Healthcare Course-end Project 2

February 25, 2023

1 Healthcare Course-end Project 2 :-> By Pavan Lande

1.0.1 DESCRIPTION

1.0.2 Problem Statement

1. NIDDK (National Institute of Diabetes and Digestive and Kidney Diseases) research creates knowledge about and treatments for the most chronic, costly, and consequential diseases.

2.The dataset used in this project is originally from NIDDK. The objective is to predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset.

3.Build a model to accurately predict whether the patients in the dataset have diabetes or not.

1.0.3 Dataset Description

The datasets consists of several medical predictor variables and one target variable (Outcome). Predictor variables includes the number of pregnancies the patient has had, their BMI, insulin level, age, and more.

1.0.4 Variables Description

Pregnancies Number of times pregnant

Glucose Plasma glucose concentration in an oral glucose tolerance test

BloodPressure Diastolic blood pressure (mm Hg)

SkinThickness Triceps skinfold thickness (mm)

Insulin Two hour serum insulin

BMI Body Mass Index

DiabetesPedigreeFunction Diabetes pedigree function

Age Age in years

Outcome Class variable (either 0 or 1). 268 of 768 values are 1, and the others are 0

[1]:
```
import numpy as np
import pandas as pd
import warnings
warnings.filterwarnings("ignore")

# import plotting libraries
import matplotlib
import matplotlib.pyplot as plt
%matplotlib inline

import seaborn as sns
sns.set(color_codes=True)
sns.set(style='white')
```

[2]:
```
df= pd.read_csv(r'C:\DATA SCIENCE CLASS\Online Class Lectures\DATA SCIENCE␣
↪CLASS SEP-22 COHORT\Data Science Job Guarantee Bootcamp Capstone\Simplilearn␣
↪Project DATA Set & Solution\Project_2\health care diabetes.csv')
```

[3]:
```
df.head()  # To check the initial rows
```

[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.columns
```

[4]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

1.0.5 Project Task: Week 1

1.0.6 Data Exploration:

1. Perform descriptive analysis. Understand the variables and their corresponding values. On the columns below, a value of zero does not make sense and thus indicates missing value:

- **Glucose** • **BloodPressure** • **SkinThickness** • **Insulin** • **BMI**

[5]:
```
df.describe()  # statistical summary
```

[5]:
```
       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
```

[6]:
```
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
```

[7]:
```
df.shape
```

[7]:
```
(768, 9)
```

[8]:
```
df.isnull().sum()
```

[8]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

[9]:
```
df['Outcome'].value_counts(normalize=True)
```

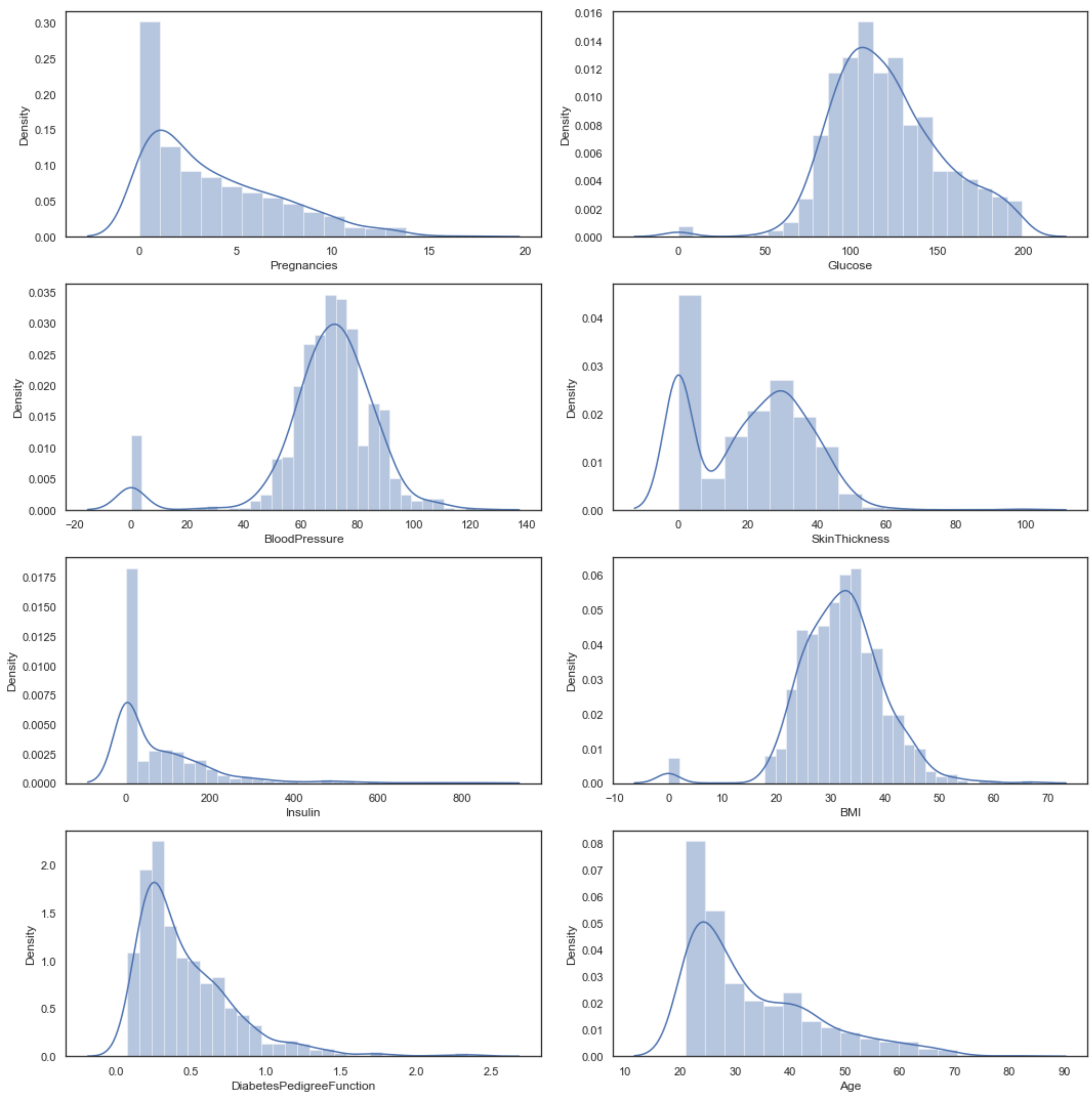
[9]:
```
0    0.651042
1    0.348958
Name: Outcome, dtype: float64
```

Findings:- 1. All are numerical variables (dtypes:- int64, float64) 2. 768 rows and 9 features (8 independant variables and 1 dependant variable) 3. No missing values are noted in the statistical summary 4. Outliers noticed in Pregnancies and Insulin feature 5. Value zero noticed in columns like 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI'. This indicates missing value and must be treated 6. Outcome is the target variable which is binary (either 0 or 1) 7. This is not an imbalanced dataset, with 65% , zero outcomes and 35% one outcomes 8. There is a need to standardize the dataset, since values of variables are in different scale

2. Visually explore these variables using histograms. Treat the missing values accordingly. Value zero is noticed in columns like 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI'. This does not makes sense. This indicates missing value and must be treated

[10]:
```
feature_cols=[col for col in df.columns if col != 'Outcome']

plt.figure(figsize=(15,15))
for i, feature in enumerate(feature_cols):
```

```
    rows = int(len(feature_cols)/2)

    plt.subplot(rows, 2, i+1)

    sns.distplot(df[feature])

plt.tight_layout()
plt.show()
```



[11]:
```
# Finding skewness in the features
from scipy.stats import skew
negative_skew=[]
positive_skew=[]
```

```
for feature in feature_cols:
    print("Skewness of {0} is {1}". format(feature, skew(df[feature])),␣
↪end='\n')
    if skew(df[feature]) <0:
        negative_skew.append(feature)
    else:
        positive_skew.append(feature)

print(end="\n")
print("Negatively skewed Features are {}".format(negative_skew), end='\n')
print("Positively skewed Features are {}".format(positive_skew), end='\n')

print("Negatively skewed feature")
```

```
Skewness of Pregnancies is 0.8999119408414357
Skewness of Glucose is 0.17341395519987735
Skewness of BloodPressure is -1.8400052311728738
Skewness of SkinThickness is 0.109158762323673
Skewness of Insulin is 2.2678104585131753
Skewness of BMI is -0.42814327880861786
Skewness of DiabetesPedigreeFunction is 1.9161592037386292
Skewness of Age is 1.127389259531697

Negatively skewed Features are ['BloodPressure', 'BMI']
Positively skewed Features are ['Pregnancies', 'Glucose', 'SkinThickness',
'Insulin', 'DiabetesPedigreeFunction', 'Age']
Negatively skewed feature
```

[12]:
```
# Percantage of missing values in features
for col in feature_cols:
    df[col].replace(0,np.nan,inplace=True)
percent_missing = df.isnull().sum() * 100 / len(df)
missing_value_df = pd.DataFrame({'column_name': df.columns,
                                 'percent_missing': percent_missing})
missing_value_df.sort_values(by=['percent_missing'], inplace=True,␣
↪ascending=False)
missing_value_df.set_index(keys=['column_name'],drop=True)
```

[12]:

column_name	percent_missing
Insulin	48.697917
SkinThickness	29.557292
Pregnancies	14.453125
BloodPressure	4.557292
BMI	1.432292
Glucose	0.651042
DiabetesPedigreeFunction	0.000000

```
Age                         0.000000
Outcome                     0.000000
```

[13]:
```
# Missing value imputaion using mean
for col in feature_cols:
    df[col].fillna(int(df[col].mean()),inplace=True)
```

[14]:
```
df.isnull().sum()
```

[14]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

[15]:
```
for col in feature_cols:
    if col not in ['BMI','DiabetesPedigreeFunction']:
        df[col]=df[col].apply(lambda x:int(x))
```

3. There are integer and float data type variables in this dataset. Create a count (frequency) plot describing the data types and the count of variables.

[16]:
```
df.dtypes
```

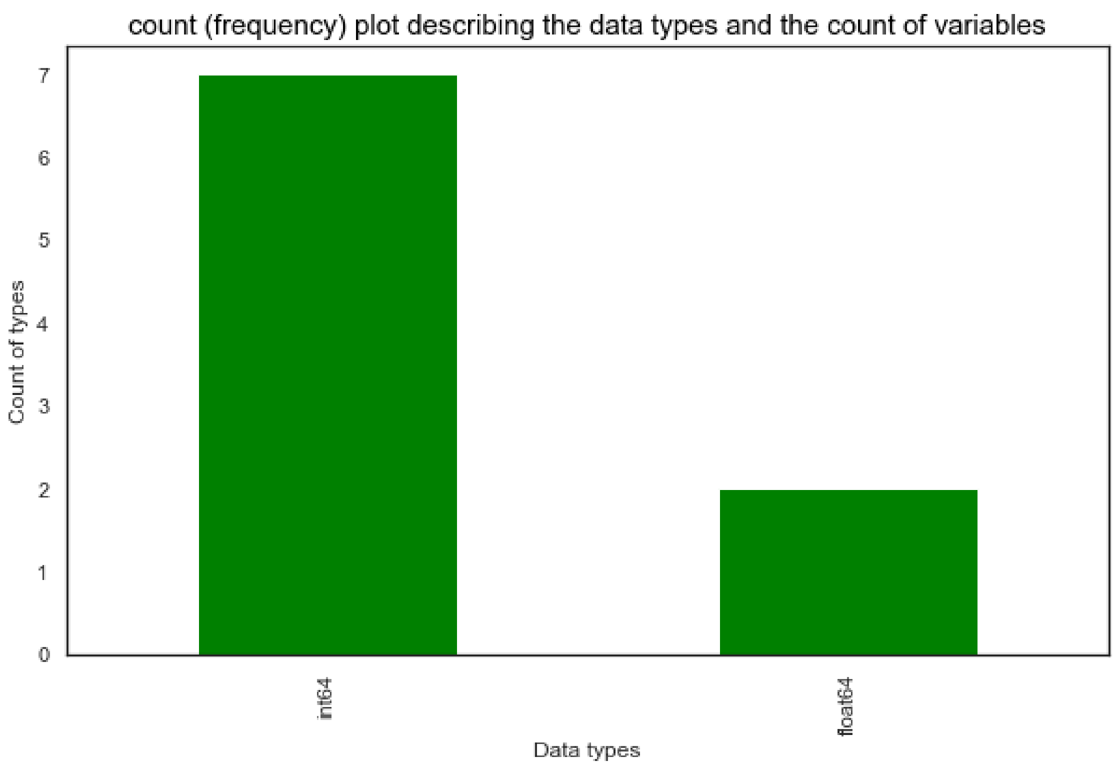
[16]:
```
Pregnancies                   int64
Glucose                       int64
BloodPressure                 int64
SkinThickness                 int64
Insulin                       int64
BMI                         float64
DiabetesPedigreeFunction    float64
Age                           int64
Outcome                       int64
dtype: object
```

[17]:
```
df.head()
```

[17]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35      155  33.6
1            1       85             66             29      155  26.6
2            8      183             64             29      155  23.3
3            1       89             66             23       94  28.1
```

```
4              4       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
```

[18]:
```
plt.figure(figsize=(10,6))
df.dtypes.value_counts().plot(kind='bar', color='green')
plt.title("count (frequency) plot describing the data types and the count of␣
 ↪variables", fontsize=15,loc='center', color='Black')
plt.xlabel("Data types")
plt.ylabel("Count of types")
plt.show()
```

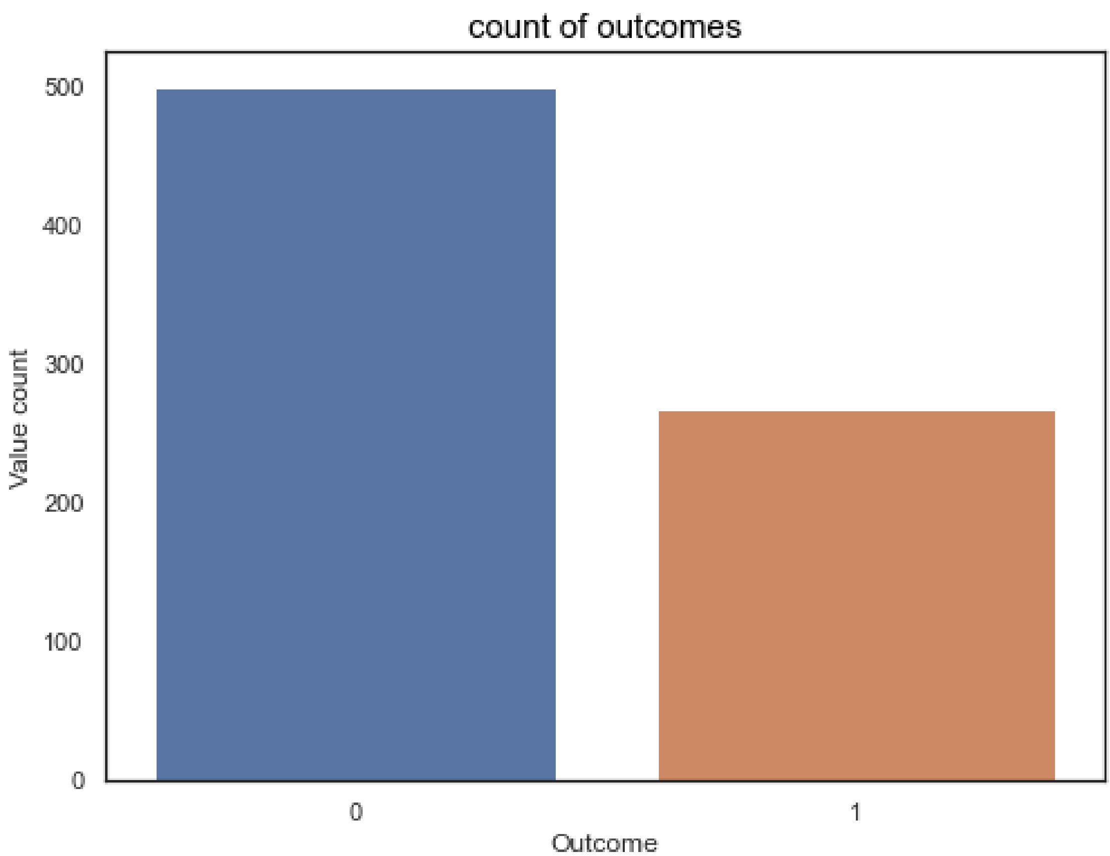


1.0.7 Project Task: Week 2

Data Exploration:

1. Check the balance of the data by plotting the count of outcomes by their value. Describe your findings and plan future course of action.

[19]:
```
plt.figure(figsize=(8,6))
sns.countplot(df['Outcome'])
plt.title("count of outcomes", fontsize=15,loc='center', color='Black')
plt.xlabel("Outcome")
plt.ylabel("Value count")
plt.show()
```

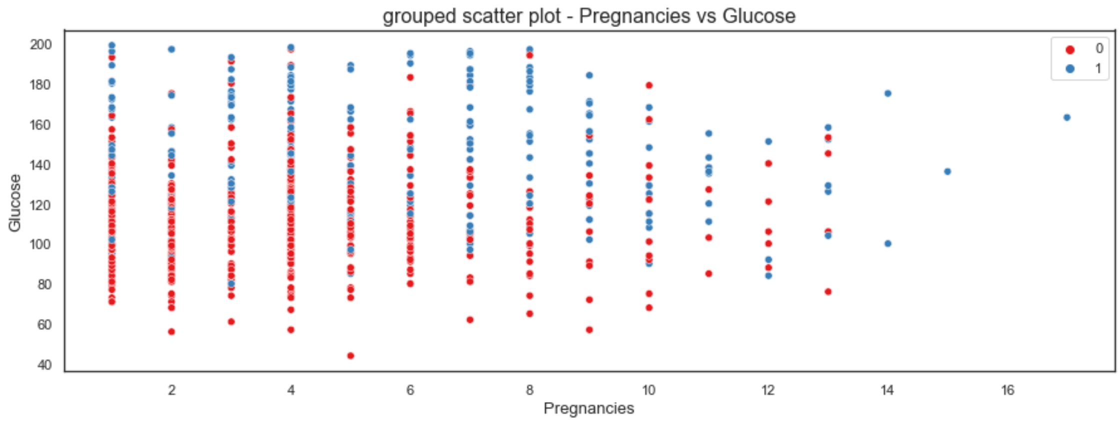


Data is not imbalanced, since both classes, majority and minority are both almost equally present in the dataset (65% & 34%)

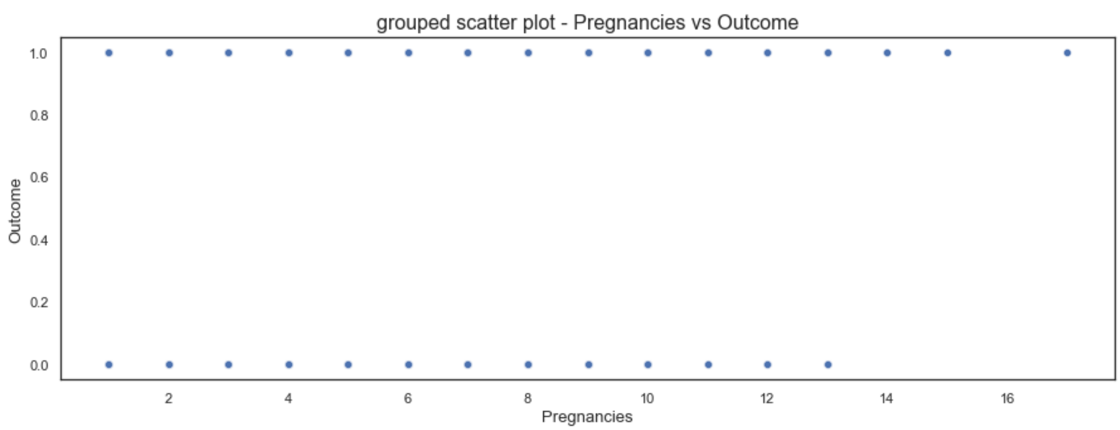
2. Create scatter charts between the pair of variables to understand the relationships. Describe your findings.

[20]:
```
plt.figure(figsize=(15,5))
sns.
 ↪scatterplot(x='Pregnancies',y='Glucose',data=df,hue='Outcome',palette="Set1")
plt.xlabel('Pregnancies', fontsize=13)
plt.ylabel('Glucose', fontsize=13)
```

```
plt.title('grouped scatter plot - Pregnancies vs Glucose',fontsize=16)
plt.legend()
plt.show()
```



[21]:
```
plt.figure(figsize=(15,5))
sns.scatterplot(x='Pregnancies',y='Outcome',data=df,palette="Set1")
plt.xlabel('Pregnancies', fontsize=13)
plt.ylabel('Outcome', fontsize=13)
plt.title('grouped scatter plot - Pregnancies vs Outcome',fontsize=16)
plt.show()
```



1. Patient can be a diabetic, irrespective of the preganancy and glucose values, since diabetic positive outcome can be noted across the dataset.

[22]:
```
sns.pairplot(df, hue='Outcome')
plt.title('grouped scatter plot - All Variables',fontsize=16)
plt.legend()
```

```
plt.show()
```

```
No artists with labels found to put in legend.  Note that artists whose label
start with an underscore are ignored when legend() is called with no argument.
```

1.Positive diabetic outcome noted for higher values of the IVs

2.BMI and skin thickness have a positive linear realtionship

3.Higher BMIs are more at risk of high values of BP, Glucose etc

4.Insulin is taken by a bigger percantage of diabetic patients

3. Perform correlation analysis. Visually explore it using a heat map.

[23]:

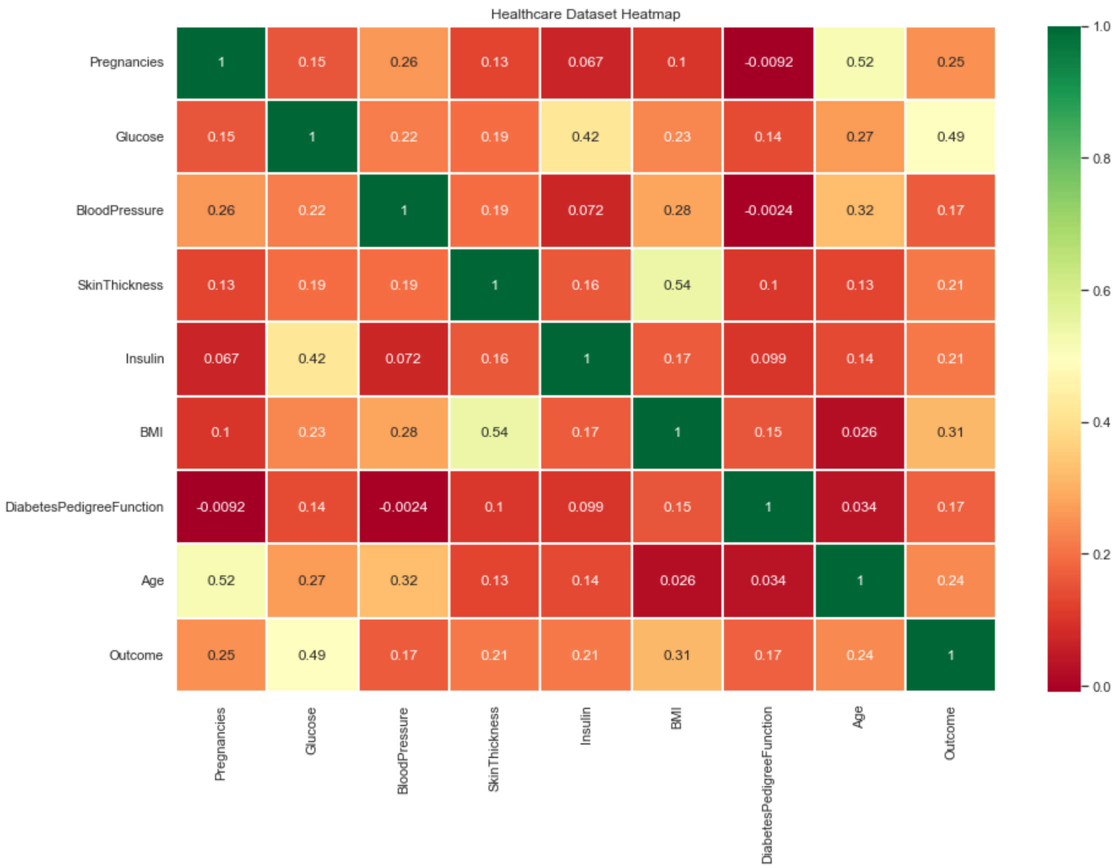
```
corr=df.corr()
corr
```

[23]:

```
                          Pregnancies   Glucose  BloodPressure  SkinThickness  \
Pregnancies                  1.000000  0.153070       0.255967       0.126082
Glucose                      0.153070  1.000000       0.218615       0.192677
BloodPressure                0.255967  0.218615       1.000000       0.191892
SkinThickness                0.126082  0.192677       0.191892       1.000000
Insulin                      0.066832  0.420301       0.072041       0.158133
BMI                          0.100746  0.231470       0.281132       0.543275
DiabetesPedigreeFunction    -0.009198  0.137100      -0.002378       0.102188
Age                          0.522303  0.266591       0.324915       0.126107
Outcome                      0.248172  0.492911       0.165723       0.214873

                           Insulin       BMI  DiabetesPedigreeFunction  \
Pregnancies               0.066832  0.100746                 -0.009198
Glucose                   0.420301  0.231470                  0.137100
BloodPressure             0.072041  0.281132                 -0.002378
SkinThickness             0.158133  0.543275                  0.102188
Insulin                   1.000000  0.166946                  0.099170
BMI                       0.166946  1.000000                  0.153506
DiabetesPedigreeFunction  0.099170  0.153506                  1.000000
Age                       0.136050  0.025744                  0.033561
Outcome                   0.214278  0.312249                  0.173844

                               Age   Outcome
Pregnancies               0.522303  0.248172
Glucose                   0.266591  0.492911
BloodPressure             0.324915  0.165723
SkinThickness             0.126107  0.214873
Insulin                   0.136050  0.214278
BMI                       0.025744  0.312249
DiabetesPedigreeFunction  0.033561  0.173844
Age                       1.000000  0.238356
Outcome                   0.238356  1.000000
```

[24]:

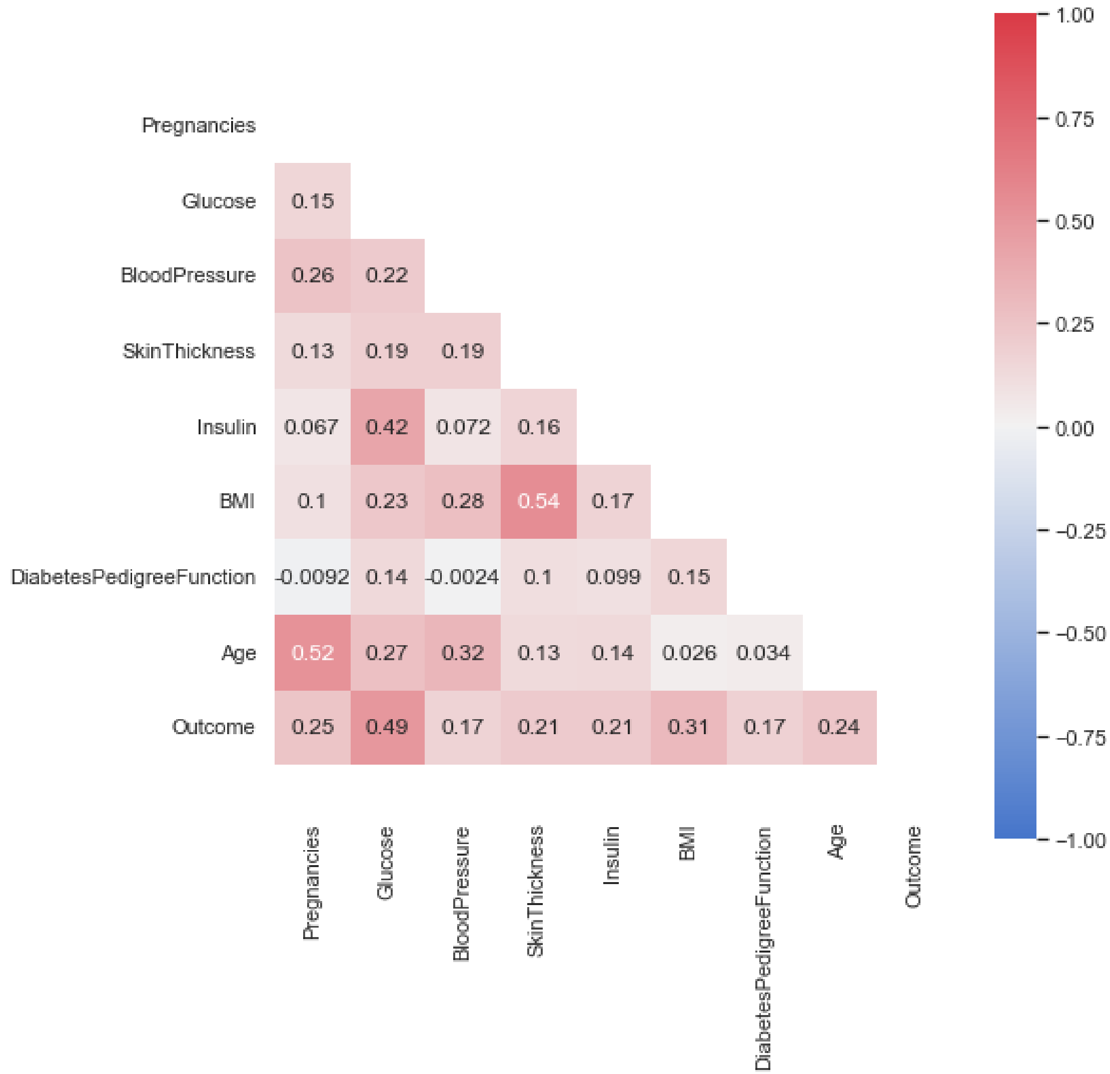
```
plt.figure(figsize=(15, 10))
sns.heatmap(corr,  annot=True,cmap='RdYlGn', linewidths=0.30)
plt.title("Healthcare Dataset Heatmap")
plt.show()

# Some strong positive correlation is noted between independant variables
```



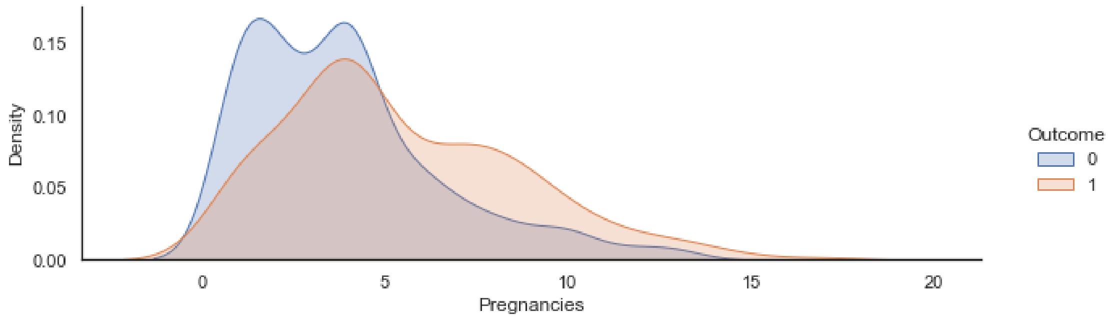
[25]:

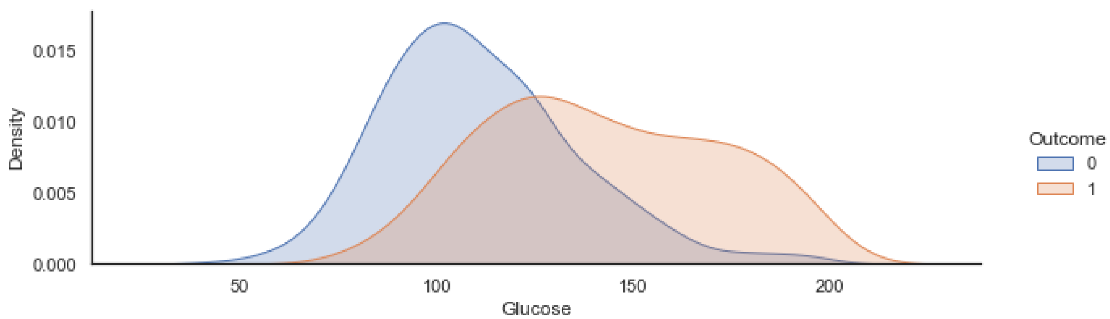
```python
# Correlation Matrix Heatmap Visualization (should run this code again after removing outliers/zero values)
sns.set(style="white")
# Generate a mask for the upper triangle
mask = np.zeros_like(df.corr(), dtype=np.bool)
mask[np.triu_indices_from(mask)] = True
# Set up the matplotlib figure to control size of heatmap
fig, ax = plt.subplots(figsize=(8,8))
# Create a custom color palette
cmap = sns.diverging_palette(255, 10, as_cmap=True)  # as_cmap returns a matplotlib colormap object rather than a list of colors
# Red=10, Green=128, Blue=255
# Plot the heatmap
sns.heatmap(df.corr(), mask=mask, annot=True, square=True, cmap=cmap , vmin=-1, vmax=1, ax=ax)  # annot display corr label
# Prevent Heatmap Cut-Off Issue
bottom, top = ax.get_ylim()
ax.set_ylim(bottom+0.5, top-0.5)
## Some strong positive correlation is noted between independant variables
```

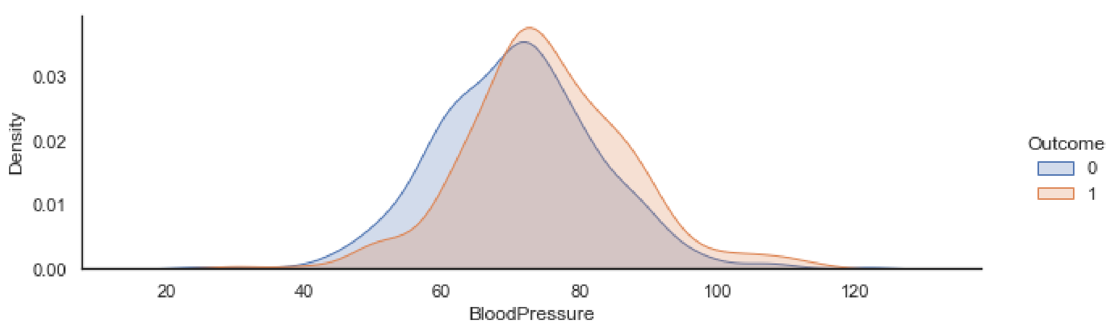
[25]: (9.5, -0.5)

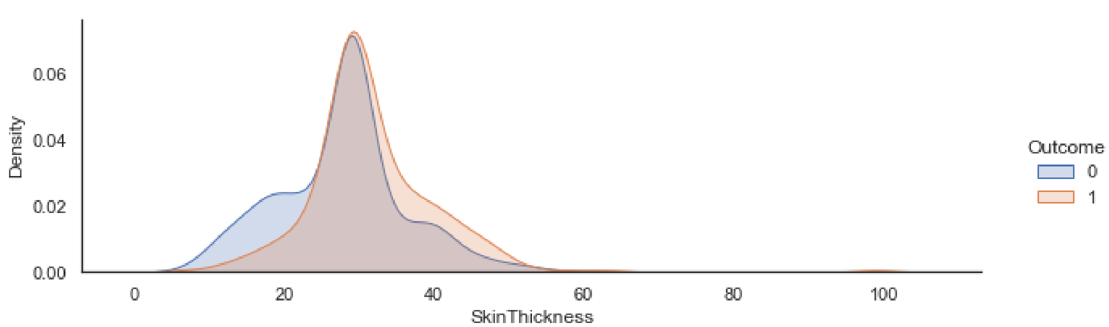


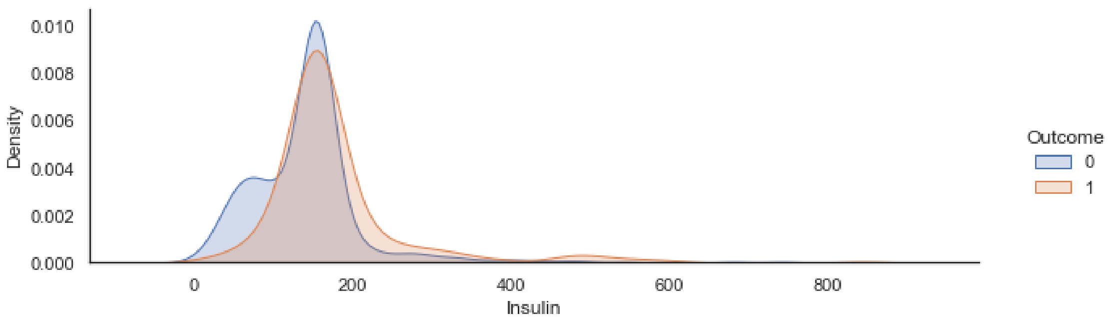
[26]:
```
for i in range(len(feature_cols)):
    sns.FacetGrid(df,hue="Outcome",aspect=3,margin_titles=True).map(sns.
↪kdeplot,feature_cols[i],shade= True).add_legend()
```

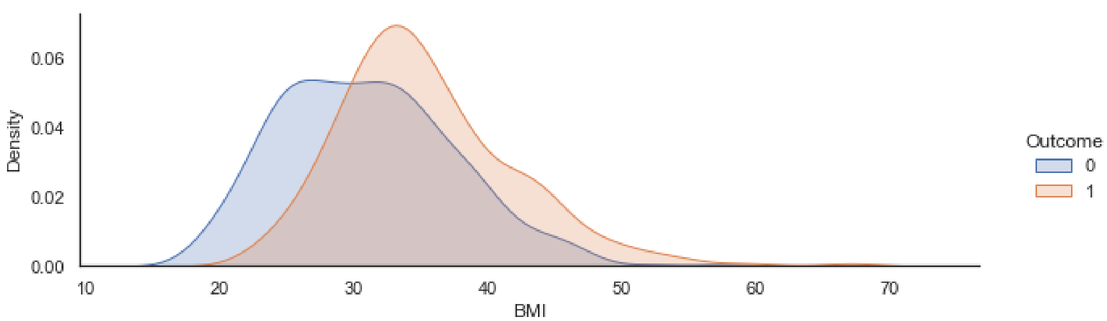

Density
0.15
0.10
0.05
0.00
0
5
10
15
20
Pregnancies
Outcome
0
1

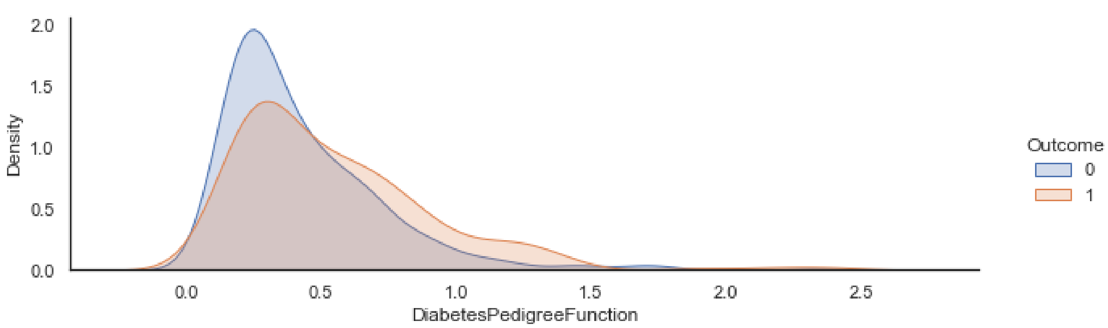

Density
0.015
0.010
0.005
0.000
50
100
150
200
Glucose
Outcome
0
1

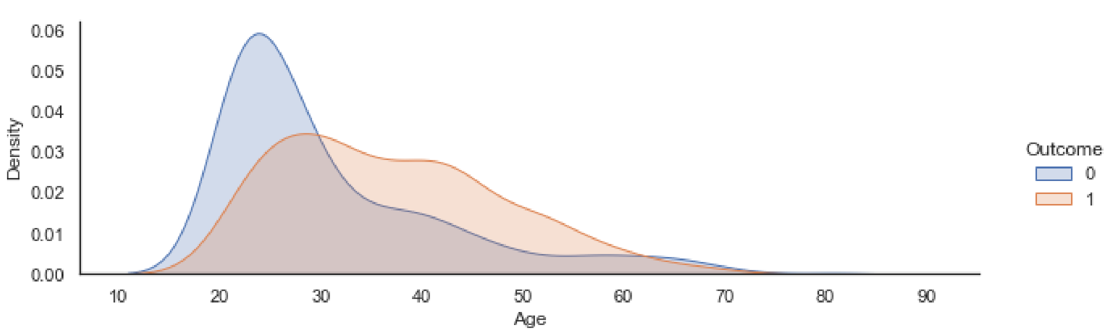

Density
0.03
0.02
0.01
0.00
20
40
60
80
100
120
BloodPressure
Outcome
0
1


Density
0.06
0.04
0.02
0.00
0
20
40
60
80
100
SkinThickness
Outcome
0
1


Density
0.010
0.008
0.006
0.004
0.002
0.000
0
200
400
600
800
Insulin
Outcome
0
1


Density
0.06
0.04
0.02
0.00
10
20
30
40
50
60
70
BMI
Outcome
0
1


Density
2.0
1.5
1.0
0.5
0.0
0.0
0.5
1.0
1.5
2.0
2.5
DiabetesPedigreeFunction
Outcome
0
1


Density
0.06
0.05
0.04
0.03
0.02
0.01
0.00
10
20
30
40
50
60
70
80
90
Age
Outcome
0
1

1.0.8 Project Task: Week 3

Data Modeling:

1. Devise strategies for model building. It is important to decide the right validation framework. Express your thought process. Strategies:- 1. Data modelling is for the prediction of a binary Outcome. Value can be either 0 or 1. 2. A supervised ML classification algorithm can be used 3. Logistic regression needs to checked, since it is good for binary classification 4. Tree based algorithms, also needs to be tried out, since the dataset has outliers. 5. Data Scaling must be done, before modeling 6. Holdout method or KFold CV can be used

[27]:
```
# import the ML algorithm
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
from statsmodels.tools.eval_measures import rmse
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import LinearSVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier

# pre-processing
from sklearn import preprocessing
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA

# import libraries for model validation
from sklearn.model_selection import StratifiedKFold
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import train_test_split
from sklearn.model_selection import LeaveOneOut

# import libraries for metrics and reporting
from sklearn.metrics import confusion_matrix
from sklearn.metrics import classification_report
from sklearn.metrics import accuracy_score
from sklearn.metrics import precision_score
from sklearn.metrics import recall_score
from sklearn.metrics import f1_score
from sklearn import metrics
from sklearn.metrics import classification_report
from sklearn.metrics import roc_curve, auc
```

```
from sklearn.model_selection import GridSearchCV
```

[28]:
```
x=df[feature_cols]
y=df['Outcome']
```

[29]:
```
# Splitting the dataset into the Training set and Test set
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size = 0.3,␣
↪random_state = 0)
```

[30]:
```
#Feature Scaling
sc = StandardScaler()
x_train_scaled = sc.fit_transform(x_train)
x_test_scaled = sc.transform(x_test)
```

2. Apply an appropriate classification algorithm to build a model. Compare various models with the results from KNN algorithm.

[31]:
```
#Using Logistic Regression Algorithm to the Training Set
classifier_logreg = LogisticRegression(random_state = 0)
classifier_logreg.fit(x_train_scaled, y_train)
y_pred_logreg=classifier_logreg.predict(x_test_scaled)
print('Accuracy of Logistic regression: {}'.
↪format(accuracy_score(y_test,y_pred_logreg)))
```

```
Accuracy of Logistic regression: 0.7705627705627706
```

[32]:
```
#Using KNeighborsClassifier Method of neighbors class to use Nearest Neighbor␣
↪algorithm
from sklearn.neighbors import KNeighborsClassifier
classifier_knn = KNeighborsClassifier(n_neighbors = 13)
classifier_knn.fit(x_train_scaled, y_train)
y_pred_knn=classifier_knn.predict(x_test_scaled)
print('Accuracy of KNN : {}'.format(accuracy_score(y_test,y_pred_knn)))
```

```
Accuracy of KNN : 0.7792207792207793
```

[33]:
```
#Using SVC method of svm class to use Support Vector Machine Algorithm
from sklearn.svm import SVC
classifier_svc = SVC(kernel = 'linear', random_state = 0)
classifier_svc.fit(x_train_scaled, y_train)
y_pred_svc=classifier_svc.predict(x_test_scaled)
print('Accuracy of SVM-linear: {}'.format(accuracy_score(y_test,y_pred_svc)))
```

```
Accuracy of SVM-linear: 0.7662337662337663
```

[34]:
```
#Using SVC-Kernel method of svm class to use Support Vector Machine Algorithm
from sklearn.svm import SVC
classifier_svc_rbf = SVC(kernel = 'rbf', random_state = 0,C=1)
classifier_svc_rbf.fit(x_train_scaled, y_train)
y_pred_svc_rbf=classifier_svc_rbf.predict(x_test_scaled)
print('Accuracy of SVM-RBF: {}'.format(accuracy_score(y_test,y_pred_svc_rbf)))
```

```
Accuracy of SVM-RBF: 0.7445887445887446
```

[35]:
```
#Using Naive Bayes to use Support Vector Machine Algorithm
# GaussianNB
classifier_nb = GaussianNB()
classifier_nb.fit(x_train_scaled, y_train)
y_pred_nb=classifier_nb.predict(x_test_scaled)
print('Accuracy of Naive Bayes-Gaussian: {}'.
 ↪format(accuracy_score(y_test,y_pred_nb)))
```

```
Accuracy of Naive Bayes-Gaussian: 0.7532467532467533
```

[36]:
```
#Using DecisionTreeClassifier of tree class to use Decision Tree Algorithm

from sklearn.tree import DecisionTreeClassifier
classifier_dec = DecisionTreeClassifier(criterion = 'entropy', random_state = 0)
classifier_dec.fit(x_train, y_train)
y_pred_dec=classifier_dec.predict(x_test)
print('Accuracy of Decision Tree Classifier: {}'.
 ↪format(accuracy_score(y_test,y_pred_dec)))
```

```
Accuracy of Decision Tree Classifier: 0.7445887445887446
```

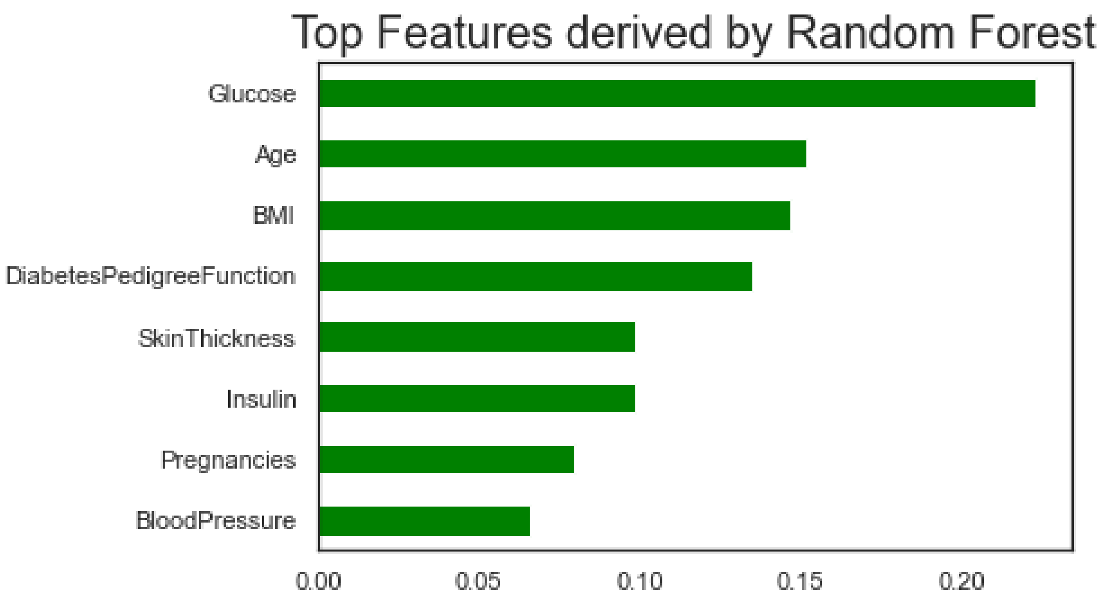
[37]:
```
#Using RandomForestClassifier method of ensemble class to use Random Forest␣
 ↪Classification algorithm

from sklearn.ensemble import RandomForestClassifier
classifier_rnd = RandomForestClassifier(n_estimators = 9, criterion =␣
 ↪'entropy', random_state = 0)
classifier_rnd.fit(x_train_scaled, y_train)
y_pred_rnd=classifier_rnd.predict(x_test_scaled)
print('Accuracy of Random Forest Classifier: {}'.
 ↪format(accuracy_score(y_test,y_pred_rnd)))
```

```
Accuracy of Random Forest Classifier: 0.7878787878787878
```

[38]:
```
feature_imp=sorted(list(zip(feature_cols,classifier_rnd.
 ↪feature_importances_)),key=lambda x:x[1],reverse=True)
feature_imp[:10] # Top 10 important features
```

[38]:
```
[('Glucose', 0.2228201379776521),
 ('Age', 0.1517873256817099),
 ('BMI', 0.14719738003933125),
 ('DiabetesPedigreeFunction', 0.13511585970768406),
 ('SkinThickness', 0.09879866678114017),
 ('Insulin', 0.09843081839304385),
 ('Pregnancies', 0.08010429797887891),
 ('BloodPressure', 0.06574551344055982)]
```

[39]:
```
# Plot the top features based on its importance
pd.Series(classifier_rnd.feature_importances_,index=x.columns).nlargest(10).
 ↪plot(kind='barh',color='green').invert_yaxis()
plt.title('Top Features derived by Random Forest', size=20)
plt.show()
```



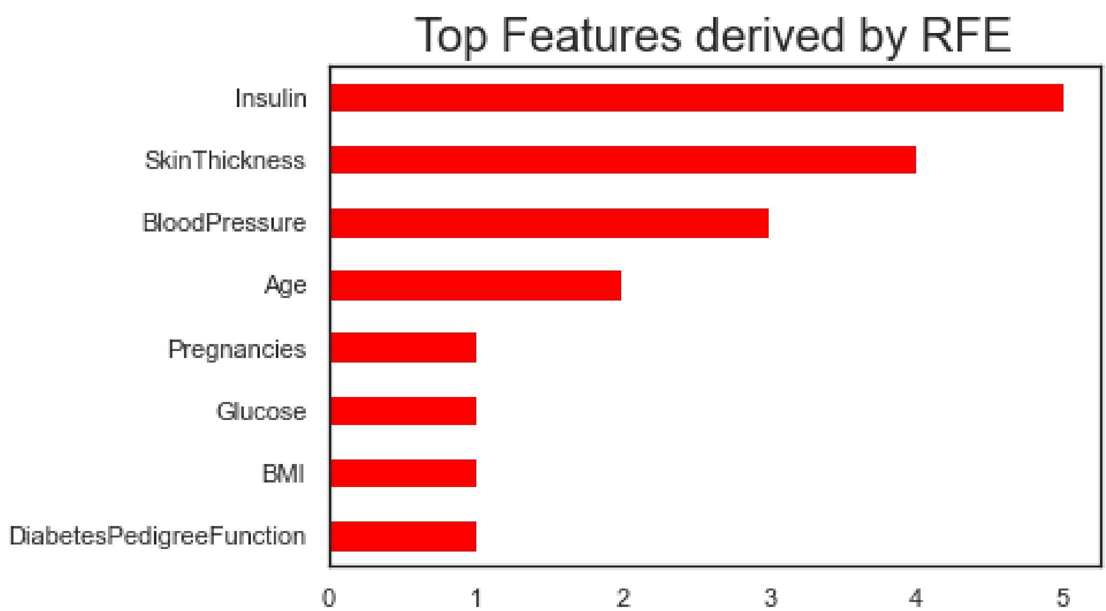
[40]:
```
# Feature Selection using RFE
from sklearn.feature_selection import RFE
```

[41]:
```
rfe=RFE(estimator=classifier_logreg,n_features_to_select=4)
rfe.fit(x,y)
for i in sorted(list(zip(feature_cols,rfe.ranking_)), key=lambda x:
 ↪x[1],reverse=True):
      print(i)
```

```
('Insulin', 5)
('SkinThickness', 4)
('BloodPressure', 3)
```

```
('Age', 2)
('Pregnancies', 1)
('Glucose', 1)
('BMI', 1)
('DiabetesPedigreeFunction', 1)
```

[42]:
```
pd.Series(rfe.ranking_,index=x.columns).nlargest(10).
 ↪plot(kind='barh',color='red').invert_yaxis()
plt.title('Top Features derived by RFE', size=20)
plt.show()
```



[43]:
```
# Using the selected fetures to predict outcome
features_selected␣
 ↪=['Insulin','SkinThickness','Age','BloodPressure','Pregnancies']
x_train_new= x_train[features_selected]
x_test_new=x_test[features_selected]
```

[44]:
```
x_train_scaled_new =sc.fit_transform(x_train_new)
x_test_scaled_new=sc.fit_transform(x_test_new)
```

[45]:
```
classifier_rnd_new = RandomForestClassifier(n_estimators = 9, criterion =␣
 ↪'entropy', random_state = 0)
classifier_rnd_new.fit(x_train_scaled_new, y_train)
y_pred_rnd_new=classifier_rnd_new.predict(x_test_scaled_new)
print('Accuracy of Random Forest Classifier with Selected Features: {}'.
 ↪format(accuracy_score(y_test,y_pred_rnd_new)))
```

```
Accuracy of Random Forest Classifier with Selected Features: 0.6536796536796536
```

[46]:
```
# create a model building fn for easy comparison
kf = StratifiedKFold(n_splits=5, shuffle=True, random_state=100)

def baseline_model(model,x_train_scaled,y_train,x_test_scaled,y_test,name):
    model.fit(x_train_scaled,y_train)

    accuracy     = np.mean(cross_val_score(model, x_train_scaled, y_train,␣
 ↪cv=kf, scoring='accuracy'))
    precision    = np.mean(cross_val_score(model, x_train_scaled, y_train,␣
 ↪cv=kf, scoring='precision'))
    recall       = np.mean(cross_val_score(model, x_train_scaled, y_train,␣
 ↪cv=kf, scoring='recall'))
    f1score      = np.mean(cross_val_score(model, x_train_scaled, y_train,␣
 ↪cv=kf, scoring='f1'))
    rocauc       = np.mean(cross_val_score(model, x_train_scaled, y_train,␣
 ↪cv=kf, scoring='roc_auc'))

    y_pred = model.predict(x_test_scaled)

    df_models = pd.DataFrame({'model'        : [name],
                             'accuracy'     : [accuracy],
                             'precision'    : [precision],
                             'recall'       : [recall],
                             'f1score'      : [f1score],
                             'rocauc'       : [rocauc],
                              })   # metrics to be used for comparison later
    return df_models

df_models=pd.
 ↪concat([baseline_model(classifier_logreg,x_train_scaled,y_train,x_test_scaled,y_test,'Logis
 ↪Regression'),
                  ␣
 ↪baseline_model(classifier_knn,x_train_scaled,y_train,x_test_scaled,y_test,'KNN␣
 ↪Classifer'),
                  ␣
 ↪baseline_model(classifier_svc,x_train_scaled,y_train,x_test_scaled,y_test,'Linear␣
 ↪SVC'),
                  ␣
 ↪baseline_model(classifier_svc_rbf,x_train_scaled,y_train,x_test_scaled,y_test,'SVC-RBF'),
                  ␣
 ↪baseline_model(classifier_nb,x_train_scaled,y_train,x_test_scaled,y_test,'Gaussian␣
 ↪NB'),
                  ␣
 ↪baseline_model(classifier_dec,x_train_scaled,y_train,x_test_scaled,y_test,'Decision␣
 ↪Tree'),
```

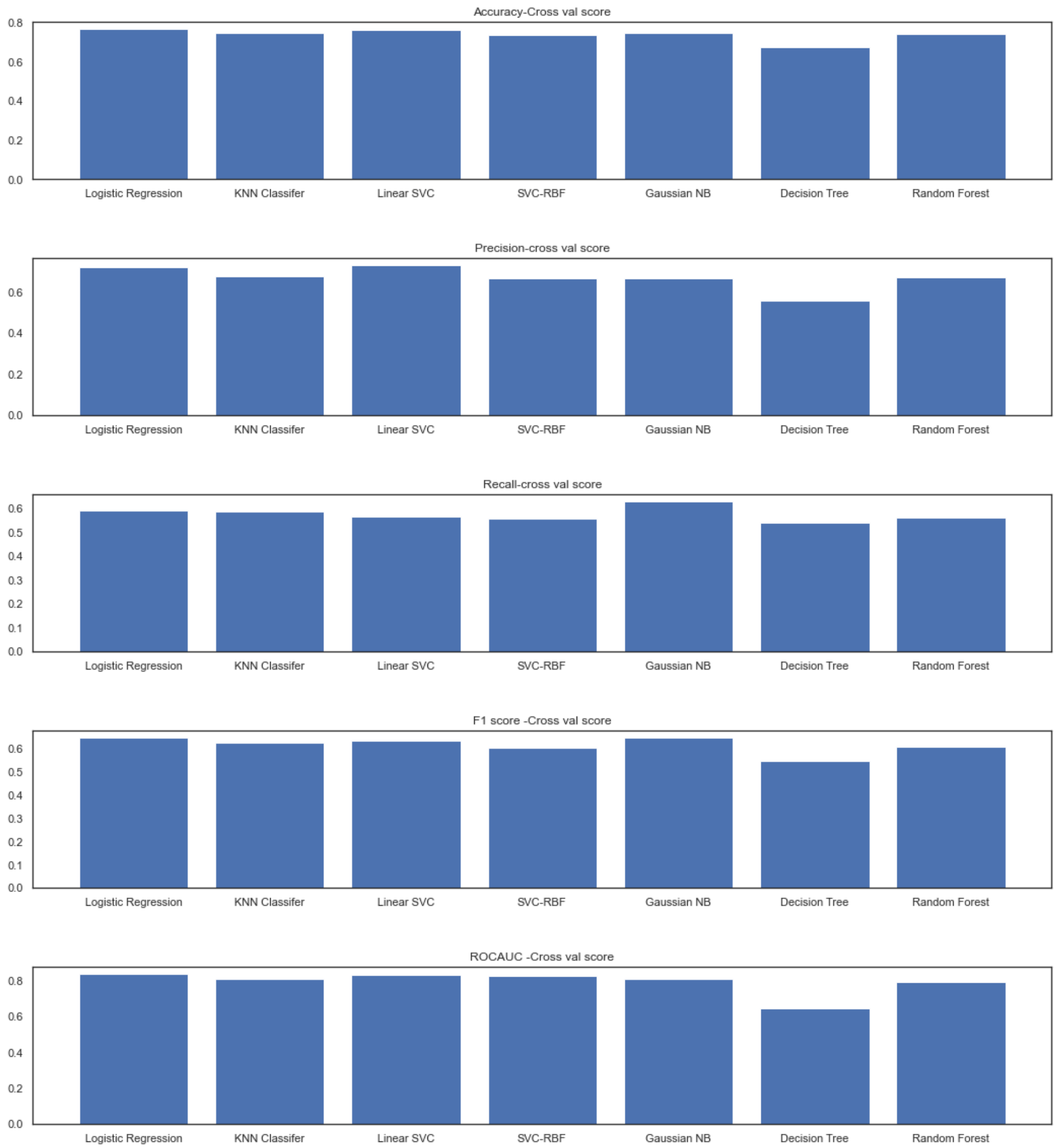
```
                     ␣
↪baseline_model(classifier_rnd,x_train_scaled,y_train,x_test_scaled,y_test,'Random␣
↪Forest')],
                   axis=0).reset_index()

df_models = df_models.drop('index', axis=1)
df_models
```

[46]:

	model	accuracy	precision	recall	f1score	rocauc
0	Logistic Regression	0.767065	0.721360	0.592173	0.647155	0.835375
1	KNN Classifer	0.748529	0.675292	0.587449	0.627657	0.809642
2	Linear SVC	0.763361	0.729954	0.566532	0.634171	0.833505
3	SVC-RBF	0.737349	0.665880	0.556140	0.603961	0.824643
4	Gaussian NB	0.750242	0.668436	0.628475	0.646598	0.810263
5	Decision Tree	0.675891	0.559716	0.541430	0.547777	0.646589
6	Random Forest	0.741035	0.672384	0.561538	0.610556	0.791475

[47]:

```
## plot the performance metric scores
fig, ax = plt.subplots(5, 1, figsize=(18, 20))

ax[0].bar(df_models.model, df_models.accuracy)
ax[0].set_title('Accuracy-Cross val score')

ax[1].bar(df_models.model, df_models.precision)
ax[1].set_title('Precision-cross val score')

ax[2].bar(df_models.model, df_models.recall)
ax[2].set_title('Recall-cross val score')

ax[3].bar(df_models.model, df_models.f1score)
ax[3].set_title('F1 score -Cross val score')

ax[4].bar(df_models.model, df_models.rocauc)
ax[4].set_title('ROCAUC -Cross val score')

# Fine-tune figure; make subplots farther from each other, or nearer to each␣
↪other.
fig.subplots_adjust(hspace=0.5, wspace=0.5)
```



1.0.9 Project Task: Week 4

Data Modeling:

1. Create a classification report by analyzing sensitivity, specificity, AUC (ROC curve), etc. Please be descriptive to explain what values of these parameter you have used.

Random Forest Classifer Evaluation

[48]:
```
print(classification_report(y_test,y_pred_rnd))
```

```
              precision    recall  f1-score   support

           0       0.83      0.87      0.85       157
           1       0.69      0.61      0.65        74

    accuracy                           0.79       231
   macro avg       0.76      0.74      0.75       231
weighted avg       0.78      0.79      0.78       231
```

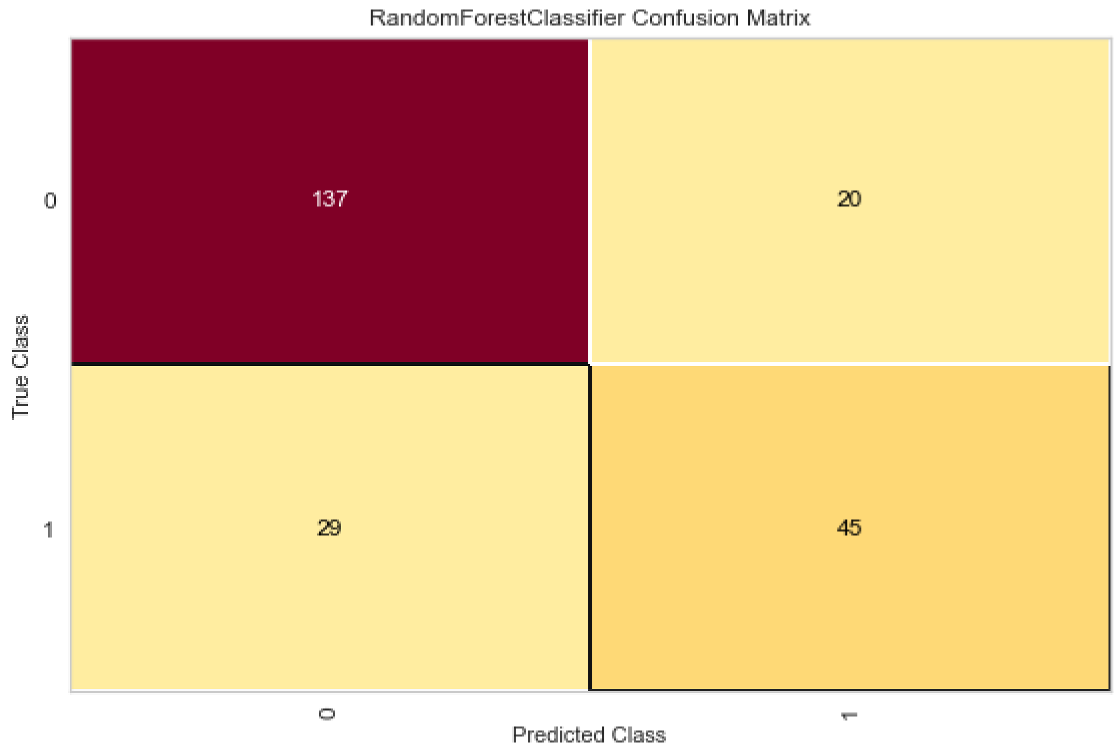
[49]:
```
print(confusion_matrix(y_test,y_pred_rnd))
```

```
[[137  20]
 [ 29  45]]
```

[70]:
```
#pip install yellowbrick
```

[51]:
```
from yellowbrick.classifier import ConfusionMatrix
```

[52]:
```
cm=ConfusionMatrix(classifier_rnd)
cm.fit(x_train_scaled,y_train)
cm.score(x_test_scaled,y_test)
cm.show()
# TP=45, FP=20
# TN=137,FN=29
```




```
[52]: <AxesSubplot:title={'center':'RandomForestClassifier Confusion Matrix'},
      xlabel='Predicted Class', ylabel='True Class'>
```

K Nearest Neighbors Classifier Evluation:-

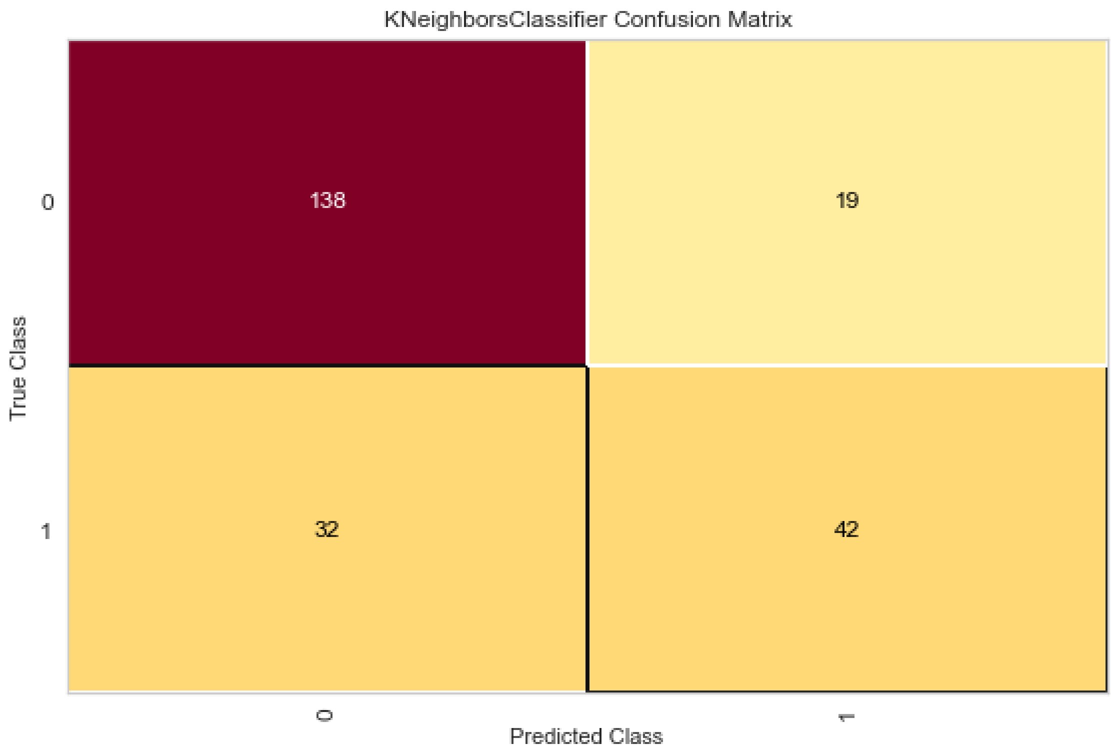
```
[53]: print(classification_report(y_test,y_pred_knn))
```

```
              precision    recall  f1-score   support

           0       0.81      0.88      0.84       157
           1       0.69      0.57      0.62        74

    accuracy                           0.78       231
   macro avg       0.75      0.72      0.73       231
weighted avg       0.77      0.78      0.77       231
```

```
[54]: print(confusion_matrix(y_test,y_pred_knn))
```

```
[[138  19]
 [ 32  42]]
```

[55]:
```
cm=ConfusionMatrix(classifier_knn)
cm.fit(x_train_scaled,y_train)
cm.score(x_test_scaled,y_test)
cm.show()
# TP=42, FP=19
# TN=138,FN=32
```



[55]:
```
<AxesSubplot:title={'center':'KNeighborsClassifier Confusion Matrix'},
xlabel='Predicted Class', ylabel='True Class'>
```

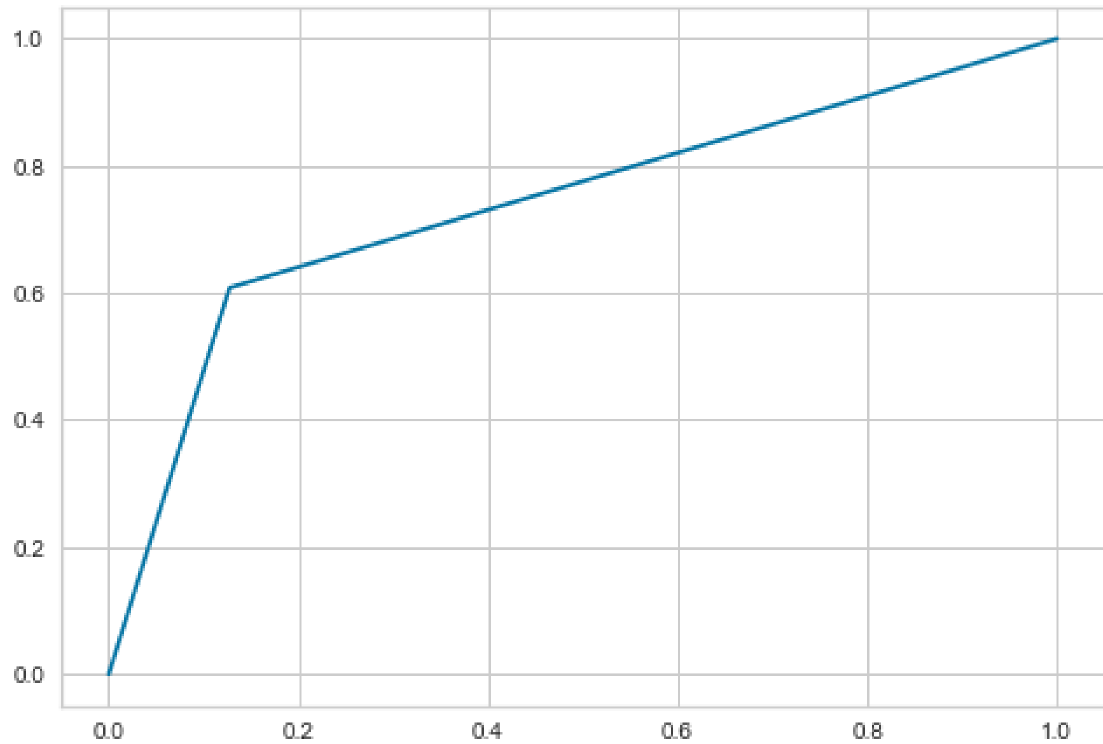
Compared to KNN Classifer, the random forest classifer gives better metrics

[56]:
```
fpr, tpr, thresholds=roc_curve(y_test,y_pred_rnd)
auc(fpr,tpr)
```

[56]:
```
0.7403597865381305
```

[57]:
```
plt.plot(fpr,tpr)
```

[57]:
```
[<matplotlib.lines.Line2D at 0x1cd0f9a25b0>]
```

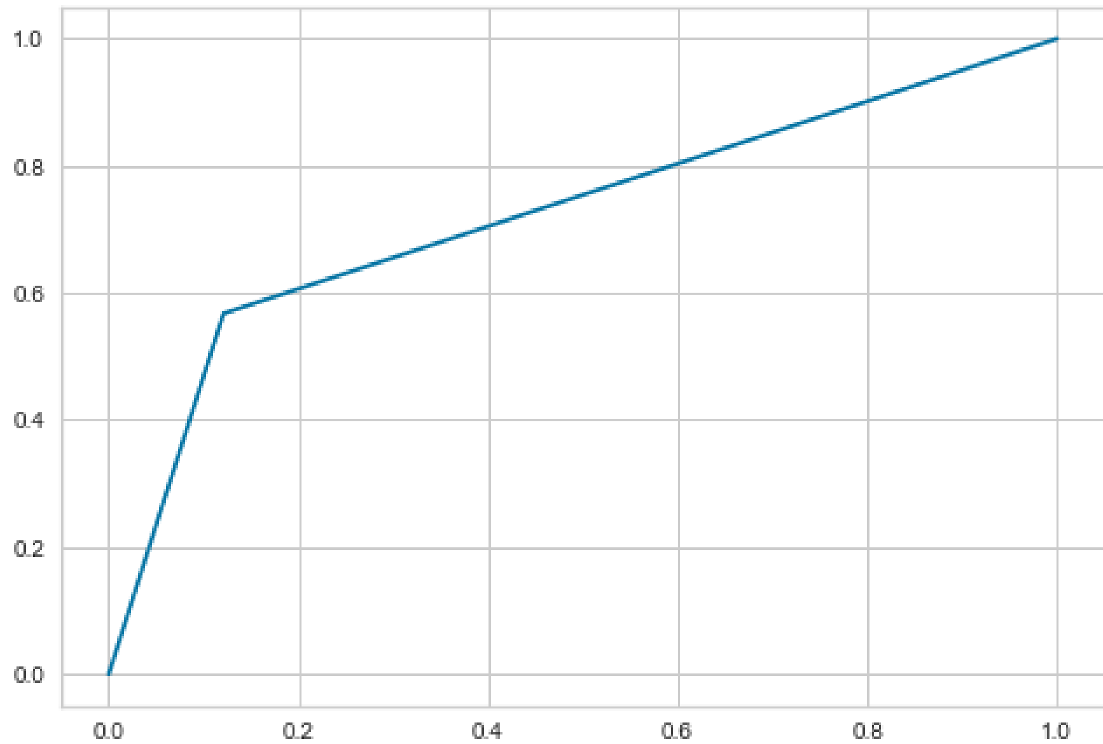


[58]:
```
fpr, tpr, thresholds=roc_curve(y_test,y_pred_knn)
auc(fpr,tpr)
```

[58]: 0.7232742296436564

[59]:
```
plt.plot(fpr,tpr)
```

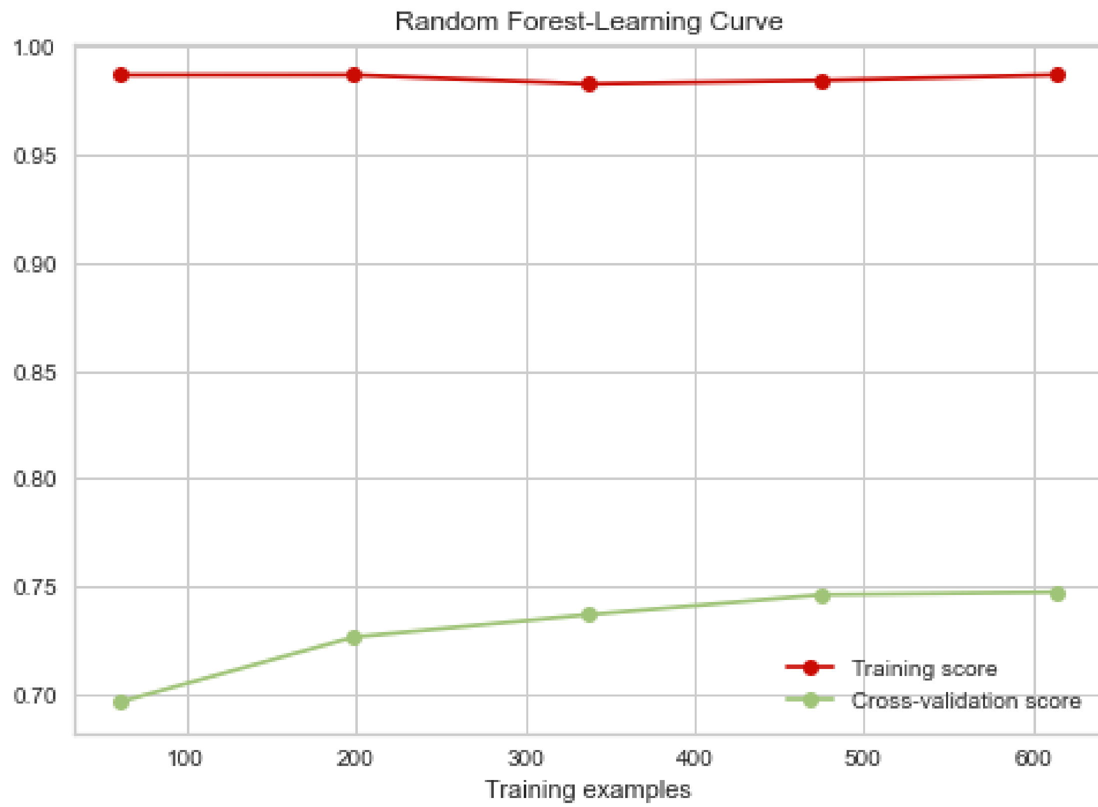
[59]: [<matplotlib.lines.Line2D at 0x1cd12348b20>]



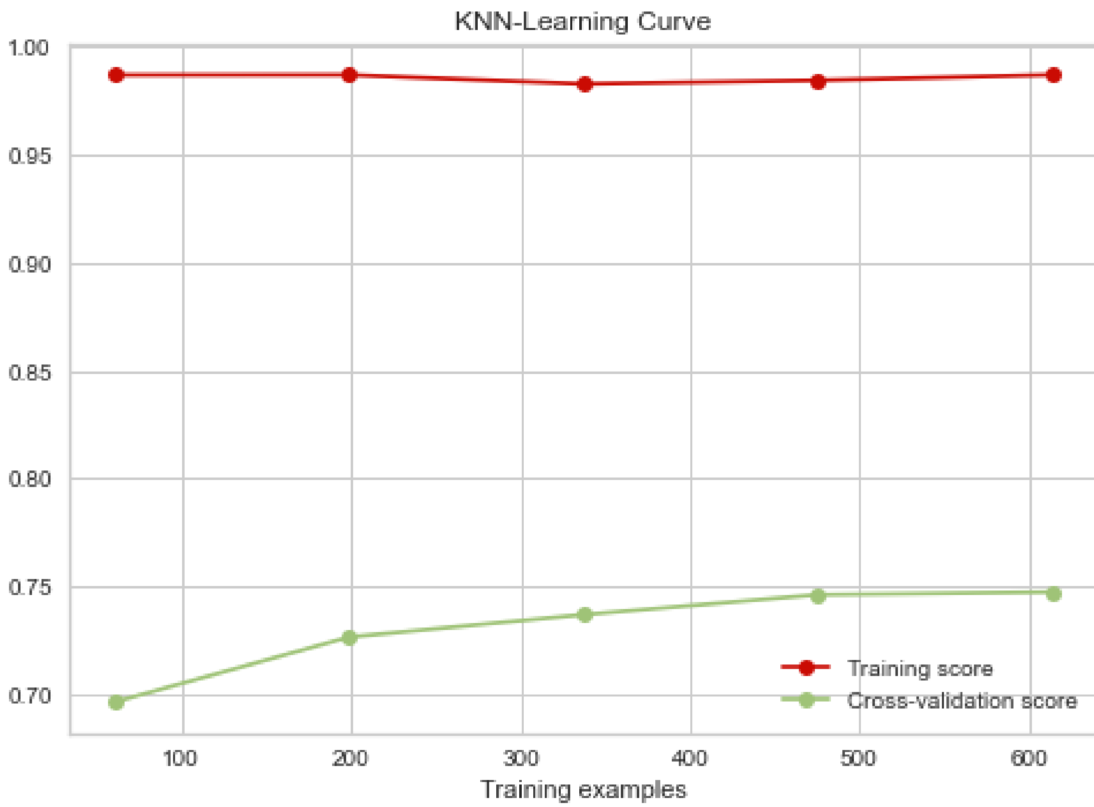
AUC value for Random Forest is better than KNN. (74% compared to 72%)

[60]:
```
from sklearn.model_selection import learning_curve
```

[61]:
```
train_sizes, train_scores, test_scores = learning_curve(classifier_rnd, x, y,␣
↪n_jobs=-1, cv=5,
                                                        verbose=0)

train_scores_mean = np.mean(train_scores, axis=1)
test_scores_mean = np.mean(test_scores, axis=1)

plt.figure()
plt.title("Random Forest-Learning Curve")
plt.xlabel("Training examples")
# plot the average training and test score lines at each training set size
plt.plot(train_sizes, train_scores_mean, 'o-', color="r", label="Training␣
↪score")
plt.plot(train_sizes, test_scores_mean, 'o-', color="g",␣
↪label="Cross-validation score")
plt.legend()
plt.show()
```



[62]:
```
train_sizes, train_scores, test_scores = learning_curve(classifier_rnd, x, y,␣
↪n_jobs=-1, cv=5,
                                                        verbose=0)

train_scores_mean = np.mean(train_scores, axis=1)
test_scores_mean = np.mean(test_scores, axis=1)

plt.figure()
plt.title("KNN-Learning Curve")
plt.xlabel("Training examples")
# plot the average training and test score lines at each training set size
plt.plot(train_sizes, train_scores_mean, 'o-', color="r", label="Training␣
↪score")
plt.plot(train_sizes, test_scores_mean, 'o-', color="g",␣
↪label="Cross-validation score")
plt.legend()
plt.show()
```



[63]:
```
train_sizes, train_scores, test_scores = learning_curve(classifier_logreg, x,␣
 ↪y, n_jobs=-1, cv=5,
                                                        verbose=0)

train_scores_mean = np.mean(train_scores, axis=1)
test_scores_mean = np.mean(test_scores, axis=1)

plt.figure()
plt.title("Logistic Regression-Learning Curve")
plt.xlabel("Training examples")
# plot the average training and test score lines at each training set size
plt.plot(train_sizes, train_scores_mean, 'o-', color="r", label="Training␣
 ↪score")
plt.plot(train_sizes, test_scores_mean, 'o-', color="g",␣
 ↪label="Cross-validation score")
plt.legend()
plt.show()
```

Data models are clearly overfit, since there is a big variance between train scores and test scores. The techniques used ot reduce overfitting are

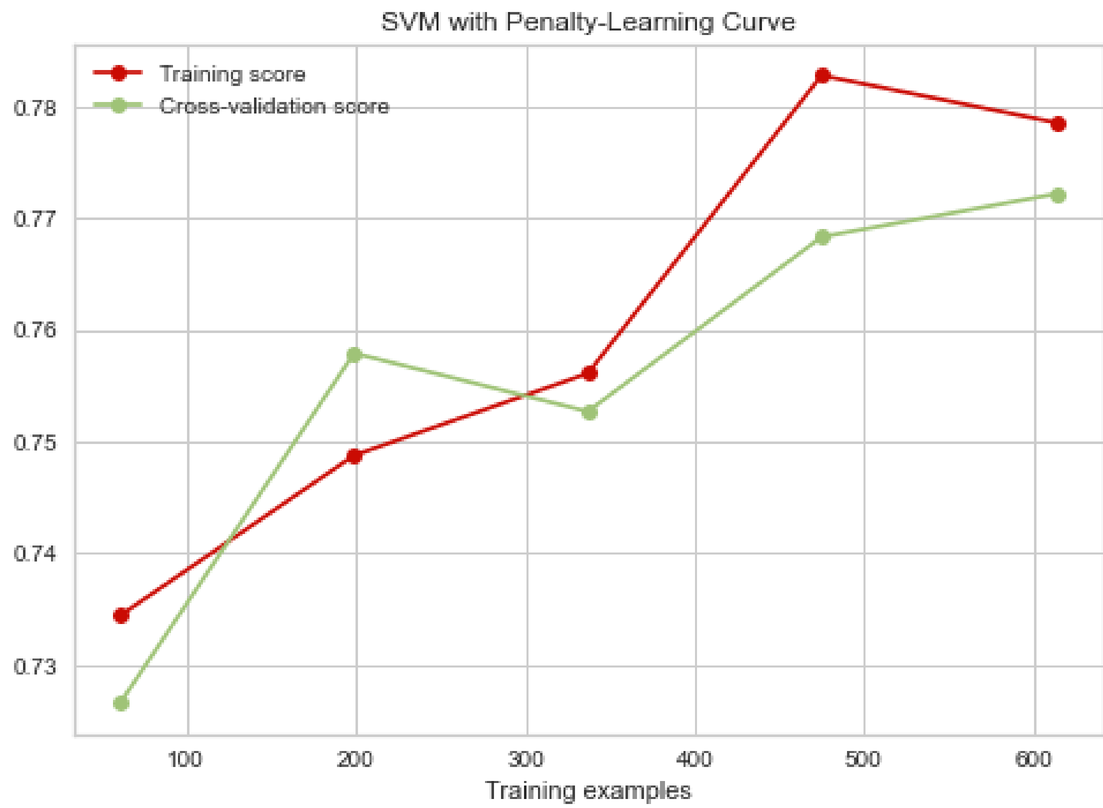
1. cross validation
2. Regularization
3. Feature Selection
4. Dimensionality Reduction

[64]:
```
classifier_svc_reg = SVC(kernel = 'linear', random_state = 0,C=100)
classifier_svc_reg.fit(x_train_scaled, y_train)
y_pred_svc_reg=classifier_svc_reg.predict(x_test_scaled)
print('Accuracy of SVM-linear with Regularization: {}'.
 ↪format(accuracy_score(y_test,y_pred_svc_reg)))
```

```
Accuracy of SVM-linear with Regularization: 0.7662337662337663
```

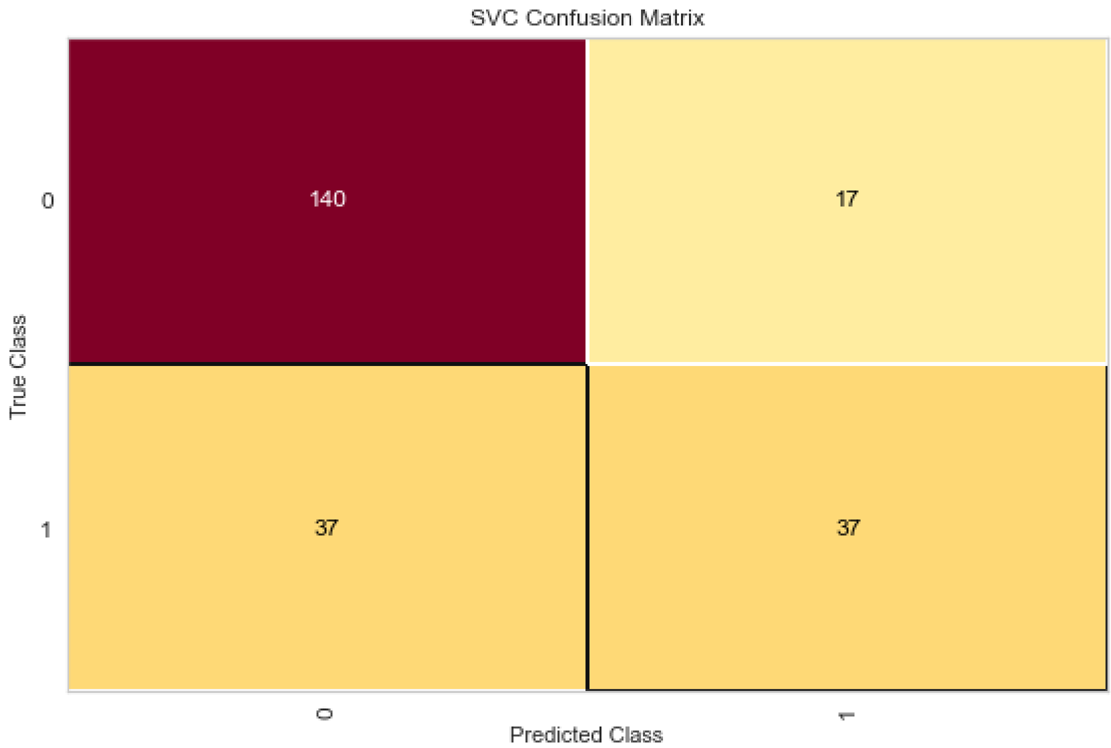
[65]:
```
train_sizes, train_scores, test_scores = learning_curve(classifier_svc_reg, x,␣
 ↪y, n_jobs=-1, cv=5,
                                                        verbose=0)

train_scores_mean = np.mean(train_scores, axis=1)
test_scores_mean = np.mean(test_scores, axis=1)
```

```
plt.figure()
plt.title("SVM with Penalty-Learning Curve")
plt.xlabel("Training examples")
# plot the average training and test score lines at each training set size
plt.plot(train_sizes, train_scores_mean, 'o-', color="r", label="Training␣
↪score")
plt.plot(train_sizes, test_scores_mean, 'o-', color="g",␣
↪label="Cross-validation score")
plt.legend()
plt.show()
```



Model gives good bias variance tradeoff.

[66]:
```
cm=ConfusionMatrix(classifier_svc_reg)
cm.fit(x_train_scaled,y_train)
cm.score(x_test_scaled,y_test)
cm.show()
# TP=37, FP=37
# TN=140,FN=17
```



[66]: <AxesSubplot:title={'center':'SVC Confusion Matrix'}, xlabel='Predicted Class', ylabel='True Class'>

[67]:
```
print(classification_report(y_test,y_pred_svc_reg))
```

```
              precision    recall  f1-score   support

           0       0.79      0.89      0.84       157
           1       0.69      0.50      0.58        74

    accuracy                           0.77       231
   macro avg       0.74      0.70      0.71       231
weighted avg       0.76      0.77      0.75       231
```

[68]:
```
'''
# Handling imbalance data - Rerunning above with resampled data - using␣
↪oversampling
# create fake sample data into the imbalanced side to balance it out.
from imblearn.over_sampling import SMOTE
sm = SMOTE(random_state = SEED)
x_train_sm, y_train_sm = sm.fit_sample(x_train, y_train.ravel())
```

```
print('X_train_sm.shape:', x_train_sm.shape)
print(pd.value_counts(pd.Series(y_train_sm)))

lassifier_svc_reg_sm = classifier_svc_reg.fit(x_train_sm, y_train_sm)
y_pred = classifier_svc_reg_sm.predict(x_test)
print('Model accuracy is', accuracy_score(y_test, y_pred))
print(classification_report(y_test, y_pred))
print(confusion_matrix(y_test, y_pred))
'''
```

[68]:

```
"\n# Handling imbalance data - Rerunning above with resampled data - using
oversampling\n# create fake sample data into the imbalanced side to balance it
out.\nfrom imblearn.over_sampling import SMOTE\nsm = SMOTE(random_state =
SEED)\nx_train_sm, y_train_sm = sm.fit_sample(x_train,
y_train.ravel())\n\nprint('X_train_sm.shape:', x_train_sm.shape)\nprint(pd.value
_counts(pd.Series(y_train_sm)))\n\nlassifier_svc_reg_sm =
classifier_svc_reg.fit(x_train_sm, y_train_sm)\ny_pred =
classifier_svc_reg_sm.predict(x_test)\nprint('Model accuracy is',
accuracy_score(y_test, y_pred))\nprint(classification_report(y_test,
y_pred))\nprint(confusion_matrix(y_test, y_pred))\n"
```

Linear Support Vector Machine, with regularization is best suited to predict the diabetic outcome

[69]:

```
# The most suitable model for the prediction is
# classifier_svc_reg = SVC(kernel = 'linear', random_state = 0,C=100)
# Accuracy of SVM-linear with Regularization: 0.7662337662337663
# Model gives good bias variance tradeoff.
# TP=37, FP=37
# TN=140,FN=17
```