Capstone Project - "Healthcare_Prediction of Diabetes"

In [1]:
```
#Import all the necessary libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
```

In [2]:
```
#input the dataset
data = pd.read_csv("health care diabetes.csv")
dataframe = data
```

In [3]:
```
#Let us check the first 5 rows of the dataframe
data.head()
```

Out[3]:

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

In [4]:
```
#Let us find the number of rows and columns
data.shape
```

Out[4]:
```
(768, 9)
```

In [5]:
```
data.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    int64  
 2   BloodPressure             768 non-null    int64  
 3   SkinThickness             768 non-null    int64  
 4   Insulin                   768 non-null    int64  
 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(2), int64(7)
memory usage: 54.1 KB
```

In [6]:
```
d1 = data.duplicated(keep='first')  #check for duplicate data. if yes, retain the first one.
d1                                 #There are no duplicate values as all the 768 rows are present.
```

Out[6]:
```
0      False
1      False
2      False
3      False
4      False
       ...  
763    False
764    False
765    False
766    False
767    False
Length: 768, dtype: bool
```

In [7]:
```
#check for missing values
d2 = data.isnull().sum()
d2                      #There are no missing values
```

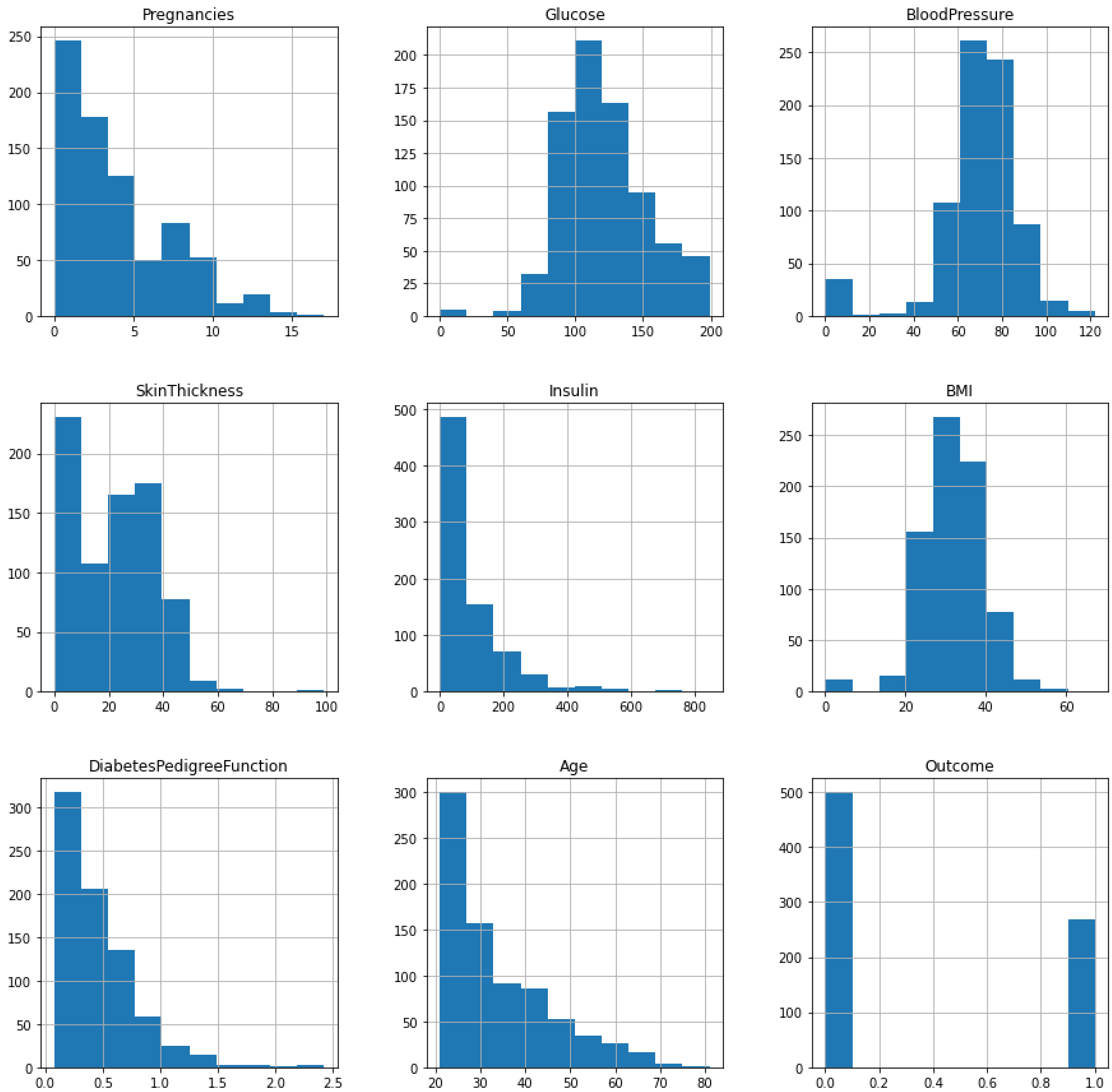
Out[7]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [8]:
```
data.describe()   #statistical analysis
```

Out[8]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

In [9]:
```
#let us visualize the data
data.hist(figsize = (15,15));
```



From the above histograms, we can see that the columns, "Pregnancies", "Insulin", "Age", "Diabetes Pedigree Function", are right skewed. Also, in the columns, "Glucose", "Blood Pressure", "Skin Thickness", "Blood Pressure", "Insulin" and "BMI" have "0" values which is not possible.

Exploratory data analysis:

Let us select the columns with "0" values and replace them with the mean values of the respective columns

In [10]:
```
df = dataframe.iloc[:,1:-3]            #Save the five columns in 'df' dataframe
df = df.mask(df == 0).fillna(df.mean())  #after masking the rows with 0's take the mean of rest of the
                                        #rows and replace the 0's.
```

In [11]:
```
df.head()   # display the first five rows of the cleaned data
```

Out[11]:

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

In [12]:
```
df1 = dataframe.iloc[:,0]   #Save the "Pregnancies" in df1
df2 = dataframe.iloc[:,-3:] # Save the rest of the 3 columns in df2
df1 = df1.to_frame()
print(df1.head())
df2.head()
```

```
   Pregnancies
0            6
1            1
2            8
3            1
4            0
```

Out[12]:

	DiabetesPedigreeFunction	Age	Outcome
0	0.627	50	1
1	0.351	31	0
2	0.672	32	1
3	0.167	21	0
4	2.288	33	1

In [13]:
```
new_data = pd.concat([df1, df, df2], axis = 1) #combine df1, df and df2 into a single dataframe
new_data
```

Out[13]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.0	35.000000	79.799479	33.6	0.627	50	1
1	1	85.0	66.0	29.000000	79.799479	26.6	0.351	31	0
2	8	183.0	64.0	20.536458	79.799479	23.3	0.672	32	1
3	1	89.0	66.0	23.000000	94.000000	28.1	0.167	21	0
4	0	137.0	40.0	35.000000	168.000000	43.1	2.288	33	1
...	...	...	...	...	...	...	...	...	...
763	10	101.0	76.0	48.000000	180.000000	32.9	0.171	63	0
764	2	122.0	70.0	27.000000	79.799479	36.8	0.340	27	0
765	5	121.0	72.0	23.000000	112.000000	26.2	0.245	30	0
766	1	126.0	60.0	20.536458	79.799479	30.1	0.349	47	1
767	1	93.0	70.0	31.000000	79.799479	30.4	0.315	23	0

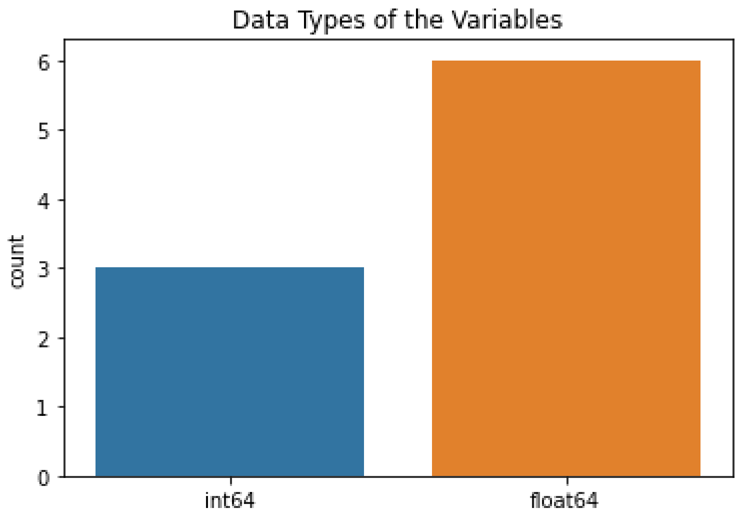
768 rows × 9 columns

In [14]:
```
x = new_data.dtypes
print(x)
```

```
Pregnancies                   int64
Glucose                     float64
BloodPressure               float64
SkinThickness               float64
Insulin                     float64
BMI                         float64
DiabetesPedigreeFunction    float64
Age                           int64
Outcome                       int64
dtype: object
```

In [15]:
```
import seaborn as sns   #import the seaborn library for visualization
```

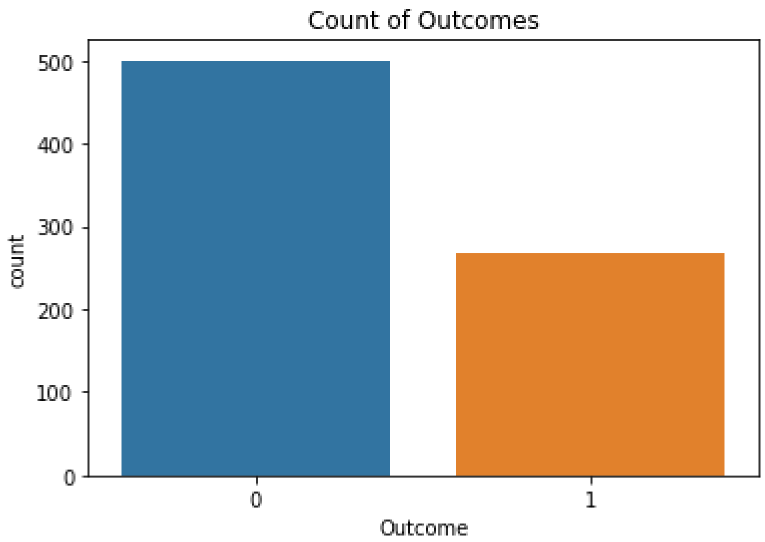
In [16]:
```
#display the countplot to find the data types
sns.countplot(x = x, data = new_data)
plt.title("Data Types of the Variables")
plt.show()
```



3 variables are of integer type and the rest 6 variables are of float type

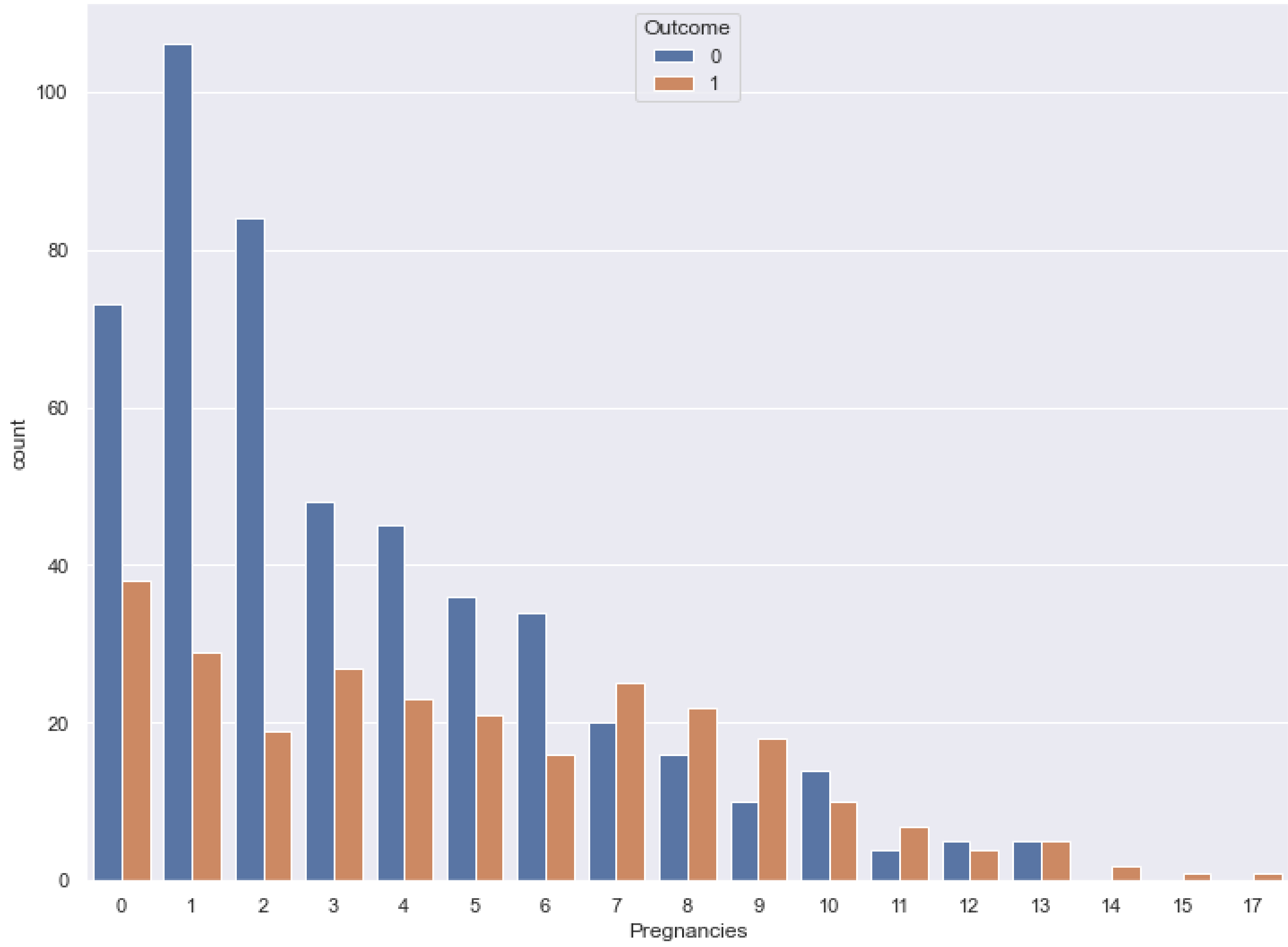
In [17]:
```
#Plot the count of Diabetic and Non-diabetic population. '0' means Non-diabetic. '1' means Diabetic.
sns.countplot(new_data.Outcome)
plt.title("Count of Outcomes");
```

```
C:\Users\meetu\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following variable as a k
eyword arg: x. From version 0.12, the only valid positional argument will be `data`, and passing other arguments withou
t an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```



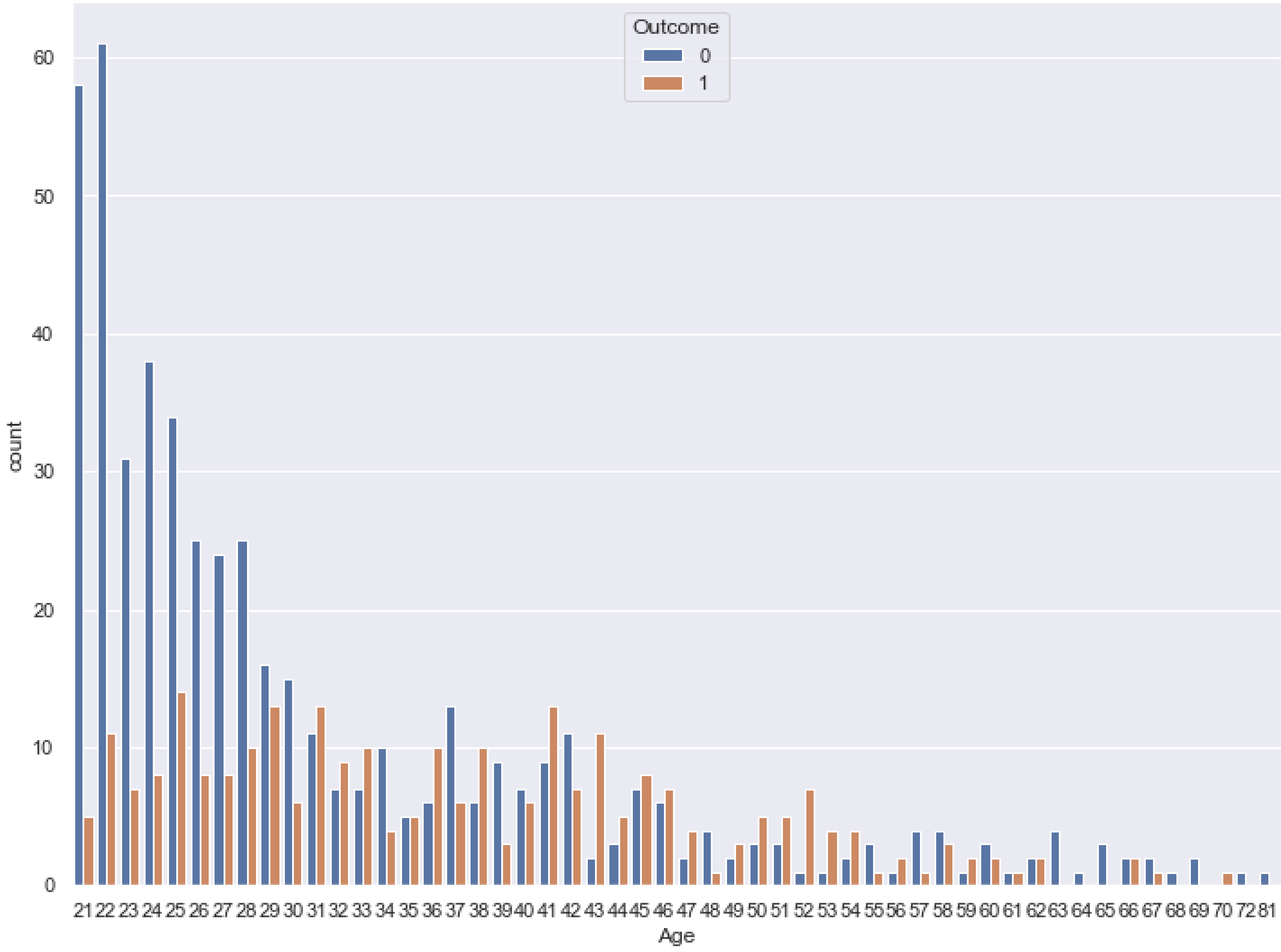
From the above countplot we can see that of the 768 patients, 500 patients do not have diabetes and the rest of 268 have diabetes

In [18]:
```
sns.set(rc = {'figure.figsize': (12,9)})
sns.countplot(x = 'Pregnancies', data = new_data, hue = 'Outcome');
```



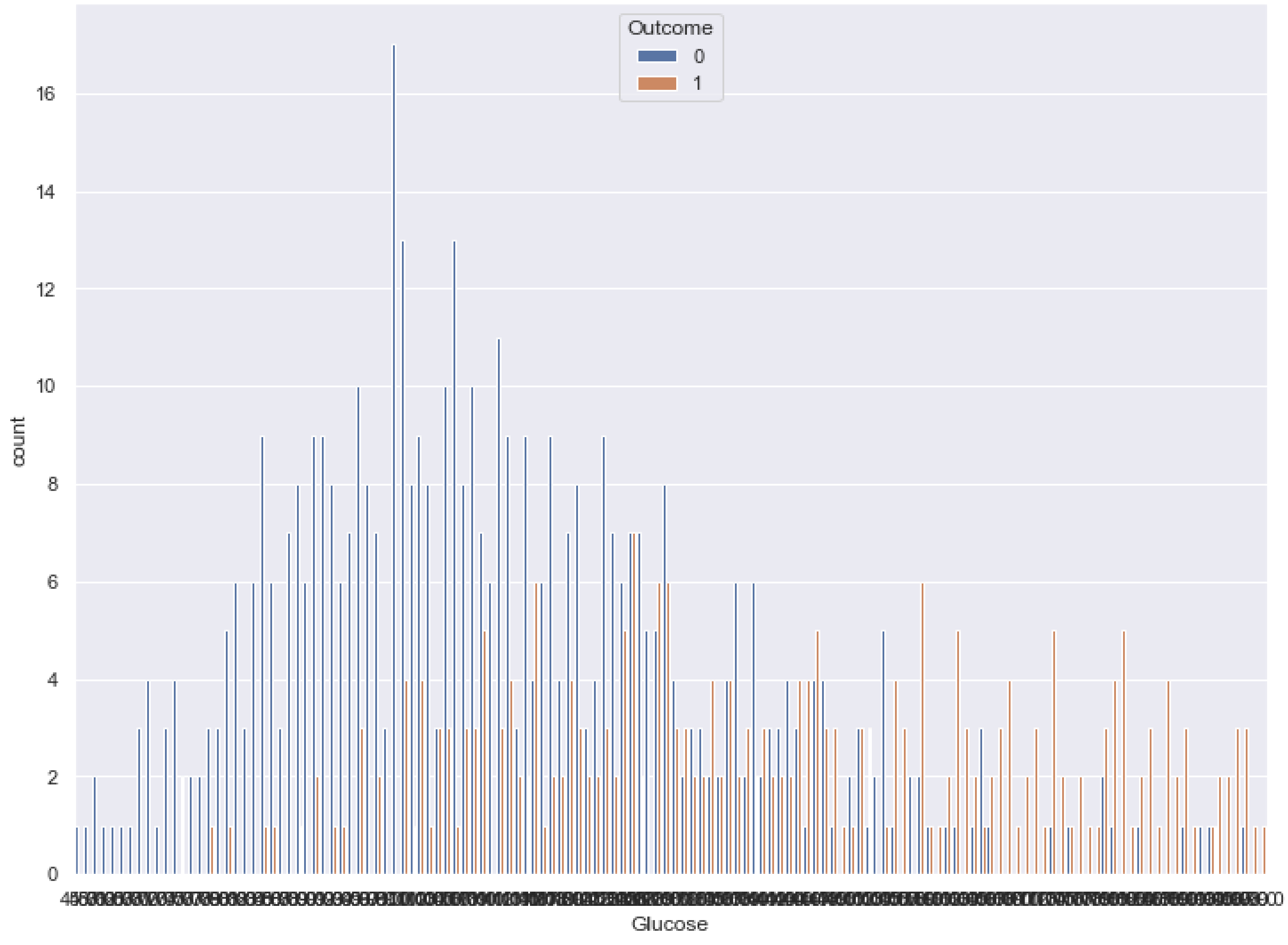
The countplot of Pregnancies shows that it is right skewed. Patients who have had pregnancies between 7 and 9 are prone to Diabetes.

In [19]:
```
sns.countplot(x = 'Age', data = new_data, hue = 'Outcome');
```



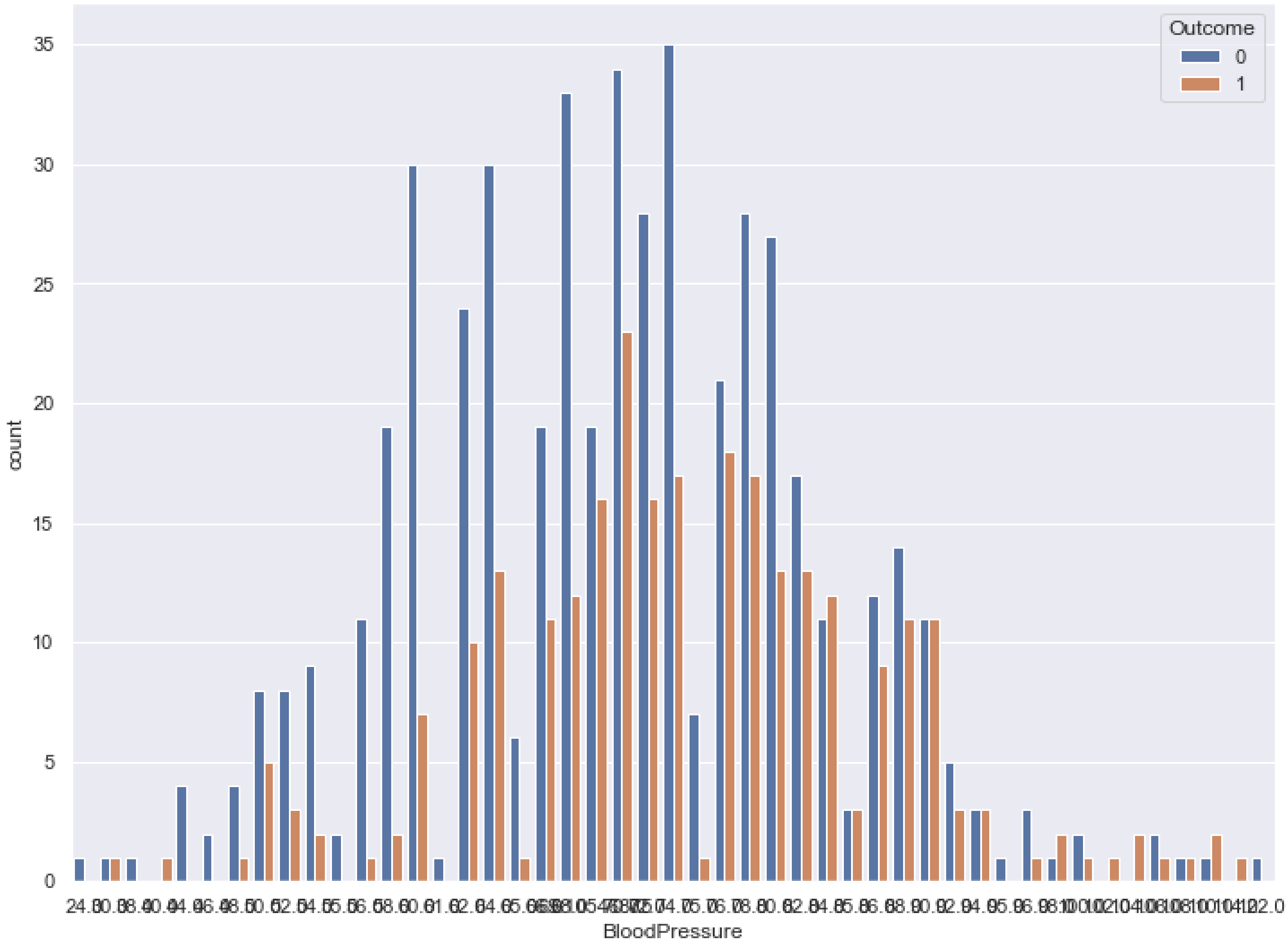
The count plot of age shows that above the age of 30 years and below 56 years, people are prone to get diabetes.

In [20]:
```
sns.countplot(x = 'Glucose', data = new_data, hue = 'Outcome');
```



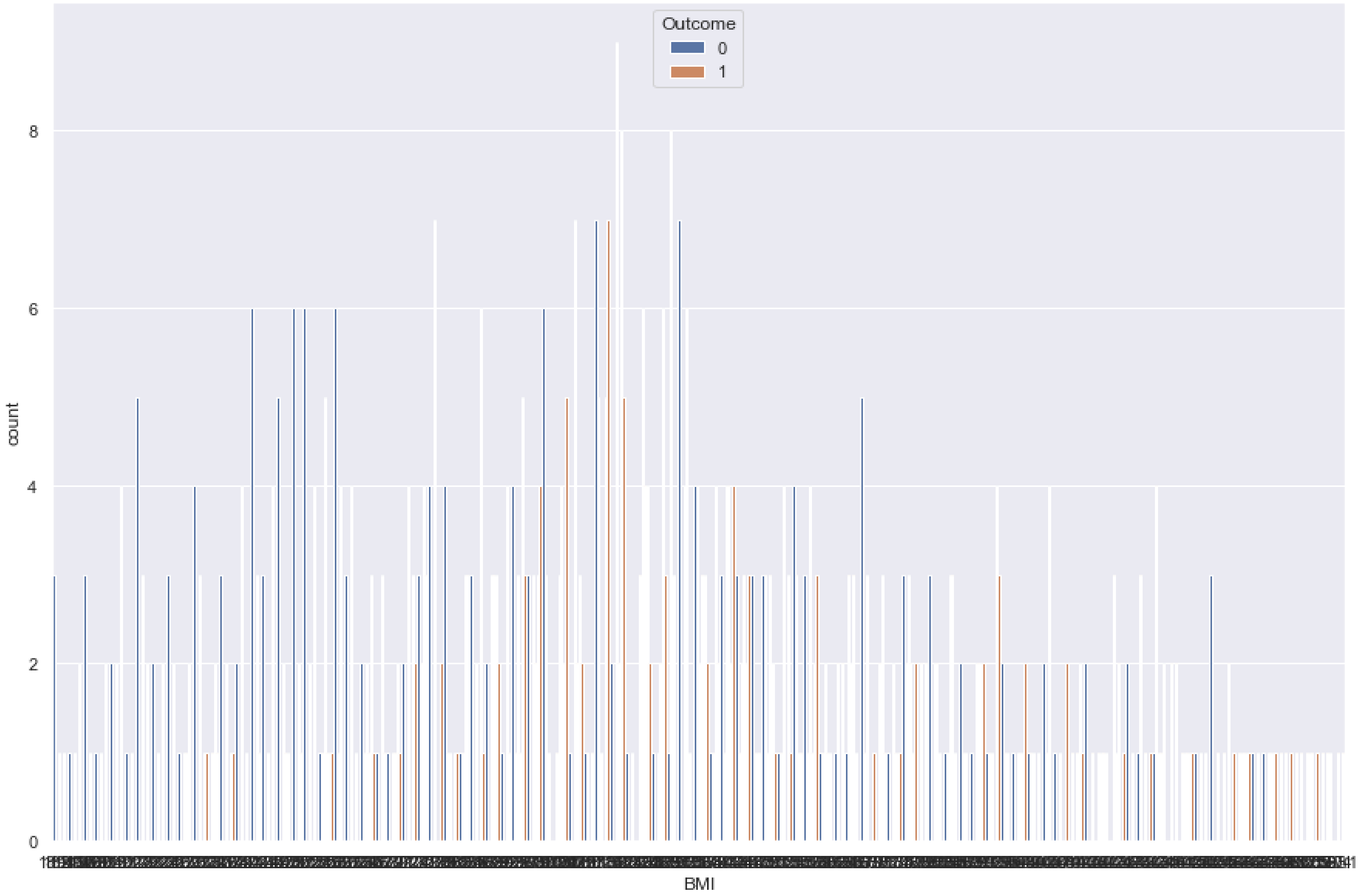
From the above countplot, we can see that a high level of glucose is an indicative of Diabetes.

In [21]:
```
sns.countplot(x = 'BloodPressure', data = new_data, hue = 'Outcome');
```



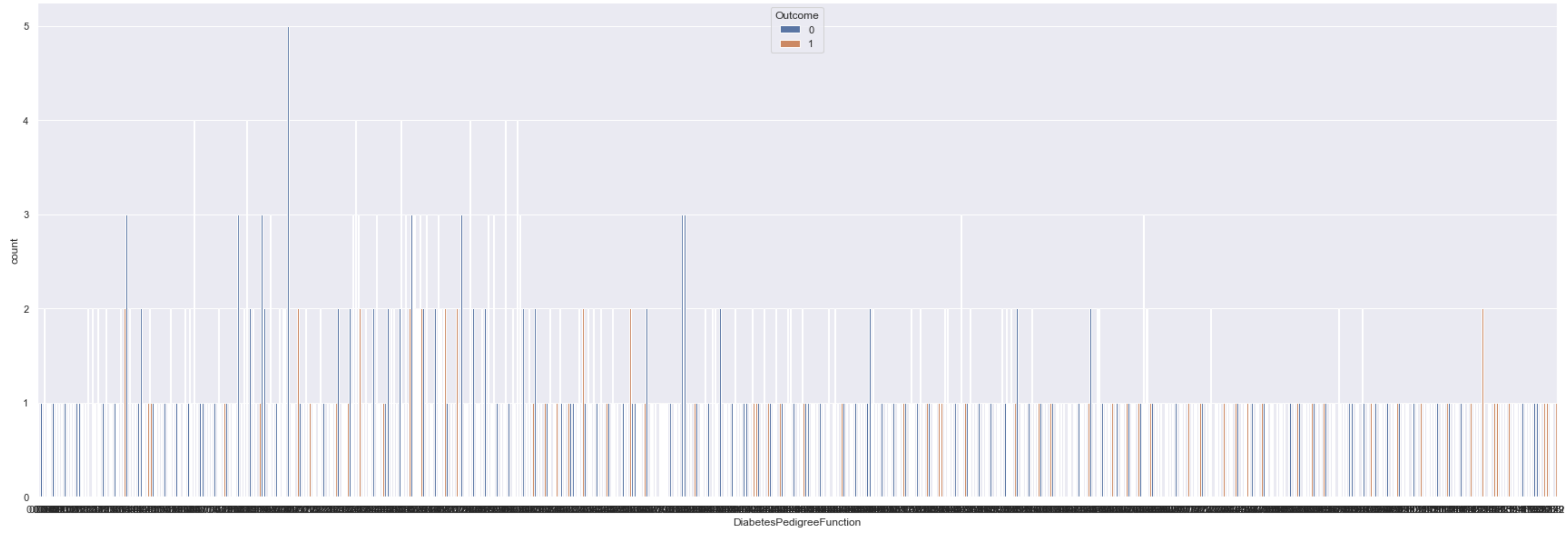
The countplot shows that Diabetes has no correlation with Blood Pressure

In [22]:
```
plt.subplots(figsize = (15,10))
sns.countplot(x = 'BMI', data = new_data, hue = 'Outcome');
```



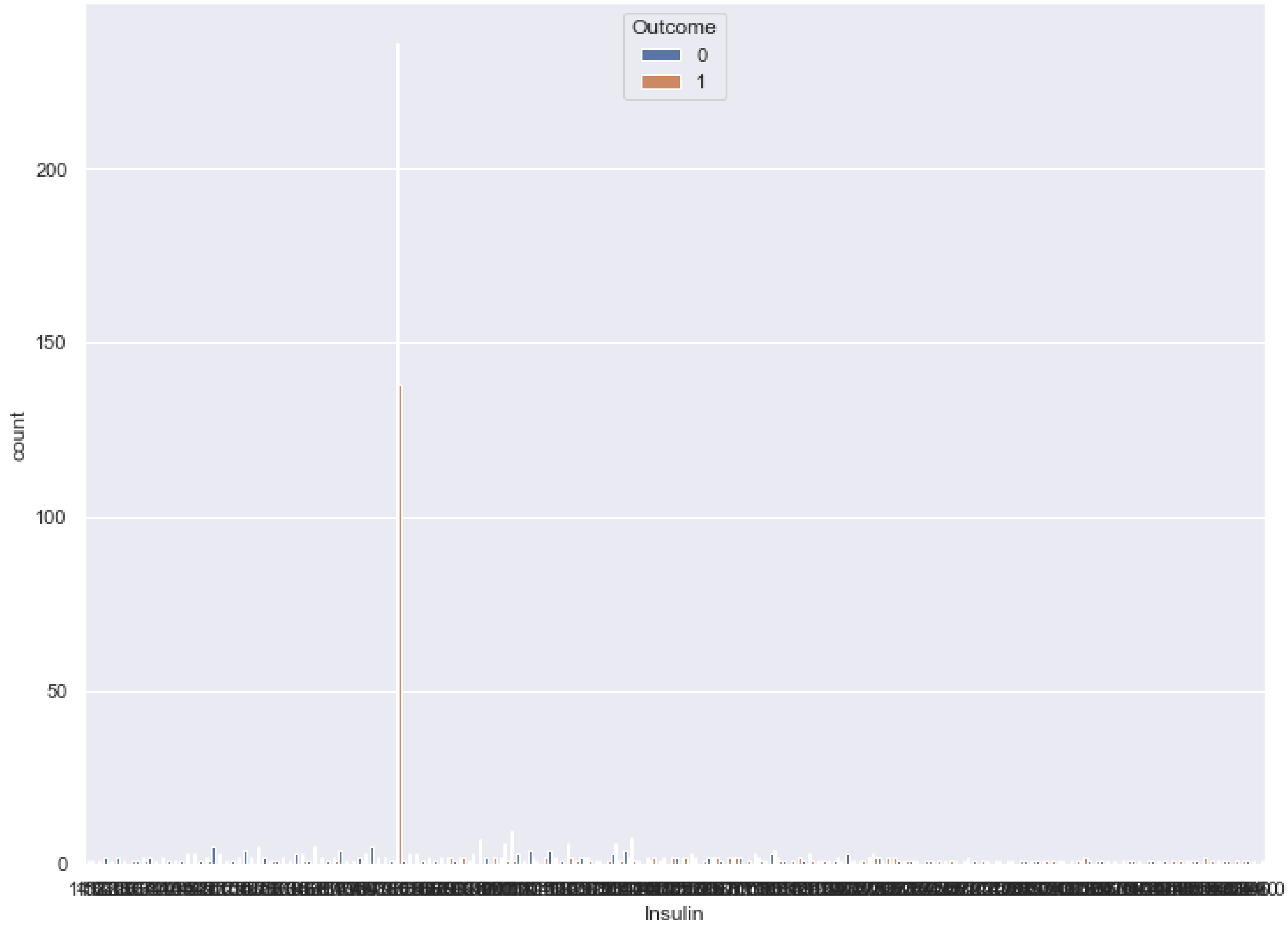
A high BMI value has a possibility of having Diabetes

In [23]:
```
plt.subplots(figsize = (30,10))
sns.countplot(x = 'DiabetesPedigreeFunction', data = new_data, hue = 'Outcome');
```



Diabetes Pedigree Function has no correlation with Diabetes

In [24]:
```
sns.countplot(x = 'Insulin', data = new_data, hue = 'Outcome');
```



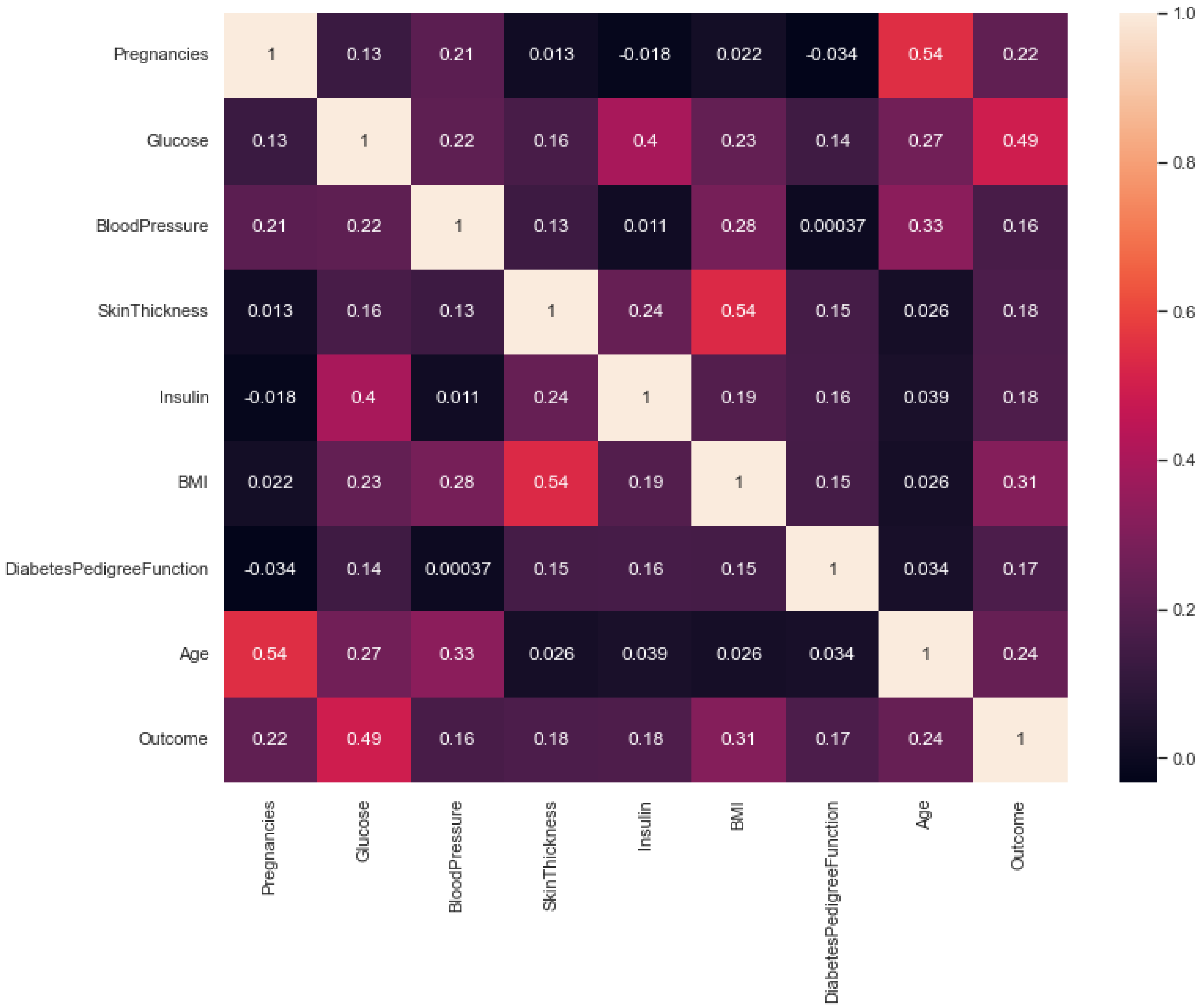
Insulin has minimum effect on the Outcome

In [25]:
```
#plotting of a Pairplot to understand the relationship between the variables
sns.pairplot(new_data);
```

- From the above Pairplot, we can clearly see that the Variables, 'BMI and Skin Thickness', 'Age and Pregnancies', 'Glucose and Insulin', 'Blood Pressure and BMI' ,and Variables 'Age and Blood Pressure' are **positively correlated**.
- Variable 'Age' has **no correlation** with the variables, 'Insulin, Skin Thickness, BMI and Diabetes Pedigree Function'.
- Variable 'Pregnancies' is **negatively correlated** with 'Insulin' and 'Diabetes Pedigree Function'.

Correlation Analysis:

In [26]:
```python
# Heatmap
sns.set(rc = {'figure.figsize':(12,9)})
sns.heatmap(new_data.corr(), annot = True)
plt.show()
```



Heatmap shows correlation between the variables. lighter the the colour, more the correlation.

For training a model, we need to select the features that are correlated. we shall find features that have correlation greater than or equal to 0.5 and select those features and train the model.

In [27]:
```python
correlation = new_data.corr()
correlation[correlation > 0.4]
```

Out[27]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1.000000	NaN	NaN	NaN	NaN	NaN	NaN	0.544341	NaN
Glucose	NaN	1.000000	NaN	NaN	NaN	NaN	NaN	NaN	0.492908
BloodPressure	NaN	NaN	1.0	NaN	NaN	NaN	NaN	NaN	NaN
SkinThickness	NaN	NaN	NaN	1.000000	NaN	0.535703	NaN	NaN	NaN
Insulin	NaN	NaN	NaN	NaN	1.0	NaN	NaN	NaN	NaN
BMI	NaN	NaN	NaN	0.535703	NaN	1.000000	NaN	NaN	NaN
DiabetesPedigreeFunction	NaN	NaN	NaN	NaN	NaN	NaN	1.0	NaN	NaN
Age	0.544341	NaN	NaN	NaN	NaN	NaN	NaN	1.000000	NaN
Outcome	NaN	0.492908	NaN	NaN	NaN	NaN	NaN	NaN	1.000000

The variables, Pregnancies, Age, Skin Thickness, BMI and Glucose have correlation greater than or equal to 0.5.

In [28]:
```
#Let us create an alias of the selected features
selected_data = new_data[["Pregnancies","Glucose", "BMI", "SkinThickness","Age"]]
print(selected_data)
```

```
     Pregnancies  Glucose   BMI  SkinThickness  Age
0              6    148.0  33.6      35.000000   50
1              1     85.0  26.6      29.000000   31
2              8    183.0  23.3      20.536458   32
3              1     89.0  28.1      23.000000   21
4              0    137.0  43.1      35.000000   33
..           ...      ...   ...            ...  ...
763           10    101.0  32.9      48.000000   63
764            2    122.0  36.8      27.000000   27
765            5    121.0  26.2      23.000000   30
766            1    126.0  30.1      20.536458   47
767            1     93.0  30.4      31.000000   23

[768 rows x 5 columns]
```

In [29]:
```
#Let us standardise the data using Standard Scaler, where are the variables are converted to the format, Mean=0 and Stanc
#Import standard scaler from sklearn library
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
model = scaler.fit(selected_data)
scaled_data = model.transform(selected_data)
print(scaled_data)
```

```
[[ 0.63994726  0.86527574  0.16725546  0.87205698  1.4259954 ]
 [-0.84488505 -1.20598931 -0.85153454  0.2486783  -0.19067191]
 [ 1.23388019  2.01597855 -1.33182125 -0.6306536  -0.10558415]
 ...
 [ 0.3429808  -0.02240928 -0.90975111 -0.37470037 -0.27575966]
 [-0.84488505  0.14197684 -0.34213954 -0.6306536   1.17073215]
 [-0.84488505 -0.94297153 -0.29847711  0.45647119 -0.87137393]]
```

In [30]:
```
# let us split the data into training and testing sample
from sklearn.model_selection import train_test_split
```

In [31]:
```
X = scaled_data
y = new_data['Outcome']
```

In [32]:
```
print(X.shape)
print(y.shape)
```

```
(768, 5)
(768,)
```

In [33]:
```
# Split the train test data in the ratio of 80:20
X_train,X_test,y_train,y_test=train_test_split(X,y, test_size=0.2, random_state=1)
```

In [34]:
```
# Import the Logistic Regression model
from sklearn.linear_model import LogisticRegression
logreg = LogisticRegression()
logreg.fit(X_train, y_train)
```

Out[34]:
```
LogisticRegression()
```

In [35]:
```
# Check the accuracy of the model, f1 score and generate the classification report.
accuracy = logreg.score(X_test, y_test)
print('Accuracy of Logistic Regression :  ', accuracy*100)

from sklearn.metrics import f1_score, classification_report, confusion_matrix
y_pred = logreg.predict(X_test)
f1 = f1_score(y_pred, y_test)
print('f1_score : ', f1)
con_mat = confusion_matrix(y_test, y_pred)
print()
print('Confusion Matrix: \n ', con_mat)
print()
print(classification_report(y_pred, y_test))
```

```
Accuracy of Logistic Regression :   76.62337662337663
f1_score :  0.6326530612244898

Confusion Matrix:
  [[87 12]
 [24 31]]

              precision    recall  f1-score   support

           0       0.88      0.78      0.83       111
           1       0.56      0.72      0.63        43

    accuracy                           0.77       154
   macro avg       0.72      0.75      0.73       154
weighted avg       0.79      0.77      0.77       154
```

In [36]:
```
# Let us train a Decision Tree model ad check its accuracy and f1 score
from sklearn.tree import DecisionTreeClassifier
classifier = DecisionTreeClassifier()
classifier.fit(X_train, y_train)
y_predict = classifier.predict(X_test)
```

In [37]:
```
from sklearn.metrics import f1_score, classification_report, confusion_matrix, accuracy_score
accu = accuracy_score(y_test, y_predict)
print("Accuracy of Decision Tree Classifier", accu*100)

f1score = f1_score(y_predict, y_test)
print('f1 score :', f1score)
con_mat1 = confusion_matrix(y_test, y_predict)
print(confusion_matrix(y_test, y_predict))
print(classification_report(y_test, y_predict))
```

```
Accuracy of Decision Tree Classifier 72.07792207792207
f1 score : 0.6126126126126126
[[77 22]
 [21 34]]
              precision    recall  f1-score   support

           0       0.79      0.78      0.78        99
           1       0.61      0.62      0.61        55

    accuracy                           0.72       154
   macro avg       0.70      0.70      0.70       154
weighted avg       0.72      0.72      0.72       154
```

In [38]:
```
# Let us use a Random Forest Classifier and check the scores
from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier(n_estimators = 30, random_state = 0)
rfc.fit(X_train,y_train)
y_predicted = rfc.predict(X_test)
```

In [39]:
```python
from sklearn.metrics import f1_score, classification_report, confusion_matrix, accuracy_score
acc = accuracy_score(y_test, y_predicted)
print("Accuracy of Random Forest Classifier: ", acc*100)
F1score = f1_score(y_predicted, y_test)
print("f1 score: ", F1score)
con_mat2 = confusion_matrix(y_test, y_predicted)
print(confusion_matrix(y_test, y_predicted))
print(classification_report(y_test, y_predicted))
```

```
Accuracy of Random Forest Classifier:  75.97402597402598
f1 score:  0.6407766990291262
[[84 15]
 [22 33]]
              precision    recall  f1-score   support

           0       0.79      0.85      0.82        99
           1       0.69      0.60      0.64        55

    accuracy                           0.76       154
   macro avg       0.74      0.72      0.73       154
weighted avg       0.75      0.76      0.76       154
```

In [40]:
```python
#Usng a K-NN algorithm, let us find the accuracy and f1 score
from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier(n_neighbors=5)
knn.fit(X_train,y_train)
y_pred1 = knn.predict(X_test)
```

In [41]:
```python
from sklearn.metrics import f1_score, confusion_matrix, classification_report, accuracy_score
accu = accuracy_score(y_test, y_pred1)
print("Accuracy of K-NN algorithm: ", accu)
F1 = f1_score(y_pred1, y_test)
print("f1 score: ", F1)
con_mat3 = confusion_matrix(y_test, y_pred1)
print(confusion_matrix(y_test, y_pred1))
print(classification_report(y_test, y_pred1))
```

```
Accuracy of K-NN algorithm:  0.7402597402597403
f1 score:  0.6296296296296297
[[80 19]
 [21 34]]
              precision    recall  f1-score   support

           0       0.79      0.81      0.80        99
           1       0.64      0.62      0.63        55

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

In [42]:
```python
pip install tabulate   # To make Tables
```

```
Note: you may need to restart the kernel to use updated packages.

ERROR: Invalid requirement: '#'
```

In [43]:
```python
from tabulate import tabulate
```

In [44]:
```python
table = [['     ', 'Logistic Regression', 'Decision Tree Classifier', 'Random Forest Classifier', 'KNN algorithm'],['f1-s
```

In [45]:
```python
print(tabulate(table, headers='firstrow', tablefmt='fancy_grid'))
```

	Logistic Regression	Decision Tree Classifier	Random Forest Classifier	KNN algorithm
f1-score	0.63	0.59	0.64	0.63
Accuracy	76.62%	70.13%	75.97%	74.03%

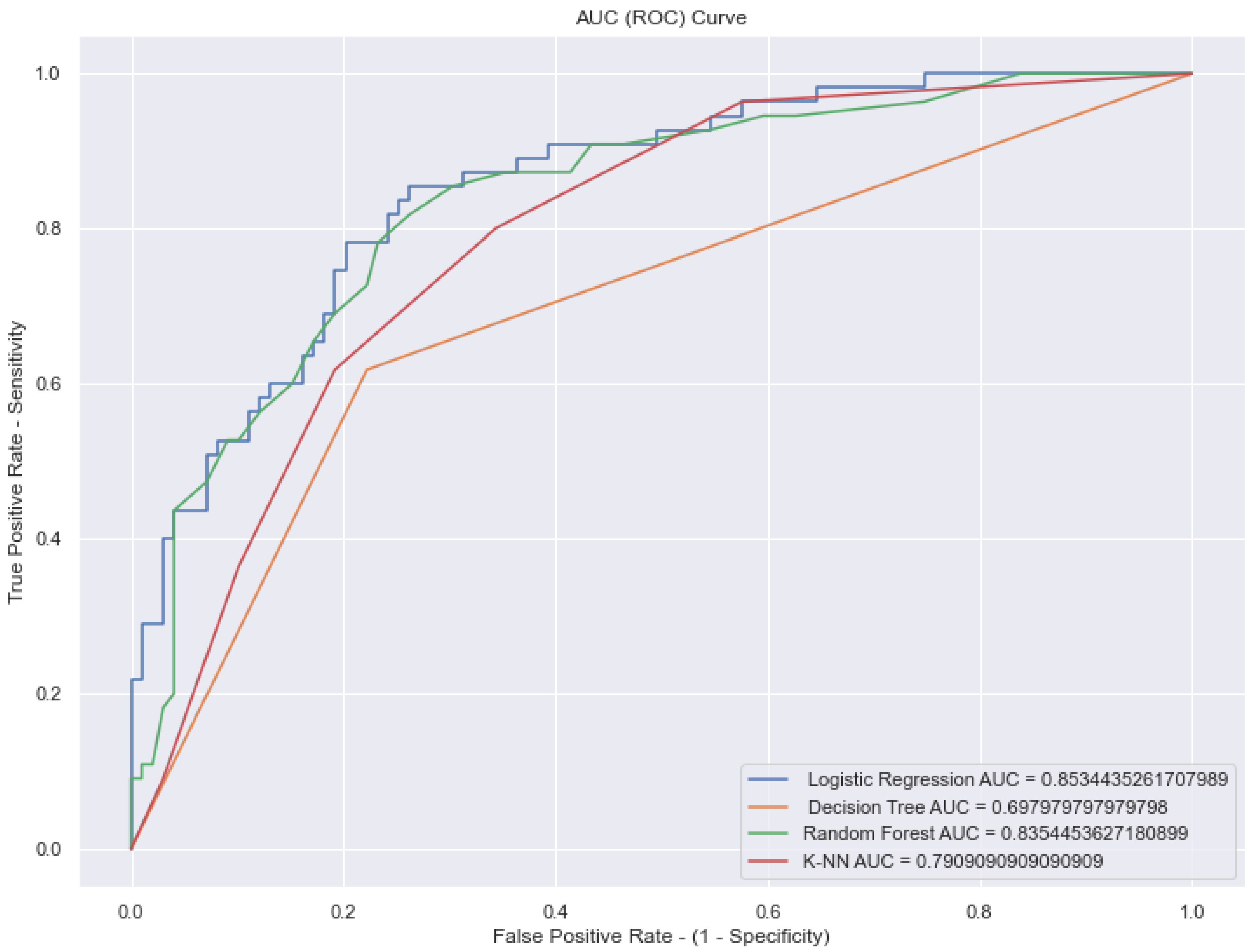
Comparing the Models with that of the KNN algorithm:

From the above table we can infer that, the Logistic Regression model and the KNN have the same f1-score of 0.63. Whereas, the Random Forest classifier is slightly better with an f1-score of 0.64. Decision tree classifier has performed poorly with an f1-score of 0.59.

AUC (ROC curve):

In [46]:
```python
from sklearn import metrics
```

In [47]:
```python
# AUC (ROC Curve) of Logistic Regression
y_pred_proba = logreg.predict_proba(X_test)[:,1]  #predict probabilities of the outcome
fpr,tpr,_ = metrics.roc_curve(y_test, y_pred_proba) # false positive rate(fpr) and true positive rate(tpr)
auc = metrics.roc_auc_score(y_test, y_pred_proba)   # Area under the ROC curve
plt.plot(fpr, tpr, label =" Logistic Regression AUC = "+str(auc))

# AUC (ROC Curve) of Decision Tree Classifier
y_predict_proba = classifier.predict_proba(X_test)[:,1]
fpr, tpr, _ = metrics.roc_curve(y_test, y_predict_proba)
auc1 = metrics.roc_auc_score(y_test, y_predict_proba)

plt.plot(fpr, tpr, label =" Decision Tree AUC = "+str(auc1))
plt.xlabel('False Positive Rate - (1 - Specificity)')
plt.ylabel('True Positive Rate - Sensitivity')
plt.title('AUC (ROC) Curve')

#AUC (ROC Curve) of Random Forest Classifier
y_predicted_proba = rfc.predict_proba(X_test)[:,1]
fpr,tpr,_ = metrics.roc_curve(y_test, y_predicted_proba)
auc2 = metrics.roc_auc_score(y_test, y_predicted_proba)
plt.plot(fpr, tpr, label =   "Random Forest AUC = "+str(auc2))

#AUC (ROC Curve) of K-NN algorithm
y_pred1_proba = knn.predict_proba(X_test)[:,1]
fpr, tpr,_ = metrics.roc_curve(y_test, y_pred1_proba)
auc3 = metrics.roc_auc_score(y_test, y_pred1_proba)
plt.plot(fpr, tpr, label = "K-NN AUC = "+str(auc3))

plt.legend()
plt.show()
```



Receiver Operating Characteristic (ROC) Curve gives the relationship between specificity and sensitivity.

In [48]:
```python
# Import required libray for accuracy, specificity, sensitivity
from sklearn.metrics import confusion_matrix, classification_report
```

In [49]:
```
# Confusion matrix of Logistic Regression
# TP = confusion_matrix[1,1] # true positive
# TN = confusion_matrix[0,0] # true negatives
# FP = confusion_matrix[0,1] # false positives
# FN = confusion_matrix[1,0] # false negatives
# Sensitivity = TP/(TP+FN)
# Specificity = TN/(TN+FP)
# Confusion Matrix of Logistic Regression
print('Confusion Matrix of Logistic Regression: ')
print(con_mat)
total1 = sum(sum(con_mat))
Accuracy1 = (con_mat[0,0] + con_mat[1,1])/total1
Sensitivity1 = con_mat[1,1]/(con_mat[1,1] + con_mat[1,0])
Specificity1 = con_mat [0,0]/(con_mat[0,0] + con_mat[0,1])
print('Accuracy = ', Accuracy1)
print('Sensitivity = ', Sensitivity1)
print('Specificity = ', Specificity1)
```

```
Confusion Matrix of Logistic Regression:
[[87 12]
 [24 31]]
Accuracy =  0.7662337662337663
Sensitivity =  0.5636363636363636
Specificity =  0.8787878787878788
```

In [50]:
```
# Confusion matrix of Decision Tree Classifier
print('Confusion Matrix of Decision Tree Classifier:')
print(con_mat1)
total2 = sum(sum(con_mat1))
Accuracy2 = (con_mat1[0,0] + con_mat1[1,1])/total2
Sensitivity2 = con_mat1[1,1]/(con_mat1[1,1] + con_mat1[1,0])
Specificity2 = con_mat1[0,0]/(con_mat1[0,0] + con_mat1[0,1])
print('Accuracy = ', Accuracy2)
print('Sensitivity = ', Sensitivity2)
print('Specificity = ', Specificity2)
```

```
Confusion Matrix of Decision Tree Classifier:
[[77 22]
 [21 34]]
Accuracy =  0.7207792207792207
Sensitivity =  0.6181818181818182
Specificity =  0.7777777777777778
```

In [51]:
```
#Confusion Matrix of Random Forest Classifier
print('Confusion Matrix of Random Forest Classifier:')
print(con_mat2)
total3 = sum(sum(con_mat2))
Accuracy3 = (con_mat2[0,0] + con_mat2[1,1])/total3
Sensitivity3 = con_mat2[1,1]/(con_mat2[1,1] + con_mat2[1,0])
Specificity3 = con_mat2[0,0]/(con_mat2[0,0] + con_mat2[0,1])
print('Accuracy = ', Accuracy3)
print('Sensitivity = ', Sensitivity3)
print('Specificity = ', Specificity3)
```

```
Confusion Matrix of Random Forest Classifier:
[[84 15]
 [22 33]]
Accuracy =  0.7597402597402597
Sensitivity =  0.6
Specificity =  0.8484848484848485
```

In [52]:
```
# Confusion Matrix of K-NN algorithm
print('Confusion Matrix of K-NN algorithm: ')
print(con_mat3)
total4 = sum(sum(con_mat3))
Accuracy4 = (con_mat3[0,0] + con_mat3[1,1])/total4
Sensitivity4 = con_mat3[1,1]/(con_mat3[1,1] + con_mat3[1,0])
Specificity4 = con_mat3[0,0]/(con_mat3[0,0] + con_mat3[0,1])
print('Accuracy = ', Accuracy4)
print('Sensitivity = ', Sensitivity4)
print('Specificity = ', Specificity4)
```

```
Confusion Matrix of K-NN algorithm:
[[80 19]
 [21 34]]
Accuracy =  0.7402597402597403
Sensitivity =  0.6181818181818182
Specificity =  0.8080808080808081
```

In [53]:
```
table1 = [['          ' , 'Logistic Regression', 'Decision Tree Clssifier', 'Random Forest Classifier', 'K-NN algorithm']
```

In [54]:
```
print(tabulate(table1, headers = 'firstrow', tablefmt = 'fancy_grid'))
```

	Logistic Regression	Decision Tree Clssifier	Random Forest Classifier	K-NN algorithm
Parameters				
Accuracy	87.20%	77.22%	75.97%	74.02%
Sensitivity	0.5636	0.6182	0.6	0.6182
Specificity	0.8788	0.7778	0.8485	0.8081
AUC	0.8534	0.6979	0.8355	0.7909

Sensitivity is the ability of a model to designate an individual with disease as positive. A highly sensitive model gives fewer false negative results. Specificity is the ability of a model to designate an individual who does not have the disease as negative.

From the above table, we can conclude that the Logistic Regression model performs better than the rest of the classifiers, since the Area Under Curve (AUC) for Logistic Regression model is the highest at 0.8534, with Sensitivity at 0.5636, Specificity at 0.8788 and an accuracy of 87.20%,

In [56]:
```
#Save the cleaned data in excel format in order to import it to Tableau for Visualization
writer = pd.ExcelWriter('pandas_simple.xlsx', engine='xlsxwriter')
new_data.to_excel(writer, sheet_name = 'raw_data.xls', index = False)
```

Data Visualization using Tableau

In [ ]:
```
<div class='tableauPlaceholder' id='viz1666259069139' style='position: relative'><noscript><a href='#'><img alt='Dashboa
```

Link for the Tableau Dashboard

https://public.tableau.com/views/DashboardHealthcare/DashboardHealthcare-DiabetesAnalysis?:language=en-GB&publish=yes&:display_count=n&:origin=viz_share_link (https://public.tableau.com/views/DashboardHealthcare/DashboardHealthcare-DiabetesAnalysis?:language=en-GB&publish=yes&:display_count=n&:origin=viz_share_link)

In [ ]: