Pima Indian Diabetes Prediction

The aim of this project to analyze the medical factors of a patient such as Glucose Level, Blood Pressure, Skin Thickness, Insulin Level and many others to predict whether the patient has diabetes or not.

About the Dataset

This dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases. The objective of the dataset is to diagnostically predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. Several constraints were placed on the selection of these instances from a larger database. In particular, all patients here are females at least 21 years old of Pima Indian heritage.

The datasets consists of several medical predictor variables and one target variable, Outcome. Predictor variables includes the number of pregnancies the patient has had, their BMI, insulin level, age, and so on.

```
#importing the libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

```
#loading the dataset
Diabetes = pd.read_csv("/content/diabetes.csv")
Diabetes.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedig
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	

Data Preprocessing

```
#shape of the dataset
Diabetes.shape
```

```
(768, 9)
```

```
#checking unique values
variables = ['Pregnancies','Glucose','BloodPressure','SkinThickness','Insulin','BMI','Diab
for i in variables:
    print(Diabetes[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]
```

```
[33.6 26.6 23.3 28.1 43.1 25.6 31.  35.3 30.5  0.  37.6 38.  27.1 30.1
 25.8 30.  45.8 29.6 43.3 34.6 39.3 35.4 39.8 29.  36.6 31.1 39.4 23.2
 22.2 34.1 36.  31.6 24.8 19.9 27.6 24.  33.2 32.9 38.2 37.1 34.  40.2
 22.7 45.4 27.4 42.  29.7 28.  39.1 19.4 24.2 24.4 33.7 34.7 23.  37.7
 46.8 40.5 41.5 25.  25.4 32.8 32.5 42.7 19.6 28.9 28.6 43.4 35.1 32.
 24.7 32.6 43.2 22.4 29.3 24.6 48.8 32.4 38.5 26.5 19.1 46.7 23.8 33.9
 20.4 28.7 49.7 39.  26.1 22.5 39.6 29.5 34.3 37.4 33.3 31.2 28.2 53.2
 34.2 26.8 55.  42.9 34.5 27.9 38.3 21.1 33.8 30.8 36.9 39.5 27.3 21.9
 40.6 47.9 50.  25.2 40.9 37.2 44.2 29.9 31.9 28.4 43.5 32.7 67.1 45.
 34.9 27.7 35.9 22.6 33.1 30.4 52.3 24.3 22.9 34.8 30.9 40.1 23.9 37.5
 35.5 42.8 42.6 41.8 35.8 37.8 28.8 23.6 35.7 36.7 45.2 44.  46.2 35.
 43.6 44.1 18.4 29.2 25.9 32.1 36.3 40.  25.1 27.5 45.6 27.8 24.9 25.3
 37.9 27.  26.  38.7 20.8 36.1 30.7 32.3 52.9 21.  39.7 25.5 26.2 19.3
 38.1 23.5 45.5 23.1 39.9 36.8 21.8 41.  42.2 34.4 27.2 36.5 29.8 39.2
 38.4 36.2 48.3 20.  22.3 45.7 23.7 22.1 42.1 42.4 18.2 26.4 45.3 37.
 24.5 32.2 59.4 21.2 26.7 30.2 46.1 41.3 38.8 35.2 42.3 40.7 46.5 33.5
 37.3 30.3 26.3 21.7 36.4 28.5 26.9 38.6 31.3 19.5 20.1 40.8 23.4 28.3
 38.9 57.3 35.6 49.6 44.6 24.1 44.5 41.2 49.3 46.3]
[0.627 0.351 0.672 0.167 2.288 0.201 0.248 0.134 0.158 0.232 0.191 0.537
 1.441 0.398 0.587 0.484 0.551 0.254 0.183 0.529 0.704 0.388 0.451 0.263
 0.205 0.257 0.487 0.245 0.337 0.546 0.851 0.267 0.188 0.512 0.966 0.42
 0.665 0.503 1.39  0.271 0.696 0.235 0.721 0.294 1.893 0.564 0.586 0.344
 0.305 0.491 0.526 0.342 0.467 0.718 0.962 1.781 0.173 0.304 0.27  0.699
 0.258 0.203 0.855 0.845 0.334 0.189 0.867 0.411 0.583 0.231 0.396 0.14
 0.391 0.37  0.307 0.102 0.767 0.237 0.227 0.698 0.178 0.324 0.153 0.165
 0.443 0.261 0.277 0.761 0.255 0.13  0.323 0.356 0.325 1.222 0.179 0.262
 0.283 0.93  0.801 0.207 0.287 0.336 0.247 0.199 0.543 0.192 0.588 0.539
 0.22  0.654 0.223 0.759 0.26  0.404 0.186 0.278 0.496 0.452 0.403 0.741
 0.361 1.114 0.457 0.647 0.088 0.597 0.532 0.703 0.159 0.268 0.286 0.318
 0.272 0.572 0.096 1.4   0.218 0.085 0.399 0.432 1.189 0.687 0.137 0.637
 0.833 0.229 0.817 0.204 0.368 0.743 0.722 0.256 0.709 0.471 0.495 0.18
```

In the dataset the variables except Pregnancies and Outcome cannot have value as 0, because it is not possible to have 0 Glucose Level or to have 0 Blood Pressure. So, this will be counted as incorrect information.

Checking the count of value 0 in the variables

```
variables = ['Glucose','BloodPressure','SkinThickness','Insulin','BMI','DiabetesPedigreeFu
for i in variables:
    c = 0
    for x in (Diabetes[i]):
        if x == 0:
            c = c + 1
    print(i,c)
```

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

Replacing the 0 value in the variables - Glucose, BloodPressure, SkinThickness, Insulin, BMI

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

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

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

Checking for missing values

```
#missing values
Diabetes.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

```
#checking descriptive statistics
Diabetes.describe()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BM
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.00000
mean	3.845052	121.681605	72.254807	26.606479	118.660163	32.45080
std	3.369578	30.436016	12.115932	9.631241	93.080358	6.87537
min	0.000000	44.000000	24.000000	7.000000	14.000000	18.20000
25%	1.000000	99.750000	64.000000	20.536458	79.799479	27.50000
50%	3.000000	117.000000	72.000000	23.000000	79.799479	32.00000

```
Diabetes.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPe
0	6	148.0	72.0	35.000000	79.799479	33.6	
1	1	85.0	66.0	29.000000	79.799479	26.6	
2	8	183.0	64.0	20.536458	79.799479	23.3	
3	1	89.0	66.0	23.000000	94.000000	28.1	
4	0	137.0	40.0	35.000000	168.000000	43.1	

Exploratory Data Analysis

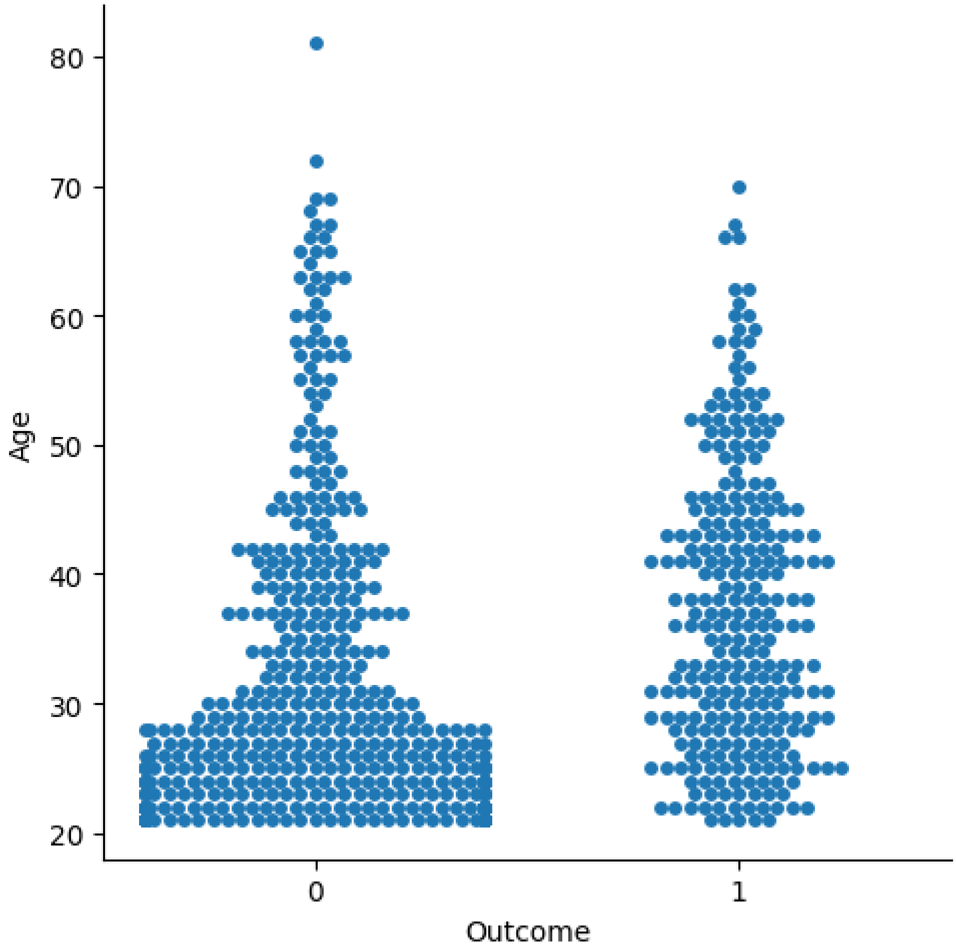
```
plt.figure(figsize=(5,5))
plt.pie(Diabetes['Outcome'].value_counts(), labels=['No Diabetes', 'Diabetes'], autopct='%
plt.title('Diabetes Outcome')
plt.show()
```

Diabetes Outcome

Age Distribution and Diabetes

```
sns.catplot(x="Outcome", y="Age", kind="swarm", data=Diabetes)
```

```
/usr/local/lib/python3.10/dist-packages/seaborn/categorical.py:3544: UserWarning:
  warnings.warn(msg, UserWarning)
<seaborn.axisgrid.FacetGrid at
0x79d105059570>/usr/local/lib/python3.10/dist-packages/seaborn/categorical.py:3544
  warnings.warn(msg, UserWarning)
```

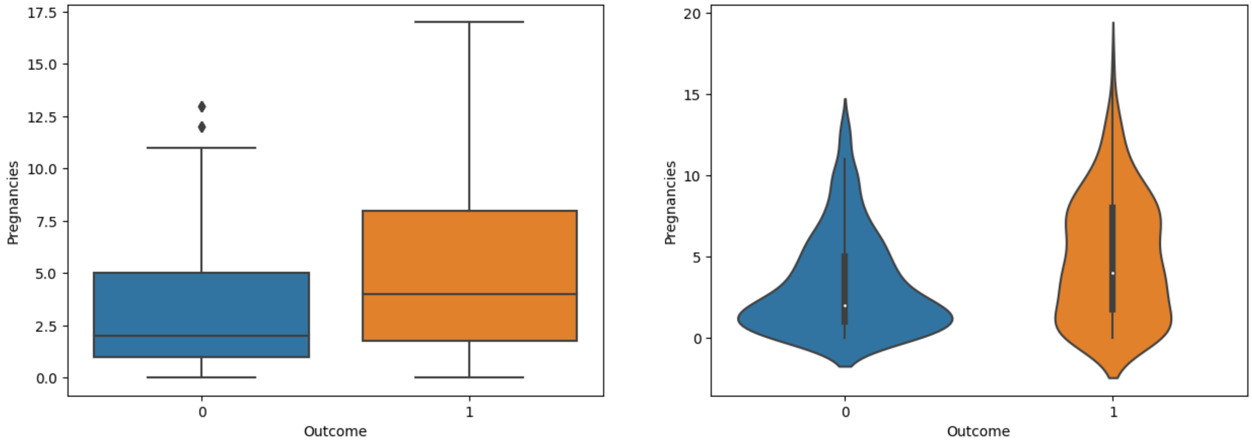


From the graph, it is quite clear that majority of the patients are adult within the age group of 20-30 years. Patients in the age range 40-55 years are more prone to diabetes, as compared to other age groups. Since the number adults in the age group 20-30 years is more, the number of patients with diabetes is also more as compared of other age groups.

Pregnancies and Diabetes

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

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

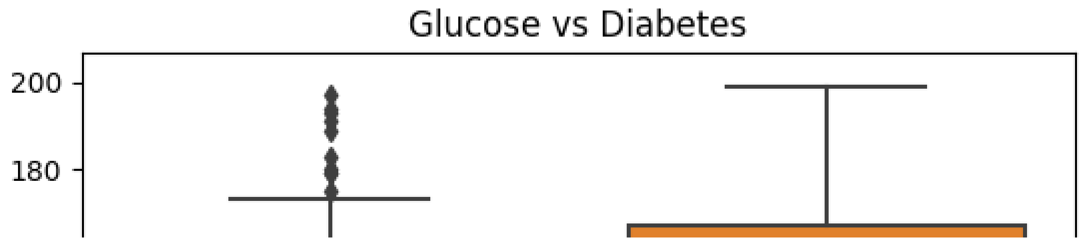


Both boxplot and violinplot shows strange relation between the number of preganacies and diabetes. According to the graphs the increased number of pregnancies highlights increased risk of diabetes.

Glucose and Diabetes

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

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

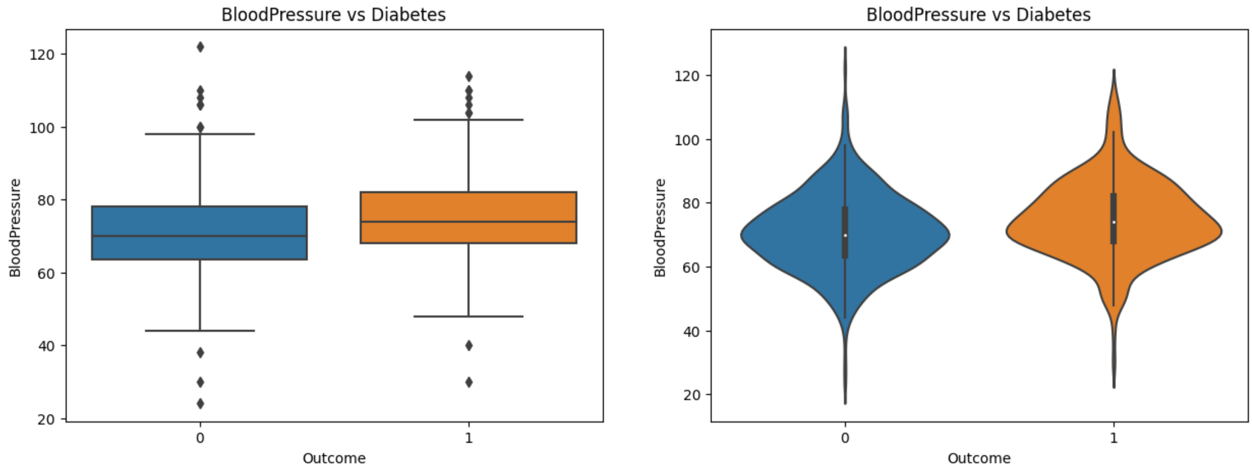


Glucose level plays a major role in determine whether the patient is diabetic or not. The patients with median gluocse level less than 120 are more likely to be non-diabetic. The patients with median gluocse level greather than 140 are more likely to be diabetic. Therefore, high gluocose levels is a good indicator of diabetes.

Blood Pressuse and Diabetes


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

```
Text(0.5, 1.0, 'BloodPressure vs Diabetes')
```

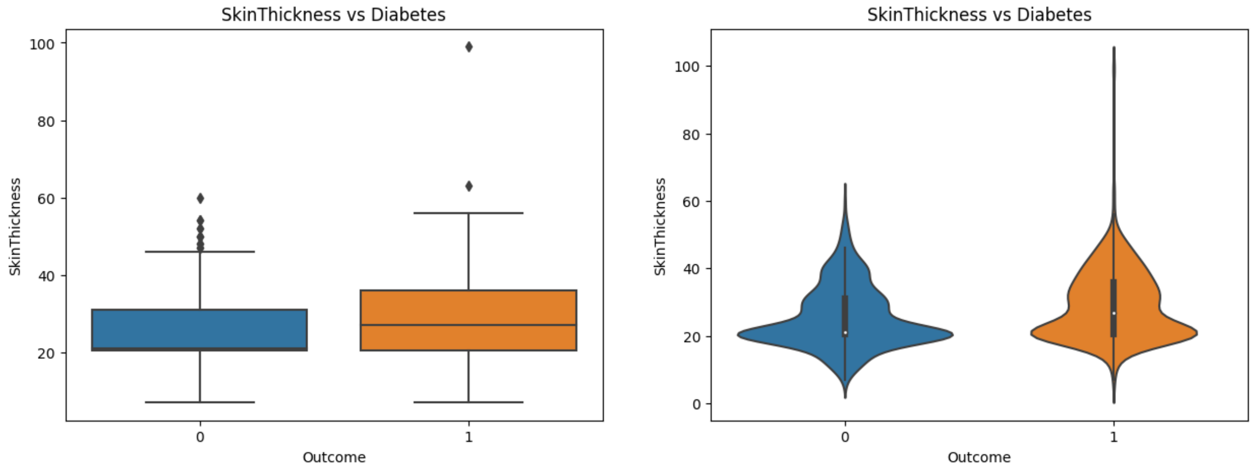


Both the boxplot and voilinplot provides clear understanding of the realtion between the blood pressure and diabetes. The boxplot shows that the median of the blood pressure for the diabetic patients is slightly higher than the non-diabetic patients. The voilinplot shows that the distribution of the blood pressure for the diabetic patients is slightly higher than the non-diabetic patients. But there has been not enough evidence to conclude that the blood pressure is a good predictor of diabetes.

Skin Thickness and Diabetes

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

```
Text(0.5, 1.0, 'SkinThickness vs Diabetes')
```



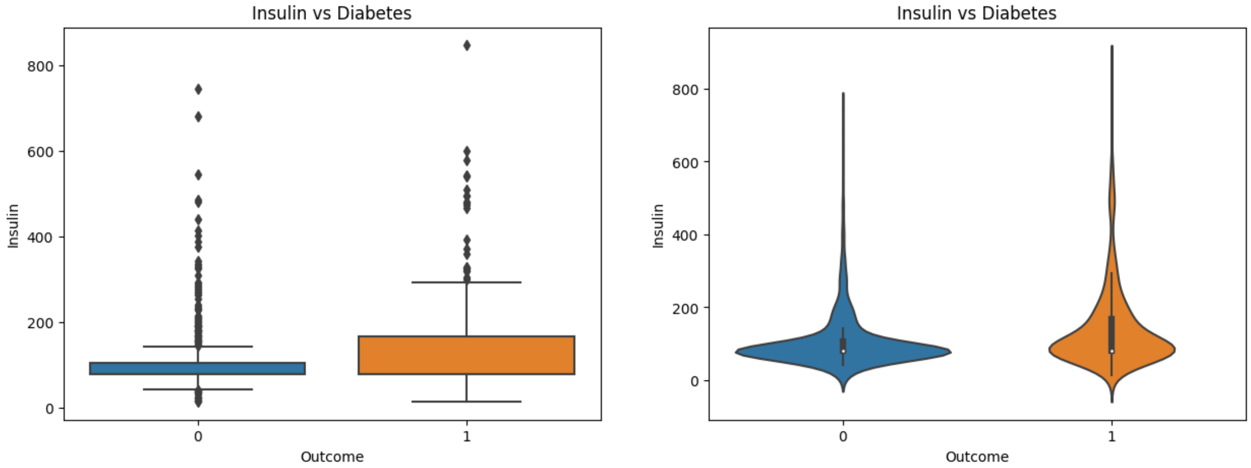
Here both the boxplot and violinplot reveals the effect of diabetes on skin thickness. As obserevd in the boxplot, the median of skin thickness is higher for the diabetic patients than the non-diabetic patients, where non diabetic patients have median skin thickness near 20 in comparison to skin thickness nearly 30 in diabetic patients. The voilinpplot shows the distribution of patients' skin thickness amoung the patients, where the non diabetic ones have greater distribution near 20 and diabetic much less distribution near 20 and increased distribution near 30. Therefore, skin thickness can be a indicator of diabetes.

Insulin and Diabetes

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

```
sns.violinplot(x='Outcome',y='Insulin',data=Diabetes,ax=ax[1]).set_title('Insulin vs Diabe
```

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

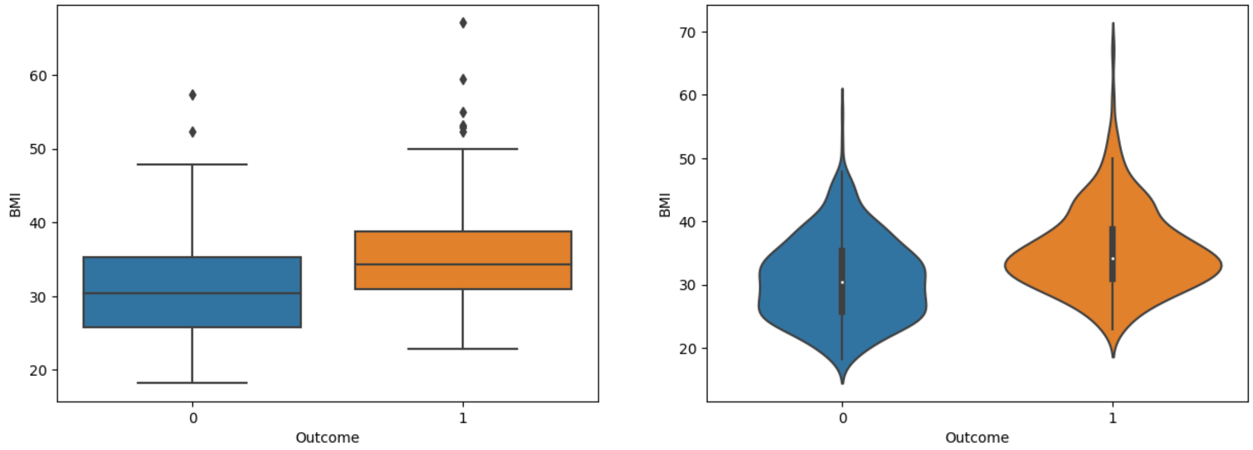


Insulin is a major body hormone that regulates glucose metabolism. Insulin is required for the body to efficiently use sugars, fats and proteins. Any change in insulin amount in the body would result in change glucose levels as well. Here the boxplot and violinplot shows the distribution of insulin level in patients. In non diabetic patients the insulin level is near to 100, whereas in diabetic patients the insulin level is near to 200. In the voilinplot we can see that the distribution of insulin level in non diabetic patients is more spread out near 100, whereas in diabetic patients the distribution is contracted and shows a little bit spread in higher insulin levels. This shows that the insulin level is a good indicator of diabetes.

BMI and Diabetes

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

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

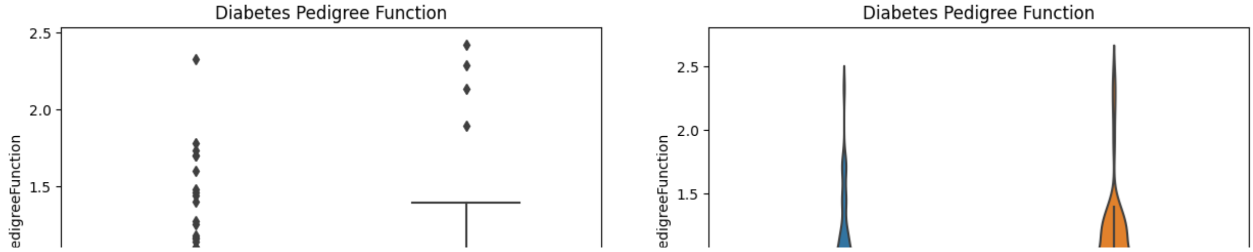


Both graphs highlights the role of BMI in diabetes prediction. Non diabetic patients have a normal BMI within the range of 25-35 whereas the diabetic patients have a BMI greater than 35. The violinplot reveals the BMI distribution, where the non dibetic patients have a increased spread from 25 to 35 with narrows after 35. However in diabetic patients there is increased spread at 35 and increased spread 45-50 as compared to non diabetic patients.Therefore BMI is a good predictor of diabetes and obese people are 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,ax=ax[0]).set_title('Di
sns.violinplot(x='Outcome',y='DiabetesPedigreeFunction',data=Diabetes,ax=ax[1]).set_title(
```

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

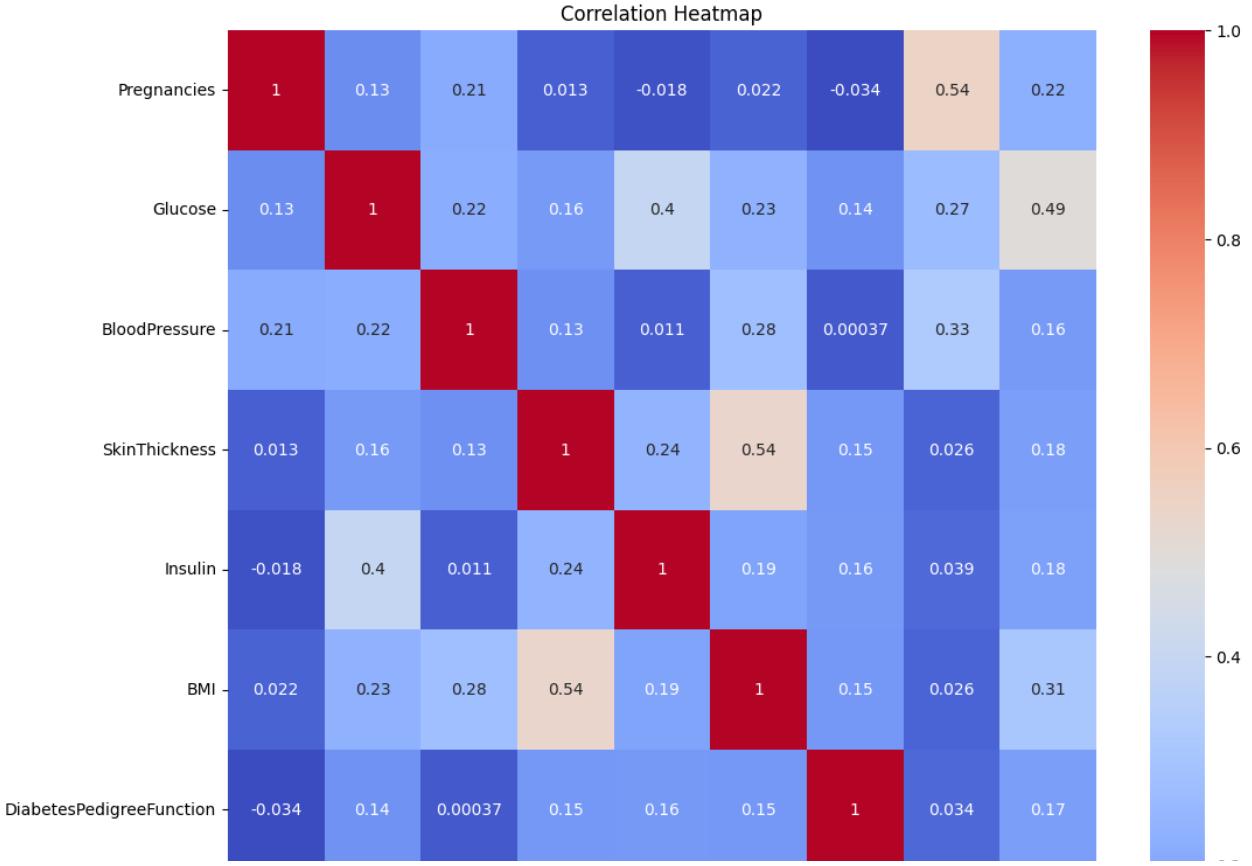


Diabetes Pedigree Function (DPF) calculates diabetes likelihood depending on the subject's age and his/her diabetic family history. From the boxplot, the patients with lower DPF, are much less likely to have diabetes. The patients with higher DPF, are much more likely to have diabetes. In the violinplot, majority of the non diabetic patients have a DPF of 0.25-0.35, whereas the diabetic patients have a increased DPF, which is shown by the their distribution in the violinplot where there is a increased spread in the DPF from 0.5 -1.5. Therefore the DPF is a good indicator of diabetes.

Coorelation Matrix Heatmap

```
#correlation heatmap
plt.figure(figsize=(12,12))
sns.heatmap(Diabetes.corr(), annot=True, cmap='coolwarm').set_title('Correlation Heatmap')
```

```
Text(0.5, 1.0, 'Correlation Heatmap')
```



Train Test Split

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(Diabetes.drop('Outcome',axis=1),Diabet
```

Diabetes Prediction

For predictiong the diabetes, I will be using the following algorithms:

Logistic Regression

Random Forest Classifier

Support Vector Machine

Logistic Regression

```
#building model
from sklearn.linear_model import LogisticRegression
```

```
lr = LogisticRegression()
lr
```

```
▾ LogisticRegression
LogisticRegression()
```

```
#training the model
lr.fit(X_train,y_train)
#training accuracy
lr.score(X_train,y_train)
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: Conver
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
0.7719869706840391
```

```
#predicted outcomes
lr_pred = lr.predict(X_test)
```

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)
```

Support Vector Machine (SVM)

```
#building model
from sklearn.svm import SVC
svm = SVC(kernel='linear', random_state=0)
svm
```

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

```
#training the model
svm.fit(X_train, y_train)
#training the model
svm.score(X_test, y_test)
```

```
0.7597402597402597
```

```
#predicting outcomes
svm_pred = svm.predict(X_test)
```

Model Evaluation

Evaluating Logistic Regression Model

Confusion Matrix Heatmap

```
from sklearn.metrics import confusion_matrix
sns.heatmap(confusion_matrix(y_test, lr_pred), annot=True, cmap='Blues')
plt.xlabel('Predicted Values')
plt.ylabel('Actual Values')
plt.title('Confusion Matrix for Logistic Regression')
plt.show()
```

The diagonal boxes shows the count of true positives for each class. The predicted value is given on top while the actual value is given on the left side. The off-diagonal boxes shows the count of false positives.

```
ax = sns.distplot(y_test, color='r',  label='Actual Value',hist=False)
sns.distplot(lr_pred, color='b', label='Predicted Value',hist=False,ax=ax)
plt.title('Actual vs Predicted Value Logistic Regression')
plt.xlabel('Outcome')
plt.ylabel('Count')
```

```
<ipython-input-36-bc104d462945>: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, color='r',  label='Actual Value',hist=False)
<ipython-input-36-bc104d462945>:2: UserWarning:
```

These distribution plot clearly visualizes the accuracy of the model. The red color represents the actual values and the blue color represents the predicted values. The more the overlapping of the two colors, the more accurate the model is.

Classification Report

```
from sklearn.metrics import classification_report
print(classification_report(y_test, lr_pred))
```

```
              precision    recall  f1-score   support

           0       0.82      0.85      0.83        99
           1       0.71      0.65      0.68        55

    accuracy                           0.78       154
   macro avg       0.76      0.75      0.76       154
weighted avg       0.78      0.78      0.78       154
```

The model has as an average f1 score of 0.755 and acuuracy of 78%.

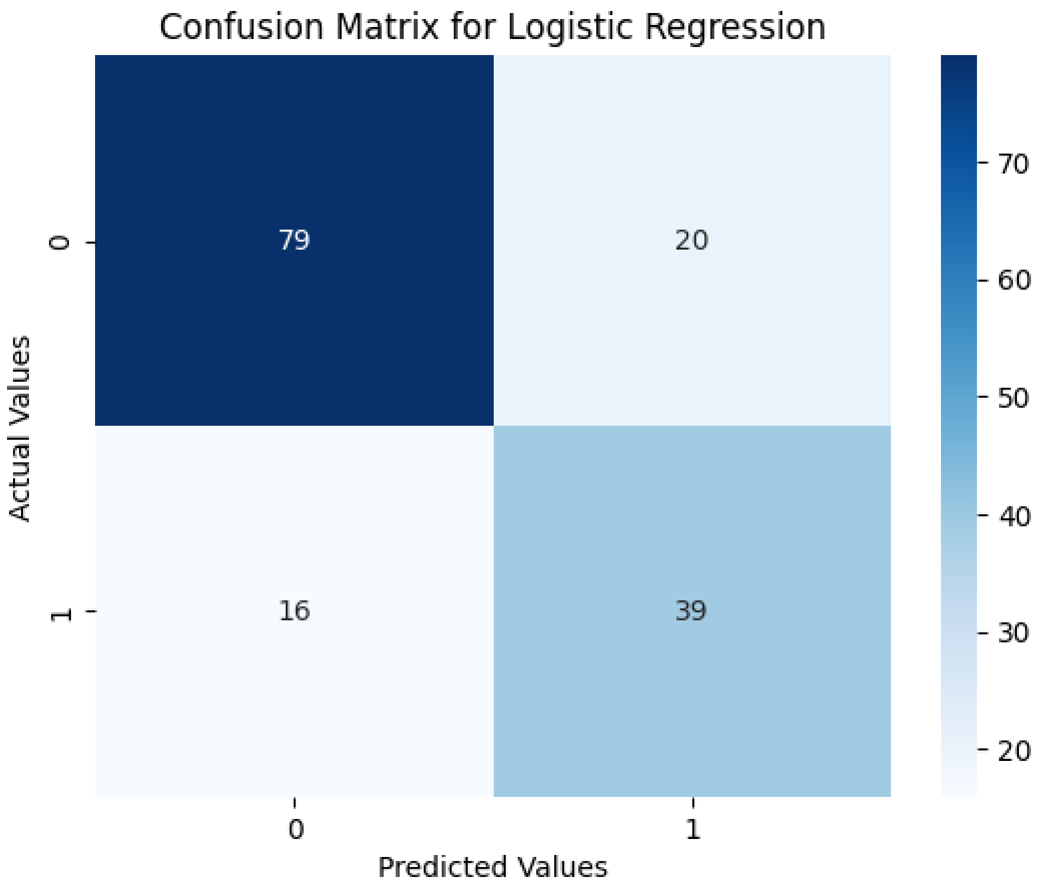
```
from sklearn.metrics import accuracy_score,mean_absolute_error,mean_squared_error,r2_score
print('Accuracy Score: ',accuracy_score(y_test,lr_pred))
print('Mean Absolute Error: ',mean_absolute_error(y_test,lr_pred))
print('Mean Squared Error: ',mean_squared_error(y_test,lr_pred))
print('R2 Score: ',r2_score(y_test,lr_pred))
```

```
Accuracy Score:  0.7792207792207793
Mean Absolute Error:  0.22077922077922077
Mean Squared Error:  0.22077922077922077
R2 Score:  0.038383838383838076
```

Evaluating Random Forest Classifier

Confusion Matrix Heatmap

```
sns.heatmap(confusion_matrix(y_test, rfc_pred), annot=True, cmap='Blues')
plt.xlabel('Predicted Values')
plt.ylabel('Actual Values')
plt.title('Confusion Matrix for Logistic Regression')
plt.show()
```

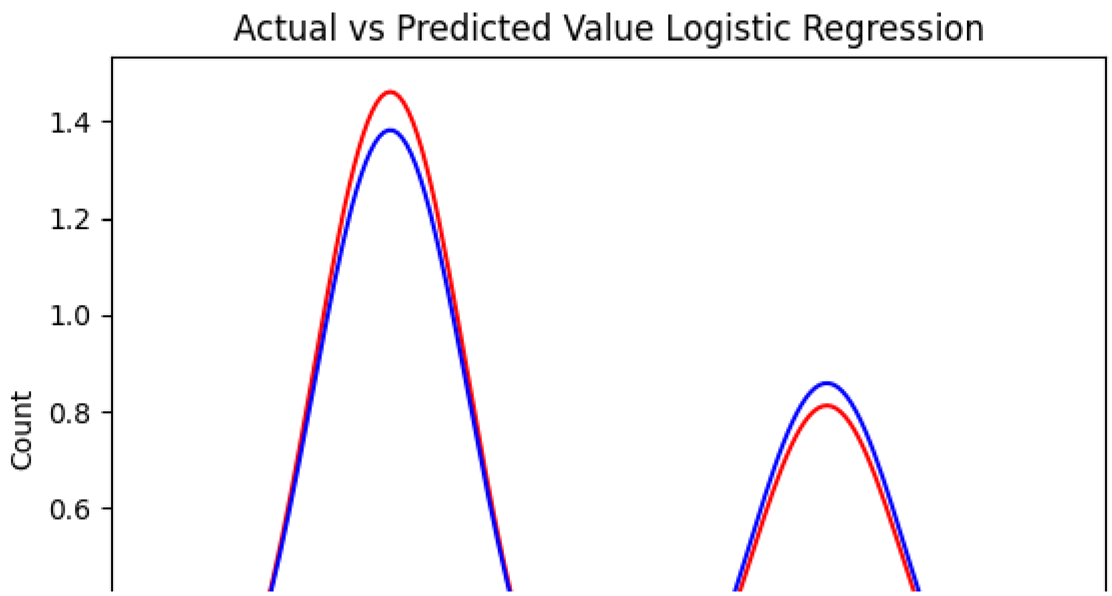


The diagonal boxes shows the count of true positives for each class. The predicted value is given on top while the actual value is given on the left side. The off-diagonal boxes shows the count of false positives.

Distribution Plot

```
ax = sns.distplot(y_test, color='r',  label='Actual Value',hist=False)
sns.distplot(rfc_pred, color='b', label='Predicted Value',hist=False,ax=ax)
plt.title('Actual vs Predicted Value Logistic Regression')
plt.xlabel('Outcome')
plt.ylabel('Count')
```

```
<ipython-input-40-9669e741e5cd>: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, color='r',  label='Actual Value',hist=False)
<ipython-input-40-9669e741e5cd>: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(rfc_pred, color='b', label='Predicted Value',hist=False,ax=ax)
Text(0, 0.5, 'Count')
```



These distribution plot clearly visualizes the accuracy of the model. The red color represents the actual values and the blue color represents the predicted values. The more the overlapping of the two colors, the more accurate the model is.

Classification Report

```
print(classification_report(y_test, rfc_pred))
```

```
              precision    recall  f1-score   support

           0       0.83      0.80      0.81        99
           1       0.66      0.71      0.68        55

    accuracy                           0.77       154
   macro avg       0.75      0.75      0.75       154
```

```
weighted avg       0.77      0.77      0.77       154
```

The model has as an average f1 score of 0.745 and acuuracy of 77% which less in comparison to Logistic Regression model.

```
print('Accuracy Score: ',accuracy_score(y_test,rfc_pred))
print('Mean Absolute Error: ',mean_absolute_error(y_test,rfc_pred))
print('Mean Squared Error: ',mean_squared_error(y_test,rfc_pred))
print('R2 Score: ',r2_score(y_test,rfc_pred))
```

```
Accuracy Score:  0.7662337662337663
Mean Absolute Error:  0.23376623376623376
Mean Squared Error:  0.23376623376623376
R2 Score:  -0.018181818181818181852
```

Evaluating SVM Model

Confusion Matrix Heatmap

```
sns.heatmap(confusion_matrix(y_test, svm_pred), annot=True, cmap='Blues')
plt.xlabel('Predicted Values')
plt.ylabel('Actual Values')
plt.title('Confusion Matrix for Logistic Regression')
plt.show()
```

Confusion Matrix for Logistic Regression

The diagonal boxes shows the count of true positives for each class. The predicted value is given on top while the actual value is given on the left side. The off-diagonal boxes shows the count of false positives.

Distribution Plot

```
ax = sns.distplot(y_test, color='r',  label='Actual Value',hist=False)
sns.distplot(svm_pred, color='b', label='Predicted Value',hist=False,ax=ax)
plt.title('Actual vs Predicted Value Logistic Regression')
plt.xlabel('Outcome')
plt.ylabel('Count')
```

```
<ipython-input-44-b9a6ee476682>: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
```

These distribution plot clearly visualizes the accuracy of the model. The red color represents the actual values and the blue color represents the predicted values. The more the overlapping of the two colors, the more accurate the model is.


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


Classification Report


```
similar flexibility) or `kdeplot` (an axes-level function for kernel density plots
```


```
print(classification_report(y_test, rfc_pred))
```

```
              precision    recall  f1-score   support

           0       0.83      0.80      0.81        99
           1       0.66      0.71      0.68        55

    accuracy                           0.77       154
   macro avg       0.75      0.75      0.75       154
weighted avg       0.77      0.77      0.77       154
```

The model has as an average f1 score of 0.745 and acuuracy of 77% which is equivalent to previous model.

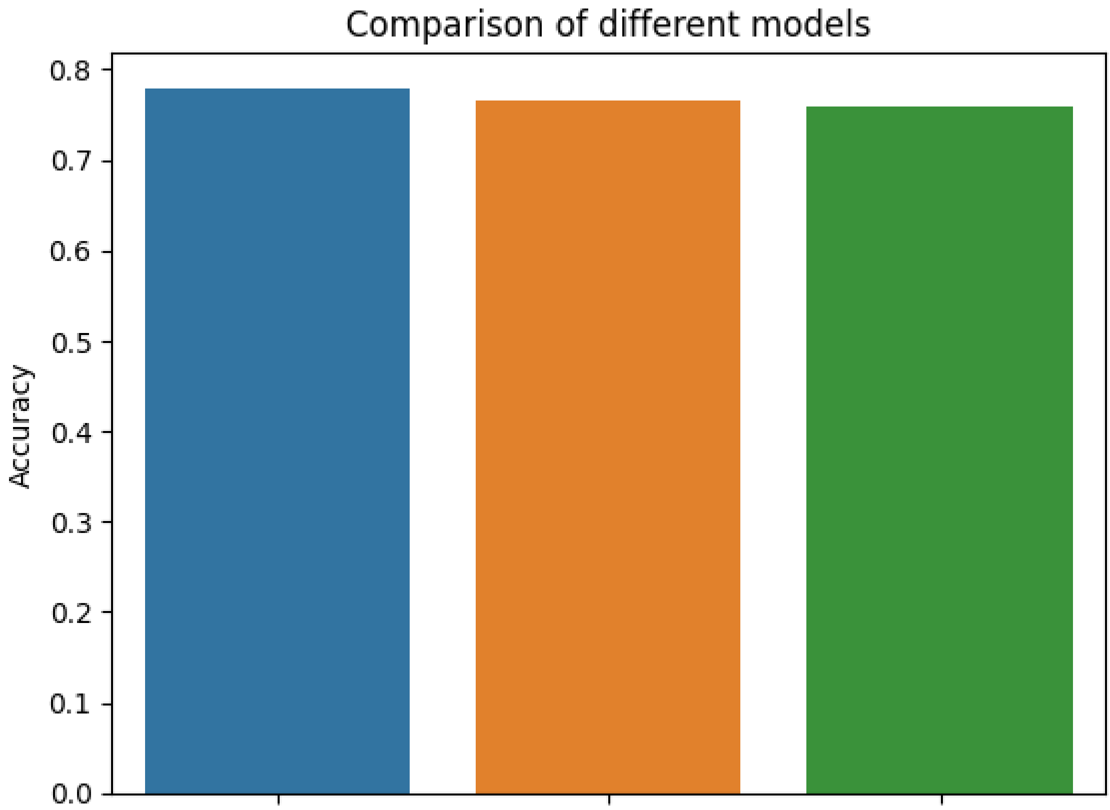
```
print('Accuracy Score: ',accuracy_score(y_test,svm_pred))
print('Mean Absolute Error: ',mean_absolute_error(y_test,svm_pred))
print('Mean Squared Error: ',mean_squared_error(y_test,svm_pred))
print('R2 Score: ',r2_score(y_test,svm_pred))
```

```
Accuracy Score:  0.7597402597402597
Mean Absolute Error:  0.24025974025974026
Mean Squared Error:  0.24025974025974026
R2 Score:  -0.046464646464646764
```

Comparing the models

```
#comparing the accuracy of different models
sns.barplot(x=['Logistic Regression', 'RandomForestClassifier', 'SVM'], y=[0.7792207792207
plt.xlabel('Classifier Models')
plt.ylabel('Accuracy')
plt.title('Comparison of different models')
```

```
Text(0.5, 1.0, 'Comparison of different models')
```



Conclusion

From the exploratory data analysis, I have concluded that the risk of diabetes depends upon the following factors:

Glucose level

Number of pregnancies

Skin Thickness

Insulin level

BMI

With in increase in Glucose level, insulin level, BMI and number of pregnancies, the risk of diabetes increases. However, the number of pregnancies have strange effect of risk of diabetes which couldn't be explained by the data. The risk of diabetes also increases with increase in skin thickness.

Coming to the classification models, Logistic Regression outperformed Random Forest and SVM with 78% accuracy. The accuracy of the model can be improved by increasing the size of the dataset. The dataset used for this project was very small and had only 768 rows.

END