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

Diabetes Binary Classification Dataset

Input Features: 'preg_count', 'glucose_concentration', 'diastolic_bp', 'triceps_skin_fold_thickness', two_hr_serum_insulin', 'bmi', 'diabetes_pedi', 'age'

Target Feature: 'diabetes_class'

Objective: Predict diabetes_class for given input features

Data Source: https://archive.ics.uci.edu/ml/datasets/pima+indians+diabetes

In [2]:
```
columns = ['diabetes_class', 'preg_count', 'glucose_concentration', 'diastolic_bp',
       'triceps_skin_fold_thickness', 'two_hr_serum_insulin', 'bmi',
       'diabetes_pedi', 'age']
```

In [3]:
```
df = pd.read_csv('pima_indians_diabetes_all.csv')
```

In [4]:
```
df.describe() # Note that most of the minima are zero. That's not good.
```

Out[4]:

	preg_count	glucose_concentration	diastolic_bp	triceps_skin_fold_thickness	two_hr_serum_insulin	bmi	diabetes_pedi	
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.00
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.24
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.76
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.00
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.00
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.00
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.00
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.00

In [17]:

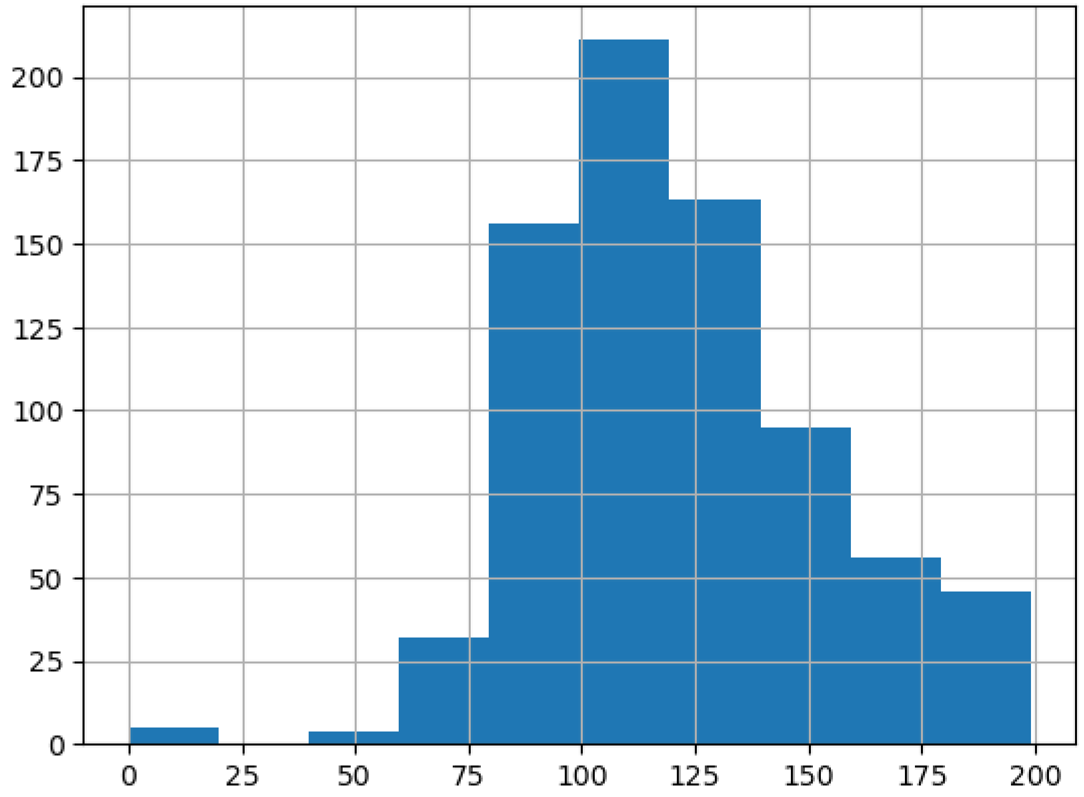
```
print(df.describe())
```

```
       preg_count  glucose_concentration  diastolic_bp  
count  768.000000             768.000000    768.000000  \
mean     3.845052             120.894531     69.105469   
std      3.369578              31.972618     19.355807   
min      0.000000               0.000000      0.000000   
25%      1.000000              99.000000     62.000000   
50%      3.000000             117.000000     72.000000   
75%      6.000000             140.250000     80.000000   
max     17.000000             199.000000    122.000000   

       triceps_skin_fold_thickness  two_hr_serum_insulin         bmi  
count                   768.000000            768.000000  768.000000  \
mean                     20.536458             79.799479   31.992578   
std                      15.952218            115.244002    7.884160   
min                       0.000000              0.000000    0.000000   
25%                       0.000000              0.000000   27.300000   
50%                      23.000000             30.500000   32.000000   
75%                      32.000000            127.250000   36.600000   
max                      99.000000            846.000000   67.100000   

       diabetes_pedi         age  diabetes_class  
count     768.000000  768.000000      768.000000  
mean        0.471876   33.240885        0.348958  
std         0.331329   11.760232        0.476951  
min         0.078000   21.000000        0.000000  
25%         0.243750   24.000000        0.000000  
50%         0.372500   29.000000        0.000000  
75%         0.626250   41.000000        1.000000  
max         2.420000   81.000000        1.000000  
```

In [5]:
```
df['glucose_concentration'].hist()
plt.show()
```

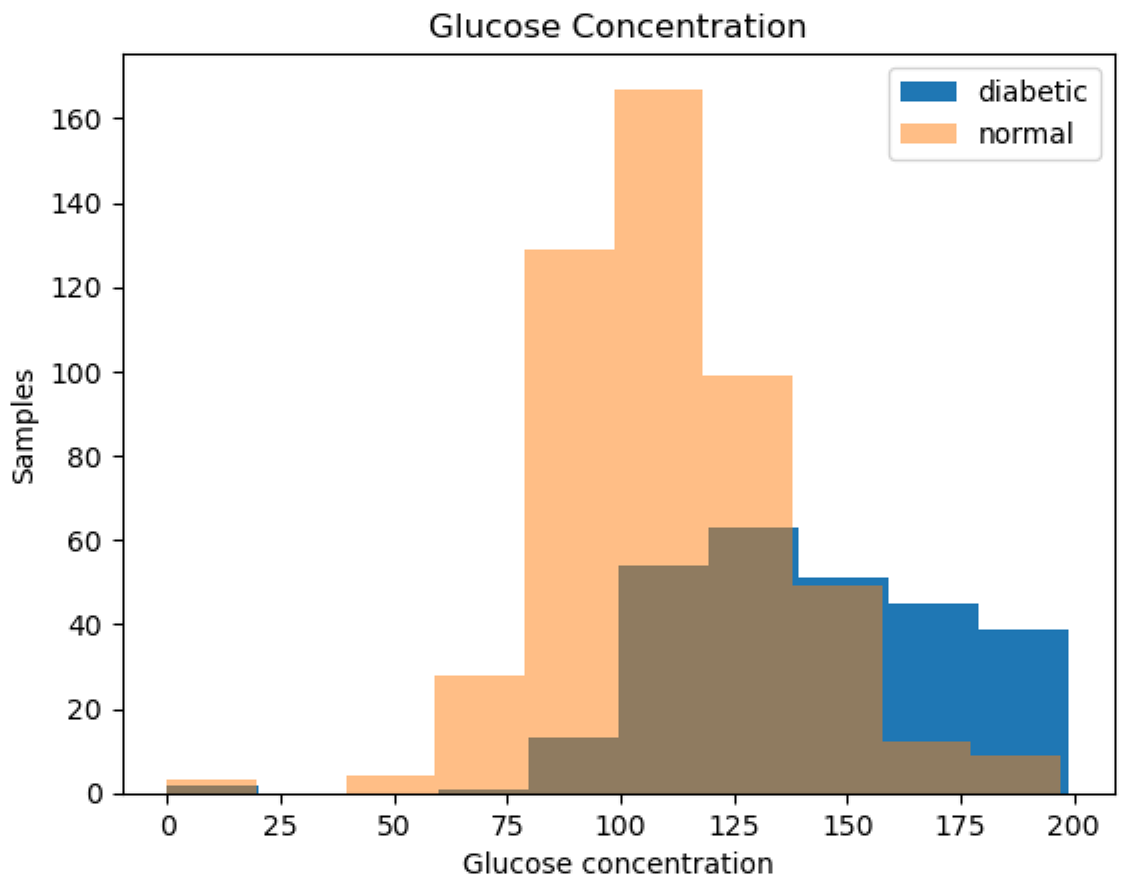


In [6]:
```
df['diabetes_class'].value_counts()
```

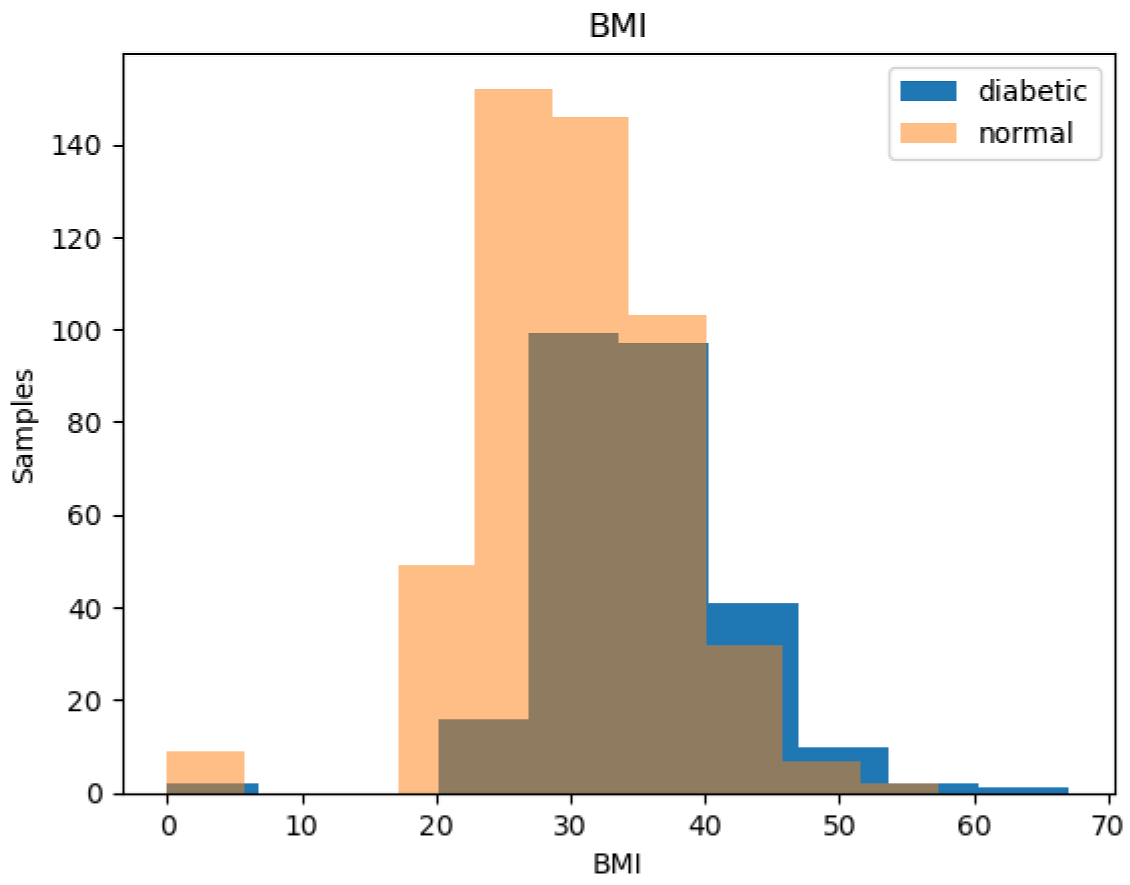
Out[6]:
```
diabetes_class
0    500
1    268
Name: count, dtype: int64
```

In [7]:
```
# Separate diabetic and normal samples
diabetic = df.diabetes_class == 1
normal = df.diabetes_class == 0
```

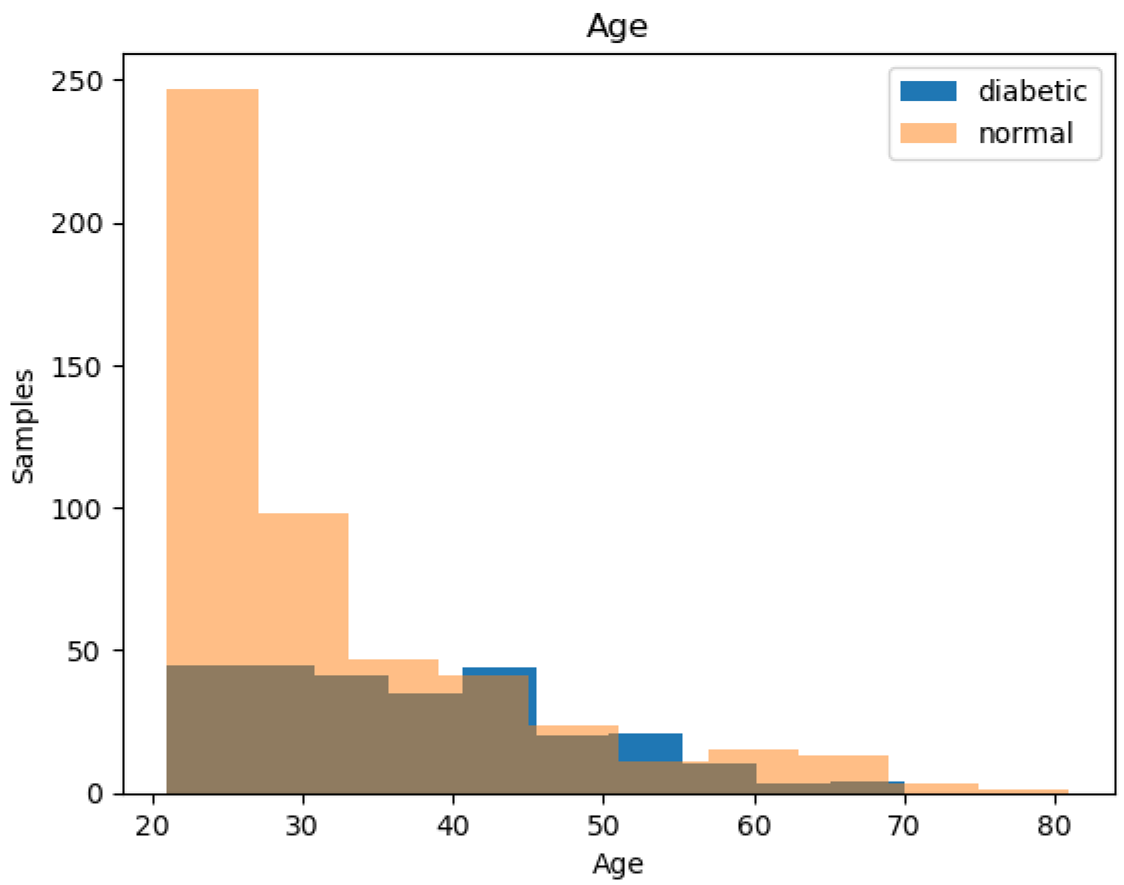
In [8]:
```
# Glucose concentration histogram
plt.hist(df[diabetic].glucose_concentration,label='diabetic')
plt.hist(df[normal].glucose_concentration,alpha=0.5,label='normal')
plt.title('Glucose Concentration')
plt.xlabel('Glucose concentration')
plt.ylabel('Samples')
plt.legend()
plt.show()
```



In [9]:
```
# BMI histogram
plt.hist(df[diabetic].bmi,label='diabetic')
plt.hist(df[normal].bmi,alpha=0.5,label='normal')
plt.title('BMI')
plt.xlabel('BMI')
plt.ylabel('Samples')
plt.legend()
plt.show()
```



In [10]:
```
# Age
plt.hist(df[diabetic].age,label='diabetic')
plt.hist(df[normal].age,alpha=0.5,label='normal')
plt.title('Age')
plt.xlabel('Age')
plt.ylabel('Samples')
plt.legend()
plt.show()
```



Training and Validation Set

Target Variable as first column followed by input features:

'diabetes_class', 'preg_count', 'glucose_concentration', 'diastolic_bp', 'triceps_skin_fold_thickness', 'two_hr_serum_insulin', 'bmi', 'diabetes_pedi', 'age'

Training, Validation files do not have a column header

In [11]:
```
# Training = 70% of the data
# Validation = 30% of the data
# Randomize the datset
np.random.seed(5)
l = list(df.index)
np.random.shuffle(l)
df = df.iloc[l]
```

In [12]:
```
rows = df.shape[0]
train = int(.7 * rows)
test = rows - train
```

In [13]:
```
rows, train, test
```

Out[13]:
```
(768, 537, 231)
```

In [14]:
```
# Write Training Set
df[:train].to_csv('diabetes_train.csv'
                          ,index=False,index_label='Row',header=False
                          ,columns=columns)
```

In [15]:
```
# Write Validation Set
df[train:].to_csv('diabetes_validation.csv'
                          ,index=False,index_label='Row',header=False
                          ,columns=columns)
```

In [16]:
```
# Write Column List
with open('diabetes_train_column_list.txt','w') as f:
    f.write(','.join(columns))
```

In [ ]: