at-5114-ai-in-hc-lp-diab-ch

March 6, 2024

```
[13]: IMPORTING LIBRARIES:
```

```
[53]: import numpy as np
      import pandas as pd
      import matplotlib.pyplot as plt
      import seaborn as sns
      from pandas.plotting import scatter_matrix
      from sklearn.preprocessing import StandardScaler
      from sklearn.model_selection import train_test_split
      from sklearn.ensemble import RandomForestClassifier
      from sklearn.tree import DecisionTreeClassifier
      from sklearn.svm import SVC
      from sklearn.feature_selection import RFE
      from sklearn.metrics import confusion_matrix, classification_report,␣
        ↪accuracy_score
      import warnings

      warnings.filterwarnings('ignore')
      %matplotlib inline
```

```
[ ]: DATASET UPLOAD:
```

```
[54]: diabetes_df = pd.read_csv('C:\\Users\\HP\\Downloads\\archive (1)\\diabetes.csv')
      diabetes_df.head()
```

```
[54]:    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

         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
```

[ ]:
```
EXPLORATORY DATA ANALYSIS:
```

[55]:
```
diabetes_df.columns
```

[55]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

[ ]:
```
INFORMATION ABOUT DATASET:
```

[56]:
```
diabetes_df.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
```

[ ]:
```
CHECKING THE NULL VALUES IN DATASET:
```

[57]:
```
diabetes_df.isnull().head(10)
```

[57]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin    BMI  \
0        False    False          False          False    False  False
1        False    False          False          False    False  False
2        False    False          False          False    False  False
3        False    False          False          False    False  False
4        False    False          False          False    False  False
5        False    False          False          False    False  False
6        False    False          False          False    False  False
7        False    False          False          False    False  False
8        False    False          False          False    False  False
9        False    False          False          False    False  False
```

```
   DiabetesPedigreeFunction    Age  Outcome
0                     False  False    False
1                     False  False    False
2                     False  False    False
3                     False  False    False
4                     False  False    False
5                     False  False    False
6                     False  False    False
7                     False  False    False
8                     False  False    False
9                     False  False    False
```

[17]:
```
diabetes_df.isnull().sum()
```

[17]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

[ ]:
```
"In the given code snippet, the approach to handling missing values diverges␣
 ↪from traditional null-checking methods. Rather than explicitly checking for␣
 ↪null values using isnull() and calculating their sum, the code immediately␣
 ↪addresses potential missing data by creating a copy of the original dataset␣
 ↪(diabetes_df_copy). This copy is then subjected to imputation techniques␣
 ↪without initially distinguishing between explicit nulls and 0 values. The␣
 ↪specified columns - 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',␣
 ↪and 'BMI' - undergo mean imputation directly through fillna(diabetes_df_copy.
 ↪mean()). Consequently, missing or zero values are replaced with the mean of␣
 ↪each respective column. The subsequent display of NaN counts through␣
 ↪print(diabetes_df_copy.isnull().sum()) provides insights into the␣
 ↪effectiveness of the imputation process in handling missing or zero values␣
 ↪within the dataset."
```

[58]:
```
import numpy as np
import pandas as pd

# Load the dataset
diabetes_df = pd.read_csv('C:\\Users\\HP\\Downloads\\archive (1)\\diabetes.csv')

# Define columns to replace and create a copy of the dataframe
```

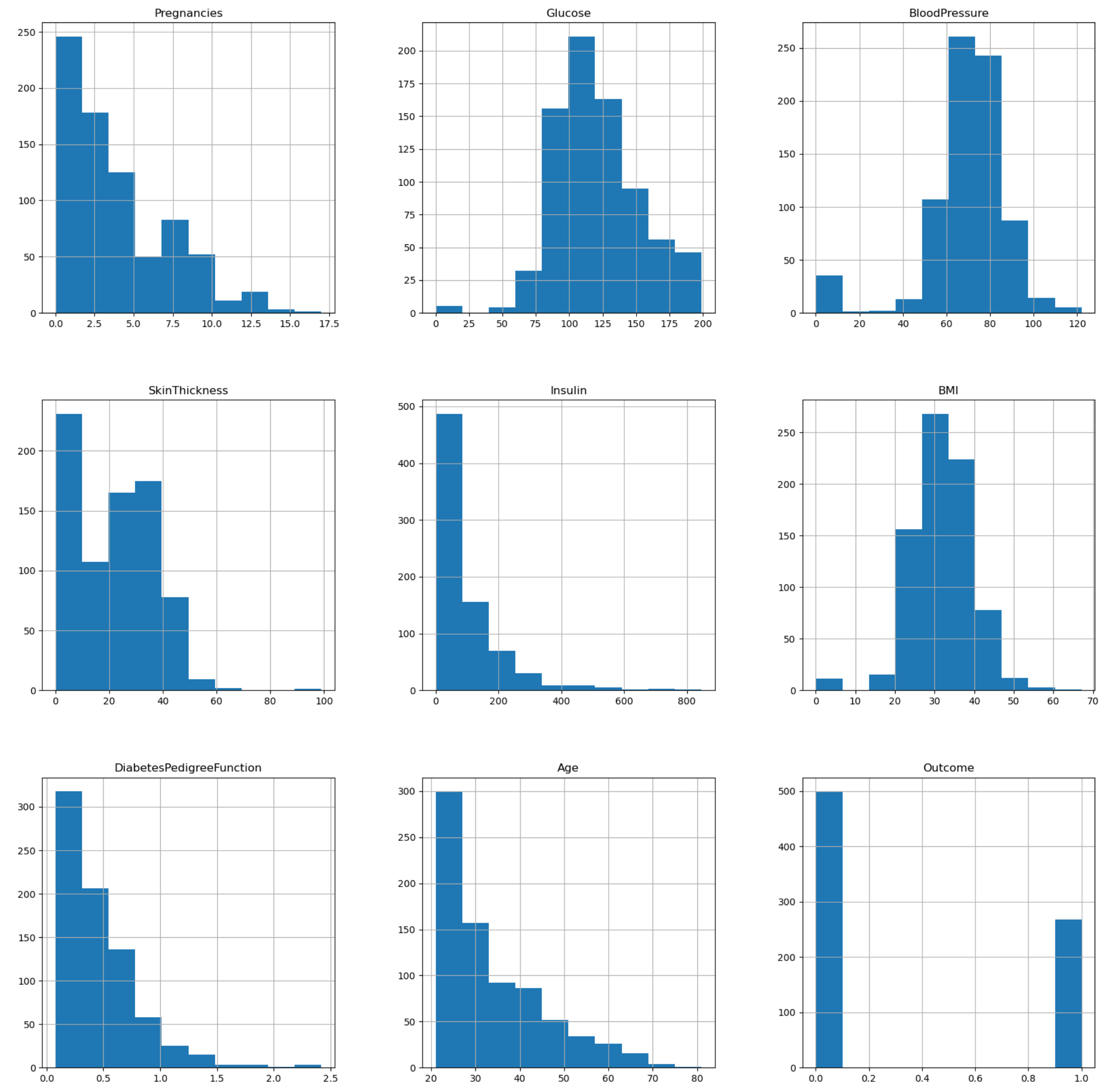
```
columns_to_replace = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',␣
 ↪'BMI']
diabetes_df_copy = diabetes_df.copy(deep=True)

# Alternatively, consider using imputation techniques for missing values
# Using mean imputation for the specified columns
diabetes_df_copy.fillna(diabetes_df_copy.mean(), inplace=True)

# Displaying the Count of NANs after imputation
print(diabetes_df_copy.isnull().sum())
```

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

[ ]:
```
DATA VISUALIZATION:
```

[ ]:
```
DATA DISTRIBUTION PLOTS BEFORE REMOVING THE NULL VALUES :
```

[59]:
```
p = diabetes_df.hist(figsize = (20,20))
```

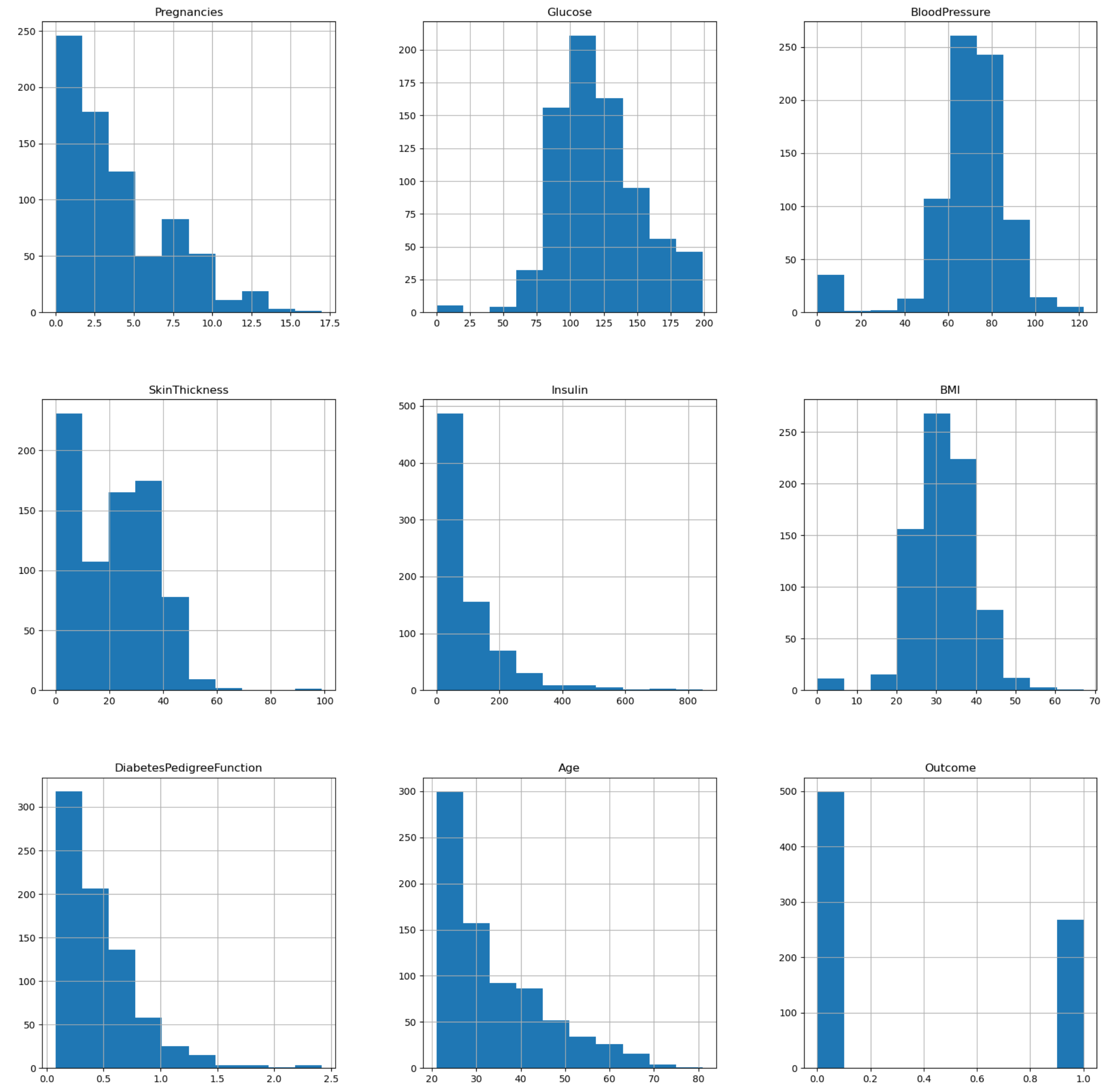


```
[ ]: Now we will be imputing the mean value of the column to each missing value of␣
      ↪that particular column.
```

```
[27]: diabetes_df_copy['Glucose'].fillna(diabetes_df_copy['Glucose'].mean(), inplace␣
       ↪= True)
      diabetes_df_copy['BloodPressure'].fillna(diabetes_df_copy['BloodPressure'].
       ↪mean(), inplace = True)
      diabetes_df_copy['SkinThickness'].fillna(diabetes_df_copy['SkinThickness'].
       ↪median(), inplace = True)
      diabetes_df_copy['Insulin'].fillna(diabetes_df_copy['Insulin'].median(),␣
       ↪inplace = True)
      diabetes_df_copy['BMI'].fillna(diabetes_df_copy['BMI'].median(), inplace = True)
```

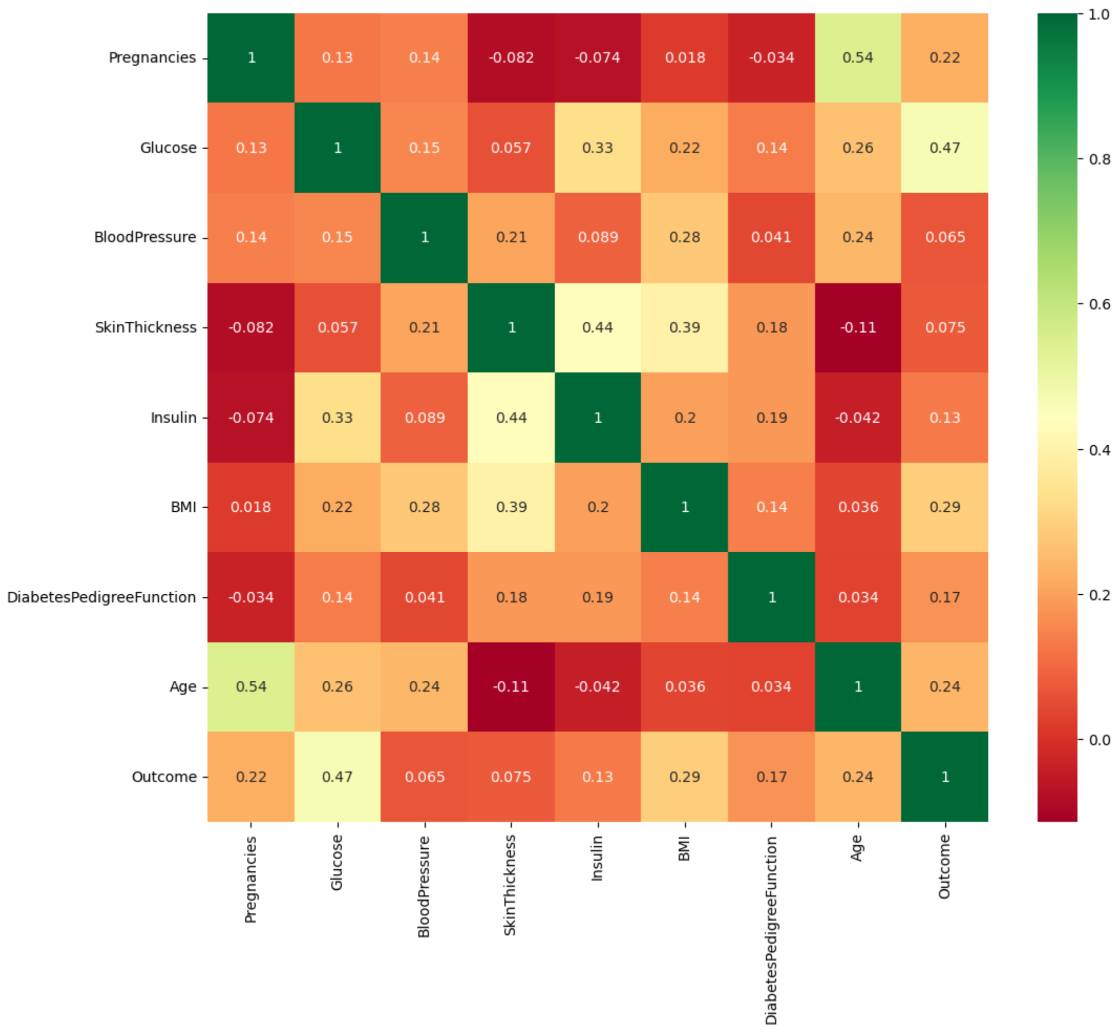
```
[ ]: DATA DISTRIBUTION PLOTS AFTER REMOVING THE NULL VALUES:
```

```
[60]: # Data Distribution Plots after imputation
      p = diabetes_df_copy.hist(figsize=(20, 20))
```



```
[ ]: FEATURES CORRELATION:
```

```
[61]: plt.figure(figsize=(12, 10))
      correlation_matrix = diabetes_df.corr()
      sns.heatmap(correlation_matrix, annot=True, cmap='RdYlGn')
      plt.show()
```



	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1	0.13	0.14	-0.082	-0.074	0.018	-0.034	0.54	0.22
Glucose	0.13	1	0.15	0.057	0.33	0.22	0.14	0.26	0.47
BloodPressure	0.14	0.15	1	0.21	0.089	0.28	0.041	0.24	0.065
SkinThickness	-0.082	0.057	0.21	1	0.44	0.39	0.18	-0.11	0.075
Insulin	-0.074	0.33	0.089	0.44	1	0.2	0.19	-0.042	0.13
BMI	0.018	0.22	0.28	0.39	0.2	1	0.14	0.036	0.29
DiabetesPedigreeFunction	-0.034	0.14	0.041	0.18	0.19	0.14	1	0.034	0.17
Age	0.54	0.26	0.24	-0.11	-0.042	0.036	0.034	1	0.24
Outcome	0.22	0.47	0.065	0.075	0.13	0.29	0.17	0.24	1

[ ]:
```
DATA SCALING:
```

[ ]:
```
Let's check the data before scaling it
```

[62]:
```
diabetes_df_copy.head()
```

[62]:
```
   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

   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
```

[ ]:
```
AFTER STANDARD SCALING:
```

[63]:
```
columns_to_scale = ['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness',␣
 ↪'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age']

sc_X = StandardScaler()
X = pd.DataFrame(sc_X.fit_transform(diabetes_df_copy[columns_to_scale]),␣
 ↪columns=columns_to_scale)
X.head()
```

[63]:
```
   Pregnancies   Glucose  BloodPressure  SkinThickness   Insulin       BMI  \
0     0.639947  0.848324       0.149641       0.907270 -0.692891  0.204013
1    -0.844885 -1.123396      -0.160546       0.530902 -0.692891 -0.684422
2     1.233880  1.943724      -0.263941      -1.288212 -0.692891 -1.103255
3    -0.844885 -0.998208      -0.160546       0.154533  0.123302 -0.494043
4    -1.141852  0.504055      -1.504687       0.907270  0.765836  1.409746

   DiabetesPedigreeFunction       Age
0                  0.468492  1.425995
1                 -0.365061 -0.190672
2                  0.604397 -0.105584
3                 -0.920763 -1.041549
4                  5.484909 -0.020496
```

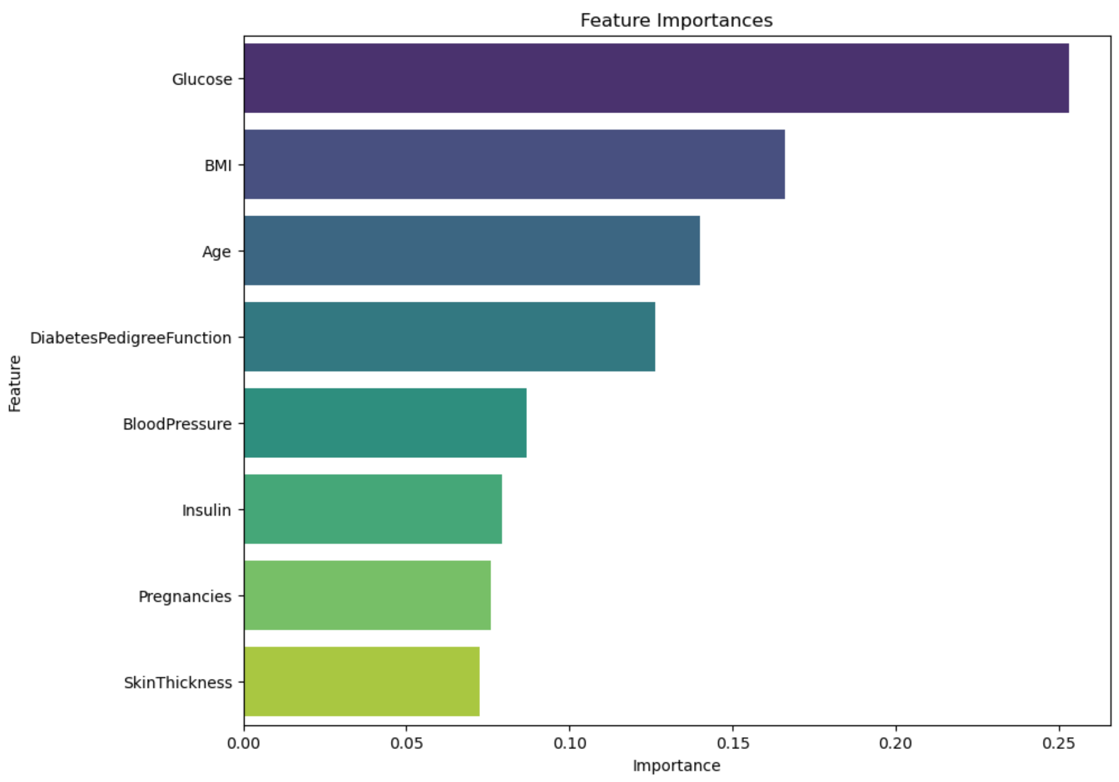
[ ]:
```
MODEL BUILDING USING ML ALGORITHMS:
```

[ ]:
```
RANDOM FOREST
```

[ ]:
```
DATA SPLITTING: (FEATURE SELECTION)
```

[64]:
```
# Feature selection using Random Forest
# Specify the features and target variable
X = diabetes_df_copy.drop('Outcome', axis=1)
y = diabetes_df_copy['Outcome']

# Perform the train-test split
random_state_value = 7  # You can change this value if needed
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.33,␣
 ↪random_state=random_state_value)

# Create and train the Random Forest Classifier for feature selection
rfc_feature_selection = RandomForestClassifier(n_estimators=200)
```

```
rfc_feature_selection.fit(X_train, y_train)

# Extract feature importances
feature_importances = rfc_feature_selection.feature_importances_

# Create a DataFrame to display feature importances
feature_importance_df = pd.DataFrame({
    'Feature': X.columns,
    'Importance': feature_importances
})

# Sort features by importance in descending order
feature_importance_df = feature_importance_df.sort_values(by='Importance',␣
 ↪ascending=False)

# Plotting the feature importances
plt.figure(figsize=(10, 8))
sns.barplot(x='Importance', y='Feature', data=feature_importance_df,␣
 ↪palette='viridis')
plt.title('Feature Importances')
plt.show()

# Select top features based on importance
threshold = 0.02  # Adjust the threshold as needed
selected_features = feature_importance_df.
 ↪loc[feature_importance_df['Importance'] > threshold]['Feature'].values

# Use only the selected features for training and testing
X_train_selected = X_train[selected_features]
X_test_selected = X_test[selected_features]
```



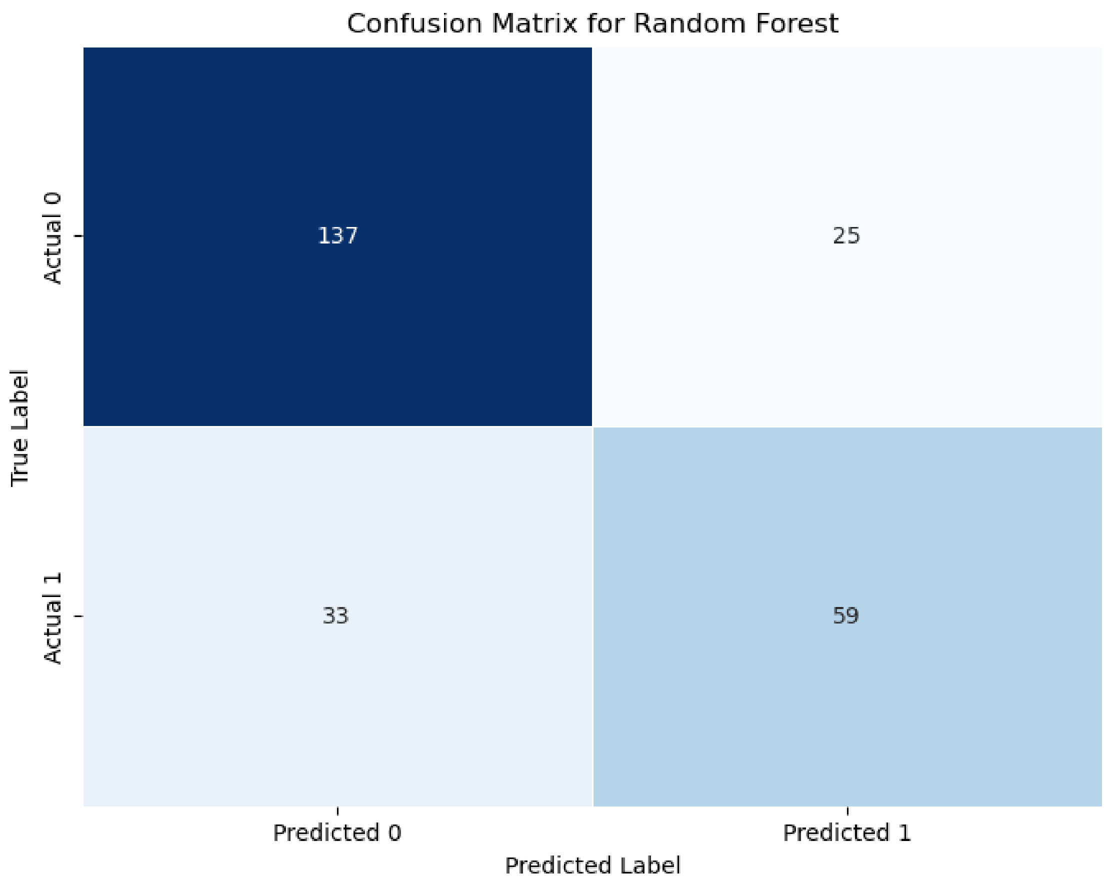
[65]:
```
# MODEL BUILDING USING ML ALGORITHMS:
# RANDOM FOREST:
# Create and train the RandomForestClassifier with selected features
rfc = RandomForestClassifier(n_estimators=200)
rfc.fit(X_train_selected, y_train)

# Predict on the test set
predictions_rfc = rfc.predict(X_test_selected)

# Calculate and print the accuracy score
accuracy_rfc = accuracy_score(y_test, predictions_rfc)
print("Random Forest Accuracy Score =", format(accuracy_rfc))
```

```
Random Forest Accuracy Score = 0.7716535433070866
```

[ ]:
```
CLASSIFICATION REPORT & CONFUSION MATRIX:
```

[66]:
```
# Confusion Matrix:
cm_rfc = confusion_matrix(y_test, predictions_rfc)

# Create a heatmap for the confusion matrix
plt.figure(figsize=(8, 6))
```

```
sns.heatmap(cm_rfc, annot=True, fmt='d', cmap='Blues', linewidths=.5,␣
 ↪cbar=False,
            xticklabels=['Predicted 0', 'Predicted 1'], yticklabels=['Actual␣
 ↪0', 'Actual 1'])
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix for Random Forest')
plt.show()

# Classification Report:
classification_report_rfc = classification_report(y_test, predictions_rfc)
print("Classification Report for Random Forest:\n", classification_report_rfc)
```

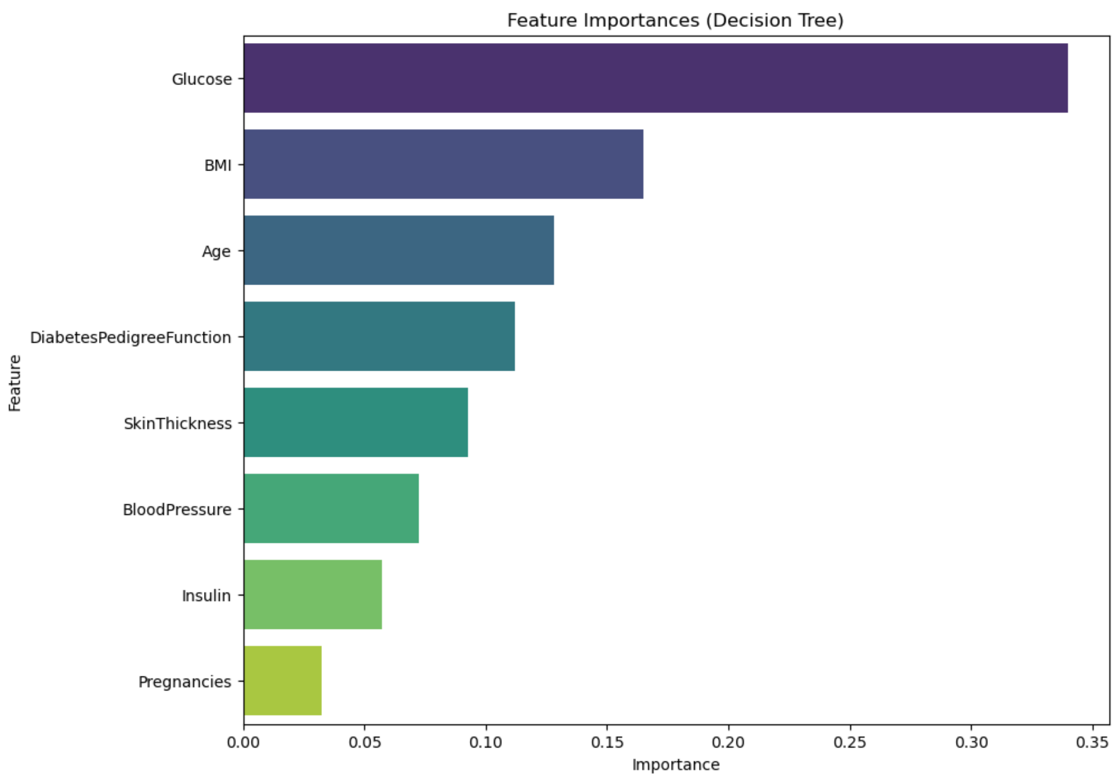


```
Classification Report for Random Forest:
               precision    recall  f1-score   support

           0       0.81      0.85      0.83       162
           1       0.70      0.64      0.67        92
```

```
    accuracy                           0.77       254
   macro avg       0.75      0.74      0.75       254
weighted avg       0.77      0.77      0.77       254
```

[ ]:
```
DECISION TREE:
```

[67]:
```
# Create and train the DecisionTreeClassifier for feature selection
dtree_feature_selection = DecisionTreeClassifier()
dtree_feature_selection.fit(X_train, y_train)

# Extract feature importances
feature_importances_dtree = dtree_feature_selection.feature_importances_

# Create a DataFrame to display feature importances
feature_importance_df_dtree = pd.DataFrame({
    'Feature': X.columns,
    'Importance': feature_importances_dtree
})

# Sort features by importance in descending order
feature_importance_df_dtree = feature_importance_df_dtree.
 ↪sort_values(by='Importance', ascending=False)

# Plotting the feature importances for Decision Tree
plt.figure(figsize=(10, 8))
sns.barplot(x='Importance', y='Feature', data=feature_importance_df_dtree,␣
 ↪palette='viridis')
plt.title('Feature Importances (Decision Tree)')
plt.show()

# Select top features based on importance
threshold_dtree = 0.02  # Adjust the threshold as needed
selected_features_dtree = feature_importance_df_dtree.loc[
    feature_importance_df_dtree['Importance'] > threshold_dtree]['Feature'].
 ↪values

# Use only the selected features for training and testing for Decision Tree
X_train_selected_dtree = X_train[selected_features_dtree]
X_test_selected_dtree = X_test[selected_features_dtree]
```



[68]:
```python
from sklearn.tree import DecisionTreeClassifier

# Create and train the DecisionTreeClassifier
dtree = DecisionTreeClassifier()
dtree.fit(X_train, y_train)
```

[68]:
```
DecisionTreeClassifier()
```

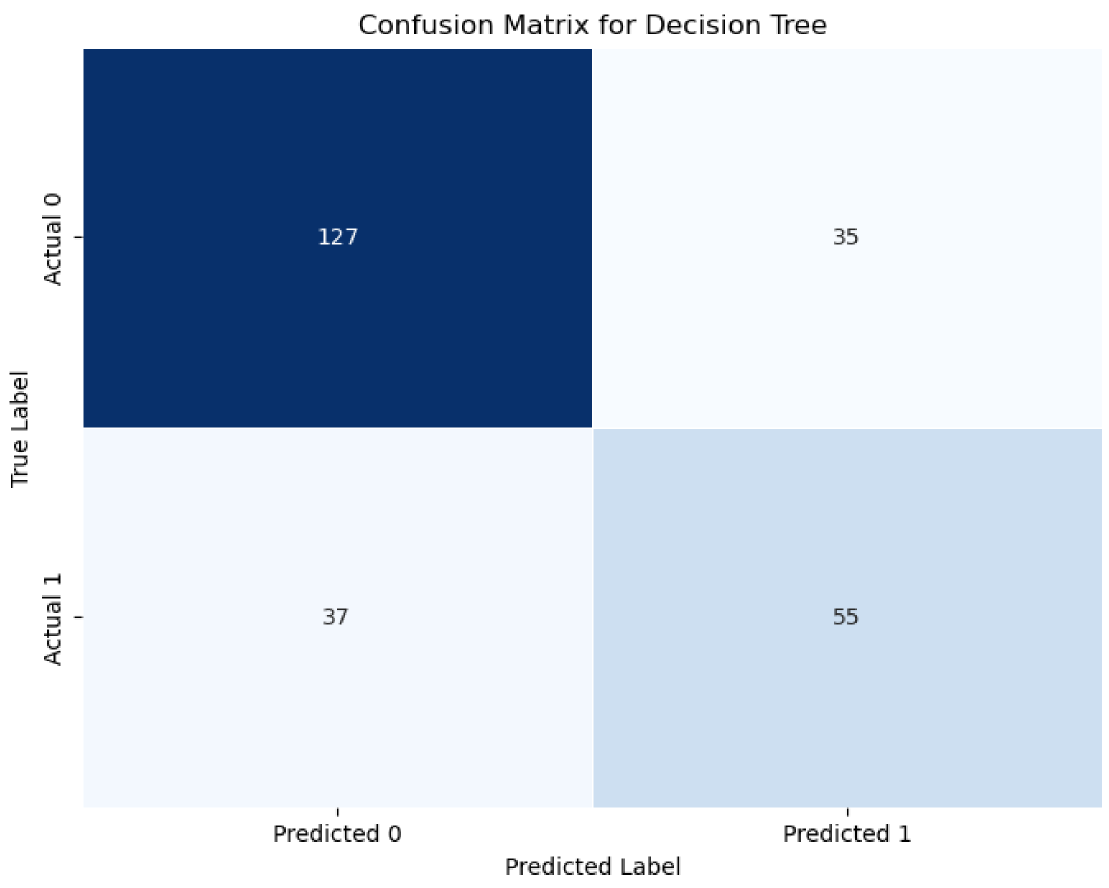
[ ]:
```
CHECKING THE ACCURACY SCORE ON TESTING SET:
```

[69]:
```python
# Create and train the DecisionTreeClassifier with selected features
dtree = DecisionTreeClassifier()
dtree.fit(X_train_selected_dtree, y_train)

# Predict on the test set for Decision Tree
predictions_dtree = dtree.predict(X_test_selected_dtree)

# Calculate and print the accuracy score for Decision Tree
accuracy_dtree = accuracy_score(y_test, predictions_dtree)
print("Decision Tree Accuracy Score =", format(accuracy_dtree))
```

```
Decision Tree Accuracy Score = 0.7165354330708661
```

```
[ ]: CLASSIFICATION REPORT & CONFUSION MATRIX:
```

```
[70]: # Assuming 'X_test' contains the testing features with the same columns as␣
       ↪'X_train'

      # Train Decision Tree Classifier
      dtree = DecisionTreeClassifier()
      dtree.fit(X_train, y_train)

      # Predict on the test set with the same features used for training
      predictions_dtree = dtree.predict(X_test)

      # Confusion Matrix:
      cm_dtree = confusion_matrix(y_test, predictions_dtree)

      # Create a heatmap for the confusion matrix
      plt.figure(figsize=(8, 6))
      sns.heatmap(cm_dtree, annot=True, fmt='d', cmap='Blues', linewidths=.5,␣
       ↪cbar=False,
                  xticklabels=['Predicted 0', 'Predicted 1'], yticklabels=['Actual␣
       ↪0', 'Actual 1'])
      plt.xlabel('Predicted Label')
      plt.ylabel('True Label')
      plt.title('Confusion Matrix for Decision Tree')
      plt.show()

      # Classification Report:
      classification_report_dtree = classification_report(y_test, predictions_dtree)
      print("Classification Report for Decision Tree:\n", classification_report_dtree)
```



```
Classification Report for Decision Tree:
              precision    recall  f1-score   support

           0       0.77      0.78      0.78       162
           1       0.61      0.60      0.60        92

    accuracy                           0.72       254
   macro avg       0.69      0.69      0.69       254
weighted avg       0.72      0.72      0.72       254
```

[ ]:
```
SUPPORT VECTOR MACHINE (SVM):
```

[71]:
```
# Feature selection using Recursive Feature Elimination (RFE) for Support␣
↪Vector Machines (SVM)
from sklearn.svm import SVC, LinearSVC
from sklearn.feature_selection import RFE
from sklearn.model_selection import train_test_split
```

```
# Specify the features and target variable
X = diabetes_df_copy.drop('Outcome', axis=1)
y = diabetes_df_copy['Outcome']

# Perform the train-test split
random_state_value = 7  # You can change this value if needed
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.33,␣
↪random_state=random_state_value)

# Create and train the LinearSVC model
linear_svc_model = LinearSVC()
linear_svc_model.fit(X_train, y_train)

# Use Recursive Feature Elimination (RFE) for feature selection
num_features_to_select = 5  # Adjust the number of features as needed
rfe = RFE(linear_svc_model, n_features_to_select=num_features_to_select)
rfe.fit(X_train, y_train)

# Extract selected features
selected_features = X_train.columns[rfe.support_]

# Use only the selected features for training and testing
X_train_selected = X_train[selected_features]
X_test_selected = X_test[selected_features]

# Display the selected features
print("Selected Features:", selected_features)
```

```
Selected Features: Index(['Pregnancies', 'BloodPressure', 'SkinThickness',
'BMI',
       'DiabetesPedigreeFunction'],
      dtype='object')
```

[72]:
```
from sklearn.svm import SVC
from sklearn import metrics

# Assuming 'X_test' contains the testing features
svc_model = SVC()
svc_model.fit(X_train, y_train)
```

[72]:
```
SVC()
```

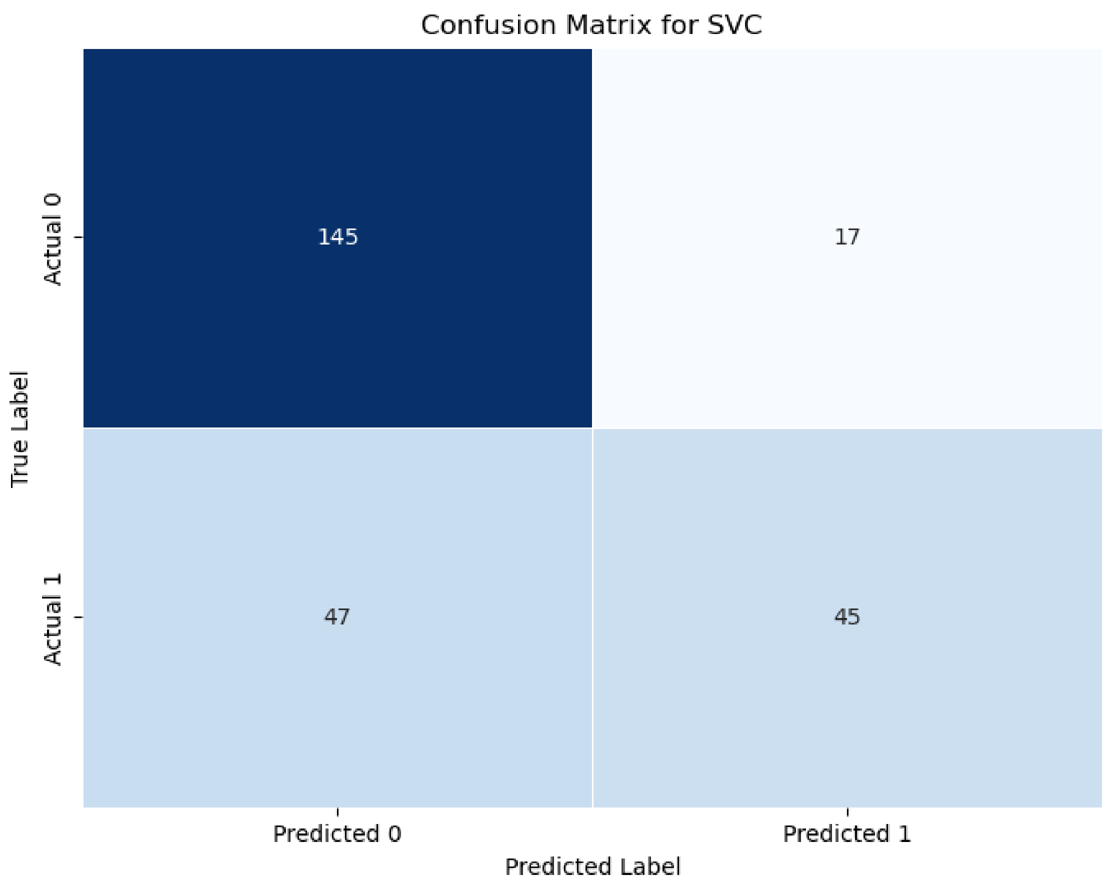
[76]:
```
from sklearn.metrics import accuracy_score

# Assuming 'y_test' contains the true labels and 'svc_pred' contains the␣
↪predicted labels
svc_pred = svc_model.predict(X_test)
```

```
# Calculate Accuracy Score for SVC
accuracy_score_svc = accuracy_score(y_test, svc_pred)

# Display the Accuracy Score
print("Accuracy Score for SVC:", accuracy_score_svc)
```

```
Accuracy Score for SVC: 0.7480314960629921
```

[78]:
```
from sklearn.metrics import confusion_matrix, classification_report

# Assuming 'y_test' contains the true labels and 'svc_pred' contains the␣
↪predicted labels
svc_pred = svc_model.predict(X_test)

# Confusion Matrix for SVC
cm_svc = confusion_matrix(y_test, svc_pred)
print("Confusion Matrix for SVC:\n", cm_svc)

# Create a heatmap for the confusion matrix
plt.figure(figsize=(8, 6))
sns.heatmap(cm_svc, annot=True, fmt='d', cmap='Blues', linewidths=.5,␣
↪cbar=False,
            xticklabels=['Predicted 0', 'Predicted 1'], yticklabels=['Actual␣
↪0', 'Actual 1'])
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix for SVC')
plt.show()

# Classification Report for SVC
classification_report_svc = classification_report(y_test, svc_pred)
print("Classification Report for SVC:\n", classification_report_svc)
```

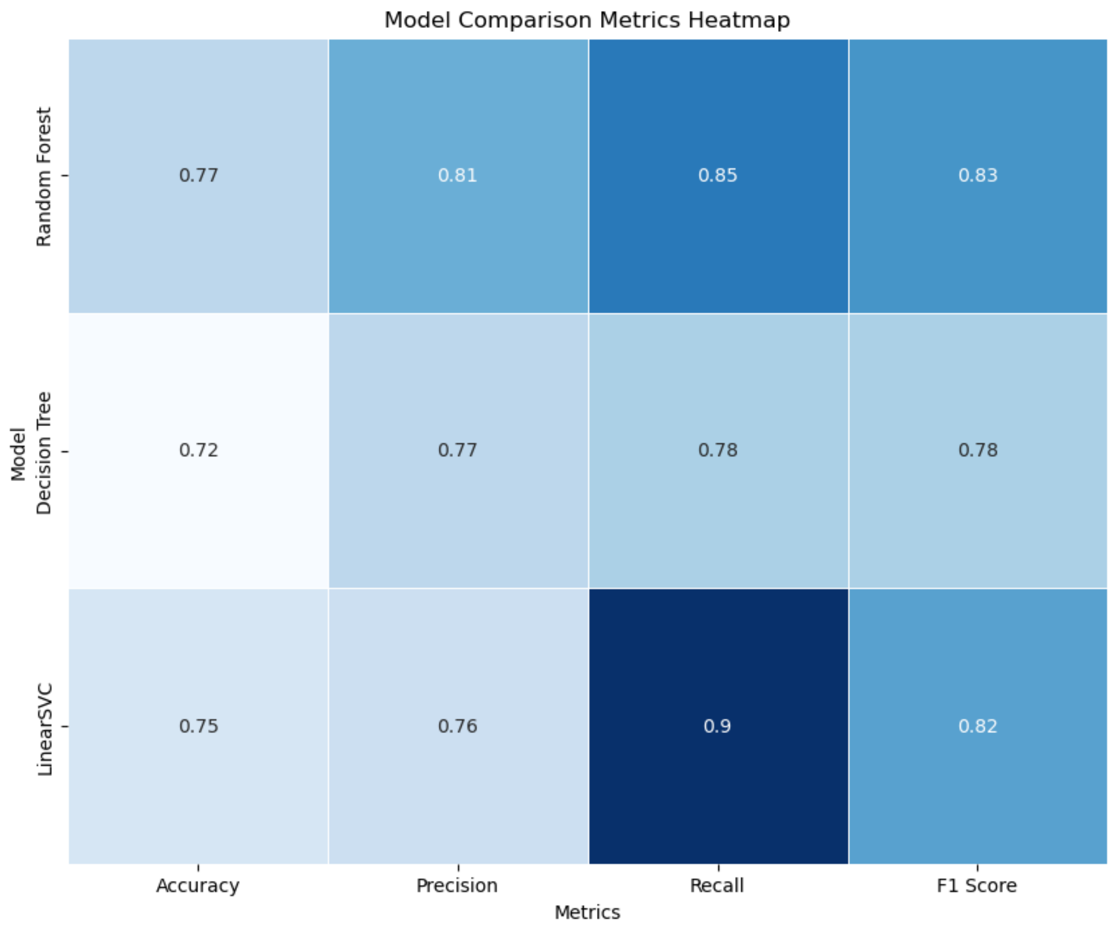
```
Confusion Matrix for SVC:
 [[145  17]
 [ 47  45]]
```



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

           0       0.76      0.90      0.82       162
           1       0.73      0.49      0.58        92

    accuracy                           0.75       254
   macro avg       0.74      0.69      0.70       254
weighted avg       0.74      0.75      0.73       254
```

[84]:
```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt

# Example: Replace these with your actual metric values
model_names = ['Random Forest', 'Decision Tree', 'LinearSVC']
accuracy_list = [0.77, 0.72, 0.75]
precision_list = [0.81, 0.77, 0.76]
```

```
recall_list = [0.85, 0.78, 0.90]
f1_score_list = [0.83, 0.78, 0.82]

# Create a DataFrame for model comparison metrics
model_comparison_metrics = pd.DataFrame({
    'Model': model_names,
    'Accuracy': accuracy_list,
    'Precision': precision_list,
    'Recall': recall_list,
    'F1 Score': f1_score_list
})

# Create a heatmap for model comparison metrics
plt.figure(figsize=(10, 8))
sns.heatmap(model_comparison_metrics.set_index('Model')[['Accuracy',␣
 ↪'Precision', 'Recall', 'F1 Score']], annot=True, cmap='Blues', linewidths=.
 ↪5, cbar=False)
plt.xlabel('Metrics')
plt.ylabel('Model')
plt.title('Model Comparison Metrics Heatmap')
plt.show()
```


Model Comparison Metrics Heatmap
Random Forest
Decision Tree
LinearSVC
Model
0.77
0.81
0.85
0.83
0.72
0.77
0.78
0.78
0.75
0.76
0.9
0.82
Accuracy
Precision
Recall
F1 Score
Metrics