
According to this dataset, **Males** are more susceptible to get Heart Disease than **Females**.



- There are four types of chest pain, typical, non typical, asymptomatic and nonanginal.
- Most of the Heart Disease patients are found to have asymptomatic chest pain
 - ♦ Value 1: typical
 - ♦ Value 2: non typical
 - ♦ Value 3: asymptomatic
 - ♦ Value 4: nonanginal



Heart Disease is very common in the seniors which is composed of **age group 60 and above** and common among adults which belong to the age group of **41 to 60**. But it's rare among the age group of **19 to 40** and very rare among the age group of 0 to 18.



5. Prepare Data for Modeling

```
features = data.drop(columns='AHD', axis=1)
target = data['AHD']
```

6. Splitting the data

```
In [35]:
1     from sklearn.model_selection import train_test_split
2     X_train, X_test, y_train, y_test = train_test_split(features, target,test_size=0.25, random_state=45)

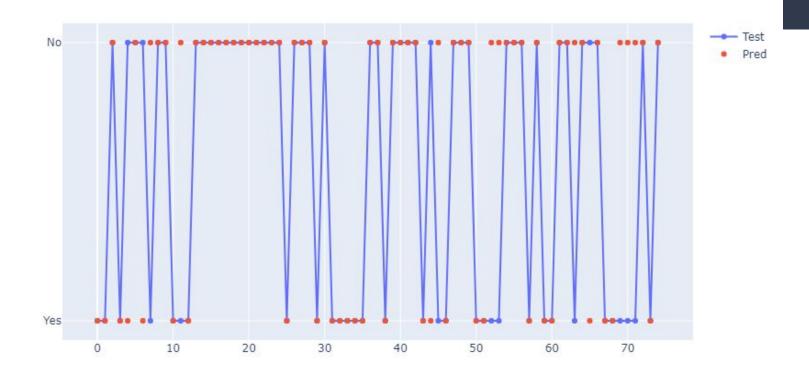
In [36]:
1     print(f'features.shape: {features.shape}, X_train.shape: {X_train.shape}, X_test.shape: {X_test.shape}'

features.shape: (299, 13), X_train.shape: (224, 13), X_test.shape: (75, 13)
```

7. Fitting into Model

8. Prediction and plotting 'predicted and actual' graph

```
y_pred = model.predict(X_test)
   actual = []
   predcition = []
   for i, j in zip(y_test, y_pred):
       actual.append(i)
       predcition.append(j)
   dic = {
        'Actual': actual,
       'Prediction': predcition
   result = pd.DataFrame(dic)
   import plotly.graph_objects as go
fig = go.Figure()
   fig.add_trace(go.Scatter(x=np.arange(0,len(y_test)), y=y_test,
                       mode='markers+lines',
                       name='Test'))
fig.add trace(go.Scatter(x=np.arange(0,len(y test)), y=y pred,
                       mode='markers',
                       name='Pred'))
```



- The red dots represent the predicted values that are either 0 or 1 and the blue line & and dot represents the actual value of that particular patient.
- In the places where the red dot and blue dot do not overlap are the wrong predictions and where the both dots overlap those are the right predicted values.

9. Model Evaluation

```
In [40]: 1 from sklearn.metrics import accuracy_score
In [41]: 1 # accuracy on training data
2 X_train_prediction = model.predict(X_train)
3 training_data_accuracy = accuracy_score(X_train_prediction, y_train)
In [42]: 1 print('Accuracy on Training data : ', training_data_accuracy)
Accuracy on Training data : 0.8705357142857143
```

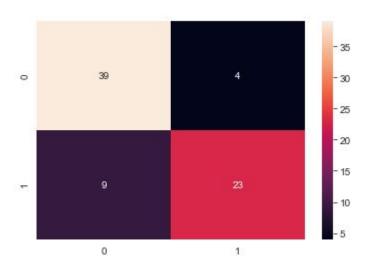
Accuracy on Training data: 0.8705357142857143

Accuracy on Testing data: 0.826666666666667

Classification Report:

```
from sklearn.metrics import classification_report
    print(classification_report(y_test,y_pred))
            precision
                       recall f1-score
                                        support
        No
                0.81
                         0.91
                                  0.86
                                            43
                0.85
                         0.72
                                  0.78
                                            32
       Yes
                                  0.83
                                            75
   accuracy
  macro avg
                0.83
                         0.81
                                  0.82
                                            75
weighted avg
                0.83
                                  0.82
                                            75
                         0.83
```

Confusion Matrix



Thank You!

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Confusion Matrix

Predicted

Actual

	Negative	Positive
Negative	True Negative	False Positive
Positive	False Negative	True Positive

Confusion Matrix:

True Positive (TP) — model correctly predicts the positive class (prediction and actual both are positive). In the above example, 10 people who have tumors are predicted positively by the model.

True Negative (TN) — model correctly predicts the negative class (prediction and actual both are negative). In the above example, 60 people who don't have tumors are predicted negatively by the model.

False Positive (FP) — model gives the wrong prediction of the negative class (predicted-positive, actual-negative). In the above example, 22 people are predicted as positive of having a tumor, although they don't have a tumor. FP is also called a TYPE I error.

False Negative (FN) — model wrongly predicts the positive class (predicted-negative, actual-positive). In the above example, 8 people who have tumors are predicted as negative. FN is also called a TYPE II error.

Precision:

Precision talks about how precise/accurate your model is out of those predicted positive, how many of them are actual positive.

	Predicted	
	Negative	Positive
Negative	True Negative	False Positive
Positive	False Negative	True Positive
		Negative Negative True Negative

$$Precision = \frac{True \ Positive}{True \ Positive + False \ Positive}$$
$$= \frac{True \ Positive}{Total \ Predicted \ Positive}$$

Recall:

Recall actually calculates how many of the Actual Positives our model capture through labeling it as Positive (True Positive)

Actual Positive Positive Positive False Positive True Negative True Positive True Positive

$$\begin{aligned} \text{Recall} &= \frac{\textit{True Positive}}{\textit{True Positive} + \textit{False Negative}} \\ &= \frac{\textit{True Positive}}{\textit{Total Actual Positive}} \end{aligned}$$

F1 Score:

F1 Score is needed when you want to seek a balance between Precision and Recall.

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