Supervised Learning - Project

In this Project, we are going to perform a full supervised learning machine learning project on a "Diabetes" 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 a patient has diabetes, based on certain diagnostic measurements included in the dataset.

Kaggle Dataset

Part I : EDA - Exploratory Data Analysis

For this task, you are required to conduct an exploratory data analysis on the diabetes dataset. You have the freedom to choose the visualizations you want to use, but your analysis should cover the following tasks mostly:

- Are there any missing values in the dataset?
- How are the predictor variables related to the outcome variable?
- What is the correlation between the predictor variables?
- What is the distribution of each predictor variable?
- Are there any outliers in the predictor variables?
- How are the predictor variables related to each other?
- Is there any interaction effect between the predictor variables?
- What is the average age of the individuals in the dataset?
- What is the average glucose level for individuals with diabetes and without diabetes?
- What is the average BMI for individuals with diabetes and without diabetes?
- How does the distribution of the predictor variables differ for individuals with diabetes and without diabetes?
- Are there any differences in the predictor variables between males and females (if gender information is available)?

In [ ]:

```
import pandas as pd
from matplotlib import pyplot as plt
import plotly.express as px
import numpy as np
import seaborn as sns
import statistics
from scipy import stats
import statsmodels.api as sm
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import log_loss, roc_auc_score, recall_score, precision_score,
```

In [ ]:
```python
df = pd.read_csv('diabetes.csv')
df.head()
```

Out[ ]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunc
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	2

In [ ]:
```python
df.describe()
# Avg age is 33 years old
```

Out[ ]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Dial
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 [ ]:
```python
df[(df['Outcome']== 1)].mean()
# Average glucose level for individuals with diabetes is 141
# Average BMI for individuals with diabetes is 35
```

Out[ ]:
```
Pregnancies                   4.865672
Glucose                     141.257463
BloodPressure                70.824627
SkinThickness                22.164179
Insulin                     100.335821
BMI                          35.142537
DiabetesPedigreeFunction      0.550500
Age                          37.067164
Outcome                       1.000000
dtype: float64
```

In [ ]:
```python
df[(df['Outcome']== 0)].mean()
# Average glucose level for individuals without diabetes is 110
# Average BMI for individuals without diabetes is 30
```

```
Out[ ]: Pregnancies                   3.298000
        Glucose                     109.980000
        BloodPressure                68.184000
        SkinThickness                19.664000
        Insulin                      68.792000
        BMI                          30.304200
        DiabetesPedigreeFunction      0.429734
        Age                          31.190000
        Outcome                       0.000000
        dtype: float64
```

```
In [ ]: df.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 [ ]: # There is no missing value
        df.isnull().sum()
        # no
```

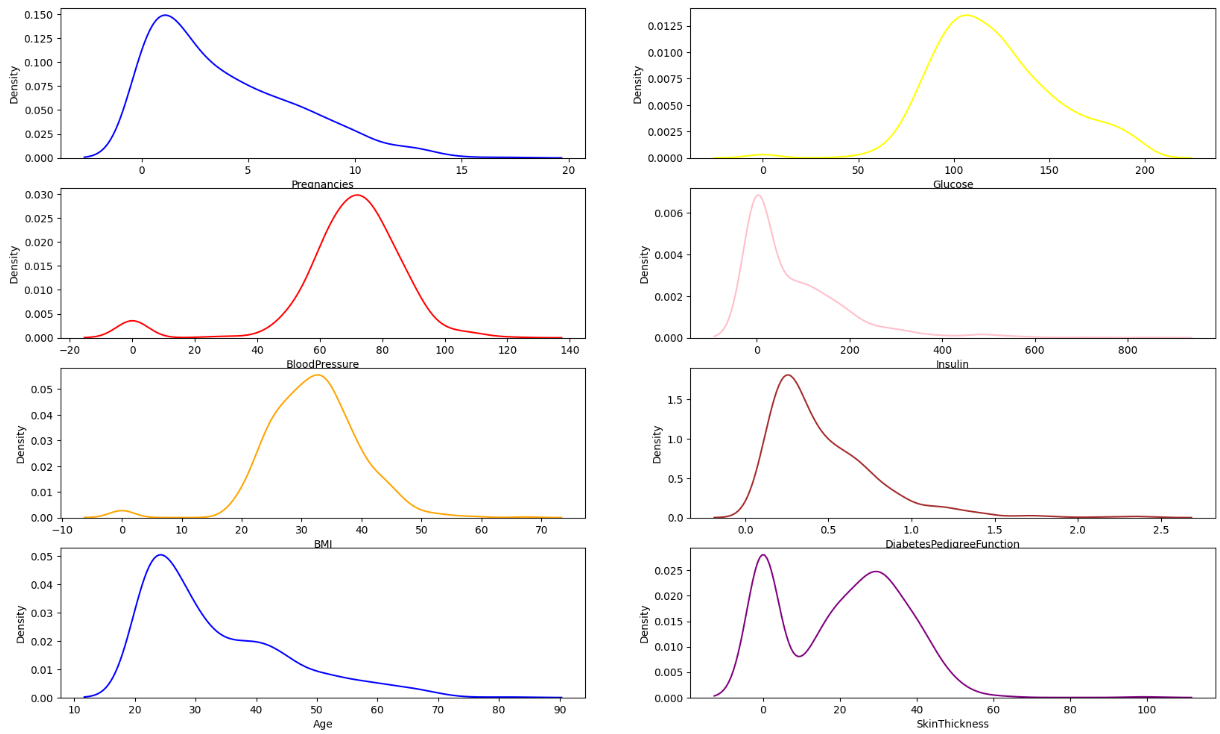
```
Out[ ]: Pregnancies                 0
        Glucose                     0
        BloodPressure               0
        SkinThickness               0
        Insulin                     0
        BMI                         0
        DiabetesPedigreeFunction    0
        Age                   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

```
In [ ]: # No duplication
        df.duplicated().sum()
```

```
Out[ ]: 0
```

```
In [ ]: fig, axes = plt.subplots(nrows=4, ncols=2, figsize=(20, 12))
        ax = sns.kdeplot(data=df, x="Pregnancies", ax=axes[0,0], color='blue')
        ax = sns.kdeplot(data=df, x="Glucose", ax=axes[0,1], color='yellow')
        ax = sns.kdeplot(data=df, x="BloodPressure", ax=axes[1,0], color='red')
        ax = sns.kdeplot(data=df, x="Insulin", ax=axes[1,1], color='pink')
        ax = sns.kdeplot(data=df, x="BMI", ax=axes[2,0], color='orange')
```

```
ax = sns.kdeplot(data=df, x="DiabetesPedigreeFunction", ax=axes[2,1], color='brown'
ax = sns.kdeplot(data=df, x="Age", ax=axes[3,0], color='blue')
ax = sns.kdeplot(data=df, x="SkinThickness", ax=axes[3,1], color='purple')
```



In [ ]:
```
stat, p = stats.shapiro(df['BMI'])
print('%0.30f' % p)
if p > 0.05:
    print('Probably normally distributed')
else:
    print('Probably not normally distributed')
```

```
0.000000000000001840758660204126
Probably not normally distributed
```

In [ ]:
```
stat, p = stats.shapiro(df['Glucose'])
print('%0.30f' % p)
if p > 0.05:
    print('Probably normally distributed')
else:
    print('Probably not normally distributed')
```

```
0.000000000019874648801709859924
Probably not normally distributed
```

Part II : Preprocessing & Feature Engineering

You need to perform preprocessing on the given dataset. Please consider the following tasks and carry out the necessary steps accordingly.

- Handling missing values

- Handling outliers
- Scaling and normalization
- Feature Engineering
- Handling imbalanced data

In [ ]:
```
# there is one outlier (Glucose = 0)
fig = px.box(df, y='Glucose',width=600, height=400)
fig.show()
```

In [ ]:
```
df[df['Glucose']== 0]
```

Out[ ]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFu
75	1	0	48	20	0	24.7	
182	1	0	74	20	23	27.7	
342	1	0	68	35	0	32.0	
349	5	0	80	32	0	41.0	
502	6	0	68	41	0	39.0	

In [ ]:
```
df_G_1 = df[(df['Glucose'] > 0) & (df['Outcome']== 1)]
df_G_0 = df[(df['Glucose'] > 0) & (df['Outcome']== 0)]
```

In [ ]:
```
# Glucose level can't be zero, so will impute the value using the median becuase gl
df['Glucose'] = df.apply(lambda x:statistics.median(df_G_1['Glucose']) if ((x['Gluc
df['Glucose'] = df.apply(lambda x:statistics.median(df_G_0['Glucose']) if ((x['Gluc
```

In [ ]:
```
# There are some outliers in BloodPressure
fig = px.box(df, y='BloodPressure',width=600, height=400)
fig.show()
```

In [ ]:
```
df[df['BloodPressure']== 0]
```

Out[ ]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFu
7	10	115.0	0	0	0	35.3	
15	7	100.0	0	0	0	30.0	
49	7	105.0	0	0	0	0.0	
60	2	84.0	0	0	0	0.0	
78	0	131.0	0	0	0	43.2	
81	2	74.0	0	0	0	0.0	
172	2	87.0	0	23	0	28.9	
193	11	135.0	0	0	0	52.3	
222	7	119.0	0	0	0	25.2	
261	3	141.0	0	0	0	30.0	
266	0	138.0	0	0	0	36.3	
269	2	146.0	0	0	0	27.5	
300	0	167.0	0	0	0	32.3	
332	1	180.0	0	0	0	43.3	
336	0	117.0	0	0	0	33.8	
347	3	116.0	0	0	0	23.5	
357	13	129.0	0	30	0	39.9	
426	0	94.0	0	0	0	0.0	
430	2	99.0	0	0	0	22.2	
435	0	141.0	0	0	0	42.4	
453	2	119.0	0	0	0	19.6	
468	8	120.0	0	0	0	30.0	
484	0	145.0	0	0	0	44.2	
494	3	80.0	0	0	0	0.0	
522	6	114.0	0	0	0	0.0	
533	6	91.0	0	0	0	29.8	
535	4	132.0	0	0	0	32.9	
589	0	73.0	0	0	0	21.1	
601	6	96.0	0	0	0	23.7	
604	4	183.0	0	0	0	28.4	

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFu
619	0	119.0	0	0	0	32.4	
643	4	90.0	0	0	0	28.0	
697	0	99.0	0	0	0	25.0	
703	2	129.0	0	0	0	38.5	
706	10	115.0	0	0	0	0.0	

In [ ]:
```
df_B_1 = df[(df['BloodPressure'] > 0) & (df['Outcome']== 1)]
df_B_0 = df[(df['BloodPressure'] > 0) & (df['Outcome']== 0)]
```

In [ ]:
```
# BloodPressure level can't be zero, so will impute the value using the median becu
df['BloodPressure'] = df.apply(lambda x:statistics.median(df_B_1['BloodPressure'])
df['BloodPressure'] = df.apply(lambda x:statistics.median(df_B_0['BloodPressure'])
```

In [ ]:
```
# There are some outliers in Age, but it's okay
fig = px.box(df, y='Age',width=600, height=400)
fig.show()
```

In [ ]:
```
# There are some outliers in inaulin
fig = px.box(df, y='Insulin',width=600, height=400)
fig.show()
```

In [ ]:
```
fig = px.box(df, y='BMI',width=600, height=400)
fig.show()
```

In [ ]:
```
df[df['BMI']== 0]
```

Out[ ]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFu
9	8	125.0	96.0	0	0	0.0	
49	7	105.0	70.0	0	0	0.0	
60	2	84.0	70.0	0	0	0.0	
81	2	74.0	70.0	0	0	0.0	
145	0	102.0	75.0	23	0	0.0	
371	0	118.0	64.0	23	89	0.0	
426	0	94.0	70.0	0	0	0.0	
494	3	80.0	70.0	0	0	0.0	
522	6	114.0	70.0	0	0	0.0	
684	5	136.0	82.0	0	0	0.0	
706	10	115.0	74.5	0	0	0.0	

In [ ]:

```
df_BMI_1 = df[(df['BMI'] > 0) & (df['Outcome']== 1)]
df_BMI_0 = df[(df['BMI'] > 0) & (df['Outcome']== 0)]
```

In [ ]:

```
# BMI level can't be zero, so will impute the value using the median
df['BMI'] = df.apply(lambda x:statistics.median(df_BMI_1['BMI']) if ((x['BMI'] ==0)
df['BMI'] = df.apply(lambda x:statistics.median(df_BMI_0['BMI']) if ((x['BMI'] ==0)
```

In [ ]:

```
fig = px.box(df, y='DiabetesPedigreeFunction',width=600, height=400)
fig.show()
```

In [ ]:

```
fig = px.box(df, y='Pregnancies',width=600, height=400)
fig.show()
```

In [ ]:

```
fig = px.box(df, y='SkinThickness',width=600, height=400)
fig.show()
```

In [ ]:

```
df[df['SkinThickness']== 0]
```

Out[ ]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFu
2	8	183.0	64.0	0	0	23.3	
5	5	116.0	74.0	0	0	25.6	
7	10	115.0	70.0	0	0	35.3	
9	8	125.0	96.0	0	0	34.3	
10	4	110.0	92.0	0	0	37.6	
...	...	...	...	...	...	...	
757	0	123.0	72.0	0	0	36.3	
758	1	106.0	76.0	0	0	37.5	
759	6	190.0	92.0	0	0	35.5	
762	9	89.0	62.0	0	0	22.5	
766	1	126.0	60.0	0	0	30.1	

227 rows × 9 columns

In [ ]:

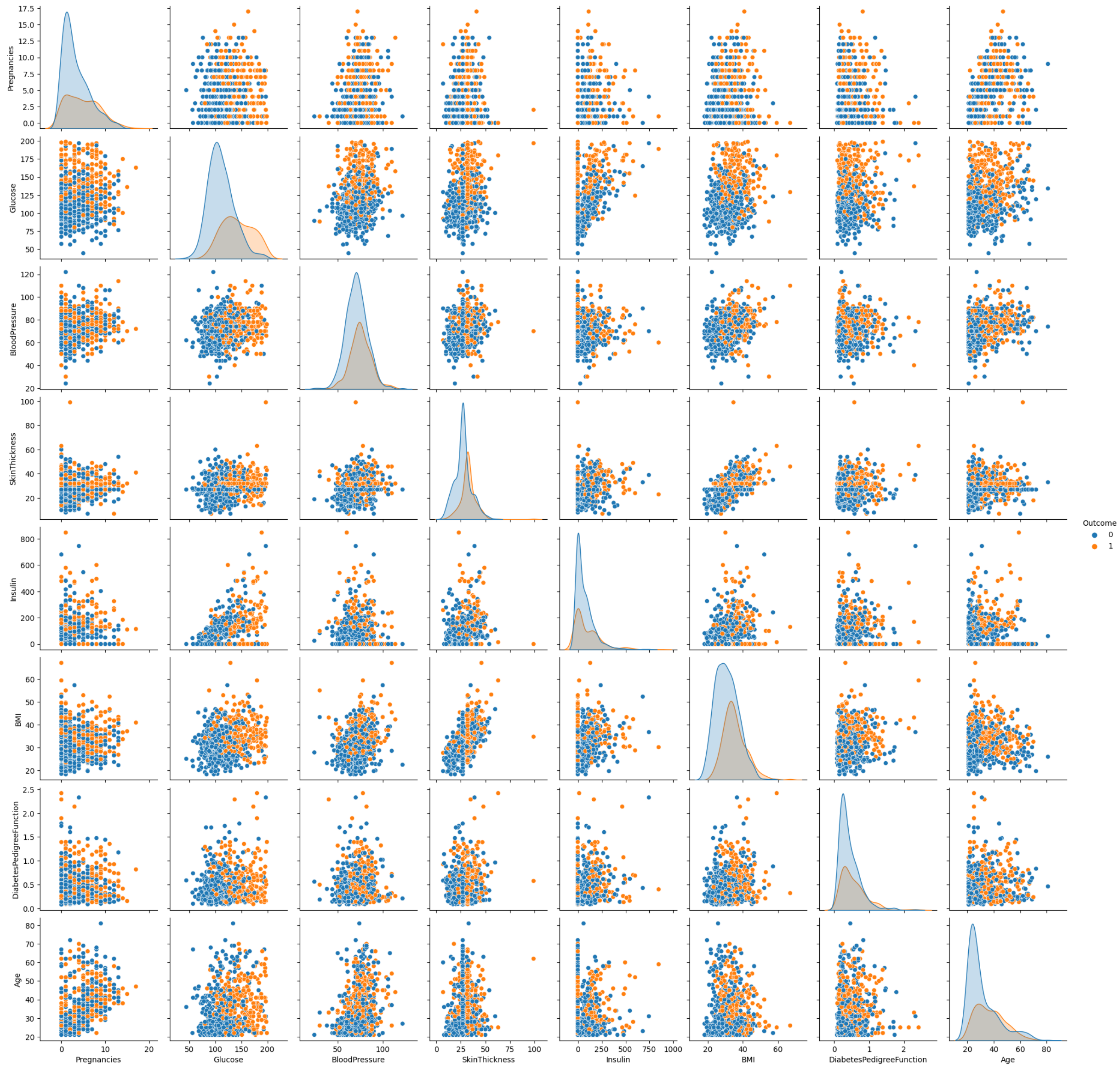
```
df_ST_1 = df[(df['SkinThickness'] > 0) & (df['Outcome']== 1)]
df_ST_0 = df[(df['SkinThickness'] > 0) & (df['Outcome']== 0)]
```

In [ ]:

```
# SkinThickness level can't be zero, so will impute the value using the median becu
df['SkinThickness'] = df.apply(lambda x:statistics.median(df_ST_1['SkinThickness'])
df['SkinThickness'] = df.apply(lambda x:statistics.median(df_ST_0['SkinThickness'])
```

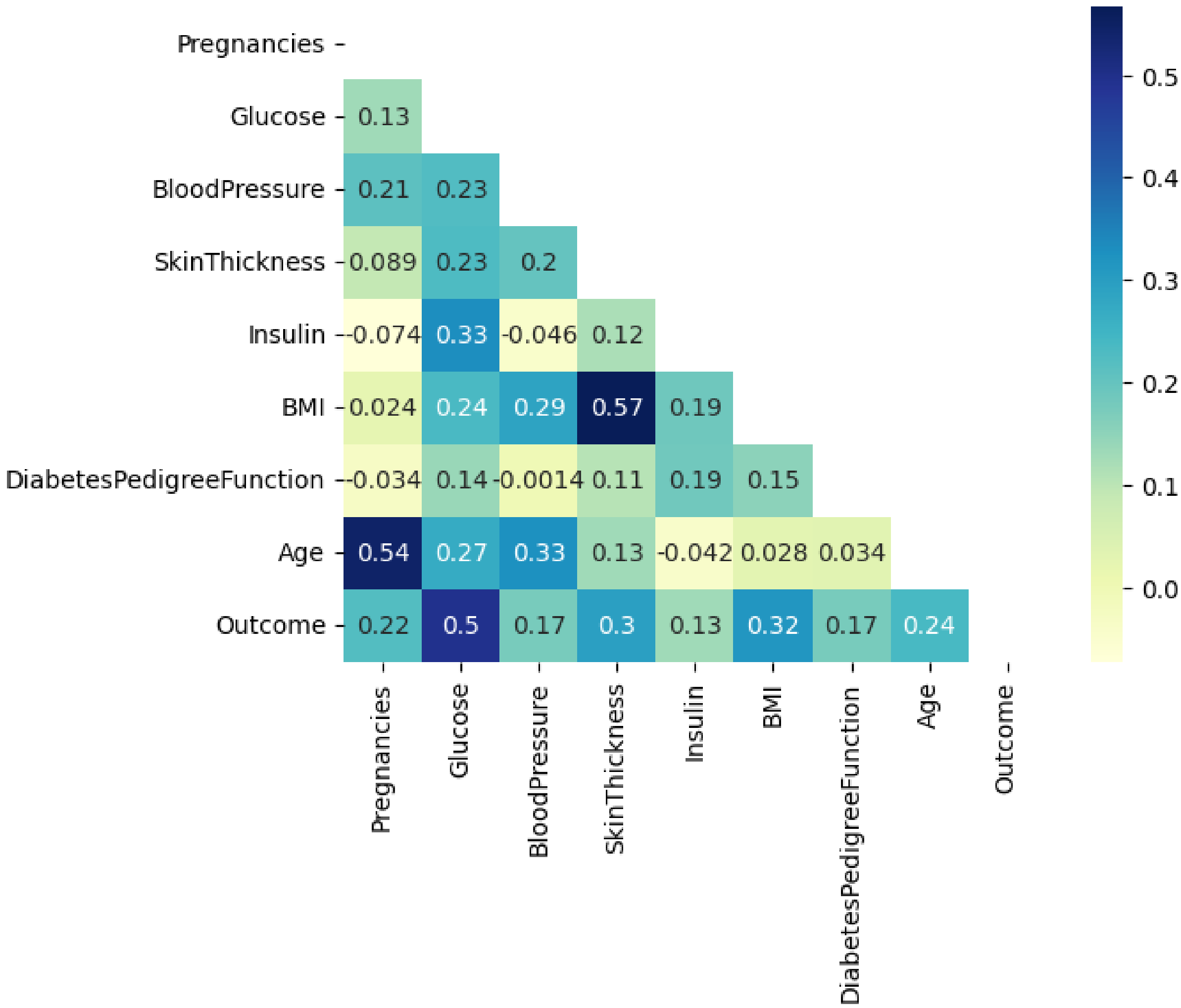
In [ ]:

```
sns.pairplot(df, hue="Outcome")
plt.show()
```



In [ ]:

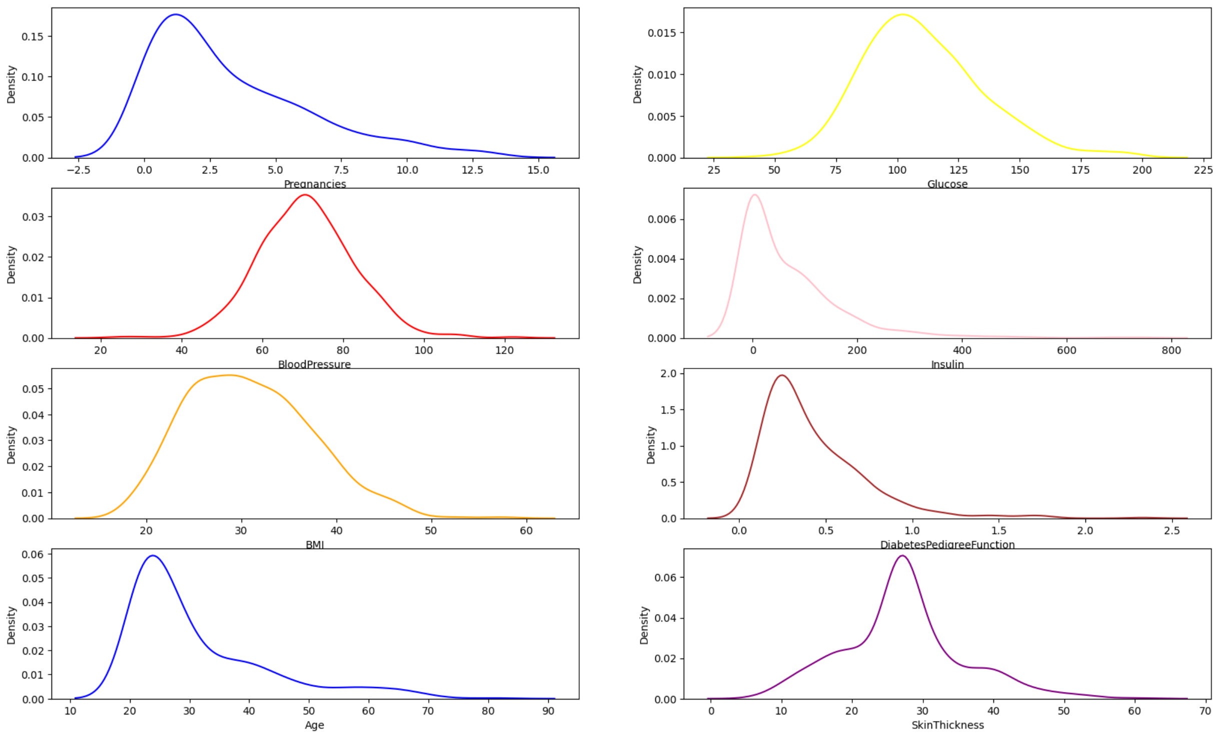
```
mask = np.triu(np.ones_like(df.corr(), dtype=bool))
#df.corr()
dataplot = sns.heatmap(df.corr(), mask=mask, cmap="YlGnBu", annot=True)
plt.show()
```



There is a correalion between Age & Pregancies, SkinThickness & BMI, Glucose & Outcome

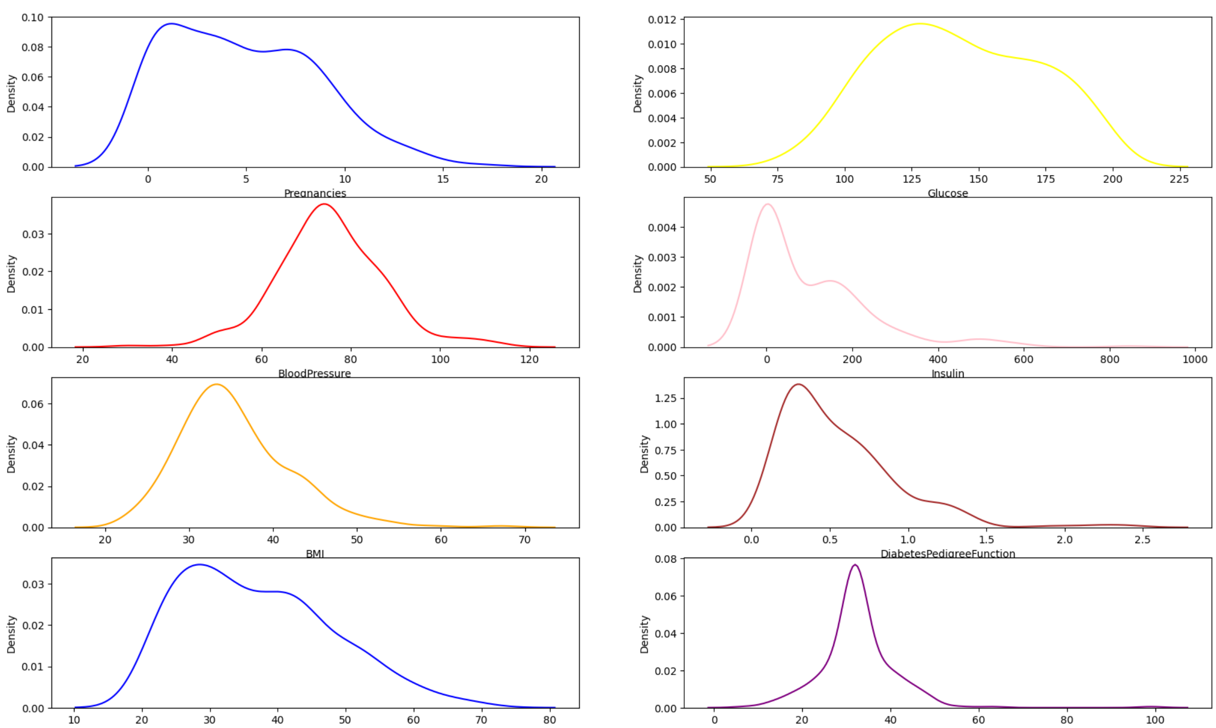
In [ ]:
```
df_0 = df[df.Outcome == 0] # without diabetes
df_1 = df[df.Outcome == 1] # with diabetes
```

In [ ]:
```
# without diabetes distribution
fig, axes = plt.subplots(nrows=4, ncols=2, figsize=(20, 12))
ax = sns.kdeplot(data=df_0, x="Pregnancies", ax=axes[0,0], color='blue')
ax = sns.kdeplot(data=df_0, x="Glucose", ax=axes[0,1], color='yellow')
ax = sns.kdeplot(data=df_0, x="BloodPressure", ax=axes[1,0], color='red')
ax = sns.kdeplot(data=df_0, x="Insulin", ax=axes[1,1], color='pink')
ax = sns.kdeplot(data=df_0, x="BMI", ax=axes[2,0], color='orange')
ax = sns.kdeplot(data=df_0, x="DiabetesPedigreeFunction", ax=axes[2,1], color='brow
ax = sns.kdeplot(data=df_0, x="Age", ax=axes[3,0], color='blue')
ax = sns.kdeplot(data=df_0, x="SkinThickness", ax=axes[3,1], color='purple')
```



In [ ]:

```python
# with diabetes distribution
fig, axes = plt.subplots(nrows=4, ncols=2, figsize=(20, 12))
ax = sns.kdeplot(data=df_1, x="Pregnancies", ax=axes[0,0], color='blue')
ax = sns.kdeplot(data=df_1, x="Glucose", ax=axes[0,1], color='yellow')
ax = sns.kdeplot(data=df_1, x="BloodPressure", ax=axes[1,0], color='red')
ax = sns.kdeplot(data=df_1, x="Insulin", ax=axes[1,1], color='pink')
ax = sns.kdeplot(data=df_1, x="BMI", ax=axes[2,0], color='orange')
ax = sns.kdeplot(data=df_1, x="DiabetesPedigreeFunction", ax=axes[2,1], color='brow
ax = sns.kdeplot(data=df_1, x="Age", ax=axes[3,0], color='blue')
ax = sns.kdeplot(data=df_1, x="SkinThickness", ax=axes[3,1], color='purple')
```



In [ ]:
```
fig = px.histogram(df, x='Outcome', color_discrete_map= {1:'orange', 2:'green'}, co
fig.show()
# dataset is imbalanced
```

In [ ]:
```
# Separate features from target
X = df[['Pregnancies','Glucose','BloodPressure','SkinThickness','Insulin','BMI','Di
y= df['Outcome']
```

In [ ]:
```
# Scale the data
from sklearn import preprocessing
MinMaxScaler = preprocessing.MinMaxScaler()
X_minmax = MinMaxScaler.fit_transform(X)
```

In [ ]:
```
X = pd.DataFrame(X_minmax,columns=['Pregnancies','Glucose','BloodPressure','SkinThi
X.head()
```

Out[ ]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigr
0	0.352941	0.670968	0.489796	0.304348	0.000000	0.314928	
1	0.058824	0.264516	0.428571	0.239130	0.000000	0.171779	
2	0.470588	0.896774	0.408163	0.271739	0.000000	0.104294	
3	0.058824	0.290323	0.428571	0.173913	0.111111	0.202454	
4	0.000000	0.600000	0.163265	0.304348	0.198582	0.509202	

In [ ]:
```
mn = sm.MNLogit(y,sm.add_constant(X))
```

In [ ]:
```
model = mn.fit()
print_model = model.summary()
print(print_model)
```

```
Optimization terminated successfully.
         Current function value: 0.456015
         Iterations 6
                          MNLogit Regression Results
==============================================================================
Dep. Variable:                Outcome   No. Observations:                  768
Model:                        MNLogit   Df Residuals:                      759
Method:                           MLE   Df Model:                            8
Date:                Thu, 03 Aug 2023   Pseudo R-squ.:                  0.2950
Time:                        23:19:54   Log-Likelihood:                -350.22
converged:                       True   LL-Null:                       -496.74
Covariance Type:            nonrobust   LLR p-value:                 1.243e-58
====================================================================================
========
               Outcome=1       coef    std err          z      P>|z|      [0.025
0.975]
------------------------------------------------------------------------------------
--------
const                      -6.1411      0.549    -11.192      0.000      -7.216
-5.066
Pregnancies                 2.0326      0.552      3.679      0.000       0.950
3.115
Glucose                     6.0122      0.604      9.954      0.000       4.828
7.196
BloodPressure              -0.9308      0.856     -1.088      0.277      -2.608
0.746
SkinThickness               3.4816      1.265      2.752      0.006       1.002
5.961
Insulin                    -1.3657      0.716     -1.907      0.057      -2.769
0.038
BMI                         3.5979      0.879      4.092      0.000       1.875
5.321
DiabetesPedigreeFunction    2.1601      0.710      3.042      0.002       0.769
3.552
Age                         0.6106      0.572      1.068      0.286      -0.510
1.732
====================================================================================
========
```

All features are statistically significant except for the Age and BloodPressure. For now we will keep them in the model.

Part III : Training ML Model

For this task, you are required to build a machine learning model to predict the outcome variable. This will be a binary classification task, as the target variable is binary. You should select at least two models, one of which should be an ensemble model, and compare their performance.

- Train the models: Train the selected models on the training set.
- Model evaluation: Evaluate the trained models on the testing set using appropriate evaluation metrics, such as accuracy, precision, recall, F1-score, and ROC-AUC.

- Model comparison: Compare the performance of the selected models and choose the best-performing model based on the evaluation metrics. You can also perform additional analysis, such as model tuning and cross-validation, to improve the model's performance.

In [ ]:
```
# Separate features from target
X = df[['Pregnancies','Glucose','BloodPressure','SkinThickness','Insulin','BMI','Di
y= df['Outcome']
```

In [ ]:
```
# balance the dataset
from imblearn.over_sampling import RandomOverSampler
OverSample=RandomOverSampler(random_state=0, sampling_strategy='minority')
X_over,y_over=OverSample.fit_resample(X,y)
```

In [ ]:
```
from sklearn.model_selection import train_test_split
X_OS_train, X_OS_test, y_OS_train, y_OS_test = train_test_split(X_over, y_over, tes
```

Build Logistic Regression this will be our bench mark

In [ ]:
```
from sklearn.linear_model import LogisticRegression
logre = LogisticRegression(max_iter=10000)
logre.fit(X_OS_train, y_OS_train)
```

Out[ ]:
```
▾ LogisticRegression
LogisticRegression(max_iter=10000)
```

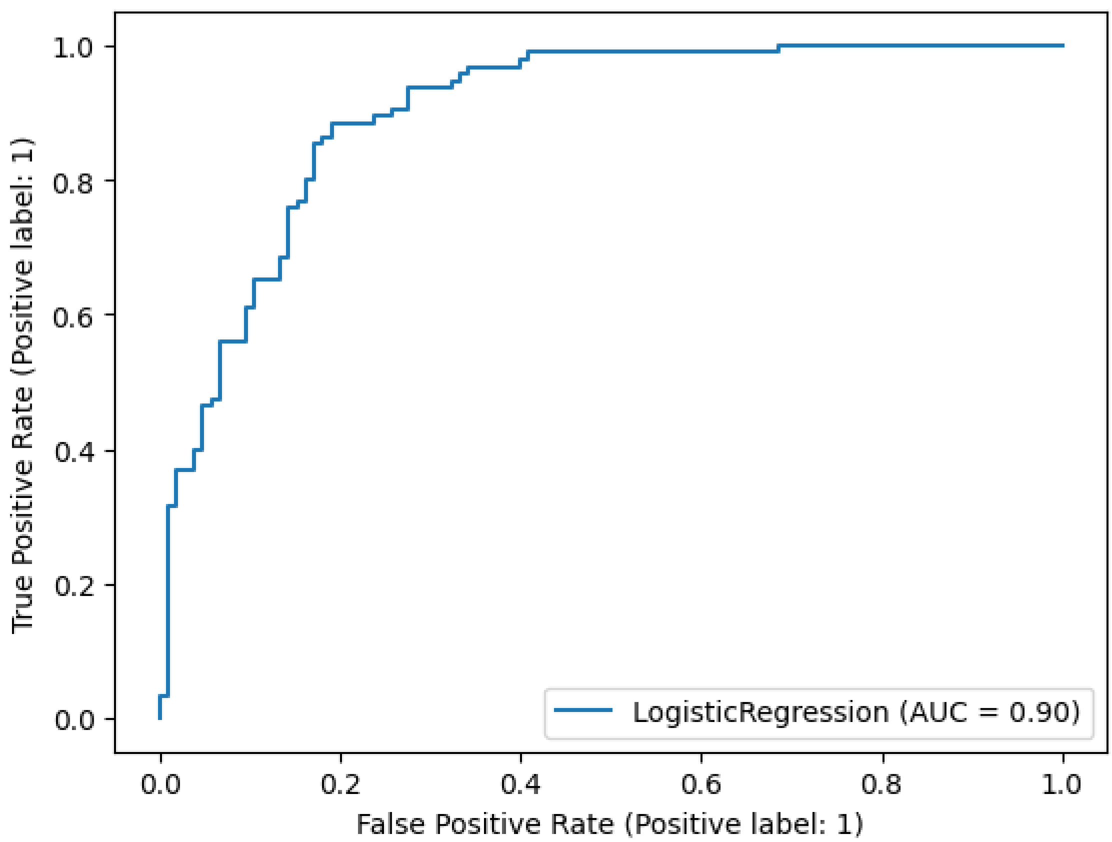
In [ ]:
```
y_logpred = logre.predict(X_OS_test)
```

In [ ]:
```
print('Log loss = {:.5f}'.format(log_loss(y_OS_test, y_logpred)))
print('AUC = {:.5f}'.format(roc_auc_score(y_OS_test, y_logpred)))
print('Average Precision = {:.5f}'.format(average_precision_score(y_OS_test, y_logp
print('\nUsing 0.5 as threshold:')
print('Accuracy = {:.5f}'.format(accuracy_score(y_OS_test, y_logpred)))
print('Precision = {:.5f}'.format(precision_score(y_OS_test, y_logpred)))
print('Recall = {:.5f}'.format(recall_score(y_OS_test, y_logpred)))
print('F1 score = {:.5f}'.format(f1_score(y_OS_test, y_logpred)))

print('\nClassification Report')
print(classification_report(y_OS_test, y_logpred))
```

```
Log loss = 5.76698
AUC = 0.84060
Average Precision = 0.76761

Using 0.5 as threshold:
Accuracy = 0.84000
Precision = 0.81818
Recall = 0.85263
F1 score = 0.83505

Classification Report
              precision    recall  f1-score   support

           0       0.86      0.83      0.84       105
           1       0.82      0.85      0.84        95

    accuracy                           0.84       200
   macro avg       0.84      0.84      0.84       200
weighted avg       0.84      0.84      0.84       200
```

In [ ]:
```
RocCurveDisplay.from_estimator(logre, X_OS_test, y_OS_test)
```

Out[ ]: <sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x1d2149b70d0>



Decision Tree Model

In [ ]:
```
from sklearn.tree import DecisionTreeClassifier
dtc = DecisionTreeClassifier(max_depth=5)
```

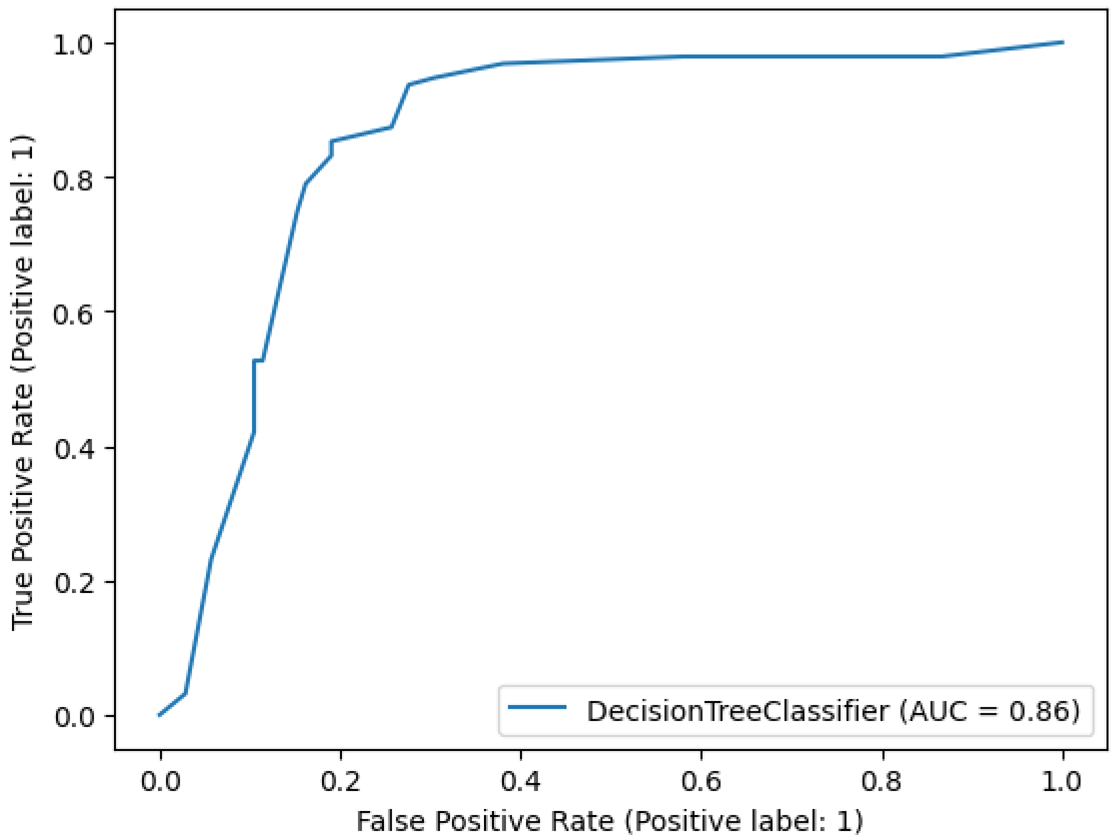
```
dtc.fit(X_OS_train, y_OS_train)
y_dtcpred = dtc.predict(X_OS_test)
```

In [ ]:
```
print('Log loss = {:.5f}'.format(log_loss(y_OS_test, y_dtcpred)))
print('AUC = {:.5f}'.format(roc_auc_score(y_OS_test, y_dtcpred)))
print('Average Precision = {:.5f}'.format(average_precision_score(y_OS_test, y_dtcp
print('\nUsing 0.5 as threshold:')
print('Accuracy = {:.5f}'.format(accuracy_score(y_OS_test, y_dtcpred)))
print('Precision = {:.5f}'.format(precision_score(y_OS_test, y_dtcpred)))
print('Recall = {:.5f}'.format(recall_score(y_OS_test, y_dtcpred)))
print('F1 score = {:.5f}'.format(f1_score(y_OS_test, y_dtcpred)))

print('\nClassification Report')
print(classification_report(y_OS_test, y_dtcpred))
```

```
Log loss = 6.66808
AUC = 0.81378
Average Precision = 0.74359

Using 0.5 as threshold:
Accuracy = 0.81500
Precision = 0.81522
Recall = 0.78947
F1 score = 0.80214

Classification Report
              precision    recall  f1-score   support

           0       0.81      0.84      0.83       105
           1       0.82      0.79      0.80        95

    accuracy                           0.81       200
   macro avg       0.82      0.81      0.81       200
weighted avg       0.82      0.81      0.81       200
```

In [ ]:
```
RocCurveDisplay.from_estimator(dtc, X_OS_test, y_OS_test)
```

Out[ ]:
```
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x1d21bca3e20>
```



Random Forest Tree Model

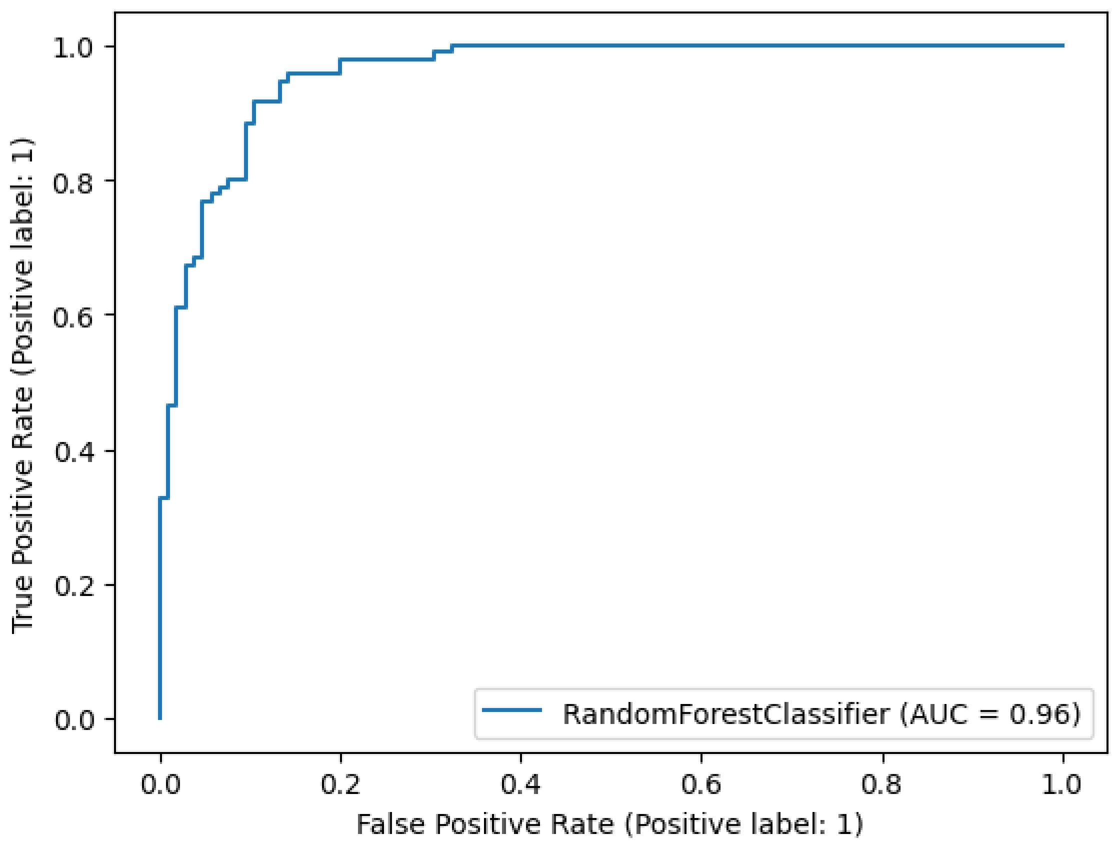
In [ ]:
```
rft = RandomForestClassifier(n_estimators=100, max_depth=5, random_state= 45)
rft.fit(X_OS_train, y_OS_train)
y_rftpred = rft.predict(X_OS_test)
```

In [ ]:
```
print('Log loss = {:.5f}'.format(log_loss(y_OS_test, y_rftpred)))
print('AUC = {:.5f}'.format(roc_auc_score(y_OS_test, y_rftpred)))
print('Average Precision = {:.5f}'.format(average_precision_score(y_OS_test, y_rftp
print('\nUsing 0.5 as threshold:')

print('Accuracy = {:.5f}'.format(accuracy_score(y_OS_test, y_rftpred)))
print('Precision = {:.5f}'.format(precision_score(y_OS_test, y_rftpred)))
print('Recall = {:.5f}'.format(recall_score(y_OS_test, y_rftpred)))
print('F1 score = {:.5f}'.format(f1_score(y_OS_test, y_rftpred)))

print('\nClassification Report')
print(classification_report(y_OS_test, y_rftpred))
```

```
Log loss = 3.78458
AUC = 0.89799
Average Precision = 0.82712

Using 0.5 as threshold:
Accuracy = 0.89500
Precision = 0.84259
Recall = 0.95789
F1 score = 0.89655

Classification Report
              precision    recall  f1-score   support

           0       0.96      0.84      0.89       105
           1       0.84      0.96      0.90        95

    accuracy                           0.90       200
   macro avg       0.90      0.90      0.89       200
weighted avg       0.90      0.90      0.89       200
```

In [ ]:
```
RocCurveDisplay.from_estimator(rft, X_OS_test, y_OS_test)
```

Out[ ]: <sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x1d2166277f0>



In [ ]:
```
feature_scores = pd.Series(rft.feature_importances_, index=X_OS_train.columns).sort
feature_scores
```

```
Out[ ]: SkinThickness               0.274307
        Glucose                     0.242430
        BMI                         0.121540
        Age                         0.112810
        Insulin                     0.092289
        DiabetesPedigreeFunction    0.076688
        Pregnancies                 0.046933
        BloodPressure               0.033002
        dtype: float64
```

```
In [ ]: #remove Age and BloodPressure
        X = df[['Pregnancies','Glucose','SkinThickness','Insulin','BMI','DiabetesPedigreeFu
        y= df['Outcome']
```

```
In [ ]: OverSample=RandomOverSampler(random_state=0, sampling_strategy='minority')
        X_over,y_over=OverSample.fit_resample(X,y)
```

```
In [ ]: X_OS_train, X_OS_test, y_OS_train, y_OS_test = train_test_split(X_over, y_over, tes
```

```
In [ ]: rft = RandomForestClassifier(n_estimators=100, max_depth=5, random_state= 45)
        rft.fit(X_OS_train, y_OS_train)
        y_rftpred = rft.predict(X_OS_test)
```

```
In [ ]: print('Log loss = {:.5f}'.format(log_loss(y_OS_test, y_rftpred)))
        print('AUC = {:.5f}'.format(roc_auc_score(y_OS_test, y_rftpred)))
        print('Average Precision = {:.5f}'.format(average_precision_score(y_OS_test, y_rftp
        print('\nUsing 0.5 as threshold:')

        print('Accuracy = {:.5f}'.format(accuracy_score(y_OS_test, y_rftpred)))
        print('Precision = {:.5f}'.format(precision_score(y_OS_test, y_rftpred)))
        print('Recall = {:.5f}'.format(recall_score(y_OS_test, y_rftpred)))
        print('F1 score = {:.5f}'.format(f1_score(y_OS_test, y_rftpred)))

        print('\nClassification Report')
        print(classification_report(y_OS_test, y_rftpred))
```

```
Log loss = 4.68567
AUC = 0.87318
Average Precision = 0.79494

Using 0.5 as threshold:
Accuracy = 0.87000
Precision = 0.81651
Recall = 0.93684
F1 score = 0.87255

Classification Report
              precision    recall  f1-score   support

           0       0.93      0.81      0.87       105
           1       0.82      0.94      0.87        95

    accuracy                           0.87       200
   macro avg       0.88      0.87      0.87       200
weighted avg       0.88      0.87      0.87       200
```

Part IV : Conclusion

From the machine learning models developed and the exploratory data analysis (EDA) conducted, generate four bullet points as your findings.

- The dataset has no missing values, but it has a lot of unrealistic information. e.g. BMI = 0.
- Random Forest Tree gives the best result with 84% accuracy.
- Insulin is the most important feature.
- BloodPressure is the least important, which surprise me!!

In [ ]: