

## ▼ Multiple Linear Regression

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn import datasets
from sklearn.linear_model import LinearRegression
from sklearn import metrics
```

```
db_dataset = datasets.load_diabetes()
db = pd.DataFrame(db_dataset.data, columns=db_dataset.feature_names)
#db.describe()
#print(db_dataset.DESCR)
```

```
Y = db_dataset.target # Y is the target data provided or the quantitative measure of disease
```

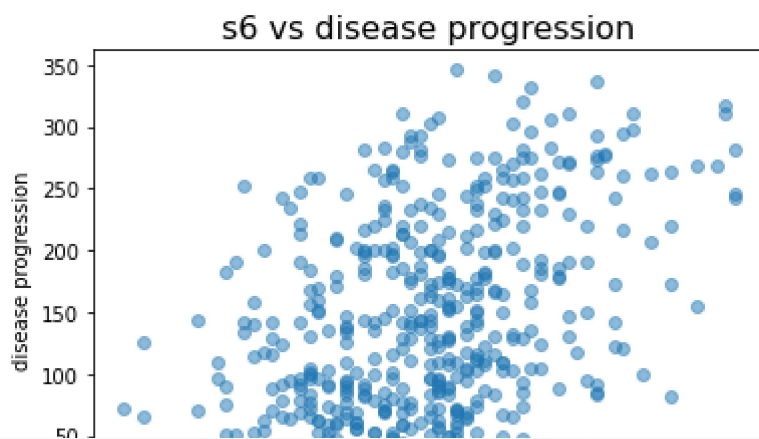
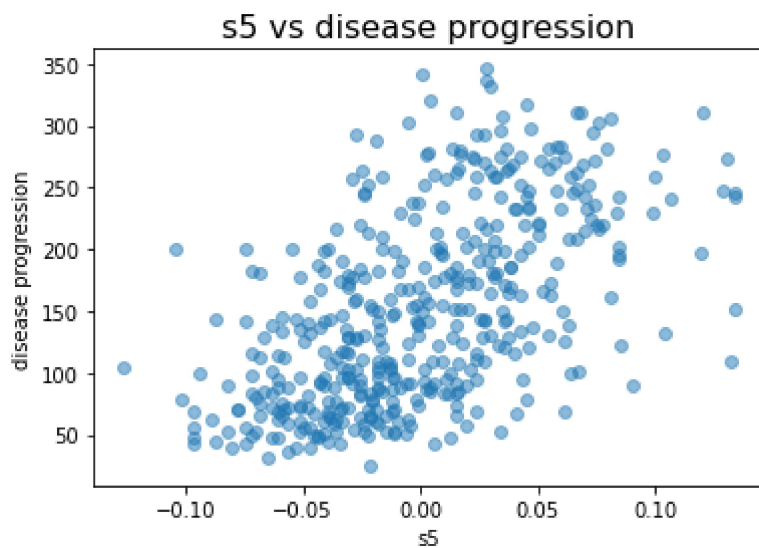
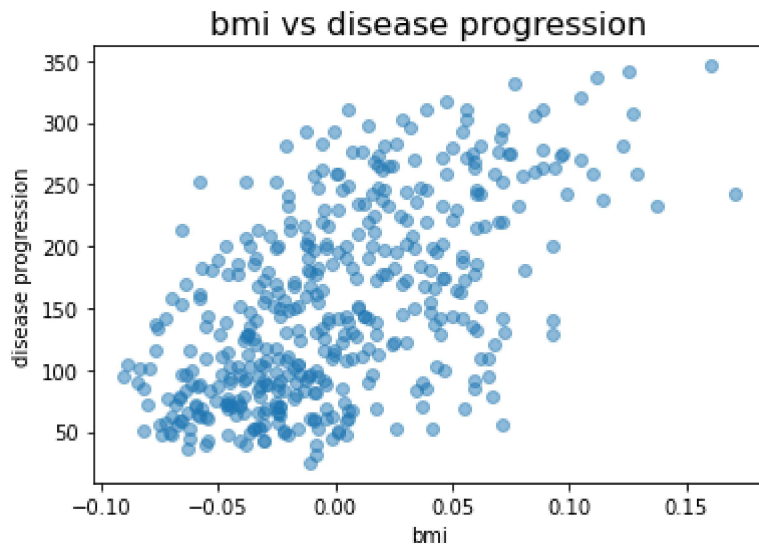
## ▼ Problem

Determine the percentage of how bmi, s5 (possibly log of serum triglycerides level), and s6 (sugar level) of the patient could explain the values of the disease progression one year after baseline.

```
plt.scatter(x=db['bmi'],y=Y,alpha=0.5)
plt.title('bmi vs disease progression', fontsize=16)
plt.xlabel('bmi')
plt.ylabel('disease progression')
plt.show()
```

```
plt.scatter(x=db['s5'],y=Y,alpha=0.5)
plt.title('s5 vs disease progression', fontsize=16)
plt.xlabel('s5')
plt.ylabel('disease progression')
plt.show()
```

```
plt.scatter(x=db['s6'],y=Y,alpha=0.5)
plt.title('s6 vs disease progression', fontsize=16)
plt.xlabel('s6')
plt.ylabel('disease progression')
plt.show()
```



```
X = pd.DataFrame(np.c_[db['bmi'], db['s6'],db['s5']], columns=['bp','s6','s5'])  
y = db_dataset.target
```

```
# We are using 80% of the data to build the training set and 20% for test set  
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random_state=1)
```

```
model = LinearRegression() #Defining linear regression model  
model.fit(X_train, y_train) #Building training model
```

```
LinearRegression(copy_X=True, fit_intercept=True, n_jobs=None, normalize=False)
```

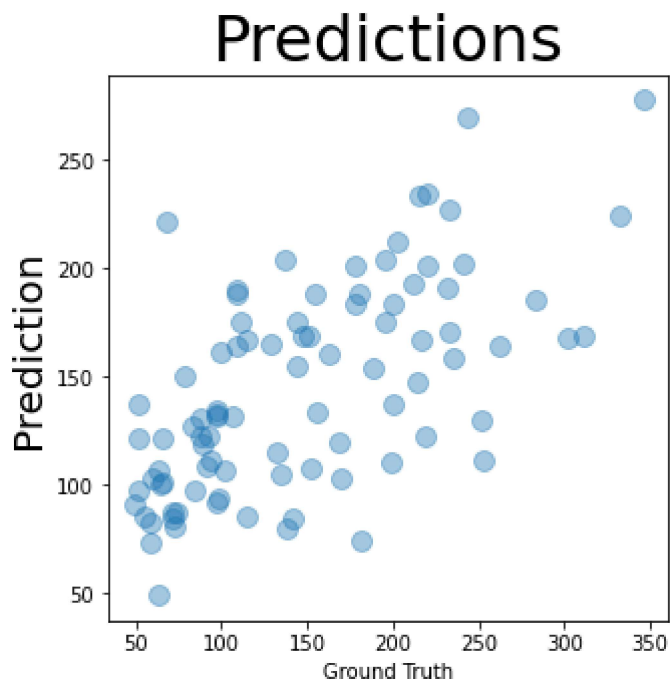
```
model_summary = pd.DataFrame(X.columns, columns=['Features'])
model_summary['Weights Raw'] = model.coef_.reshape(3,1) # Coefficient of each Features
model_summary = model_summary.append({'Features':'Intercept', 'Weights Raw':float(model.inter
model_summary
```

|   | Features  | Weights Raw |
|---|-----------|-------------|
| 0 | bp        | 678.324727  |
| 1 | s6        | 85.890837   |
| 2 | s5        | 571.126807  |
| 3 | Intercept | 151.646552  |

```
preds = model.predict(X_test) # applying trained model to make prediction using test set
out = pd.DataFrame({'Actual': y_test, 'Predicted': preds})
```

```
plt.figure(figsize=(5,5))
plt.title('Predictions', fontsize=32)
plt.scatter(y_test, preds, s = 100, alpha=0.4)
plt.xlabel('Ground Truth')
plt.ylabel('Prediction', fontsize=20)
```

```
Text(0, 0.5, 'Prediction')
```



```
def adjr2(r2,x):
    n = x.shape[0]
    p = x.shape[1]
```

```

adjusted_r2 = 1-(1-r2)*(n-1)/(n-p-1)
return adjusted_r2

```

```

MSE = metrics.mean_squared_error(y_test, preds)
RMSE = np.sqrt(MSE)
R2 = metrics.r2_score(y_test, preds)
AR2 = adjr2(R2,X_train)
model_metrics = pd.DataFrame([[ 'MSE'],[ 'RMSE'],[ 'R^2'],
                                [ 'Adjusted R^2']],
                                columns=[ 'Metrics'])
model_metrics['Multiple Regression'] = MSE, RMSE, R2, AR2
model_metrics

```

|   | Metrics      | Multiple Regression |
|---|--------------|---------------------|
| 0 | MSE          | 3230.174342         |
| 1 | RMSE         | 56.834623           |
| 2 | R^2          | 0.393846            |
| 3 | Adjusted R^2 | 0.388636            |

The correlation of disease progression with the BMI, s5 (possible log of serum triglycerides level), and s6 (sugar level) was shown above. It can be concluded that the quantitative measure of disease progression one year after baseline was affected only to a certain degree of the BMI, s5, and s6 of the patient which is proven by relatively small R^2 which is 0.39. Therefore, the BMI, s5, and s6 could explain the measure of disease progression values by only 39%

## ▼ Polynomial Regression

```

from sklearn.preprocessing import PolynomialFeatures

```

```

def adjr2(r2,x):
    n = x.shape[0]
    p = x.shape[1]
    adjusted_r2 = 1-(1-r2)*(n-1)/(n-p-1)
    return adjusted_r2

```

```

X = pd.DataFrame(np.c_[db['bmi'], db['s6'],db['s5']], columns=['bp','s6','s5'])
y = db_dataset.target
X_train, X_test, y_train, y_test = train_test_split(X,y,test_size = 0.2,random_state = 1)

```

```

quad_features = PolynomialFeatures(degree=2)
x_quad = quad_features.fit_transform(X_train)

```

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

```
LinearRegression(copy_X=True, fit_intercept=True, n_jobs=None, normalize=False)
```

```
preds = model.predict(quad_features.fit_transform(X_test))
```

```
poly_MSE = metrics.mean_squared_error(y_test,preds)
poly_RMSE = np.sqrt(poly_MSE)
poly_R2 = metrics.r2_score(y_test,preds)
poly_AR2 = adjr2(poly_R2,X_train)
model_metrics = pd.DataFrame([[ 'MSE'],[ 'RMSE'],[ 'R^2'],
                                [ 'Adjusted R^2']],
                                columns=[ 'Metrics'])
model_metrics['Polynomial Regression'] = poly_MSE, poly_RMSE, poly_R2, poly_AR2
model_metrics
```



|   | Metrics      | Polynomial Regression |
|---|--------------|-----------------------|
| 0 | MSE          | 3194.420746           |
| 1 | RMSE         | 56.519207             |
| 2 | R^2          | 0.400556              |
| 3 | Adjusted R^2 | 0.395403              |

Using the polynomial regression improves the R^2 by 1% and lessen the MSE and this is because we can have now a curve hence more data points can be reached. Therefore, the BMI, s5, and s6 could explain the measure of disease progression values by 40% now.

## ▼ Linear Regression using Normal Equation

$$\theta = (X^T X)^{-1} X^T y$$

(Normal Equation)

```
X = pd.DataFrame(np.c_[db['bmi'], db['s6'],db['s5']], columns=[ 'bp', 's6', 's5'])
y = db_dataset.target
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random_state=1)
```

```
X=X_train
y=y_train
```

```

ones = np.ones((X.shape[0], 1)) # Appending a column of ones in X to add the bias term.
X = np.concatenate((ones, X), axis=1)
XTX = np.dot(X.T,X)
XTX_inv = np.linalg.inv(XTX)
XTy = ((X.T).dot(y))
inter_weights = np.dot(XTX_inv,XTy)
intercept = inter_weights[0]
print("The intercept is:",intercept)
weights = inter_weights[1:8]
print("The weights are:",weights)

```

```

The intercept is: 151.6465519307307
The weights are: [678.32472659  85.89083682 571.12680662]

```

```

ones = np.ones((X_test.shape[0], 1))# Appending a column of ones in X to add the bias term.
X = np.concatenate((ones, X_test), axis=1)
preds = np.dot(X,inter_weights)

```

```

normal_MSE = metrics.mean_squared_error(y_test, preds)
normal_RMSE = np.sqrt(normal_MSE)
normal_R2 = metrics.r2_score(y_test, preds)
normal_AR2 = adjr2(normal_R2,X_train)
model_metrics = pd.DataFrame([['MSE'],['RMSE'],['R^2'],
                               ['Adjusted R^2']],
                              columns=['Metrics'])
model_metrics['Normal Equation'] = normal_MSE, normal_RMSE, normal_R2, normal_AR2
model_metrics

```

|   | Metrics      | Normal Equation |
|---|--------------|-----------------|
| 0 | MSE          | 3230.174342     |
| 1 | RMSE         | 56.834623       |
| 2 | R^2          | 0.393846        |
| 3 | Adjusted R^2 | 0.388636        |

The result of linear regression using the normal equation is just the same with MLR because this is just another way of solving MLR.

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