MSDS Practicum II - Diabetes Data Analysis

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0.3.1 Spring 2020

0.3.2 Purpose of project:

Showcase skills in data manipulation and engineering, exploratory data analysis, visualizations and Machine leaning.

0.3.3 The problems to solve are:

1. What factors are best for predicting that someone has diabetes?
2. Which machine learning tool is best for predicting the outcome?

0.3.4 About the Dataset:

The dataset was contributed to Kaggle.com by Rahul. Data can be found at "https://www.kaggle.com/rahulsah06/machine-learning-for-diabetes-with-python"

0.3.5 Other Resources used:

"Pandas for Everyone' by Daniel Chen

https://www.kaggle.com/sagira/logistic-regression-math-behind-without-sklearn

https://www.kaggle.com/kwisatzhaderach/simple-mlp-approach

https://www.kaggle.com/aljojose/pima-indians-diabetes-my-first-project

https://towardsdatascience.com/feature-selection-techniques-in-machine-learning-with-python-f24e7da3f36e

https://www.kaggle.com/saurav9786/eda-makes-sense

https://www.kaggle.com/uciml/pima-indians-diabetes-database

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 or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. Several constraints were placed on the selection of these instances from a larger database. In particular, all patients here are females at least 21 years old of Pima Indian heritage.

0.4 Variables

Pregnancies - Number of times pregnant

Glucose - Plasma glucose concentration a 2 hours in an oral glucose tolerance test

BloodPressure - Diastolic blood pressure (mm Hg)

SkinThickness - Triceps skin fold thickness (mm)

Insulin - 2-Hour serum insulin (mu U/ml)

BMI - Body mass index (weight in kg/(height in m)^2)

DiabetesPedigreeFunction - Diabetes pedigree function

Age - Age (years)

Outcome

0.4.1 Import Libraries

[1]:
```
# import numpy, pandas. seaborn and matplotlib

import numpy as np
import pandas as pd
import seaborn as sns
sns.set()
import matplotlib.pyplot as plt
%matplotlib inline

# import warnings filter
import warnings
warnings.filterwarnings('ignore')
```

0.4.2 Upload Data

[2]:
```
# Use pandas to read the csv file

data= pd.read_csv('C:/Users/spbro/OneDrive/Desktop/diabetes_data.csv')
```

0.4.3 Eploratory Data Analysis

[3]:
```
# List the column names for the dataset
data.columns
```

[3]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

[4]:
```
# drop DiabetesPedigreeFunction column. Description does not appear to
# indicate what it really means and the purpose in the analysis

data.drop(['DiabetesPedigreeFunction'],axis=1,inplace=True)
```

[5]:
```
# use rename() to change column names

data = data.rename(columns = {'Pregnancies':'pregnancies'})
data = data.rename(columns = {'Glucose':'glucose'})
data = data.rename(columns = {'BloodPressure':'bloodpressure'})
data = data.rename(columns = {'Insulin':'insulin'})
data = data.rename(columns = {'Age':'age'})
data = data.rename(columns = {'Outcome':'outcome'})
data = data.rename(columns = {'SkinThickness':'skinthickness'})
data = data.rename(columns = {'BMI':'bmi'})
```

[6]:
```
# Display first 5 rows

data.head()
```

[6]:
```
   pregnancies  glucose  bloodpressure  skinthickness  insulin   bmi  age  \
0            6      148             72             35        0  33.6   50
1            1       85             66             29        0  26.6   31
2            8      183             64              0        0  23.3   32
3            1       89             66             23       94  28.1   21
4            0      137             40             35      168  43.1   33

   outcome
0        1
1        0
2        1
3        0
4        1
```

[7]:
```
# display columns

data.columns
```

[7]:
```
Index(['pregnancies', 'glucose', 'bloodpressure', 'skinthickness', 'insulin',
       'bmi', 'age', 'outcome'],
      dtype='object')
```

[8]:
```
# Display last 5 rows

data.tail()
```

[8]:
```
     pregnancies  glucose  bloodpressure  skinthickness  insulin   bmi  age  \
763           10      101             76             48      180  32.9   63
764            2      122             70             27        0  36.8   27
765            5      121             72             23      112  26.2   30
766            1      126             60              0        0  30.1   47
767            1       93             70             31        0  30.4   23

     outcome
763        0
764        0
765        0
766        1
767        0
```

[9]:
```
data.shape

# There are 768 rows and 9 columns
```

[9]:
```
(768, 8)
```

[10]:
```
# A statistical description of each column

data.describe()
```

[10]:
```
       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         age     outcome
count  768.000000  768.000000  768.000000
mean    31.992578   33.240885    0.348958
std      7.884160   11.760232    0.476951
min      0.000000   21.000000    0.000000
25%     27.300000   24.000000    0.000000
50%     32.000000   29.000000    0.000000
75%     36.600000   41.000000    1.000000
max     67.100000   81.000000    1.000000
```

[11]:
```
# check if data contains any null values

data.isnull().any()
```

[11]:
```
pregnancies      False
glucose          False
bloodpressure    False
skinthickness    False
insulin          False
bmi              False
age              False
outcome          False
dtype: bool
```

[12]:
```
# display more descriptive stats using .info()
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 8 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   age            768 non-null    int64
 7   outcome        768 non-null    int64
dtypes: float64(1), int64(7)
memory usage: 48.1 KB
```

[13]:
```
# how many instances of diabetes using count

data['outcome'].value_counts()
```

[13]:
```
0    500
1    268
Name: outcome, dtype: int64
```

[14]:
```
# Use groupby to explore number of people with diabetes per each observation␣
↪using mean values

data.groupby('outcome').mean()
```

[14]:
```
         pregnancies     glucose  bloodpressure  skinthickness     insulin  \
outcome
0           3.298000  109.980000      68.184000      19.664000   68.792000
1           4.865672  141.257463      70.824627      22.164179  100.335821

               bmi        age
outcome
0        30.304200  31.190000
1        35.142537  37.067164
```

Although the data info shows that there are no missing values, I can tell that the data is skwed because of unusual number of zeros. It appears unsual that Glucose, BloodPressure, SkinThickness, Insulin, and BMI will have zeros. I will concentrate on these five attributes and replace the zeros with NaN and then replace with the mean values.

[15]:
```
#Replace 0 with NaN

d=data[['glucose','bloodpressure','skinthickness','insulin','bmi']]=data[['glucose','bloodpres
 ↪replace(0,np.nan)
d.head()
```

[15]:
```
   glucose  bloodpressure  skinthickness  insulin   bmi
0    148.0           72.0           35.0      NaN  33.6
1     85.0           66.0           29.0      NaN  26.6
2    183.0           64.0            NaN      NaN  23.3
3     89.0           66.0           23.0     94.0  28.1
4    137.0           40.0           35.0    168.0  43.1
```

[16]:
```
#Replace NaN with mean values

data['glucose'].fillna(data['glucose'].median(),inplace=True)
data['bloodpressure'].fillna(data['bloodpressure'].median(),inplace=True)
data['skinthickness'].fillna(data['skinthickness'].median(),inplace=True)
data['insulin'].fillna(data['insulin'].median(),inplace=True)
data['bmi'].fillna(data['bmi'].median(),inplace=True)
data.head()
```

[16]:
```
   pregnancies  glucose  bloodpressure  skinthickness  insulin   bmi  age  \
0            6    148.0           72.0           35.0    125.0  33.6   50
1            1     85.0           66.0           29.0    125.0  26.6   31
2            8    183.0           64.0           29.0    125.0  23.3   32
3            1     89.0           66.0           23.0     94.0  28.1   21
4            0    137.0           40.0           35.0    168.0  43.1   33

   outcome
0        1
1        0
```

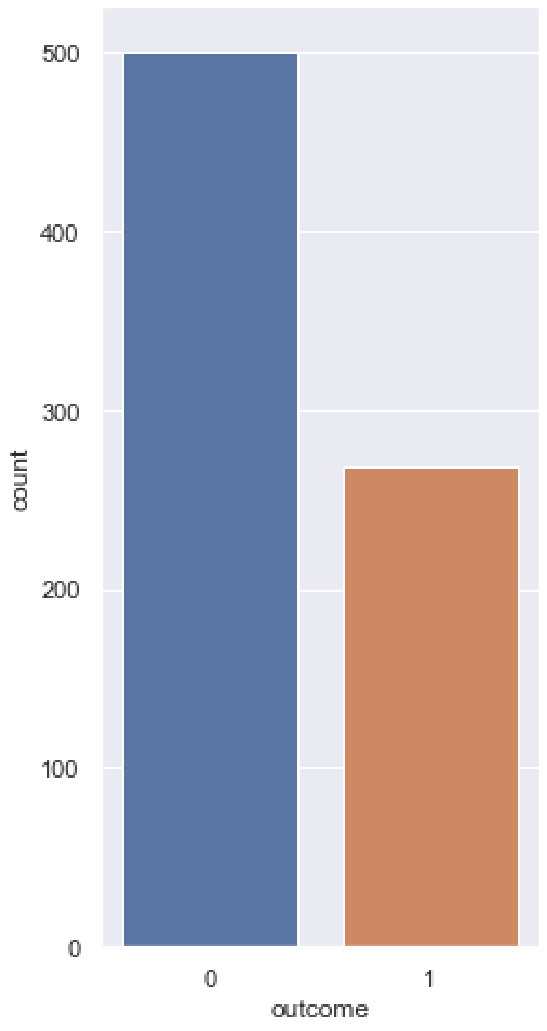
```
2         1
3         0
4         1
```

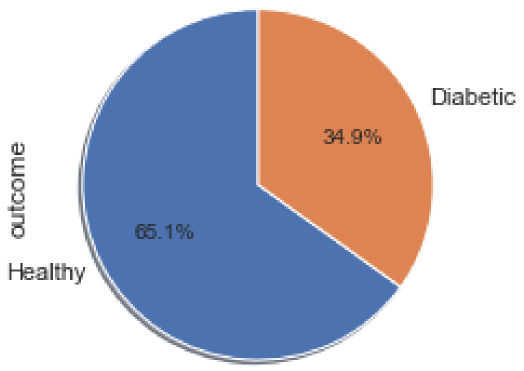
0.5 Data Visualization

0.6 BAR PLOT

[17]:
```
# The plot shows the amount of individuals that have diabetes and those who␣
↪dont.

# countplot----Plot the frequency of the Outcome

fig1, ax1 = plt.subplots(1,2,figsize=(8,8))

#It shows the count of observations in each categorical bin using bars

sns.countplot(data['outcome'],ax=ax1[0])

#Find the % of diabetic and Healthy person

labels = 'Healthy', 'Diabetic'

data.outcome.value_counts().plot.pie(labels=labels, autopct='%1.
↪1f%%',shadow=True, startangle=90)
```

[17]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x23bf994b188>
```

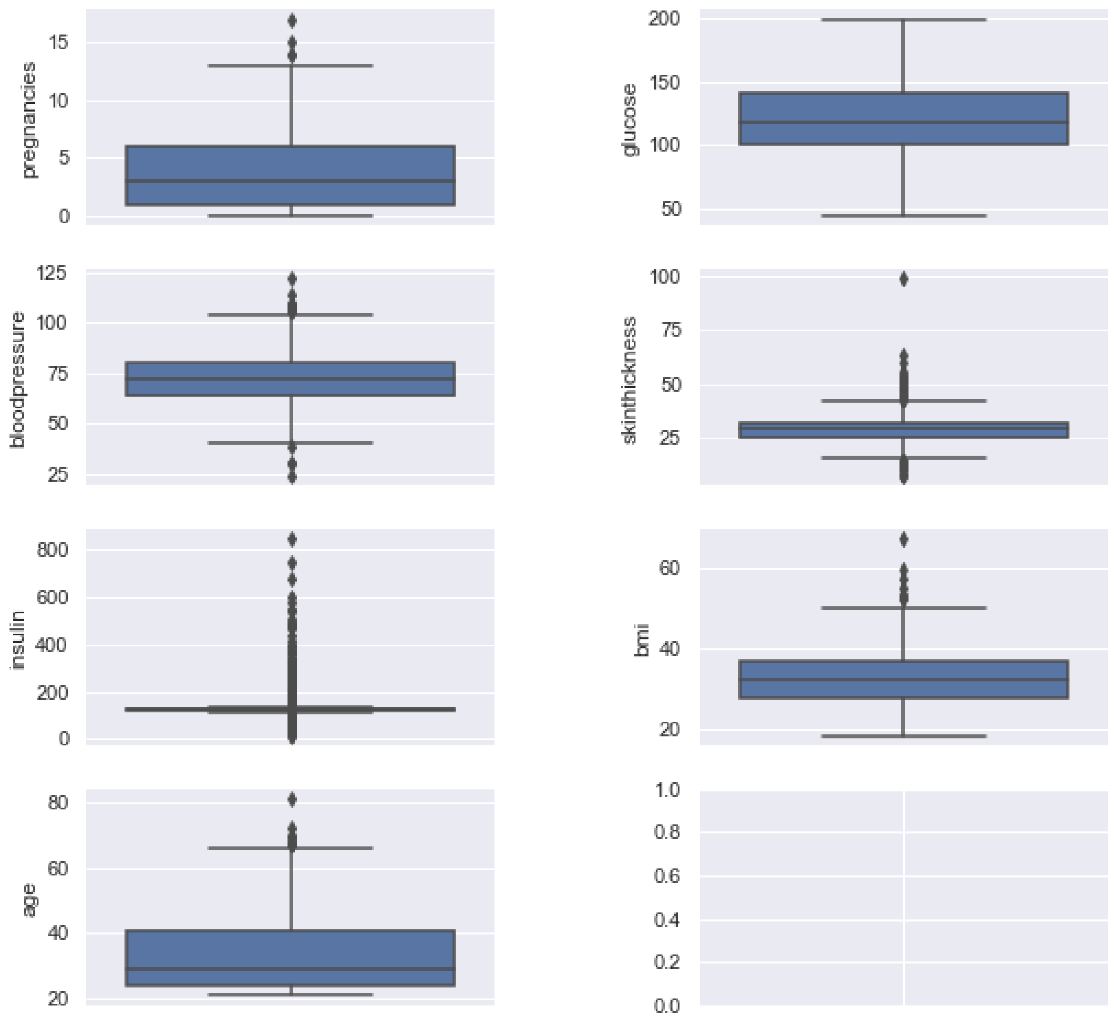




0.6.1 BOXPLOTS

[18]:
```
f, axes = plt.subplots(4,2, figsize=(10,10), sharex=True)

plt.subplots_adjust(wspace=0.5) # adjust the space between the plots

sns.despine(left=True)

# plot a boxplot of eacb observation to see if there are outliers

sns.boxplot( x= 'pregnancies',  data=data, orient='v',ax=axes[0,0])

sns.boxplot( x= 'glucose',  data=data, orient='v',ax=axes[0,1])

sns.boxplot( x= 'bloodpressure',  data=data, orient='v',ax=axes[1,0])
sns.boxplot( x= 'skinthickness',  data=data, orient='v',ax=axes[1,1])

sns.boxplot( x= 'insulin',  data=data, orient='v',ax=axes[2,0])

sns.boxplot( x= 'bmi',  data=data, orient='v',ax=axes[2,1])

sns.boxplot( x= 'age',  data=data, orient='v',ax=axes[3,0])
```

```
[18]: <matplotlib.axes._subplots.AxesSubplot at 0x23bf9b5f048>
```

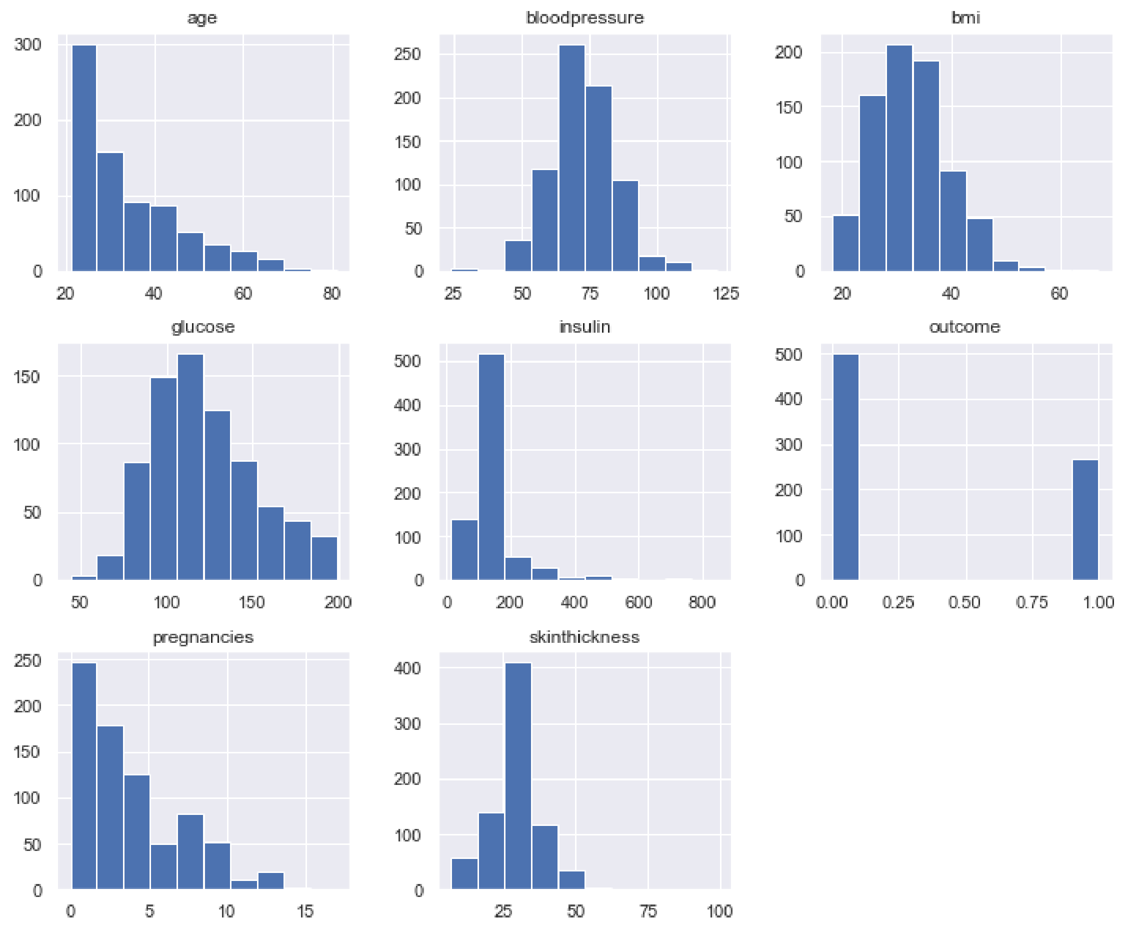


0.7 Observation

Although we have replaced zeros, the boxplots show outliers in all attributes.

0.8 HISTOGRAM

[19]:
```
data.hist(figsize=(12,10));
```



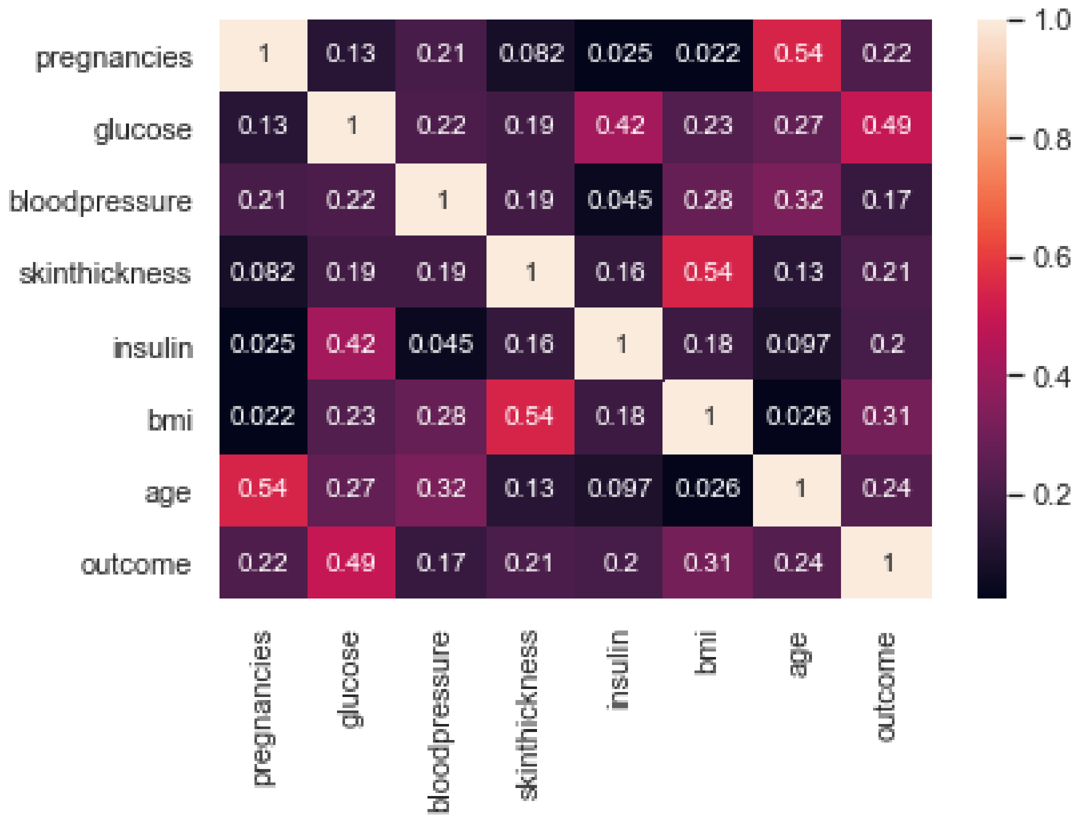
0.9 OBSERVATION

The plots show that Glucose, Blood Pressure, BMI are normally distributed.Pregnancies, Insulin,and Age are rightly skewed.

0.10 CORRELATION PLOT

[20]:
```
# corrlation matrix

cor=data.corr()

# correlation plot---heatmap

sns.heatmap(cor,annot=True)
```

```
[20]: <matplotlib.axes._subplots.AxesSubplot at 0x23bfa521e08>
```



	pregnancies	glucose	bloodpressure	skinthickness	insulin	bmi	age	outcome
pregnancies	1	0.13	0.21	0.082	0.025	0.022	0.54	0.22
glucose	0.13	1	0.22	0.19	0.42	0.23	0.27	0.49
bloodpressure	0.21	0.22	1	0.19	0.045	0.28	0.32	0.17
skinthickness	0.082	0.19	0.19	1	0.16	0.54	0.13	0.21
insulin	0.025	0.42	0.045	0.16	1	0.18	0.097	0.2
bmi	0.022	0.23	0.28	0.54	0.18	1	0.026	0.31
age	0.54	0.27	0.32	0.13	0.097	0.026	1	0.24
outcome	0.22	0.49	0.17	0.21	0.2	0.31	0.24	1

0.11 OBSERVATION

This shows that glucose is the most correlated with the outcome. Also, bimi, insulin and age appear to be next on the correlation scale.

Other correlation pairs are pregnancy to age, insulin to glucose, bmi and skinthickness, age and glucose.

0.12 MACHINE LEARNING (ML)

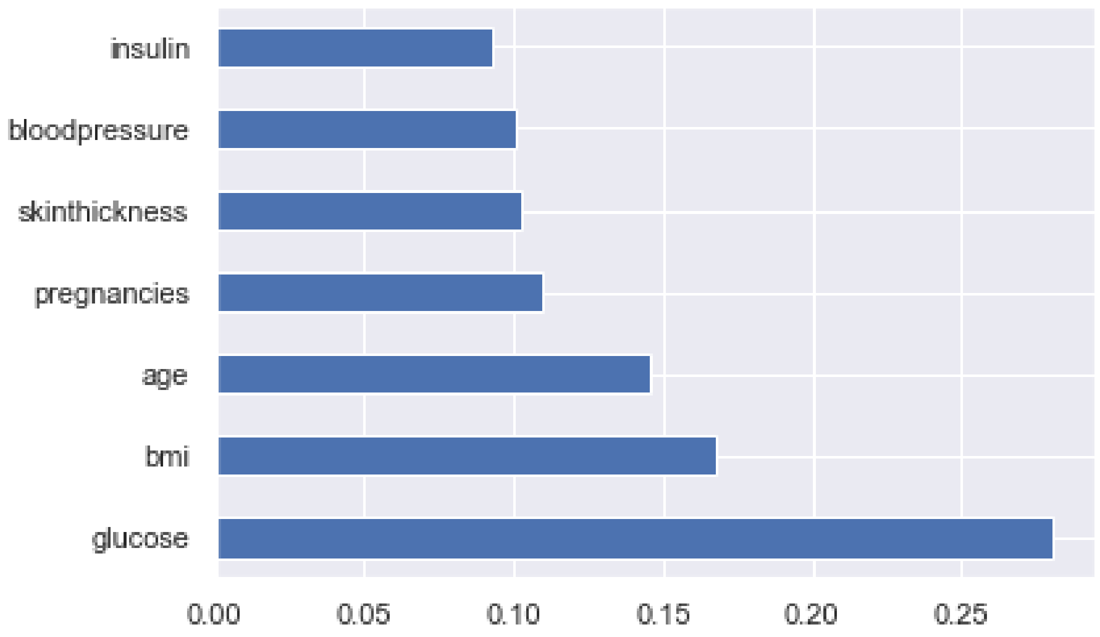
```
[21]: # Split data into X = observation and y = outcome

attributes = list(data.columns[:7])
X = data[attributes].values
y= data['outcome'].values

from sklearn import preprocessing

# Get column names first
```

```
names = data.columns[:7]# Create the Scaler object
scaler = preprocessing.StandardScaler()# Fit your data on the scaler object
scaled_df = scaler.fit_transform(X)
X = pd.DataFrame(scaled_df, columns=names)
```

Use ExtraTreesClassifier to determine feature or observation importance

[22]:
```
from sklearn.ensemble import ExtraTreesClassifier
model = ExtraTreesClassifier()
model.fit(X,y)
print(model.feature_importances_)

#plot graph of feature importances for better visualization
feat_importances = pd.Series(model.feature_importances_, index=X.columns)
feat_importances.nlargest(10).plot(kind='barh')
plt.show()
```

```
[0.10963028 0.28086509 0.10084644 0.10237593 0.09284294 0.16765796
 0.14578137]
```



0.13 OBSERVATION

It was supprising to me based on reseach that insuline and blodpressure will be lower on the scale to predict the outcome. Pregnancy was a bit more of a prefered predictor of the outcome than bloodpressure. The attribute that has a better predictability of the outcome was glucose.

Given that most of the observations were skewed, I decided to standardize the dataset in preparation for machine learning. This will be simply achived using StandardScaler from Sklearn.preprocessing.

[23]:
```
# Split into train and test sets for machine learning.
# test set was split at 20% and random_state set to 42

from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.20,␣
↪random_state = 42)
```

0.14 MODELS for ML

[24]:
```
# Import suite of algorithms.
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.svm import SVC
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis,␣
↪QuadraticDiscriminantAnalysis
from sklearn.ensemble import RandomForestClassifier, AdaBoostClassifier,␣
↪BaggingClassifier, GradientBoostingClassifier
from sklearn.calibration import CalibratedClassifierCV
```

[25]:
```
# Create objects of required models.
models = []
models.append(("KNN",KNeighborsClassifier()))
models.append(("DecisionTree",DecisionTreeClassifier()))
models.append(("QDA",  QuadraticDiscriminantAnalysis()))
models.append(("AdaBoost", AdaBoostClassifier()))
models.append(("SVM Linear",SVC(kernel="linear")))
models.append(("Random Forest",  RandomForestClassifier()))
models.append(("Bagging",BaggingClassifier()))
```

[26]:
```
# Find accuracy of models.
results = []
for name,model in models:
    kfold = KFold(n_splits=10, random_state=123)
    cv_result = cross_val_score(model,X_train,y_train, cv = kfold,scoring =␣
↪"accuracy")
    results.append(tuple([name,cv_result.mean(), cv_result.std()]))

results.sort(key=lambda x: x[1], reverse = True)
for i in range(len(results)):
    print('{:20s} {:2.2f} (+/-) {:2.2f} '.format(results[i][0] , results[i][1]␣
↪* 100, results[i][2] * 100))
```

```
SVM Linear          75.41 (+/-) 4.19
Bagging             75.09 (+/-) 2.93
AdaBoost            75.08 (+/-) 4.48
Random Forest       73.95 (+/-) 3.48
QDA                 73.78 (+/-) 6.01
KNN                 73.30 (+/-) 6.82
DecisionTree        71.99 (+/-) 4.22
```

0.15 FIND BEST PARAMETERS TO OPTIMIZE BEST MODEL

[27]:
```
### SVM Linear was the best model.
### find the parameters for SVM that will optimize the model
### using GridSearchCV.



from sklearn.model_selection import GridSearchCV
model = SVC()
paramaters = [
             {'C' : [0.001, 0.01, 0.1, 1, 10, 100, 1000], 'kernel' : ['linear']}
             ]
grid_search = GridSearchCV(estimator = model,
                           param_grid = paramaters,
                           scoring = 'accuracy',
                           cv = 10,
                           n_jobs = -1)
grid_search = grid_search.fit(X_train, y_train)
best_accuracy = grid_search.best_score_
best_parameters = grid_search.best_params_

print('Best accuracy : ', grid_search.best_score_)
print('Best parameters :', grid_search.best_params_  )
```

```
Best accuracy :  0.758957654723127
Best parameters : {'C': 0.01, 'kernel': 'linear'}
```

C = It controls the trade off between smooth decision boundary and classifying training points correctly. A large value of c means you will get more training points correctly.

Kernel = type of hyperplane used to separate the data

0.16 OPTIMIZE MODEL

0.16.1 Use the Best parameters : {'C': 0.01, 'kernel': 'linear'} to optimize the model

[28]:
```
# Predict output for test set.
final_model = SVC(C = 0.01, kernel = 'linear')
final_model.fit(X_train, y_train)
y_pred = final_model.predict(X_test)
```

```
from sklearn.metrics import confusion_matrix, accuracy_score
cf = confusion_matrix(y_test, y_pred)
print(cf)
print(accuracy_score(y_test, y_pred) * 100)

from sklearn.metrics import classification_report
report = classification_report(y_test, y_pred)
print(report)
```

```
[[87 12]
 [23 32]]
77.27272727272727
              precision    recall  f1-score   support

           0       0.79      0.88      0.83        99
           1       0.73      0.58      0.65        55

    accuracy                           0.77       154
   macro avg       0.76      0.73      0.74       154
weighted avg       0.77      0.77      0.77       154
```

0.16.2 Machine learning with Added Column - random numbers

[29]:
```
# copy and modify original dataset for analysis
data2 = data

np.random.seed(42)

# create new column with the random number generator

data2['randNumCol'] = np.random.randint(10,40, size=len(data2))
```

[30]:
```
# Rearrage columns so it is easier to split X and Y for analysis

data2=data2[['pregnancies', 'glucose', 'bloodpressure', 'skinthickness',␣
 ↪'insulin',
       'bmi', 'age', 'randNumCol', 'outcome']]
```

[31]:
```
# display first five rows
data2.head()
```

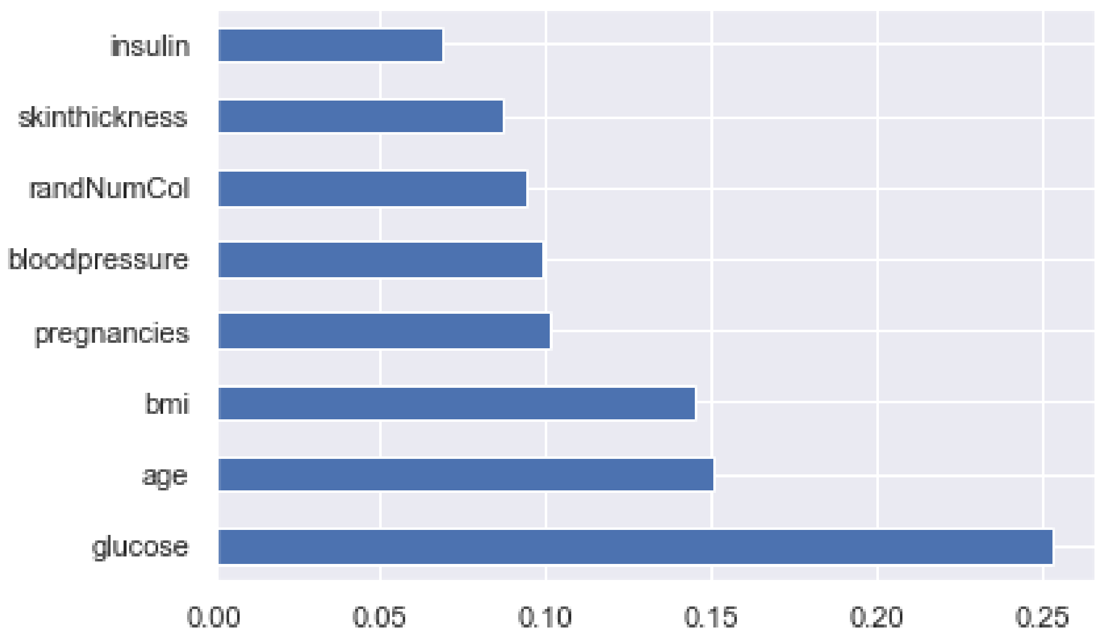
[31]:
```
   pregnancies  glucose  bloodpressure  skinthickness  insulin   bmi  age  \
0            6    148.0           72.0           35.0    125.0  33.6   50
1            1     85.0           66.0           29.0    125.0  26.6   31
2            8    183.0           64.0           29.0    125.0  23.3   32
3            1     89.0           66.0           23.0     94.0  28.1   21
```

```
4             0    137.0            40.0           35.0    168.0  43.1   33

   randNumCol  outcome
0          16        1
1          29        0
2          38        1
3          24        0
4          20        1
```

[32]:
```
# Split new data into X = observation and y = outcome

attributes = list(data2.columns[:8])
X = data2[attributes].values
y= data2['outcome'].values

from sklearn import preprocessing

# Get column names first
names = data2.columns[:8]# Create the Scaler object
scaler = preprocessing.StandardScaler()# Fit your data on the scaler object
scaled_df = scaler.fit_transform(X)
X = pd.DataFrame(scaled_df, columns=names)
```

[33]:
```
# Use ExtraTreesClassifier to determine order of importance for attributes.

from sklearn.ensemble import ExtraTreesClassifier
model = ExtraTreesClassifier()
model.fit(X,y)
print(model.feature_importances_)

#plot graph of feature importances for better visualization
feat_importances = pd.Series(model.feature_importances_, index=X.columns)
feat_importances.nlargest(10).plot(kind='barh')
plt.show()
```

```
[0.10138801 0.25342595 0.09905497 0.08679671 0.06879194 0.1451958
 0.15091407 0.09443254]
```



0.16.3 OBSERVATION

The attributes that show up after the random number attribute shows the cut of teh feature importance. This appears to indicate that the random number attribute is a better predictor of the outcome than the attributes that come after that.

```
[34]: # drop all attributes that placed below and including the random number column

      X.drop(['insulin', 'skinthickness', 'randNumCol'],axis=1,inplace=True)
```

```
[35]: X.head()
```

```
[35]:    pregnancies   glucose  bloodpressure       bmi       age
      0     0.639947  0.866045      -0.031990  0.166619  1.425995
      1    -0.844885 -1.205066      -0.528319 -0.852200 -0.190672
      2     1.233880  2.016662      -0.693761 -1.332500 -0.105584
      3    -0.844885 -1.073567      -0.528319 -0.633881 -1.041549
      4    -1.141852  0.504422      -2.679076  1.549303 -0.020496
```

```
[36]: # Split feature importamce attributes into train and test sets for machine␣
       ↪learning.
      # test set was split at 20% and random_state set to 42

      from sklearn.model_selection import train_test_split
      X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.20,␣
       ↪random_state = 42)
```

```
[37]: # Use Optimized model of ML to test prediction of the feature importance␣
       ↪attributes.
      # Predict output for test set.
      final_model = SVC(C = 0.1, kernel = 'linear')
      final_model.fit(X_train, y_train)
      y_pred = final_model.predict(X_test)

      from sklearn.metrics import confusion_matrix, accuracy_score
      cf = confusion_matrix(y_test, y_pred)
      print(cf)
      print(accuracy_score(y_test, y_pred) * 100)

      from sklearn.metrics import classification_report
      report = classification_report(y_test, y_pred)
      print(report)
```

```
[[85 14]
 [20 35]]
77.92207792207793
              precision    recall  f1-score   support

           0       0.81      0.86      0.83        99
           1       0.71      0.64      0.67        55

    accuracy                           0.78       154
   macro avg       0.76      0.75      0.75       154
weighted avg       0.78      0.78      0.78       154
```

0.16.4 Compare the two Predictions

The model improved after removing attributes that appear to not contribute much to the prediction. It incressed from about 76% to 78%. Upon closer observation it appears that the imporovement in the model was only reflected in prdiction True negatives.Therefore it was not a significant change when the features or attributes were taken out. Further, given that the "C" paramenter in SVM linear is used to determine how acurate a prediction should be versus the smoothness level of the classifications, a higher value of "C" provides stonger accuracy in predictions. This appears to explain why myb accuracy for the model is at about 78%.