DIABETES PREDICTION MODEL (Using Logistic Regression)

This project focuses on building a machine learning model to predict the likelihood of diabetes in patients using the PIMA Indians Diabetes Dataset. Although the initial plan was to implement a Support Vector Machine (SVM) classifier, multiple models were trained and evaluated to identify the most effective approach. After comprehensive training and performance comparison, Logistic Regression emerged as the best-performing model, achieving an accuracy of 78%.

PROBLEM STATEMENT AND MOTIVATION

Diabetes is a condition where the body cannot properly control blood sugar levels, which can lead to serious health problems. Early prediction helps prevent complications and allows timely intervention for high-risk individuals. Machine learning can analyze patient data to identify patterns and predict diabetes efficiently, supporting faster and more accurate decision making.

> Why Machine Learning?

Machine learning techniques provide an efficient way to analyze medical datasets, uncover underlying patterns, and make accurate predictions. By applying predictive models to patient data, healthcare decision-making can be enhanced through faster and more reliable risk assessment.

Model Selection and Rationale

Initially, a Support Vector Machine (SVM) model was selected due to its effectiveness in handling complex and high-dimensional data. However, to ensure optimal performance, three different classification models were trained and evaluated:

- Logistic Regression
- Random Forest Classifier
- Support Vector Machine (SVM)

The Random Forest Classifier performed poorly relative to the other models, which may be attributed to the small dataset size and potential overfitting. Both SVM and Logistic Regression demonstrated strong predictive performance, but Logistic Regression achieved the highest accuracy of 78%, making it the most suitable model for this task.

About the Dataset

This dataset originates from the National Institute of Diabetes and Digestive and Kidney Diseases. The data was carefully selected from a larger database, with specific criteria: all patients are female, at least 21 years old, and of Pima Indian heritage.

The dataset includes multiple medical predictor variables such as the number of pregnancies, BMI, insulin level, and age along with a taget variable, Outcome, which indicates the presence or absence od Diabetes.

```
# Importing Libraries

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

Data Collection and Analysis

PIMA Diabetes Dataset

```
# Loading the Dataset
diabetes_dataset = pd.read_csv('/content/diabetes.csv')
diabetes_dataset
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1
...	...	...	...	...	...	...	...	...	...
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

768 rows × 9 columns

Next steps: Generate code with diabetes_dataset New interactive sheet

```
diabetes_dataset.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

Next steps: Generate code with diabetes_dataset New interactive sheet

```
# number of rows and Columns in this dataset
diabetes_dataset.shape
```

```
(768, 9)
```

```
# checking the unique values
variables = ['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin']
for i in variables:
  print(diabetes_dataset[i].unique())
```

```
[ 6  1  8  0  5  3 10  2  4  7  9 11 13 15 17 12 14]
[148  85 183  89 137 116  78 115 197 125 110 168 139 189 166 100 118 107
 103 126  99 196 119 143 147  97 145 117 109 158  88  92 122 138 102  90
 111 180 133 106 171 159 146  71 105 101 176 150  73 187  84  44 141 114
  95 129  79   0  62 131 112 113  74  83 136  80 123  81 134 142 144  93
 163 151  96 155  76 160 124 162 132 120 173 170 128 108 154  57 156 153
 188 152 104  87  75 179 130 194 181 135 184 140 177 164  91 165  86 193
 191 161 167  77 182 157 178  61  98 127  82  72 172  94 175 195  68 186
 198 121  67 174 199  56 169 149  65 190]
[ 72  66  64  40  74  50   0  70  96  92  80  60  84  30  88  90  94  76
  82  75  58  78  68 110  56  62  85  86  48  44  65 108  55 122  54  52
  98 104  95  46 102 100  61  24  38 106 114]
[35 29  0 23 32 45 19 47 38 30 41 33 26 15 36 11 31 37 42 25 18 24 39 27
 21 34 10 60 13 20 22 28 54 40 51 56 14 17 50 44 12 46 16  7 52 43 48  8
 49 63 99]
[  0  94 168  88 543 846 175 230  83  96 235 146 115 140 110 245  54 192
 207  70 240  82  36  23 300 342 304 142 128  38 100  90 270  71 125 176
  48  64 228  76 220  40 152  18 135 495  37  51  99 145 225  49  50  92
 325  63 284 119 204 155 485  53 114 105 285 156  78 130  55  58 160 210
 318  44 190 280  87 271 129 120 478  56  32 744 370  45 194 680 402 258
 375 150  67  57 116 278 122 545  75  74 182 360 215 184  42 132 148 180
 205  85 231  29  68  52 255 171  73 108  43 167 249 293  66 465  89 158
  84  72  59  81 196 415 275 165 579 310  61 474 170 277  60  14  95 237
 191 328 250 480 265 193  79  86 326 188 106  65 166 274  77 126 330 600
 185  25  41 272 321 144  15 183  91  46 440 159 540 200 335 387  22 291
 392 178 127 510  16 112]
```

In the dataset all the variables except Pregnancies and Outcome cannot have a value of 0, as it is not possible to have a glucose level or blood pressure of zero. Such values are therefore considered invalid or incorrect data.

```
# Checking the count of value 0 in the variables
variables = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age']
for i in variables:
    c = 0
    for x in diabetes_dataset[i]:
        if x == 0:
            c += 1
    print(i, c)
```

```
Glucose 5
BloodPressure 35
SkinThickness 227
Insulin 374
BMI 11
DiabetesPedigreeFunction 0
Age 0
```

Now I have to replace all the incorrect values

```
# replacing the missing values with the mean
variables = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']
for i in variables:
  diabetes_dataset[i].replace(0, diabetes_dataset[i].mean(), inplace=True)
```

```
/tmp/ipython-input-606313552.py:4: FutureWarning: A value is trying to be set on a copy of a DataFrame or Series through cha
The behavior will change in pandas 3.0. This inplace method will never work because the intermediate object on which we are

For example, when doing 'df[col].method(value, inplace=True)', try using 'df.method({col: value}, inplace=True)' or df[col]


  diabetes_dataset[i].replace(0, diabetes_dataset[i].mean(), inplace=True)
```

```
# checking to make sure that the incorrect values are replaced
for i in variables:
    c = 0
    for x in diabetes_dataset[i]:
        if x == 0:
            c += 1
    print(i, c)
```

```
Glucose 0
BloodPressure 0
SkinThickness 0
Insulin 0
BMI 0
```

Checking for missing values

```
diabetes_dataset.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    float64
 2   BloodPressure             768 non-null    float64
 3   SkinThickness             768 non-null    float64
 4   Insulin                   768 non-null    float64
 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(6), int64(3)
memory usage: 54.1 KB
```

Descriptive Statistics

```
# getting the statistical measures of data
diabetes_dataset.describe()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	76
mean	3.845052	121.681605	72.254807	26.606479	118.660163	32.450805	0.471876	33.240885	
std	3.369578	30.436016	12.115932	9.631241	93.080358	6.875374	0.331329	11.760232	
min	0.000000	44.000000	24.000000	7.000000	14.000000	18.200000	0.078000	21.000000	
25%	1.000000	99.750000	64.000000	20.536458	79.799479	27.500000	0.243750	24.000000	
50%	3.000000	117.000000	72.000000	23.000000	79.799479	32.000000	0.372500	29.000000	
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	

```
diabetes_dataset.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.0	35.000000	79.799479	33.6	0.627	50	1
1	1	85.0	66.0	29.000000	79.799479	26.6	0.351	31	0
2	8	183.0	64.0	20.536458	79.799479	23.3	0.672	32	1
3	1	89.0	66.0	23.000000	94.000000	28.1	0.167	21	0
4	0	137.0	40.0	35.000000	168.000000	43.1	2.288	33	1

Next steps: Generate code with diabetes_dataset New interactive sheet

```
diabetes_dataset['Outcome'].value_counts()
```

	count
Outcome	
0	500
1	268

dtype: int64

0 --> Non-Diabetic

1 --> Diabetic

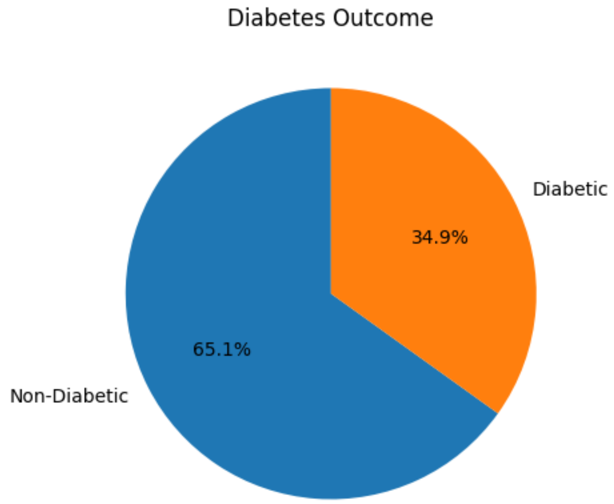
```
diabetes_dataset.groupby('Outcome').mean()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
Outcome								
0	3.298000	110.705367	70.810008	25.373135	106.457354	30.880066	0.429734	31.190000
1	4.865672	142.159661	74.950326	28.907494	141.426597	35.381288	0.550500	37.067164

Exploratory Data Analysis

During the EDA, I'll be exploring how the data is distributed, investigate patterns and correlations among the features, and examine how each feature relates to the target variable. The process will begin by analyzing the overall distribution of the data, and then move on to study the relationships between the independent variables and the outcome.

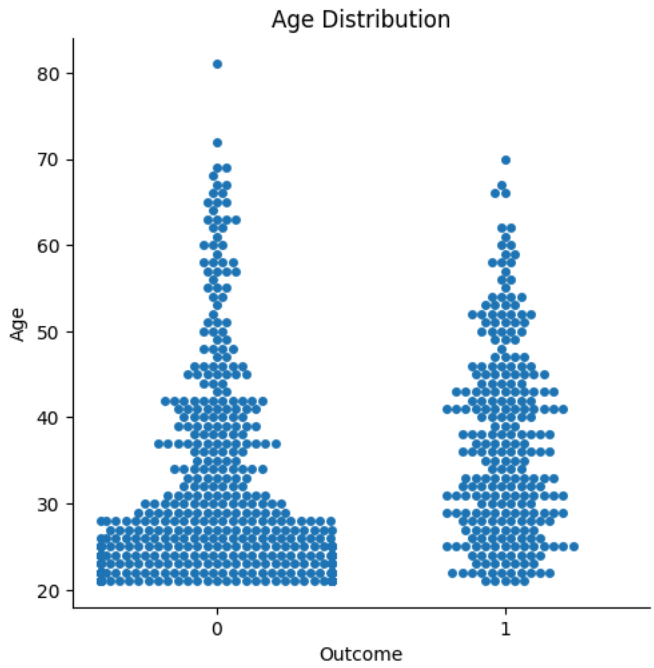
```
plt.figure(figsize=(6, 5))
plt.pie(diabetes_dataset['Outcome'].value_counts(), labels=['Non-Diabetic', 'Diabetic'], autopct='%1.1f%%', startangle=90)
plt.title('Diabetes Outcome')
plt.show()
```



Age Distribution and Diabetes

```
sns.catplot(x='Outcome', y='Age', data=diabetes_dataset, kind='swarm')
plt.title('Age Distribution')
plt.show()
```

```
/usr/local/lib/python3.12/dist-packages/seaborn/categorical.py:3399: UserWarning: 6.6% of the points cannot be placed; you m
  warnings.warn(msg, UserWarning)
/usr/local/lib/python3.12/dist-packages/seaborn/categorical.py:3399: UserWarning: 22.4% of the points cannot be placed; you
  warnings.warn(msg, UserWarning)
/usr/local/lib/python3.12/dist-packages/seaborn/categorical.py:3399: UserWarning: 21.6% of the points cannot be placed; you
  warnings.warn(msg, UserWarning)
```

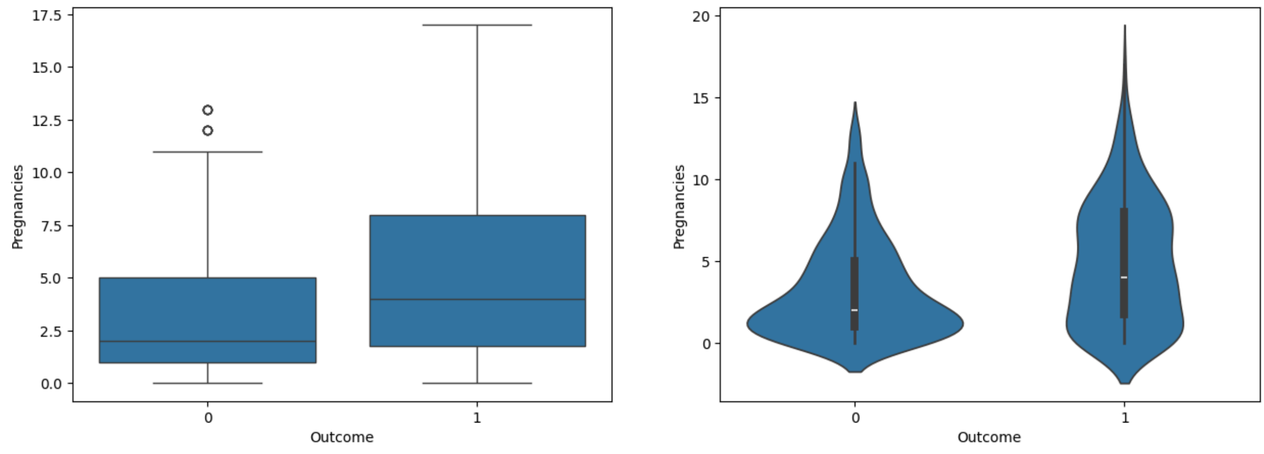


The graph shows that most patients are adults between 20 and 30 years old. While individuals aged 40 50 50 years appear more susceptible to diabetes, the higher number of adults in the 20-30 gap group results in a greater overall count of diabetes cases within the younder group.

Pregnancies and Diabetes

```
fig,ax = plt.subplots(1,2,figsize=(15,5))
sns.boxplot(x='Outcome',y='Pregnancies',data=diabetes_dataset,ax=ax[0])
sns.violinplot(x='Outcome',y='Pregnancies',data=diabetes_dataset,ax=ax[1])
```

```
<Axes: xlabel='Outcome', ylabel='Pregnancies'>
```

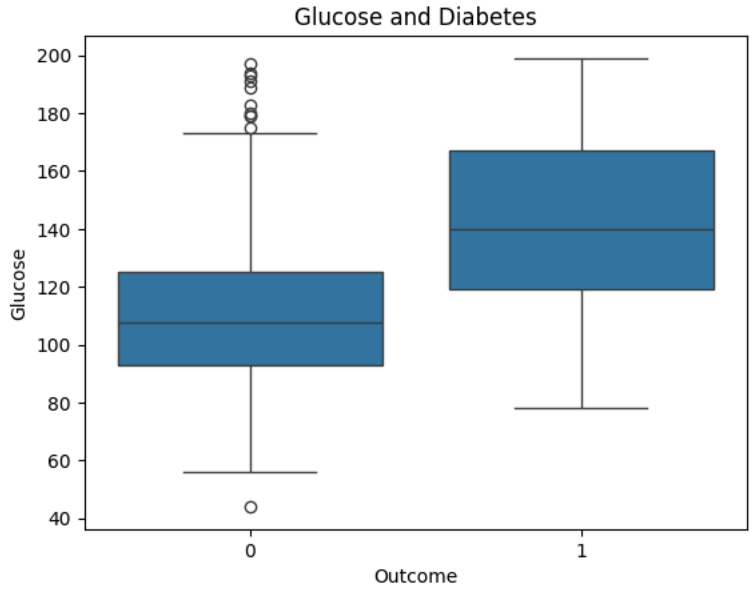


Both reveal an interesting relationship between the number of pregnancies and diabetes. The graphs suggest that a higher number of pregnancies is associated with an increased risk of developing diabetes.

Glucose and Diabetes

```
sns.boxplot(x='Outcome', y='Glucose', data=diabetes_dataset).set_title('Glucose and Diabetes')
```

```
Text(0.5, 1.0, 'Glucose and Diabetes')
```

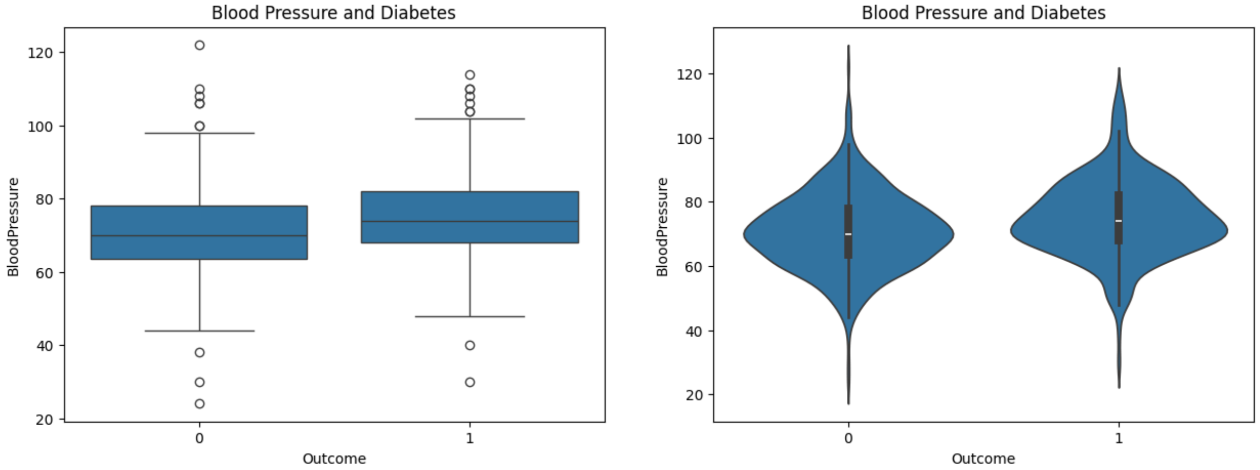


Glucose levels plays a major role in determining whether the patient is diabetic or not. Patients with a median glucose level below 120 are more likely to be non-diabetic, while those with a median glucose level above 140 are more likely to be diabetic. Therefore, high glucose levels are a strong indicator of diabetes.

Blood Pressure and Diabetes

```
fig,ax = plt.subplots(1,2,figsize=(15,5))
sns.boxplot(x='Outcome', y='BloodPressure', data=diabetes_dataset, ax=ax[0]).set_title('Blood Pressure and Diabetes')
sns.violinplot(x='Outcome', y='BloodPressure', data=diabetes_dataset, ax=ax[1]).set_title('Blood Pressure and Diabetes')
```

```
Text(0.5, 1.0, 'Blood Pressure and Diabetes')
```

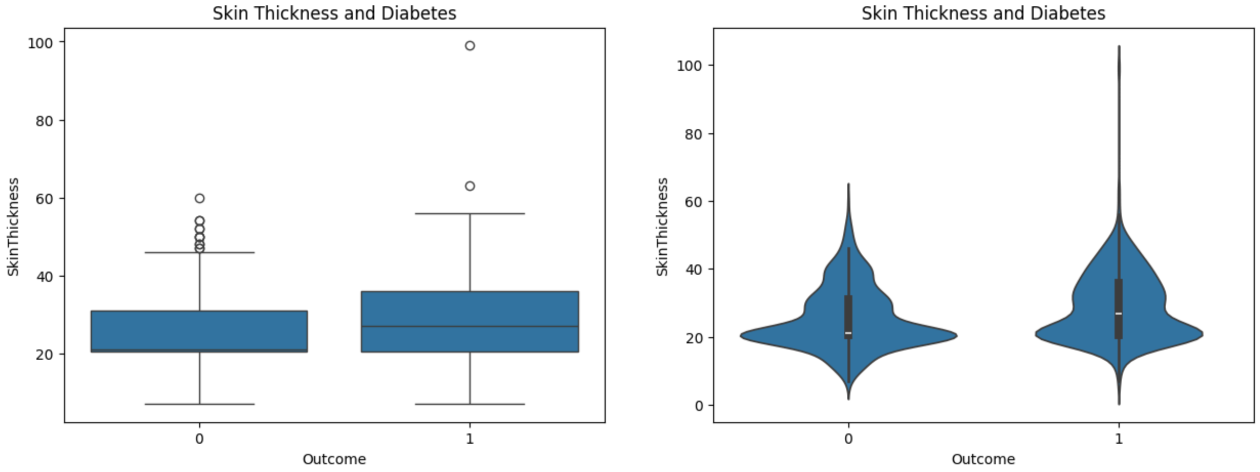


The boxplot and violin plot show that diabeticpatients have slightly higher blood pressure than non-diabetic patients. However, the difference is small and blood pressure alone is not a strong predictor of diabetes.

Skin Thickness and Diabetes

```
fig,ax = plt.subplots(1,2,figsize=(15,5))
sns.boxplot(x='Outcome', y='SkinThickness', data=diabetes_dataset, ax=ax[0]).set_title('Skin Thickness and Diabetes')
sns.violinplot(x='Outcome', y='SkinThickness', data=diabetes_dataset, ax=ax[1]).set_title('Skin Thickness and Diabetes')
```

```
Text(0.5, 1.0, 'Skin Thickness and Diabetes')
```

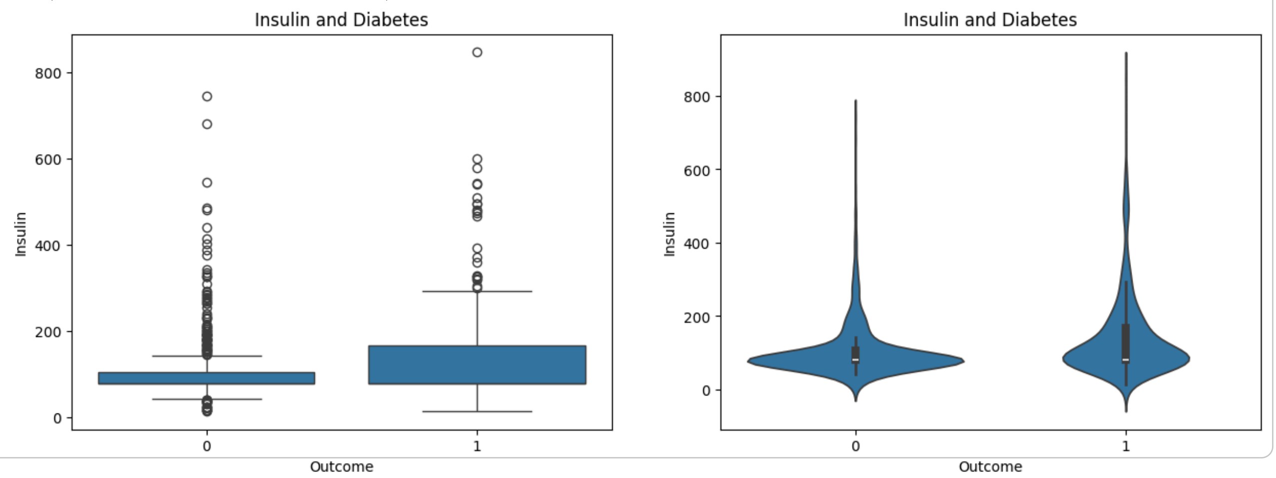


Both the boxplot and violin plot show the effect of diabetes on skin thickness. The boxplot indicates that diabetic patients have a higher median skin thickness(around 30) compared to non-diabetic patients (around 20). The violin plot also shows a higher distribution of skin thickness values around 30 for diabetic patients. Therefore, skin thickness can be an indicator of diabetes.

Insulin and Diabetes

```
fig,ax = plt.subplots(1,2,figsize=(15,5))
sns.boxplot(x='Outcome', y='Insulin', data=diabetes_dataset, ax=ax[0]).set_title('Insulin and Diabetes')
sns.violinplot(x='Outcome', y='Insulin', data=diabetes_dataset, ax=ax[1]).set_title('Insulin and Diabetes')
```

```
Text(0.5, 1.0, 'Insulin and Diabetes')
```

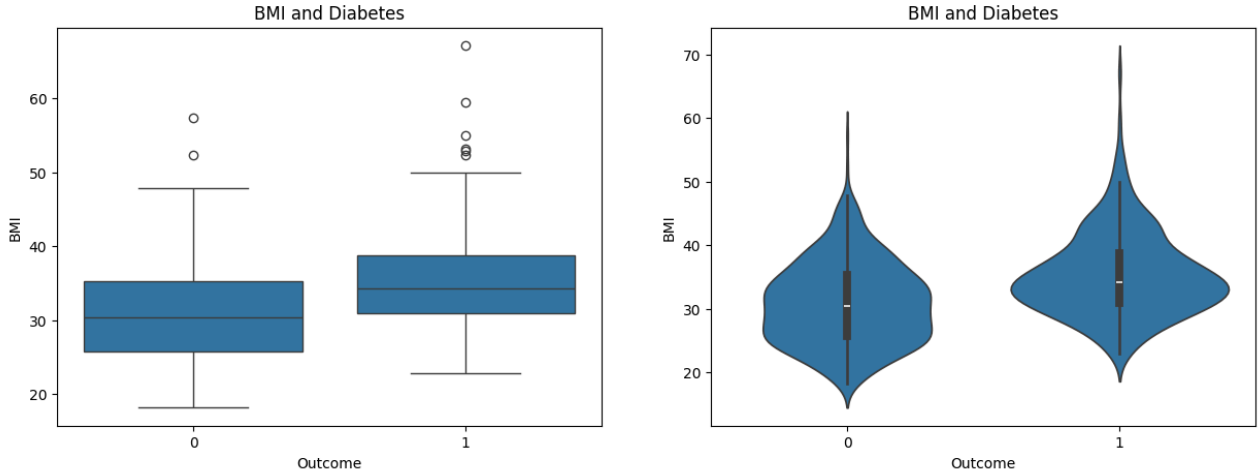


Insulin is a key hormone that regulates glucose metabolism. The boxplot and violin plot show that non-diabetic patients have insulin levels around 100, while diabetic patients have higher levels around 200. The violin plot also indicates a more concentrated distribution at higher insulin levels for diabetic patients. This suggests that insulin level is a good indicator.

BMI and Diabetes

```
fig,ax = plt.subplots(1,2,figsize=(15,5))
sns.boxplot(x='Outcome', y='BMI', data=diabetes_dataset, ax=ax[0]).set_title('BMI and Diabetes')
sns.violinplot(x='Outcome', y='BMI', data=diabetes_dataset, ax=ax[1]).set_title('BMI and Diabetes')
```

```
Text(0.5, 1.0, 'BMI and Diabetes')
```

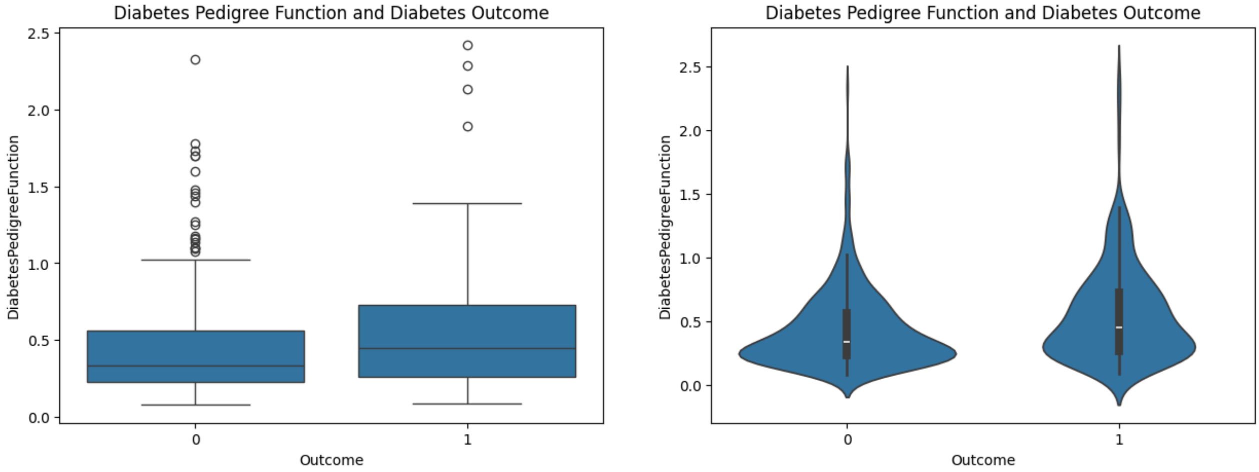


Both plots highlight the role of BMI in diabetes prediction. Non-diabetic patients mostly have BMI values between 25 and 35, while diabetic patients tend to have higher BMI values above 35. The violin plot shows greater distribution at higher BMI ranges for diabetic patients. This indicates that BMI is a strong predictor of diabetes, with obese individuals being more likely to be diabetic.

Diabetes Pedigree Function and Diabetes Outcome

```
fig,ax = plt.subplots(1,2,figsize=(15,5))
sns.boxplot(x='Outcome', y='DiabetesPedigreeFunction', data=diabetes_dataset, ax=ax[0]).set_title('Diabetes Pedigree Funct
sns.violinplot(x='Outcome', y='DiabetesPedigreeFunction', data=diabetes_dataset, ax=ax[1]).set_title('Diabetes Pedigree Fu
```

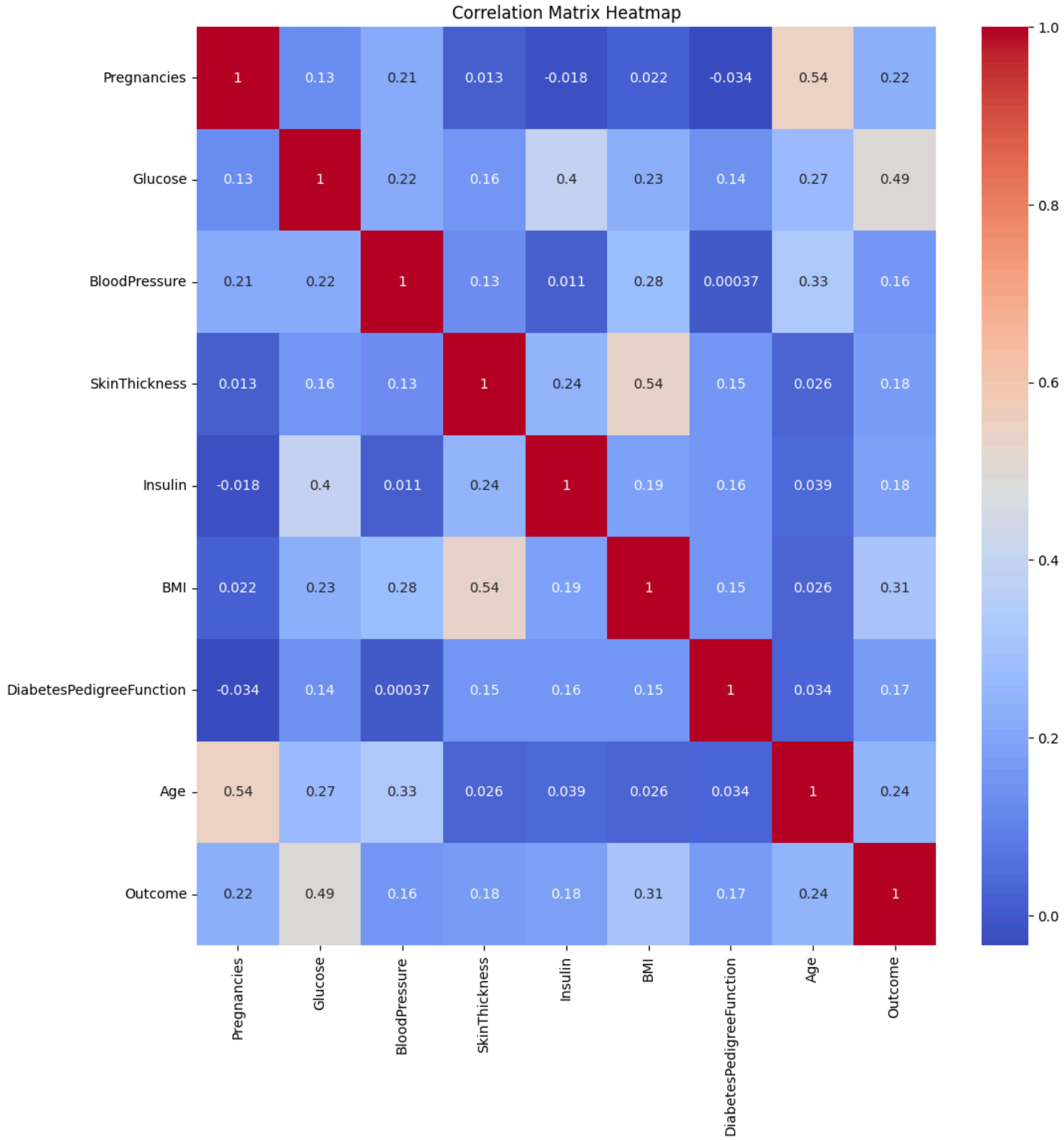
```
Text(0.5, 1.0, 'Diabetes Pedigree Function and Diabetes Outcome')
```



The Diabetes Pedigree Function (DPF) estimates diabetes risk based on family history and age. The boxplot shows that patients with lower DPF values are less likely to be diabetic, while higher DPF values are associated with diabetes. The violin plot indicates that non-diabetic patients mostly have DPF values between 0.25 and 0.35 whereas diabetic patients show higher and more spread-out DPF values. This suggest that DPF is a good indicator of diabetes.

Correlation Matrix Heatmap

```
plt.figure(figsize=(12, 12))
sns.heatmap(diabetes_dataset.corr(), annot=True, cmap='coolwarm').set_title('Correlation Matrix Heatmap')
plt.show()
```



Train, Test, Split

Data Standardization

```
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split

X = diabetes_dataset.drop(columns='Outcome', axis=1)
Y = diabetes_dataset['Outcome']

# Split first
X_train, X_test, Y_train, Y_test = train_test_split(
    X, Y, test_size=0.2, stratify=Y, random_state=2
)

# Scale after splitting
scaler = StandardScaler()
```

```
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

```
print(X.shape, X_train.shape, X_test.shape)
```

```
(768, 8) (614, 8) (154, 8)
```

For predicting diabetes, the following algorithms will be used;

1. Logistic Regression
2. Support Vector Machine
3. Random Forest Classifier(optional)

1. Logistic Regression

```
from sklearn.linear_model import LogisticRegression
logreg = LogisticRegression()
logreg
```

```
▾ LogisticRegression
LogisticRegression()
```

```
# training the model
logreg.fit(X_train, Y_train)
```

```
▾ LogisticRegression
LogisticRegression()
```

```
# training accuracy
logreg.score(X_train, Y_train)
```

```
0.7850162866449512
```

```
# accuracy score on the test data
X_test_prediction = logreg.predict(X_test)
test_data_accuracy = logreg.score(X_test, Y_test)
```

```
print('Accuracy score of the test data : ', training_data_accuracy)
```

```
Accuracy score of the test data :  0.7817589576547231
```

```
# predicted outcomes
logreg_pred = logreg.predict(X_test)
logreg_pred
```

```
array([0, 0, 1, 1, 0, 0, 0, 1, 0, 1, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0,
       1, 0, 0, 0, 1, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1,
       0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0,
       0, 1, 1, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0,
       1, 0, 0, 0, 1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       1, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1,
       1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1])
```

2. Support Vector Machine

```
classifier = svm.SVC(kernel='linear', random_state=0)
```

```
# training the support vector Machine Classifier
classifier.fit(X_train, Y_train)
```

```
▾ SVC
SVC(kernel='linear', random_state=0)
```

```
# accuracy score on the training data
X_train_prediction = classifier.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, Y_train)
```

```
print('Accuracy score of the training data : ', training_data_accuracy)
```

```
Accuracy score of the training data :  0.7817589576547231
```

```
# accuracy score on the test data
svm_pred = classifier.predict(X_test)
test_data_accuracy = classifier.score(X_test, Y_test)
```

```
print('Accuracy score of the test data : ', test_data_accuracy)
```

```
Accuracy score of the test data :  0.7792207792207793
```

Random Forest Classifier

```
#buidling model
from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier(n_estimators=100,random_state=42)
rfc
```

```
▾ RandomForestClassifier ⓘ ?
RandomForestClassifier(random_state=42)
```

```
#training model
rfc.fit(X_train, Y_train)
#training accuracy
rfc.score(X_train, Y_train)
```

```
1.0
```

```
#predicted outcomes
rfc_pred = rfc.predict(X_test)
test_data_accuracy = rfc.score(X_test, Y_test)
```

```
print('Accuracy score of the test data : ', test_data_accuracy)
```

```
Accuracy score of the test data :  0.7402597402597403
```

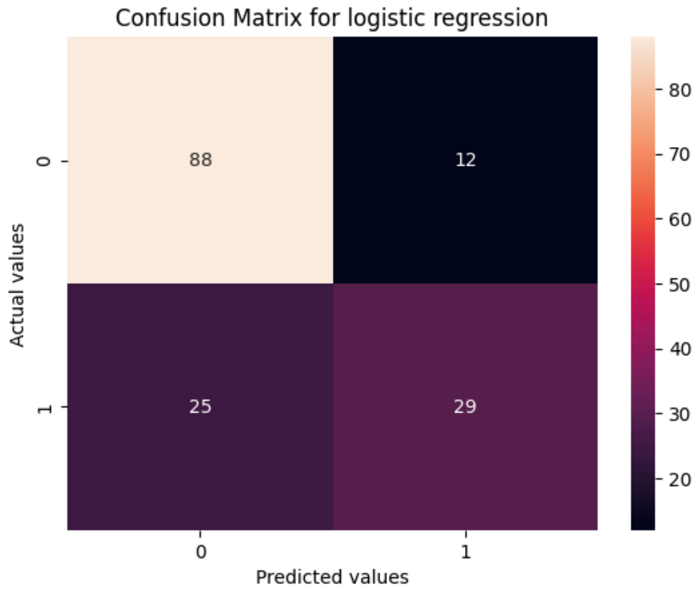
performed poorly, DROPPED!!!

Model Evaluation

Evaluating Logistic Regression model

Confusion Matrix Heatmap

```
from sklearn.metrics import confusion_matrix
sns.heatmap(confusion_matrix(Y_test, logreg_pred), annot=True, fmt='g')
plt.xlabel('Predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for logistic regression')
plt.show()
```



The diagonal cells show the number of correct predictions for each class, with predicted values on the top and actual values on the left. The off-diagonal cells represent incorrect predictions.

Distribution plot

```
ax = sns.distplot(Y_test, hist=False, color="r", label="Actual Value")
sns.distplot(logreg_pred, hist=False, color="b", label="Predicted Values", ax=ax)
plt.title('Actual vs Predicted Values for Logistic Regression')
plt.xlabel('Outcome')
plt.ylabel('Count')
plt.legend()
plt.show()
```

```
/tmp/ipython-input-2135419208.py:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `kdeplot` (an axes-level function for kernel density plots).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  ax = sns.distplot(Y_test, hist=False, color="r", label="Actual Value")
/tmp/ipython-input-2135419208.py:2: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `kdeplot` (an axes-level function for kernel density plots).

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https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  sns.distplot(logreg_pred, hist=False, color="b", label="Predicted Values", ax=ax)
```
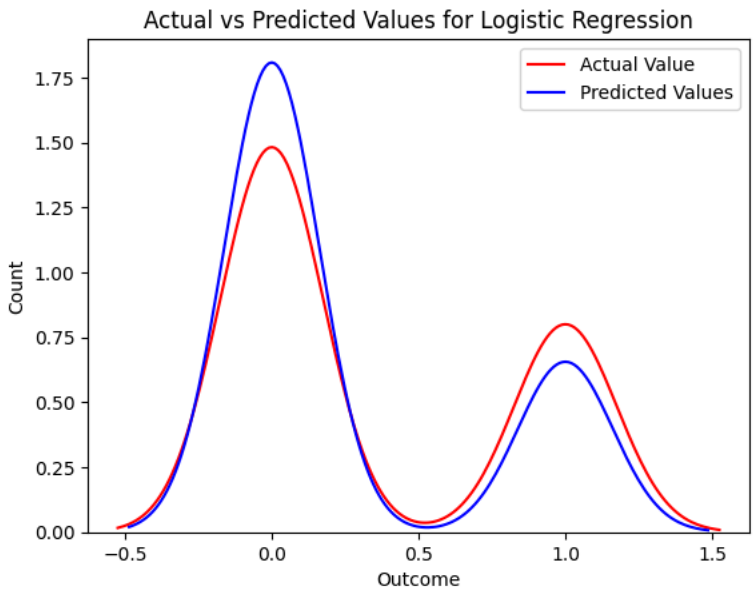



The prediction plots visualize the model's accuracy, where red represents actual values and blue represents predicted values. Greater overlap between the two indicates better model performance.

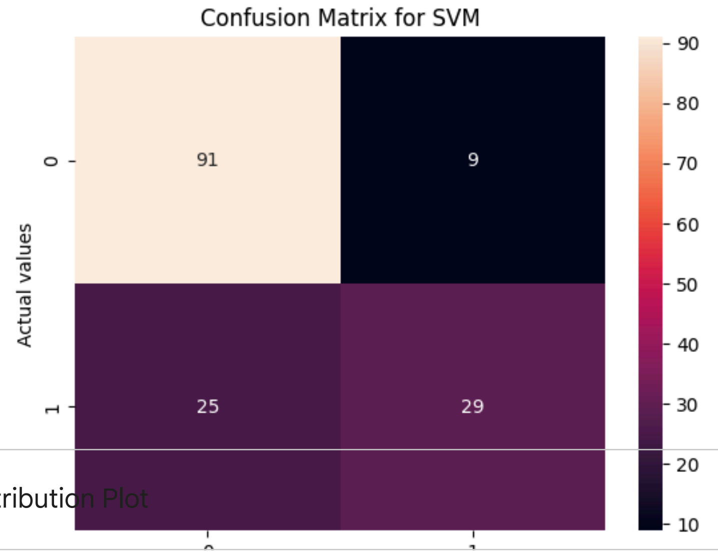
```
## Classification Report
from sklearn.metrics import classification_report
print(classification_report(Y_test, logreg_pred))
```

```
              precision    recall  f1-score   support

           0       0.78      0.88      0.83       100
           1       0.71      0.54      0.61        54

    accuracy                           0.76       154
   macro avg       0.74      0.71      0.72       154
weighted avg       0.75      0.76      0.75       154
```

Evaluating SVM Model

Confusion Matrix Heatmap

```
sns.heatmap(confusion_matrix(Y_test, svm_pred), annot=True, fmt='g')
plt.xlabel('Predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for SVM')
plt.show()
```



Distribution Plot

```
ax = sns.distplot(Y_test, hist=False, color="r", label="Actual Value")
sns.distplot(X_test_prediction, hist=False, color="b", label="Predicted Values", ax=ax)
plt.title('Actual vs Predicted Values for SVM')
plt.xlabel('Outcome')
plt.ylabel('Count')
plt.legend()
plt.show()
```

```
/tmp/ipython-input-769744288.py:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `kdeplot` (an axes-level function for kernel density plots).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  ax = sns.distplot(Y_test, hist=False, color="r", label="Actual Value")
/tmp/ipython-input-769744288.py:2: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `kdeplot` (an axes-level function for kernel density plots).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  sns.distplot(X_test_prediction, hist=False, color="b", label="Predicted Values", ax=ax)
```