Goals

- implement the model $f_{w,b}$ for linear regression with one variable
- implement and explore the cost function for linear regression with one variable.

1. Model Representation

Notation

Here is a summary of some of the notation you will encounter.

General Notation	Description	Python (if applicable)
a	scalar, non bold	
$\mathbf{a}$	vector, bold	
Regression		
$\mathbf{x}$	Training Example feature values	`x_train`
$\mathbf{y}$	Training Example targets	`y_train`
$x^{(i)}$, $y^{(i)}$	i_{th}Training Example	`x_i`, `y_i`
m	Number of training examples	`m`
w	parameter: weight	`w`
b	parameter: bias	`b`
$f_{w,b}(x^{(i)})$	The result of the model evaluation at $x^{(i)}$ parameterized by w, b: $f_{w,b}(x^{(i)}) = wx^{(i)} + b$	`f_wb`

Tools

In this assignment you will make use of:

- NumPy, a popular library for scientific computing
- Matplotlib, a popular library for plotting data

In [1]:
```
import numpy as np
import matplotlib.pyplot as plt
```

Problem Statement

As in the lecture, you will use the motivating example of diabetes progression prediction. This assignment will use a simple data set with only two data points shown below. These two points will constitute our *data or training set*.

BMI	Diabetes progression
32.1	151
21.6	75

You would like to fit a linear regression model through these two points, so you can then predict diabetes progression for other patients - say, a patient with BMI = 30.5.

Please run the following code cell to create your `x_train` and `y_train` variables. The data is stored in one-dimensional NumPy arrays.

In [2]:
```
# x_train is the input variable (BMI)
# y_train is the target (diabetes progression level)
x_train = np.array([32.1, 21.6])
y_train = np.array([151, 75])
print(f"x_train = {x_train}")
print(f"y_train = {y_train}")
```

```
x_train = [32.1 21.6]
y_train = [151  75]
```

> **Note**: The course will frequently utilize the python 'f-string' output formatting described here when printing. The content between the curly braces is evaluated when producing the output.

Number of training examples `m`

You will use `m` to denote the number of training examples. Numpy arrays have a `.shape` parameter. `x_train.shape` returns a python tuple with an entry for each dimension. `x_train.shape[0]` is the length of the array and number of examples as shown below.

In [3]:
```
# m is the number of training examples
print(f"x_train.shape: {x_train.shape}")
m = x_train.shape[0]
print(f"Number of training examples is: {m}")
```

```
x_train.shape: (2,)
Number of training examples is: 2
```

One can also use the Python `len()` function as shown below.

In [4]:
```
# m is the number of training examples
m = len(x_train)

print(f"Number of training examples is: {m}")
```

```
Number of training examples is: 2
```

Training example `x_i, y_i`

You will use ($x^{(i)}$, $y^{(i)}$) to denote the i^{th} training example. Since Python is zero indexed, ($x^{(0)}$, $y^{(0)}$) is (32.1, 151) and ($x^{(1)}$, $y^{(1)}$) is (21.6, 75).

To access a value in a Numpy array, one indexes the array with the desired offset. For example the syntax to access location zero of `x_train` is `x_train[0]`. Finish the next code block below to get the i^{th} training example.

In [5]:
```
i = 0 # Change this to 1 to see (x^1, y^1)

x_i = x_train[i]   # ith feature value
y_i = y_train[i]   # ith target value
print(f"(x^({i}), y^({i})) = ({x_i}, {y_i})")
```

```
(x^(0), y^(0)) = (32.1, 151)
```

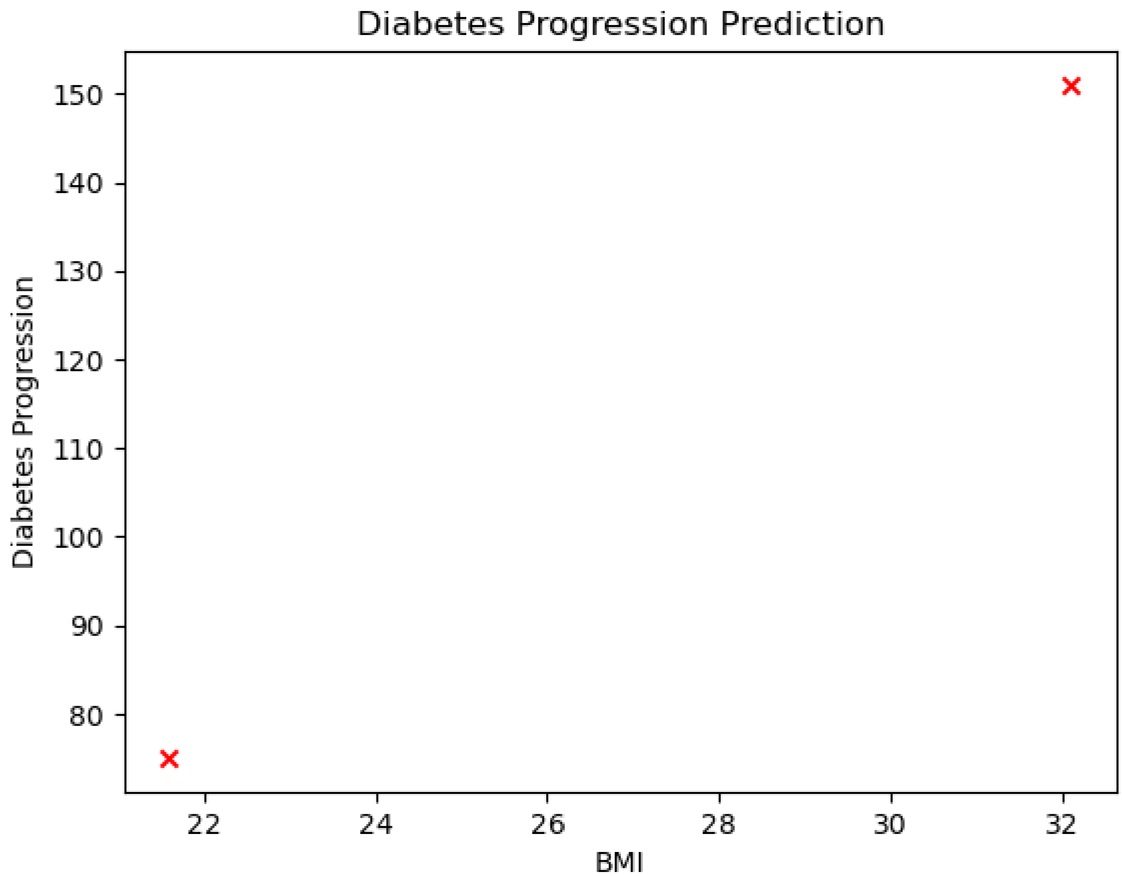
Plotting the data

You can plot these two points using the `scatter()` function in the `matplotlib` library, as shown in the cell below.

- The function arguments `marker` and `c` show the points as red crosses (the default is blue dots).

You can use other functions in the `matplotlib` library to set the title and labels to display

In [6]:
```
# Plot the data points
plt.scatter(x_train, y_train, marker='x', c='r')
# Set the title
plt.title("Diabetes Progression Prediction")
# Set the y-axis label
plt.ylabel('Diabetes Progression')
# Set the x-axis label
plt.xlabel('BMI')
plt.show()
```



Model function

As described in lecture, the model function for linear regression (which is a function that maps from `x` to `y`) is represented as

$$f_{w,b}(x^{(i)}) = wx^{(i)} + b \tag{1}$$

The formula above is how you can represent straight lines - different values of w and b give you different straight lines on the plot.

Let's try to get a better intuition for this through the code blocks below. Let's start with $w = 1$ and $b = 1$.

Note: You can come back to this cell to adjust the model's w and b parameters

In [7]:

```
w = 1
b = 1
print(f"w: {w}")
print(f"b: {b}")
```

```
w: 1
b: 1
```

Now, let's compute the value of $f_{w,b}(x^{(i)})$ for your two data points. You can explicitly write this out for each data point as -

for $x^{(0)}$, `f_wb = w * x[0] + b`

for $x^{(1)}$, `f_wb = w * x[1] + b`

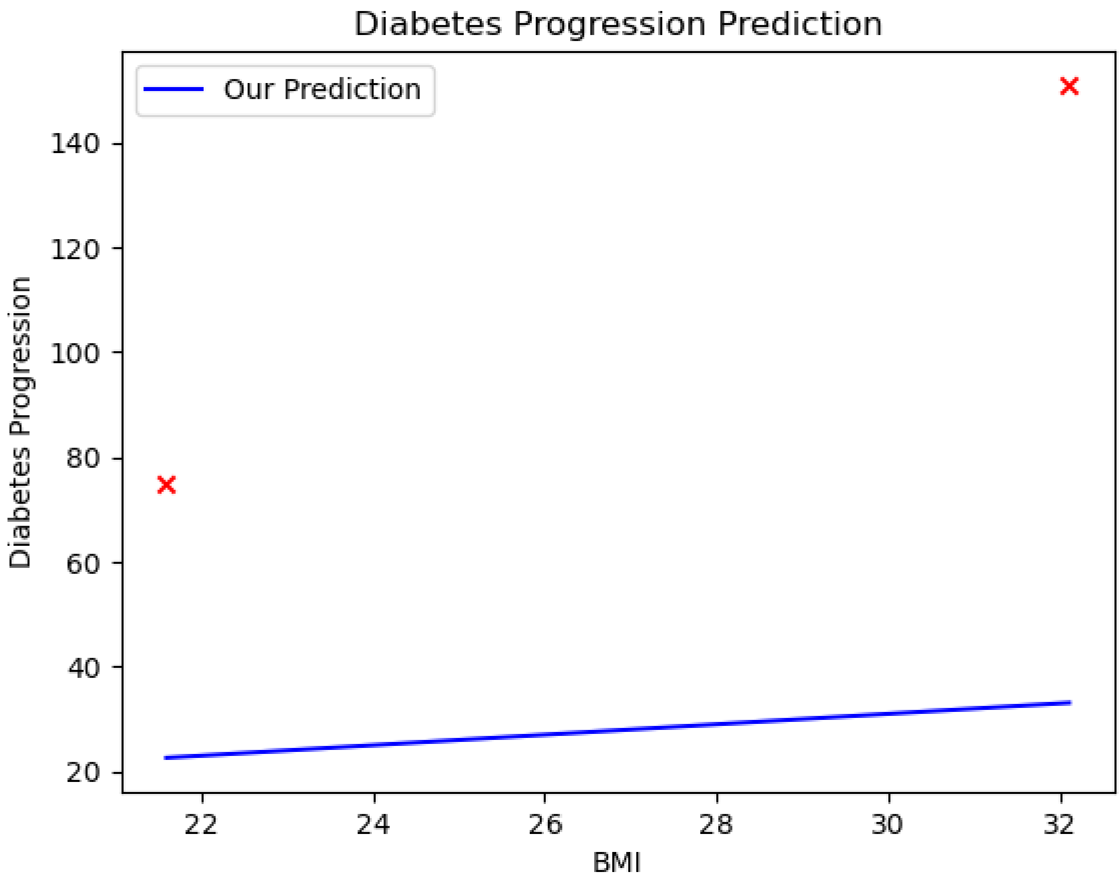
For a large number of data points, this can get unwieldy and repetitive. So instead, you can calculate the function output in a `for` loop in the `compute_model_output` function below.

> **Note**: The argument description `(ndarray (m,))` describes a Numpy n-dimensional array of shape (m,). `(scalar)` describes an argument without dimensions, just a magnitude.
> **Note**: `np.zero(n)` will return a one-dimensional numpy array with n entries

In [8]:
```
def compute_model_output(x, w, b):
    """
    Computes the prediction of a linear model
    Args:
      x (ndarray (m,)): Data, m examples
      w,b (scalar)    : model parameters
    Returns
      y (ndarray (m,)): target values
    """
    m = x.shape[0]
    f_wb = np.zeros(m)
    # write a loop to compute f_wb
    for i in range(0, m):
        f_wb[i] = w * x[i] + b

    return f_wb
```

Now let's call the `compute_model_output` function and plot the output..

In [9]:
```
tmp_f_wb = compute_model_output(x_train, w, b)      # call the compute_model_output fu

# Plot our model prediction
plt.plot(x_train, tmp_f_wb, c='b', label='Our Prediction')

# Plot the data points
plt.scatter(x_train, y_train, c='r', marker='x')

# Set the title
plt.title("Diabetes Progression Prediction")

# Set the y-axis label
plt.ylabel('Diabetes Progression')

# Set the x-axis label
plt.xlabel('BMI')

plt.legend()
plt.show()
```



As you can see, setting $w = 1$ and $b = 1$ does *not* result in a line that fits our data.

Prediction

Try experimenting with different values of w and b. What should the values be for a line that fits our data? Note that you can actually compute the theorectical values of w and b by hand given the two training examples. Put your best w and b in the prediction cell below.

Now that we have a model, we can use it to make our original prediction. Let's predict the diabetes progression of a patient with BMI=30.5. Note: your prediction value should be around 140.

In [10]:
```
w = 76/10.5                           # Your best w (7.238)
b = -32.1*76/10.5 + 151               # Your best b (-81.343)
x_i = 30.5
diabetes_progression = w*x_i + b  # prediction

print(f"${diabetes_progression:.1f}")
```

```
$139.4
```

2. Cost Function

Here, cost is a measure of how well our model is predicting the diabetes progression of a patient.

The equation for cost with one variable is:

$$J(w,b) = \frac{1}{2m} \sum\limits_{i = 0}^{m-1} (f_{w,b}(x^{(i)}) - y^{(i)})^2 \tag{2}$$

where

$$f_{w,b}(x^{(i)}) = wx^{(i)} + b \tag{3}$$

- $f_{w,b}(x^{(i)})$ is our prediction for example i using parameters w,b.
- $(f_{w,b}(x^{(i)}) - y^{(i)})^2$ is the squared difference between the target value and the prediction.
- These differences are summed over all the m examples and divided by `2m` to produce the cost, $J(w,b)$.

> Note, in lecture summation ranges are typically from 1 to m, while code will be from 0 to m-1.

The code below calculates cost by looping over each example. In each loop:

- `f_wb`, a prediction is calculated
- the difference between the target and the prediction is calculated and squared.
- this is added to the total cost.

In [11]:
```
def compute_cost(x, y, w, b):
    """
    Computes the cost function for linear regression.

    Args:
      x (ndarray (m,)): Data, m examples
      y (ndarray (m,)): target values
      w,b (scalar)    : model parameters

    Returns
        total_cost (float): The cost of using w,b as the parameters for linear regress
               to fit the data points in x and y
    """
    # number of training examples
    m = x.shape[0]
    cost_sum = 0

    # write a loop to compute the summation of the squred difference for all training

    for i in range (0, m):
        y_i = w*x[i]+b
        cost_sum += (y_i - y[i])**2

    total_cost = (1 / (2 * m)) * cost_sum

    return total_cost
```

Test your compute_cost function using x_train, y_train, and your best w and b. Your total cost should be around 0.

In [12]:
```
total_cost = compute_cost(x_train, y_train, w, b)   # call compute_cost function
print(f"Total cost is: {total_cost:.1f}")
```

```
Total cost is: 0.0
```

Redefine your x_train and y_train using a larger training set below. Test your compute_cost function again.

BMI	Diabetes progression
32.1	151
21.6	75
30.5	141
22.6	97

In [13]:
```
# Redefining x_train and y_train
x_train = np.array([32.1, 21.6, 30.5, 22.6])
y_train = np.array([151, 75, 141, 97])

total_cost = compute_cost(x_train, y_train, w, b)   # call compute_cost function
print(f"Total cost is: {total_cost:.1f}")
```

```
Total cost is: 27.6
```

In [ ]: