healthcare capstone

May 29, 2023

[1]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split, RandomizedSearchCV
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import cross_val_score, StratifiedKFold
from sklearn.metrics import classification_report, roc_auc_score, roc_curve, auc
```

[2]:
```
# 0 for Glucose, BloodPressure, SkinThickness, Insulin, BMI doesn't make sense␣
 ↪and indicates missing value
dfd=pd.read_csv('health care diabetes.csv')
dfd
```

[2]:
```
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0              6      148             72             35        0  33.6
1              1       85             66             29        0  26.6
2              8      183             64              0        0  23.3
3              1       89             66             23       94  28.1
4              0      137             40             35      168  43.1
..           …        …            …            …      …    …
763           10      101             76             48      180  32.9
764            2      122             70             27        0  36.8
765            5      121             72             23      112  26.2
766            1      126             60              0        0  30.1
767            1       93             70             31        0  30.4

     DiabetesPedigreeFunction  Age  Outcome
0                       0.627   50        1
1                       0.351   31        0
2                       0.672   32        1
3                       0.167   21        0
4                       2.288   33        1
..                        …    …      …
```

```
763                       0.171   63        0
764                       0.340   27        0
765                       0.245   30        0
766                       0.349   47        1
767                       0.315   23        0

[768 rows x 9 columns]
```

[3]:
```
dfd.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   Pregnancies               768 non-null    int64
 1   Glucose                   768 non-null    int64
 2   BloodPressure             768 non-null    int64
 3   SkinThickness             768 non-null    int64
 4   Insulin                   768 non-null    int64
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64
 8   Outcome                   768 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

[4]:
```
# dont have null values but 0 doe
dfd.isnull().sum()
```

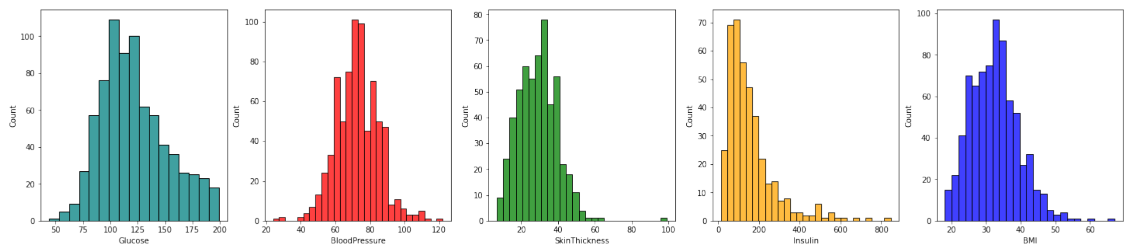
[4]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

[5]:
```
# replace 0 values with NaN for selected columns
dfd[['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']] =␣
↪dfd[['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']].
↪replace(0, np.NaN)
```

[6]:
```
# now null values show
dfd.isnull().sum().value_counts(normalize=True)
```

[6]:
```
0      0.444444
11     0.111111
227    0.111111
374    0.111111
5      0.111111
35     0.111111
dtype: float64
```

[7]:
```
# exploring these variables using histograms
x, axes = plt.subplots(1, 5, figsize=(25,5))
sns.histplot(dfd.Glucose, ax=axes[0], color='teal')
sns.histplot(dfd.BloodPressure, ax=axes[1], color='red')
sns.histplot(dfd.SkinThickness, ax=axes[2], color='green')
sns.histplot(dfd.Insulin, ax=axes[3], color='orange')
sns.histplot(dfd.BMI, ax=axes[4], color='blue')
plt.show()
```

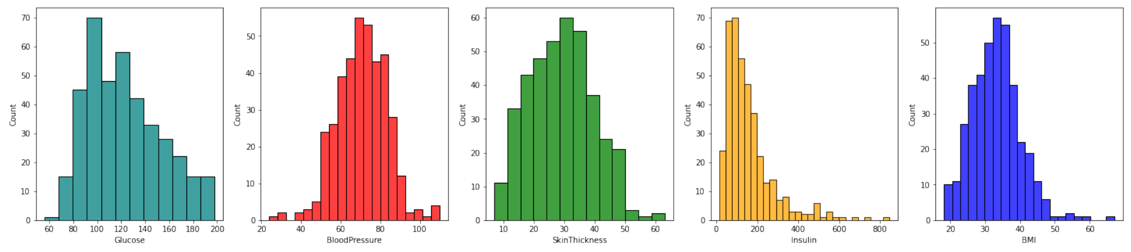


[8]:
```
dfd2=dfd.dropna()
```

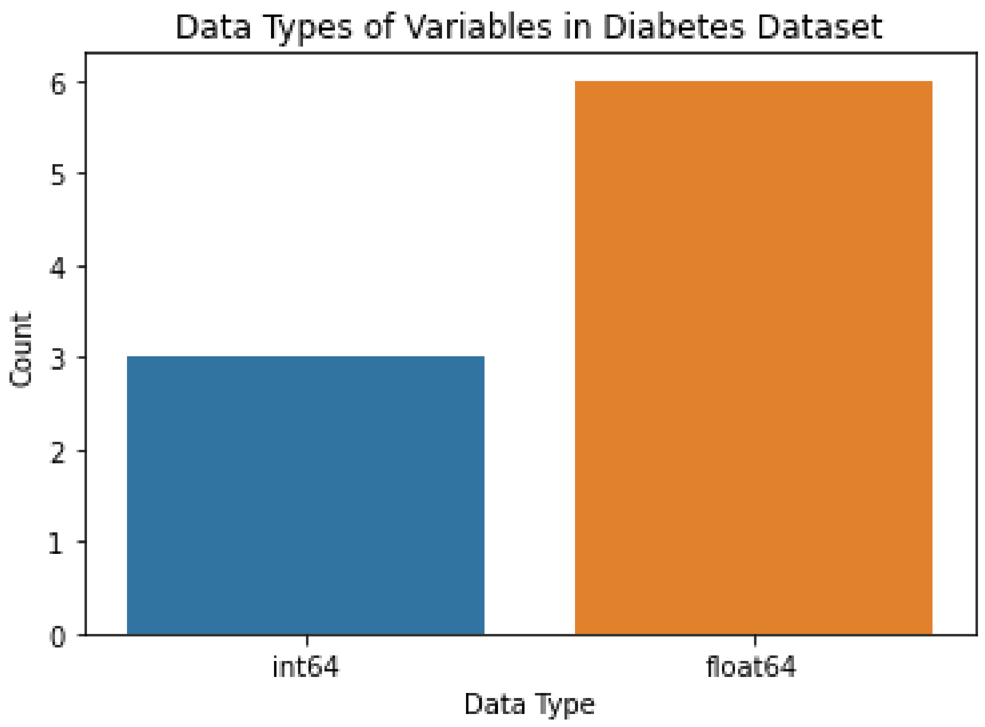
[9]:
```
dfd2.shape
```

[9]:
```
(392, 9)
```

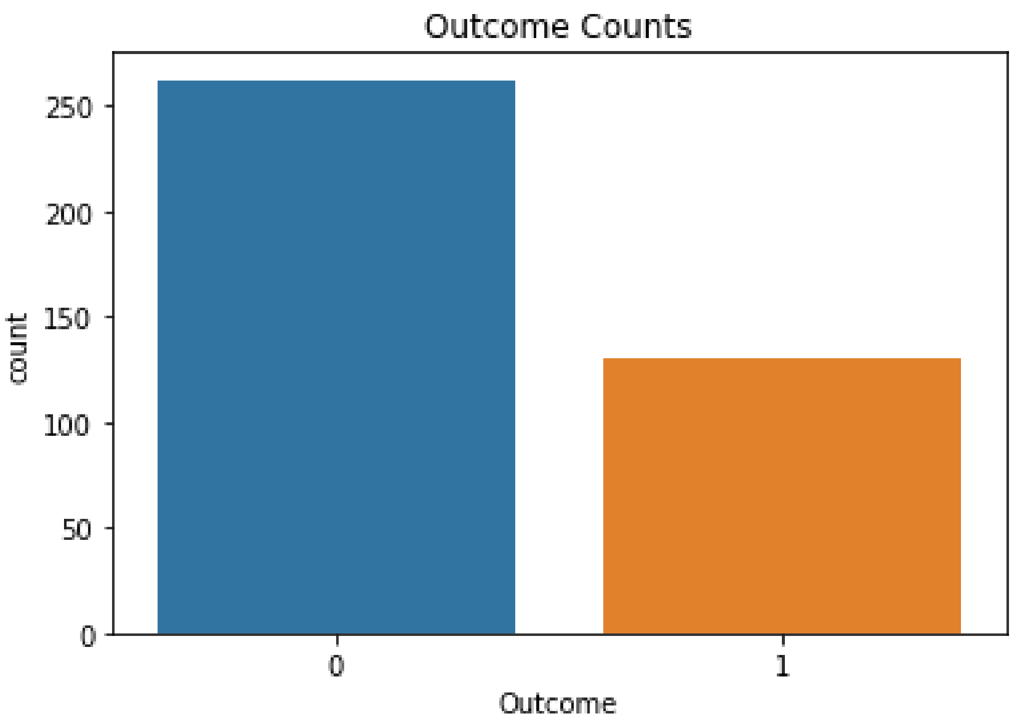
[10]:
```
# dropped the missing values
x, axes = plt.subplots(1, 5, figsize=(25,5))
sns.histplot(dfd2.Glucose, ax=axes[0], color='teal')
sns.histplot(dfd2.BloodPressure, ax=axes[1], color='red')
sns.histplot(dfd2.SkinThickness, ax=axes[2], color='green')
sns.histplot(dfd2.Insulin, ax=axes[3], color='orange')
sns.histplot(dfd2.BMI, ax=axes[4], color='blue')
plt.show()
```



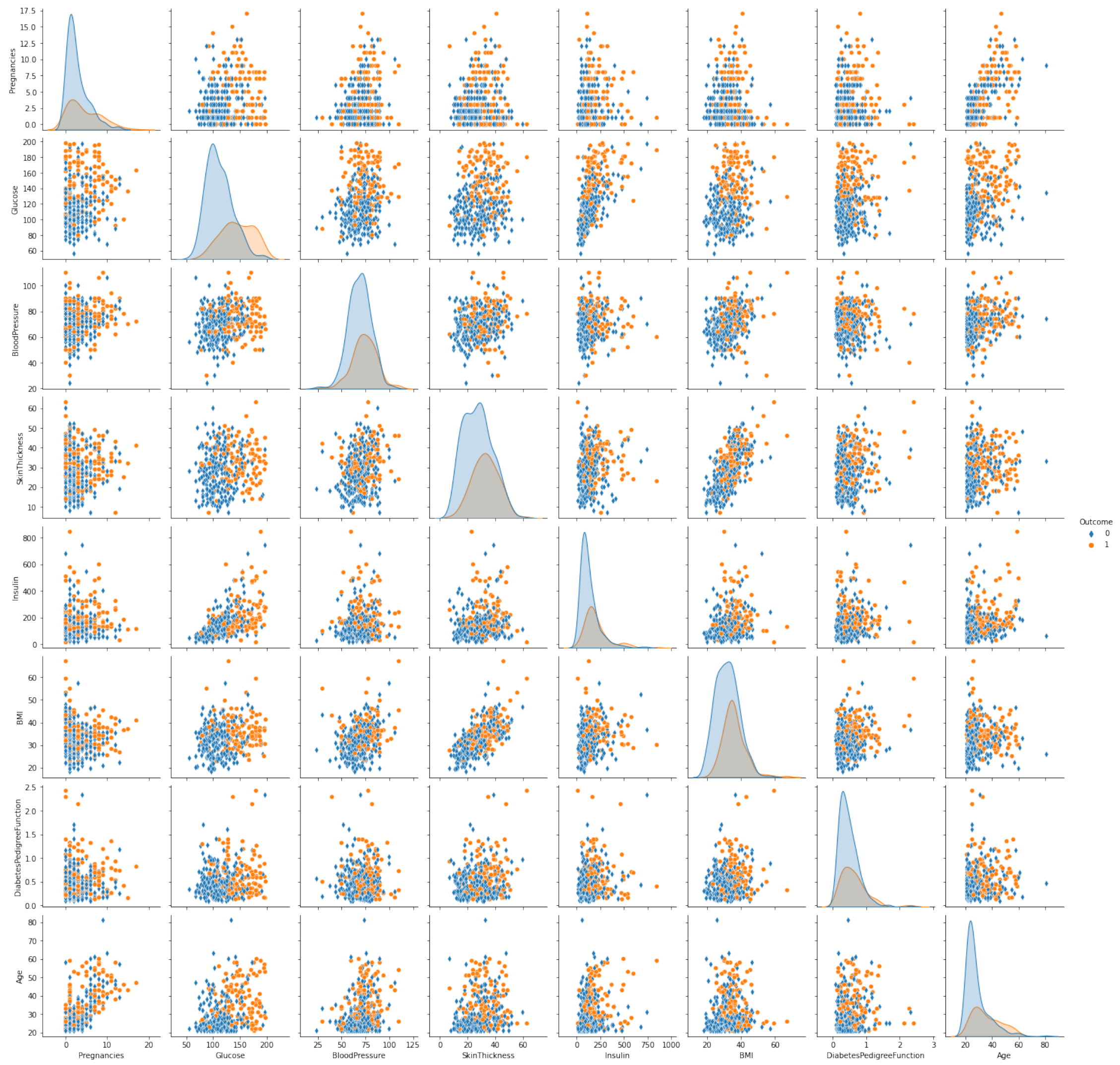
[11]:
```
# count (frequency) plot describing the data types and the count of variables
sns.countplot(data=dfd, x=dfd.dtypes)
plt.title('Data Types of Variables in Diabetes Dataset')
plt.xlabel('Data Type')
plt.ylabel('Count')
plt.show()
```



[12]:
```
# check the balance of the data
sns.countplot(x='Outcome', data=dfd2)
plt.title('Outcome Counts')
plt.show()
# the dataset is imbalanced, with more patients having an outcome of 0 (no␣
↪diabetes) than 1 (diabetes)
```



```
[13]: # scatter charts between the pair of variables to understand the relationships
      sns.pairplot(dfd2, hue='Outcome', markers=['d', 'o'])
      plt.show()
```



0.0.1 Scatterplot findings

-Age and Pregnancies shows a positive correlation. As the number of pregnancies increase, the age of the patient tends to increase as well.

-Glucose and Outcome shows a positive correlation. Patients with higher glucose levels are more likely to have diabetes.

-BloodPressure and Outcome does not show a clear correlation between the two variables.

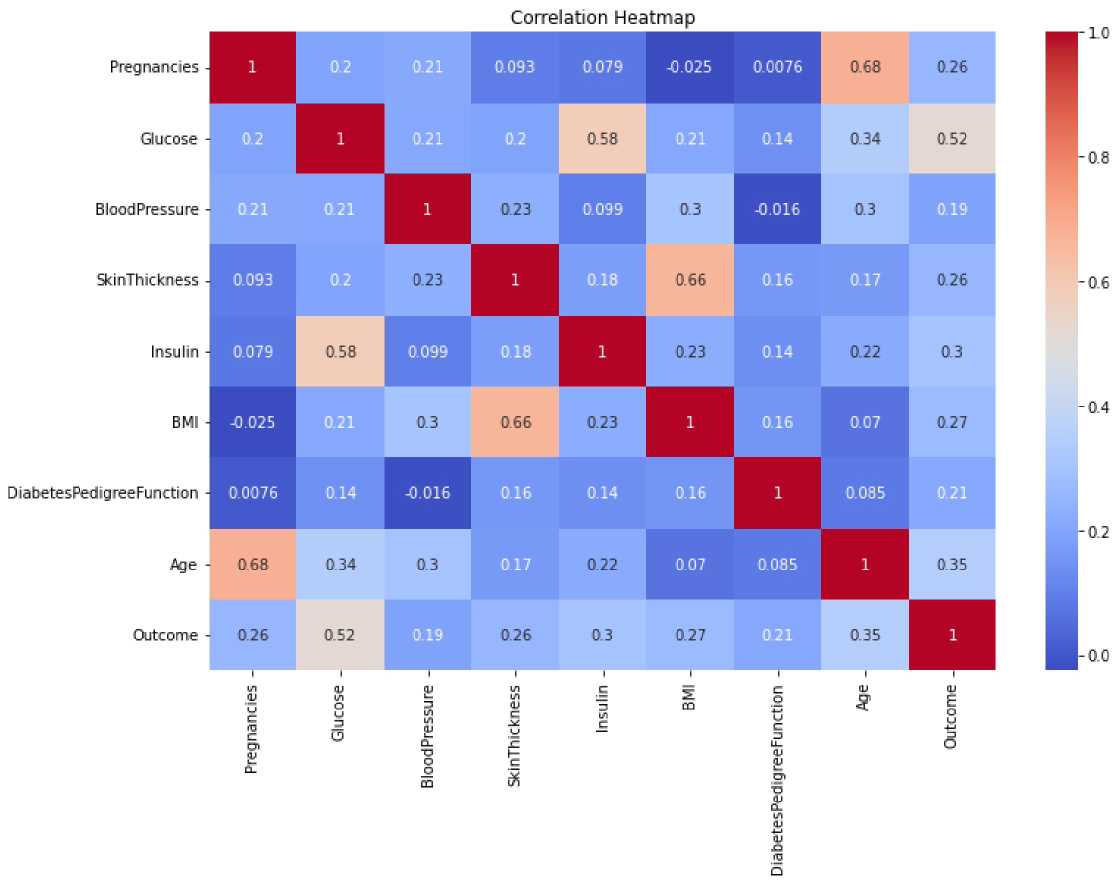
-SkinThickness and BMI shows a positive correlation. Patients with higher BMI tend to have higher skin thickness.

-Insulin and Glucose shows a positive correlation. Patients with higher glucose levels tend to have higher insulin levels.

-BMI and Outcome shows a positive correlation. Patients with higher BMI levels are more likely to have diabetes.

-DiabetesPedigreeFunction and Age shows that patients with higher diabetes pedigree function tend to be older.

[14]:
```
# correlation analysis with a heatmap
corr = dfd2.corr()
plt.figure(figsize=(12,8))
sns.heatmap(corr, annot=True, cmap='coolwarm')
plt.title('Correlation Heatmap')
plt.show()
# glucose has the biggest correlation with having diabetes
```



	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1	0.2	0.21	0.093	0.079	-0.025	0.0076	0.68	0.26
Glucose	0.2	1	0.21	0.2	0.58	0.21	0.14	0.34	0.52
BloodPressure	0.21	0.21	1	0.23	0.099	0.3	-0.016	0.3	0.19
SkinThickness	0.093	0.2	0.23	1	0.18	0.66	0.16	0.17	0.26
Insulin	0.079	0.58	0.099	0.18	1	0.23	0.14	0.22	0.3
BMI	-0.025	0.21	0.3	0.66	0.23	1	0.16	0.07	0.27
DiabetesPedigreeFunction	0.0076	0.14	-0.016	0.16	0.14	0.16	1	0.085	0.21
Age	0.68	0.34	0.3	0.17	0.22	0.07	0.085	1	0.35
Outcome	0.26	0.52	0.19	0.26	0.3	0.27	0.21	0.35	1

[15]:
```
# separate the input data from the target variable, so that the model can learn␣
↪the relationship between the two.
X = dfd2.drop('Outcome', axis=1)
# prepare data to predict outcome by setting it equal to y
y = dfd2['Outcome']
```

```
[16]: X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.20,␣
       ↪random_state=42)
      print(X_train.shape, X_test.shape)
      print(y_train.shape, y_test.shape)
```

```
(313, 8) (79, 8)
(313,) (79,)
```

```
[17]: # so we can refer to the variable name instead of having to type out the entire␣
       ↪classifier name each time we want to use it.
      knn = KNeighborsClassifier()
      lr = LogisticRegression(max_iter=1000)
      rf = RandomForestClassifier()
      svm = SVC()
```

```
[18]: # creating a dictionary named models that maps each algorithm name to its␣
       ↪corresponding model.
      models = {'KNN': knn, 'Logistic Regression': lr, 'Random Forest': rf, 'Support␣
       ↪Vector Machine': svm}
```

```
[19]: # perform cross-validation on classification models using stratified 5-fold␣
       ↪cross-validation and report the mean accuracy and standard deviation of the␣
       ↪accuracy scores for each model
      for name, model in models.items():
          kfold = StratifiedKFold(n_splits=5, shuffle=True, random_state=42)
          scores = cross_val_score(model, X, y, cv=kfold, scoring='accuracy')
          print(f'{name} Accuracy: {np.mean(scores)} +/- {np.std(scores)}')
```

```
KNN Accuracy: 0.7245050308341447 +/- 0.027375430575277974
Logistic Regression Accuracy: 0.7780266147354755 +/- 0.030093848040059545
Random Forest Accuracy: 0.7858487504057123 +/- 0.027227646289426977
Support Vector Machine Accuracy: 0.77036676403765 +/- 0.012148198212065897
```

```
[20]: # Train the model and make predictions
      model.fit(X_train, y_train)
      y_pred = model.predict(X_test)

      # check if predict_proba is available
      if hasattr(model, 'predict_proba'):
          y_prob = model.predict_proba(X_test)[:, 1]  # Probabilities for positive␣
       ↪class
      elif hasattr(model, 'decision_function'):
          y_scores = model.decision_function(X_test)  # provides confidence scores
          y_prob = (y_scores - y_scores.min()) / (y_scores.max() - y_scores.min())  #␣
       ↪Normalize to [0, 1] to make them comparable to probabilities
      else:
```

```
    raise AttributeError("Model does not have 'predict_proba' or␣
↪'decision_function' attribute.") # no predict_proba/decision_function␣
↪attribute, no probabilities or confidence scores so raise error
```

[21]:
```
# generates a classification report by comparing the predicted labels y_pred␣
↪with the true labels y_test.
report = classification_report(y_test, y_pred)
# AUC score provides a summary of the model's performance to distinguish␣
↪between positive and negative samples across different classification␣
↪thresholds.
auc = roc_auc_score(y_test, y_prob)
```

[22]:
```
# classification report is a summary of the model's performance for each class
print("Classification Report:")
print(report)
print("AUC: {:.3f}".format(auc))
```

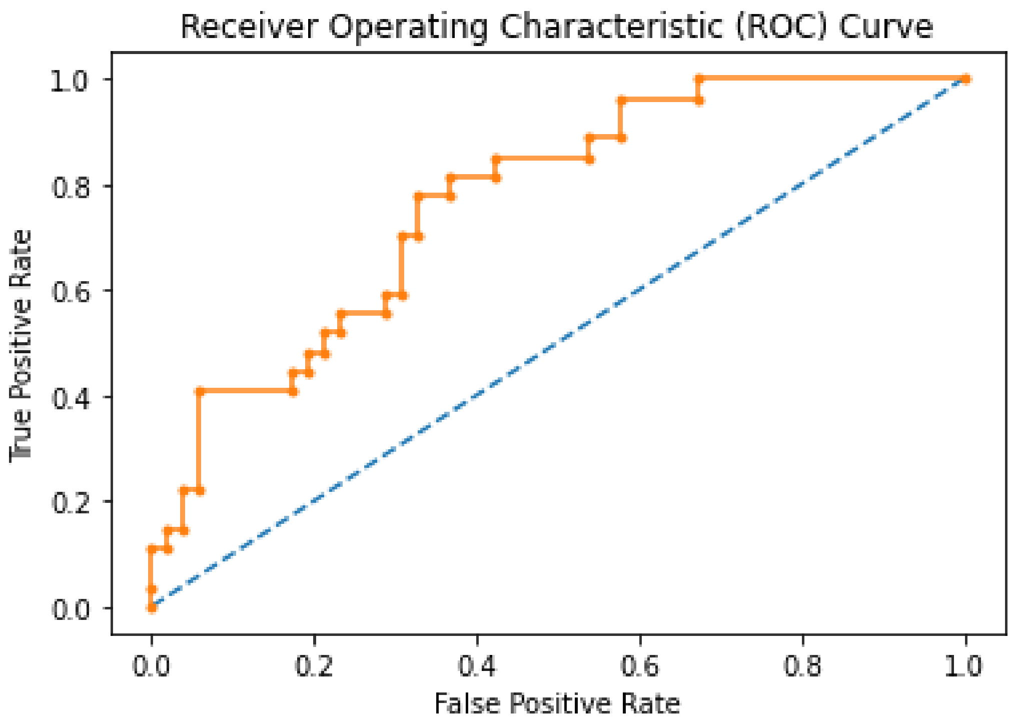
```
Classification Report:
              precision    recall  f1-score   support

           0       0.75      0.92      0.83        52
           1       0.73      0.41      0.52        27

    accuracy                           0.75        79
   macro avg       0.74      0.67      0.68        79
weighted avg       0.74      0.75      0.72        79

AUC: 0.770
```

[23]:
```
# calculate roc curve
fpr, tpr, thresholds = roc_curve(y_test, y_prob)
plt.plot([0, 1], [0, 1], linestyle='--')
plt.plot(fpr, tpr, marker='.')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.show()
```


Receiver Operating Characteristic (ROC) Curve
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0

```
[ ]:
```