DATA70121 Assignment 1 - EDA & Regression

Data Science MSc
Statistics & ML 1

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1) Data Description
We are given a dataset of 750 observations collected by the USA's Health Institute for women with variable 0/1 as Outcome showing whether person(specific-women) tested positive for Diabetes once. There are 9 columns with different medically-variable values w.r.t Diabetes.
Column Variables include -

- Pregnancies: number of times the woman has been pregnant
- Glucose: plasma glucose concentration (mg/dl) at 2 hours in an oral glucose tolerance test (OGTT)
- Blood Pressure: Diastolic blood pressure (mm Hg) Skin Thickness: Triceps skin fold thickness (mm) Serum
- Insulin: insulin concentration2 (µ U/ml) at 2 hours in an OGTT
- BMI: body mass index (weight in kg)/(height in m)2
- Diabete Pedigree: a numerical score designed tomeasure the genetic influence of both the woman's diabetic and her non-diabetic relatives on diabetes risk: higher scores mean higher risk.
- Age: in years
- Outcome: 1 if the woman eventually tested positive for diabetes, zero otherwise

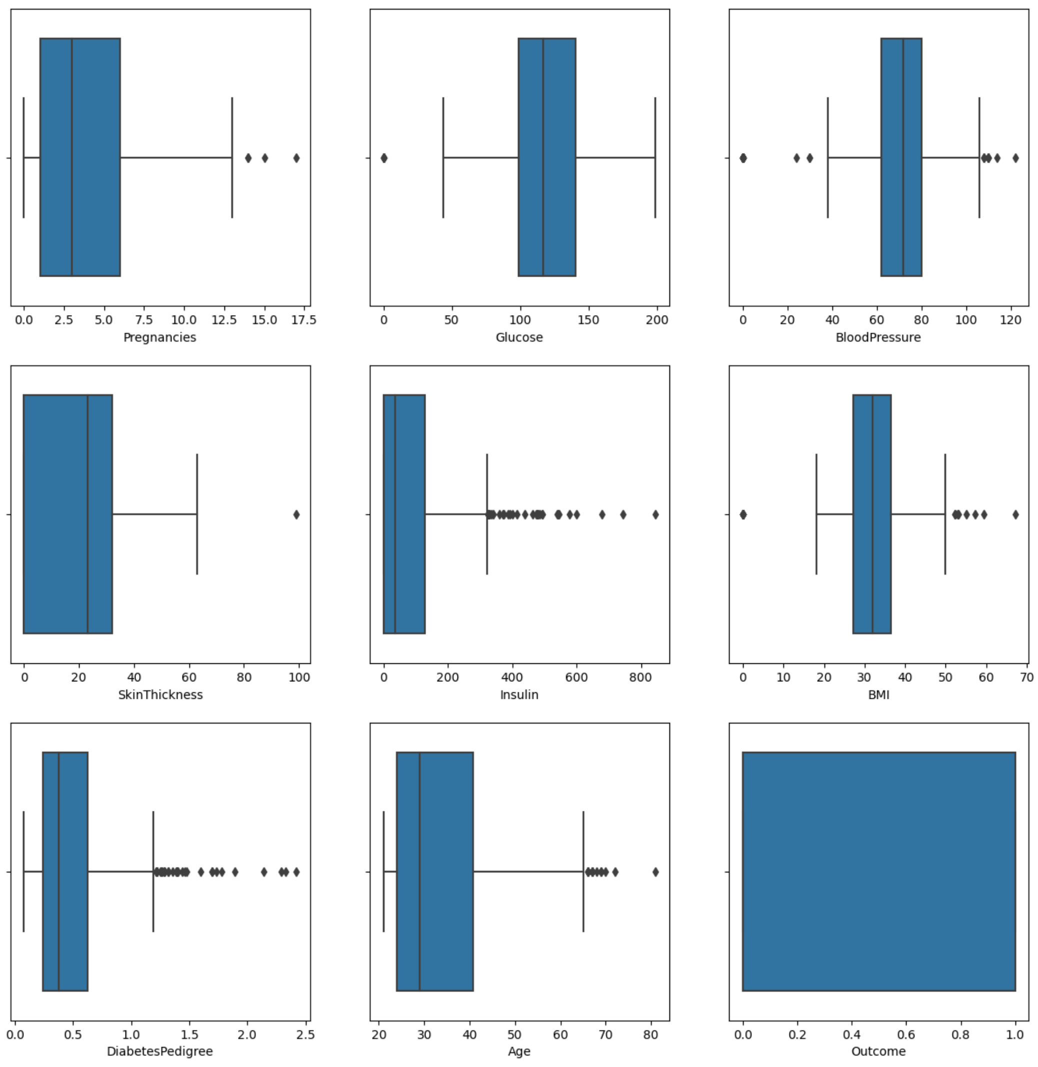

Fig 1 (Boxplot for different columns of Diabetes Dataset set)

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Fig 1) BoxPlot graph shows multiple outliers(minimum value) for different columns like Glucose, BloodPressure, SkinThickness, Insulin and BMI as 0 which is logically incorrect considering human medical records(Survival not possible for any of these values to be zero). This can be considered as missing data instead on zero and can be dropped to increase accuracy of our model or replaced by mean/median respective of their distribution. Other than this, there are no duplicate values. Dataset includes float, integer data types and is mostly quantitative. Pregnancy can be zero representing no pregnancy & 17 representing max pregnancy. Max age is 21 whereas min age is 21.

2) Exploratory Data Analysis

Median Pregnancies 3.0	Mean Pregnancies 3.844
Median Glucose 117.0	Mean Glucose 120.73733333333334
Median BloodPressure 72.0	Mean BloodPressure 68.98266666666666
Median SkinThickness 23.0	Mean SkinThickness 20.489333333333335
Median Insulin 36.5	Mean Insulin 80.37866666666666
Median BMI 32.0	Mean BMI 31.959066666666665
Median DiabetesPedigree 0.377	Mean DiabetesPedigree 0.473544
Median Age 29.0	Mean Age 33.166666666666664
Median Outcome 0.0	Mean Outcome 0.3466666666666667

EDA includes visualization of data with Boxplots & Histogram (Fig 1 &3) to see the anomalies in outliers and distributions. Before doing any further we find correlation and find in the 'Outcome' row that Glucose, BMI & Age are most correlated and BloodPressure, Insulin & DiabetesPedigree are least correlated and can be dropped. But, after looking at their distribution using Histogram created through seaborn. Columns which followed Normal Distribution have their 0 values replaced by Mean, and for Skewed Distribution zero's were replaced by median. (To increase the accuracy of model), After doing this we calculate the new correlation heatmap (Fig 2).

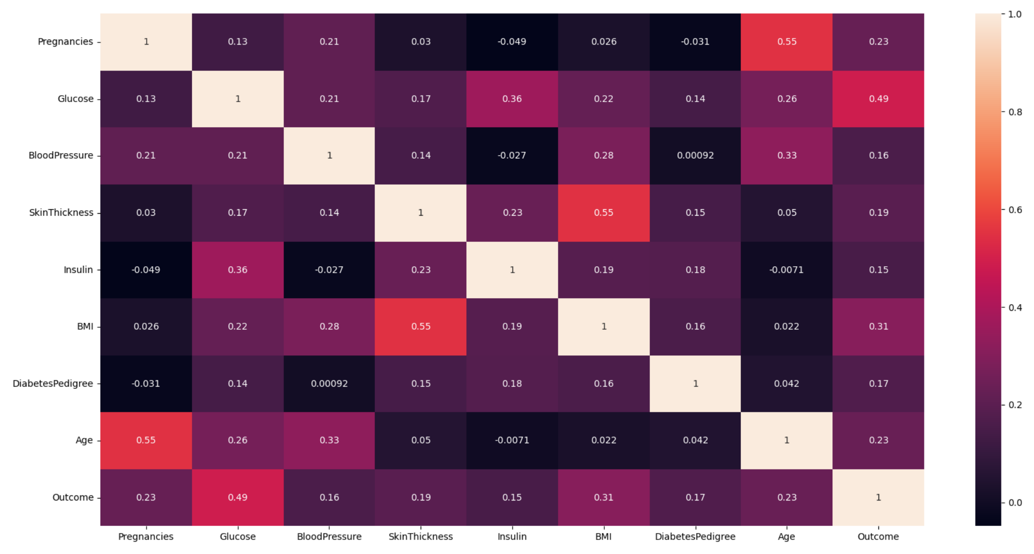


Fig 2 **(**Correlation HeatMap after Data Cleaning**)**

Outcomes are represented as 1 for Diabetes and 0 for Non-Diabetic Women, the total count and percentage of those with or without Diabetes is:
Number of Non-Diabetic cases: 490 (65.23%)
Number of Diabetes cases: 260 (34.67%)

Correlation value with respect to Outcomes in descending order are:

Outcome	1.000000	Glucose	0.486978
BMI	0.309369	Age	0.232892
Pregnancies	0.229235	SkinThickness	0.193141
DiabetesPedigree	0.170688	BloodPressure	0.159144
Insulin	0.151832	Name: Outcome, dtype: float64	

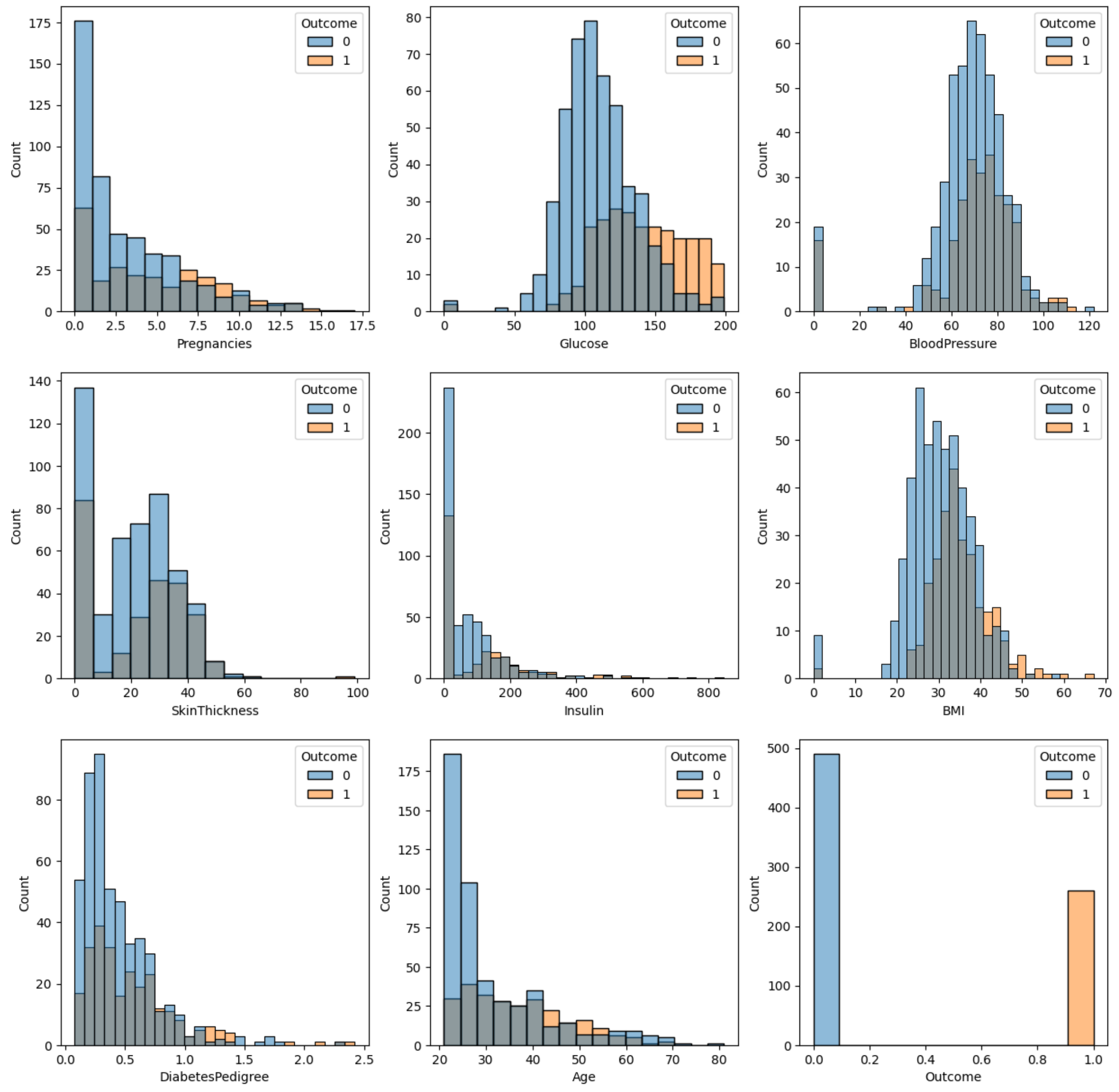
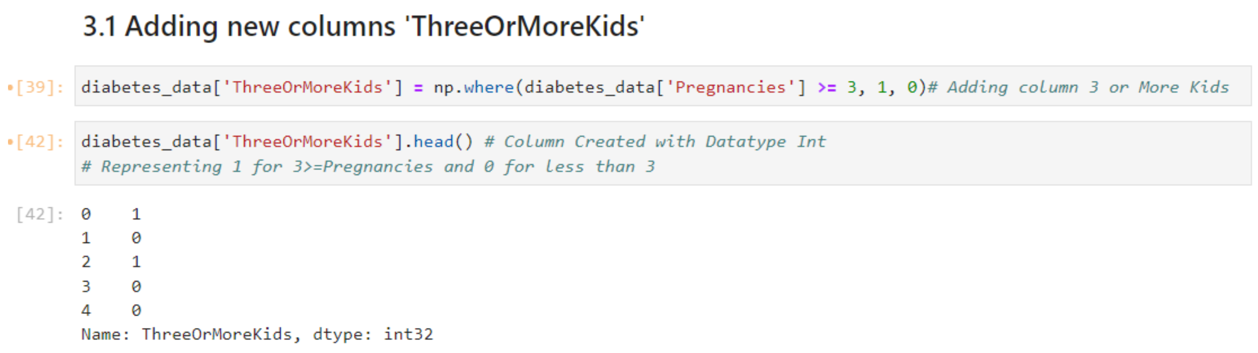


Fig 3 (Histogram for different columns/variables represents its distribution as Skewed or Normal)

3) Addition of New Column and predict Diabetes based on that column

We have 34% (approx) females in dataset suffering from Diabetes and rest approx 65% are considered healthy. This 34-65 percentage distribution of dataset is considered as a good distribution for True/False cases in dataset.
Next, using pregnancies column a new column is created 'ThreeOrMoreKids' for those females with 3 or more kids. (Fig 4)



3.1 Adding new columns 'ThreeOrMoreKids'

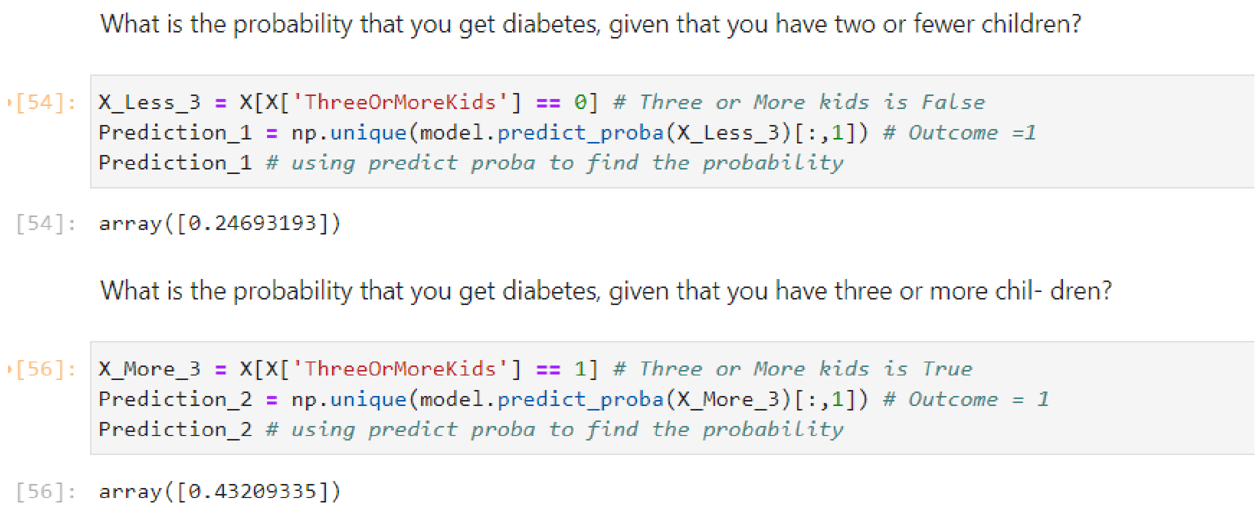
```
[39]: diabetes_data['ThreeOrMoreKids'] = np.where(diabetes_data['Pregnancies'] >= 3, 1, 0)# Adding column 3 or More Kids

[42]: diabetes_data['ThreeOrMoreKids'].head() # Column Created with Datatype Int
      # Representing 1 for 3>=Pregnancies and 0 for less than 3

[42]: 0    1
      1    0
      2    1
      3    0
      4    0
      Name: ThreeOrMoreKids, dtype: int32
```

Fig 4 (Adding new columns 'ThreeOrMoreKids' in the Diabetes_data dataset**)**

X is assigned to column 'ThreeOrMoreKids' as an array and Y is assigned to column 'Outcome". The model score using simple Logistic Regression after importing suitables packages & keywords comes to be 65.3%.
Using this model we get our answer to 3.1) & 3.2) as shown in Fig 5.



What is the probability that you get diabetes, given that you have two or fewer children?

```
[54]: X_Less_3 = X[X['ThreeOrMoreKids'] == 0] # Three or More kids is False
      Prediction_1 = np.unique(model.predict_proba(X_Less_3)[:,1]) # Outcome =1
      Prediction_1 # using predict proba to find the probability

[54]: array([0.24693193])
```

What is the probability that you get diabetes, given that you have three or more chil- dren?

```
[56]: X_More_3 = X[X['ThreeOrMoreKids'] == 1] # Three or More kids is True
      Prediction_2 = np.unique(model.predict_proba(X_More_3)[:,1]) # Outcome = 1
      Prediction_2 # using predict proba to find the probability

[56]: array([0.43209335])
```

Fig 5 (Answers to question 3.1 & 3.2**)**
From fig 5,
Probability of having Diabetes for women with less than 3 kids is 24.6% (approx)
Probability of having Diabetes for women with more than or equal to 3 kids is 43.2% (approx) (Fig 6)
Probabilities have been calculated using .predict_proba in python method instead of pen-paper calculations.
Simple Logistic Regression model is used to predict the above values and is mentioned in details in the code sheet attached below.

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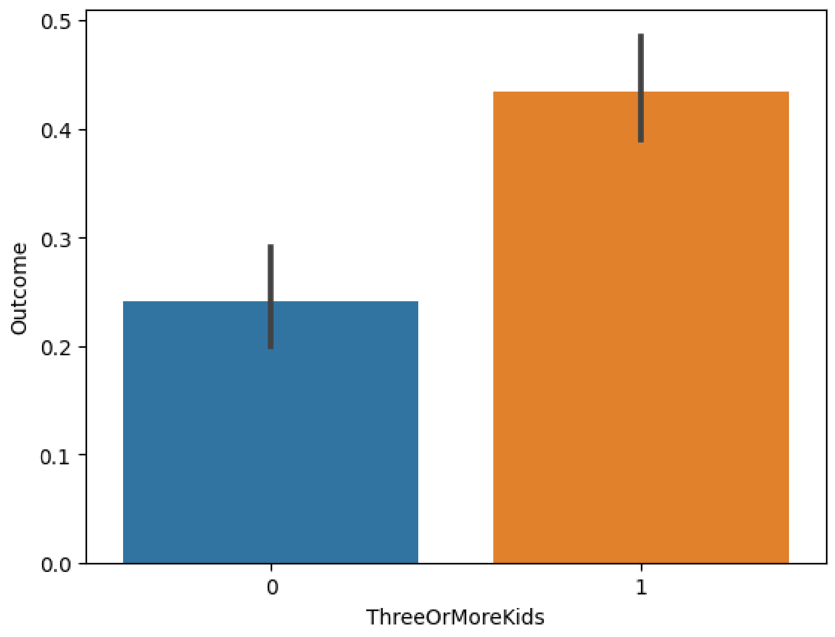
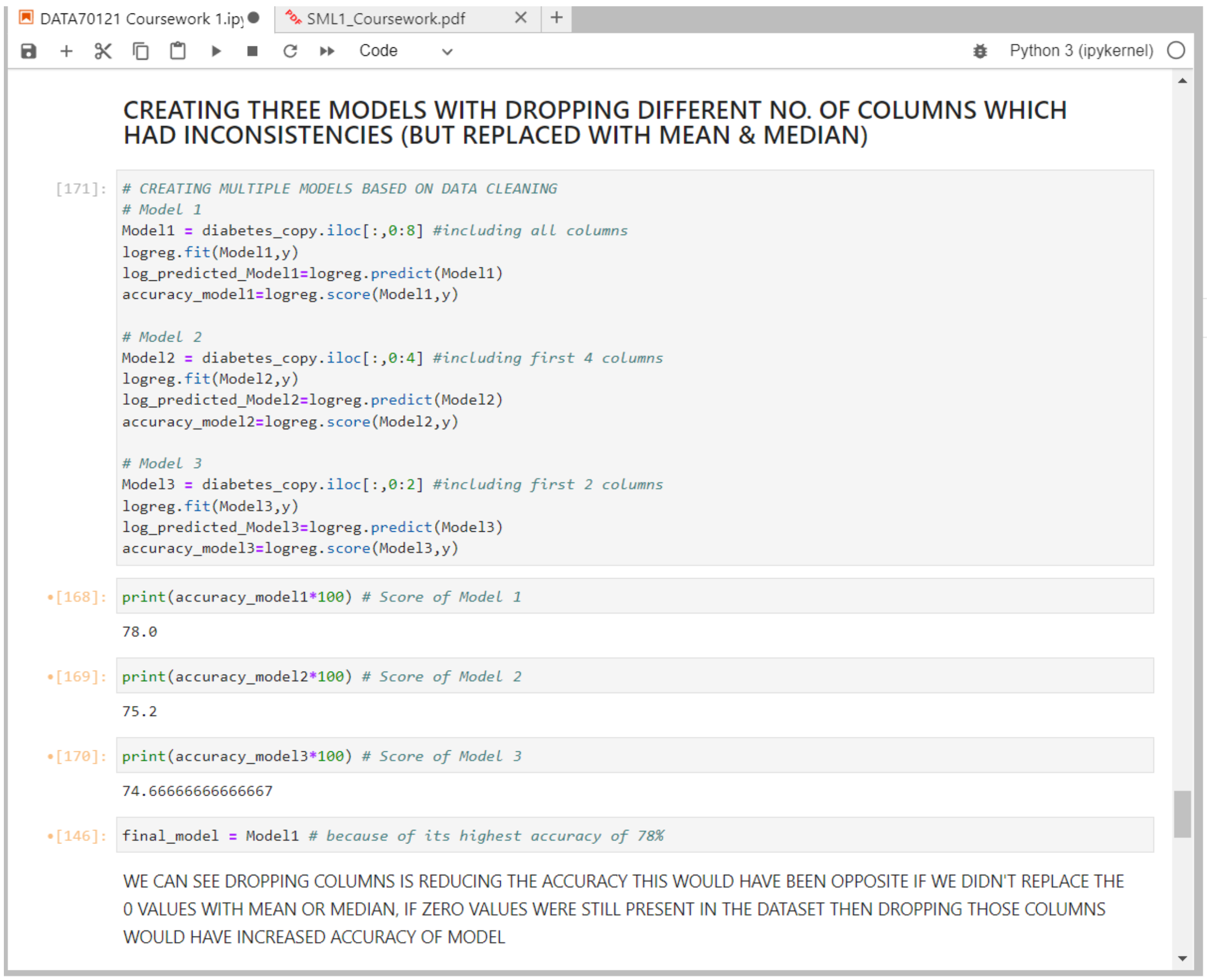


Fig 6 (Barplot visualization for Q3.1 & Q3.2 **)**

4) Comparison of Models & Prediction for New Dataset
In section 4, rather than creating a new different model, modifications have been done on the previous one to create two more logistic regression models.
Two cases have been considered -
CASE 1) When all zero's in the dataset were cleaned before building the Logistic Model (This has been followed in all the previous steps and code is also for the same)
For this method the highest accuracy of 78% was received when all columns were included in the prediction model.
For the other two models in the same case when the columns were decreased the accuracy also decreased (Fig 7)
Accuracy - Model 1 (78%) > Model 2 > Model 3

CASE 2) When zero's are not replaced before building models (Hypothetical & Code not included)
When all zeroes were kept in the dataset before and after modeling the overall accuracy decreased by significant percentage and had opposit effect than the above model. And, as soon as columns with zero values were dropped the accuracy of model started increasing.

This is mainly because of the first 2 steps in EDA where we replaced the zero values with mean/median based on their distribution increasing their accuracy as compared to a dataset where data cleaning was not started.



CREATING THREE MODELS WITH DROPPING DIFFERENT NO. OF COLUMNS WHICH HAD INCONSISTENCIES (BUT REPLACED WITH MEAN & MEDIAN)

```
[171]: # CREATING MULTIPLE MODELS BASED ON DATA CLEANING
# Model 1
Model1 = diabetes_copy.iloc[:,0:8] #including all columns
logreg.fit(Model1,y)
log_predicted_Model1=logreg.predict(Model1)
accuracy_model1=logreg.score(Model1,y)

# Model 2
Model2 = diabetes_copy.iloc[:,0:4] #including first 4 columns
logreg.fit(Model2,y)
log_predicted_Model2=logreg.predict(Model2)
accuracy_model2=logreg.score(Model2,y)

# Model 3
Model3 = diabetes_copy.iloc[:,0:2] #including first 2 columns
logreg.fit(Model3,y)
log_predicted_Model3=logreg.predict(Model3)
accuracy_model3=logreg.score(Model3,y)
```

```
[168]: print(accuracy_model1*100) # Score of Model 1
78.0
```

```
[169]: print(accuracy_model2*100) # Score of Model 2
75.2
```

```
[170]: print(accuracy_model3*100) # Score of Model 3
74.66666666666667
```

```
[146]: final_model = Model1 # because of its highest accuracy of 78%
```

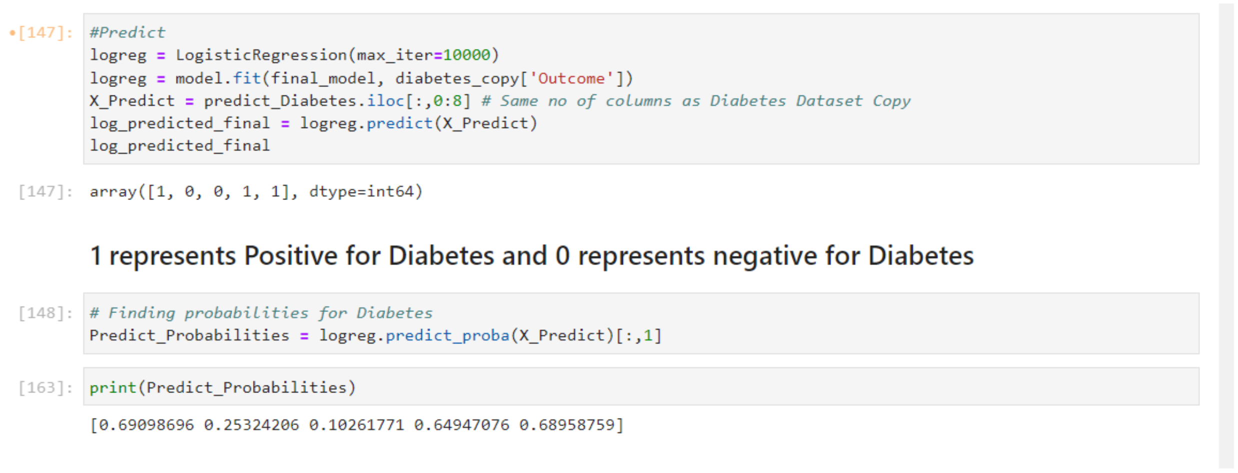
WE CAN SEE DROPPING COLUMNS IS REDUCING THE ACCURACY THIS WOULD HAVE BEEN OPPOSITE IF WE DIDN'T REPLACE THE 0 VALUES WITH MEAN OR MEDIAN, IF ZERO VALUES WERE STILL PRESENT IN THE DATASET THEN DROPPING THOSE COLUMNS WOULD HAVE INCREASED ACCURACY OF MODEL

Fig 7 (Creating 3 Logistics Regression by changing the column attribute**) -** CASE 1

To predict, how likely women in dataset 2 will develop diabetes we use our Model1 as final_model. We load the predict data and predict it using logreg.predict property of Logistic Regression.
Output Array: [1,0,0,1,1]
We again calculate their respective probability on Python using .predict_proba function and the get respective probability as

Women 1	Outcome: 1	Prob(Developing Diabetes): 69.1%
Women 2	Outcome: 0	Prob(Developing Diabetes): 25.3%
Women 3	Outcome: 0	Prob(Developing Diabetes): 10.3%
Women 4	Outcome: 1	Prob(Developing Diabetes): 64.9%
Women 5	Outcome: 1	Prob(Developing Diabetes): 68.9%

(in Predict Dataset) refer Fig 8



```
•[147]: #Predict
        logreg = LogisticRegression(max_iter=10000)
        logreg = model.fit(final_model, diabetes_copy['Outcome'])
        X_Predict = predict_Diabetes.iloc[:,0:8] # Same no of columns as Diabetes Dataset Copy
        log_predicted_final = logreg.predict(X_Predict)
        log_predicted_final

 [147]: array([1, 0, 0, 1, 1], dtype=int64)
```

1 represents Positive for Diabetes and 0 represents negative for Diabetes

```
 [148]: # Finding probabilities for Diabetes
        Predict_Probabilities = logreg.predict_proba(X_Predict)[:,1]

 [163]: print(Predict_Probabilities)

        [0.69098696 0.25324206 0.10261771 0.64947076 0.68958759]
```

Fig 8 (Predicting the Outcome value of predictData using the Model with Highest Accuracy**) -** CASE 1

JUPYTER NOTEBOOK CONVERTED TO PDF AND MERGED WITH REPORT

AUTOMATIC CONVERSION OF NOTEBOOK TO PDF MIGHT CREATE SOME MISALIGNMENTS ETC.

In [ ]:
```
import numpy as np # Loading suitable packages for
import pandas as pd # Importing dataset,visualizing data
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.preprocessing import StandardScaler #importing ML packages
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn import metrics
from sklearn.metrics import confusion_matrix, classification_report;
from sklearn.linear_model import LogisticRegression
```

In [5]:
```
diabetes_data = pd.read_csv('PimaDiabetes.csv')#Importing given dataset
```

2) EDA - EXPLORATORY DATA ANALYSIS

In [6]:
```
diabetes_data.info() #finding different datatypes & null count
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 750 entries, 0 to 749
Data columns (total 9 columns):
 #   Column            Non-Null Count  Dtype  
---  ------            --------------  -----  
 0   Pregnancies       750 non-null    int64  
 1   Glucose           750 non-null    int64  
 2   BloodPressure     750 non-null    int64  
 3   SkinThickness     750 non-null    int64  
 4   Insulin           750 non-null    int64  
 5   BMI               750 non-null    float64
 6   DiabetesPedigree  750 non-null    float64
 7   Age               750 non-null    int64  
 8   Outcome           750 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 52.9 KB
```

In [7]:
```
diabetes_data.describe()#finding count,mean,std,min,quartile and max values
```

Out[7]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree	Ag
count	750.000000	750.000000	750.000000	750.000000	750.000000	750.000000	750.000000	750.0000
mean	3.844000	120.737333	68.982667	20.489333	80.378667	31.959067	0.473544	33.1666
std	3.370085	32.019671	19.508814	15.918828	115.019198	7.927399	0.332119	11.7088
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.0000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.244000	24.0000
50%	3.000000	117.000000	72.000000	23.000000	36.500000	32.000000	0.377000	29.0000
75%	6.000000	140.750000	80.000000	32.000000	129.750000	36.575000	0.628500	40.7500
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.0000

In [8]:
```
diabetes_data.head()#Looking at first 5 values of dataset
```

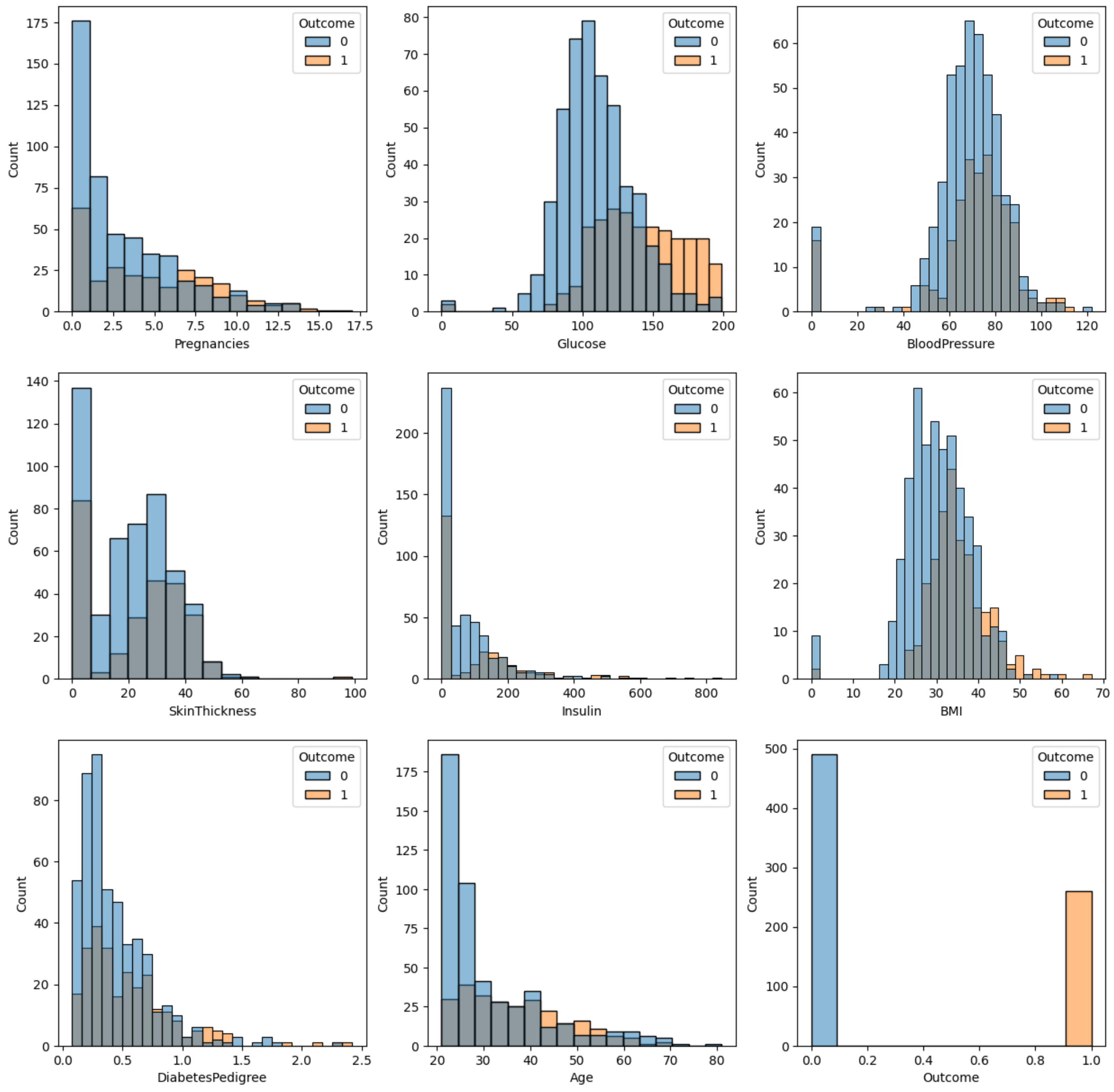
Out[8]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree	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

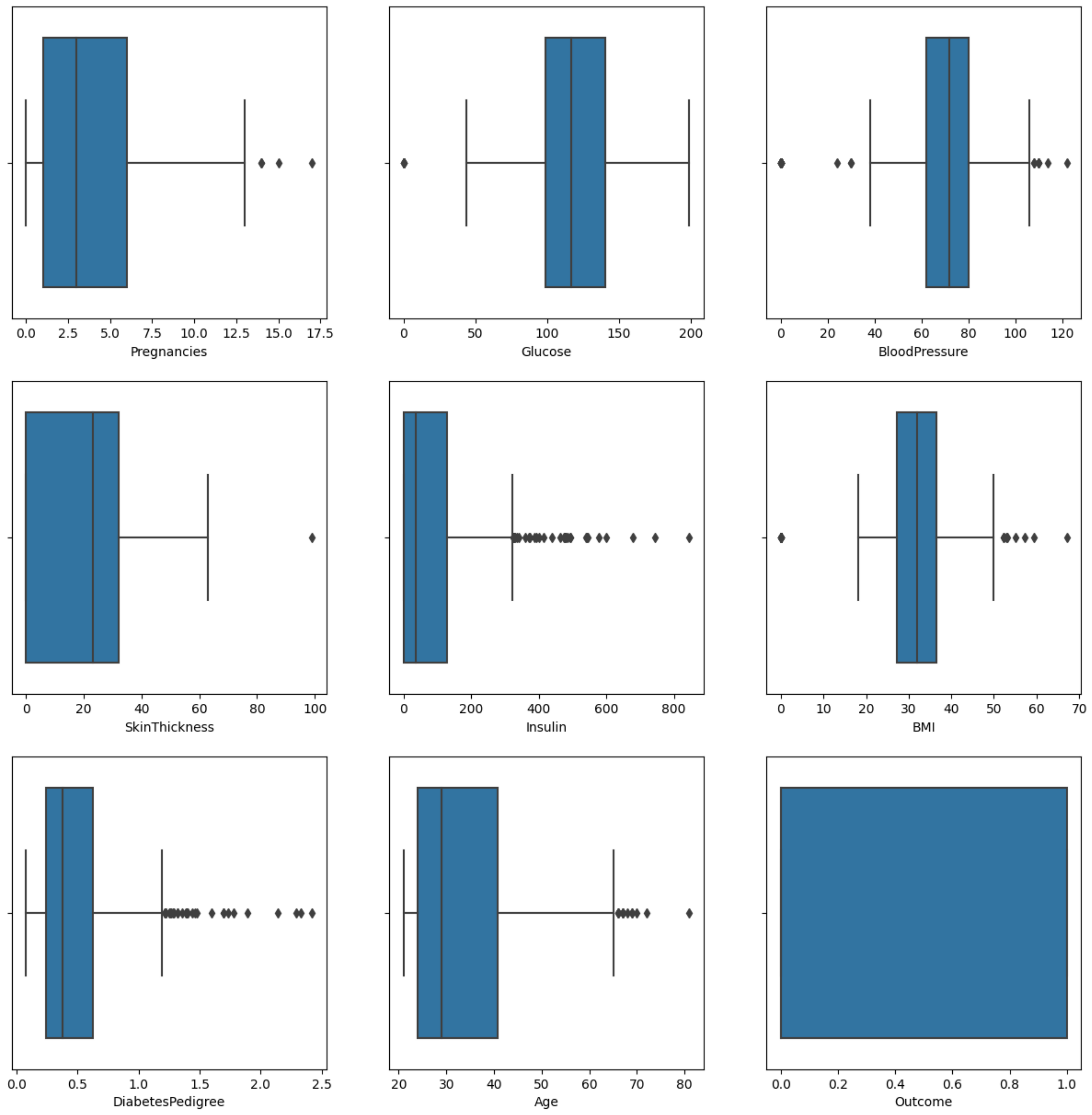
In [9]:
```
diabetes_data.shape #Finding the shape of dataset 750 ROWS/ 9 Columns
```

Out[9]:
```
(750, 9)
```

In [18]:
```
plt.figure(figsize=(15, 15)) #To find the distributions of different columns
i = 1                        # We can see Normal & Skewed distributions
for column_name in diabetes_data.columns:
    plt.subplot(3, 3, i) # Using Histogram from Seaborn Library
    sns.histplot(data=diabetes_data, x=col_name, hue="Outcome")
    i += 1
plt.show()
```



In [19]:
```
plt.figure(figsize=(15, 15)) # to find outliers and abnormality
i = 1        # of dataset for different columns
for column_name in diabetes_data.columns:
    plt.subplot(3, 3, i) # Using boxplot from Seaborn Library
    sns.boxplot(data=diabetes_data, x=col_name, hue="Outcome")
    i += 1
plt.show()
```



In [25]:
```
i = 1 # To find mean - median of the respective columns
for column_name in diabetes_data.columns:
    print("Median "+ column_name, diabetes_data[column_name].median())
    print("Mean " + column_name, diabetes_data[column_name].mean())
i += 1
```

```
Median Pregnancies 3.0
Mean Pregnancies 3.844
Median Glucose 117.0
Mean Glucose 120.73733333333334
Median BloodPressure 72.0
Mean BloodPressure 68.98266666666666
Median SkinThickness 23.0
Mean SkinThickness 20.489333333333335
Median Insulin 36.5
Mean Insulin 80.37866666666666
Median BMI 32.0
Mean BMI 31.959066666666665
Median DiabetesPedigree 0.377
Mean DiabetesPedigree 0.473544
Median Age 29.0
Mean Age 33.166666666666664
Median Outcome 0.0
Mean Outcome 0.3466666666666667
```

In [26]:
```
diabetes_data.isnull().sum() #To find any null values from dataset
#diabetes_data.isnull().any() # Same can be achieved using this 2 formula's
#diabetes_data.isnull().all()
```

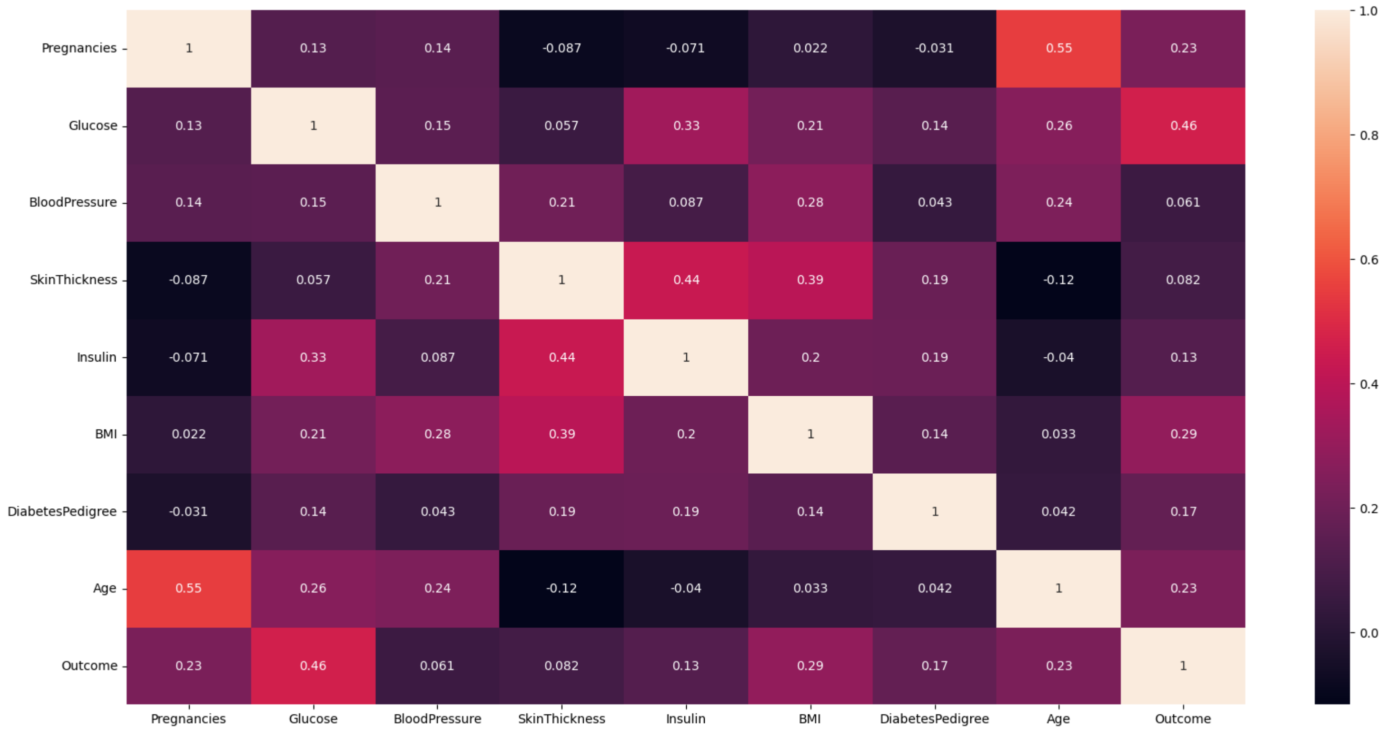
Out[26]:
```
Pregnancies         0
Glucose             0
BloodPressure       0
SkinThickness       0
Insulin             0
BMI                 0
DiabetesPedigree    0
Age                 0
Outcome             0
dtype: int64
```

In [13]:
```
corr=diabetes_data.corr()
corr ## to find correlation before any data cleaning
## We can see some abnormal or not so good correlation values
```

Out[13]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree	
Pregnancies	1.000000	0.129594	0.142453	-0.087047	-0.070822	0.021739	-0.031085	0.5
Glucose	0.129594	1.000000	0.145972	0.056647	0.333005	0.214316	0.140364	0.2
BloodPressure	0.142453	0.145972	1.000000	0.205494	0.086750	0.278569	0.042922	0.2
SkinThickness	-0.087047	0.056647	0.205494	1.000000	0.436093	0.394615	0.189191	-0.1
Insulin	-0.070822	0.333005	0.086750	0.436093	1.000000	0.195726	0.191289	-0.0
BMI	0.021739	0.214316	0.278569	0.394615	0.195726	1.000000	0.143798	0.0
DiabetesPedigree	-0.031085	0.140364	0.042922	0.189191	0.191289	0.143798	1.000000	0.0
Age	0.547124	0.259797	0.237693	-0.115862	-0.040152	0.032972	0.041807	1.0
Outcome	0.229235	0.460310	0.060860	0.082205	0.130928	0.289832	0.170688	0.2

In [14]:
```
plt.subplots(figsize=(20, 10)) #Graphical Representation of Uncleaned Data
sns.heatmap(data=corr, annot=True) # using Heatmap from Seaborn Library
plt.show()
```



In [15]:
```
corr["Outcome"].sort_values(ascending=False) #Correlation values in Descending order wrt Outcome
```

Out[15]:
```
Outcome             1.000000
Glucose             0.460310
BMI                 0.289832
Age                 0.232892
Pregnancies         0.229235
DiabetesPedigree    0.170688
Insulin             0.130928
SkinThickness       0.082205
BloodPressure       0.060860
Name: Outcome, dtype: float64
```

In [28]:
```
for i in diabetes_data.columns[:-1]: # The data didn't have null values but multiple 0 values
# Zero which are not possible and cause medical anomalies hence we find no. of zero values
    print(f" {i} = {len(diabetes_data[diabetes_data[i]==0])}, 0 values")
```

```
 Pregnancies = 109, 0 values
 Glucose = 5, 0 values
 BloodPressure = 35, 0 values
 SkinThickness = 221, 0 values
 Insulin = 362, 0 values
 BMI = 11, 0 values
 DiabetesPedigree = 0, 0 values
 Age = 0, 0 values
```

In [29]:
```
#Based on the distribution histogram seen above
#replacing 0 values with mean/median of that column based on their distribution
diabetes_data['Glucose']=diabetes_data['Glucose'].replace(0,diabetes_data['Glucose'].mean())#norr
diabetes_data['BloodPressure']=diabetes_data['BloodPressure'].replace(0,diabetes_data['BloodPres
diabetes_data['SkinThickness']=diabetes_data['SkinThickness'].replace(0,diabetes_data['SkinThick
diabetes_data['Insulin']=diabetes_data['Insulin'].replace(0,diabetes_data['Insulin'].median())#sl
diabetes_data['BMI']=diabetes_data['BMI'].replace(0,diabetes_data['BMI'].median())#skewed
# Pregnancies and Outcome have not been included as it is part of datasets and both are possible
# Pregnancies 0 = No kids
# Outcome 0 = No diabetes
```

In [30]:
```
for i in diabetes_data.columns[:-1]: # Now the zero values have been cleaned up
    print(f" {i} = {len(diabetes_data[diabetes_data[i]==0])}, 0 values")
```

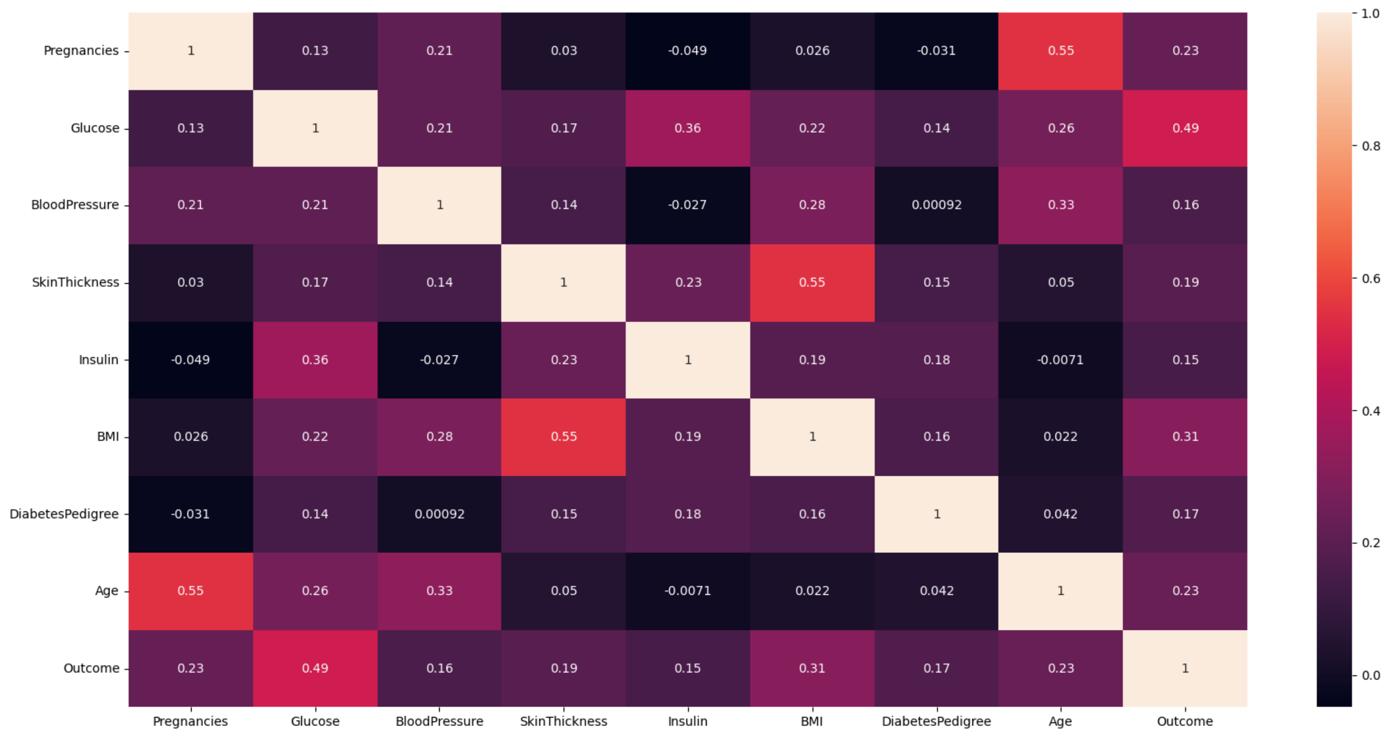
```
Pregnancies = 109, 0 values
Glucose = 0, 0 values
BloodPressure = 0, 0 values
SkinThickness = 0, 0 values
Insulin = 0, 0 values
BMI = 0, 0 values
DiabetesPedigree = 0, 0 values
Age = 0, 0 values
```

In [31]:
```
corr_new=diabetes_data.corr() # Saving and find new correlation
corr_new
```

Out[31]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree	
Pregnancies	1.000000	0.128068	0.211608	0.029973	-0.048568	0.026288	-0.031085	0.5
Glucose	0.128068	1.000000	0.210672	0.171486	0.363157	0.223783	0.140153	0.2
BloodPressure	0.211608	0.210672	1.000000	0.144606	-0.026548	0.276076	0.000924	0.3
SkinThickness	0.029973	0.171486	0.144606	1.000000	0.230233	0.548834	0.147981	0.0
Insulin	-0.048568	0.363157	-0.026548	0.230233	1.000000	0.185733	0.183242	-0.0
BMI	0.026288	0.223783	0.276076	0.548834	0.185733	1.000000	0.156929	0.0
DiabetesPedigree	-0.031085	0.140153	0.000924	0.147981	0.183242	0.156929	1.000000	0.0
Age	0.547124	0.262853	0.325834	0.050201	-0.007071	0.022102	0.041807	1.0
Outcome	0.229235	0.486978	0.159144	0.193141	0.151832	0.309369	0.170688	0.2

In [167…
```
plt.subplots(figsize=(20, 10))#Visualizing the new correlation heatmap
sns.heatmap(data=corr_new, annot=True) # using Seaborn's heatmap
plt.show()
```

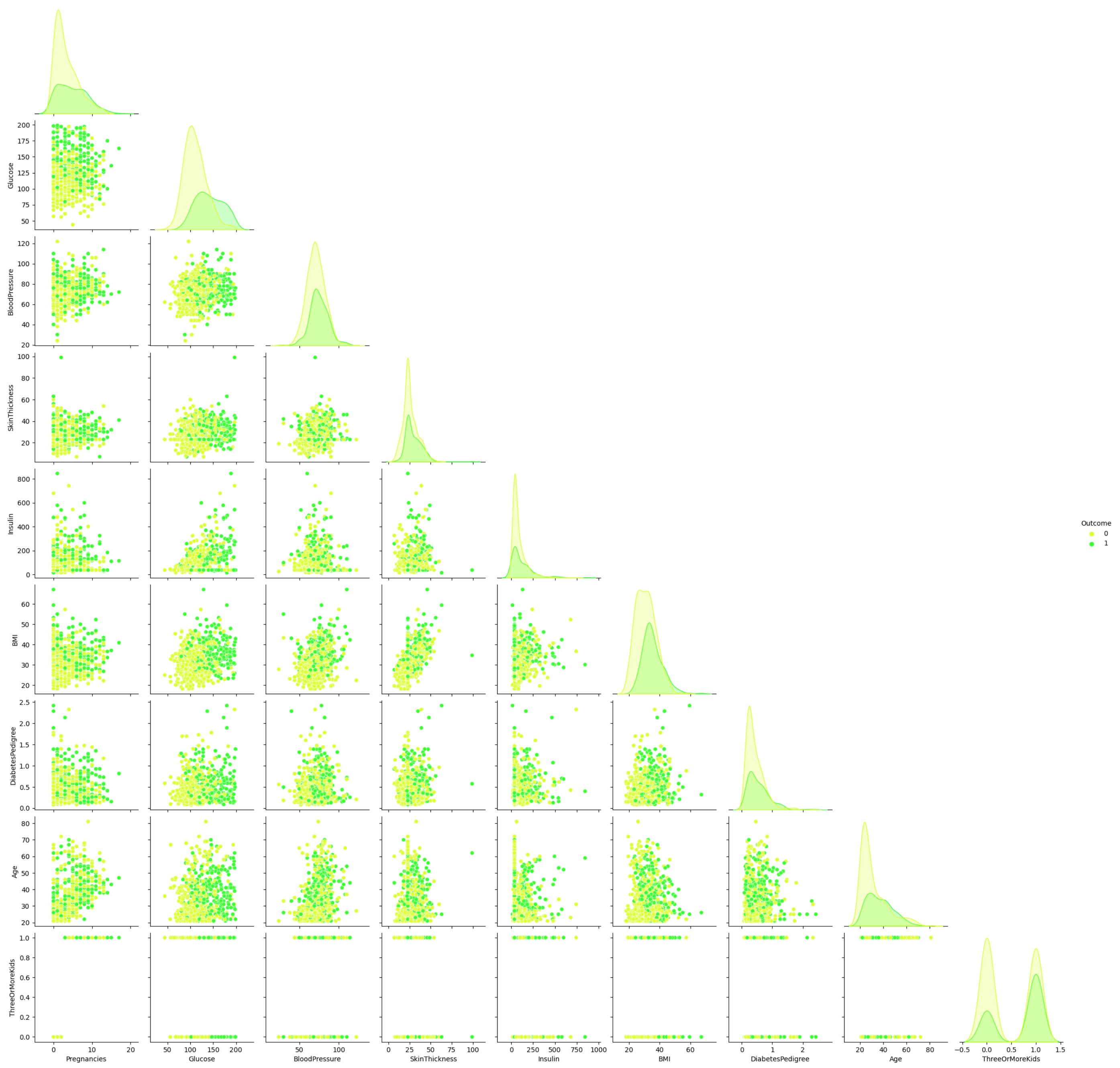


In [172…
```
corr_new["Outcome"].sort_values(ascending=False) #Correlation values in Descending order wrt Out
```

```
Out[172]: Outcome             1.000000
          Glucose             0.486978
          BMI                 0.309369
          Age                 0.232892
          Pregnancies         0.229235
          SkinThickness       0.193141
          DiabetesPedigree    0.170688
          BloodPressure       0.159144
          Insulin             0.151832
          Name: Outcome, dtype: float64
```

```
In [166…: sns.pairplot(diabetes_data, hue='Outcome', corner=True, palette=('#DDFF33','#3CFF33'))
          #Using Seaborn's pair plot to show plots based on Hue as Outcome
```

```
Out[166]: <seaborn.axisgrid.PairGrid at 0x170ccbb2710>
```



```
In [35]: diabetes_data['Outcome'].value_counts() #Finding Diabetic and Non Diabetic Patients
```

```
Out[35]: 0    490
         1    260
         Name: Outcome, dtype: int64
```

```
In [173…: diabetes = len(diabetes_data.loc[diabetes_data['Outcome'] == 1]) # Finding the percentage ratio
          no_diabetes = len(diabetes_data.loc[diabetes_data['Outcome'] == 0])
          print("Number of Non-Diabetic cases: {0} ({1:2.2f}%)".format(no_diabetes, (diabetes / (diabetes
          print("Number of Diabetes cases: {0} ({1:2.2f}%)".format(diabetes, (diabetes / (diabetes + no_di
```

```
Number of Non-Diabetic cases: 490 (34.67%)
Number of Diabetes cases: 260 (34.67%)
```

3) Adding a Column 'ThreeOrMoreKids' and fitting appropriate Regression Model

3.1 Adding new columns 'ThreeOrMoreKids'

```
In [39]: diabetes_data['ThreeOrMoreKids'] = np.where(diabetes_data['Pregnancies'] >= 3, 1, 0)# Adding col
```

```
In [42]: diabetes_data['ThreeOrMoreKids'].head() # Column Created with Datatype Int
         # Representing 1 for 3>=Pregnancies and 0 for less than 3
```

```
Out[42]: 0    1
         1    0
         2    1
         3    0
         4    0
         Name: ThreeOrMoreKids, dtype: int32
```

3.2 Creating Appropriate Model

```
In [47]: X = diabetes_data[['ThreeOrMoreKids']] #Converting one variable into suitable array
         # to avoid reshaping error later during model creation
         Y = diabetes_data['Outcome']
         #X = X.reshape(-1,1)
         # No need to reshape or convert the second variable
```

```
In [48]: model = LogisticRegression(solver = 'liblinear',random_state = 0)
```

```
In [49]: model.fit(X,Y)
```

```
Out[49]: ▾ LogisticRegression
         LogisticRegression(random_state=0, solver='liblinear')
```

```
In [50]: model.score(X,Y)
```

```
Out[50]: 0.6533333333333333
```

```
In [51]: model.predict(X)
```

```
Out[51]: array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                0, 0], dtype=int64)
```

What is the probability that you get diabetes, given that you have two or fewer children?

```
In [54]: X_Less_3 = X[X['ThreeOrMoreKids'] == 0] # Three or More kids is False
         Prediction_1 = np.unique(model.predict_proba(X_Less_3)[:,1]) # Outcome =1
         Prediction_1 # using predict proba to find the probability
```

```
Out[54]: array([0.24693193])
```

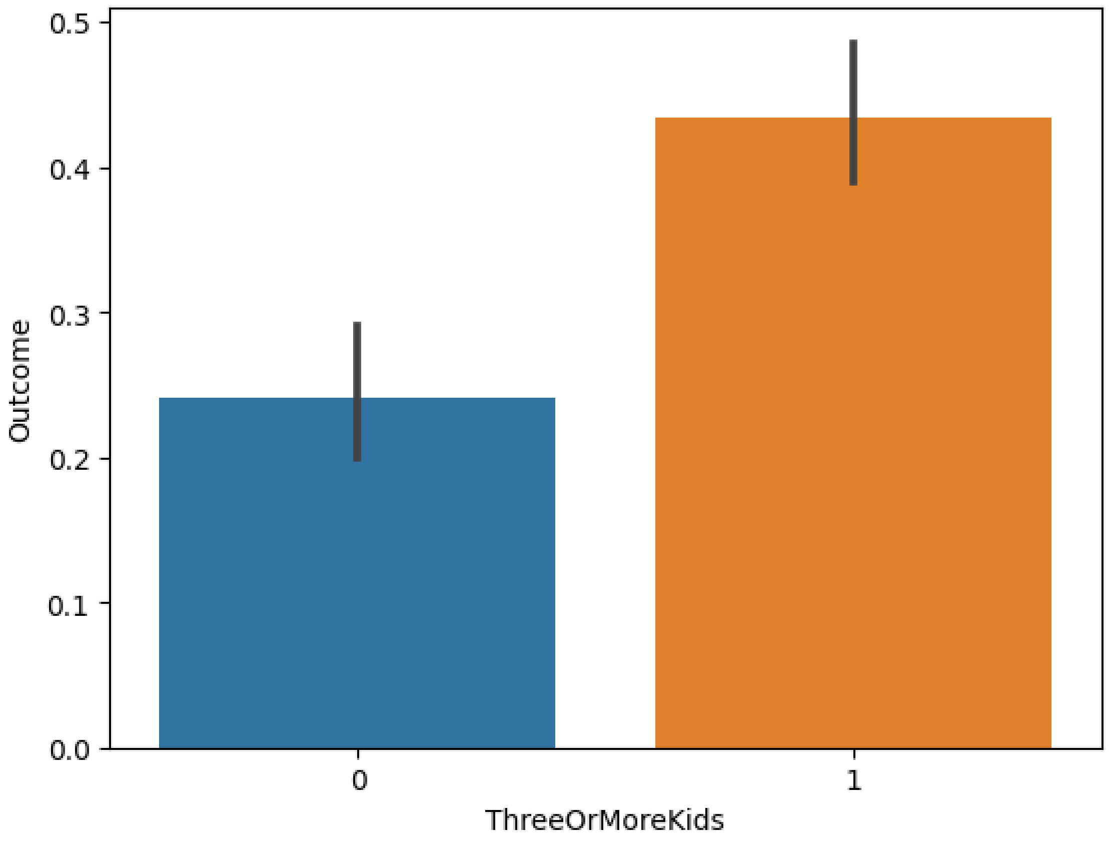
What is the probability that you get diabetes, given that you have three or more chil- dren?

```
In [56]: X_More_3 = X[X['ThreeOrMoreKids'] == 1] # Three or More kids is True
         Prediction_2 = np.unique(model.predict_proba(X_More_3)[:,1]) # Outcome = 1
         Prediction_2 # using predict proba to find the probability
```

```
Out[56]: array([0.43209335])
```

```
In [80]: sns.barplot(data=diabetes_data, x="ThreeOrMoreKids", y="Outcome")
```

```
Out[80]: <AxesSubplot: xlabel='ThreeOrMoreKids', ylabel='Outcome'>
```



4 CREATING MULTIPLE LOGISTIC MODEL BY REMOVING INCONSISTENT COLUMNS

In [62]:
```
# # Fit the model on train Logistic Regression Code to Be Followed
# model = LogisticRegression(solver="liblinear")
# model.fit(x_train, y_train)
# #predict on test
# y_predict = model.predict(x_test)
```

In [174…
```
# Loading the Logistics Regression Prediction Model to Calculate Accuracy of Different Models
logreg=LogisticRegression()
logreg.fit(X_train,y_train)
y_pred=logreg.predict(X_test)
```

In [86]:
```
diabetes_copy=diabetes_data.copy(deep=True) #Creating a copy to create multiple models
```

In [62]:
```
scaler=StandardScaler() # Standardisation made no difference
```

In [141…
```
diabetes_copy.head()
```

Out[141]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree	Age	Outcome	ThreeOrN
0	6	148.0	72.0	35	36.5	33.6	0.627	50	1	
1	1	85.0	66.0	29	36.5	26.6	0.351	31	0	
2	8	183.0	64.0	23	36.5	23.3	0.672	32	1	
3	1	89.0	66.0	23	94.0	28.1	0.167	21	0	
4	0	137.0	40.0	35	168.0	43.1	2.288	33	1	

CREATING THREE MODELS WITH DROPPING DIFFERENT NO. OF COLUMNS WHICH HAD INCONSISTENCIES (BUT REPLACED WITH MEAN & MEDIAN)

In [171...

```
# CREATING MULTIPLE MODELS BASED ON DATA CLEANING
# Model 1
Model1 = diabetes_copy.iloc[:,0:8] #including all columns
logreg.fit(Model1,y)
log_predicted_Model1=logreg.predict(Model1)
accuracy_model1=logreg.score(Model1,y)

# Model 2
Model2 = diabetes_copy.iloc[:,0:4] #including first 4 columns
logreg.fit(Model2,y)
log_predicted_Model2=logreg.predict(Model2)
accuracy_model2=logreg.score(Model2,y)

# Model 3
Model3 = diabetes_copy.iloc[:,0:2] #including first 2 columns
logreg.fit(Model3,y)
log_predicted_Model3=logreg.predict(Model3)
accuracy_model3=logreg.score(Model3,y)
```

In [168...

```
print(accuracy_model1*100) # Score of Model 1
```

```
78.0
```

In [169...

```
print(accuracy_model2*100) # Score of Model 2
```

```
75.2
```

In [170...

```
print(accuracy_model3*100) # Score of Model 3
```

```
74.66666666666667
```

In [146...

```
final_model = Model1 # because of its highest accuracy of 78%
```

WE CAN SEE DROPPING COLUMNS IS REDUCING THE ACCURACY THIS WOULD HAVE BEEN OPPOSITE IF WE DIDN'T REPLACE THE 0 VALUES WITH MEAN OR MEDIAN, IF ZERO VALUES WERE STILL PRESENT IN THE DATASET THEN DROPPING THOSE COLUMNS WOULD HAVE INCREASED ACCURACY OF MODEL

In [134...

```
predict_Diabetes =pd.read_csv("ToPredict.csv")
```

In [99]:

```
predict_Diabetes.head()
```

Out[99]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree	Age
0	4	136	70	0	0	31.2	1.182	22
1	1	121	78	39	74	39.0	0.261	28
2	3	108	62	24	0	26.0	0.223	25
3	0	181	88	44	510	43.3	0.222	26
4	8	154	78	32	0	32.4	0.443	45

In [100...

```
predict_Diabetes.describe()
```

Out[100]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree	Age
count	5.000000	5.00000	5.000000	5.000000	5.000000	5.000000	5.000000	5.000000
mean	3.200000	140.00000	75.200000	27.800000	116.800000	34.380000	0.466200	29.200000
std	3.114482	28.62691	9.757049	17.268468	222.128791	6.803822	0.410425	9.093954
min	0.000000	108.00000	62.000000	0.000000	0.000000	26.000000	0.222000	22.000000
25%	1.000000	121.00000	70.000000	24.000000	0.000000	31.200000	0.223000	25.000000
50%	3.000000	136.00000	78.000000	32.000000	0.000000	32.400000	0.261000	26.000000
75%	4.000000	154.00000	78.000000	39.000000	74.000000	39.000000	0.443000	28.000000
max	8.000000	181.00000	88.000000	44.000000	510.000000	43.300000	1.182000	45.000000

In [101…

```
#replacing 0 values with median of that column for the following small data and distribution chec
predict_Diabetes['SkinThickness']=predict_Diabetes['SkinThickness'].replace(0,predict_Diabetes['S
predict_Diabetes['Insulin']=predict_Diabetes['Insulin'].replace(0,predict_Diabetes['Insulin'].med
predict_Diabetes['BMI']=predict_Diabetes['BMI'].replace(0,predict_Diabetes['BMI'].median())
```

In [147…

```
#Predict
logreg = LogisticRegression(max_iter=10000)
logreg = model.fit(final_model, diabetes_copy['Outcome'])
X_Predict = predict_Diabetes.iloc[:,0:8] # Same no of columns as Diabetes Dataset Copy
log_predicted_final = logreg.predict(X_Predict)
log_predicted_final
```

Out[147]:

```
array([1, 0, 0, 1, 1], dtype=int64)
```

1 represents Positive for Diabetes and 0 represents negative for Diabetes

In [148…

```
# Finding probabilities for Diabetes
Predict_Probabilities = logreg.predict_proba(X_Predict)[:,1]
```

In [163…

```
print(Predict_Probabilities)
```

```
[0.69098696 0.25324206 0.10261771 0.64947076 0.68958759]
```

Assumptions

Few assumptions have been considered while creating the above models and code -

- Logistic Model have been considered both as a Regression model & Classifier.
- Comments have been added in the jupyter notebook file for explanation.
- Code is attached in the end after converting the Jupyter Notebook file to PDF, using NBconvert, as it automatically converts it, the orientation of Images and tables get little bit misaligned or have extra low/high margins.
- Majority of Code is attached in the code section of report and not explained in between the report section to keep the word limit and remove duplicates.

References

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