In [2]:
```
#Let's start with importing necessary libraries

import pandas as pd
import numpy as np
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model  import Ridge,Lasso,RidgeCV, LassoCV, ElasticNet, ElasticNetCV
from sklearn.model_selection import train_test_split
from statsmodels.stats.outliers_influence import variance_inflation_factor
from sklearn.metrics import accuracy_score, confusion_matrix, roc_curve, roc_auc_score
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')

#import scikitplot as skl
sns.set()
```

In [3]:
```
# Let's use the handy function we created
def adj_r2(x,y,r2):
    n = x.shape[0]
    p = x.shape[1]
    adjusted_r2 = 1-(1-r2)*(n-1)/(n-p-1)
    return adjusted_r2
```

In [4]:
```
data = pd.read_csv(r"D:\INEURONE\MachineLARNING\Logistic-regression_final\diabetes.csv
data.head()
```

Out[4]:

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

In [5]:
```
data.describe()
```

Out[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesF
count	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	
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	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 [ ]:
```
# what standard deviation tells us
# agar zero hai toh sare data point ek hi number se full hai
# agar sare data point 1-50 k bichme hai toh SD inmese hi hoga leking ek bhi point mene 100
# so high value of SD says that data is higly spread and low value of Sd says that ki apka sara
```

In [61]:
```
data.info()
```

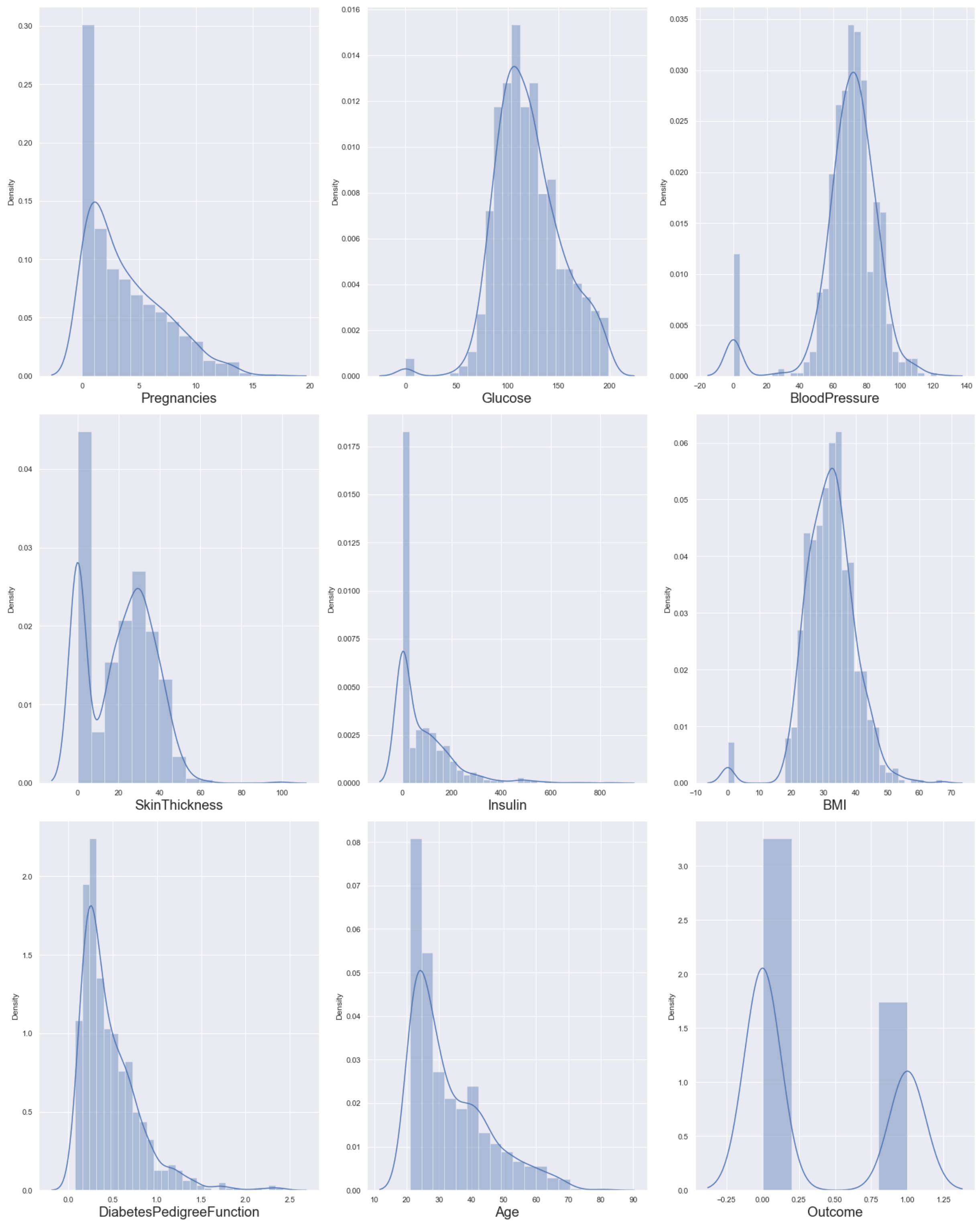
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               768 non-null    int64  
 1   Glucose                   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 [62]:
```
data.isnull().sum()
```

Out[62]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

Seems like there is no missing values in our data. Great, let's see the distribution of data:

In [63]:
```
# let's see how data is distributed for every column
plt.figure(figsize=(20,25), facecolor='white')
plotnumber = 1

for column in data:
    if plotnumber<=9 :
        ax = plt.subplot(3,3,plotnumber)
        sns.distplot(data[column])
        plt.xlabel(column,fontsize=20)
        #plt.ylabel('Salary',fontsize=20)
    plotnumber+=1
plt.tight_layout()
```

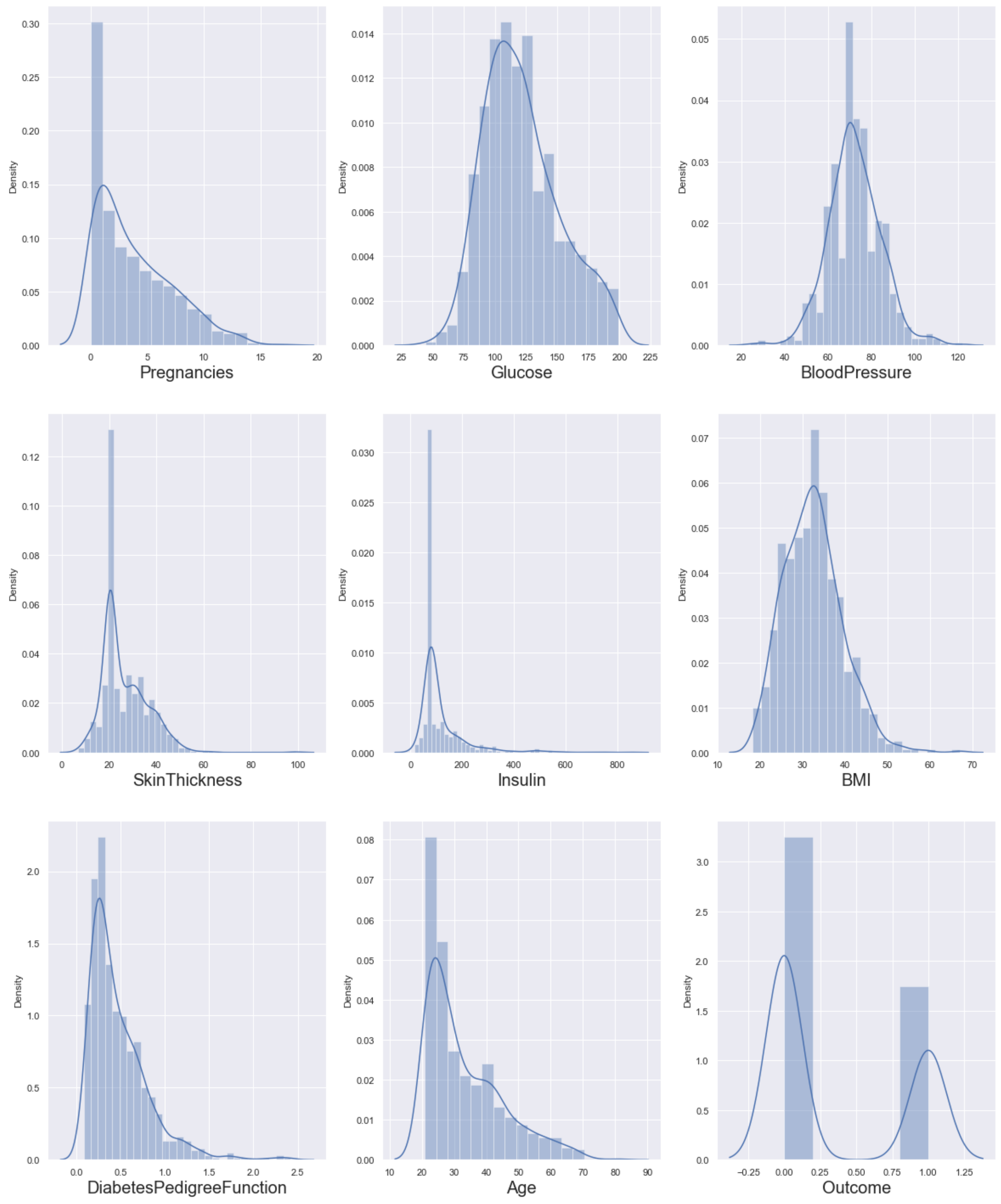


We can see there is some skewness in the data, let's deal with data.

Also, we can see there few data for columns Glucose , Insulin, skin thickenss, BMI and Blood Pressure which have value as 0. That's not possible,right? you can do a quick search to see that one cannot have 0 values for these. Let's deal with that. we can either remove such data or simply replace it with their respective mean values. Let's do the latter.

In [64]:
```
# replacing zero values with the mean of the column
data['BMI'] = data['BMI'].replace(0,data['BMI'].mean())
data['BloodPressure'] = data['BloodPressure'].replace(0,data['BloodPressure'].mean())
data['Glucose'] = data['Glucose'].replace(0,data['Glucose'].mean())
data['Insulin'] = data['Insulin'].replace(0,data['Insulin'].mean())
data['SkinThickness'] = data['SkinThickness'].replace(0,data['SkinThickness'].mean())
#pregrnancies data also look skewed towards left because of some outliers, let's remove them
# q = data['Pregnancies'].quantile(0.95)
# data_cleaned = data[data['Pregnancies']<q]

```

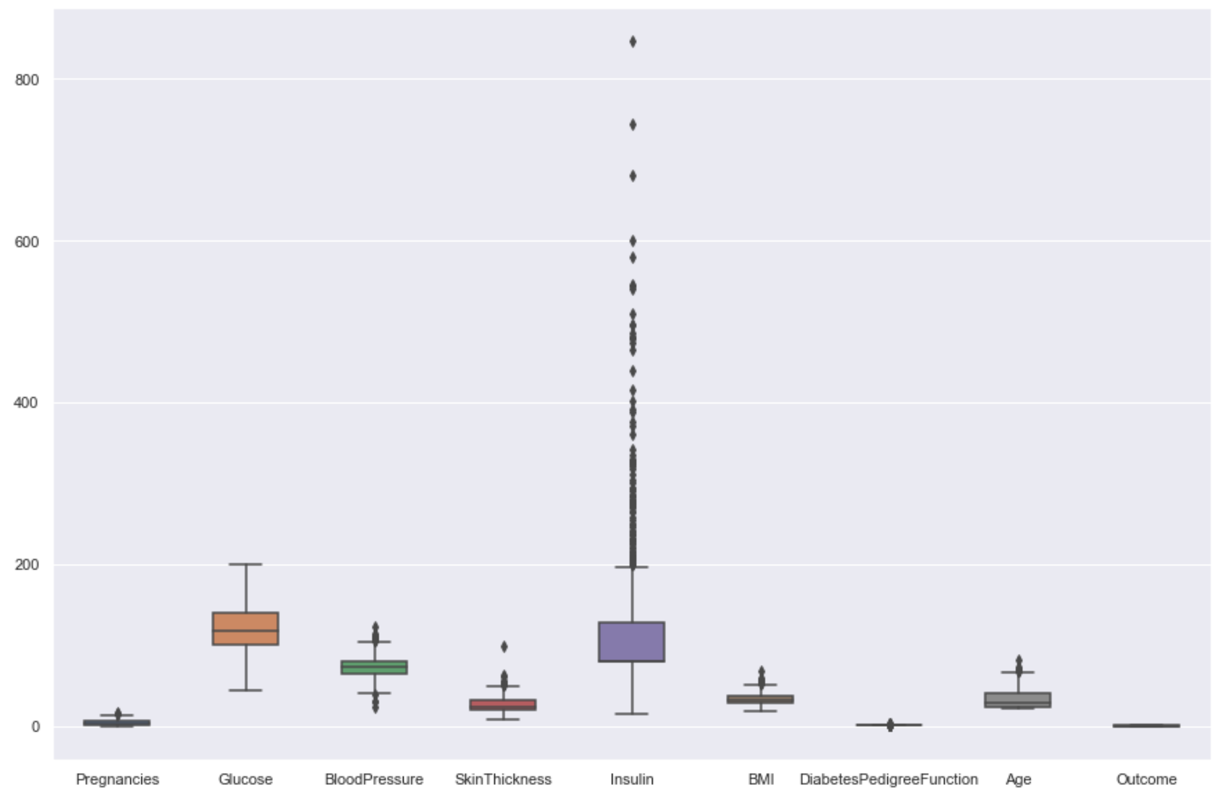
In [65]:
```
# let's see how data is distributed for every column
plt.figure(figsize=(20,25), facecolor='white')
plotnumber = 1

for column in data:
    if plotnumber<=9 :
        ax = plt.subplot(3,3,plotnumber)
        sns.distplot(data[column])
        plt.xlabel(column,fontsize=20)
        #plt.ylabel('Salary',fontsize=20)
    plotnumber+=1
plt.show()
```



Great, now we have dealt with the 0 values and data looks better. But, there still are outliers present in some columns. let's deal with them.

In [66]:
```
fig,ax = plt.subplots(figsize= (15,10))
sns.boxplot(data = data ,width = 0.5 , ax = ax,fliersize = 5)
```

Out[66]: <AxesSubplot:>



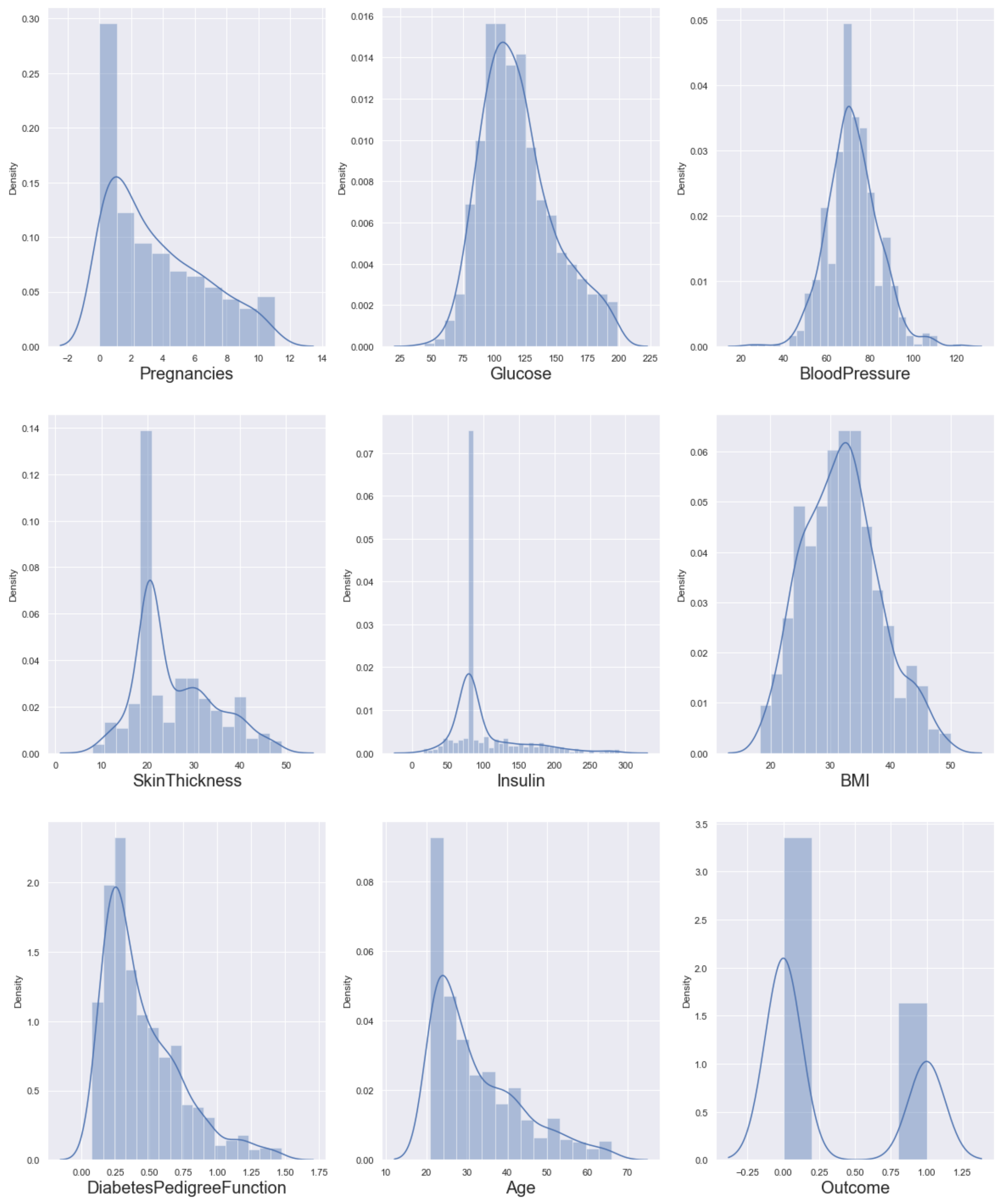
In [67]:
```
q = data['Pregnancies'].quantile(0.98)
# we are removing the top 2% data from the Pregnancies column
data_cleaned = data[data['Pregnancies']<q]
q = data_cleaned['BMI'].quantile(0.99)
# we are removing the top 1% data from the BMI column
data_cleaned  = data_cleaned[data_cleaned['BMI']<q]
q = data_cleaned['SkinThickness'].quantile(0.99)
# we are removing the top 1% data from the SkinThickness column
data_cleaned  = data_cleaned[data_cleaned['SkinThickness']<q]
q = data_cleaned['Insulin'].quantile(0.95)
# we are removing the top 5% data from the Insulin column
data_cleaned  = data_cleaned[data_cleaned['Insulin']<q]
q = data_cleaned['DiabetesPedigreeFunction'].quantile(0.99)
# we are removing the top 1% data from the DiabetesPedigreeFunction column
data_cleaned  = data_cleaned[data_cleaned['DiabetesPedigreeFunction']<q]
q = data_cleaned['Age'].quantile(0.99)
# we are removing the top 1% data from the Age column
data_cleaned  = data_cleaned[data_cleaned['Age']<q]
```

yaha mujhe doubt hai ki ek column k outlier ko nikalne k chakker me baki ke column bhi uda diye , toh kya ye sahi tarika hai?

In [68]:
```
data.shape
```
Out[68]:
```
(768, 9)
```

In [69]:
```
data_cleaned.shape
```
Out[69]:
```
(674, 9)
```

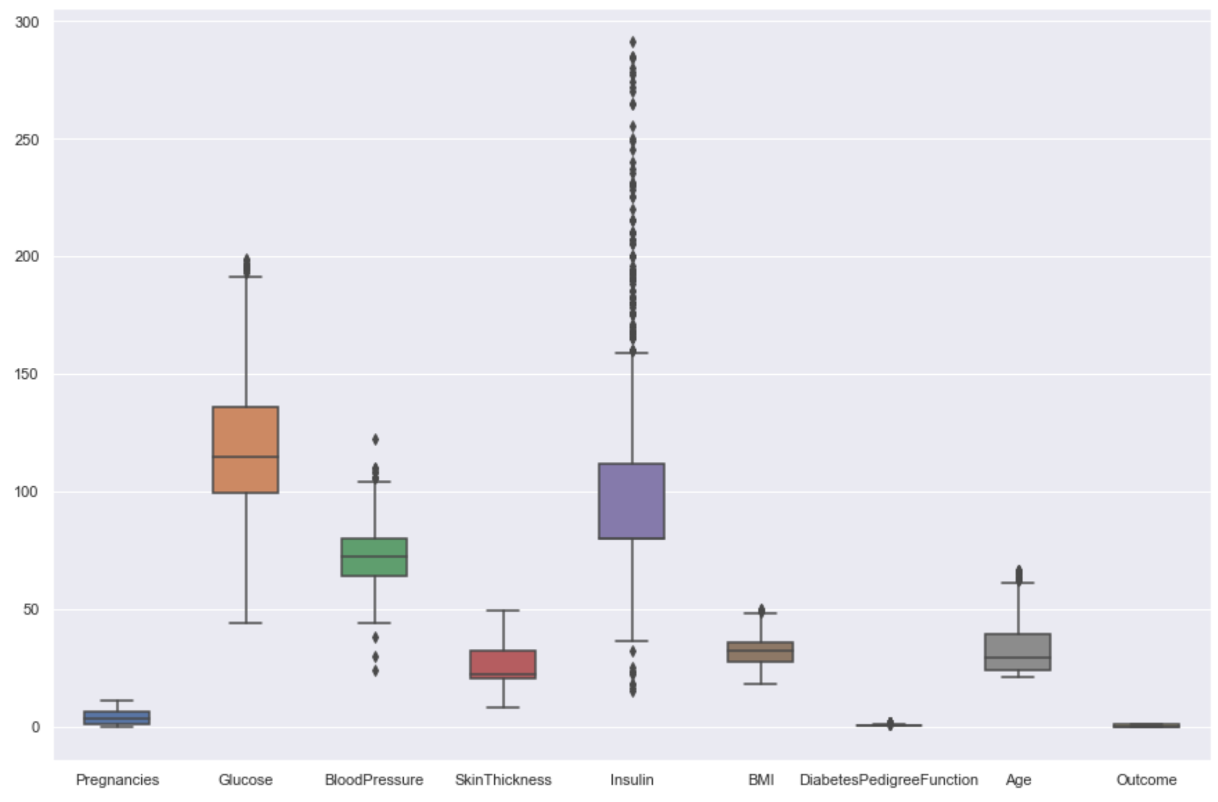
In [70]:
```
# let's see how data is distributed for every column
plt.figure(figsize=(20,25), facecolor='white')
plotnumber = 1

for column in data_cleaned:
    if plotnumber<=9 :
        ax = plt.subplot(3,3,plotnumber)
        sns.distplot(data_cleaned[column])
        plt.xlabel(column,fontsize=20)
        #plt.ylabel('Salary',fontsize=20)
    plotnumber+=1
plt.show()

```



The data looks much better now than before. We will start our analysis with this data now as we don't want to loose important information. If our model doesn't work with accuracy, we will come back for more preprocessing.

In [71]:
```
fig,ax = plt.subplots(figsize= (15,10))
sns.boxplot(data = data_cleaned ,width = 0.5 , ax = ax,fliersize = 5)
```

Out[71]:
```
<AxesSubplot:>
```



In [72]:
```
# we can try log transformatiion or box-cox
```

In [73]:
```
X = data_cleaned.drop(columns = ['Outcome'])
y = data_cleaned['Outcome']
```

In [74]:
```
X.head()
```

Out[74]:

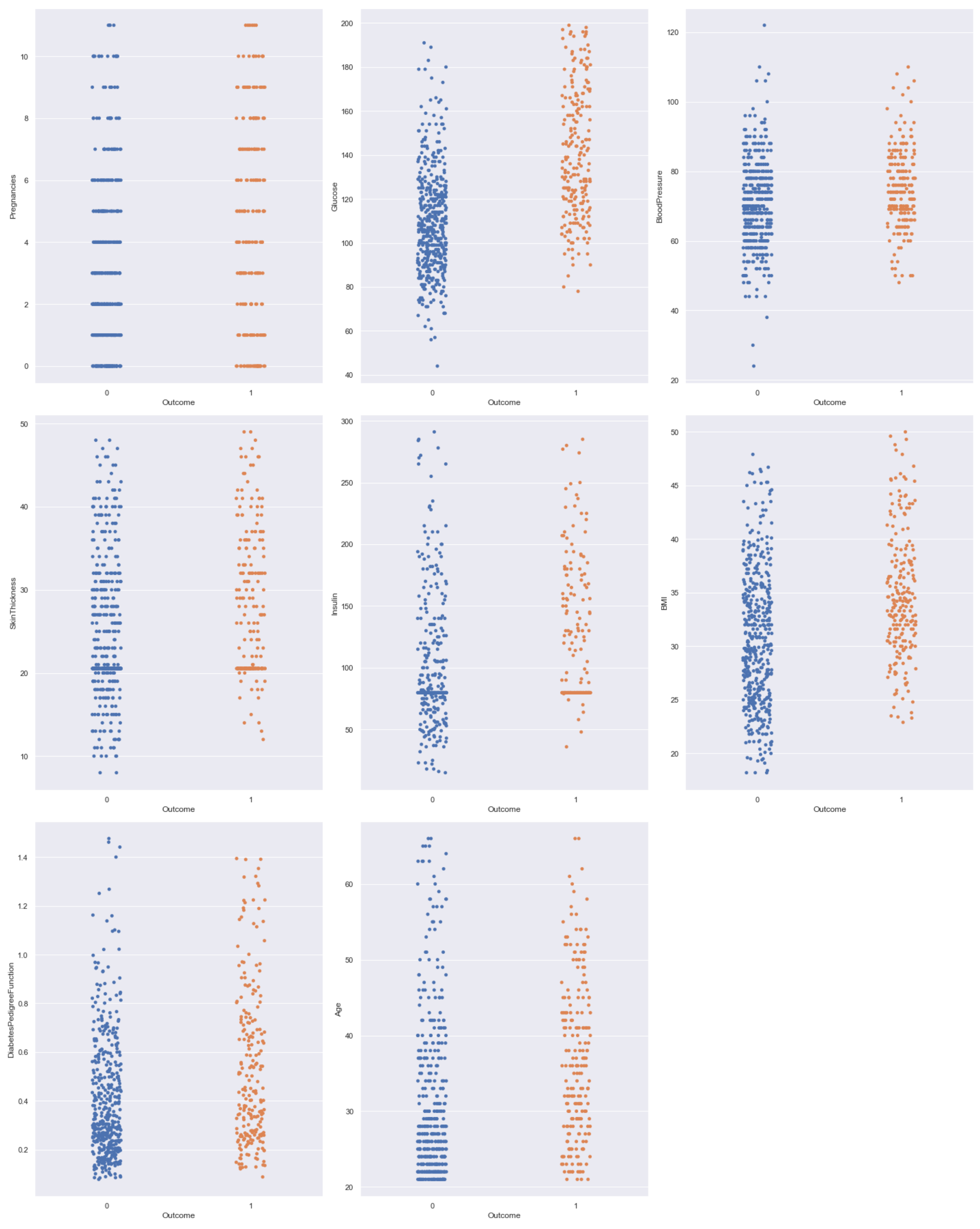
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
0	6	148.0	72.0	35.000000	79.799479	33.6	0.62
1	1	85.0	66.0	29.000000	79.799479	26.6	0.35
2	8	183.0	64.0	20.536458	79.799479	23.3	0.67
3	1	89.0	66.0	23.000000	94.000000	28.1	0.16
5	5	116.0	74.0	20.536458	79.799479	25.6	0.20

In [75]:
```
y.head()
```

Out[75]:
```
0    1
1    0
2    1
3    0
5    0
Name: Outcome, dtype: int64
```

Before we fit our data to a model, let's visualize the relationship between our independent variables and the categories.

In [76]:
```
# let's see how data is distributed for every column
plt.figure(figsize=(20,25), facecolor='white')
plotnumber = 1

for column in X:
    if plotnumber<=9 :
        ax = plt.subplot(3,3,plotnumber)
        sns.stripplot(y,X[column])
        #plt.xlabel(column,fontsize=20)
        #plt.ylabel('Salary',fontsize=20)
    plotnumber+=1
plt.tight_layout()
```



Great!! Let's proceed with checking multicollineairty in the dependent variables. Before that, we should scale our data. Let's use standardscaler for that.

In [77]:
```
scalar = StandardScaler()
X_scaled = scalar.fit_transform(X)
```

This is how our data looks now after scaling. Great, now we will check for multicollinearity using VIF(Variance Inflation factor)

In [78]:
```
X_scaled
```

Out[78]:
```
array([[ 7.96753910e-01,  9.83984062e-01,  4.52611463e-04, ...,
         2.65819648e-01,  6.30484542e-01,  1.60141519e+00],
       [-8.64793539e-01, -1.16977621e+00, -5.04474494e-01, ...,
        -8.31445036e-01, -3.38078670e-01, -1.32706484e-01],
       [ 1.46137289e+00,  2.18051755e+00, -6.72783529e-01, ...,
        -1.34872696e+00,  7.88402456e-01, -4.14369227e-02],
       ...,
       [ 4.64444420e-01,  6.09439465e-02,  4.52611463e-04, ...,
        -8.94145875e-01, -7.10063091e-01, -2.23976046e-01],
       [-8.64793539e-01,  2.31877301e-01, -1.00940160e+00, ...,
        -2.82812694e-01, -3.45097244e-01,  1.32760650e+00],
       [-8.64793539e-01, -8.96282840e-01, -1.67856424e-01, ...,
        -2.35787064e-01, -4.64413001e-01, -8.62862978e-01]])
```

In [79]:
```
#multicoliner propertie
vif = pd.DataFrame()
vif["vif"] = [variance_inflation_factor(X_scaled,i) for i in range(X_scaled.shape[1])]
vif["Features"] = X.columns

#let's check the values
vif

```

Out[79]:

	vif	Features
0	1.449056	Pregnancies
1	1.304263	Glucose
2	1.262686	BloodPressure
3	1.470049	SkinThickness
4	1.271017	Insulin
5	1.513160	BMI
6	1.042300	DiabetesPedigreeFunction
7	1.662728	Age

Great, all the vif values are less than 5 and are very low. That means no multicollinearity. Now we can go ahead with fitting our data in the model. Before that let's split our data in test and training set.

In [ ]:
```
# agar 5 se jada hai toh vo column remove kr stke hai , tho uske liye Correlaton check karege
# jiska bhi corr "y"  k sath jada hoga usko rehne dege baki ko remove kardege
# ek or chiz sikhi ki 2 column ko multply krdiya or jo column VIF high btare the dono ko hta diy
#(check youtube Unfold Data Science)
```

In [80]:
```
x_train,x_test,y_train,y_test = train_test_split(X_scaled,y, test_size= 0.25, random_state = 35
```

In [81]:
```
log_reg = LogisticRegression()

log_reg.fit(x_train,y_train)
```

Out[81]:
```
LogisticRegression()
```

In [82]:
```
## model saving or pickling our model
import pickle
with open('modelforprediction','wb') as f:
    pickle.dump(log_reg,f)

with open('standardscalar.sav','wb')  as f:
    pickle.dump(scalar,f)

'''with open('modelforprediction','rb') as f:
    pickle.load(f)'''   # to load the model
```

Out[82]:
```
"with open('modelforprediction','rb') as f:\n    pickle.load(f)"
```

In [83]:
```
# r2 score
log_reg.score(x_train,y_train)
```

Out[83]:
```
0.7742574257425743
```

In [84]:
```
# adj_r2 score

adj_r2(x_train,y_train,log_reg.score(x_train,y_train))
```

Out[84]:
```
0.7706164164803577
```

Great, our adjusted r2 score is almost same as r2 score, thus we are not being penalized for use of many features.

let's see how well our model performs on the test data set.

In [85]:
```
y_pred = log_reg.predict(x_test)
```

In [86]:
```
accuracy = accuracy_score(y_test,y_pred)
accuracy
```

Out[86]:
```
0.834319526627219
```

In [87]:
```
conf_mat = confusion_matrix(y_test,y_pred)
conf_mat
```

Out[87]:
```
array([[109,   8],
       [ 20,  32]], dtype=int64)
```

In [88]:
```
true_positive = conf_mat[0][0]
false_positive = conf_mat[0][1]
false_negative = conf_mat[1][0]
true_negative = conf_mat[1][1]
```

In [89]:
```
Accuracy = (true_positive + true_negative) / (true_positive +false_positive + false_negative + t
Accuracy
```

Out[89]:
```
0.834319526627219
```

In [90]:
```
Precision = true_positive/(true_positive+false_positive)
Precision
```

Out[90]:
```
0.9316239316239316
```

In [91]:
```
Recall = true_positive/(true_positive+false_negative)
Recall
```

Out[91]:
```
0.8449612403100775
```

In [92]:
```
F1_Score = 2*(Recall * Precision) / (Recall + Precision)
F1_Score
```

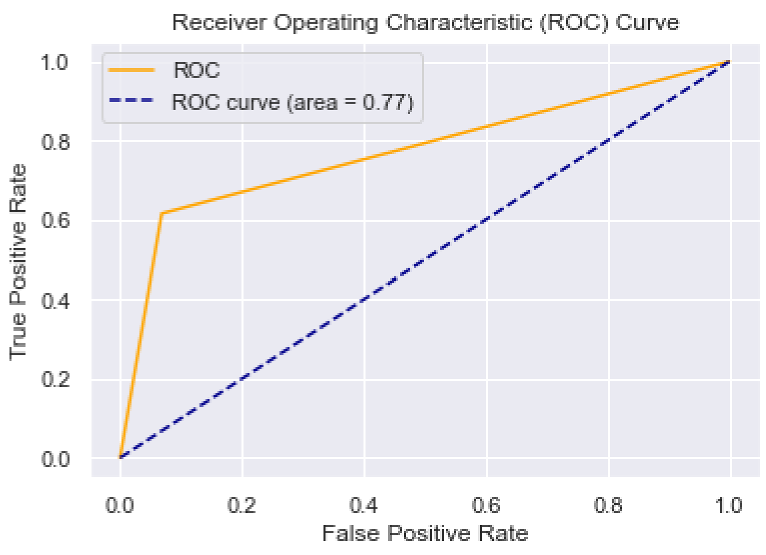
Out[92]:
```
0.8861788617886178
```

In [93]:
```
auc = roc_auc_score(y_test, y_pred)
auc
```

Out[93]:
```
0.7735042735042735
```

In [94]:
```
fpr, tpr, thresholds = roc_curve(y_test, y_pred)
```

In [95]:
```
plt.plot(fpr, tpr, color='orange', label='ROC')
plt.plot([0, 1], [0, 1], color='darkblue', linestyle='--',label='ROC curve (area = %0.2f)' % auc)
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.legend()
plt.show()
```



In [ ]:
```

```