IME672A: DATA MINING AND KNOWLEDGE DISCOVERY

Decision Tree using Python

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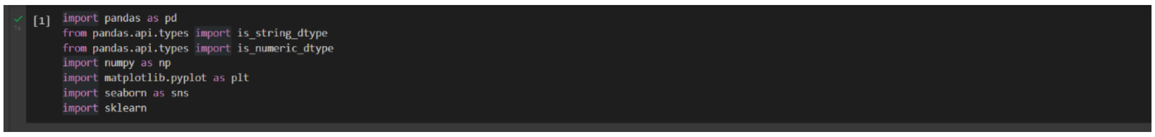
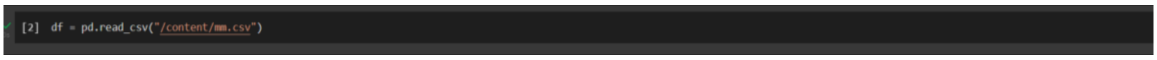
The data set includes information about the content of the heart-disease directory. The dataset is obtained from UCI machine learning repository (https://archive.ics.uci.edu/ml/datasets/heart+disease).

Importing libraries

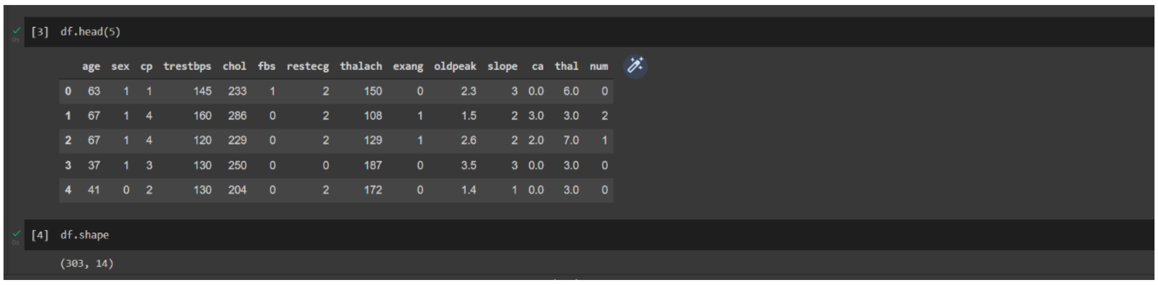


```
[1] import pandas as pd
    from pandas.api.types import is_string_dtype
    from pandas.api.types import is_numeric_dtype
    import numpy as np
    import matplotlib.pyplot as plt
    import seaborn as sns
    import sklearn
```



```
[2] df = pd.read_csv("/content/mm.csv")
```

Data Analysis



```
[3] df.head(5)
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	num
0	63	1	1	145	233	1	2	150	0	2.3	3	0.0	6.0	0
1	67	1	4	160	286	0	2	108	1	1.5	2	3.0	3.0	2
2	67	1	4	120	229	0	2	129	1	2.6	2	2.0	7.0	1
3	37	1	3	130	250	0	0	187	0	3.5	3	0.0	3.0	0
4	41	0	2	130	204	0	2	172	0	1.4	1	0.0	3.0	0

```
[4] df.shape

(303, 14)
```

There are 303 rows and 14 features in original dataset.

Description of features in dataset:

1. age: age in years
2. sex: sex (1 = male; 0 = female)
3. cp: chest pain type
   - Value 1: typical angina
   - Value 2: atypical angina
   - Value 3: non-anginal pain
   - Value 4: asymptomatic
4. trestbps: resting blood pressure (in mm Hg on admission to the hospital)
5. chol: serum cholestoral in mg/dl
6. fbs: (fasting blood sugar > 120 mg/dl) (1 = true; 0 = false)
7. restecg: resting electrocardiographic results

- Value 0: normal

- Value 1: having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV)

- Value 2: showing probable or definite left ventricular hypertrophy by Estes' criteria

8. thalach: maximum heart rate achieved
9. exang: exercise induced angina (1 = yes; 0 = no)
10. oldpeak = ST depression induced by exercise relative to rest
11. slope: the slope of the peak exercise ST segment

- Value 1: upsloping

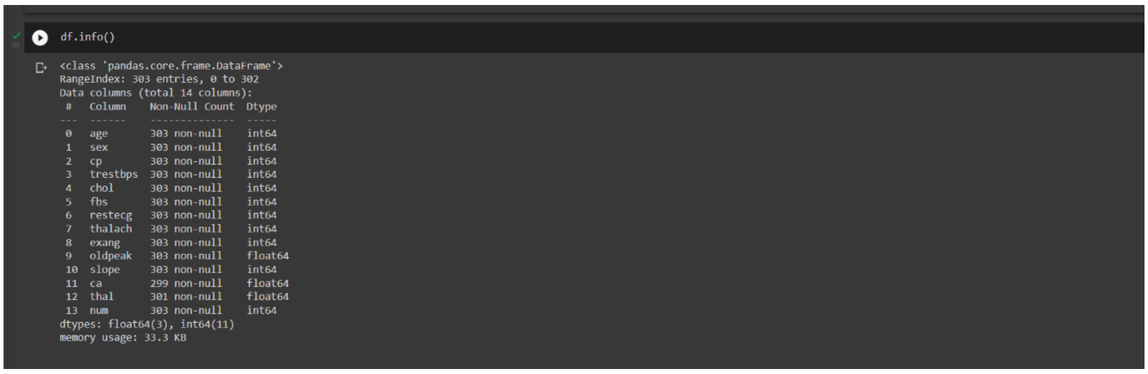
- Value 2: flat

- Value 3: downsloping

12. ca: number of major vessels (0-3) colored by flourosopy
13. thal: 3 = normal; 6 = fixed defect; 7 = reversable defect
14. num: diagnosis of heart disease (angiographic disease status)

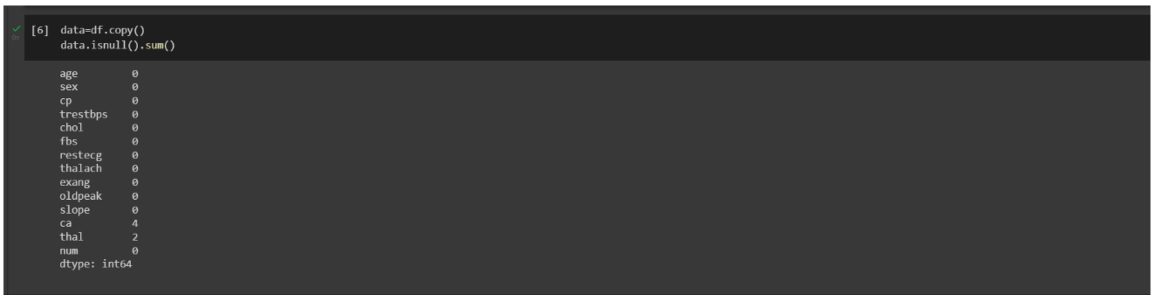
- Value 0: < 50% diameter narrowing

- Value 1: > 50% diameter narrowing



```
df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       303 non-null    int64  
 1   sex       303 non-null    int64  
 2   cp        303 non-null    int64  
 3   trestbps  303 non-null    int64  
 4   chol      303 non-null    int64  
 5   fbs       303 non-null    int64  
 6   restecg   303 non-null    int64  
 7   thalach   303 non-null    int64  
 8   exang     303 non-null    int64  
 9   oldpeak   303 non-null    float64
 10  slope     303 non-null    int64  
 11  ca        299 non-null    float64
 12  thal      301 non-null    float64
 13  num       303 non-null    int64  
dtypes: float64(3), int64(11)
memory usage: 33.3 KB
```

An easy way to check for missing values is to use the method isnull. We will get a data frame with true (1) and false (0) values, so we will sum the values and we can see in which column we have missing values.

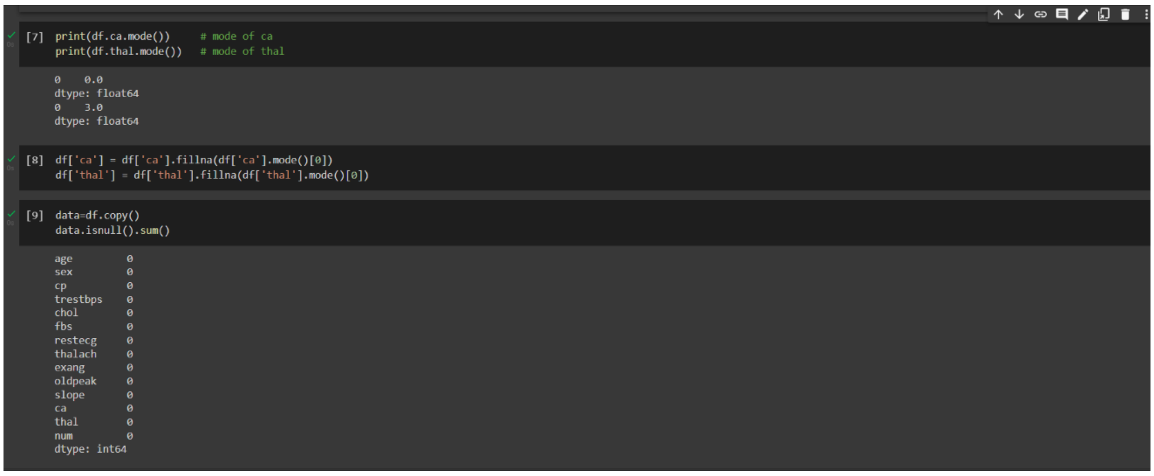


```
[6] data=df.copy()
    data.isnull().sum()

    age         0
    sex         0
    cp          0
    trestbps    0
    chol        0
    fbs         0
    restecg     0
    thalach     0
    exang       0
    oldpeak     0
    slope       0
    ca          4
    thal        2
    num         0
    dtype: int64
```

We can see that there are 2 and 4 missing values in attributes 'ca' and 'thal' respectively.

The data we get is rarely homogenous. Sometimes data can be missing, and it needs to be handled so that it does not reduce the performance of our machine learning model. To do this we need to replace the missing data by the Mean or Mode or Median of the entire column.

Here, the missing values are replaced with the mode value or most frequent value of the entire feature column.

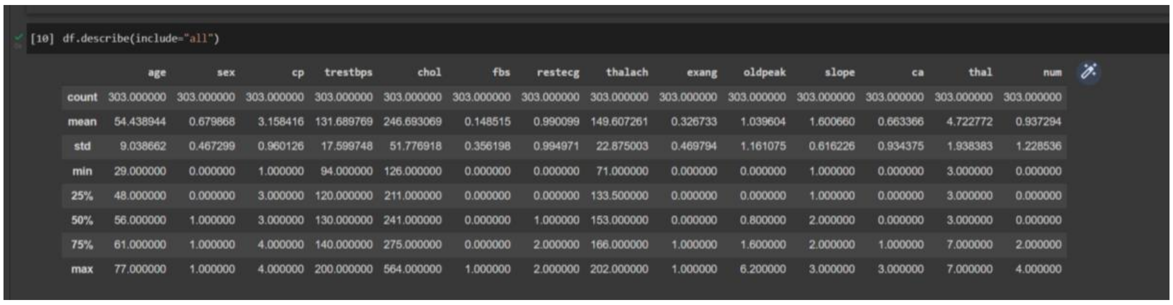


```
[7]  print(df.ca.mode())     # mode of ca
     print(df.thal.mode())   # mode of thal

     0    0.0
     dtype: float64
     0    3.0
     dtype: float64
```

```
[8]  df['ca'] = df['ca'].fillna(df['ca'].mode()[0])
     df['thal'] = df['thal'].fillna(df['thal'].mode()[0])
```

```
[9]  data=df.copy()
     data.isnull().sum()

     age         0
     sex         0
     cp          0
     trestbps    0
     chol        0
     fbs         0
     restecg     0
     thalach     0
     exang       0
     oldpeak     0
     slope       0
     ca          0
     thal        0
     num         0
     dtype: int64
```

We can see now that there aren't any missing values now.



```
[10] df.describe(include="all")
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	num
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.438944	0.679868	3.158416	131.689769	246.693069	0.148515	0.990099	149.607261	0.326733	1.039604	1.600660	0.663366	4.722772	0.937294
std	9.038662	0.467299	0.960126	17.599748	51.776918	0.356198	0.994971	22.875003	0.469794	1.161075	0.616226	0.934375	1.938383	1.228536
min	29.000000	0.000000	1.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000	0.000000	1.000000	0.000000	3.000000	0.000000
25%	48.000000	0.000000	3.000000	120.000000	211.000000	0.000000	0.000000	133.500000	0.000000	0.000000	1.000000	0.000000	3.000000	0.000000
50%	56.000000	1.000000	3.000000	130.000000	241.000000	0.000000	1.000000	153.000000	0.000000	0.800000	2.000000	0.000000	3.000000	0.000000
75%	61.000000	1.000000	4.000000	140.000000	275.000000	0.000000	2.000000	166.000000	1.000000	1.600000	2.000000	1.000000	7.000000	2.000000
max	77.000000	1.000000	4.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000	6.200000	3.000000	3.000000	7.000000	4.000000

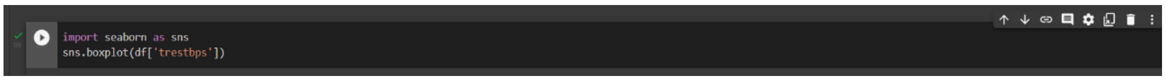
Outliers are observations that lie on abnormal distance from other observations in the data and they will affect the regression dramatically. Because of this, the regression will try to place the line closer to these values.

The minimum value for 'trestbps' is 94, the maximum is 200 and the mean value is 131.689769. Also, we can see that 25% of the values are under 120 and 75% are under 140.

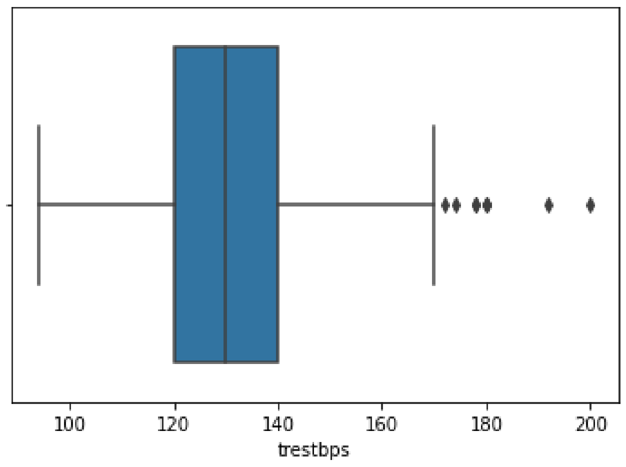
Similarly, the minimum value for 'chol' is 126, the maximum is 564 and the mean value is 246.693069. Also, we can see that 25% of the values are under 211 and 75% are under 275.

So, in this case both trestbps and chol contains outliers.

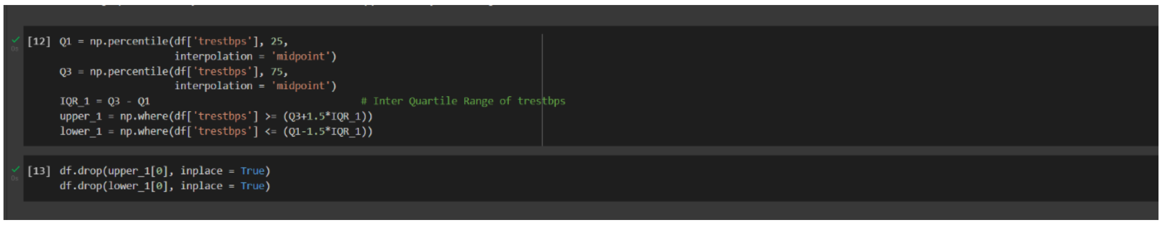
Boxplot captures the summary of the data effectively and efficiently with only a simple box and whiskers. It summarizes sample data using 25th, 50th, and 75th percentiles.



```
import seaborn as sns
sns.boxplot(df['trestbps'])
```

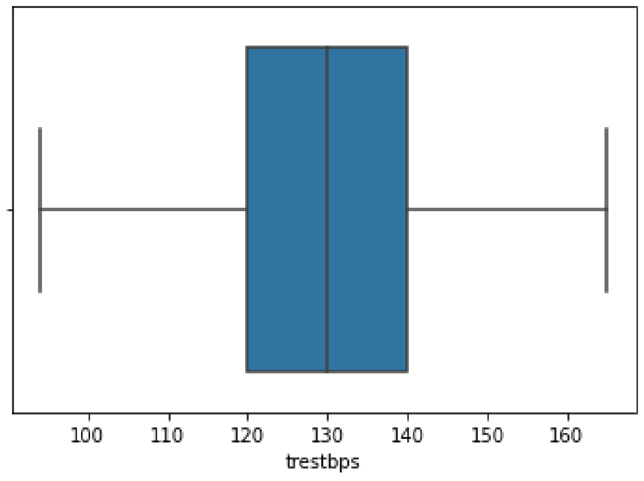


In the above graph, can clearly see those values above 170 approximately are acting as the outliers.



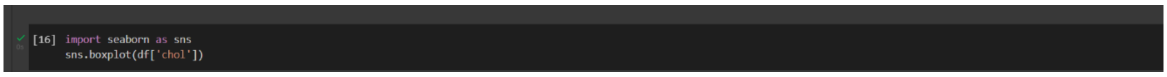
```
[12] Q1 = np.percentile(df['trestbps'], 25,
                        interpolation = 'midpoint')
     Q3 = np.percentile(df['trestbps'], 75,
                        interpolation = 'midpoint')
     IQR_1 = Q3 - Q1                                 # Inter Quartile Range of trestbps
     upper_1 = np.where(df['trestbps'] >= (Q3+1.5*IQR_1))
     lower_1 = np.where(df['trestbps'] <= (Q1-1.5*IQR_1))

[13] df.drop(upper_1[0], inplace = True)
     df.drop(lower_1[0], inplace = True)
```

Boxplot of 'trestbps' after removing outliers.

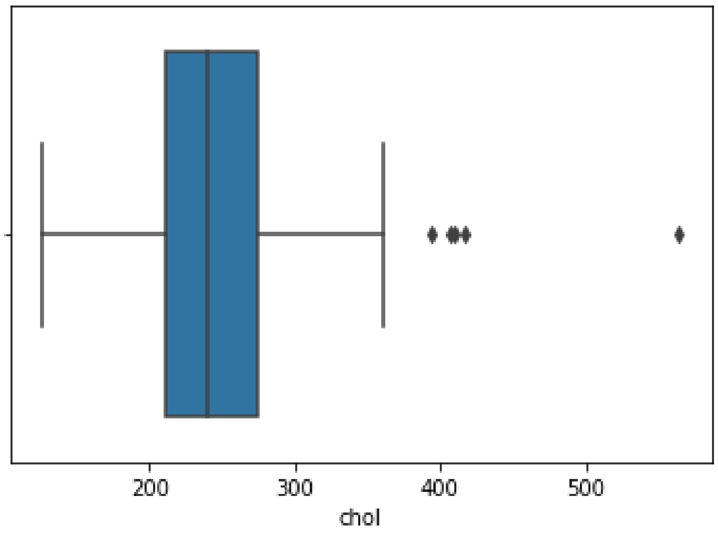


```
[15] df.shape

     (290, 14)
```

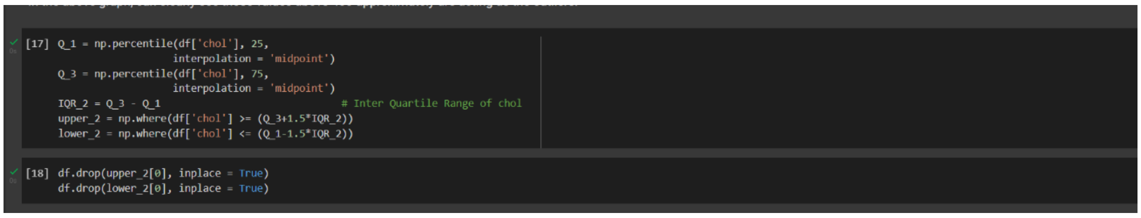
There are 290 rows and 14 features in the dataset after removing outliers of 'trestbps'.



```
[16] import seaborn as sns
     sns.boxplot(df['chol'])
```



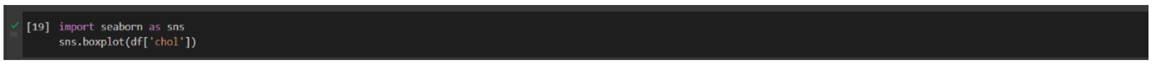
In the above graph, can clearly see those values above 400 approximately are acting as the outliers.



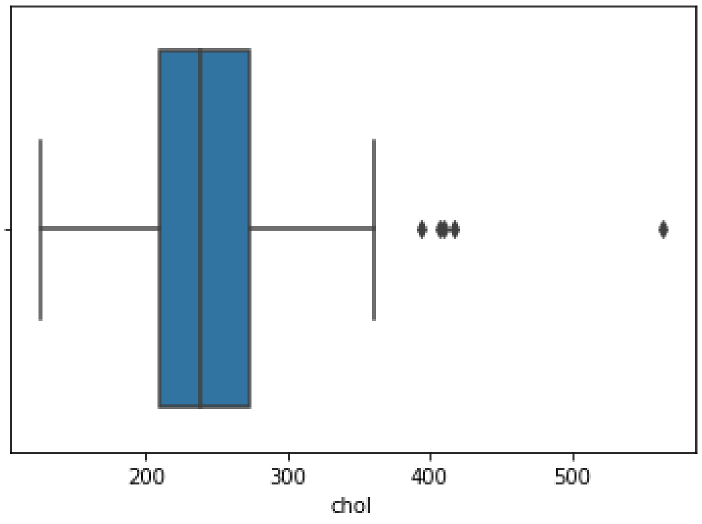
```
[17] Q_1 = np.percentile(df['chol'], 25,
                    interpolation = 'midpoint')
     Q_3 = np.percentile(df['chol'], 75,
                    interpolation = 'midpoint')
     IQR_2 = Q_3 - Q_1                          # Inter Quartile Range of chol
     upper_2 = np.where(df['chol'] >= (Q_3+1.5*IQR_2))
     lower_2 = np.where(df['chol'] <= (Q_1-1.5*IQR_2))
```

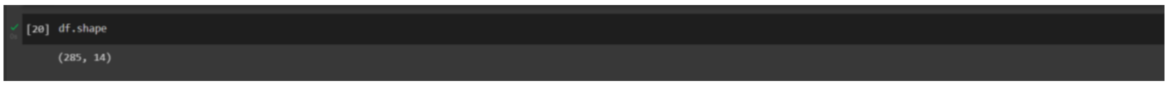
```
[18] df.drop(upper_2[0], inplace = True)
     df.drop(lower_2[0], inplace = True)
```

Boxplot of 'chol' after removing outliers.



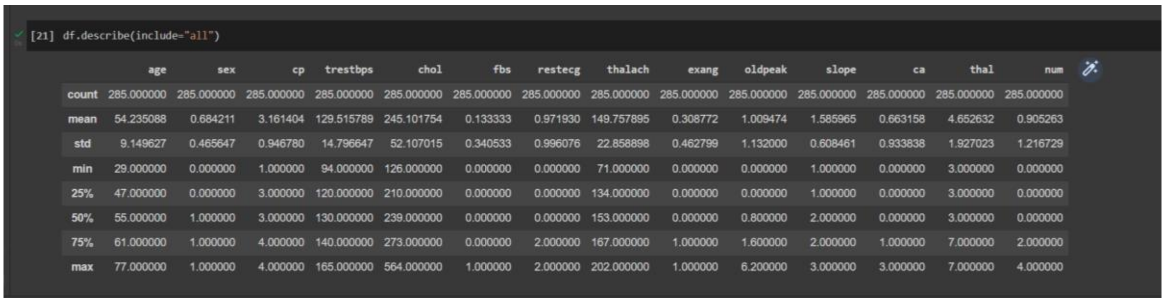
```
[19] import seaborn as sns
     sns.boxplot(df['chol'])
```





```
[20] df.shape
     (285, 14)
```

There are 285 rows and 14 features in the dataset after removing outliers of 'chol'.

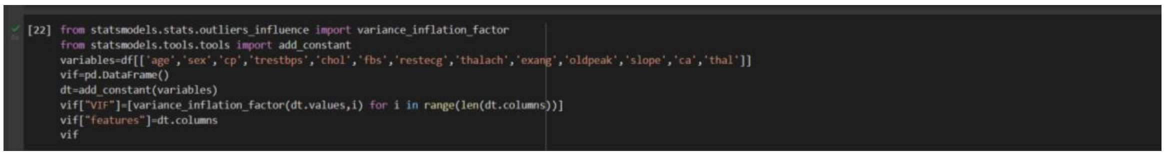


```
[21] df.describe(include="all")
```

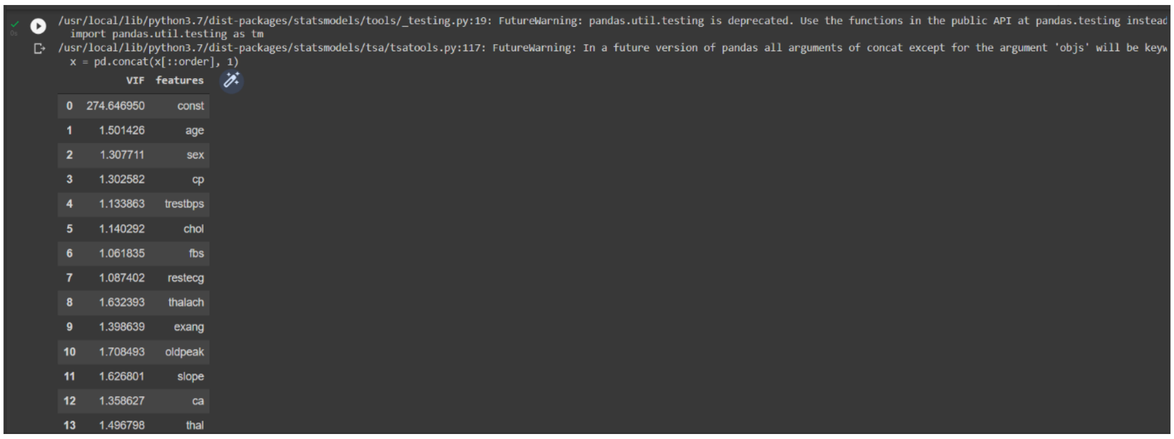
	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	num
count	285.000000	285.000000	285.000000	285.000000	285.000000	285.000000	285.000000	285.000000	285.000000	285.000000	285.000000	285.000000	285.000000	285.000000
mean	54.235088	0.684211	3.161404	129.515789	245.101754	0.133333	0.971930	149.757895	0.308772	1.009474	1.585965	0.663158	4.652632	0.905263
std	9.149627	0.465647	0.946780	14.796647	52.107015	0.340533	0.996076	22.858898	0.462799	1.132000	0.608461	0.933838	1.927023	1.216729
min	29.000000	0.000000	1.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000	0.000000	1.000000	0.000000	3.000000	0.000000
25%	47.000000	0.000000	3.000000	120.000000	210.000000	0.000000	0.000000	134.000000	0.000000	0.000000	1.000000	0.000000	3.000000	0.000000
50%	55.000000	1.000000	3.000000	130.000000	239.000000	0.000000	0.000000	153.000000	0.000000	0.800000	2.000000	0.000000	3.000000	0.000000
75%	61.000000	1.000000	4.000000	140.000000	273.000000	0.000000	2.000000	167.000000	1.000000	1.600000	2.000000	1.000000	7.000000	2.000000
max	77.000000	1.000000	4.000000	165.000000	564.000000	1.000000	2.000000	202.000000	1.000000	6.200000	3.000000	3.000000	7.000000	4.000000

The maximum value is still far away from the mean, but it is acceptably closer.

Multicollinearity exists whenever an independent variable is highly correlated with one or more of the other independent variables in a multiple regression equation. Multicollinearity is a problem because it undermines the statistical significance of an independent variable. When VIF value is equal to 1, there is no multicollinearity at all. Values between 1 and 5 are considered perfectly okay. VIFs greater than 5 represent critical levels of multicollinearity where the coefficients are poorly estimated, and the p-values are questionable.



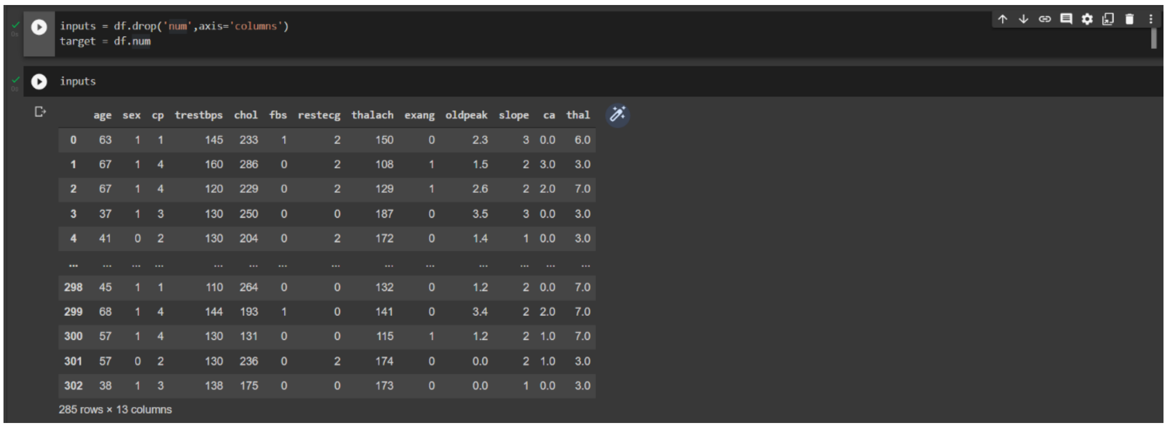
```
[22] from statsmodels.stats.outliers_influence import variance_inflation_factor
     from statsmodels.tools.tools import add_constant
     variables=df[['age','sex','cp','trestbps','chol','fbs','restecg','thalach','exang','oldpeak','slope','ca','thal']]
     vif=pd.DataFrame()
     dt=add_constant(variables)
     vif["VIF"]=[variance_inflation_factor(dt.values,i) for i in range(len(dt.columns))]
     vif["features"]=dt.columns
     vif
```



```
/usr/local/lib/python3.7/dist-packages/statsmodels/tools/_testing.py:19: FutureWarning: pandas.util.testing is deprecated. Use the functions in the public API at pandas.testing instead
  import pandas.util.testing as tm
/usr/local/lib/python3.7/dist-packages/statsmodels/tsa/tsatools.py:117: FutureWarning: In a future version of pandas all arguments of concat except for the argument 'objs' will be keyw
  x = pd.concat(x[::order], 1)
```

	VIF	features
0	274.646950	const
1	1.501426	age
2	1.307711	sex
3	1.302582	cp
4	1.133863	trestbps
5	1.140292	chol
6	1.061835	fbs
7	1.087402	restecg
8	1.632393	thalach
9	1.398639	exang
10	1.708493	oldpeak
11	1.626801	slope
12	1.358627	ca
13	1.496798	thal

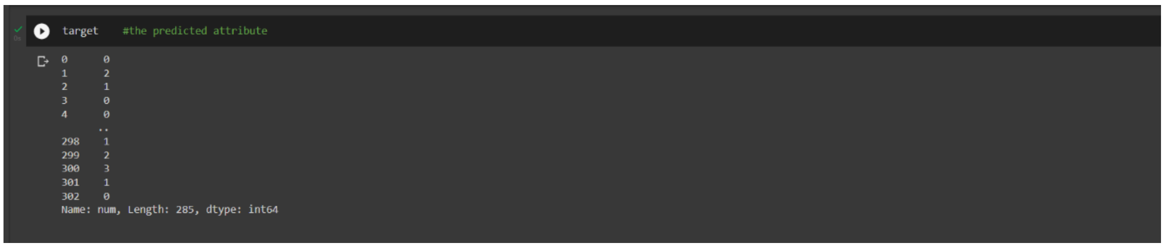
These results show that our model doesn't have multicollinearity for any of the independent variables.



```
inputs = df.drop('num',axis='columns')
target = df.num
```

```
inputs
```

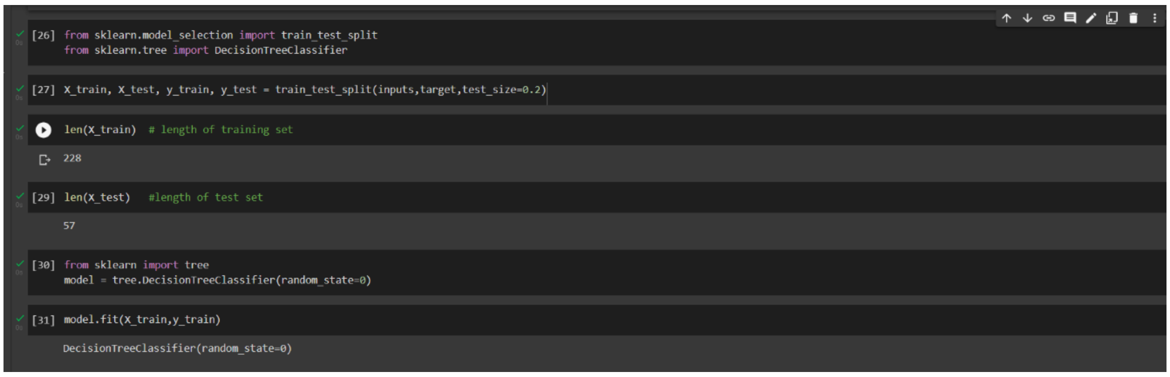
```
     age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  slope   ca  thal
0     63    1   1       145   233    1        2      150      0      2.3      3  0.0   6.0
1     67    1   4       160   286    0        2      108      1      1.5      2  3.0   3.0
2     67    1   4       120   229    0        2      129      1      2.6      2  2.0   7.0
3     37    1   3       130   250    0        0      187      0      3.5      3  0.0   3.0
4     41    0   2       130   204    0        2      172      0      1.4      1  0.0   3.0
...  ...  ...  ...      ...   ...  ...      ...      ...    ...      ...    ...  ...   ...
298   45    1   1       110   264    0        0      132      0      1.2      2  0.0   7.0
299   68    1   4       144   193    1        0      141      0      3.4      2  2.0   7.0
300   57    1   4       130   131    0        0      115      1      1.2      2  1.0   7.0
301   57    0   2       130   236    0        2      174      0      0.0      2  1.0   3.0
302   38    1   3       138   175    0        0      173      0      0.0      1  0.0   3.0
285 rows × 13 columns
```



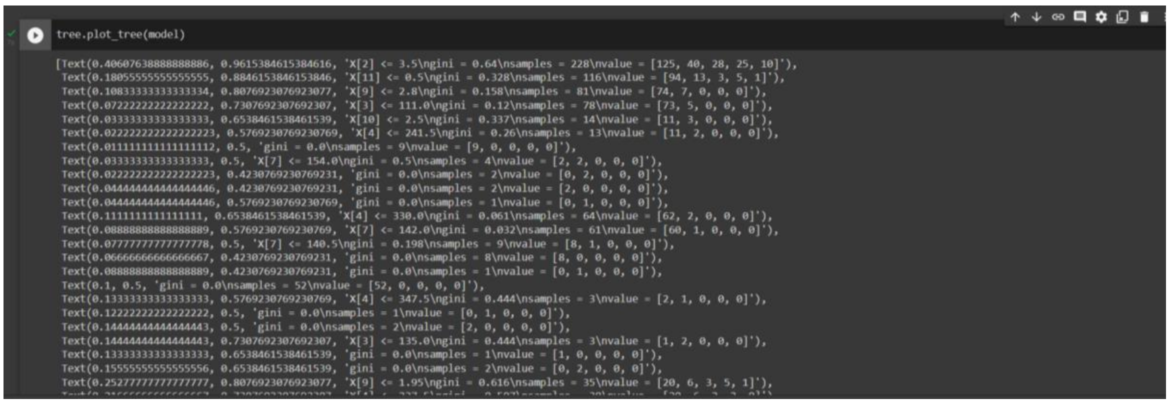
```
target     #the predicted attribute
```

```
0      0
1      2
2      1
3      0
4      0
      ..
298    1
299    2
300    3
301    1
302    0
Name: num, Length: 285, dtype: int64
```

Divide data into training and test sets.

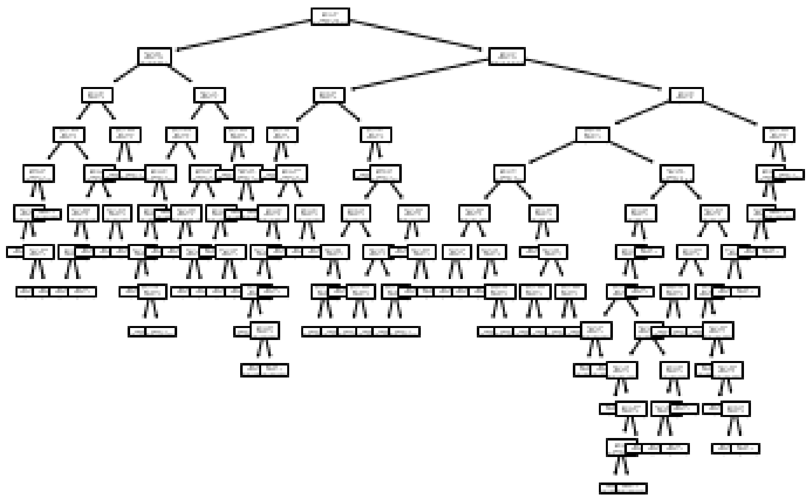


```
[26] from sklearn.model_selection import train_test_split
     from sklearn.tree import DecisionTreeClassifier

[27] X_train, X_test, y_train, y_test = train_test_split(inputs,target,test_size=0.2)

     len(X_train)  # length of training set

     228

[29] len(X_test)   #length of test set

     57

[30] from sklearn import tree
     model = tree.DecisionTreeClassifier(random_state=0)

[31] model.fit(X_train,y_train)

     DecisionTreeClassifier(random_state=0)
```

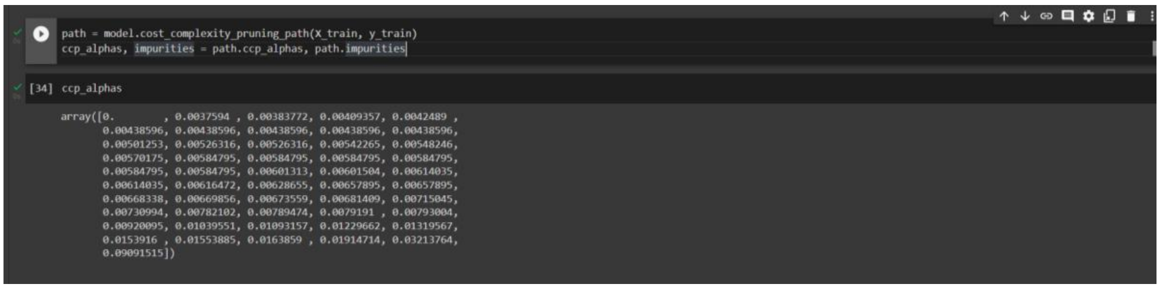


```
tree.plot_tree(model)
```

```
[Text(0.40607638888888886, 0.9615384615384616, 'X[2] <= 3.5\ngini = 0.64\nsamples = 228\nvalue = [125, 40, 28, 25, 10]'),
 Text(0.18055555555555555, 0.8846153846153846, 'X[11] <= 0.5\ngini = 0.328\nsamples = 116\nvalue = [94, 13, 3, 5, 1]'),
 Text(0.10833333333333334, 0.8076923076923077, 'X[9] <= 2.8\ngini = 0.158\nsamples = 81\nvalue = [74, 7, 0, 0, 0]'),
 Text(0.07222222222222222, 0.7307692307692307, 'X[3] <= 111.0\ngini = 0.12\nsamples = 78\nvalue = [73, 5, 0, 0, 0]'),
 Text(0.03333333333333333, 0.6538461538461539, 'X[10] <= 2.5\ngini = 0.337\nsamples = 14\nvalue = [11, 3, 0, 0, 0]'),
 Text(0.022222222222222223, 0.5769230769230769, 'X[4] <= 241.5\ngini = 0.26\nsamples = 13\nvalue = [11, 2, 0, 0, 0]'),
 Text(0.011111111111111112, 0.5, 'gini = 0.0\nsamples = 9\nvalue = [9, 0, 0, 0, 0]'),
 Text(0.03333333333333333, 0.5, 'X[7] <= 154.0\ngini = 0.5\nsamples = 4\nvalue = [2, 2, 0, 0, 0]'),
 Text(0.022222222222222223, 0.4230769230769231, 'gini = 0.0\nsamples = 2\nvalue = [0, 2, 0, 0, 0]'),
 Text(0.044444444444444446, 0.4230769230769231, 'gini = 0.0\nsamples = 2\nvalue = [2, 0, 0, 0, 0]'),
 Text(0.044444444444444446, 0.5769230769230769, 'gini = 0.0\nsamples = 1\nvalue = [0, 1, 0, 0, 0]'),
 Text(0.1111111111111111, 0.6538461538461539, 'X[4] <= 330.0\ngini = 0.061\nsamples = 64\nvalue = [62, 2, 0, 0, 0]'),
 Text(0.08888888888888889, 0.5769230769230769, 'X[7] <= 142.0\ngini = 0.032\nsamples = 61\nvalue = [60, 1, 0, 0, 0]'),
 Text(0.07777777777777778, 0.5, 'X[7] <= 140.5\ngini = 0.198\nsamples = 9\nvalue = [8, 1, 0, 0, 0]'),
 Text(0.06666666666666667, 0.4230769230769231, 'gini = 0.0\nsamples = 8\nvalue = [8, 0, 0, 0, 0]'),
 Text(0.08888888888888889, 0.4230769230769231, 'gini = 0.0\nsamples = 1\nvalue = [0, 1, 0, 0, 0]'),
 Text(0.1, 0.5, 'gini = 0.0\nsamples = 52\nvalue = [52, 0, 0, 0, 0]'),
 Text(0.13333333333333333, 0.5769230769230769, 'X[4] <= 347.5\ngini = 0.444\nsamples = 3\nvalue = [2, 1, 0, 0, 0]'),
 Text(0.12222222222222222, 0.5, 'gini = 0.0\nsamples = 1\nvalue = [0, 1, 0, 0, 0]'),
 Text(0.14444444444444443, 0.5, 'gini = 0.0\nsamples = 2\nvalue = [2, 0, 0, 0, 0]'),
 Text(0.14444444444444443, 0.7307692307692307, 'X[3] <= 135.0\ngini = 0.444\nsamples = 3\nvalue = [1, 2, 0, 0, 0]'),
 Text(0.13333333333333333, 0.6538461538461539, 'gini = 0.0\nsamples = 1\nvalue = [1, 0, 0, 0, 0]'),
 Text(0.15555555555555556, 0.6538461538461539, 'gini = 0.0\nsamples = 2\nvalue = [0, 2, 0, 0, 0]'),
 Text(0.25277777777777777, 0.8076923076923077, 'X[9] <= 1.95\ngini = 0.616\nsamples = 35\nvalue = [20, 6, 3, 5, 1]'),
```



Minimal cost complexity pruning recursively finds the node with the "weakest link". The weakest link is characterized by an effective alpha, where the nodes with the smallest effective alpha are pruned first. As alpha increases, more of the tree is pruned, which increases the total impurity of its leaves.

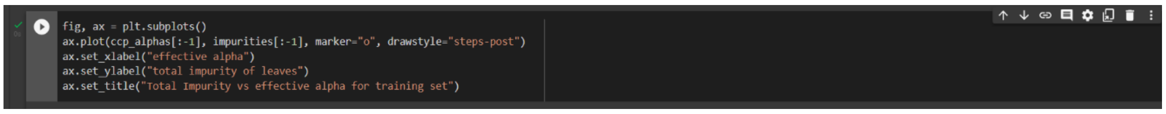


```
path = model.cost_complexity_pruning_path(X_train, y_train)
ccp_alphas, impurities = path.ccp_alphas, path.impurities
```

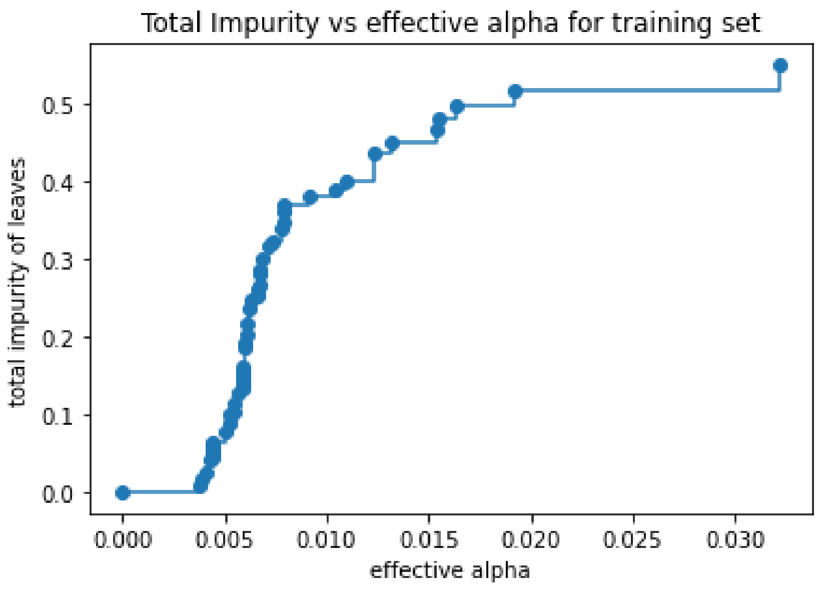
```
[34] ccp_alphas
```

```
array([0.        , 0.0037594 , 0.00383772, 0.00409357, 0.0042489 ,
       0.00438596, 0.00438596, 0.00438596, 0.00438596, 0.00438596,
       0.00501253, 0.00526316, 0.00526316, 0.00542265, 0.00548246,
       0.00570175, 0.00584795, 0.00584795, 0.00584795, 0.00584795,
       0.00584795, 0.00584795, 0.00601313, 0.00601504, 0.00614035,
       0.00614035, 0.00616472, 0.00628655, 0.00657895, 0.00657895,
       0.00668338, 0.00669856, 0.00673559, 0.00681409, 0.00715045,
       0.00730994, 0.00782102, 0.00789474, 0.0079191 , 0.00793004,
       0.00920095, 0.01039551, 0.01093157, 0.01229662, 0.01319567,
       0.0153916 , 0.01553885, 0.0163859 , 0.01914714, 0.03213764,
       0.09091515])
```

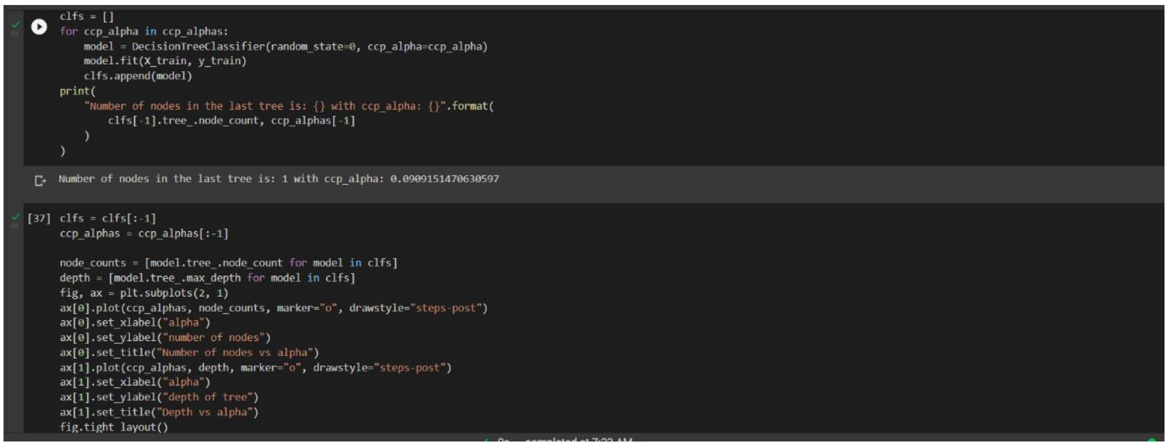
In the following plot, the maximum effective alpha value is removed, because it is the trivial tree with only one node.



```
fig, ax = plt.subplots()
ax.plot(ccp_alphas[:-1], impurities[:-1], marker="o", drawstyle="steps-post")
ax.set_xlabel("effective alpha")
ax.set_ylabel("total impurity of leaves")
ax.set_title("Total Impurity vs effective alpha for training set")
```



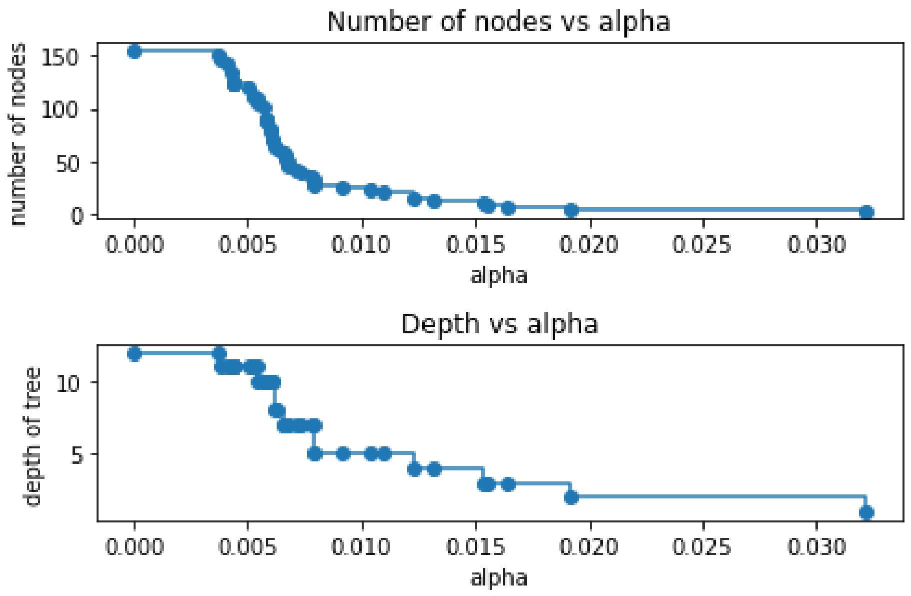
Next, we train a decision tree using the effective alphas. The last value in ccp_alphas is the alpha value that prunes the whole tree, leaving the tree, clfs[-1], with one node.



```
clfs = []
for ccp_alpha in ccp_alphas:
    model = DecisionTreeClassifier(random_state=0, ccp_alpha=ccp_alpha)
    model.fit(X_train, y_train)
    clfs.append(model)
print(
    "Number of nodes in the last tree is: {} with ccp_alpha: {}".format(
        clfs[-1].tree_.node_count, ccp_alphas[-1]
    )
)
```

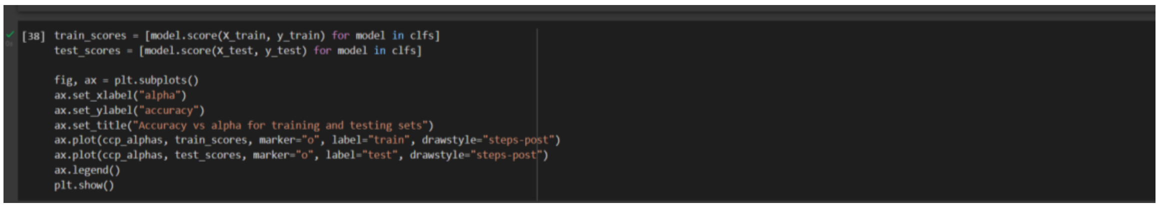
```
Number of nodes in the last tree is: 1 with ccp_alpha: 0.0909151470630597
```

```
[37] clfs = clfs[:-1]
     ccp_alphas = ccp_alphas[:-1]

     node_counts = [model.tree_.node_count for model in clfs]
     depth = [model.tree_.max_depth for model in clfs]
     fig, ax = plt.subplots(2, 1)
     ax[0].plot(ccp_alphas, node_counts, marker="o", drawstyle="steps-post")
     ax[0].set_xlabel("alpha")
     ax[0].set_ylabel("number of nodes")
     ax[0].set_title("Number of nodes vs alpha")
     ax[1].plot(ccp_alphas, depth, marker="o", drawstyle="steps-post")
     ax[1].set_xlabel("alpha")
     ax[1].set_ylabel("depth of tree")
     ax[1].set_title("Depth vs alpha")
     fig.tight_layout()
```

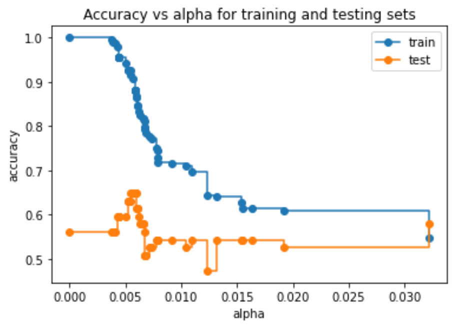


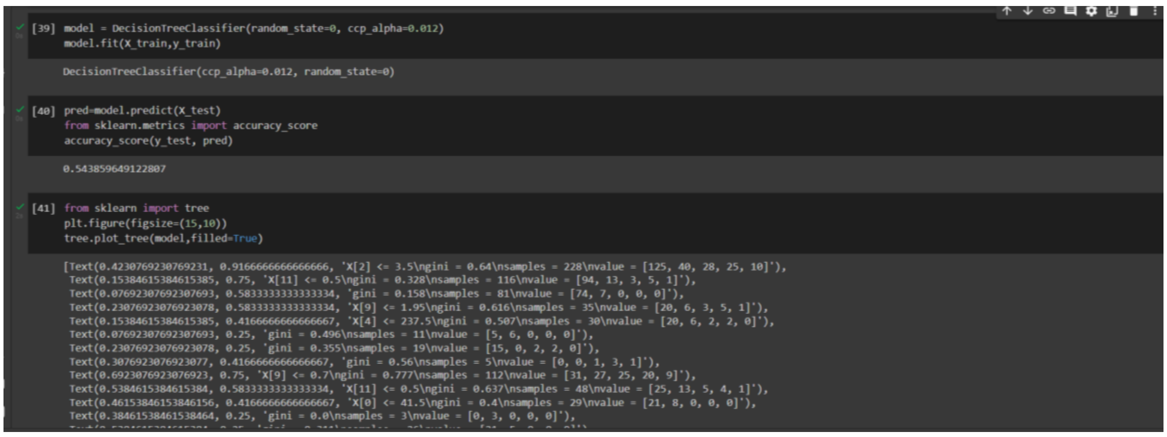
Here we observe that the number of nodes and tree depth decreases as alpha increases.

As alpha increases, more of the tree is pruned, thus creating a decision tree that generalizes better.

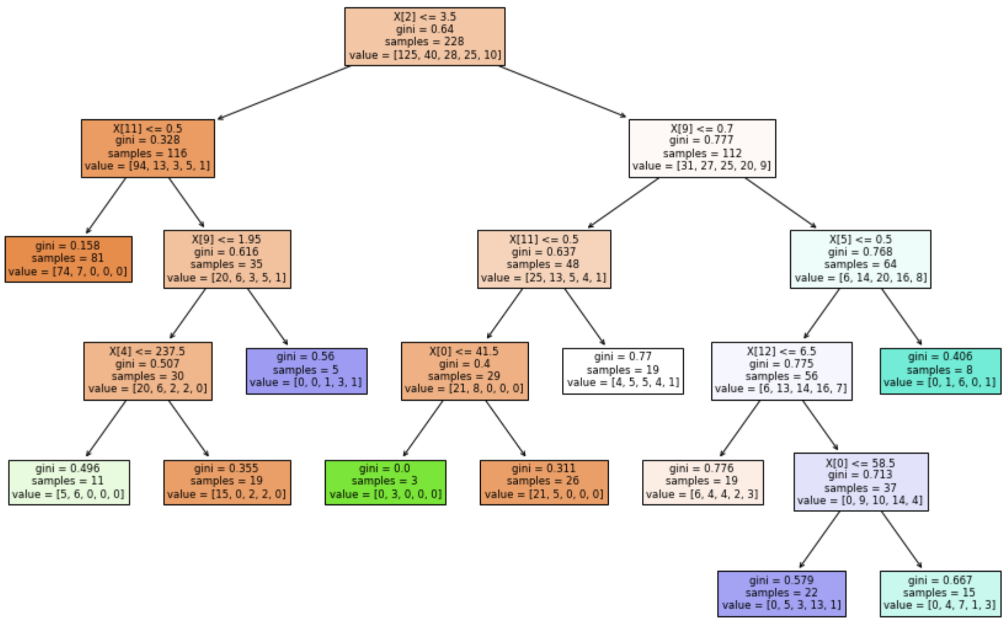


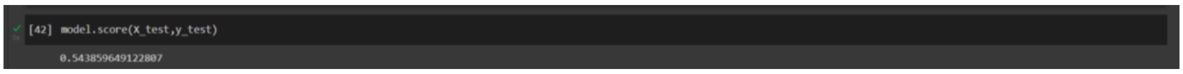
```
[38] train_scores = [model.score(X_train, y_train) for model in clfs]
     test_scores = [model.score(X_test, y_test) for model in clfs]

     fig, ax = plt.subplots()
     ax.set_xlabel("alpha")
     ax.set_ylabel("accuracy")
     ax.set_title("Accuracy vs alpha for training and testing sets")
     ax.plot(ccp_alphas, train_scores, marker="o", label="train", drawstyle="steps-post")
     ax.plot(ccp_alphas, test_scores, marker="o", label="test", drawstyle="steps-post")
     ax.legend()
     plt.show()
```





```
[39] model = DecisionTreeClassifier(random_state=0, ccp_alpha=0.012)
     model.fit(X_train,y_train)

     DecisionTreeClassifier(ccp_alpha=0.012, random_state=0)

[40] pred=model.predict(X_test)
     from sklearn.metrics import accuracy_score
     accuracy_score(y_test, pred)

     0.543859649122807

[41] from sklearn import tree
     plt.figure(figsize=(15,10))
     tree.plot_tree(model,filled=True)

     [Text(0.4230769230769231, 0.9166666666666666, 'X[2] <= 3.5\ngini = 0.64\nsamples = 228\nvalue = [125, 40, 28, 25, 10]'),
      Text(0.15384615384615385, 0.75, 'X[11] <= 0.5\ngini = 0.328\nsamples = 116\nvalue = [94, 13, 3, 5, 1]'),
      Text(0.07692307692307693, 0.5833333333333334, 'gini = 0.158\nsamples = 81\nvalue = [74, 7, 0, 0, 0]'),
      Text(0.23076923076923078, 0.5833333333333334, 'X[9] <= 1.95\ngini = 0.616\nsamples = 35\nvalue = [20, 6, 3, 5, 1]'),
      Text(0.15384615384615385, 0.4166666666666667, 'X[4] <= 237.5\ngini = 0.507\nsamples = 30\nvalue = [20, 6, 2, 2, 0]'),
      Text(0.07692307692307693, 0.25, 'gini = 0.496\nsamples = 11\nvalue = [5, 6, 0, 0, 0]'),
      Text(0.23076923076923078, 0.25, 'gini = 0.355\nsamples = 19\nvalue = [15, 0, 2, 2, 0]'),
      Text(0.3076923076923077, 0.4166666666666667, 'gini = 0.56\nsamples = 5\nvalue = [0, 0, 1, 3, 1]'),
      Text(0.6923076923076923, 0.75, 'X[9] <= 0.7\ngini = 0.777\nsamples = 112\nvalue = [31, 27, 25, 20, 9]'),
      Text(0.5384615384615384, 0.5833333333333334, 'X[11] <= 0.5\ngini = 0.637\nsamples = 48\nvalue = [25, 13, 5, 4, 1]'),
      Text(0.46153846153846156, 0.4166666666666667, 'X[0] <= 41.5\ngini = 0.4\nsamples = 29\nvalue = [21, 8, 0, 0, 0]'),
      Text(0.38461538461538464, 0.25, 'gini = 0.0\nsamples = 3\nvalue = [0, 3, 0, 0, 0]'),
```





```
[42] model.score(X_test,y_test)

     0.543859649122807
```