Task 2

Disease PREDICTION

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INITIALIZING

Libraries importing

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score, confusion_matrix
```

Loading the Data

```
# Load the dataset
data = pd.read_csv('data.csv')
testdata = pd.read_csv('test_data.csv')
# Display the first few rows of the dataset
print(data.head())
```

DATASET

[5 rows x 25 columns]

- Glucose,
- Cholesterol,
- Hemoglobin,
- Platelets,
- White Blood Cells,
- Red Blood Cells,
- Hematocrit,
- Mean Corpuscular Volume,
- Mean Corpuscular Hemoglobin,
- Mean Corpuscular Hemoglobin Concentration,
- Insulin,
- BMI,
- Systolic Blood Pressure,
- Diastolic Blood Pressure,
- Triglycerides,
- HbA1c,
- LDL Cholesterol,
- HDL Cholesterol,
- ALT,
- AST,
- Heart Rate,
- · Creatinine,
- Troponin,
- C-reactive Protein,
- Disease

```
Red Blood Cells Hematocrit Mean Corpuscular Volume
       0.529895
                  0.290006
                                           0.631045
      0.403033
                  0.164216
                                           0.307553
      0.382021
                  0.625267
                                           0.295122
      0.166214
                  0.073293
                                           0.668719
      0.439851
                                           0.442159
                  0.894991
Mean Corpuscular Hemoglobin Mean Corpuscular Hemoglobin Concentration \
                  0.001328
                                                             0.795829
                  0.207938
                                                             0.505562
                  0.868369
                                                             0.026808
                  0.125447
                                                             0.501051
                  0.257288
                                                             0.805987
       HbA1c LDL Cholesterol HDL Cholesterol
                                                     ALT
                                                               AST \
... 0.502665
                     0.215560
                                      0.512941 0.064187 0.610827
                     0.652465
... 0.856810
                                      0.106961 0.942549 0.344261
... 0.466795
                     0.387332
                                      0.421763 0.007186 0.506918
... 0.016256
                     0.040137
                                      0.826721 0.265415 0.594148
... 0.429431
                     0.146294
                                      0.221574 0.015280 0.567115
Heart Rate Creatinine Troponin C-reactive Protein
 0.939485
             0.095512 0.465957
                                           0.769230
                                                     Healthy
 0.666368
             0.659060 0.816982
                                           0.401166 Diabetes
 0.431704
             0.417295 0.799074
                                           0.779208
                                                    Thalasse
 0.225756
                  NaN 0.637061
                                           0.354094
                                                      Anemia
             0.153350 0.794008
                                           0.094970
                                                    Thalasse
```

DATA PREPROCESSING

Data Preprocessing

```
# Check for missing values
print(data.isnull().sum())
# Fill missing values if any (for simplicity, using mean of the columns here)
data = data.fillna(data.mean())
# Separate features and target variable
X_train = data.drop('Disease', axis=1)
y_train = data['Disease']

X_test = testdata.drop('Disease', axis=1)
y_test = testdata['Disease']

disease_classes = y_train.unique() # Assuming all disease classes are present in the training set
# Define the mapping dictionary
mapping = {disease_class: 1 for disease_class in disease_classes}

# Apply the mapping to both the training and test target variables
y_train = y_train.apply(lambda x: 0 if x == 'Healthy' else 1)
y_test = y_test.apply(lambda x: 0 if x == 'Healthy' else 1)
```

```
# Standardize the features
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
# will have a mean of 0 and a standard deviation of 1 after transformation.
```

OUR MODEL

Building and Training the Model

```
from sklearn.ensemble import AdaBoostClassifier
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score

# Initialize the SVM base estimator
base_estimator = SVC(kernel='linear', probability=True)
# Initialize the AdaBoost classifier with SVM as the base estimator
adaboost_svm_classifier = AdaBoostClassifier(base_estimator=base_estimator, n_estimators=50, random_state=42)
# Train the AdaBoost classifier
adaboost_svm_classifier.fit(X_train, y_train)
```

PREDICTION

Making Predictions and Evaluating the Model

```
y_pred = adaboost_svm_classifier.predict(X_test)
accuracy = accuracy_score(y_test, y_pred)
precision = precision_score(y_test, y_pred, average='weighted')
recall = recall score(y test, y pred, average='weighted')
f1 = f1 score(y test, y pred, average='weighted')
print(f'Accuracy: {accuracy * 100:.2f}%')
print(f'Precision: {precision* 100:.2f}%')
print(f'Recall: {recall:.2f}')
print(f'F1 Score: {f1:.2f}')
conf_matrix = confusion_matrix(y_test, y_pred)
sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='Blues')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix')
plt.show()
```

ACCURACY

Accuracy: 98.97%

Precision: 97.95%

Recall: 98.97%

F1 Score: 98.46%



