In [2]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import StandardScaler  #to standardized the data to a common
from sklearn.model_selection import train_test_split #to split our data into training an
from sklearn import svm #supervised learning algorithm
from sklearn.metrics import accuracy_score #it calculates the accuracy of a classificati

import warnings
warnings.filterwarnings('ignore', category=UserWarning)
```

Data Collection

In [4]:
```
#loading the dataset to pandas dataframe

data = pd.read_csv('diabetes.csv')
```

In [5]:
```
#first five rows
data.head()
```

Out[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcom
0	6	148	72	35	0	33.6	0.627	50	
1	1	85	66	29	0	26.6	0.351	31	
2	8	183	64	0	0	23.3	0.672	32	
3	1	89	66	23	94	28.1	0.167	21	
4	0	137	40	35	168	43.1	2.288	33	

In [6]:
```
#number of rows and columns
data.shape
```

Out[6]:
```
(768, 9)
```

In [7]:
```
#checking for missing values

data.isnull().sum()
```

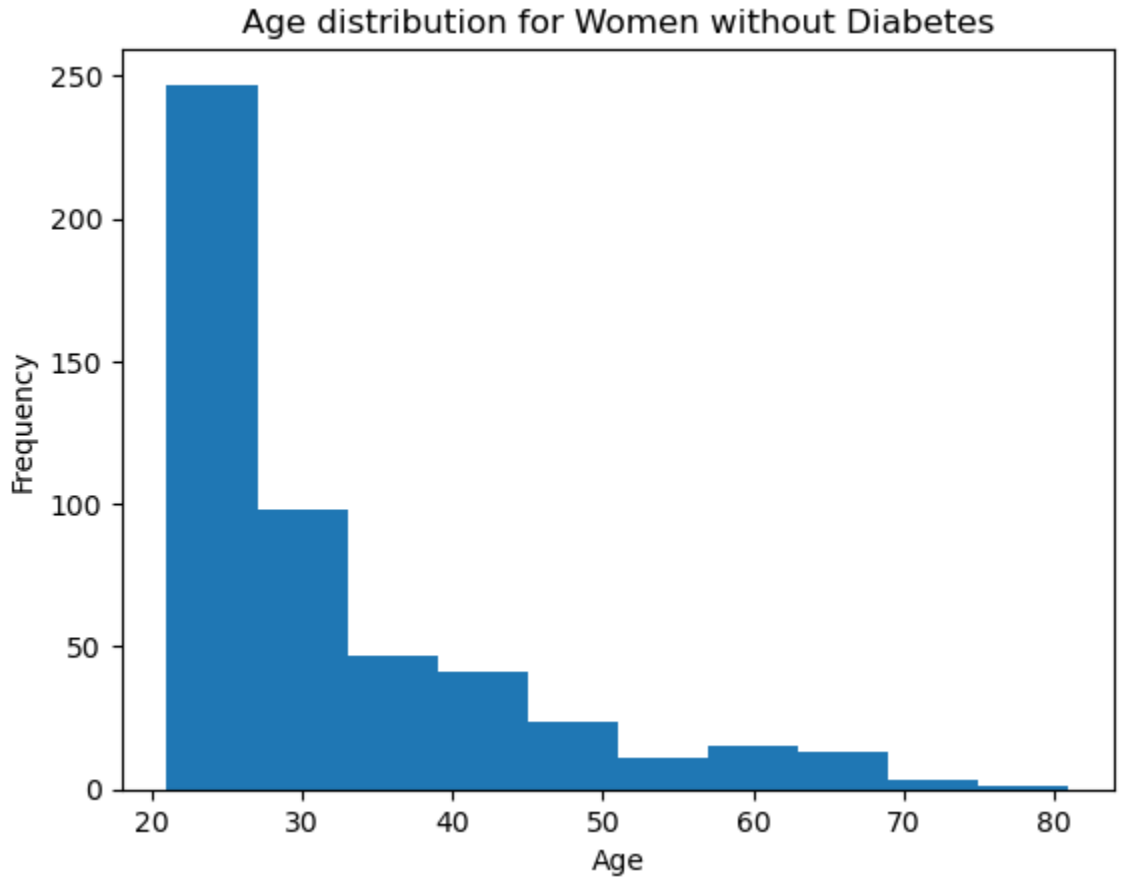
Out[7]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [8]:
```
#checking the data types
data.info()
```

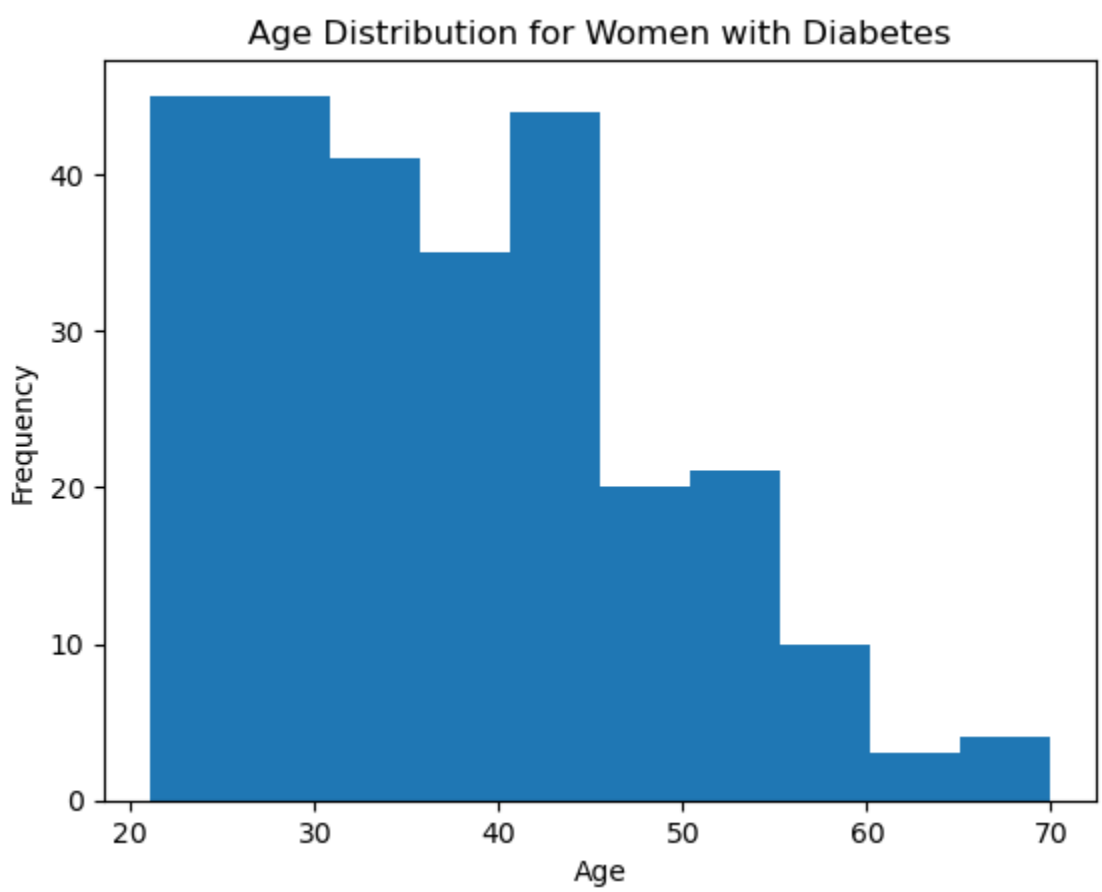
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   Pregnancies               768 non-null    int64
```

```
 1   Glucose                   768 non-null    int64
 2   BloodPressure             768 non-null    int64
 3   SkinThickness             768 non-null    int64
 4   Insulin                   768 non-null    int64
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64
 8   Outcome                   768 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

In [9]:
```
plt.hist(data[data['Outcome']==0]['Age'], bins = 10)
plt.title('Age distribution for Women without Diabetes')
plt.xlabel('Age')
plt.ylabel('Frequency')
plt.show()
```



In [10]:
```
plt.hist(data[data['Outcome']==1]['Age'], bins = 10)
plt.title('Age Distribution for Women with Diabetes')
plt.xlabel('Age')
plt.ylabel('Frequency')
plt.show()
```



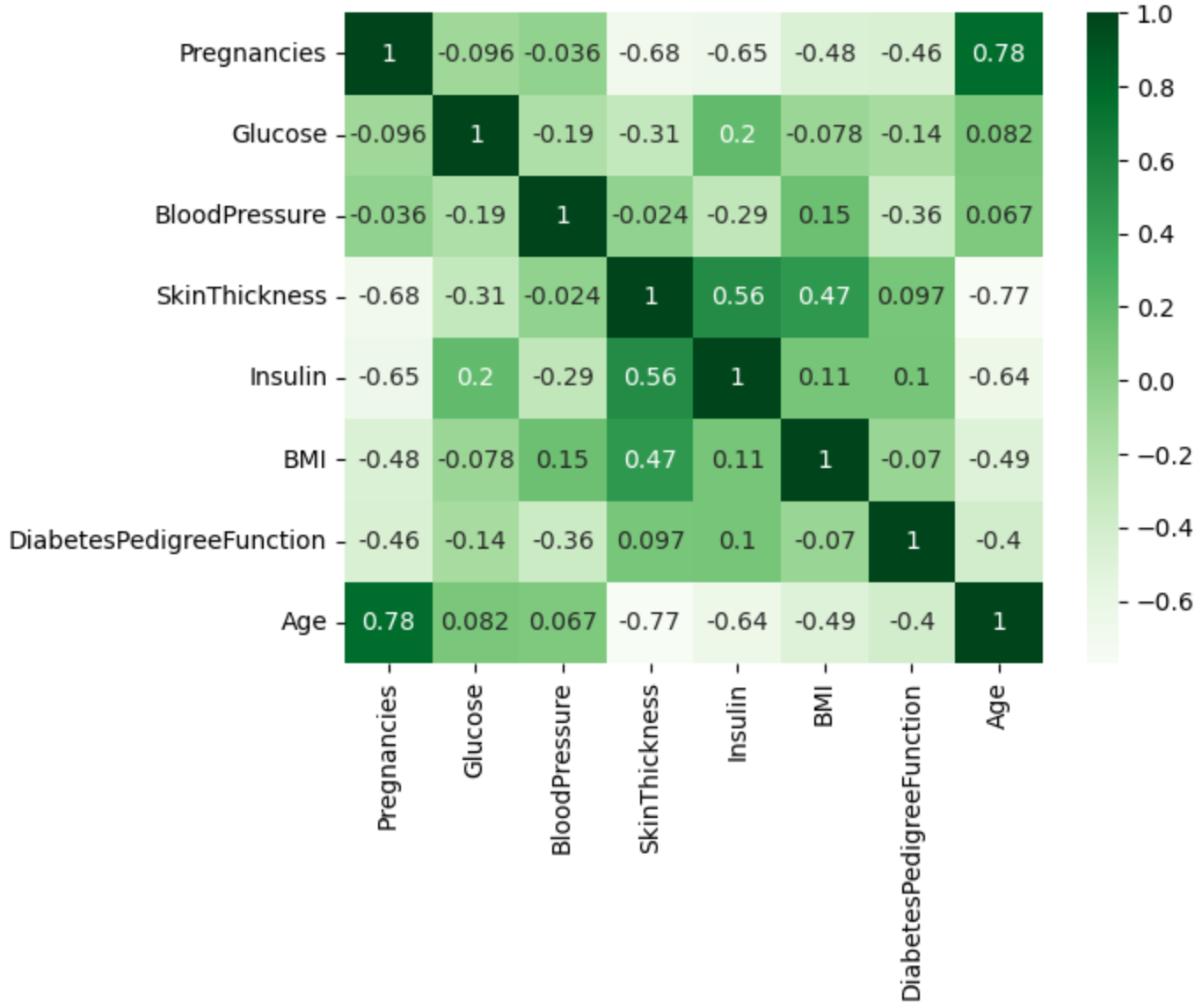
In [81]:
```
#Correlation
correlation = data.iloc[:,0:8].corr()

correlation
```

Out[81]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Diabetes
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.017683	
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.221071	
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.281805	
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.392573	
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.197859	
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.000000	
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.140647	
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.036242	

In [85]:
```
 #heatmap showing the correlation between two variables
sns.heatmap(correlation.corr(numeric_only=True).iloc[:,0:8], annot=True, cmap='Greens');
```



In [13]:
```
#statistics of the data
data.describe()
```

Out[13]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFuncti
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.0000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.4718
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.3313
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.0780
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.2437
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.3725
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.6262
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.4200

In [14]:
```
#number of diabetes and non-diabetes patients
#  0 = Non-diabetic patients
#  1 = Diabetic patients
data['Outcome'].value_counts()
```

Out[14]:
```
Outcome
0    500
1    268
Name: count, dtype: int64
```

In [15]:
```
#Mean value of the dataset by diabetic and non diabetic patients groupby 'Outcome'
data.groupby('Outcome').mean()
```

Out[15]:

Outcome	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFun
0	3.298000	109.980000	68.184000	19.664000	68.792000	30.304200	0.42
1	4.865672	141.257463	70.824627	22.164179	100.335821	35.142537	0.55

In [16]:
```
#Seperating features from label

x = data.drop(columns = 'Outcome', axis = 1)
y = data['Outcome']
```

In [17]:
```
print(x)
```

```
     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
..           ...      ...            ...            ...      ...   ...
763           10      101             76             48      180  32.9
764            2      122             70             27        0  36.8
765            5      121             72             23      112  26.2
766            1      126             60              0        0  30.1
767            1       93             70             31        0  30.4

     DiabetesPedigreeFunction  Age
0                       0.627   50
1                       0.351   31
2                       0.672   32
3                       0.167   21
4                       2.288   33
..                        ...  ...
763                     0.171   63
764                     0.340   27
765                     0.245   30
766                     0.349   47
767                     0.315   23

[768 rows x 8 columns]
```

In [18]:
```
print(y)
```

```
0      1
1      0
2      1
3      0
4      1
      ..
763    0
764    0
765    0
766    1
767    0
Name: Outcome, Length: 768, dtype: int64
```

Data Standardization

In [19]:
```
#Data standardization; to convert the values to a common range between 0 & 1 for our ML
```

```
scaler = StandardScaler()
```

In [20]:
```
#Fitting and transforming the 'x' data into the scaler to be in a common range
standardized_data = scaler.fit_transform(x)
```

In [21]:
```
#Printing the 'standardized_data' data
print(standardized_data)
```

```
[[ 0.63994726  0.84832379  0.14964075 ...  0.20401277  0.46849198
   1.4259954 ]
 [-0.84488505 -1.12339636 -0.16054575 ... -0.68442195 -0.36506078
  -0.19067191]
 [ 1.23388019  1.94372388 -0.26394125 ... -1.10325546  0.60439732
  -0.10558415]
 ...
 [ 0.3429808   0.00330087  0.14964075 ... -0.73518964 -0.68519336
  -0.27575966]
 [-0.84488505  0.1597866  -0.47073225 ... -0.24020459 -0.37110101
   1.17073215]
 [-0.84488505 -0.8730192   0.04624525 ... -0.20212881 -0.47378505
  -0.87137393]]
```

In [22]:
```
x = standardized_data
y = data['Outcome']
```

Spliting the Data into Training and Test Data.

In [24]:
```
# test_size 0.2 = 20% data,
#y = stratify it ensures that the distribution of y is maintained in both y_train and x_
#random_state = the same data split is generated everytime I run the code

x_train, x_test, y_train, y_test = train_test_split(x, y, test_size = 0.2, stratify = y,
```

In [25]:
```
#Checking the shape of the data
#x_train = 80%
#x_test = 20%

print(x.shape, x_train.shape, x_test.shape)
```

```
(768, 8) (614, 8) (154, 8)
```

In [26]:
```
#Training the model, using our support vector machine linear classifier
#I'm using linear because the data can be classified into two clases 'diabetes and non-d

classifier = svm.SVC(kernel = 'linear')
```

Algorithm

In [28]:
```
#Fitting our training data into the classifier
# x_training data and y_train is the label

classifier.fit(x_train, y_train)
```

Out[28]:
```
SVC
SVC(kernel='linear')
```

Model Evaluation

In [30]:
```
#Evaluating the model to know the accuracy the training data
```

```
x_train_prediction = classifier.predict(x_train)

training_data_accuracy = accuracy_score(x_train_prediction, y_train)
```

In [31]:
```
#Accuracy score of the train data

print('Accuracy score of the training data is:', training_data_accuracy)
```

```
Accuracy score of the training data is: 0.7866449511400652
```

In [32]:
```
#Evaluating the model to know the accuracy the test data

x_test_prediction = classifier.predict(x_test)

test_data_accuracy = accuracy_score(x_test_prediction, y_test)
```

In [33]:
```
#Accuracy score of the Test Data

print('Accuracy score of the test data is:', test_data_accuracy)
```

```
Accuracy score of the test data is: 0.7727272727272727
```

Predictive System

In [35]:
```
#Making a predictive system
input_data = (10,168,74,0,0,38,0.537,34)

#Changing the input data to numpy arrray since the processing is more efficient
convert_data_to_numpy = np.asarray(input_data)

#reshaping the array as we are predicting for one data point
#parameter for reshaping ==> '.reshape(1, -1)'
reshape_input_data = convert_data_to_numpy.reshape(1, -1)

#standardizing the input_data
std_data = scaler.transform(reshape_input_data)
print(std_data)

prediction = classifier.predict(std_data)
print(prediction)

if prediction==0:
    print('The patient is non-diabetic')
else:
    print('The patient is diabetic')
```

```
[[ 1.82781311  1.4742667   0.25303625 -1.28821221 -0.69289057  0.76245745
   0.1966813   0.06459135]]
[1]
The patient is diabetic
```

In [36]:
```
#Making a predictive system for Non-Diabetic
input_data = (4,110,92,0,0,37.6,0.191,30)

#changing the input data to numpy arrray since the processing is more efficient
convert_data_to_numpy = np.asarray(input_data)

#reshaping the array as we are predicting for one data point
#parameter for reshaping ==> '.reshape(1, -1)'
reshape_input_data = convert_data_to_numpy.reshape(1, -1)

#standardizing the input_data
std_data = scaler.transform(reshape_input_data)
print(std_data)
```

```
prediction = classifier.predict(std_data)
print(prediction)

if prediction==[0]:
    print('The patient is non-diabetic')
else:
    print('The patient is diabetic')
```

```
[[ 0.04601433 -0.34096773  1.18359575 -1.28821221 -0.69289057  0.71168975
  -0.84827977 -0.27575966]]
[0]
The patient is non-diabetic
```

In [ ]:

In [ ]: