In [1]:	Heart Disease Classification  Import Necessary Libraries  import numpy as np
111 [1].	<pre>import pandas as pd import seaborn as sns import matplotlib.pyplot as plt  from sklearn.model_selection import train_test_split from sklearn.metrics import accuracy_score, confusion_matrix, classification_report from sklearn.linear_model import LogisticRegression from sklearn.preprocessing import StandardScaler  import warnings</pre>
	warnings.filterwarnings('ignore')
In [2]:	About Dataset  # Age: Refers to the number of years a person has lived; it is a critical factor in assessing health risks, # including heart-related conditions, as risks often increase with age. # gender: (0 for Female, 1 for Male) # # Heart Rate (Impulse): The number of times the heart beats per minute, indicating cardiovascular activity.
	# # Systolic BP (Pressurehigh): The pressure in the arteries when the heart contracts and pumps blood. # # Diastolic BP (Pressurelow): The pressure in the arteries when the heart is at rest between beats. # Blood Sugar (Glucose): The amount of glucose present in the blood, crucial for energy and metabolism. # CK-MB (KCM): An enzyme found in the heart muscle; elevated levels indicate heart muscle damage. # # Test-Troponin (Troponin): A protein released into the blood when the heart muscle is damaged, a key marker for diagnosing heart attacks.  1. Load & Data Acquisition
In [40]: Out[40]:	df = pd.read_csv("Heart Attack.csv")           age gender impluse pressurehight pressurelow glucose kcm troponin class           0         64         1         66         160         83         160.0         1.80         0.012 negative           1         21         1         94         98         46         296.0         6.75         1.060 positive           2         55         1         64         160         77         270.0         1.99         0.003 negative           3         64         1         70         120         55         270.0         13.87         0.122 positive           4         55         1         64         112         65         300.0         1.08         0.003 negative
	2. Data Preprocessing  # View the first 5 rows of the dataset df.head()  age gender impluse pressurehight pressurelow glucose kcm troponin class
In [42]:	0         64         1         66         160         83         160.0         1.80         0.012         negative           1         21         1         94         98         46         296.0         6.75         1.060         positive           2         55         1         64         160         77         270.0         1.99         0.003         negative           3         64         1         70         120         55         270.0         13.87         0.122         positive           4         55         1         64         112         65         300.0         1.08         0.003         negative   # Check for missing values
Out[42]:	<pre>age     0 gender     0 impluse     0 pressurehight    0 pressurelow    0 glucose     0 kcm      0 troponin     0 class     0 dtype: int64</pre>
In [43]: Out[43]:	# summary of the df df.describe()    age   gender   impluse   pressurehight   pressurelow   glucose   kcm   troponin     count   1319.000000   1319.000000   1319.000000   1319.000000   1319.000000   1319.000000   1319.000000   1319.000000   1319.000000   1319.000000   1319.000000     mean   56.191812   0.659591   78.336619   127.170584   72.269143   146.634344   15.274306   0.360942     std   13.647315   0.474027   51.630270   26.122720   14.033924   74.923045   46.327083   1.154568
In [44]:	min       14.000000       0.000000       20.000000       42.000000       38.000000       0.0321000       0.001000         25%       47.000000       0.000000       64.000000       110.000000       98.000000       1.655000       0.006000         50%       58.000000       1.000000       74.000000       124.000000       72.000000       116.000000       2.850000       0.014000         75%       65.000000       1.000000       85.000000       143.000000       541.000000       58.05000       0.085500         max       103.000000       1.000000       1111.000000       223.000000       541.000000       300.000000       10.300000
	Cclass 'pandas.core.frame.DataFrame'>           RangeIndex: 1319 entries, 0 to 1318           Data columns (total 9 columns):           # Column Non-Null Count Cou
In [45]:	6 kcm 1319 non-null float64 7 troponin 1319 non-null float64 8 class 1319 non-null object dtypes: float64(3), int64(5), object(1) memory usage: 92.9+ KB  EDA (Exploratory Data Analysis)  fig = plt.figure(figsize = (15, 4))
	<pre>plt.pie(df[['class']].groupby('class').size(), labels =['Negative', 'Positive'], explode=(0, 0.1), autopct='%1.1f%%', shadow=True) plt.show()  Negative 38.6%</pre>
	61.4%
In [46]: Out[46]:	<pre>sns.displot(data = df,x = 'age',kind = 'kde',fill = True) <seaborn.axisgrid.facetgrid 0x2119f11f810="" at=""></seaborn.axisgrid.facetgrid></pre>
	0.025 - 0.020 - 21 0.015 -
	0.005
In [47]:	<pre>columns = df.columns[3:6]  for col in columns:     sns.displot(df[col], kind = 'kde', color='blue')     plt.title(f'Distribution of {col}')     plt.xlabel(col)     plt.show()</pre>
	0.016 - 0.014 - 0.012 -
	0.000 - 0.006 - 0.004 -
	0.000  Distribution of pressurelow
	0.025 -
	0.015 - 0.010 - 0.005 -
	0.000 40 60 80 100 120 140 160 pressurelow  Distribution of glucose
	0.000 - O.000
	0.002 -
In [48]: Out[48]:	0 100 200 300 400 500 600  Glucose  Outliers Handling  sns.boxplot (data = df, y = 'age')
	100 -
	90 - 40 - 20 - 40 - 40 - 40 - 40 - 40 - 4
In [62]:	<pre># Function to remove outliers using the IQR method def remove_outliers(df):     for column in df.select_dtypes(include=['number']).columns: # Numerical columns only         Q1 = df[column].quantile(0.25)         Q3 = df[column].quantile(0.75)         IQR = Q3 - Q1         lower_bound = Q1 - 1.5 * IQR         upper_bound = Q3 + 1.5 * IQR</pre>
In [73]:	<pre>df = df[(df[column] &gt;= lower_bound) &amp; (df[column] &lt;= upper_bound)]     return df  # Remove outliers from the dataset df = remove_outliers(df)  def Boxplot(df):     for column in df.select_dtypes(include=['number']).columns:         sns.boxplot(df[column])         plt.title(f"Boxplot of {column}")         plt.show()</pre>
	# Call the function Boxplot (df)  Boxplot of age  90 -
	70 - 60 - 50 - 40 -
	30 - 20 - Boxplot of gender 1.0 -
	0.6 -
	0.2 - 0.0 - 0
	Boxplot of impluse  110 -
	80 - 70 - 60 - 50 -
	Boxplot of pressurehight  180 - 160 -
	120 -
	Boxplot of pressurelow
	100 - 90 - 80 - 70 -
	60 - 50 - 40 - 0
	225 - 200 - 175 - 150 -
	125 - 100 - 75 -
	50
	5 - 4 - 3 - 2 -
	Boxplot of troponin
	0.030 - 0.025 - 0.020 - 0.015 -
	0.010 - 0.005 - 0
In [89]:	<pre># Initialize StandardScaler scaler = StandardScaler()  # Select feature columns to scale feature_columns = ['age', 'gender', 'impluse', 'pressurehight', 'pressurelow', 'glucose',</pre>
	<pre># Apply StandardScaler df[feature_columns] = scaler.fit_transform(df[feature_columns])  # Separate features (X) and target (y) X = df.drop(columns=["class"]) y = df["class"]  # Split data into training and testing sets X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)  print(X_train.shape) print(X_test.shape)</pre>
Out[84]: In [85]:	LogisticRegression(random_state=42)  # Make predictions y_pred = model.predict(X_test)
In [90]: Out[90]:	<pre>comparison_df = pd.DataFrame({"Actual":y_test, "Predicted":y_pred}) comparison_df  Actual Predicted  1253 positive positive  1201 positive positive  541 negative negative  1208 positive positive</pre>
	1133 negative negative   197 negative negative  1197 negative negative  1102 negative negative  68 negative negative  766 negative negative
In [86]:	# Evaluate the model accuracy = accuracy_score(y_test, y_pred) print(f"Accuracy: {accuracy:.2f}")  Accuracy: 0.91  # Classification report and confusion matrix print("\nClassification Report:") print(classification_report(y_test, y_pred))
	Classification_report(y_test, y_pred))  Classification Report:     precision    recall f1-score    support  negative    0.91    0.96    0.94    77 positive    0.91    0.81    0.86    37  accuracy
In [144	<pre>print("\nConfusion Matrix:") conf_matrix = confusion_matrix(y_test, y_pred) sns.heatmap(conf_matrix, annot=True, fmt="d", cmap="Reds", xticklabels=["No Disease", "Disease"], yticklabels=["No Disease", "Disease"]) plt.xlabel("Predicted") plt.ylabel("Actual") plt.title("Confusion Matrix") plt.show()</pre> Confusion Matrix:  Confusion Matrix
	- 70 - 60 - 50
	- 30 - 20 - 10
In [116 In [117	No Disease Disease Predicted  Naive Bayes  from sklearn.naive_bayes import GaussianNB  nb = GaussianNB()
Out[117]: In [118	<pre>nb.fit(X_train,y_train)  v GaussianNB GaussianNB()  y_pred = nb.predict(X_test)  print("\nNaive Bayes Model")</pre>
In [124	print("Accuracy: ",accuracy_score(y_test,y_pred))  Naive Bayes Model Accuracy: 0.9210526315789473  Random Forest  from sklearn.ensemble import RandomForestClassifier
In [126 Out[126]:	# Initialize Random Forest classifier  rf_model = RandomForestClassifier(n_estimators=100, random_state=42)  # Train the model  rf_model.fit(X_train,y_train)  V RandomForestClassifier  RandomForestClassifier(random_state=42)
	y_pred = rf_model.predict(X_test)  print("\nRandom Forest Classifier") print("Accuracy: ",accuracy_score(y_test,y_pred))  Random Forest Classifier Accuracy: 0.9736842105263158  Support Vector Classiffier
	<pre>from sklearn.svm import SVC  # Initialize Support Vector Machine classifier svm_model = SVC(kernel='linear', random_state=42) # 'linear' kernel for linear SVM svm_model.fit(X_train,y_train)</pre> <pre>v</pre>
In [140	<pre>SVC(kernel='linear', random_state=42)  y_pred = svm_model.predict(X_test)  print("\nSupport Vector Classifier") print("Accuracy: ",accuracy_score(y_test,y_pred))  Support Vector Classifier Accuracy: 0.9298245614035088</pre>
In [115	<pre>def predict_heart_disease():     print("Please enter the following details:")  # Step 1: Taking input from the user     age = int(input("Enter age: "))     gender = int(input("Enter Gender: "))     impluse = float(input("Enter impluse: "))     pressurehight = float(input("Enter pressurehight: "))     pressurelow = float(input("Enter pressurehight: "))     glucose = float(input("Enter Glucose: "))     kcm = float(input("Enter kcm: "))     troponin = float(input("Enter troponin: "))</pre>
	<pre>troponin = float(input("Enter troponin: "))  # Step 2: Create a feature vector from the user input input_data = np.array([[age, gender, impluse, pressurehight, pressurelow, glucose,</pre>
	<pre># Step 5: Output the result print(f"\nPredicted Class: {prediction}")  # Call the function predict_heart_disease()  Please enter the following details: Enter age: 90 Enter Gender: 0 Enter impluse: 25 Enter pressurehight: 120 Enter pressurehight: 120 Enter pressurelow: 80 Enter pressurelow: 80</pre>
In [141	<pre>Enter Glucose: 200 Enter kcm: 0.2 Enter troponin: 0.01  Predicted Class: negative  from sklearn.svm import SVC kernels = ['linear', 'poly', 'rbf', 'sigmoid']  for kernel in kernels:     svm_model = SVC(kernel=kernel)     svm_model.fit(X_train, y_train) # Assuming you have training data</pre>
In [ ]:	