

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.

Data Dictionary

Feature	Description
Pregnancies	Number of times pregnant
Glucose	Plasma glucose concentration a 2 hours in an oral glucose tolerance test
BloodPressure	Diastolic blood pressure (mm Hg)
SkinThickness	Triceps skin fold thickness (mm)
Insulin	2-Hour serum insulin (mu U/ml)
BMI	Body mass index (weight in kg/(height in m)^2)
DiabetesPedigreeFunction	Diabetes pedigree function
Age	Age (years)
Outcome	Class variable (0 or 1)

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

```
In [ ]: #Loading the dataset
df = pd.read_csv("diabetes.csv")
df.head()
```

Out[]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeF
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

In []: `#shape of the dataset
df.shape`

Out[]: (768, 9)

Checking the unique values for each variable in the dataset

In []: `#checking unique values
variables = ['Pregnancies','Glucose','BloodPressure','SkinThickness','Insulin','
for i in variables:
 print(df[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
0.542 0.773 0.678 0.719 0.382 0.319 0.19 0.956 0.084 0.725 0.299 0.244
0.745 0.615 1.321 0.64 0.142 0.374 0.383 0.578 0.136 0.395 0.187 0.905
0.15 0.874 0.236 0.787 0.407 0.605 0.151 0.289 0.355 0.29 0.375 0.164]
```

```

0.431 0.742 0.514 0.464 1.224 1.072 0.805 0.209 0.666 0.101 0.198 0.652
2.329 0.089 0.645 0.238 0.394 0.293 0.479 0.686 0.831 0.582 0.446 0.402
1.318 0.329 1.213 0.427 0.282 0.143 0.38 0.284 0.249 0.926 0.557 0.092
0.655 1.353 0.612 0.2 0.226 0.997 0.933 1.101 0.078 0.24 1.136 0.128
0.422 0.251 0.677 0.296 0.454 0.744 0.881 0.28 0.259 0.619 0.808 0.34
0.434 0.757 0.613 0.692 0.52 0.412 0.84 0.839 0.156 0.215 0.326 1.391
0.875 0.313 0.433 0.626 1.127 0.315 0.345 0.129 0.527 0.197 0.731 0.148
0.123 0.127 0.122 1.476 0.166 0.932 0.343 0.893 0.331 0.472 0.673 0.389
0.485 0.349 0.279 0.346 0.252 0.243 0.58 0.559 0.302 0.569 0.378 0.385
0.499 0.306 0.234 2.137 1.731 0.545 0.225 0.816 0.528 0.509 1.021 0.821
0.947 1.268 0.221 0.66 0.239 0.949 0.444 0.463 0.803 1.6 0.944 0.196
0.241 0.161 0.135 0.376 1.191 0.702 0.674 1.076 0.534 1.095 0.554 0.624
0.219 0.507 0.561 0.421 0.516 0.264 0.328 0.233 0.108 1.138 0.147 0.727
0.435 0.497 0.23 0.955 2.42 0.658 0.33 0.51 0.285 0.415 0.381 0.832
0.498 0.212 0.364 1.001 0.46 0.733 0.416 0.705 1.022 0.269 0.6 0.571
0.607 0.17 0.21 0.126 0.711 0.466 0.162 0.419 0.63 0.365 0.536 1.159
0.629 0.292 0.145 1.144 0.174 0.547 0.163 0.738 0.314 0.968 0.409 0.297
0.525 0.154 0.771 0.107 0.493 0.717 0.917 0.501 1.251 0.735 0.804 0.661
0.549 0.825 0.423 1.034 0.16 0.341 0.68 0.591 0.3 0.121 0.502 0.401
0.601 0.748 0.338 0.43 0.892 0.813 0.693 0.575 0.371 0.206 0.417 1.154
0.925 0.175 1.699 0.682 0.194 0.4 0.1 1.258 0.482 0.138 0.593 0.878
0.157 1.282 0.141 0.246 1.698 1.461 0.347 0.362 0.393 0.144 0.732 0.115
0.465 0.649 0.871 0.149 0.695 0.303 0.61 0.73 0.447 0.455 0.133 0.155
1.162 1.292 0.182 1.394 0.217 0.631 0.88 0.614 0.332 0.366 0.181 0.828
0.335 0.856 0.886 0.439 0.253 0.598 0.904 0.483 0.565 0.118 0.177 0.176
0.295 0.441 0.352 0.826 0.97 0.595 0.317 0.265 0.646 0.426 0.56 0.515
0.453 0.785 0.734 1.174 0.488 0.358 1.096 0.408 1.182 0.222 1.057 0.766
0.171]
[50 31 32 21 33 30 26 29 53 54 34 57 59 51 27 41 43 22 38 60 28 45 35 46
56 37 48 40 25 24 58 42 44 39 36 23 61 69 62 55 65 47 52 66 49 63 67 72
81 64 70 68]
[1 0]

```

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

```

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

```

```

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

```

Now, I have count of incorrect values in the variables, I will be replacing these values

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

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

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

Glucose 0
 BloodPressure 0
 SkinThickness 0
 Insulin 0
 BMI 0

Now, I have replace the incorrect values

Checking for missing values

```
In [ ]: #missing values
df.info()
```

#	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

```
In [ ]: #checking descriptive statistics
df.describe()
```

Out[]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	121.681605	72.254807	26.606479	118.660163	32.450805
std	3.369578	30.436016	12.115932	9.631241	93.080358	6.875374
min	0.000000	44.000000	24.000000	7.000000	14.000000	18.200000
25%	1.000000	99.750000	64.000000	20.536458	79.799479	27.500000
50%	3.000000	117.000000	72.000000	23.000000	79.799479	32.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000

◀ ▶

In []: df.head()

Out[]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedig
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	

◀ ▶

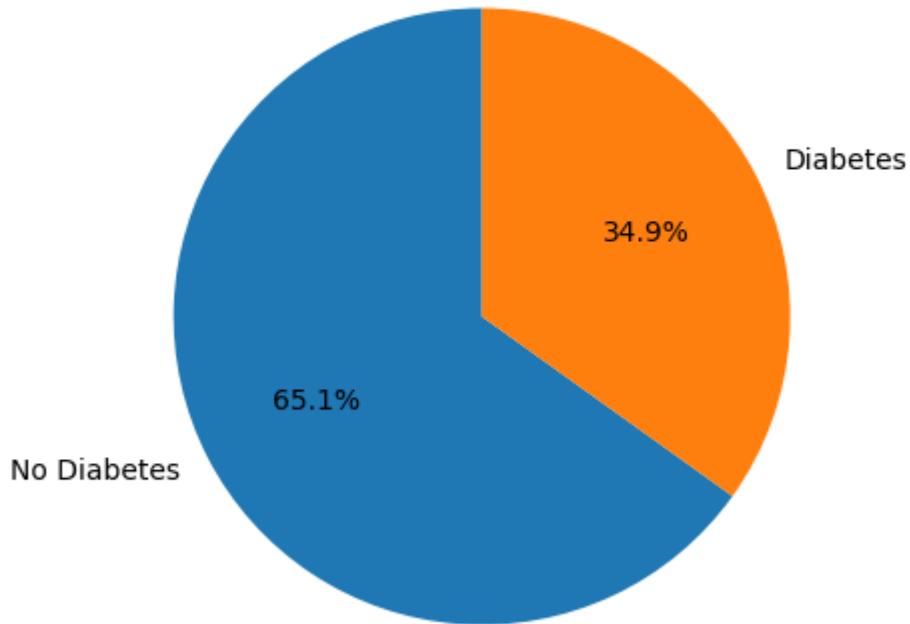
Exploratory Data Analysis

In the exploratory data analysis, I will be looking at the distribution of the data, the correlation between the features, and the relationship between the features and the target variable. I will start by looking at the distribution of the data, followed by relationship between the target variable and independent variables.

In []:

```
plt.figure(figsize=(5,5))
plt.pie(df['Outcome'].value_counts(), labels=['No Diabetes', 'Diabetes'], autopct='%1.1f%%')
plt.title('Diabetes Outcome')
plt.show()
```

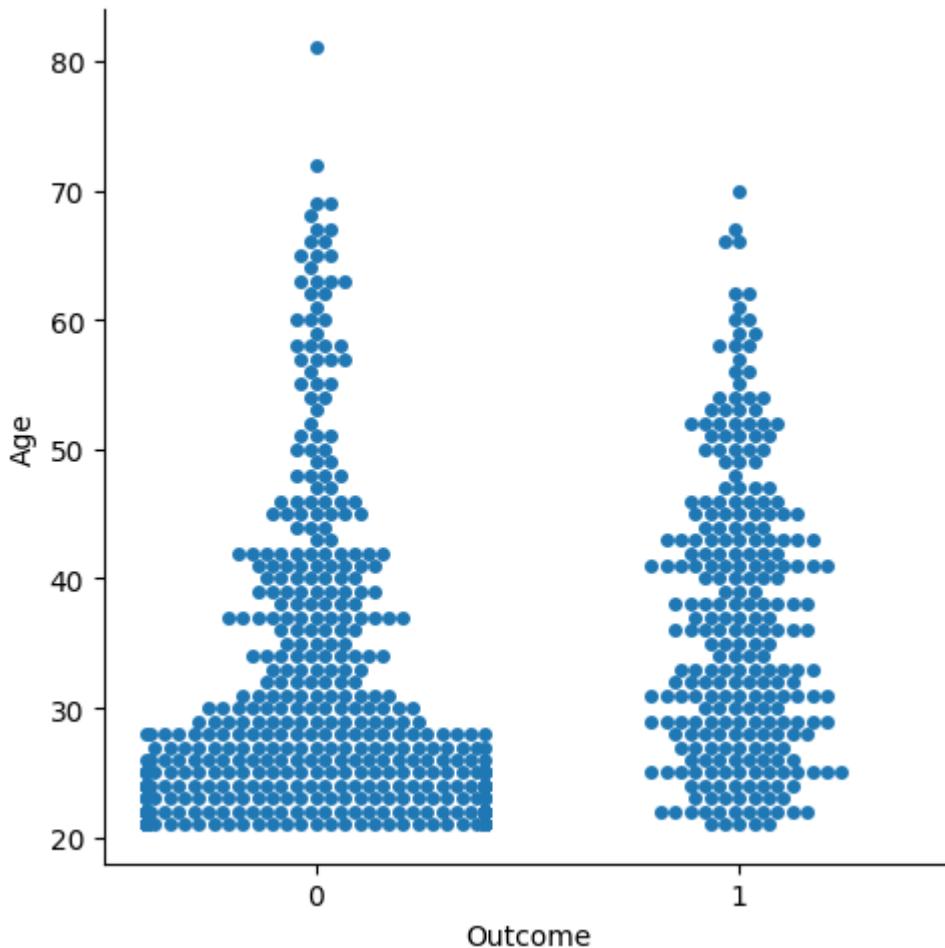
Diabetes Outcome



Age Distribution and Diabetes

```
In [ ]: sns.catplot(x="Outcome", y="Age", kind="swarm", data=df)
```

```
Out[ ]: <seaborn.axisgrid.FacetGrid at 0x2c9111178d0>
```

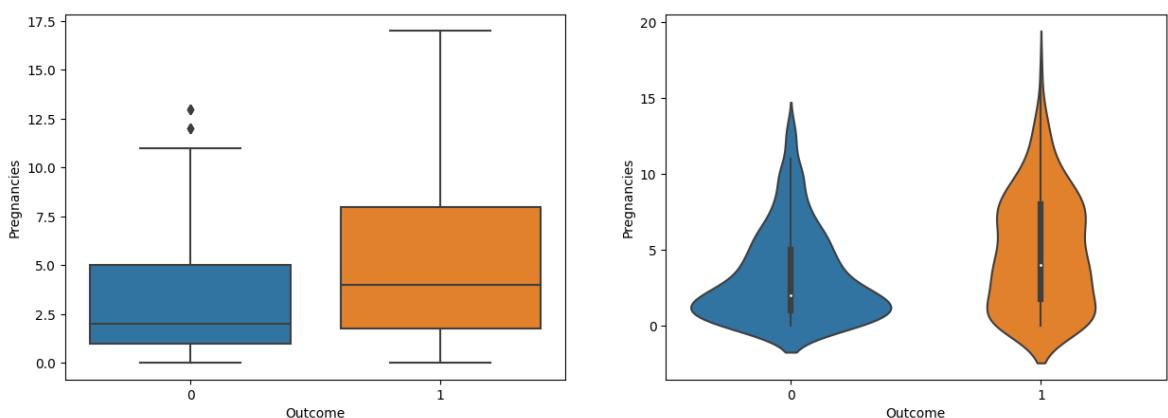


From the graph, it is quite clear that majority of the patients are adult within the age group of 20-30 years. Patients in the age range 40-55 years are more prone to diabetes, as compared to other age groups. Since the number adults in the age group 20-30 years is more, the number of patients with diabetes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

Pregnancies and Diabetes

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

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

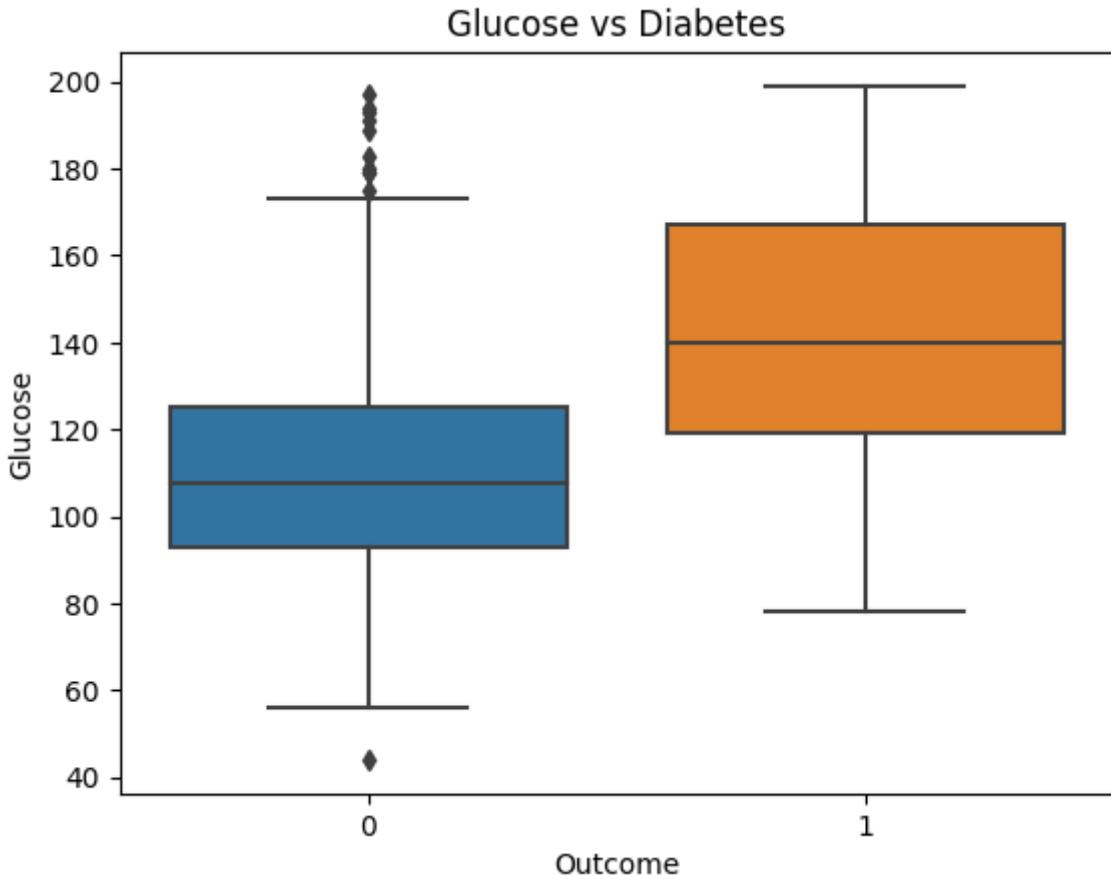


Both boxplot and violinplot shows strange relation between the number of pregnancies and diabetes. According to the graphs the increased number of pregnancies highlights increased risk of diabetes.

Glucose and Diabetes

```
In [ ]: sns.boxplot(x='Outcome', y='Glucose', data=df).set_title('Glucose vs Diabetes')
```

```
Out[ ]: Text(0.5, 1.0, 'Glucose vs Diabetes')
```

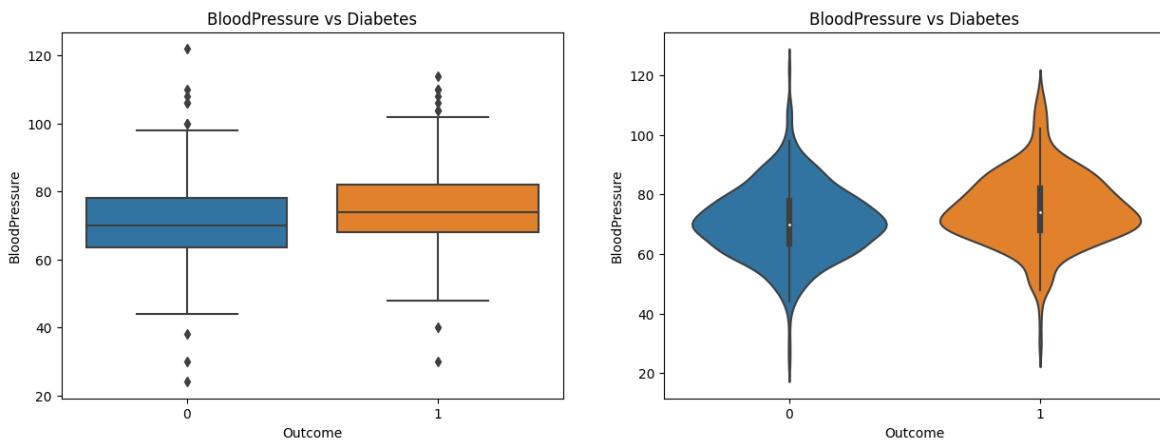


Glucose level plays a major role in determine whether the patient is diabetic or not. The patients with median gluocse level less than 120 are more likely to be non-diabetic. The patients with median gluocse level greater than 140 are more likely to be diabetic. Therefore, high glucose levels is a good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

Blood Pressuse and Diabetes

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

```
Out[ ]: Text(0.5, 1.0, 'BloodPressure vs Diabetes')
```

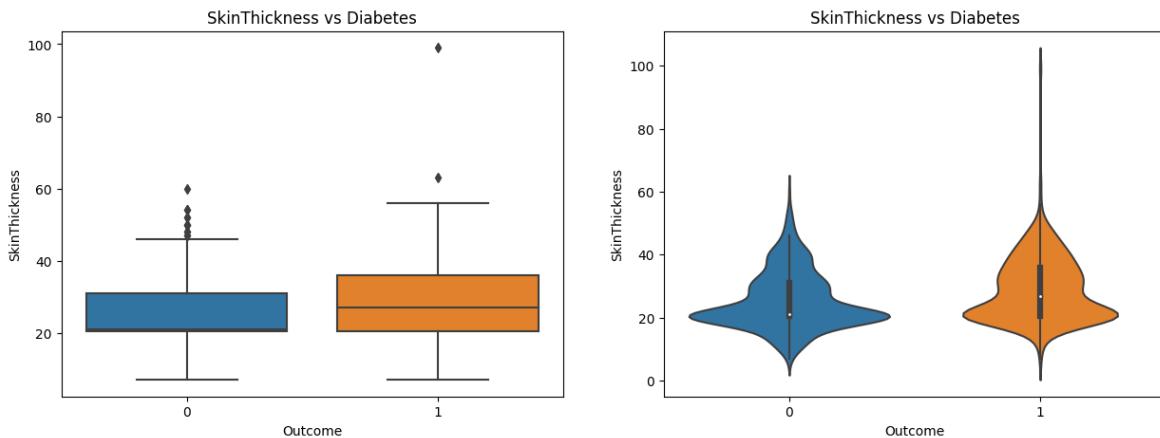


Both the boxplot and violinplot provides clear understanding of the realtion between the blood pressure and diabetes. The boxplot shows that the median of the blood pressure for the diabetic patients is slightly higher than the non-diabetic patients. The violinplot shows that the distribution of the 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

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

Out[]: Text(0.5, 1.0, 'SkinThickness vs Diabetes')

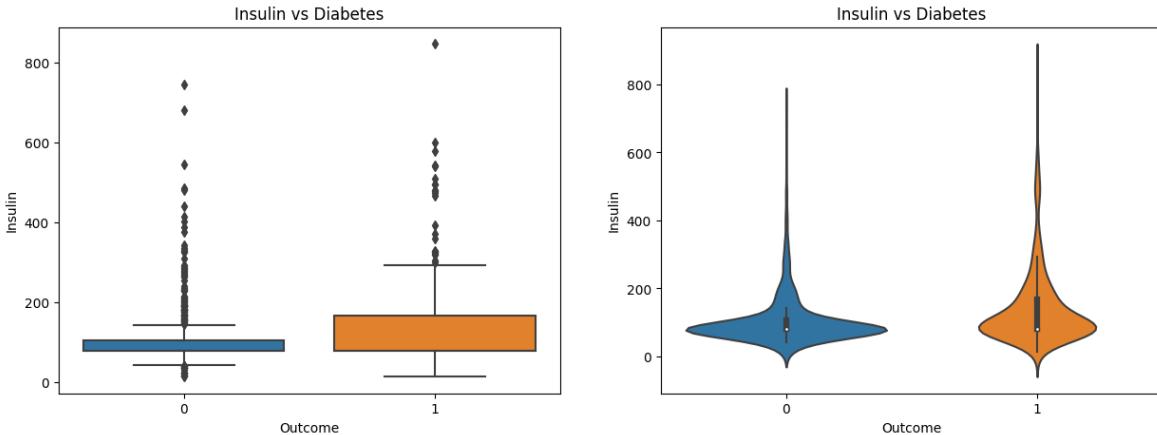


Here both the boxplot and violinplot reveals the effect of diabetes on skin thickness. As obseved in the boxplot, the median of skin thickness is higher for the diabetic patients than the non-diabetic patients, where non diabetic patients have median skin thickness near 20 in comparison to skin thickness nearly 30 in diabetic patients. The violinplot 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

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

Out[]: Text(0.5, 1.0, 'Insulin vs Diabetes')

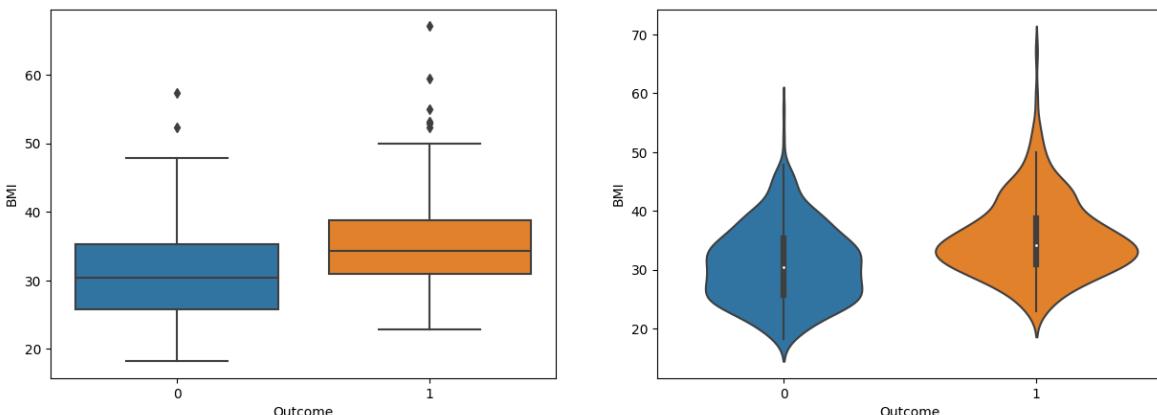


Insulin is a major body hormone that regulates glucose metabolism. Insulin is required for the body to efficiently use sugars, fats and proteins. Any change in insulin amount in the body would result in change glucose levels as well. Here the boxplot and violinplot shows the distribution of insulin level 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 violinplot 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

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

Out[]: <Axes: xlabel='Outcome', ylabel='BMI'>



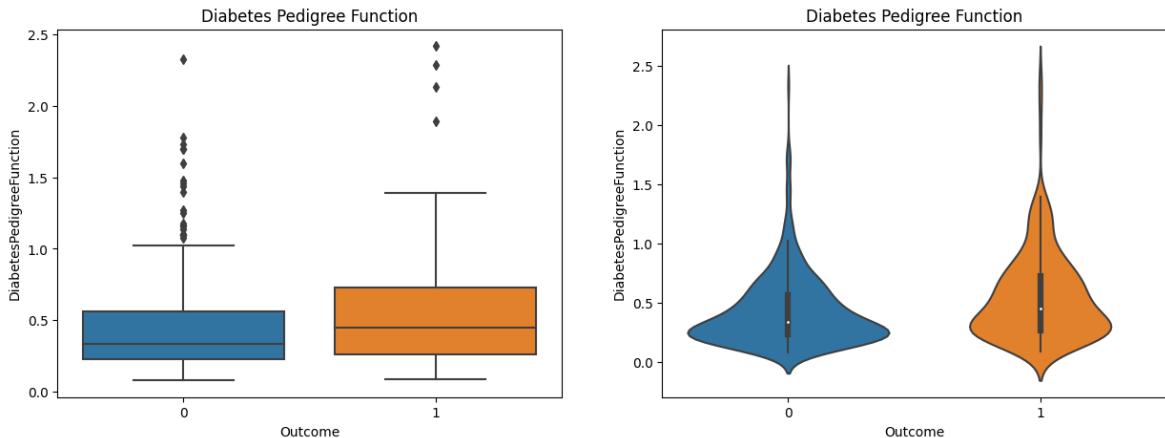
Both graphs highlights the role of BMI in diabetes prediction. Non diabetic patients have a normal BMI within the range of 25-35 whereas the diabetic patients have a BMI greater than 35. The violinplot reveals the BMI distribution, where the non diabetic patients have a increased spread from 25 to 35 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

```
In [ ]: fig,ax = plt.subplots(1,2,figsize=(15,5))
sns.boxplot(x='Outcome',y='DiabetesPedigreeFunction',data=df,ax=ax[0]).set_title('Boxplot')
sns.violinplot(x='Outcome',y='DiabetesPedigreeFunction',data=df,ax=ax[1]).set_title('Violinplot')
```

```
Out[ ]: Text(0.5, 1.0, 'Diabetes Pedigree Function')
```



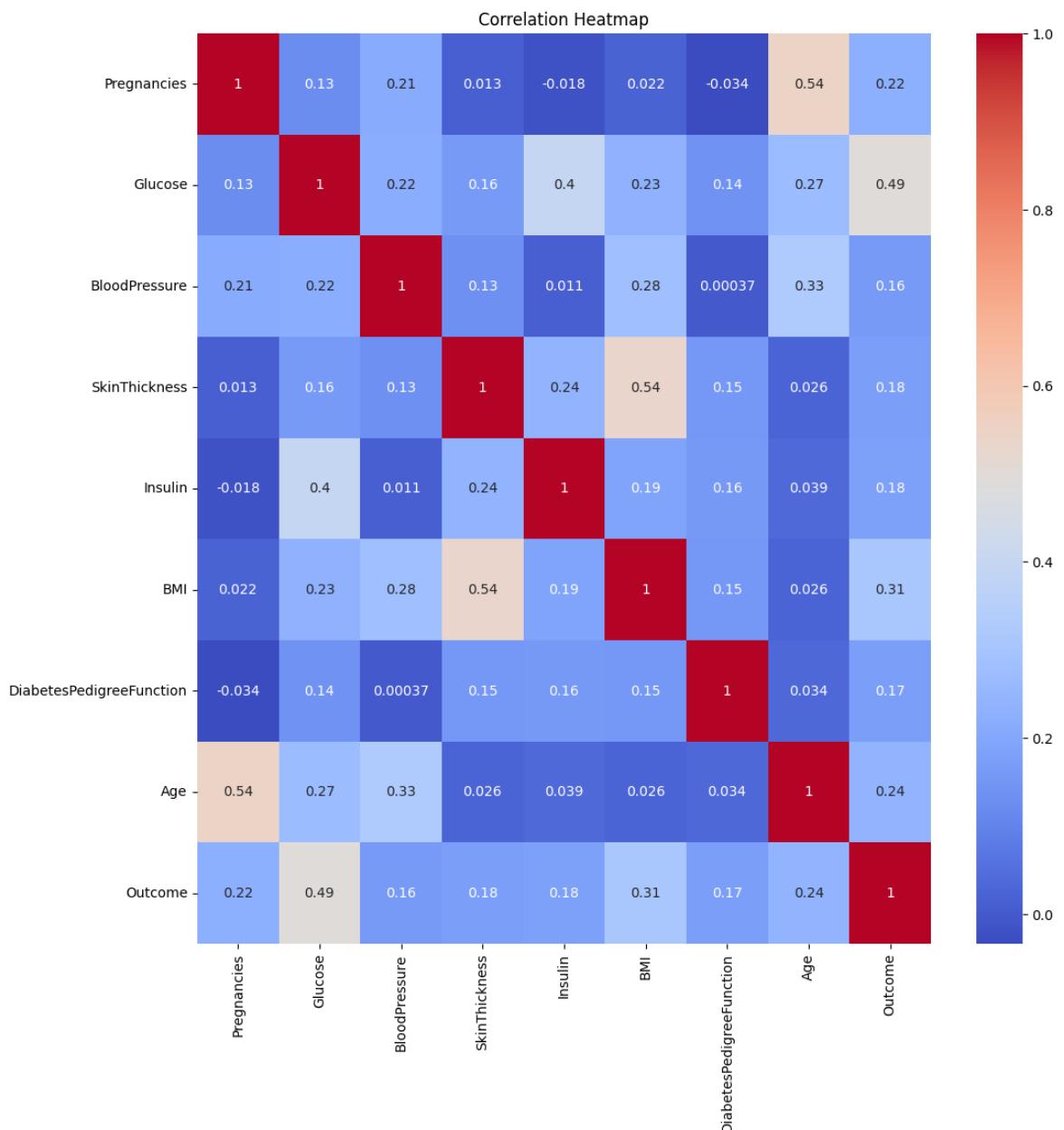
Diabetes Pedigree Function (DPF) calculates diabetes likelihood depending on the subject's age and his/her diabetic family history. From the boxplot, the patients with lower DPF, are much less likely to have diabetes. The patients with higher DPF, are much more likely to have diabetes. In the violinplot, 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.

Correlation Matrix Heatmap

```
In [ ]: #correlation heatmap
plt.figure(figsize=(12,12))
sns.heatmap(df.corr(), annot=True, cmap='coolwarm').set_title('Correlation Heatmap')
```

```
Out[ ]: Text(0.5, 1.0, 'Correlation Heatmap')
```

Diabetes Prediction



Train Test Split

```
In [ ]: from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(df.drop('Outcome', axis=1), df['Outcome'])
```

Diabetes Prediction

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

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

Logistic Regression

```
In [ ]: #building model
from sklearn.linear_model import LogisticRegression
lr = LogisticRegression()
lr
```

```
Out[ ]: ▾ LogisticRegression
LogisticRegression()
```

```
In [ ]: #training the model
lr.fit(X_train,y_train)
#training accuracy
lr.score(X_train,y_train)
```

```
Out[ ]: 0.7719869706840391
```

```
In [ ]: #predicted outcomes
lr_pred = lr.predict(X_test)
```

Random Forest Classifier

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

```
Out[ ]: ▾ RandomForestClassifier
RandomForestClassifier(random_state=42)
```

```
In [ ]: #training model
rfc.fit(X_train, y_train)
#training accuracy
rfc.score(X_train, y_train)
```

```
Out[ ]: 1.0
```

```
In [ ]: #predicted outcomes
rfc_pred = rfc.predict(X_test)
```

Support Vector Machine (SVM)

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

```
Out[ ]: ▾ SVC
SVC(kernel='linear', random_state=0)
```

```
In [ ]: #training the model
svm.fit(X_train, y_train)
```

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

Out[]: 0.7597402597402597

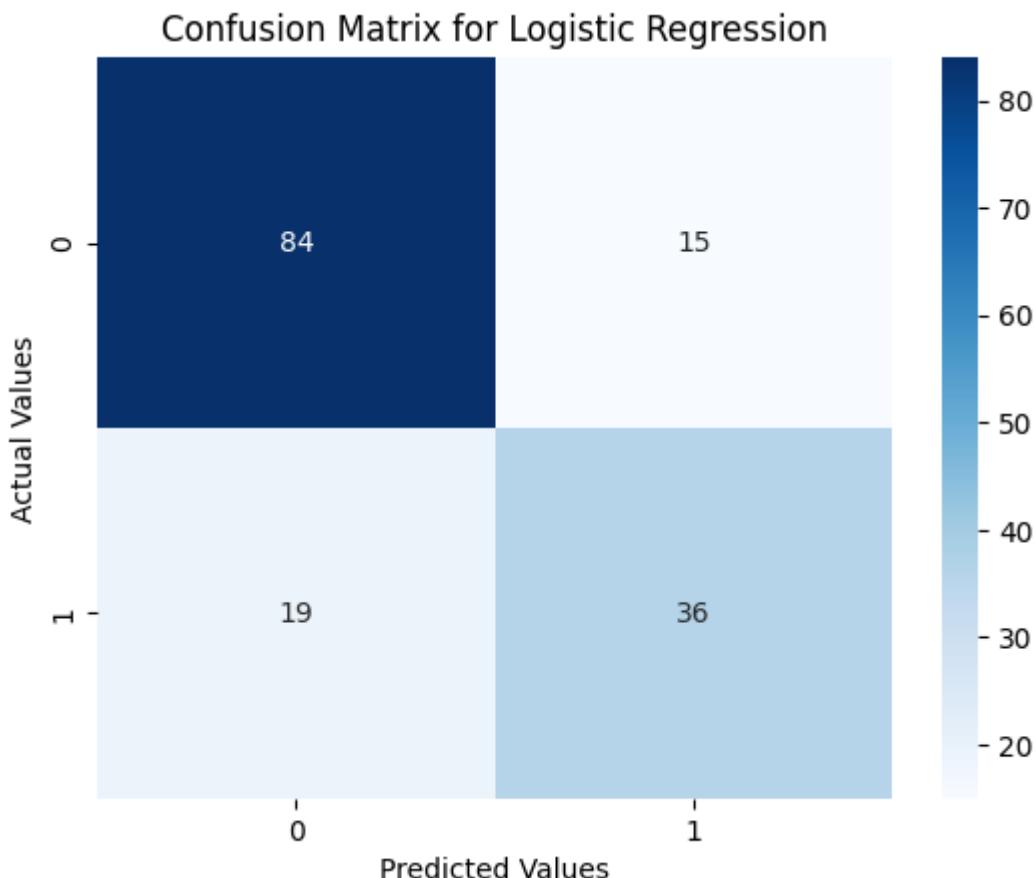
```
#predicting outcomes
svm_pred = svm.predict(X_test)
```

Model Evaluation

Evaluating Logistic Regression Model

Confusion Matrix Heatmap

```
In [ ]: 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()
```

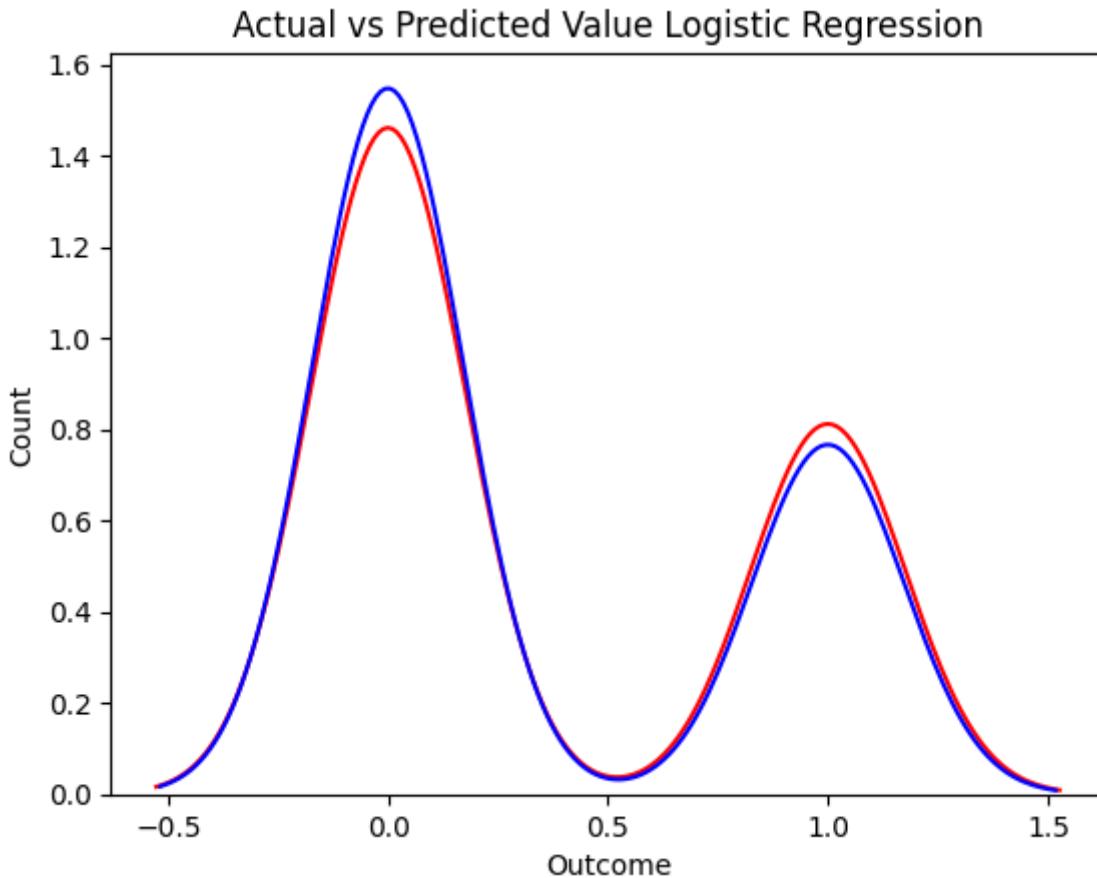


The diagonal boxes shows the count of true positives for each class. The predicted value is given on top while the actual value is given on the left side. The off-diagonal boxes shows the count of false positives.

Distribution plot

```
In [ ]: 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')
```

Out[]: 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

```
In [ ]: 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 an average f1 score of 0.755 and accuracy of 78%.

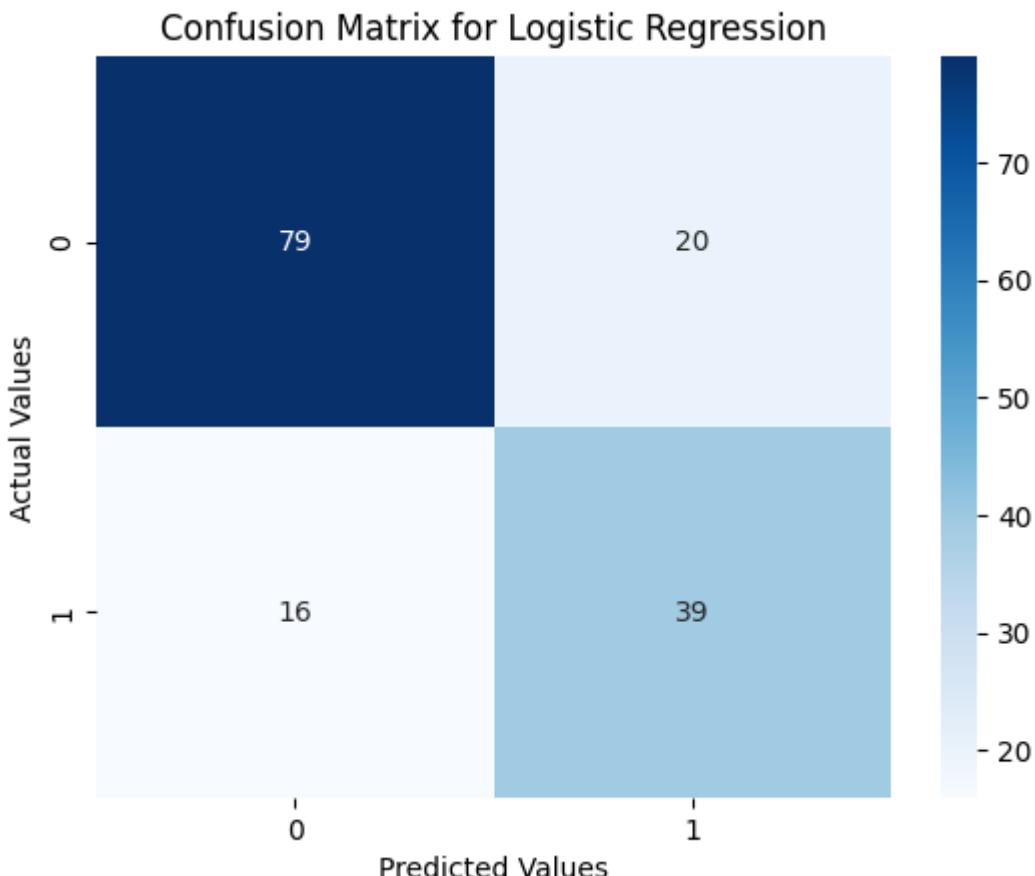
```
In [ ]: from sklearn.metrics import accuracy_score,mean_absolute_error,mean_squared_error
print('Accuracy Score: ',accuracy_score(y_test,lr_pred))
print('Mean Absolute Error: ',mean_absolute_error(y_test,lr_pred))
print('Mean Squared Error: ',mean_squared_error(y_test,lr_pred))
print('R2 Score: ',r2_score(y_test,lr_pred))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

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

```
In [ ]: 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()
```



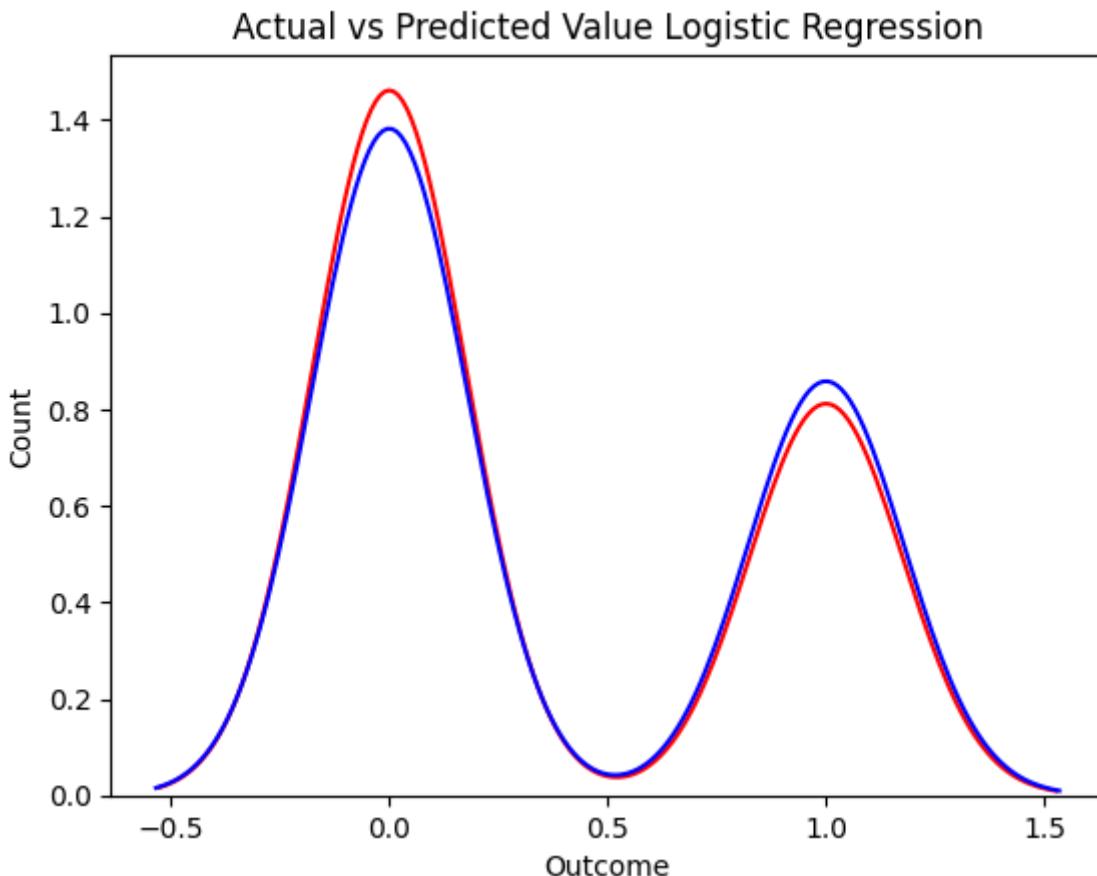
The diagonal boxes shows the count of true positives for each class. The predicted value is given on top while the actual value is given on the left side. The off-diagonal boxes shows the count of false positives.

Distribution Plot

```
In [ ]: 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')
```

Out[]: 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

In []: `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 an average f1 score of 0.745 and accuracy of 77% which is less in comparison to Logistic Regression model.

In []: `print('Accuracy Score: ',accuracy_score(y_test,rfc_pred))
print('Mean Absolute Error: ',mean_absolute_error(y_test,rfc_pred))`

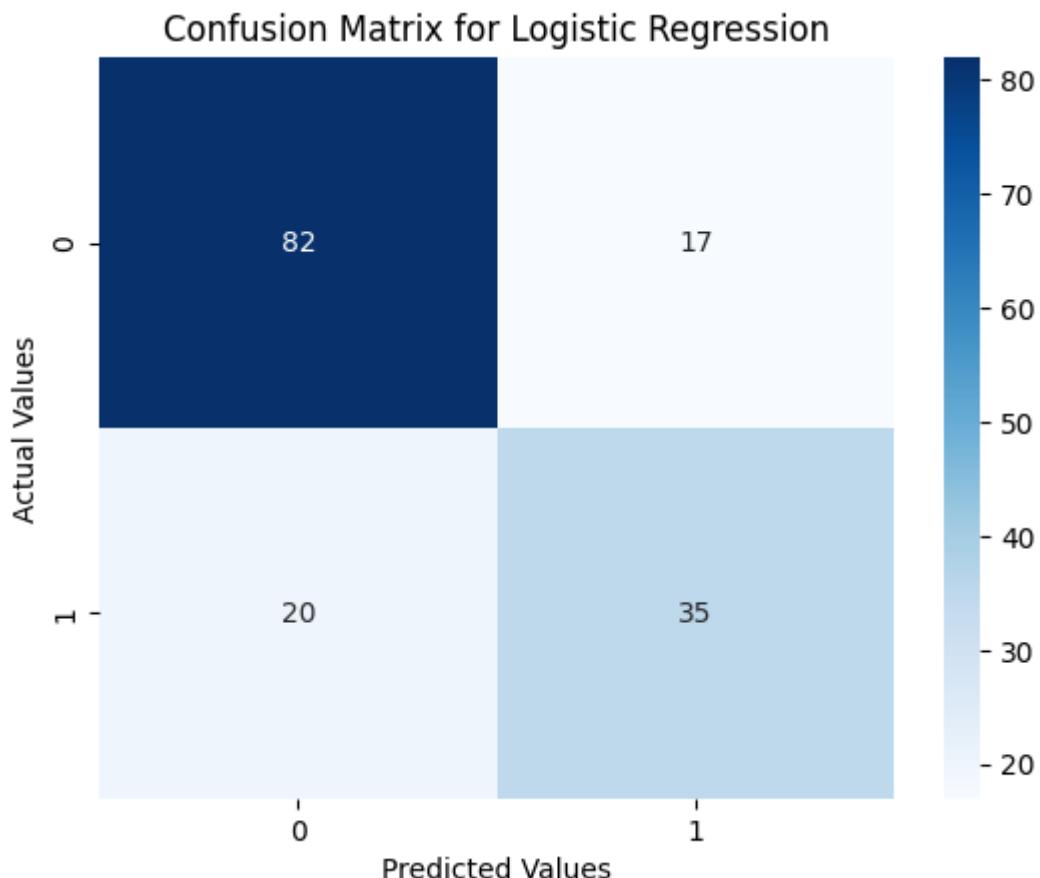
```
print('Mean Squared Error: ',mean_squared_error(y_test,rfc_pred))
print('R2 Score: ',r2_score(y_test,rfc_pred))
```

Accuracy Score: 0.766233766233766
 Mean Absolute Error: 0.23376623376623376
 Mean Squared Error: 0.23376623376623376
 R2 Score: -0.01818181818181852

Evaluating SVM Model

Confusion Matrix Heatmap

```
In [ ]: 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()
```

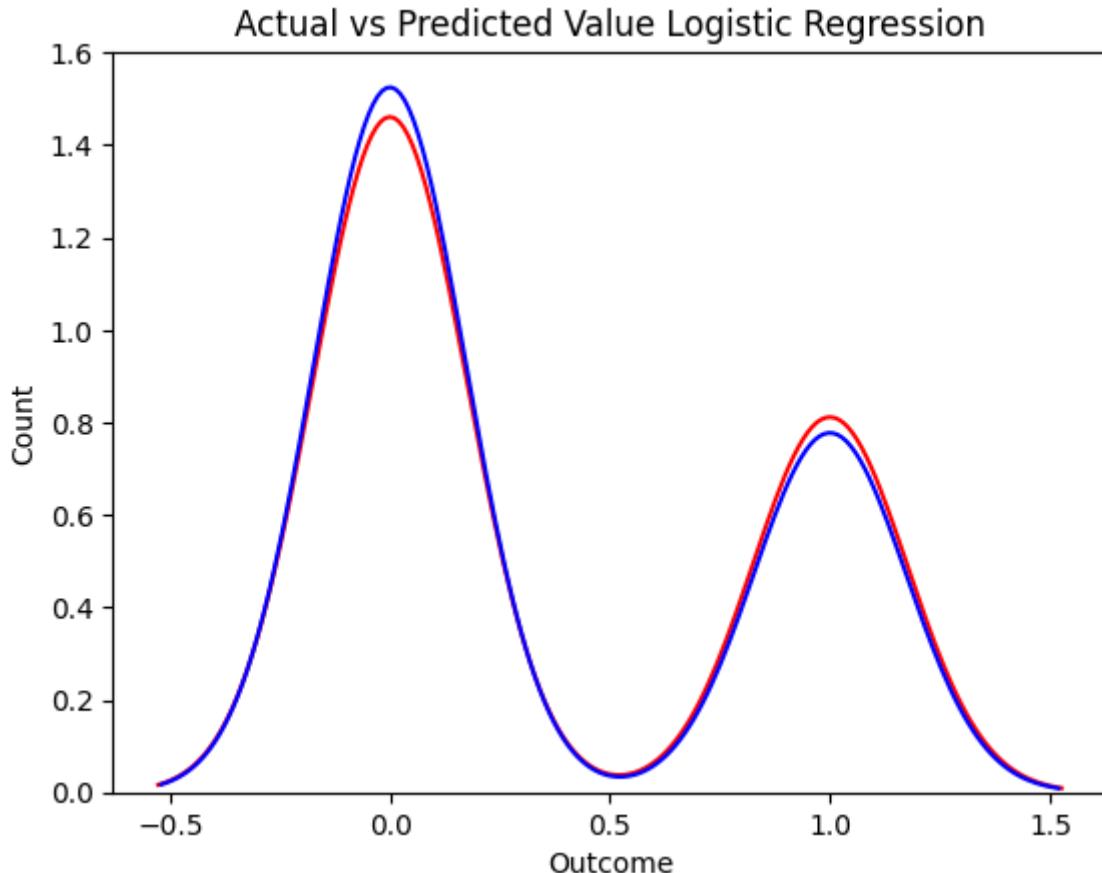


The diagonal boxes shows the count of true positives for each class. The predicted value is given on top while the actual value is given on the left side. The off-diagonal boxes shows the count of false positives.

Distribution Plot

```
In [ ]: 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')
```

```
Out[ ]: 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

```
In [ ]: 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 an average f1 score of 0.745 and accuracy of 77% which is equivalent to previous model.

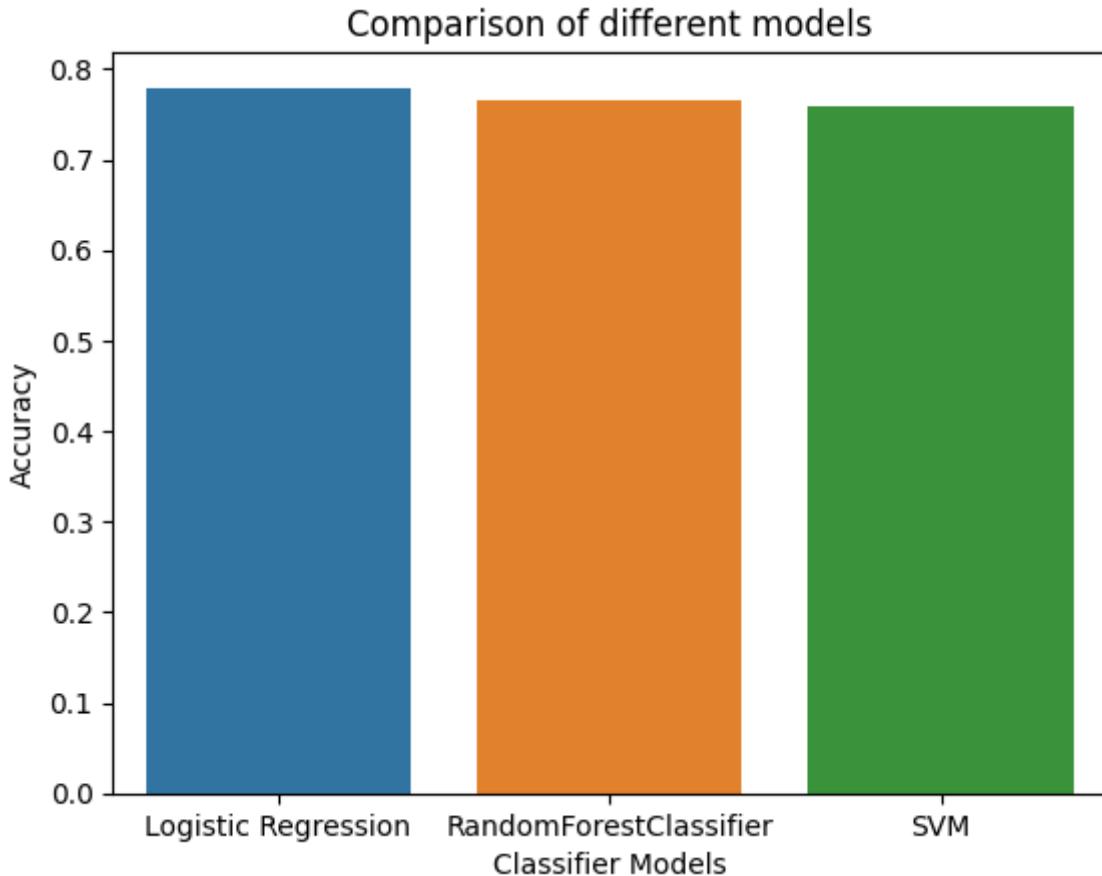
```
In [ ]: print('Accuracy Score: ',accuracy_score(y_test,svm_pred))
print('Mean Absolute Error: ',mean_absolute_error(y_test,svm_pred))
print('Mean Squared Error: ',mean_squared_error(y_test,svm_pred))
print('R2 Score: ',r2_score(y_test,svm_pred))
```

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

Comparing the models

```
In [ ]: #comparing the accuracy of different models
sns.barplot(x=['Logistic Regression', 'RandomForestClassifier', 'SVM'], y=[0.779, 0.774, 0.765])
plt.xlabel('Classifier Models')
plt.ylabel('Accuracy')
plt.title('Comparison of different models')

Out[ ]: 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:

1. Glucose level
2. Number of pregnancies
3. Skin Thickness
4. Insulin level
5. BMI

With an increase in Glucose level, insulin level, BMI and number of pregnancies, the risk of diabetes increases. However, the number of pregnancies have a strange effect on the 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.