Project1

March 22, 2020

1 Project 1

Use the data *diabetes2.csv* for this project. More information about the dataset can be found here: https://www.kaggle.com/kandij/diabetes-dataset

1.1 Linear Regression

Can you predict BMI based on other features in the dataset?

1. Explore the Data
2. Build your Model
   - Build a Linear Regression Model using train_test_split() for your cross-validation
   - Standardize your continuous predictors
3. Evaluate your model
   - How did your model do? What metrics do you use to support this?
4. Interpret the coefficients to your model
   - In the context of this problem, what do the coefficients represent?

[1]:
```
import warnings
warnings.filterwarnings('ignore')

import pandas as pd
import numpy as np

import matplotlib.pyplot as plt
from plotnine import *
import seaborn as sns

from sklearn.linear_model import LinearRegression, LogisticRegression # Linear␣
↪Regression Model
from sklearn.preprocessing import StandardScaler, LabelBinarizer
from sklearn.metrics import accuracy_score, precision_score, recall_score,␣
↪confusion_matrix, roc_curve,mean_squared_error, r2_score, roc_auc_score␣
↪#model eval
from sklearn.model_selection import train_test_split # simple TT split cv
from sklearn.model_selection import KFold # k-fold cv
#from sklearn.model_selection import LeaveOneOut #LOO cv
from sklearn.model_selection import cross_val_score # cross validation metrics
from sklearn.model_selection import cross_val_predict # cross validation metrics
```

```
get_ipython().run_line_magic('matplotlib', 'inline')
```

[2]:
```
diabetes = pd.read_csv('data/diabetes2.csv')
print(diabetes.head())
print(diabetes.describe())
print(diabetes.info())
print(diabetes.isnull().sum())
#diabetes.loc[diabetes['SkinThickness'] == 0]
#diabetes.loc[diabetes['Weight'].isnull()]
```

```
   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
       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
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
Pregnancies                 768 non-null int64
```

```
Glucose                     768 non-null int64
BloodPressure               768 non-null int64
SkinThickness               768 non-null int64
Insulin                     768 non-null int64
BMI                         768 non-null float64
DiabetesPedigreeFunction    768 non-null float64
Age                         768 non-null int64
Outcome                     768 non-null int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
None
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

Removing 0 values to improve model metrics

[3]:
```
diabetes = diabetes[diabetes.BloodPressure != 0] #removed 0 values to avoid␣
 ↪throwing off the model
diabetes = diabetes[diabetes.SkinThickness != 0]
diabetes = diabetes[diabetes.Insulin != 0]
diabetes = diabetes[diabetes.BMI != 0]
diabetes = diabetes[diabetes.Glucose != 0]

diabetes = diabetes.reset_index(drop = True)
print(diabetes.shape)
print(diabetes.describe())
```

```
(392, 9)
       Pregnancies     Glucose  BloodPressure  SkinThickness     Insulin  \
count   392.000000  392.000000     392.000000     392.000000  392.000000
mean      3.301020  122.627551      70.663265      29.145408  156.056122
std       3.211424   30.860781      12.496092      10.516424  118.841690
min       0.000000   56.000000      24.000000       7.000000   14.000000
25%       1.000000   99.000000      62.000000      21.000000   76.750000
50%       2.000000  119.000000      70.000000      29.000000  125.500000
75%       5.000000  143.000000      78.000000      37.000000  190.000000
max      17.000000  198.000000     110.000000      63.000000  846.000000

              BMI  DiabetesPedigreeFunction         Age     Outcome
count  392.000000                392.000000  392.000000  392.000000
```

```
mean    33.086224                    0.523046   30.864796    0.331633
std      7.027659                    0.345488   10.200777    0.471401
min     18.200000                    0.085000   21.000000    0.000000
25%     28.400000                    0.269750   23.000000    0.000000
50%     33.200000                    0.449500   27.000000    0.000000
75%     37.100000                    0.687000   36.000000    1.000000
max     67.100000                    2.420000   81.000000    1.000000
```

[ ]:

```
#g = sns.pairplot(diabetes)
```

[4]:

```
diabetes.loc[diabetes['BMI'] < 18.5, 'Weight'] = 'Underweight'
diabetes.loc[diabetes['BMI'].between(18.5,24.999), 'Weight'] = 'Normal'
diabetes.loc[diabetes['BMI'].between(25,29.999), 'Weight'] = 'Overweight'
diabetes.loc[diabetes['BMI'] >= 30, 'Weight'] = 'Obese'

diabetes["Weight"] = diabetes["Weight"].astype('category')

label_binary = LabelBinarizer()
lb_results = label_binary.fit_transform(diabetes["Weight"])
column_names = label_binary.classes_
# lb_results.shape
# column_names

lb_df = pd.DataFrame(lb_results, columns = column_names)
#print(lb_df)

diabetes = diabetes.join(lb_df, lsuffix='index', rsuffix='index')

diabetes.head(20)



# diabetes["Weight_cat"] = diabetes["Weight"].cat.codes

# print(diabetes.describe(include = "all"))
# diabetes.head(20)
```

[4]:

```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            1       89             66             23       94  28.1
1            0      137             40             35      168  43.1
2            3       78             50             32       88  31.0
3            2      197             70             45      543  30.5
4            1      189             60             23      846  30.1
5            5      166             72             19      175  25.8
6            0      118             84             47      230  45.8
7            1      103             30             38       83  43.3
8            1      115             70             30       96  34.6
9            3      126             88             41      235  39.3
```

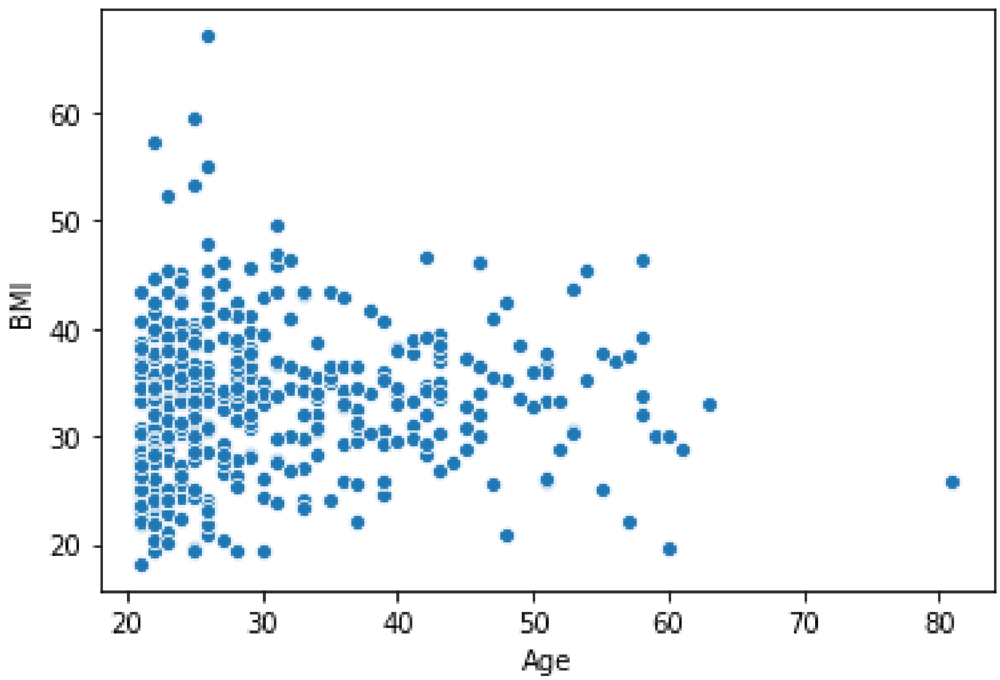
10	11	143	94	33	146	36.6
11	10	125	70	26	115	31.1
12	1	97	66	15	140	23.2
13	13	145	82	19	110	22.2
14	3	158	76	36	245	31.6
15	3	88	58	11	54	24.8
16	4	103	60	33	192	24.0
17	4	111	72	47	207	37.1
18	3	180	64	25	70	34.0
19	9	171	110	24	240	45.4

	DiabetesPedigreeFunction	Age	Outcome	Weight	Normal	Obese	\
0	0.167	21	0	Overweight	0	0	
1	2.288	33	1	Obese	0	1	
2	0.248	26	1	Obese	0	1	
3	0.158	53	1	Obese	0	1	
4	0.398	59	1	Obese	0	1	
5	0.587	51	1	Overweight	0	0	
6	0.551	31	1	Obese	0	1	
7	0.183	33	0	Obese	0	1	
8	0.529	32	1	Obese	0	1	
9	0.704	27	0	Obese	0	1	
10	0.254	51	1	Obese	0	1	
11	0.205	41	1	Obese	0	1	
12	0.487	22	0	Normal	1	0	
13	0.245	57	0	Normal	1	0	
14	0.851	28	1	Obese	0	1	
15	0.267	22	0	Normal	1	0	
16	0.966	33	0	Normal	1	0	
17	1.390	56	1	Obese	0	1	
18	0.271	26	0	Obese	0	1	
19	0.721	54	1	Obese	0	1	

	Overweight	Underweight
0	1	0
1	0	0
2	0	0
3	0	0
4	0	0
5	1	0
6	0	0
7	0	0
8	0	0
9	0	0
10	0	0
11	0	0
12	0	0

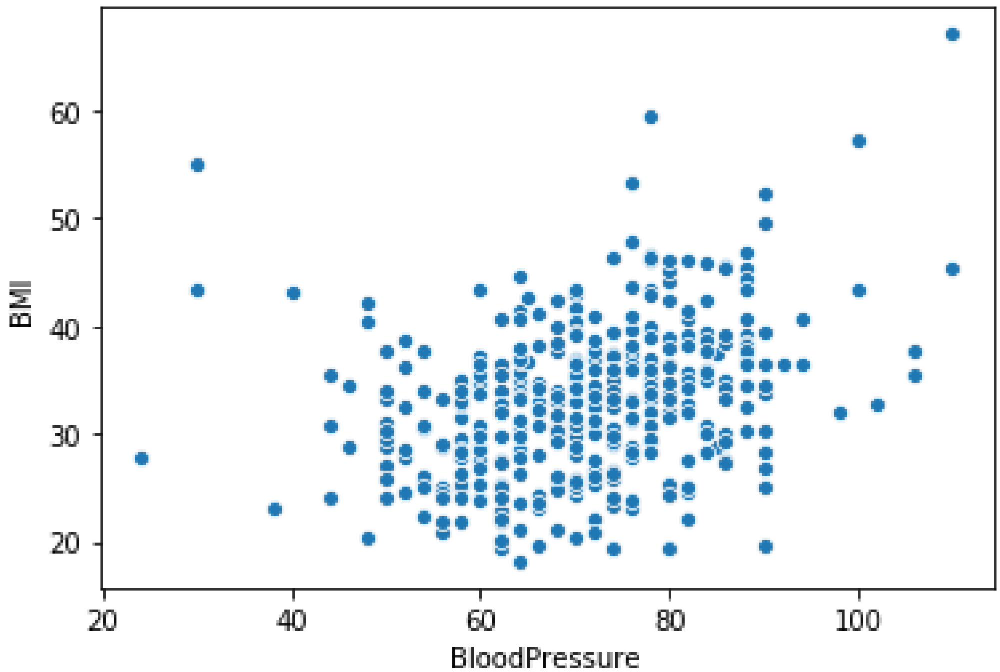
13	0	0
14	0	0
15	0	0
16	0	0
17	0	0
18	0	0
19	0	0

[5]:
```
g = sns.scatterplot(data = diabetes,x = 'Age', y = 'BMI',
                    sizes=(20, 200), hue_norm=(0, 7), legend = False)
```



Seems like age doesnt play too much of a factor on BMI. I figured there would be lower BMI's in older women

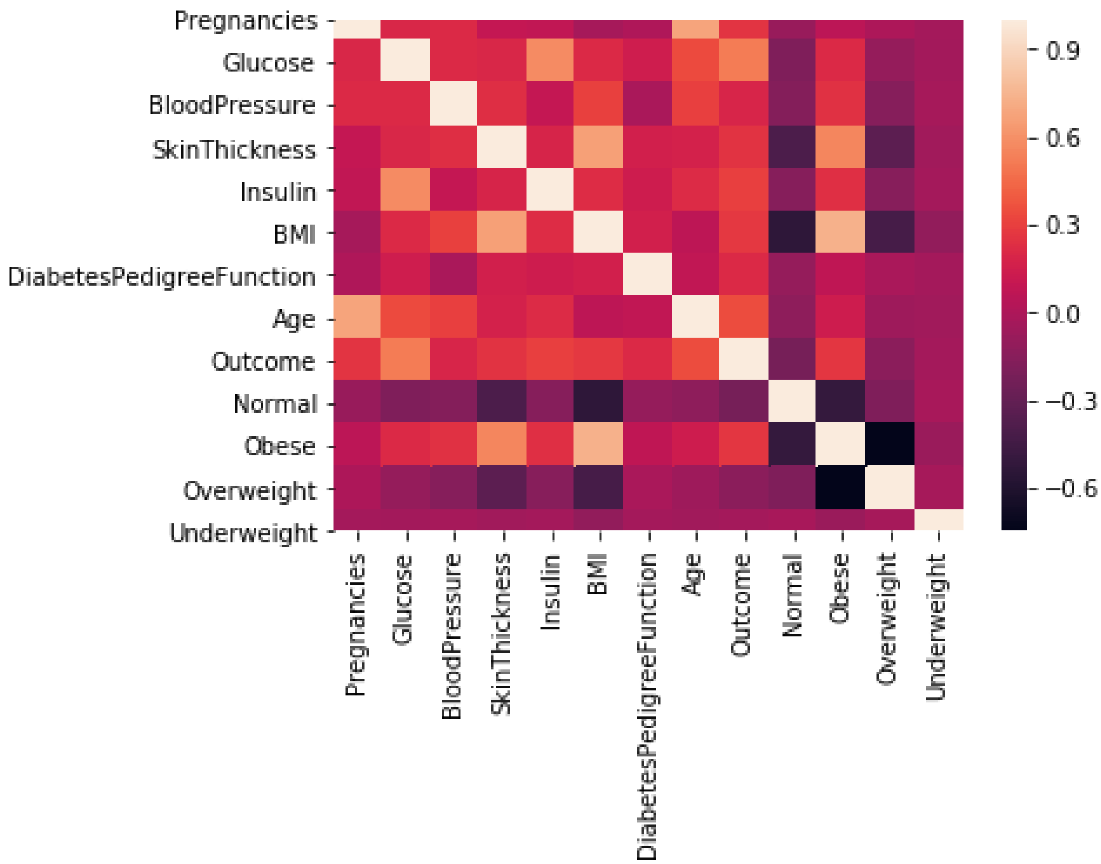
[6]:
```
g = sns.scatterplot(data = diabetes,x = 'BloodPressure', y = 'BMI',
                    sizes=(20, 200), hue_norm=(0, 7), legend = False)
```



It seems like there are many women of with both above average (31) BMI and above average blood pressure (69)

[7]:
```
corr = diabetes.corr()
sns.heatmap(corr,xticklabels=corr.columns, yticklabels=corr.columns)
```

[7]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x1cbcde7d988>
```



Correlation matrix shows strong relationships between a few variables. The darker the color the more negative a relationship and the lighter means the more positive relationship. Examples of negative relationships are highlighed in the Normal weight range. Notice how nearly all squares are dark indicating that a normal weight range has a negative relationship with nearly all other variables. The opposite can be seen in the obese weight range where colors are lighter and signify a positive relationship between obesity and variables such as glucose and insulin.

[8]:
```
predictors = ['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness',␣
↪'Insulin', 'DiabetesPedigreeFunction', 'Age', 'Outcome']
```

[9]:
```
X_train, X_test, y_train, y_test = train_test_split(diabetes[predictors],␣
↪diabetes["BMI"], test_size=0.2)
```

[10]:
```
zscore = StandardScaler()
zscore.fit(X_train)
Xz_train = zscore.transform(X_train)
Xz_test = zscore.transform(X_test)
```

[11]:
```
model = LinearRegression()
model.fit(X_train, y_train)
```

[11]: LinearRegression(copy_X=True, fit_intercept=True, n_jobs=None, normalize=False)

[12]:
```
train_pred = model.predict(X_train)
test_pred = model.predict(X_test)
```

[13]:
```
print('training r2 is:', model.score(X_train, y_train)) #training R2
print('testing r2 is:', model.score(X_test, y_test)) #testing R2

print('\ntrain mse is: ', mean_squared_error(y_train,train_pred))
print('test mse is: ', mean_squared_error(y_test,test_pred))
```

```
training r2 is: 0.5110376027308636
testing r2 is: 0.45045548584951967

train mse is:  24.921856244482562
test mse is:  23.25531849828658
```

[14]:
```
coefficients = pd.DataFrame({"Coef":model.coef_,
              "Name": predictors})

coefficients = coefficients.append({"Coef": model.intercept_,
               "Name": "intercept"}, ignore_index = True)

coefficients
```

[14]:

	Coef	Name
0	-0.172751	Pregnancies
1	-0.007750	Glucose
2	0.106797	BloodPressure
3	0.400753	SkinThickness
4	0.006368	Insulin
5	0.722948	DiabetesPedigreeFunction
6	-0.069595	Age
7	1.932546	Outcome
8	15.653319	intercept

How did your model do? What metrics do you use to support this? The model did well given decent r-squared scores in both training and testing sets. MSE in both training and test set are within one point of each other signifying a good fit. A way to improve this model might be to include a better cross validation method as well as getting more data.

[ ]:

In the context of this problem, what do the coefficients represent? The coefficients represent the value that BMI increases or decreases for every one standard deviation for its corresponding variable. For example, for every one standard deviation in pregnancy a woman is, her BMI is predicted to go down by her number of pregnancies multiplied by -.17. The strongest predictor in our model is whether the person is diabetic or not, if a woman were to be diabetic, our model adds 1.93 to her predicted BMI. Second highest variable is the diabetes pedigree funtion meaning that family history plays a large role in a womans BMI.

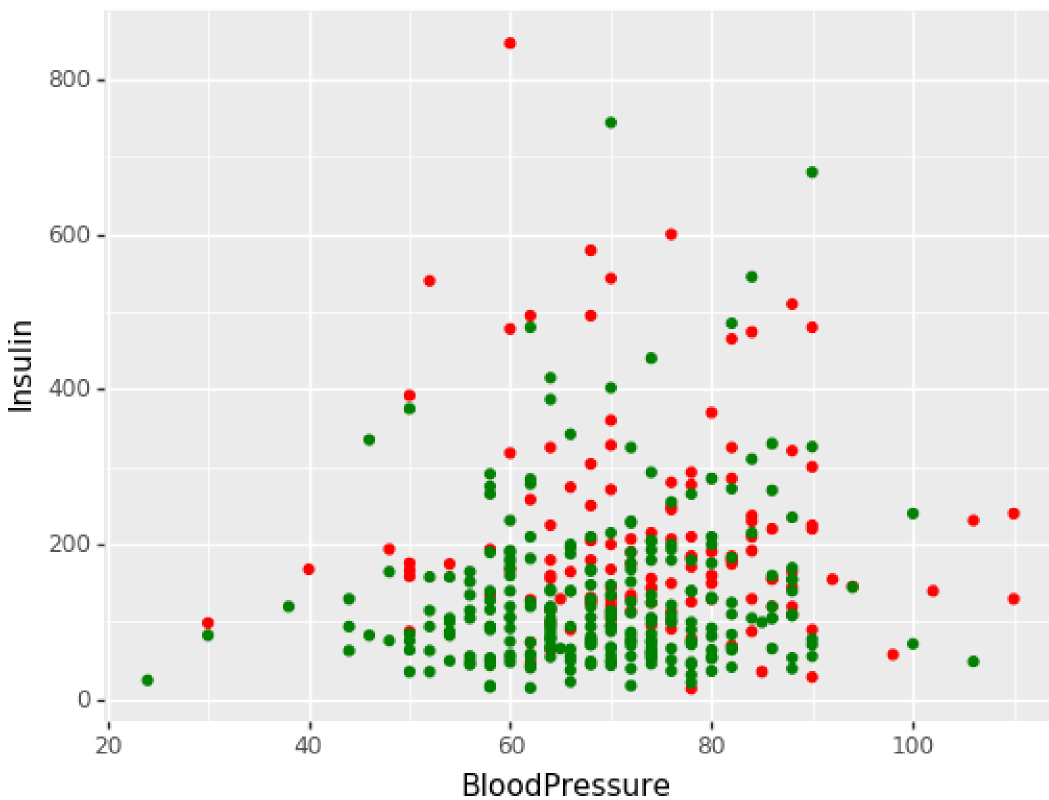
1.2 Logistic Regression

Can you predict Diabetes (Outcome) based on other features in the dataset?

1. Explore the Data (if using different variables from Linear Regression)
2. Build your Model
    - Build a Logistic Regression Model using cross-validation
        - What cross-val method did you choose, why?
    - Standardize your continuous predictors
3. Evaluate your model
    - How did your model do? What metrics do you use to support this?

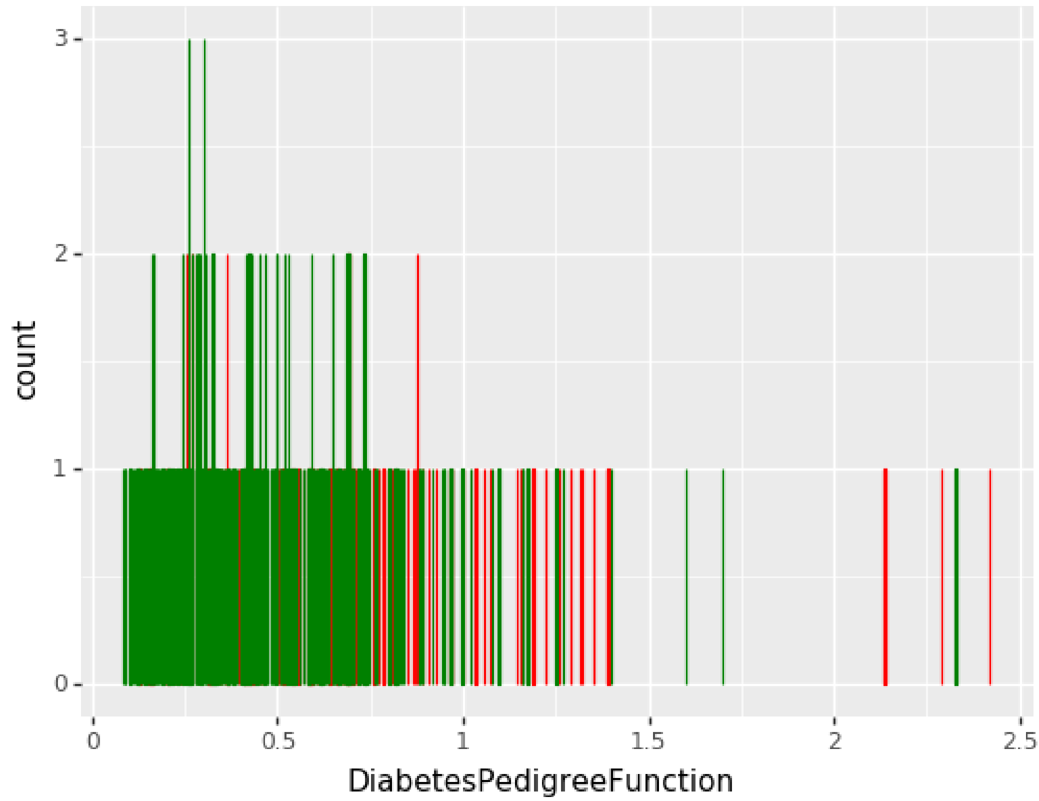
[15]:
```
yes = diabetes[diabetes['Outcome'] == 1]
no = diabetes[diabetes['Outcome'] == 0]
```

[16]:
```
(ggplot()
+geom_point(yes, aes(x = 'BloodPressure' ,y = 'Insulin'), color = 'red')
+geom_point(no, aes(x = 'BloodPressure' ,y = 'Insulin'), color = 'green'))
```



[16]: <ggplot: (-9223371913426926004)>

[17]:
```
(ggplot()
+geom_bar(yes, aes(x = 'DiabetesPedigreeFunction'), color = 'red')
+geom_bar(no, aes(x = 'DiabetesPedigreeFunction'), color = 'green'))
```



[17]: <ggplot: (-9223371913425881564)>

[18]:
```
predictors = ['Normal','Pregnancies', 'BMI', 'BloodPressure', 'SkinThickness',␣
↪'Glucose', 'Insulin', 'DiabetesPedigreeFunction', 'Age']
X = diabetes[predictors]
y = diabetes["Outcome"]
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)
```

[39]:
```
# create k-fold object
kf = KFold(n_splits = 5)
kf.split(X)


lr = LogisticRegression()
```

```
acc = [] #create empty list to store accuracy for each fold
predictedVals = []
```

[ ]:
```
#print(diabetes.isnull().sum())
#print(diabetes.isna().sum())
#diabetes.replace([np.inf, -np.inf], np.nan).dropna(axis=1)
```

[40]:
```
for train_indices, test_indices in kf.split(X):
    # Get your train/test for this fold
    y=y.reset_index(drop=True)
    X_train = X.iloc[train_indices] #iloc used to find col index
    X_test  = X.iloc[test_indices]
    y_train = y[train_indices]
    y_test  = y[test_indices]

    #standardize
    zscore = StandardScaler()
    zscore.fit(X_train)

    Xs_train = zscore.transform(X_train)
    Xs_test = zscore.transform(X_test)

    # model
    model = lr.fit(Xs_train, y_train)
    # record accuracy and predictions

    acc.append(accuracy_score(y_test, model.predict(Xs_test)))

print(acc)
np.mean(acc)
```

```
0
0
0
0
0
[0.8481012658227848, 0.620253164556962, 0.8205128205128205, 0.8461538461538461,
0.8333333333333334]
```

[40]:
```
0.7936708860759494
```

What cross-val method did you choose, why? I chose a k-fold validation method with 5 folds because k-fold reduces bias when constructing a model and limits the variance our model is exposed to in training.

[41]:
```
predictedVals = model.predict(Xs_test) #predic
accuracy_score(y_test,predictedVals)
```

[41]: 0.8333333333333334

[42]:
```
cnf_matrix = confusion_matrix(y_test, predictedVals)
cnf_matrix
```

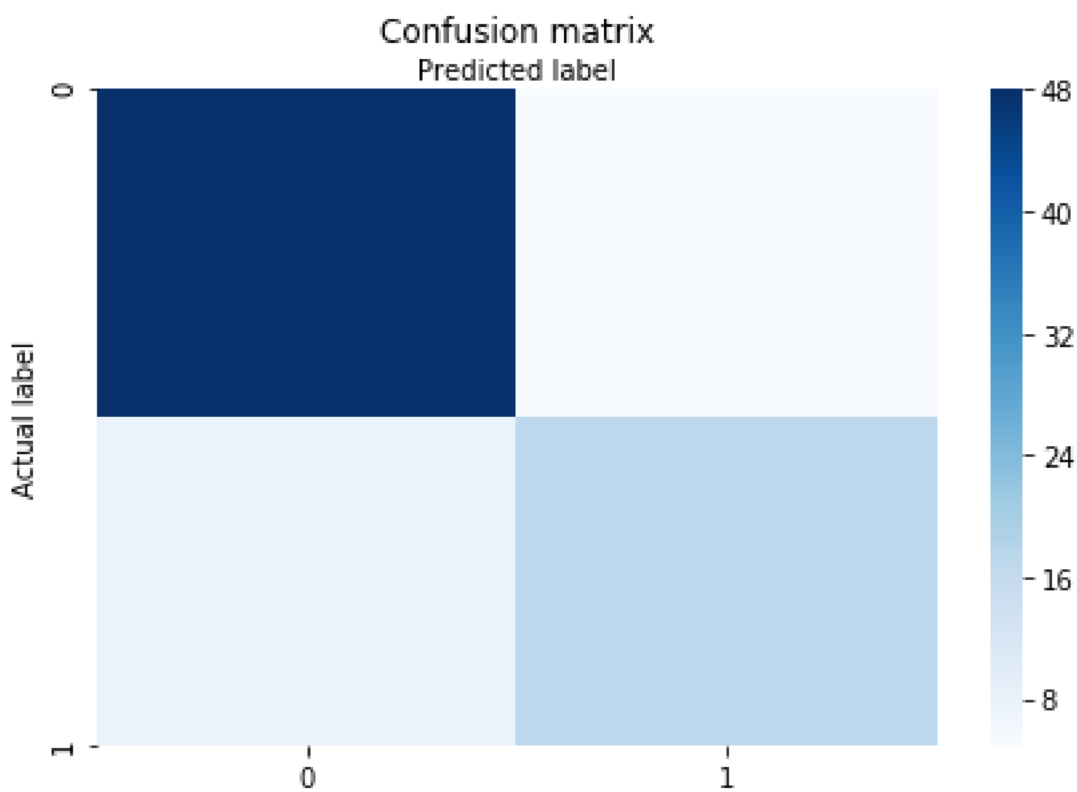
[42]:
```
array([[48,  5],
       [ 8, 17]], dtype=int64)
```

[43]:
```
class_names=[0,1]
fig, ax = plt.subplots()
tick_marks = np.arange(len(class_names))
plt.xticks(tick_marks, class_names)
plt.yticks(tick_marks, class_names)

# create heatmap

sns.heatmap(pd.DataFrame(cnf_matrix), annot=False, cmap="Blues")
ax.xaxis.set_label_position("top")
plt.tight_layout()
plt.title('Confusion matrix', y=1.1)
plt.ylabel('Actual label')
plt.xlabel('Predicted label')
```

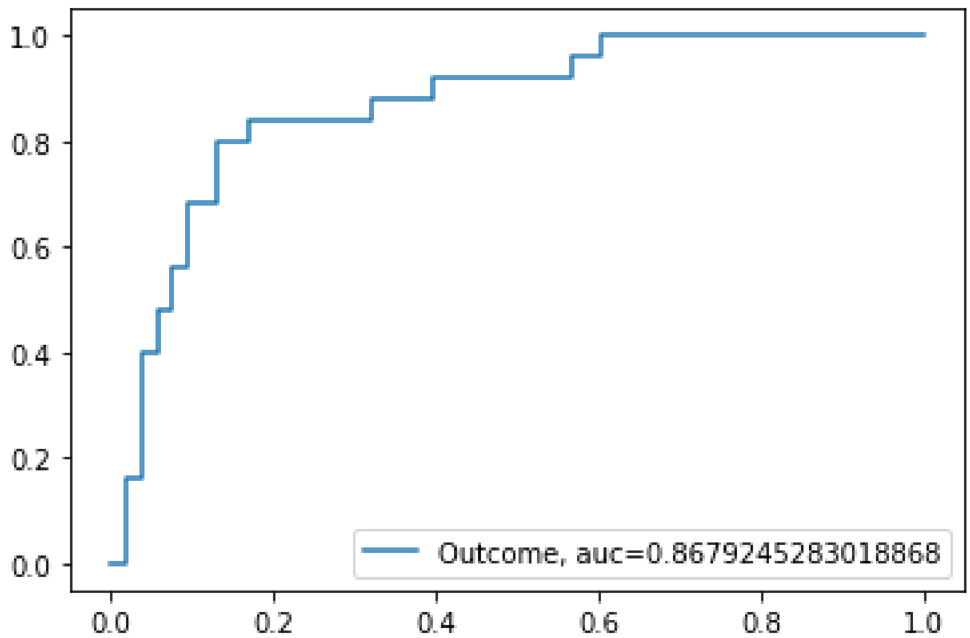
[43]:
```
Text(0.5, 257.44, 'Predicted label')
```



```
[44]: print("Accuracy - TP+TN/TP+FP+FN+TN:",accuracy_score(y_test, predictedVals))
print("Precision - TP/TP+FP:",precision_score(y_test, predictedVals)) #relates␣
↪to low false positivity
print("Recall/Sensitivity/TPR - TP/TP+FN:",recall_score(y_test, predictedVals))
```

```
Accuracy - TP+TN/TP+FP+FN+TN: 0.8333333333333334
Precision - TP/TP+FP: 0.7727272727272727
Recall/Sensitivity/TPR - TP/TP+FN: 0.68
```

```
[45]: y_pred_proba = model.predict_proba(Xs_test)[::,1]
fpr, tpr, _ = roc_curve(y_test,  y_pred_proba)
auc = roc_auc_score(y_test, y_pred_proba)
plt.plot(fpr,tpr,label="Outcome, auc="+str(auc))
plt.legend(loc=4)
plt.show()
```

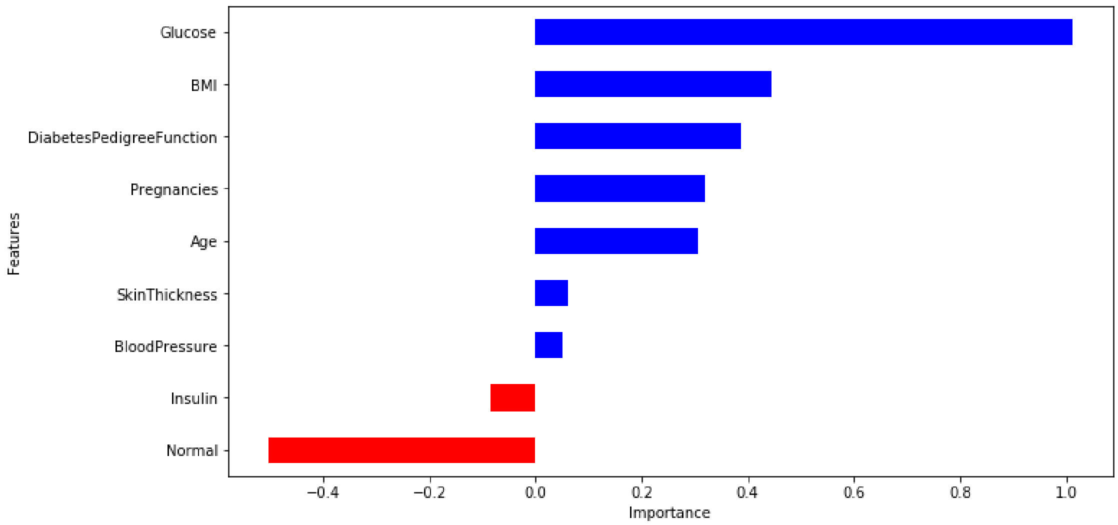


How did your model do? What metrics do you use to support this? The model did well accurately predicting 83% of our test data and having an auc score of 87%. However our models true positive rate is 68% meaning that 32% percent of women would be given a false negative report when they actually do have diabetes.

```
[27]: coeff = list(model.coef_[0])
labels = list(X_test.columns)
features = pd.DataFrame()
```

```
features['Features'] = labels
features['importance'] = coeff
features.sort_values(by=['importance'], ascending=True, inplace=True)
features['positive'] = features['importance'] > 0
features.set_index('Features', inplace=True)
features.importance.plot(kind='barh', figsize=(11, 6),color = features.positive.
 ↪map({True: 'blue', False: 'red'}))
plt.xlabel('Importance')
```

[27]: Text(0.5, 0, 'Importance')



1.3 Data Viz

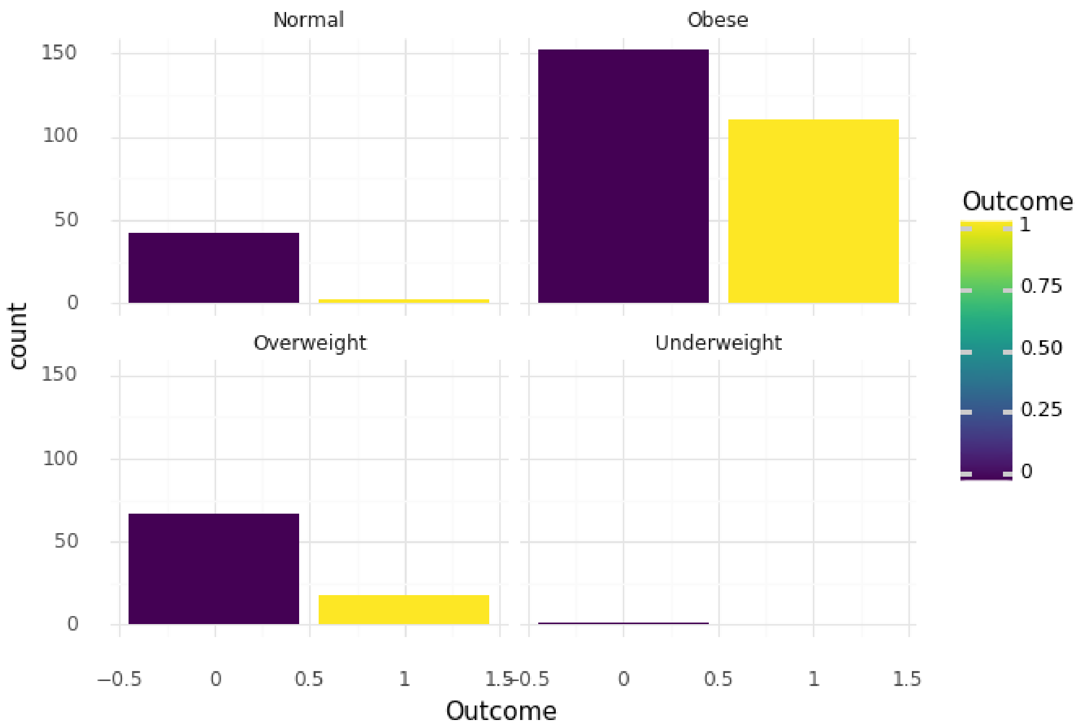
Based on your new understanding of the data create 2 graphs using ggplot/plotnine. These should **not** be graphs you made in the Explore phase of either the Logistic or Linear Regression portion.

Make sure you include at **least** 3 out of these 5 elements in your at least one of your graphs:

1. Custom x-axis labels, y-axis labels and titles
2. Fill and/or Color by a variable
3. Use facet_wrap()
4. Layer multiple geoms
5. Change the theme of your graph (see: https://plotnine.readthedocs.io/en/stable/generated/plotnine.themes.t

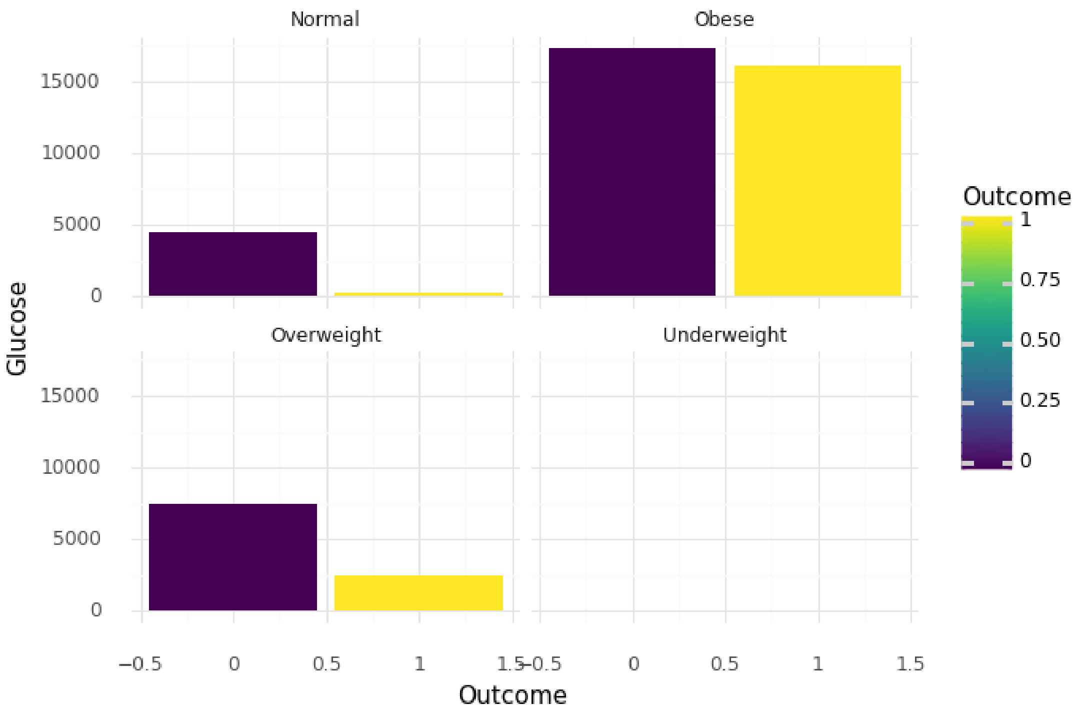
[46]:
```
diabetes['count'] = 1

(ggplot(diabetes,aes(x = 'Outcome', y = 'count', fill = 'Outcome')) #fill
+geom_bar(stat = 'identity')
+facet_wrap('~Weight') #facet wrap
+theme_minimal()) #theme
```



[46]: <ggplot: (-9223371913425484496)>

[47]:
```
(ggplot(diabetes,aes(x = 'Outcome', y = 'Glucose', fill = 'Outcome')) #fill
+geom_bar(stat = 'identity')
+facet_wrap('~Weight') #facet wrap
+theme_minimal()) #theme
```



[47]: <ggplot: (-9223371913425824696)>

[ ]: