In [34]:

```
"""
Classifiaction problem related to Pima Indians Diabetes Database.

Authors:
-------

Group-123

Snigdha Tarua - 2019ab04171
Sanka Mahesh Sai - 2019ab04135
Aravapalli Chandra Sekhar Gupta - 2019ab04187

"""
```

Out[34]:

```
'\nClassifiaction problem related to Pima Indians Diabetes Databas
e.\n\nAuthors:\n-------\n\nGroup-123\n\nSnigdha Tarua - 2019ab04171
\nSanka Mahesh Sai - 2019ab04135\nAravapalli Chandra Sekhar Gupta -
2019ab04187\n\n'
```

Table of Contents

Pima Indians Diabetes Database

Attribute Information:

```
    1. Number of times pregnant
    2. Plasma glucose concentration a 2 hours in an oral glucose tolerance
test
    3. Diastolic blood pressure (mm Hg)
    4. Triceps skin fold thickness (mm)
    5. 2-Hour serum insulin (mu U/ml)
    6. Body mass index (weight in kg/(height in m)^2)
    7. Diabetes pedigree function
    8. Age (years)
    9. Class variable (0 or 1)
```

Class Variable interpretation:

- class value 1 is interpreted as "tested positive for diabetes"

Objective:

- To perform basic analysis on the dataset and to classify based on the provided class label

- Import the data from Indian diabetes dataset (Links to an external site.) and find dataset description from here (Links to an external site.) (2 points)
- Consider all columns as independent variables and assign to variable X except the last column and consider the last column as the dependent variable and assign to variable y. Remove columns which don't help the problem statement. (1 point)
- Compute some basic statistical details like percentile, mean, standard deviation of dataset (1 point)
- Do Feature Scaling on Independent variables (2 points)
- Split the data into train and test dataset (1 point)
- Use sklearn library to train on train dataset on logistic regression and predict on test dataset (3 points)
- Compute the accuracy and confusion matrix. (2 points)

In [35]:

```
# importing required libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report,confusion_matrix, accuracy_sco
re
```

In [36]:

```
pd.options.display.float_format = "{:.2f}".format
```

Import the data from Indian diabetes dataset (Links to an external site.) and find dataset description from here (Links to an external site.) (2 points)

In [37]:

```
data = pd.read_csv("https://raw.githubusercontent.com/jbrownlee/Datasets/master/
pima-indians-diabetes.data.csv", header=None)
data.head()
```

Out[37]:

	0	1	2	3	4	5	6	7	8
0	6	148	72	35	0	33.60	0.63	50	1
1	1	85	66	29	0	26.60	0.35	31	0
2	8	183	64	0	0	23.30	0.67	32	1
3	1	89	66	23	94	28.10	0.17	21	0
4	0	137	40	35	168	43.10	2.29	33	1

In [38]:

```
# Adding column names to the above dataframe

data.columns = ["num_pregnant", "plasma_conc", "blood_pressure", "skin_thicknes
s", "serum_insulin", \
                "bmi", "diabaties_function", "age", "has_diabetes"]

data.head()
```

Out[38]:

	num_pregnant	plasma_conc	blood_pressure	skin_thickness	serum_insulin	bmi	diaba
0	6	148	72	35	0	33.60	
1	1	85	66	29	0	26.60	
2	8	183	64	0	0	23.30	
3	1	89	66	23	94	28.10	
4	0	137	40	35	168	43.10	

Compute some basic statistical details like percentile, mean, standard deviation of dataset

In [39]:

```
# to get a basic descreptive stat summary of the data
data.describe()
```

Out[39]:

	num_pregnant	plasma_conc	blood_pressure	skin_thickness	serum_insulin	bmi
count	768.00	768.00	768.00	768.00	768.00	768.00
mean	3.85	120.89	69.11	20.54	79.80	31.99
std	3.37	31.97	19.36	15.95	115.24	7.88
min	0.00	0.00	0.00	0.00	0.00	0.00
25%	1.00	99.00	62.00	0.00	0.00	27.30
50%	3.00	117.00	72.00	23.00	30.50	32.00
75%	6.00	140.25	80.00	32.00	127.25	36.60
max	17.00	199.00	122.00	99.00	846.00	67.10

In [40]:

```
# checking for null values
data.isnull().sum()
```

Out[40]:

```
num_pregnant          0
plasma_conc           0
blood_pressure        0
skin_thickness        0
serum_insulin         0
bmi                   0
diabaties_function    0
age                   0
has_diabetes          0
dtype: int64
```

In [41]:

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column              Non-Null Count  Dtype  
---  ------              --------------  -----  
 0   num_pregnant        768 non-null    int64  
 1   plasma_conc         768 non-null    int64  
 2   blood_pressure      768 non-null    int64  
 3   skin_thickness      768 non-null    int64  
 4   serum_insulin       768 non-null    int64  
 5   bmi                 768 non-null    float64
 6   diabaties_function  768 non-null    float64
 7   age                 768 non-null    int64  
 8   has_diabetes        768 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

Exploratory data analysis

Understanding the split of dependent variable

In [42]:

```
data['has_diabetes'].value_counts()
```

Out[42]:

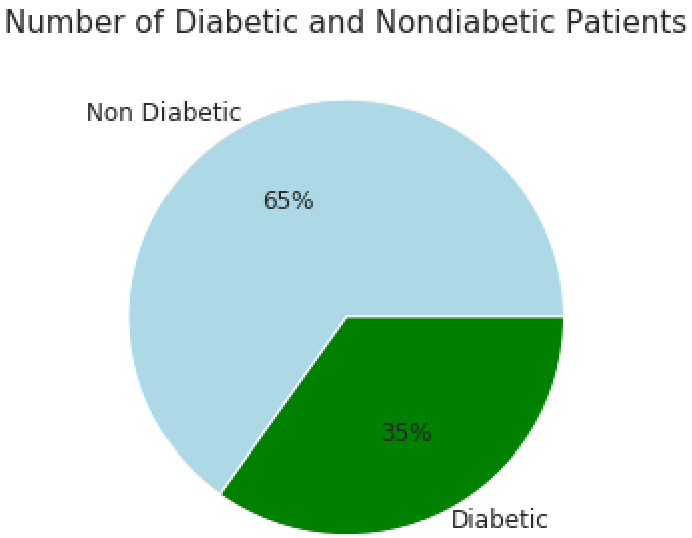
```
0    500
1    268
Name: has_diabetes, dtype: int64
```

In [43]:

```
diabetic_count = data['has_diabetes'].value_counts()[0]
non_diabetic_count = data['has_diabetes'].value_counts()[1]
```

In [44]:

```
plt.figure(figsize=(5,5))
plt.pie(x=[diabetic_count,non_diabetic_count], labels=[ 'Non Diabetic', 'Diabeti
c'], autopct='%1.0f%%',pctdistance=0.6,labeldistance=1.05,textprops={'fontsize':
12},colors=['lightblue','green'])
plt.title('Number of Diabetic and Nondiabetic Patients',loc='center', fontsize=1
5)
plt.show()
```



Pair plot

Independent variables vs dependent variable

In [45]:

```
sns.pairplot(data,hue='has_diabetes')
plt.show()
```

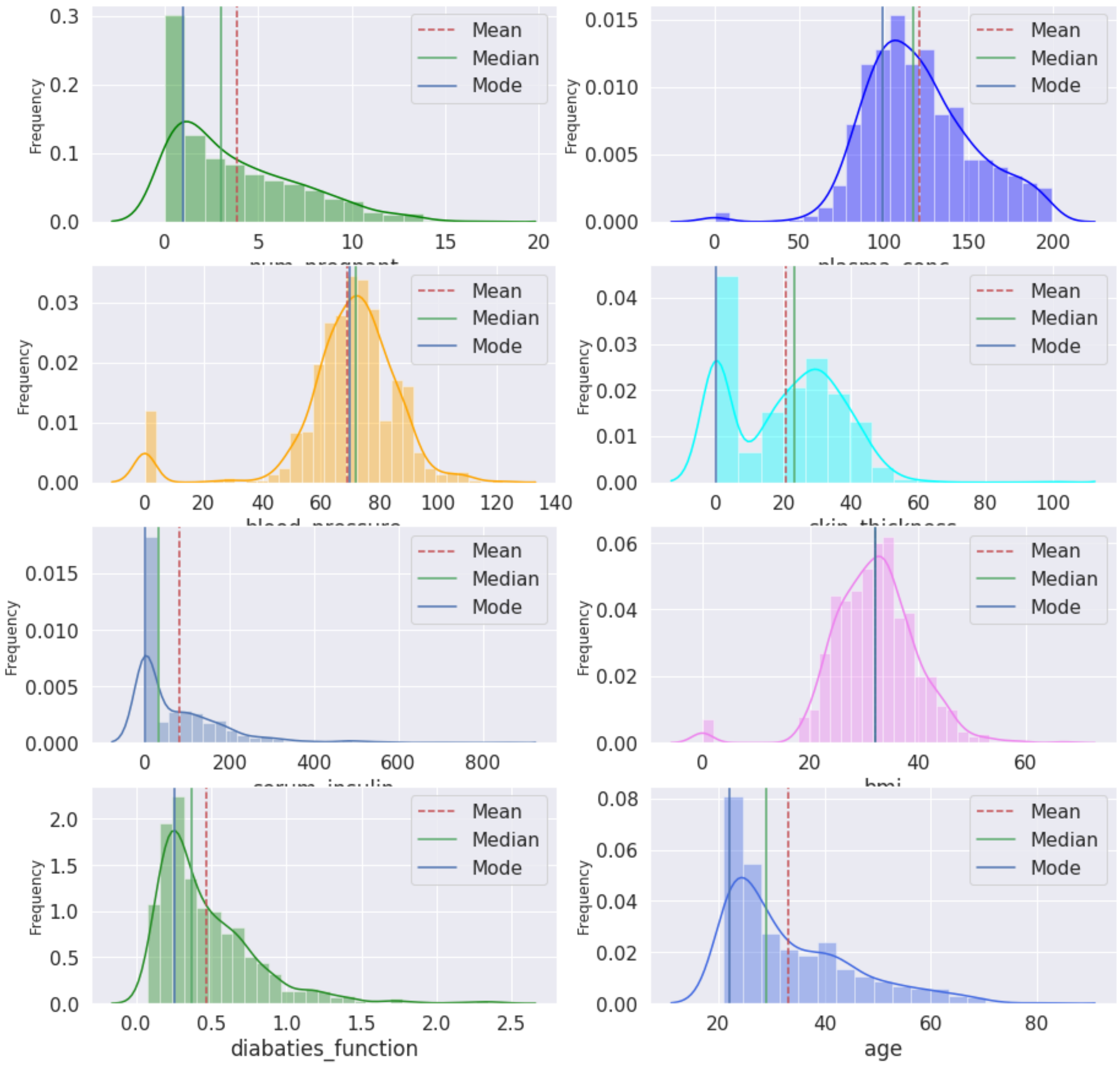
The pairs plot builds on two basic figures, the histogram and the scatter plot. The histogram on the diagonal allows us to see the distribution of a single variable while the scatter plots on the upper and lower triangles show the relationship (or lack thereof) between two variables.

Distribution Plot of all independent variables

In [46]:

```
plt.figure(figsize=(15,15))

plt.subplot(4,2,1)
sns.distplot(data['num_pregnant'], color='green')
mean = data['num_pregnant'].mean()
median = data['num_pregnant'].median()
mode = data['num_pregnant'].mode()[0]
plt.axvline(mean, color='r', linestyle='--')
plt.axvline(median, color='g', linestyle='-')
plt.axvline(mode, color='b', linestyle='-')
plt.legend({'Mean':mean,'Median':median,'Mode':mode})
plt.ylabel('Frequency', fontsize=12)

plt.subplot(4,2,2)
sns.distplot(data['plasma_conc'], color='blue')
mean = data['plasma_conc'].mean()
median = data['plasma_conc'].median()
mode = data['plasma_conc'].mode()[0]
plt.axvline(mean, color='r', linestyle='--')
plt.axvline(median, color='g', linestyle='-')
plt.axvline(mode, color='b', linestyle='-')
plt.legend({'Mean':mean,'Median':median,'Mode':mode})
plt.ylabel('Frequency', fontsize=12)

plt.subplot(4,2,3)
sns.distplot(data['blood_pressure'], color='orange')
mean = data['blood_pressure'].mean()
median = data['blood_pressure'].median()
mode = data['blood_pressure'].mode()[0]
plt.axvline(mean, color='r', linestyle='--')
plt.axvline(median, color='g', linestyle='-')
plt.axvline(mode, color='b', linestyle='-')
plt.legend({'Mean':mean,'Median':median,'Mode':mode})
plt.ylabel('Frequency', fontsize=12)

plt.subplot(4,2,4)
sns.distplot(data['skin_thickness'], color='cyan')
mean = data['skin_thickness'].mean()
median = data['skin_thickness'].median()
mode = data['skin_thickness'].mode()[0]
plt.axvline(mean, color='r', linestyle='--')
plt.axvline(median, color='g', linestyle='-')
plt.axvline(mode, color='b', linestyle='-')
plt.legend({'Mean':mean,'Median':median,'Mode':mode})
plt.ylabel('Frequency', fontsize=12)

plt.subplot(4,2,5)
sns.distplot(data['serum_insulin'])
mean = data['serum_insulin'].mean()
median = data['serum_insulin'].median()
mode = data['serum_insulin'].mode()[0]
plt.axvline(mean, color='r', linestyle='--')
plt.axvline(median, color='g', linestyle='-')
plt.axvline(mode, color='b', linestyle='-')
plt.legend({'Mean':mean,'Median':median,'Mode':mode})
plt.ylabel('Frequency', fontsize=12)

plt.subplot(4,2,6)
sns.distplot(data['bmi'], color='violet')
```

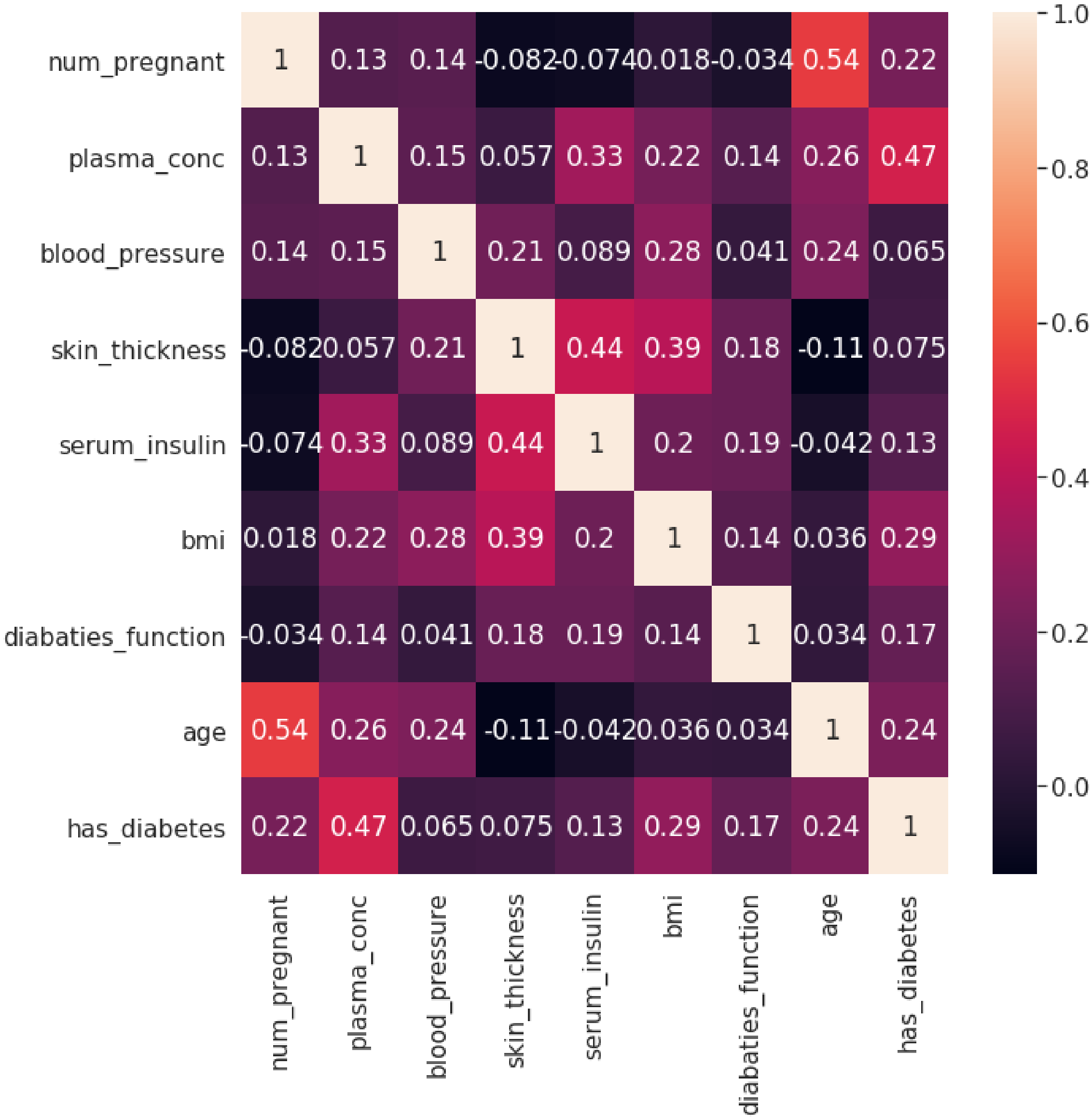
```
mean = data['bmi'].mean()
median = data['bmi'].median()
mode = data['bmi'].mode()[0]
plt.axvline(mean, color='r', linestyle='--')
plt.axvline(median, color='g', linestyle='-')
plt.axvline(mode, color='b', linestyle='-')
plt.legend({'Mean':mean,'Median':median,'Mode':mode})
plt.ylabel('Frequency', fontsize=12)

plt.subplot(4,2,7)
sns.distplot(data['diabaties_function'], color='forestgreen')
mean = data['diabaties_function'].mean()
median = data['diabaties_function'].median()
mode = data['diabaties_function'].mode()[0]
plt.axvline(mean, color='r', linestyle='--')
plt.axvline(median, color='g', linestyle='-')
plt.axvline(mode, color='b', linestyle='-')
plt.legend({'Mean':mean,'Median':median,'Mode':mode})
plt.ylabel('Frequency', fontsize=12)

plt.subplot(4,2,8)
sns.distplot(data['age'], color='royalblue')
mean = data['age'].mean()
median = data['age'].median()
mode = data['age'].mode()[0]
plt.axvline(mean, color='r', linestyle='--')
plt.axvline(median, color='g', linestyle='-')
plt.axvline(mode, color='b', linestyle='-')
plt.legend({'Mean':mean,'Median':median,'Mode':mode})
plt.ylabel('Frequency', fontsize=12)
plt.show()
```


Mean
Median
Mode
Frequency
diabaties_function
age

Correlation Plot

In [47]:

```
plt.figure(figsize=(10,10))
corrMatrix = data.corr()
sns.heatmap(corrMatrix, annot=True)
plt.show()
```



Remove columns which don’t help the problem statement.

From the correlation plot, we removed the columns that are **less than 0.15** correlated with the **has_diabetes** column. The columns that to be removed are **blood_pressure**, **skin_thickness** and **serum_insulin**

In [48]:

```
# dropping blood_pressure and skin_thickness columns

data = data.drop(['blood_pressure','skin_thickness','serum_insulin'],axis=1)
```

Standaradizing the data

In [49]:

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 6 columns):
 #   Column              Non-Null Count  Dtype  
---  ------              --------------  -----  
 0   num_pregnant        768 non-null    int64  
 1   plasma_conc         768 non-null    int64  
 2   bmi                 768 non-null    float64
 3   diabaties_function  768 non-null    float64
 4   age                 768 non-null    int64  
 5   has_diabetes        768 non-null    int64  
dtypes: float64(2), int64(4)
memory usage: 36.1 KB
```

Do Feature Scaling on Independent variables

In [50]:

```
ss = StandardScaler()
ss.fit(data.drop(['has_diabetes'], axis=1))
scaled=ss.transform(data.drop(['has_diabetes'], axis=1))
scaled_data=pd.DataFrame(data=scaled, columns=data.columns[:-1])
scaled_data
```

Out[50]:

	num_pregnant	plasma_conc	bmi	diabaties_function	age
0	0.64	0.85	0.20	0.47	1.43
1	-0.84	-1.12	-0.68	-0.37	-0.19
2	1.23	1.94	-1.10	0.60	-0.11
3	-0.84	-1.00	-0.49	-0.92	-1.04
4	-1.14	0.50	1.41	5.48	-0.02
...	...	...	...	...	...
763	1.83	-0.62	0.12	-0.91	2.53
764	-0.55	0.03	0.61	-0.40	-0.53
765	0.34	0.00	-0.74	-0.69	-0.28
766	-0.84	0.16	-0.24	-0.37	1.17
767	-0.84	-0.87	-0.20	-0.47	-0.87

768 rows × 5 columns

Splitting the data

Consider all columns as independent variables and assign to variable X except the last column and consider the last column as the dependent variable and assign to variable y.

In [51]:

```
X= scaled_data
y= data['has_diabetes']
```

Split the data into train and test dataset

In [52]:

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_
state=0)
```

Fitting Logistic Regression

Use sklearn library to train on train dataset on logistic regression and predict on test dataset.

In [53]:

```
clf = LogisticRegression(random_state=0).fit(X_train, y_train)
```

In [54]:

```
y_pred = clf.predict(X_test)
y_pred_prob = clf.predict_proba(X_test)
```

In [55]:

```
clf.score(X_train, y_train)
```

Out[55]:

```
0.7746741154562383
```

In [56]:

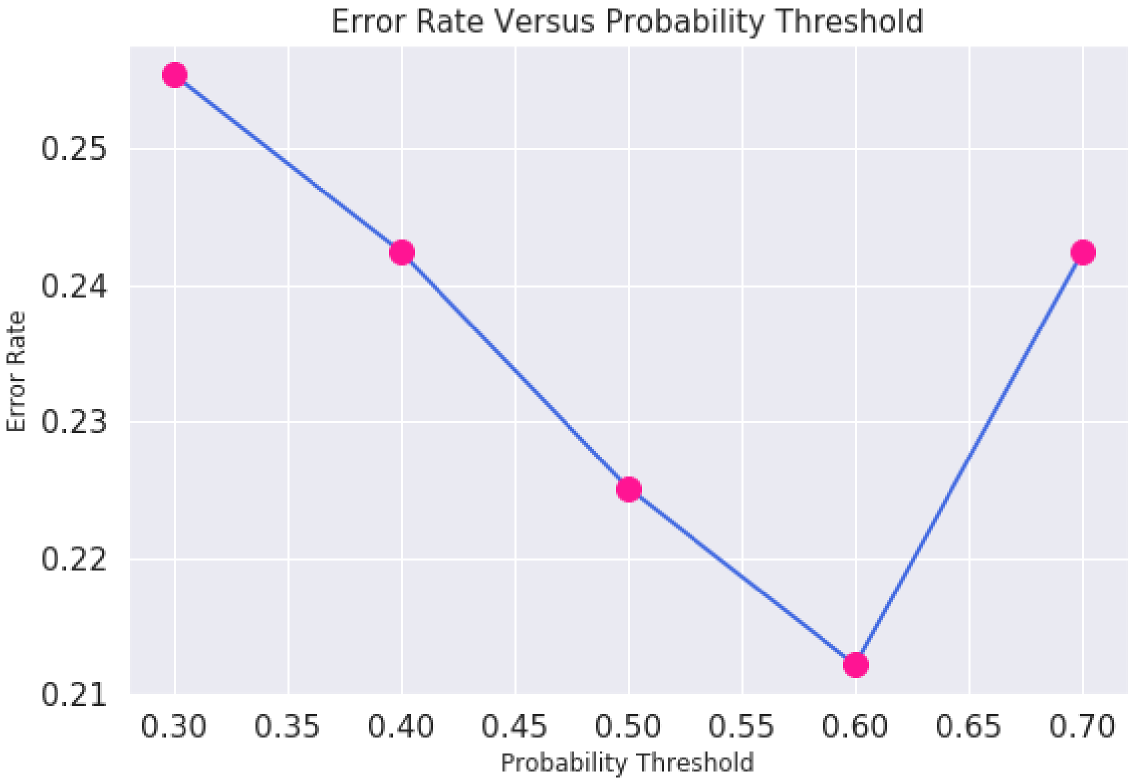
```
clf = LogisticRegression().fit(X_train, y_train)
y_pred_prob = clf.predict_proba(X_test)
y_pred_prob = list(pd.DataFrame(y_pred_prob)[1])
```

Elbow plot

In [57]:

```
error_rate=[]
thresh_values = [0.3,0.4,0.5,0.6,0.7]
for threshold in thresh_values:
    y_pred = [1 if x > threshold else 0 for x in y_pred_prob]
    error_rate.append(np.mean(y_pred!=y_test))
print(error_rate)
plt.figure(figsize=(9,6))
plt.plot(thresh_values, error_rate,color='royalblue', marker='o', linewidth=2, m
arkersize=12, markerfacecolor='deeppink', markeredgecolor='deeppink' )
plt.xlabel('Probability Threshold', fontsize=12)
plt.ylabel('Error Rate', fontsize=12)
plt.title('Error Rate Versus Probability Threshold', fontsize=15)
plt.show()
```

```
[0.2554112554112554, 0.24242424242424243, 0.22510822510822512, 0.212
12121212121213, 0.24242424242424243]
```



Optimal Thresold is 0.6 from above graph so considering that to evaluate our model.

In [58]:

```
y_pred = [1 if x > 0.60 else 0 for x in y_pred_prob]
```

Compute the accuracy and confusion matrix.

Metrics Calculation

In [59]:

```
from sklearn.metrics import accuracy_score, f1_score,recall_score, precision_sco
re, classification_report, confusion_matrix
```

In [60]:

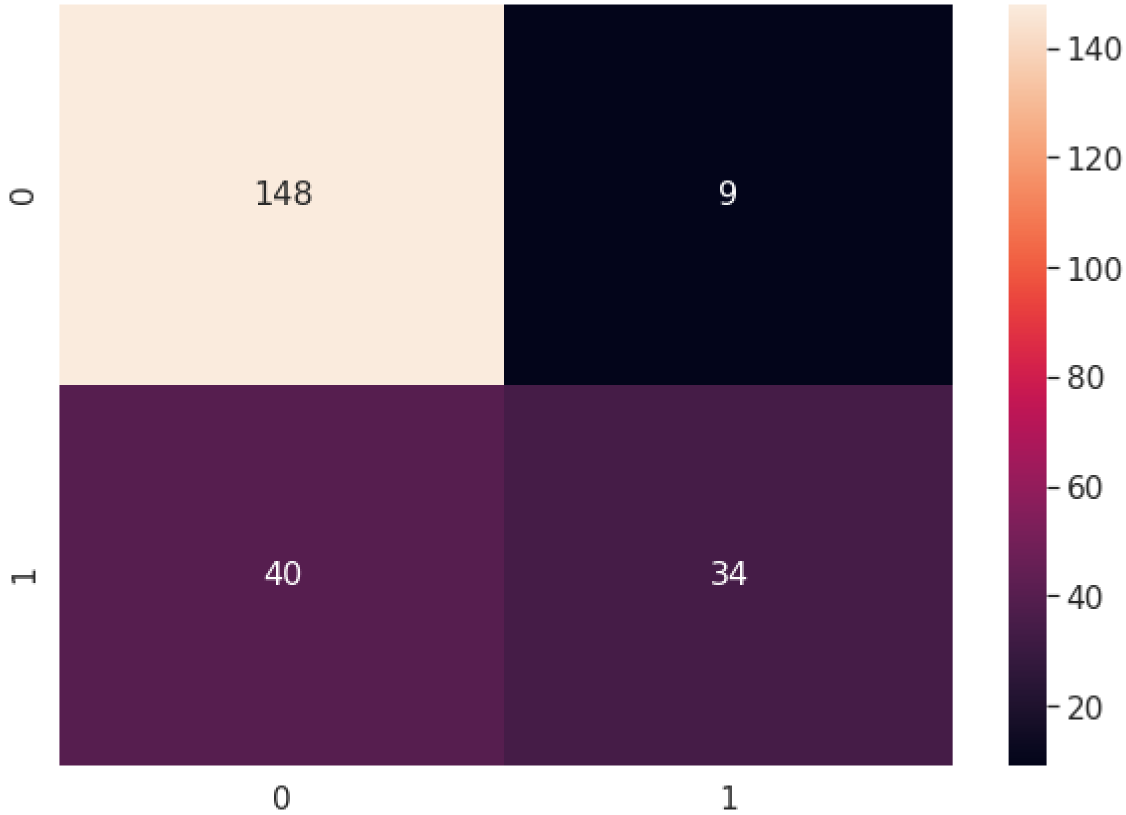
```
print('Accuracy:', accuracy_score(y_test, y_pred))

print('F1 score:', f1_score(y_test, y_pred,
                            average='weighted'))

print('Recall:', recall_score(y_test, y_pred,
                              average='weighted'))

print('Precision:', precision_score(y_test, y_pred,
                                    average='weighted'))

print('\n clasification report:\n', classification_report(y_test, y_pred))

print('\n confussion matrix:\n',confusion_matrix(y_test, y_pred))
```

```
Accuracy: 0.7878787878787878
F1 score: 0.7693073432203867
Recall: 0.7878787878787878
Precision: 0.7883436042763108

 clasification report:
               precision    recall  f1-score   support

           0       0.79      0.94      0.86       157
           1       0.79      0.46      0.58        74

    accuracy                           0.79       231
   macro avg       0.79      0.70      0.72       231
weighted avg       0.79      0.79      0.77       231


 confussion matrix:
 [[148   9]
 [ 40  34]]
```

```
   True Negatives : 144
   False Negatives : 40
   False Positives : 9
   True Positives : 34
```

In [61]:

```
confusion_matrix_data = pd.DataFrame(confusion_matrix(y_test, y_pred), range(2),
range(2))
plt.figure(figsize=(10,7))
sns.set(font_scale=1.4) # for label size
sns.heatmap(confusion_matrix_data, annot=True, annot_kws={"size": 16},fmt='g') #
font size

plt.show()
```



We have tried to answer all the asked questions and highlighted them in blue where we have answered.