Project 1

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


import pandas as pd
import numpy as np
from plotnine import *
import statsmodels.api as sm

from sklearn.linear_model import LinearRegression # Linear Regression Mo
del
from sklearn.preprocessing import StandardScaler #Z-score variables
from sklearn.metrics import mean_squared_error, r2_score #model evaluati
on

from sklearn.linear_model import LogisticRegression # Logistic Regressio
n Model
from sklearn.preprocessing import StandardScaler #Z-score variables
from sklearn.metrics import accuracy_score, confusion_matrix

from sklearn.model_selection import train_test_split # simple TT split c
v
from sklearn.model_selection import KFold # k-fold cv
from sklearn.model_selection import cross_val_score # cross validation m
etrics
from sklearn.model_selection import cross_val_predict # cross validation
metrics


%matplotlib inline
```

In [2]:
```
# Read in data

data = pd.read_csv('https://raw.githubusercontent.com/cmparlettpellerit
i/CPSC392ParlettPelleriti/master/Data/diabetes2.csv')
```

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 – Explore Data

In [3]:
```
data.shape
```
Out[3]:
```
(768, 9)
```

In [4]:
```
data.head()
```
Out[4]:

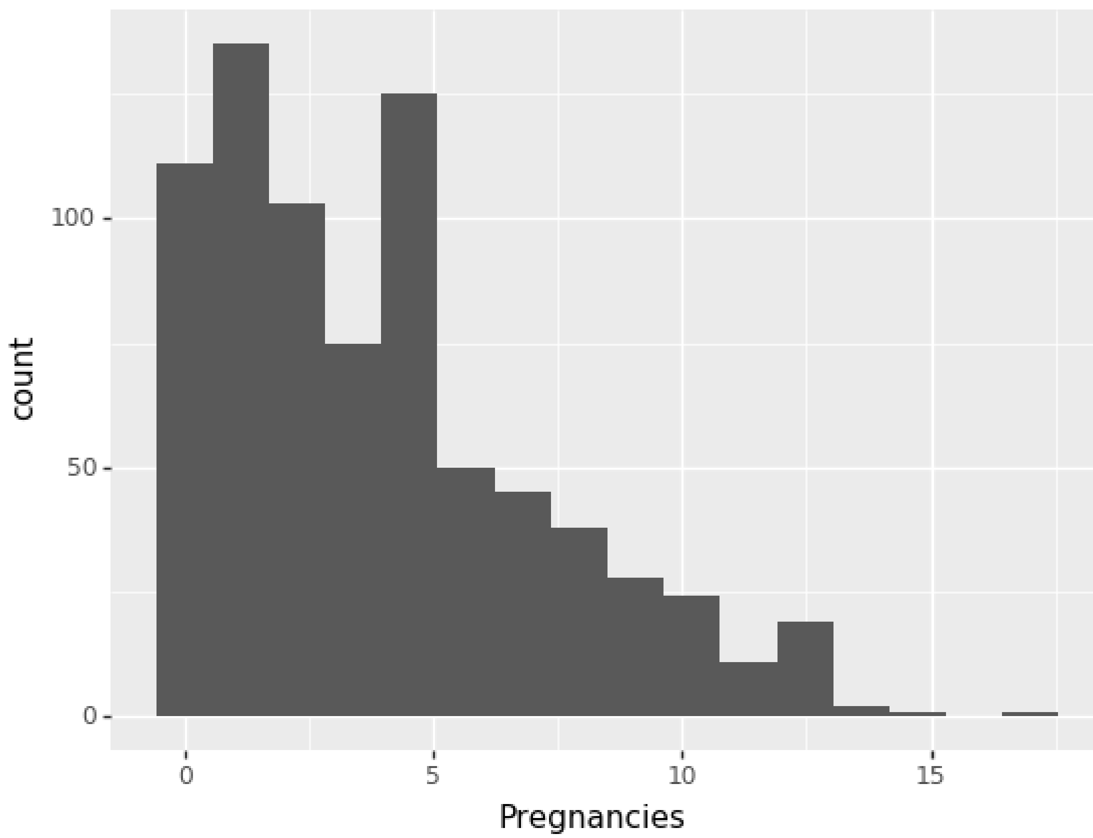
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction
0	6	148	72	35	0	33.6	0.627
1	1	85	66	29	0	26.6	0.351
2	8	183	64	0	0	23.3	0.672
3	1	89	66	23	94	28.1	0.167
4	0	137	40	35	168	43.1	2.288

In [227]:
```
data.min()
```
Out[227]:
```
Pregnancies                  0.000
Glucose                      0.000
BloodPressure                0.000
SkinThickness                0.000
Insulin                      0.000
BMI                          0.000
DiabetesPedigreeFunction     0.078
Age                         21.000
Outcome                      0.000
dtype: float64
```

In [229]:
```
data.max()
```

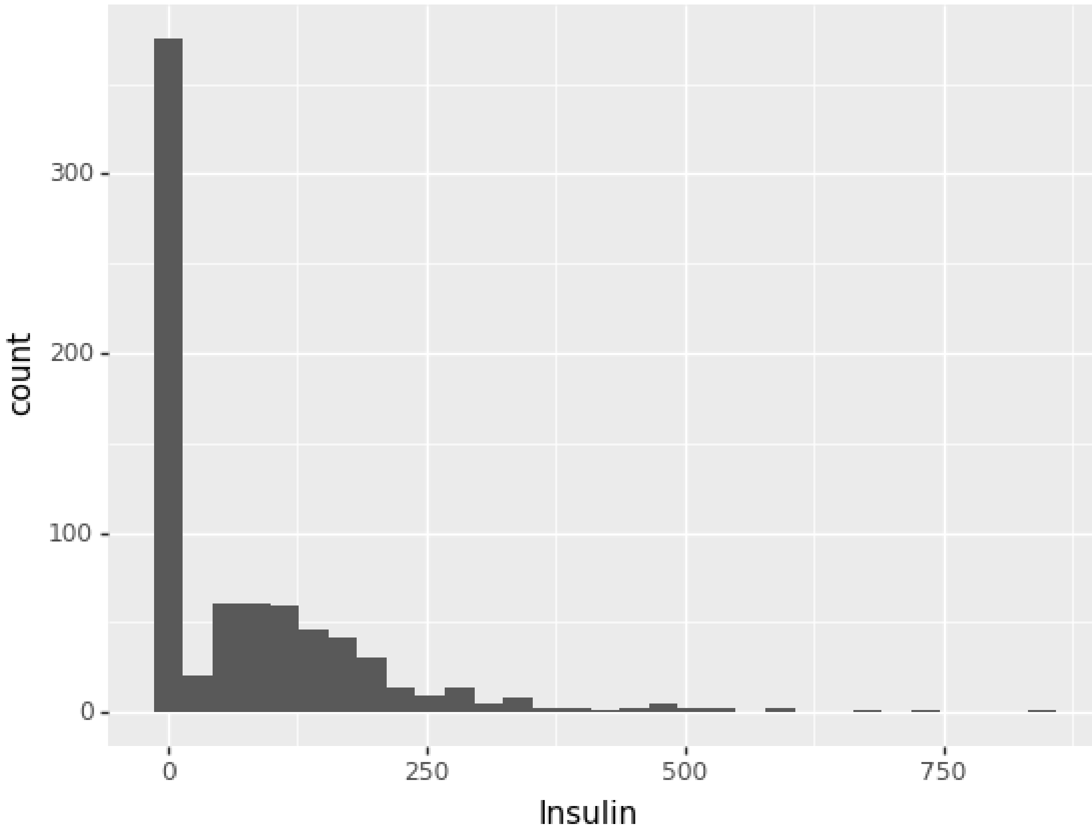
Out[229]:
```
Pregnancies                  17.00
Glucose                     199.00
BloodPressure               122.00
SkinThickness                99.00
Insulin                     846.00
BMI                          67.10
DiabetesPedigreeFunction      2.42
Age                          81.00
Outcome                       1.00
dtype: float64
```

In [233]:
```
(ggplot(data, aes('Pregnancies')) +
geom_histogram())
```



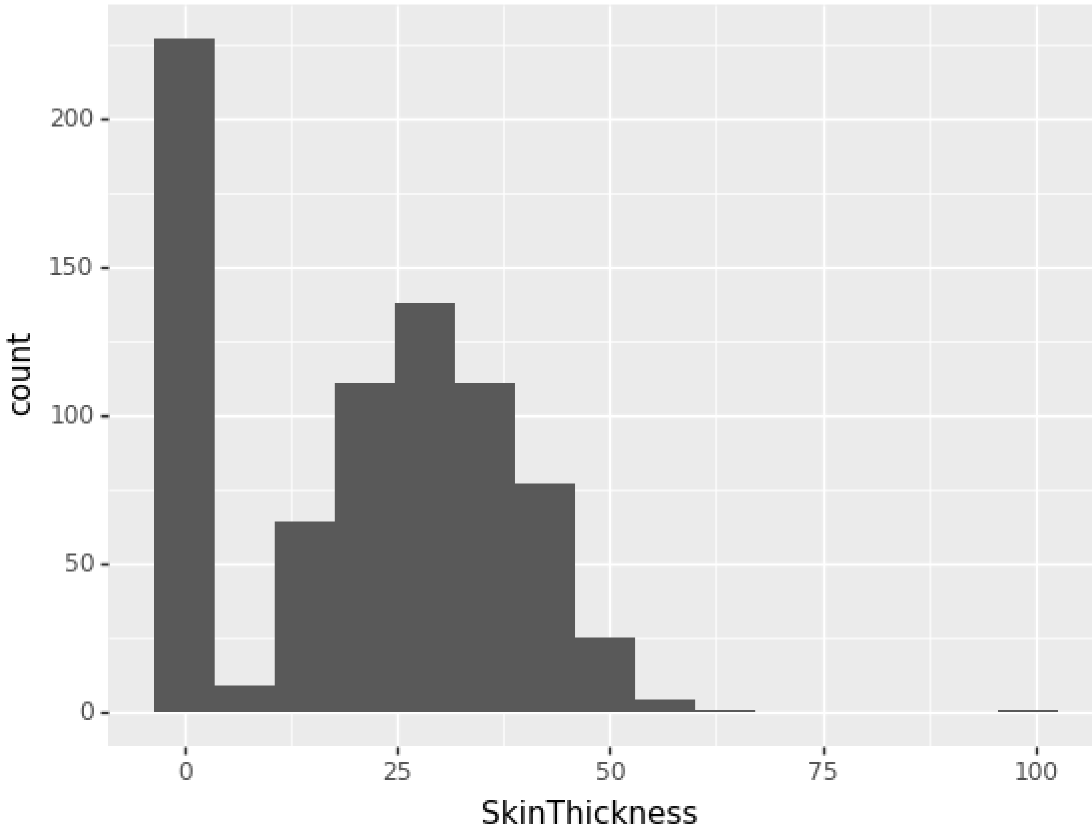
Out[233]: <ggplot: (7549948005)>

In [234]:
```
(ggplot(data, aes('Insulin')) +
geom_histogram())
```



Out[234]: <ggplot: (7549588777)>

In [235]:
```
(ggplot(data, aes('SkinThickness')) +
geom_histogram())
```



Out[235]: <ggplot: (7548102893)>

2 – Build Model

In [5]:
```
# Split

predictors = ['BloodPressure','Insulin','Age','Glucose','Pregnancies',
'SkinThickness']

X_train, X_test, y_train, y_test = train_test_split(data[predictors], da
ta["BMI"], test_size=0.2)
```

In [6]:
```
# Standardize

zScore = StandardScaler()
zScore.fit(X_train)
Xz_train = zScore.transform(X_train)
Xz_test = zScore.transform(X_test)
```

In [7]:
```
# Fit

model = LinearRegression()
model.fit(Xz_train, y_train)
```

Out[7]:
```
LinearRegression(copy_X=True, fit_intercept=True, n_jobs=None, normaliz
e=False)
```

In [8]:
```
# Predict

y_pred = model.predict(Xz_test)
y_pred[1:10]
```

Out[8]:
```
array([34.11216055, 23.54528922, 28.74205786, 31.63508272, 35.57533967,
       29.63298518, 36.74229741, 22.6737246 , 35.42091456])
```

3 – Evaluate Model

In [9]:
```
true_vs_pred = pd.DataFrame({"predict": y_pred,"trueV": y_test})
true_vs_pred.head()
```

Out[9]:

	predict	trueV
307	31.674974	24.8
691	34.112161	42.3
78	23.545289	43.2
80	28.742058	22.4
668	31.635083	34.0

In [10]:
```
model.score(Xz_test, y_test)
```

Out[10]:
```
0.2680026486648397
```

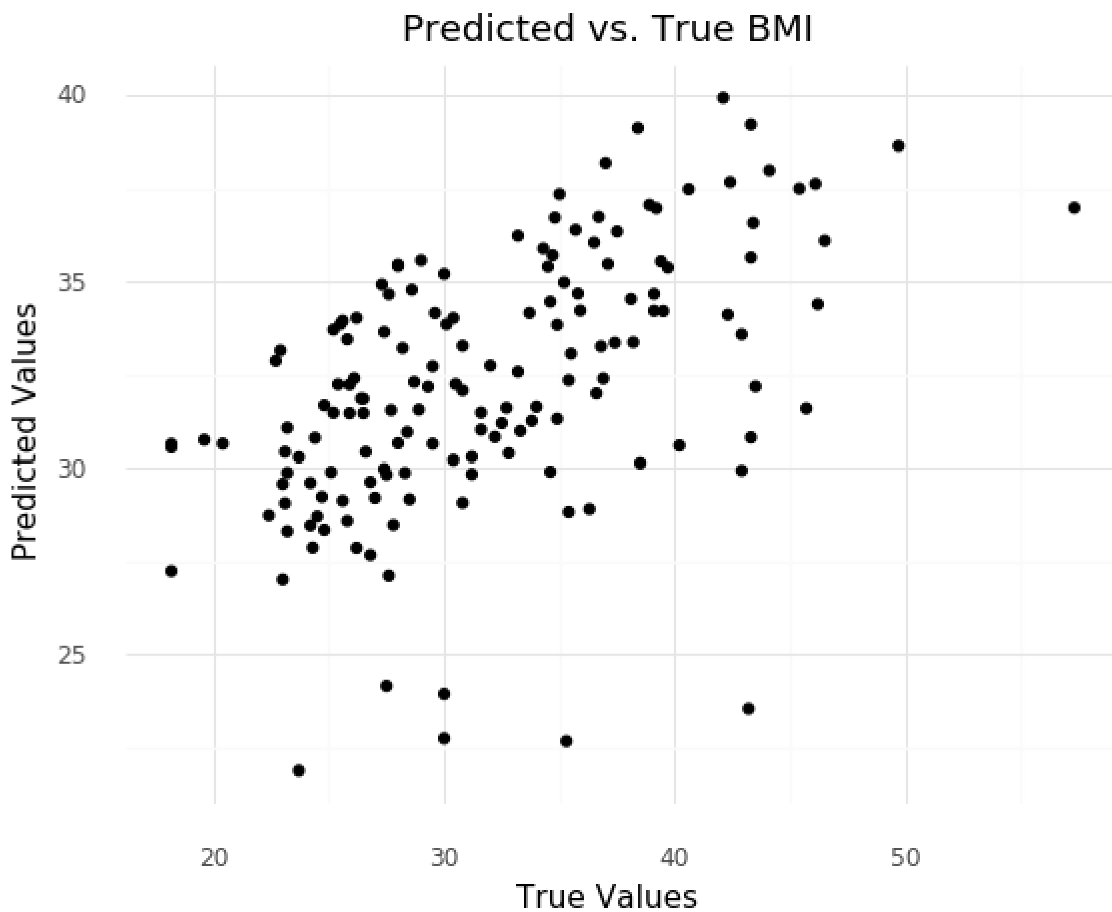
In [11]:
```
model.score(Xz_train,y_train)
```

Out[11]:
```
0.21713964199127322
```

In [12]:
```
mean_squared_error(y_test, y_pred)
```

Out[12]:
```
37.52375248654191
```

In [147]:
```
(ggplot(true_vs_pred, aes(x = "trueV", y = "predict")) +
 geom_point() +
 theme_minimal() +
 labs(x = "True Values", y = "Predicted Values", title = "Predicted vs. True BMI"))
```



Out[147]: <ggplot: (7547459061)>

How did your model do? What metrics do you use to support this?

My model did okay. The r2 and MSE aren't very high. I should have probably put in more predictors to make the model better and have better scores

4 – Interpret Coefficients

In [14]:
```
# Coefficients

coef = pd.DataFrame({"coef":model.coef_, "names":predictors})
coef
```

Out[14]:

	coef	names
0	1.671171	BloodPressure
1	-0.314993	Insulin
2	-0.217311	Age
3	1.459501	Glucose
4	-0.034476	Pregnancies
5	2.679495	SkinThickness

In the context of this problem, what do the coefficients represent?

1 unit increase in Blood Pressure is associated with the 1.671171 increase in BMI

1 unit increase in Insulin is associated with the 0.314993 decrease in BMI

1 unit increase in Age is associated with the 0.217311 decrease in BMI

1 unit increase in Glucose is associated with the 1.459501 increase in BMI

1 unit increase in Pregnancies is associated with the 0.034476 decrease in BMI

1 unit increase in Skin thickness is associated with the 2.679495 increase in BMI

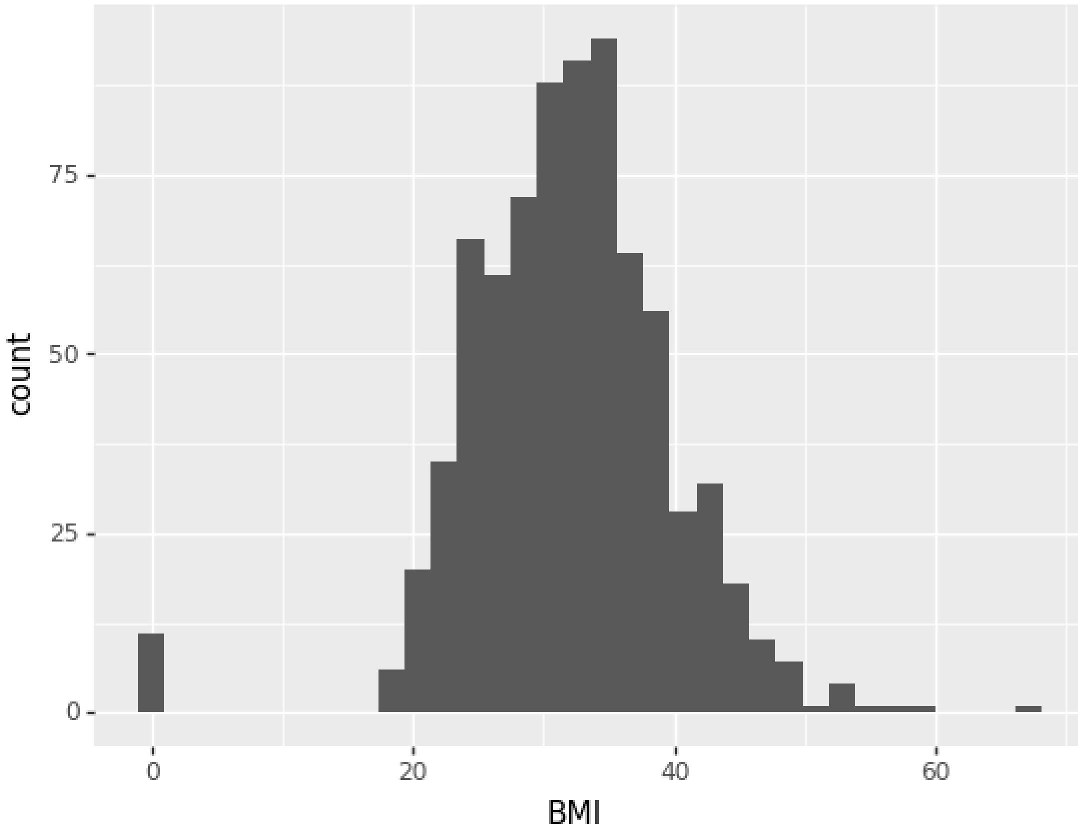
Logistic Regression

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?

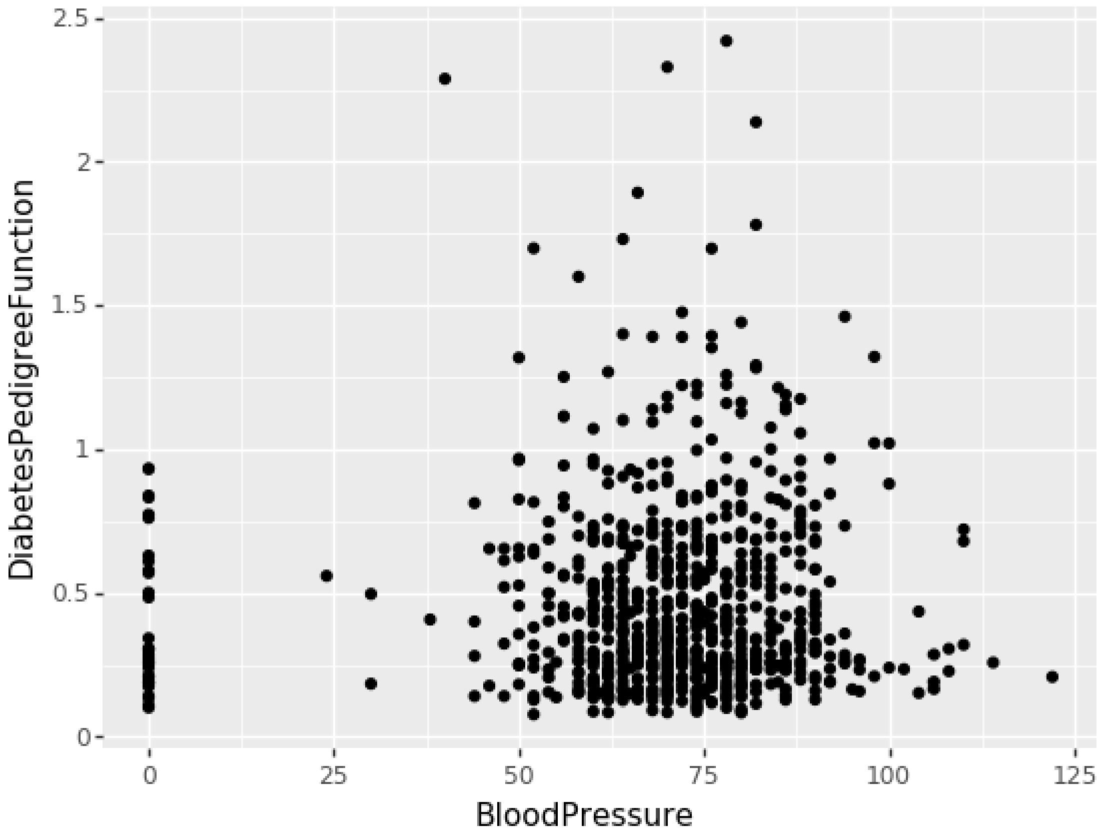
1 – Explore Data

In [236]:
```
(ggplot(data, aes('BMI')) +
geom_histogram())
```



Out[236]: <ggplot: (7548102821)>

In [238]:
```
(ggplot(data, aes('BloodPressure','DiabetesPedigreeFunction')) +
geom_point())
```



Out[238]: <ggplot: (7548091997)>

In [15]:
```
data.head()
```

Out[15]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction
0	6	148	72	35	0	33.6	0.627
1	1	85	66	29	0	26.6	0.351
2	8	183	64	0	0	23.3	0.672
3	1	89	66	23	94	28.1	0.167
4	0	137	40	35	168	43.1	2.288

2 – Build Model

In [381]:
```
# Kfold

X = data[['BloodPressure','Insulin','Age','Glucose','Pregnancies']]
y = data["Outcome"]

# create k-fold object
kf = KFold(n_splits = 5)
kf.split(X)

lr = LogisticRegression() #model

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

matrix = []  #empty list to store confusion matrix of each fold
```

In [379]:
```
# Use a for loop to loop through each fold and train a model, then add t
he accuracy to acc.

for train_indices, test_indices in kf.split(X):
    # Get your train/test for this fold
    X_train = X.iloc[train_indices]
    X_test  = X.iloc[test_indices]
    y_train = y[train_indices]
    y_test  = y[test_indices]

    #standardize
    zscore = StandardScaler()
    zscore.fit(X_train)
    Xz_train = zscore.transform(X_train)
    Xz_test = zscore.transform(X_test)

    # model
    model = lr.fit(Xz_train, y_train)

    # record accuracy
    acc.append(accuracy_score(y_test, model.predict(Xz_test)))

    # confusion matrix
    matrix.append(confusion_matrix(y_test, model.predict(Xz_test)))


#print overall acc
print(acc)
```

```
[0.7272727272727273, 0.6753246753246753, 0.7727272727272727, 0.80392156
8627451, 0.7712418300653595]
```

3 – Evaluate Model

In [60]:
```
print(np.mean(acc))
```

```
0.750097614803497
```

In [380]:
```
print(matrix)
```

```
[array([[84, 16],
       [26, 28]]), array([[75, 15],
       [35, 29]]), array([[89,  8],
       [27, 30]]), array([[101,  13],
       [ 17,  22]]), array([[89, 10],
       [25, 29]])]
```

What cross-val method did you choose, why?

I chose k-fold because leave one out would have been compuationally expensive. The data set has 700+ rows so running my code multiple times would take a long time.

How did your model do? What metrics do you use to support this?

My model did very good. From the accuracy scores of the k fold models the mean is 75%. This means that my model is about 75% accurate when it comes to predicting if someone has diabetes.

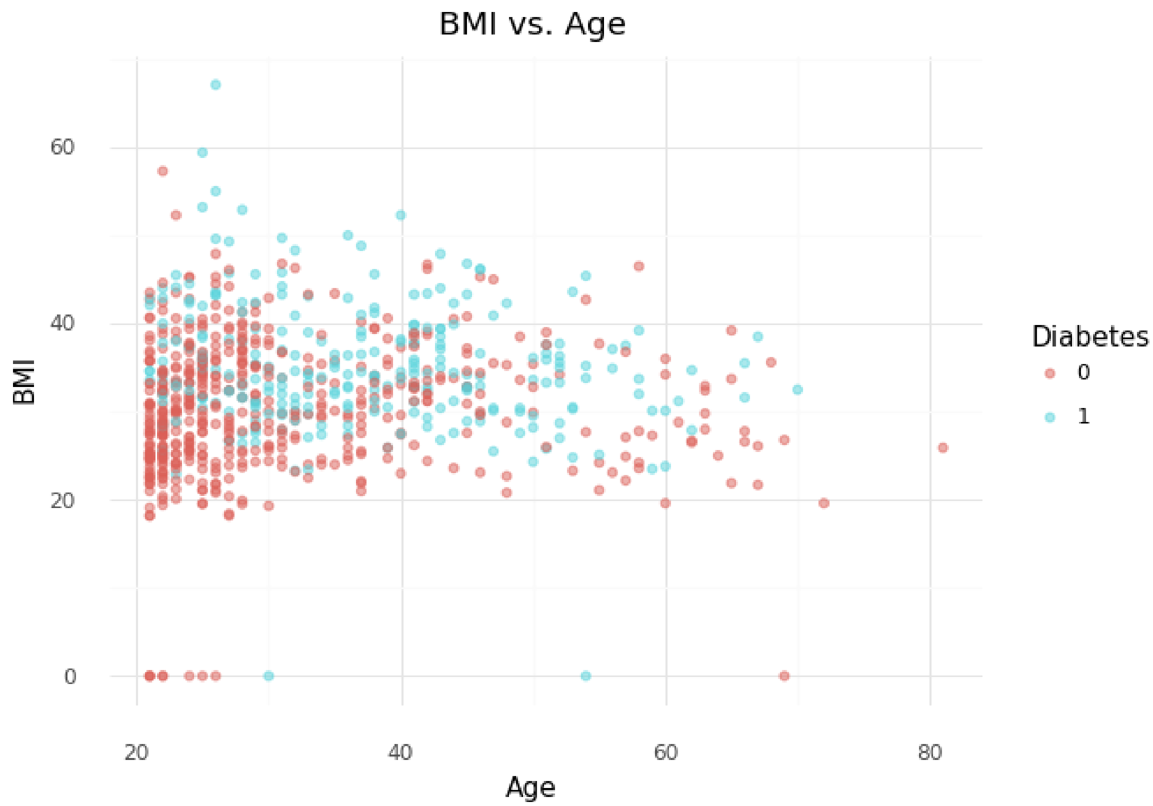
Data Viz

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:

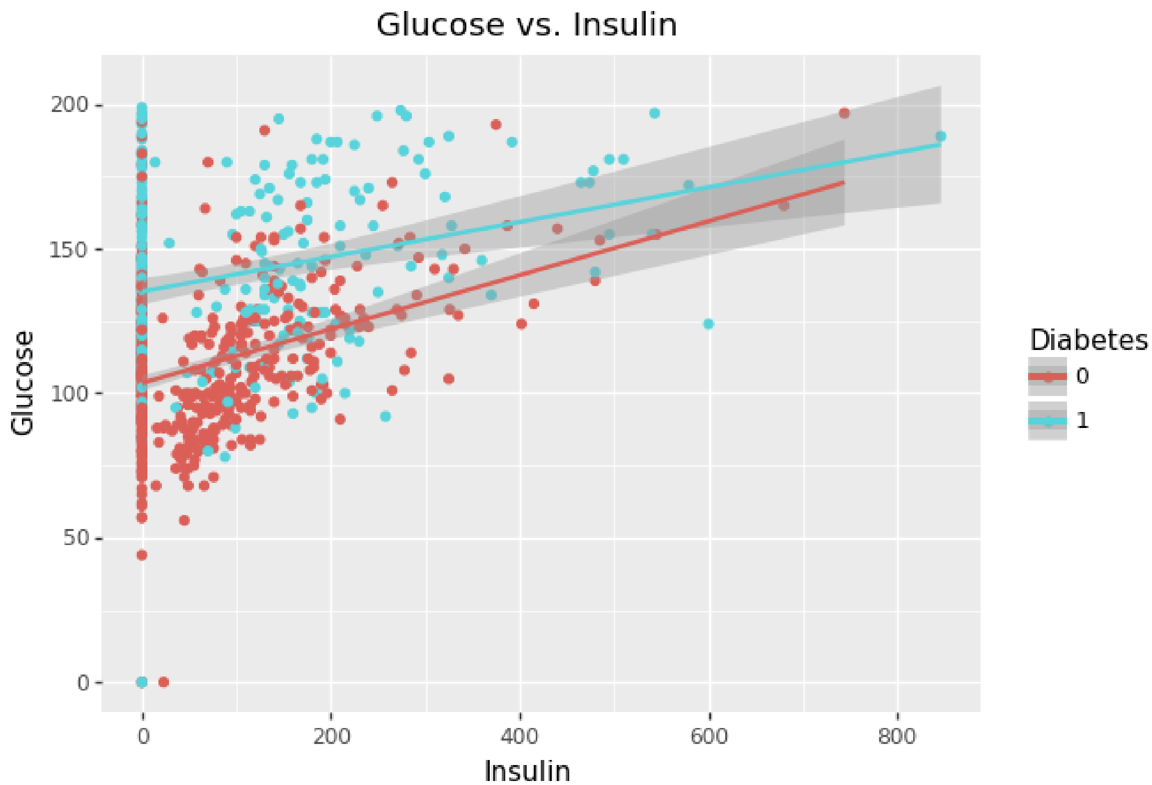
1. Custom x-axis labels, y-axis labels and titles
2. Fill and/or Color by a variable
3. Use facet_wrap()
4. Layer multiple geoms
5. Change the theme of your graph (see: https://plotnine.readthedocs.io/en/stable/generated/plotnine.themes.theme.html (https://plotnine.readthedocs.io/en/stable/generated/plotnine.themes.theme.html))

In [220]:
```
(ggplot(data, aes("Age", "BMI", color="factor(Outcome)")) +
geom_point(alpha = 0.5, size = 1.5) +
 theme_minimal() +
labs(title = "BMI vs. Age", color = "Diabetes"))
```



Out[220]: <ggplot: (7548865237)>

In [219]:
```
(ggplot(data, aes('Insulin', 'Glucose', color="factor(Outcome)")) +
 geom_point() +
theme(legend_key=element_rect(fill='#666666', alpha=.3)) +
geom_smooth(method='lm') +
labs(title = "Glucose vs. Insulin", color = "Diabetes"))
```



Out[219]: <ggplot: (7548248049)>