nce-capstone-project-health-care

October 7, 2023

0.1 Data Science Capstone Project : Health Care

[1]:
```
# Importing the libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
from matplotlib import style
import seaborn as sns
import imblearn
```

[2]:
```
# Loading the dataset

df = pd.read_csv('health care diabetes.csv')
```

0.1.1 Data Exploration:

[3]:
```
df.head() #top 5 dataset
```

[3]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
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

   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
```

[4]:
```
df.tail() #bottom 5 dataset
```

```
[4]:      Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
     763           10      101             76             48      180  32.9
     764            2      122             70             27        0  36.8
     765            5      121             72             23      112  26.2
     766            1      126             60              0        0  30.1
     767            1       93             70             31        0  30.4

          DiabetesPedigreeFunction  Age  Outcome
     763                     0.171   63        0
     764                     0.340   27        0
     765                     0.245   30        0
     766                     0.349   47        1
     767                     0.315   23        0
```

```
[5]: df.info() #concise information about a DataFrame.
```

```
<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
```

```
[6]: df.shape #Rows and columns
```

```
[6]: (768, 9)
```

```
[7]: df.describe() # statistical summary information for each numeric column
```

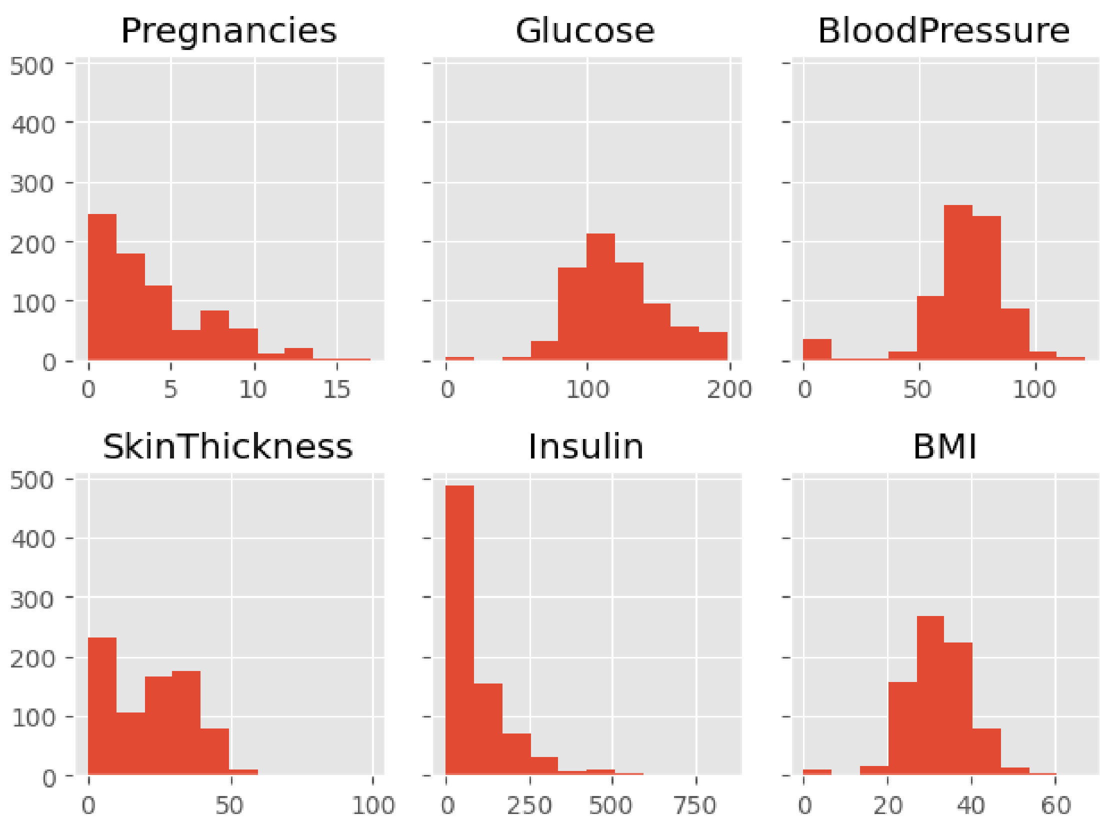
```
[7]:        Pregnancies     Glucose  BloodPressure  SkinThickness     Insulin  \
     count   768.000000  768.000000     768.000000     768.000000  768.000000
     mean      3.845052  120.894531      69.105469      20.536458   79.799479
     std       3.369578   31.972618      19.355807      15.952218  115.244002
     min       0.000000    0.000000       0.000000       0.000000    0.000000
     25%       1.000000   99.000000      62.000000       0.000000    0.000000
     50%       3.000000  117.000000      72.000000      23.000000   30.500000
     75%       6.000000  140.250000      80.000000      32.000000  127.250000
```

```
max      17.000000  199.000000     122.000000      99.000000  846.000000

             BMI  DiabetesPedigreeFunction         Age     Outcome
count  768.000000                768.000000  768.000000  768.000000
mean    31.992578                  0.471876   33.240885    0.348958
std      7.884160                  0.331329   11.760232    0.476951
min      0.000000                  0.078000   21.000000    0.000000
25%     27.300000                  0.243750   24.000000    0.000000
50%     32.000000                  0.372500   29.000000    0.000000
75%     36.600000                  0.626250   41.000000    1.000000
max     67.100000                  2.420000   81.000000    1.000000
```

- As per descriptive analysis we see that minimum value is 0 for columns such as **Pregnancies**, **Glucose**, **SkinThickness**, **Insulin**, **BMI** etc.
- which is practically impossible so we have to treat this as null value **(NAN)** hence replace with its **median** values.

[8]:
```
## Visualizations
style.use('ggplot')
fig,axs=plt.subplots(2,3,sharey=True,tight_layout=True)

axs[0,0].hist(df['Pregnancies'],bins=10)
axs[0,1].hist(df['Glucose'],bins=10)
axs[0,2].hist(df['BloodPressure'],bins=10)
axs[1,0].hist(df['SkinThickness'],bins=10)
axs[1,1].hist(df['Insulin'],bins=10)
axs[1,2].hist(df['BMI'],bins=10)

#set title
axs[0,0].set_title('Pregnancies')
axs[0,1].set_title('Glucose')
axs[0,2].set_title('BloodPressure')
axs[1,0].set_title('SkinThickness')
axs[1,1].set_title('Insulin')
axs[1,2].set_title('BMI')
```

[8]:
```
Text(0.5, 1.0, 'BMI')
```



[9]:
```
# Treating the missing values (NAN) with the meidan(50%)

df['Pregnancies'] = df['Pregnancies'].replace(0, 3.000000)
df['Glucose'] = df['Glucose'].replace(0, 117.000000)
df['BloodPressure'] = df['BloodPressure'].replace(0, 72.000000)
df['SkinThickness'] = df['SkinThickness'].replace(0, 23.000000)
df['Insulin'] = df['Insulin'].replace(0, 30.500000)
df['BMI'] = df['BMI'].replace(0, 32.000000)
```

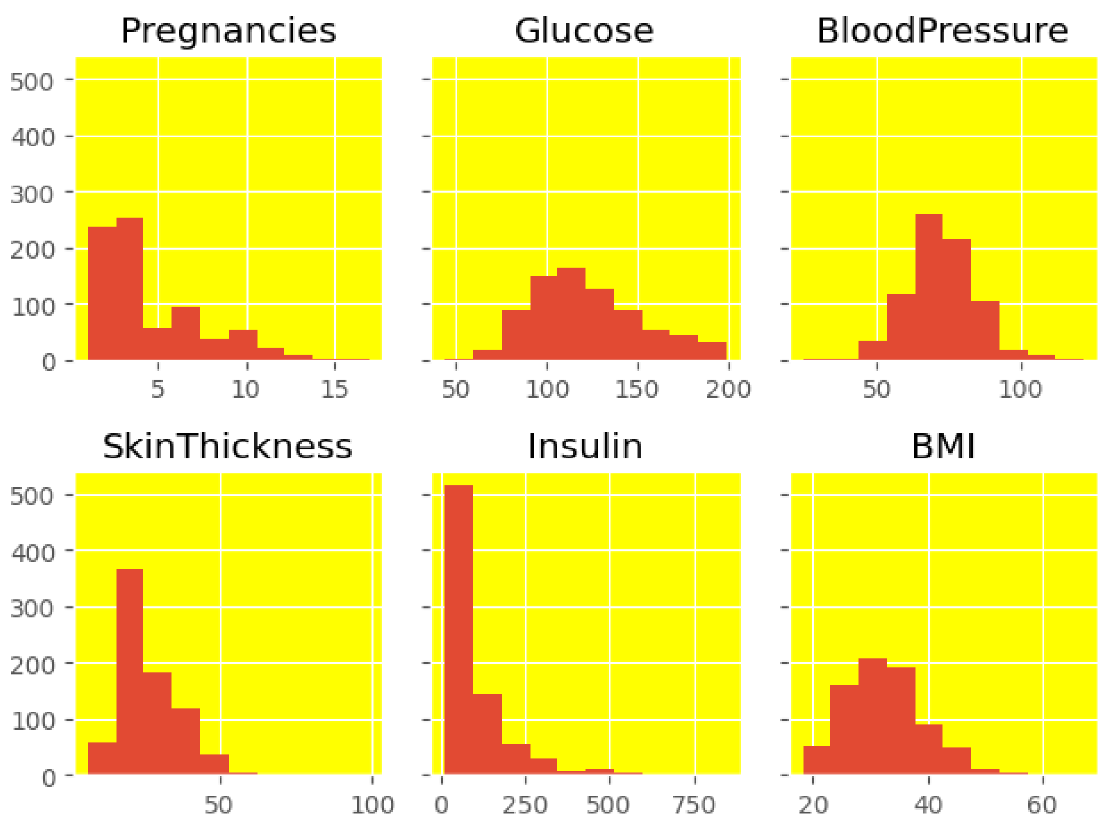
[10]:
```
df.describe()
```

[10]:
```
       Pregnancies     Glucose  BloodPressure  SkinThickness     Insulin  \
count   768.000000  768.000000     768.000000     768.000000  768.000000
mean      4.278646  121.656250      72.386719      27.334635   94.652344
std       3.021516   30.438286      12.096642       9.229014  105.547598
min       1.000000   44.000000      24.000000       7.000000   14.000000
25%       2.000000   99.750000      64.000000      23.000000   30.500000
50%       3.000000  117.000000      72.000000      23.000000   31.250000
75%       6.000000  140.250000      80.000000      32.000000  127.250000
max      17.000000  199.000000     122.000000      99.000000  846.000000
```

```
             BMI  DiabetesPedigreeFunction         Age     Outcome
count  768.000000                768.000000  768.000000  768.000000
mean    32.450911                  0.471876   33.240885    0.348958
std      6.875366                  0.331329   11.760232    0.476951
min     18.200000                  0.078000   21.000000    0.000000
25%     27.500000                  0.243750   24.000000    0.000000
50%     32.000000                  0.372500   29.000000    0.000000
75%     36.600000                  0.626250   41.000000    1.000000
max     67.100000                  2.420000   81.000000    1.000000
```

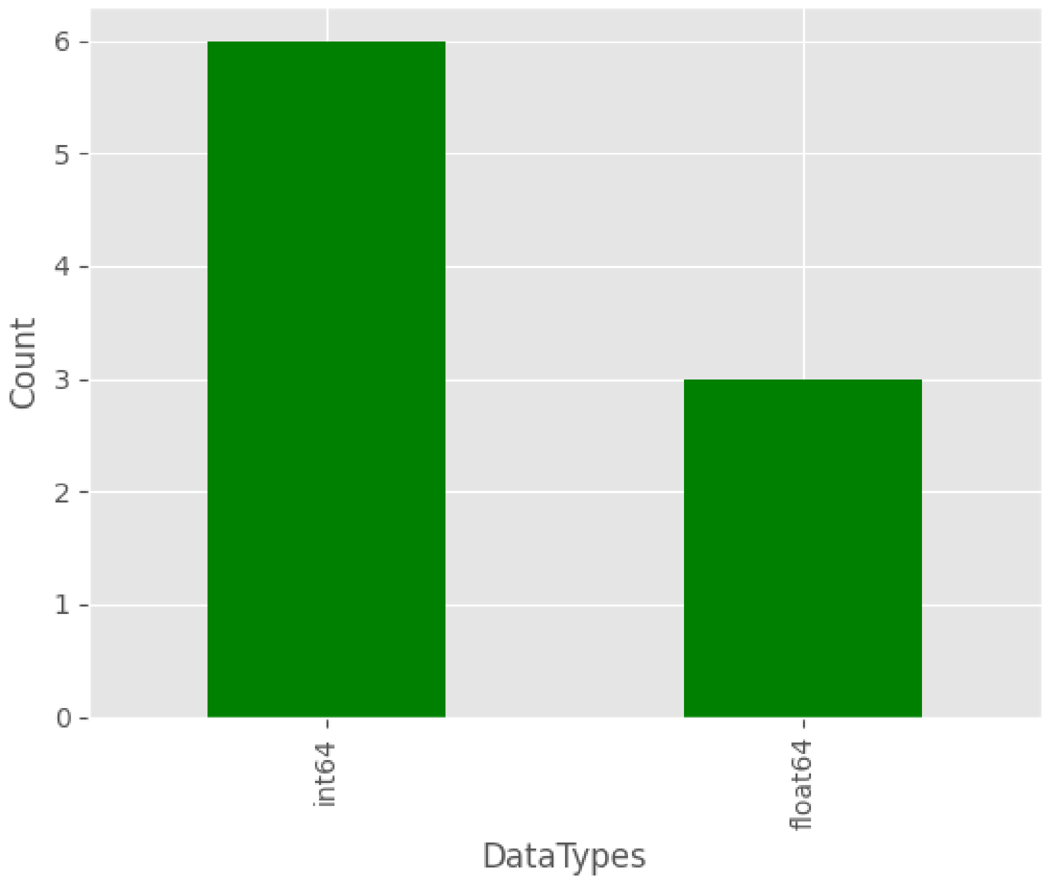
[11]:
```
## Visualizations
style.use('ggplot')
fig,axs=plt.subplots(2,3,sharey=True,tight_layout=True)
for ax in axs.flat:
    ax.set_facecolor('yellow')

axs[0,0].hist(df['Pregnancies'],bins=10)
axs[0,1].hist(df['Glucose'],bins=10)
axs[0,2].hist(df['BloodPressure'],bins=10)
axs[1,0].hist(df['SkinThickness'],bins=10)
axs[1,1].hist(df['Insulin'],bins=10)
axs[1,2].hist(df['BMI'],bins=10)

#set title
axs[0,0].set_title('Pregnancies')
axs[0,1].set_title('Glucose')
axs[0,2].set_title('BloodPressure')
axs[1,0].set_title('SkinThickness')
axs[1,1].set_title('Insulin')
axs[1,2].set_title('BMI')
```

[11]:
```
Text(0.5, 1.0, 'BMI')
```



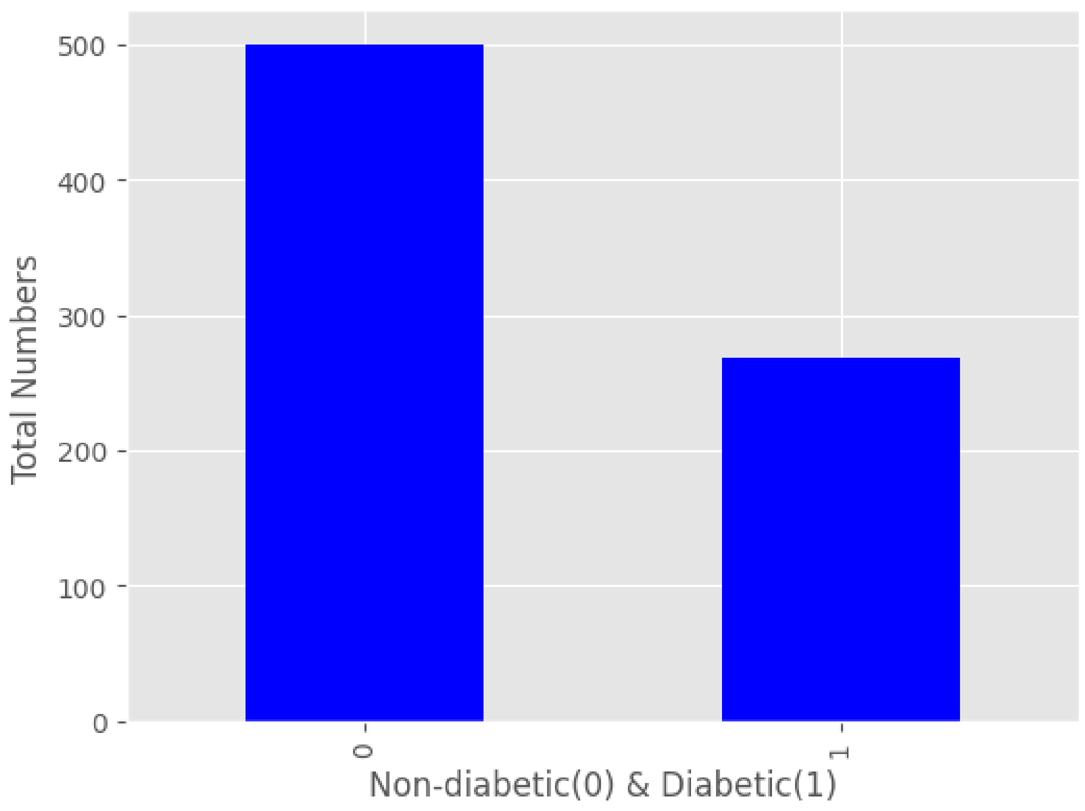
```
[12]: # Creating count(frequency) plot describing the data types and the count of␣
      ↪variables.
      style.use('ggplot')
      df.dtypes.value_counts().plot(kind='bar', color='g')
      plt.xlabel('DataTypes')
      plt.ylabel('Count')
```

```
[12]: Text(0, 0.5, 'Count')
```



```
[13]: df['Outcome'].value_counts().plot(kind='bar', color='b')
      plt.xlabel('Non-diabetic(0) & Diabetic(1)')
      plt.ylabel('Total Numbers')
```

```
[13]: Text(0, 0.5, 'Total Numbers')
```

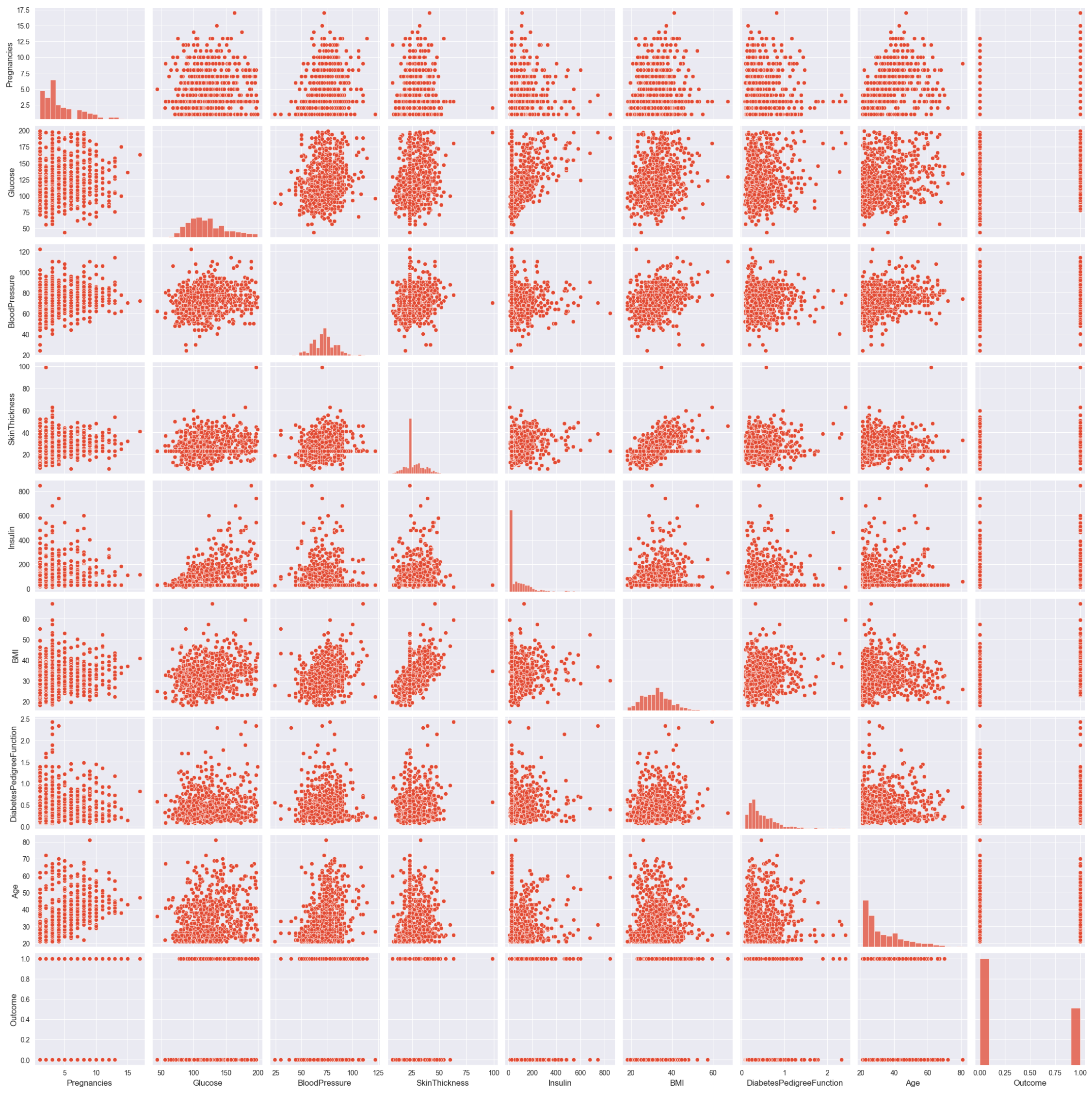


As we can see that there is an **imbalance** in data that means we might need to apply **SMOTE** moving forward.

[14]:
```
sns.set_style('darkgrid')
sns.pairplot(df)
```

```
C:\Users\Deepak Yadav\anaconda3\lib\site-packages\seaborn\axisgrid.py:118:
UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```

[14]:
```
<seaborn.axisgrid.PairGrid at 0x1df618ca050>
```



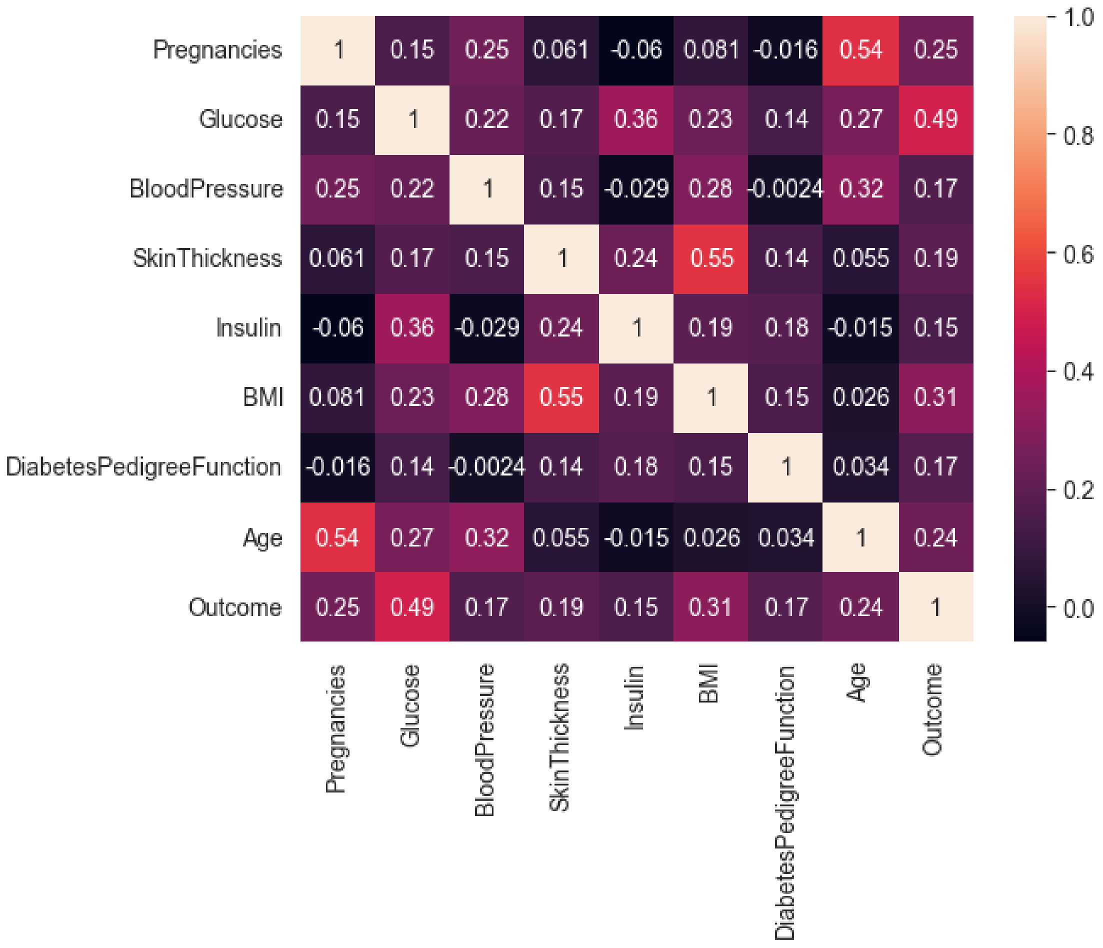
[15]:
```
df1=df.corr()
df1
```

[15]:
```
                          Pregnancies   Glucose  BloodPressure  SkinThickness  \
Pregnancies                  1.000000  0.149326       0.247530       0.060706
Glucose                      0.149326  1.000000       0.218937       0.172143
BloodPressure                0.247530  0.218937       1.000000       0.147809
SkinThickness                0.060706  0.172143       0.147809       1.000000
Insulin                     -0.059580  0.357573      -0.028721       0.238188
BMI                          0.080540  0.231400       0.281132       0.546951
DiabetesPedigreeFunction    -0.016151  0.137327      -0.002378       0.142977
Age                          0.538169  0.266909       0.324915       0.054514
Outcome                      0.245466  0.492782       0.165723       0.189065
```

```
                           Insulin       BMI  DiabetesPedigreeFunction  \
Pregnancies              -0.059580  0.080540                 -0.016151
Glucose                   0.357573  0.231400                  0.137327
BloodPressure            -0.028721  0.281132                 -0.002378
SkinThickness             0.238188  0.546951                  0.142977
Insulin                   1.000000  0.189022                  0.178029
BMI                       0.189022  1.000000                  0.153506
DiabetesPedigreeFunction  0.178029  0.153506                  1.000000
Age                      -0.015413  0.025744                  0.033561
Outcome                   0.148457  0.312249                  0.173844

                               Age   Outcome
Pregnancies               0.538169  0.245466
Glucose                   0.266909  0.492782
BloodPressure             0.324915  0.165723
SkinThickness             0.054514  0.189065
Insulin                  -0.015413  0.148457
BMI                       0.025744  0.312249
DiabetesPedigreeFunction  0.033561  0.173844
Age                       1.000000  0.238356
Outcome                   0.238356  1.000000
```

[16]:
```
sns.heatmap(df.corr(),annot=True) # Plotting the heatmap
```

[16]:
```
<Axes: >
```



	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1	0.15	0.25	0.061	-0.06	0.081	-0.016	0.54	0.25
Glucose	0.15	1	0.22	0.17	0.36	0.23	0.14	0.27	0.49
BloodPressure	0.25	0.22	1	0.15	-0.029	0.28	-0.0024	0.32	0.17
SkinThickness	0.061	0.17	0.15	1	0.24	0.55	0.14	0.055	0.19
Insulin	-0.06	0.36	-0.029	0.24	1	0.19	0.18	-0.015	0.15
BMI	0.081	0.23	0.28	0.55	0.19	1	0.15	0.026	0.31
DiabetesPedigreeFunction	-0.016	0.14	-0.0024	0.14	0.18	0.15	1	0.034	0.17
Age	0.54	0.27	0.32	0.055	-0.015	0.026	0.034	1	0.24
Outcome	0.25	0.49	0.17	0.19	0.15	0.31	0.17	0.24	1

[17]:
```
df1.to_csv('df_corr.csv')
```

[18]:
```
# Seprating 'Independent' and 'Dependent' Variables.

x=df.drop(['Outcome'],axis=1)
y=df['Outcome']
```

[19]:
```
# feature scaling

from sklearn.preprocessing import StandardScaler
```

[20]:
```
scale = StandardScaler() #Initialize the StandardScaler
x=scale.fit_transform(x)
```

Balancing dataset using **SMOTE**

[21]:
```
from imblearn.over_sampling import SMOTE
sm = SMOTE(random_state=42)
```

[22]:
```
X,Y=sm.fit_resample(x,y)
```

[23]:
```
X.shape, Y.shape
```

[23]:
```
((1000, 8), (1000,))
```

0.1.2 Data Modeling:

[24]:
```
#train test split

from sklearn.model_selection import train_test_split
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.25,␣
 ↪random_state=42)
```

Building the **Machine Learning pipeline** for different ML Classification Models like **KNN**, **logistic Regression**, **DecisionTree**, **RandomForest**, **SVM** & **NB** inorder to test multiple algorithms to see which one works best for this specific problem.

[25]:
```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.naive_bayes import GaussianNB
```

Creating a list called **model_pipeline** and appending various machine learning classifiers to it.

[26]:
```
model_pipeline=[]
model_pipeline.append(KNeighborsClassifier())
model_pipeline.append(LogisticRegression())
model_pipeline.append(DecisionTreeClassifier())
model_pipeline.append(RandomForestClassifier())
model_pipeline.append(SVC())
model_pipeline.append(GaussianNB())
```

Importing several important **metrics and functions** from scikit-learn for **evaluating machine learning models**.

[27]:
```
from sklearn.metrics import␣
 ↪accuracy_score,classification_report,confusion_matrix,roc_curve,auc
```

Creating a list of machine learning models (**model_list**) and using a list of classifiers (**model_pipeline**) to train and assess them. Evaluating metrics like **test accuracy**, **training accuracy**, **AUC**, and **confusion matrices** for each model.

[28]:
```
model_list = ['Logistic Regression', 'Decision Tree', 'Random Forest', 'SVM',␣
 ↪'KNN', 'GaussianNB']
test_acc_list = []
```

```
train_acc_list = []
auc_list = []
cm_list = []

for model in model_pipeline:
    model.fit(X_train, Y_train)
    Y_pred = model.predict(X_test)
    Y_train_pred = model.predict(X_train)
    test_acc_list.append(accuracy_score(Y_test, Y_pred))
    train_acc_list.append(accuracy_score(Y_train, Y_train_pred))
    fpr, tpr, _thresholds = roc_curve(Y_test, Y_pred)
    auc_list.append(round(auc(fpr, tpr), 2))
    cm_list.append(confusion_matrix(Y_test, Y_pred))
```

Creating a DataFrame named **result_df** containing various metrics for different machine learning models. The DataFrame includes columns for the model names, test accuracy, training accuracy, and AUC (Area Under the ROC Curve).

[29]:
```
result_df=pd.DataFrame({'model':model_list,'test_accuracy':
 ↪test_acc_list,'train_accuracy':train_acc_list,'AUC':auc_list})
```

[30]:
```
result_df
```

[30]:
```
                 model  test_accuracy  train_accuracy   AUC
0  Logistic Regression          0.756        0.836000  0.75
1        Decision Tree          0.752        0.761333  0.75
2        Random Forest          0.736        1.000000  0.74
3                  SVM          0.784        1.000000  0.78
4                  KNN          0.784        0.860000  0.78
5           GaussianNB          0.748        0.722667  0.75
```

We observe an instance of **overfitting** in the data, which prompts us to consider **cross-validation**. In this case, we opt for **K-Fold cross-validation**.

In this scenario, it's worth noting that **K-Nearest Neighbors (KNN)** exhibits lower accuracy compared to **Support Vector Machines (SVM)** and **Random Forest**. As a result, we decide to implement **K-Fold cross-validation** for the **Random Forest model**.

[31]:
```
from sklearn.ensemble import AdaBoostClassifier
base_model = RandomForestClassifier(max_depth=2)
model = AdaBoostClassifier(base_model, n_estimators=50)
model.fit(X_train, Y_train)
Y_pred = model.predict(X_test)
accuracy = accuracy_score(Y_test, Y_pred)
conf_matrix = confusion_matrix(Y_test, Y_pred)
class_report = classification_report(Y_test, Y_pred)
data = {
    'Metric': ['Accuracy', 'Confusion Matrix', 'Classification Report'],
    'Result': [accuracy, conf_matrix, class_report]
}
results_df = pd.DataFrame(data)
print(results_df)
```

```
                  Metric                                                   Result
0               Accuracy                                                    0.744
1       Confusion Matrix                                   [[89, 35], [29, 97]]
2  Classification Report                precision    recall  f1-score   …
```

[32]:
```
print(classification_report(Y_pred,Y_test))
```

```
              precision    recall  f1-score   support

           0       0.72      0.75      0.74       118
           1       0.77      0.73      0.75       132

    accuracy                           0.74       250
   macro avg       0.74      0.74      0.74       250
weighted avg       0.75      0.74      0.74       250
```

Using the **XGBoost** library (xgboost) to build a binary classification model.

[33]:
```
import xgboost as xgb
dtrain=xgb.DMatrix(X_train,label=Y_train)
params={'objective':'binary:logistic',
       'eval_metric':'logloss',
       'max_depth':3,
       'learning_rate':0.1,
       'gamma':0.2,
       'subsample':0.8,
       'colsample_bytree':0.8}
```

[34]:
```
model=xgb.train(params,dtrain,num_boost_round=100)
```

[35]:
```
dtest=xgb.DMatrix(X_test)
```

[36]:
```
Y_pred_proba=model.predict(dtest)
```

[37]:
```
Y_pred=[1 if p>=0.5 else 0 for p in Y_pred_proba]
```

[38]:
```
acc=accuracy_score(Y_test,Y_pred)
```

[39]:
```
acc
```

[39]:
```
0.76
```

In summary, we have determined that **SVM** exhibits **superior accuracy** and **AUC**. Additionally, SVM stands out as the appropriate model for this dataset due to its **absence** of **overfitting issues**.

[ ]:

```

```