CUNY MSDS DATA622 - Machine Learning & Big Data

Homework #2 : Decision Tree and Classification or Regression problem

Dataset : National Institute of Diabetes and Digestive and Kidney Diseases

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Summary

Based on the latest topics presented, bring a dataset of your choice and create a Decision Tree where you can solve a classification or regression problem and predict the outcome of a particular feature or detail of the data used. Switch variables to generate 2 decision trees and compare the results. Create a random forest for regression and analyze the results.

Based on real cases where desicion trees went wrong, and 'the bad & ugly' aspects of decision trees (https://decizone.com/blog/the-good-the-bad-the-ugly-of-using-decision-trees), how can you change this perception when using the decision tree you created to solve a real problem?

EDA Summary

Decision tree is a supervised machine learning model used to predict a target by learning decision rules from features. As the name suggests, we can think of this model as breaking down our data by making a decision based on asking a series of questions. It is a tree like structure constructed on the basis of attributes/features.

Decision tree algorithms are nothing but a series of if-else statements that can be used to predict a result based on the data set. This flowchart-like structure helps us in decision-making. The idea of a decision tree is to divide the data set into smaller data sets based on the descriptive features until we reach a small enough set that contains data points that fall under one label.

Classification and Regression Tree (CART) The decision tree has two main categories classification tree and regression tree. These two terms at a time called as CART. A classification tree is an algorithm where the target variable is fixed or categorical. The algorithm is then used to identify the “class” within which a target variable would most likely fall.

A regression tree refers to an algorithm where the target variable is and the algorithm is used to predict its value. As an example of a regression type problem, you may want to predict the selling prices of a residential house, which is a continuous dependent variable.

I will be using **National Institute of Diabetes and Digestive and Kidney Diseases** This dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases. The objective is to predict based on diagnostic measurements whether a patient has diabetes.

Several constraints were placed on the selection of these instances from a larger database. In particular, all patients here are females at least 21 years old of Pima Indian heritage.

This dataset is picked up from

- https://www.kaggle.com/datasets/mathchi/diabetes-data-set?select=diabetes.csv
- https://www.kaggle.com/datasets/mustafaali96/weight-height

Load Packages

In [1]:

```python
# Lets setup python environment and load python libraries for this EDA
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from matplotlib import pyplot
from scipy.stats import norm
from sklearn.preprocessing import StandardScaler
from scipy import stats
%matplotlib inline
from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import confusion_matrix
# Import the necessary modules and libraries
import numpy as np
from sklearn.tree import DecisionTreeRegressor

import warnings
warnings.simplefilter(action='ignore', category=Warning)
```

Diabetes Analysis & Prediction

Load Diabetes and Kidney Diseases Data

In [2]:

```python
diabetes_df = pd.read_csv("diabetes.csv")
diabetes_df.head()
```

Out[2]:

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

In [3]:

```python
diabetes_df.describe()
```

Out[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	76
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	3
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	1

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	2
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	2
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	2
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	4
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	8

Data Exploration

This dataset has following columns, few columns are unused, few are used as an inputs and treated as a feature. Class variable (0 or 1) is expected outcome

Columns :

- Pregnancies: Number of times pregnant
- Glucose: Plasma glucose concentration a 2 hours in an oral glucose tolerance test
- BloodPressure: Diastolic blood pressure (mm Hg)
- SkinThickness: Triceps skin fold thickness (mm)
- Insulin: 2-Hour serum insulin (mu U/ml)
- BMI: Body mass index (weight in kg/(height in m)^2)
- DiabetesPedigreeFunction: Diabetes pedigree function
- Age: Age (years)
- Outcome: Class variable (0 or 1)

The dependent variable is if the patient is suffering from diabetes or not. Here the dependent column contains binary variable 1 indicating the person is suffering from diabetes and 0 he is not a patient of diabetes. The data set has independent variables as several physiological parameters of a diabetes patient.

In [4]:

```
#descriptive statistics summary
diabetes_df.head() # printing first few rows of the data
```

Out[4]:

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

In [5]:

```
diabetes_df.tail()   # to show last few rows of the data
```

Out[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

In [6]:
```
diabetes_df.info() # for a quick view of the data
```

```
<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 [7]:
```
diabetes_df.sample(10)  # display a sample of 10 rows from the data
```

Out[7]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
241	4	91	70	32	88	33.1	0.446	22	0
621	2	92	76	20	0	24.2	1.698	28	0
431	3	89	74	16	85	30.4	0.551	38	0
172	2	87	0	23	0	28.9	0.773	25	0
615	3	106	72	0	0	25.8	0.207	27	0
648	11	136	84	35	130	28.3	0.260	42	1
168	4	110	66	0	0	31.9	0.471	29	0
415	3	173	84	33	474	35.7	0.258	22	1
637	2	94	76	18	66	31.6	0.649	23	0
77	5	95	72	33	0	37.7	0.370	27	0

In [8]:
```
diabetes_df.describe()    # printing summary statistics of the data
```

Out[8]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	1
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	2
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	4
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	8

```
In [9]:  pd.isnull(diabetes_df)   # check for any null values in the data
```

Out[9]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	False	False	False	False	False	False	False	False	False
1	False	False	False	False	False	False	False	False	False
2	False	False	False	False	False	False	False	False	False
3	False	False	False	False	False	False	False	False	False
4	False	False	False	False	False	False	False	False	False
...	...	...	...	...	...	...	...	...	...
763	False	False	False	False	False	False	False	False	False
764	False	False	False	False	False	False	False	False	False
765	False	False	False	False	False	False	False	False	False
766	False	False	False	False	False	False	False	False	False
767	False	False	False	False	False	False	False	False	False

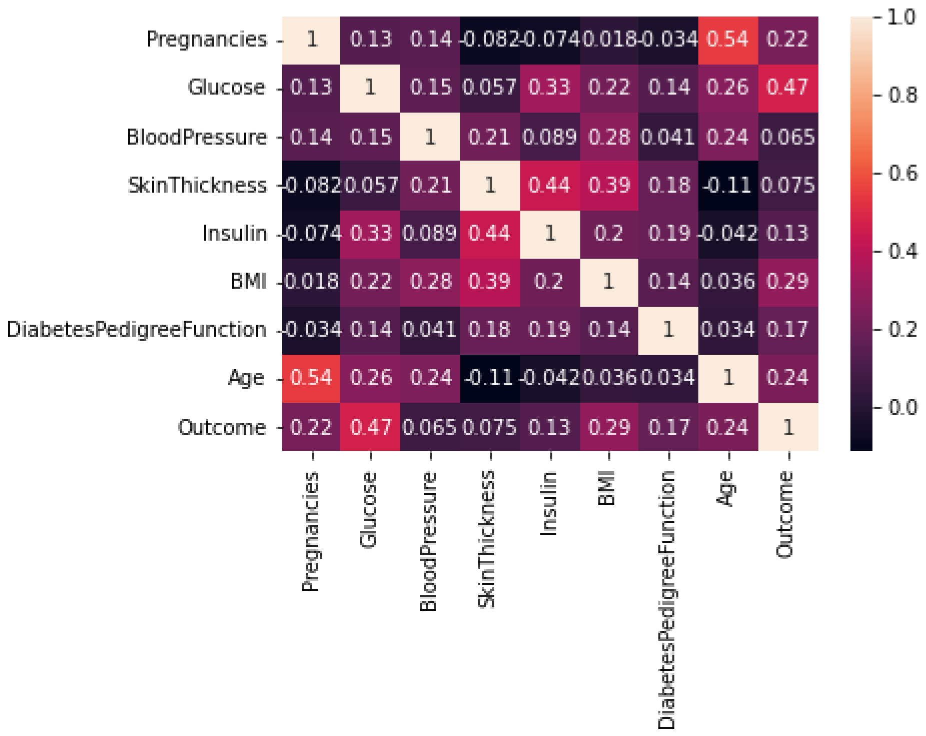
768 rows × 9 columns

The first eight columns contain the independent variables. These are some physiological variables having a correlation with diabetes symptoms. As we can see that the data frame contains nine variables in nine columns. The ninth column shows if the patient is diabetic or not. So, here the x stores the independent variables and y stores the dependent variable diabetes count.

```
In [10]: x=diabetes_df.iloc[:,:-1].values
         y=diabetes_df.iloc[:,-1].values
```

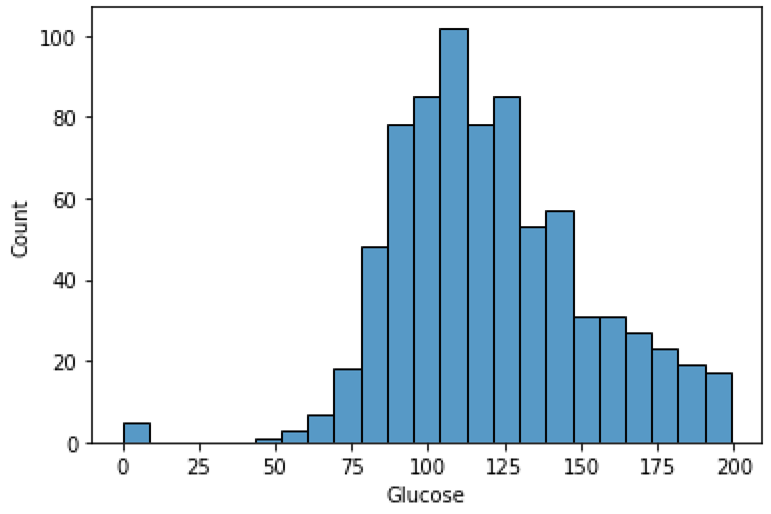
```
In [11]: corr=diabetes_df.corr()
         sns.heatmap(corr, annot=True) # an array of the same shape as data which is used to annota

Out[11]: <AxesSubplot:>
```



In [12]:

```
ax = sns.histplot(diabetes_df["Glucose"])
plt.show() # Plot histogram to show distributions of dataset
```

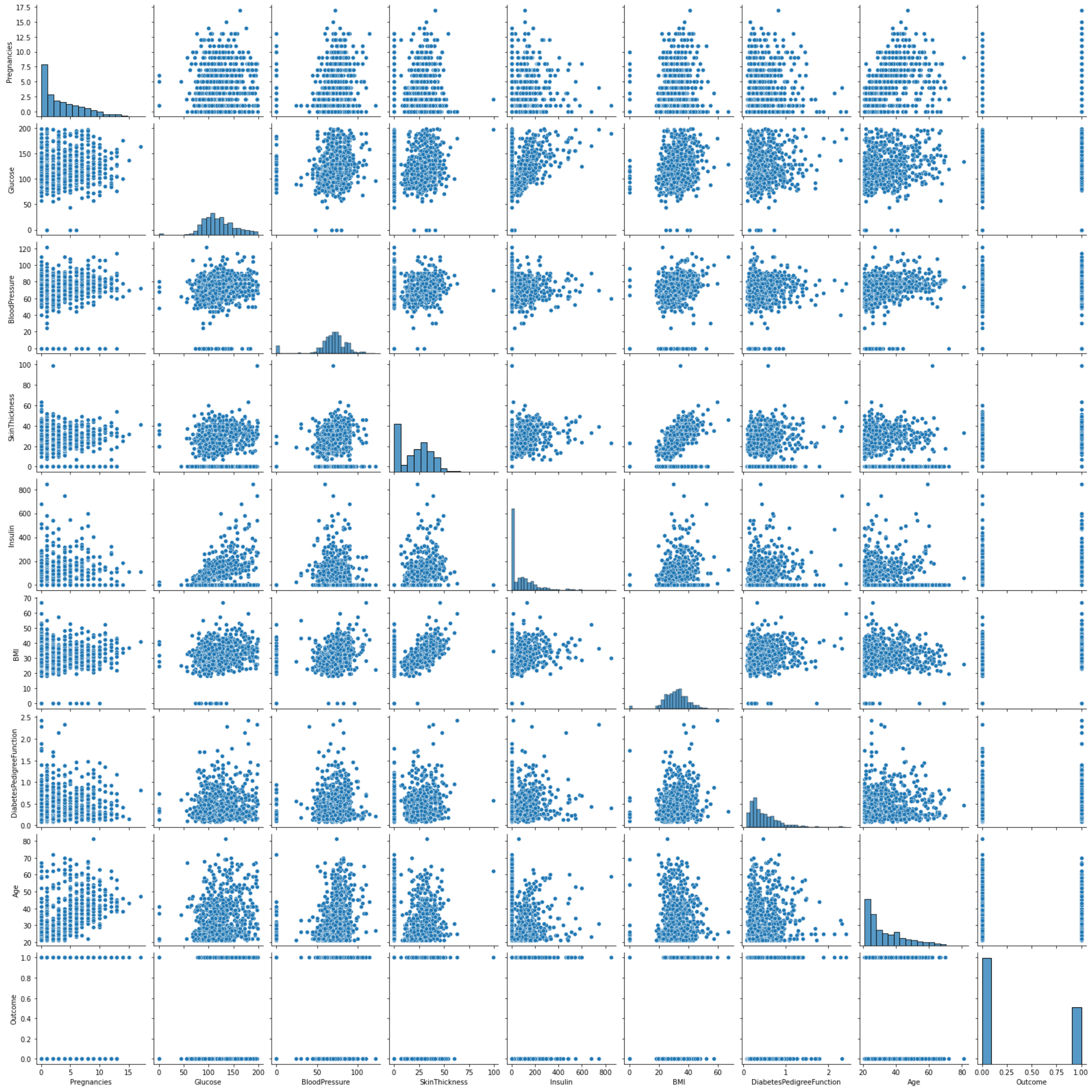


In [13]:

```
sns.pairplot(diabetes_df)
```

Out[13]:

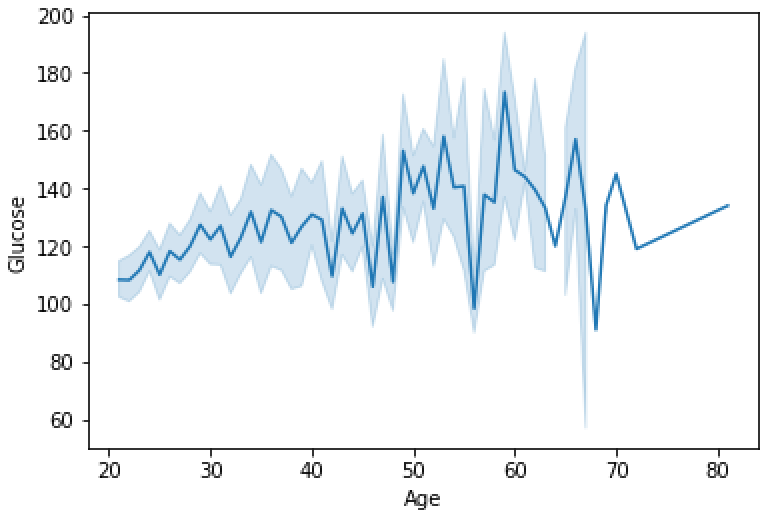
```
<seaborn.axisgrid.PairGrid at 0x1ec46d674c0>
```



Fitting the Decision Tree Regression Model to the dataset Create the Decision Tree regressor object. To do the classification we need to import the DecisionTreeClassifier() from sklearn. This special classifier is capable of classifying binary variable i.e. variable with only two classes as well as multiclass variables.

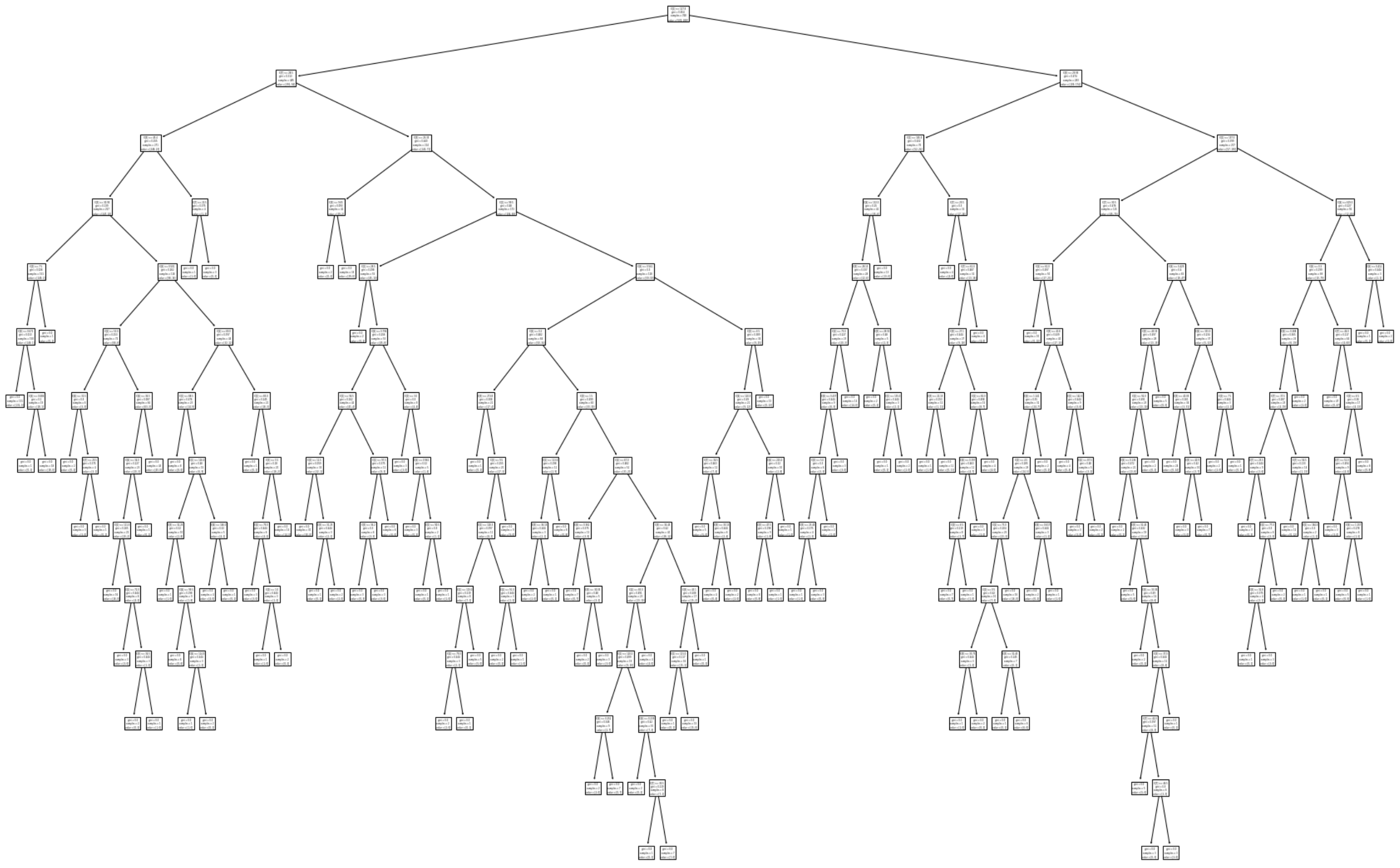
In [14]:
```
sns.lineplot(data=diabetes_df, x="Age", y="Glucose") # plot to see the rent trend
```

Out[14]:
```
<AxesSubplot:xlabel='Age', ylabel='Glucose'>
```



In [15]:
```
# Use of the classifier
from sklearn import tree
clf = tree.DecisionTreeClassifier()
clf = clf.fit(x, y)
```

In [16]:
```
plt.figure(figsize=(30,20))
tree.plot_tree(clf)
plt.show()
```



Resolutuion is not looking great, lets try something else. A high resolution and quality image of the tree is to use Graphviz format importing export_graphviz() from tree.

In [17]:
```
import os
os.environ["PATH"] += os.pathsep + 'C:/DataScience/Softwares/Graphviz/bin'
```

```
# Creating better graph
import graphviz
dot_data = tree.export_graphviz(clf, out_file=None)
graph = graphviz.Source(dot_data)
graph.render("diabetes")
```

Out[17]:

```
'diabetes.pdf'
```

Perform regression using decision

The dataset contains the height and weight of persons and a column with their genders. The original dataset has more than thousands of rows. Additional to the basic libraries we imported in a classification problem, here we will need to import the DecisionTreeRegressor() from sklearn.

In [18]:

```
wt_ht_df=pd.read_csv('weight-height.csv')
wt_ht_df.head()
```

Out[18]:

	Gender	Height	Weight
0	Male	73.847017	241.893563
1	Male	68.781904	162.310473
2	Male	74.110105	212.740856
3	Male	71.730978	220.042470
4	Male	69.881796	206.349801

In [19]:

```
wt_ht_df.describe()
```

Out[19]:

	Height	Weight
count	10000.000000	10000.000000
mean	66.367560	161.440357
std	3.847528	32.108439
min	54.263133	64.700127
25%	63.505620	135.818051
50%	66.318070	161.212928
75%	69.174262	187.169525
max	78.998742	269.989699

Create Variables

As we can see that the dataframe contains three variables in three columns. The last two columns are only of our interest. We want to regress the weight of a person using the height of him/her. So, here the independent variable height is x and the dependent variable weight is y.

In [20]:

```
x=wt_ht_df.iloc[:,1:2].values
y=wt_ht_df.iloc[:,-1].values
```

Splitting the dataset

Here we have set the test_size as 20% that means the training data set will consist 80% of the total data. This is a common practice of splitting the whole data set for creating training and testing data set. The test data set works as an independent data set when need to test the classifier after it gets trained with training data.

In [21]:
```
# Splitting the data for training and testing
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test=train_test_split(x,y, test_size=0.20, random_state=0)
```

Fitting the decision tree regression

We have here fitted decision tree regression with two different depth values two draw a comparison between them.

In [22]:
```
# Creating regression models with two different depths
regr_1 = DecisionTreeRegressor(max_depth=2)
regr_2 = DecisionTreeRegressor(max_depth=5)
regr_1.fit(x_train, y_train)
regr_2.fit(x_train, y_train)
```

Out[22]:
```
DecisionTreeRegressor(max_depth=5)
```

Prediction

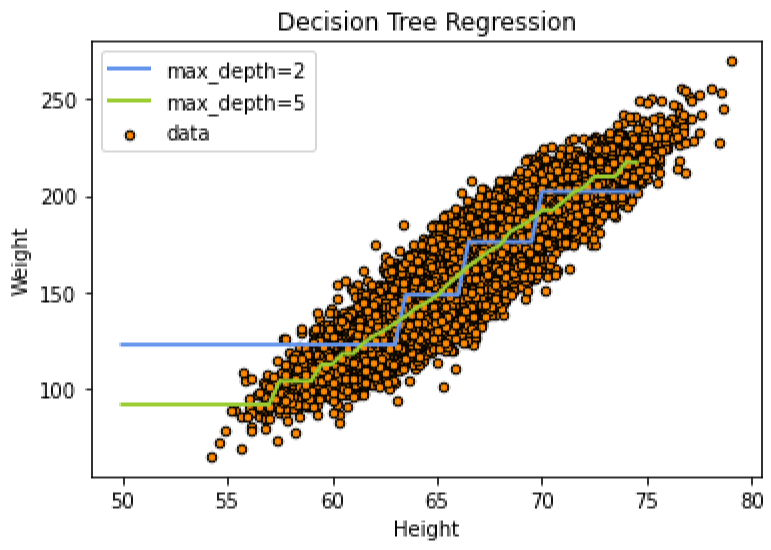
The below line of codes will give predictions from both the regression models with two different depth values using a new independent variable set X_test.

In [23]:
```
# Making prediction
X_test = np.arange(50,75, 0.5)[:, np.newaxis]
y_1 = regr_1.predict(X_test)
y_2 = regr_2.predict(X_test)
```

Visualizing prediction performance

The below line of codes will generate a height vs weight scattered plot alongwith two prediction lines created from two different regression models.

In [24]:
```
# Plot the results
plt.figure()
plt.scatter(x, y, s=20, edgecolor="black",
            c="darkorange", label="data")
plt.plot(X_test, y_1, color="cornflowerblue",
         label="max_depth=2", linewidth=2)
plt.plot(X_test, y_2, color="yellowgreen", label="max_depth=5", linewidth=2)
plt.xlabel("Height")
plt.ylabel("Weight")
plt.title("Decision Tree Regression")
plt.legend()
plt.show()
```



Reduced Data & Switched Variables

The dataset contains the height and weight of persons and a column with their genders. The original dataset has more than thousands of rows, but for this regression purpose, I have used only the first 100 rows containing data on 50 male and 50 females.

In [25]:
```
wt_ht_df=pd.read_csv('weight-height1.csv')
wt_ht_df.head()
```

Out[25]:

	Gender	Height	Weight
0	Male	73.847017	241.893563
1	Male	68.781904	162.310473
2	Male	74.110105	212.740856
3	Male	71.730978	220.042470
4	Male	69.881796	206.349801

In [26]:
```
x=wt_ht_df.iloc[:,1:2].values
y=wt_ht_df.iloc[:,-1].values
```

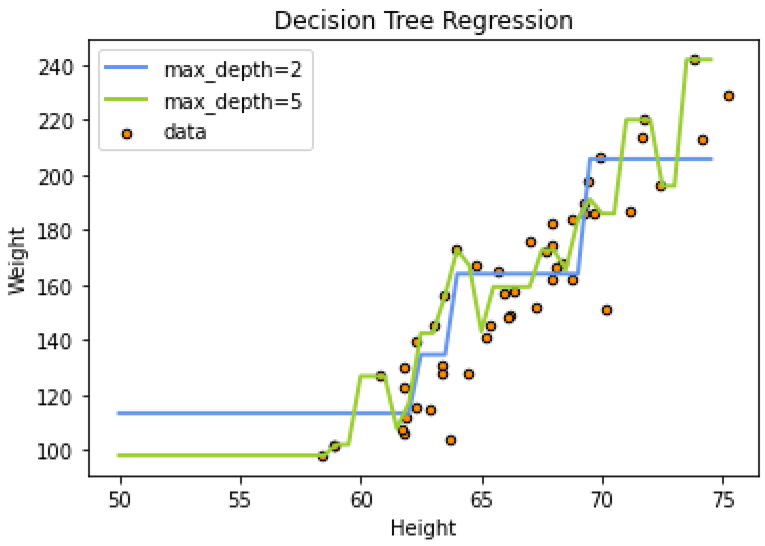
In [27]:
```
# Splitting the data for training and testing
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test=train_test_split(x,y, test_size=0.20, random_state=0)
```

In [28]:
```
# Creating regression models with two different depths
regr_1 = DecisionTreeRegressor(max_depth=2)
regr_2 = DecisionTreeRegressor(max_depth=5)
regr_1.fit(x_train, y_train)
regr_2.fit(x_train, y_train)
```

Out[28]:
```
DecisionTreeRegressor(max_depth=5)
```

In [29]:
```
# Making prediction
X_test = np.arange(50,75, 0.5)[:, np.newaxis]
y_1 = regr_1.predict(X_test)
y_2 = regr_2.predict(X_test)
```

In [30]:
```
# Plot the results
plt.figure()
plt.scatter(x, y, s=20, edgecolor="black",
            c="darkorange", label="data")
plt.plot(X_test, y_1, color="cornflowerblue",
         label="max_depth=2", linewidth=2)
plt.plot(X_test, y_2, color="yellowgreen", label="max_depth=5", linewidth=2)
plt.xlabel("Height")
plt.ylabel("Weight")
plt.title("Decision Tree Regression")
plt.legend()
plt.show()
```



Random forest for regression

In [31]:
```
diabetes_df["Glucose"]=diabetes_df["Glucose"].fillna(0)
diabetes_df["BloodPressure"]=diabetes_df["BloodPressure"].fillna(0)
diabetes_df["SkinThickness"]=diabetes_df["SkinThickness"].fillna(0)
diabetes_df["Insulin"]=diabetes_df["Insulin"].fillna(0)
diabetes_df["BMI"]=diabetes_df["BMI"].fillna(0)
diabetes_df.isna().any()
```

Out[31]:
```
Pregnancies                 False
Glucose                     False
BloodPressure               False
SkinThickness               False
Insulin                     False
BMI                         False
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

In [32]:
```
diabetes_df.head()
```

Out[32]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

In [33]:

```
x=pd.DataFrame(diabetes_df,columns=["Pregnancies","Glucose","BloodPressure","SkinThicknes
y=diabetes_df.Outcome.values.reshape(-1,1)
x.head()
```

Out[33]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
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 [34]:

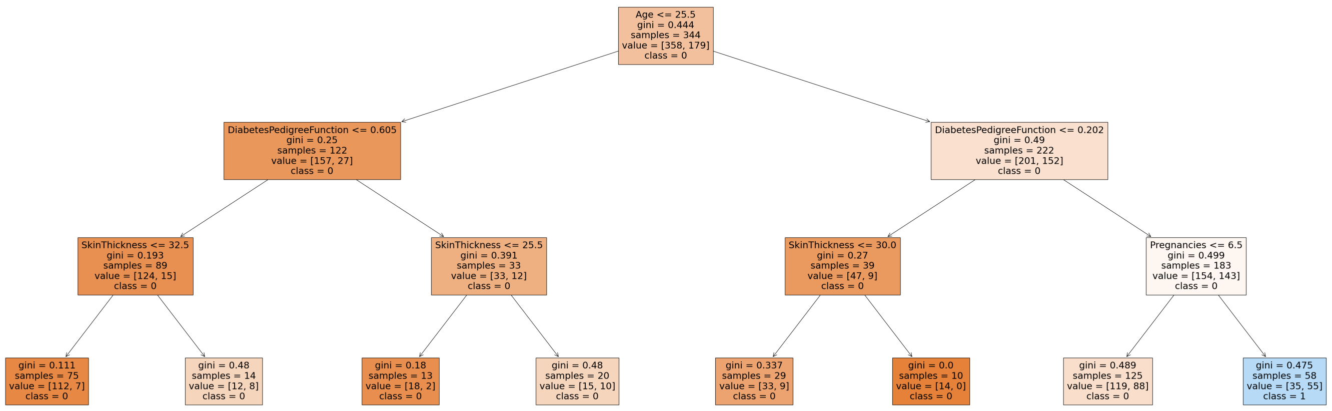
```
from sklearn.ensemble import RandomForestClassifier
from sklearn import metrics
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.3,random_state=1)
clf=RandomForestClassifier(n_estimators=150,max_depth=3)
clf=clf.fit(x_train,y_train)
y_pred=clf.predict(x_test)

print("Accuracy :",metrics.accuracy_score(y_test,y_pred))
```

```
Accuracy : 0.7835497835497836
```

In [35]:

```
f_n=["Pregnancies","Glucose","BloodPressure","SkinThickness","Insulin","BMI","DiabetesPedi
t_n=["0","1"]
fig=plt.figure(figsize=(60,20),dpi=100)
plot=tree.plot_tree(clf.estimators_[5],feature_names=f_n,class_names=t_n,filled=True)
plt.figure(figsize=(30,20))
plt.show()
fig.savefig("Tree1.png")
```



```
<Figure size 2160x1440 with 0 Axes>
```

Conclusion

As we can see in the resulting plot, the decision tree of depth 2 captures the general trend in the data. It is important to know how to choose an appropriate value for a depth of a tree to not overfit or underfit the data. Knowing how to combine decision trees to form an ensemble random forest is also useful as it usually has a better generalization performance than an individual decision tree due to randomness, which helps to decrease the model’s variance. It is also less sensitive to outliers in the dataset and doesn’t require much parameter tuning.

- We built a machine learning-based classifier that predicts if a patient is diabetic or not, based on the information provided in the database.
- While building this predictor, we learned about common preprocessing steps such as feature scaling and imputing missing values. For more detailed explanation about handling missing values in python, please refer to my article here.
- We implemented Random forest algorithm, evaluated the performance using the accuracy score, comparing the performance between train and test data.

References

https://scikit-learn.org/stable/modules/tree.html

https://www.bu.edu/sph/files/2014/05/MorganCART.pdf

In [ ]:
```

```