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CSE- 1

MACHINE LEARNING

LAB PROGRAM

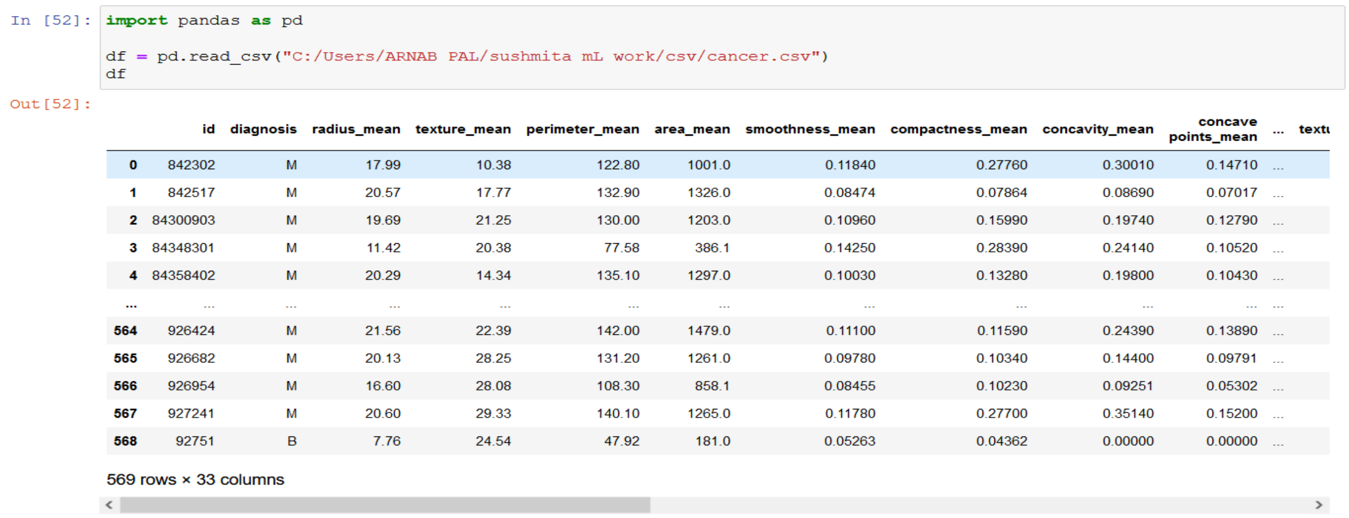
Submission -2

Github link : LAB Program - 2

PROBLEM STATEMENT - Implementation of decision tree on a breast cancer dataset using sklearn in python.

Program Code Snippet

Loading Dataset

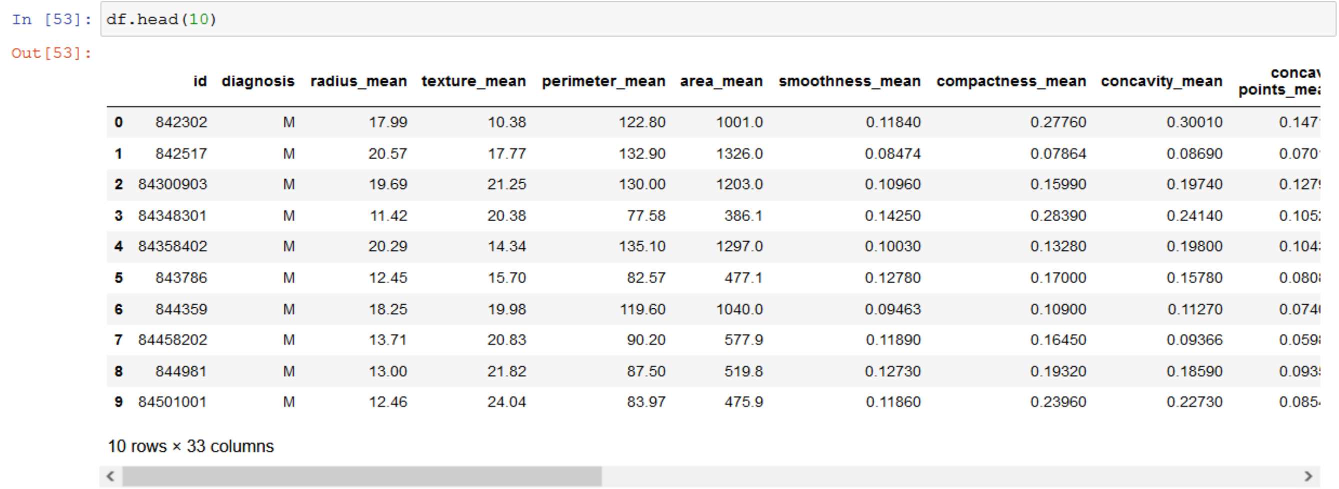


```
In [52]: import pandas as pd

         df = pd.read_csv("C:/Users/ARNAB PAL/sushmita mL work/csv/cancer.csv")
         df
```

Out[52]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...	textu
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.14710	...	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.07017	...	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.12790	...	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.10520	...	
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.10430	...	
...	...	...	...	...	...	...	...	...	...	...	...	
564	926424	M	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	...	
565	926682	M	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	...	
566	926954	M	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	...	
567	927241	M	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	...	
568	92751	B	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	...	

569 rows × 33 columns



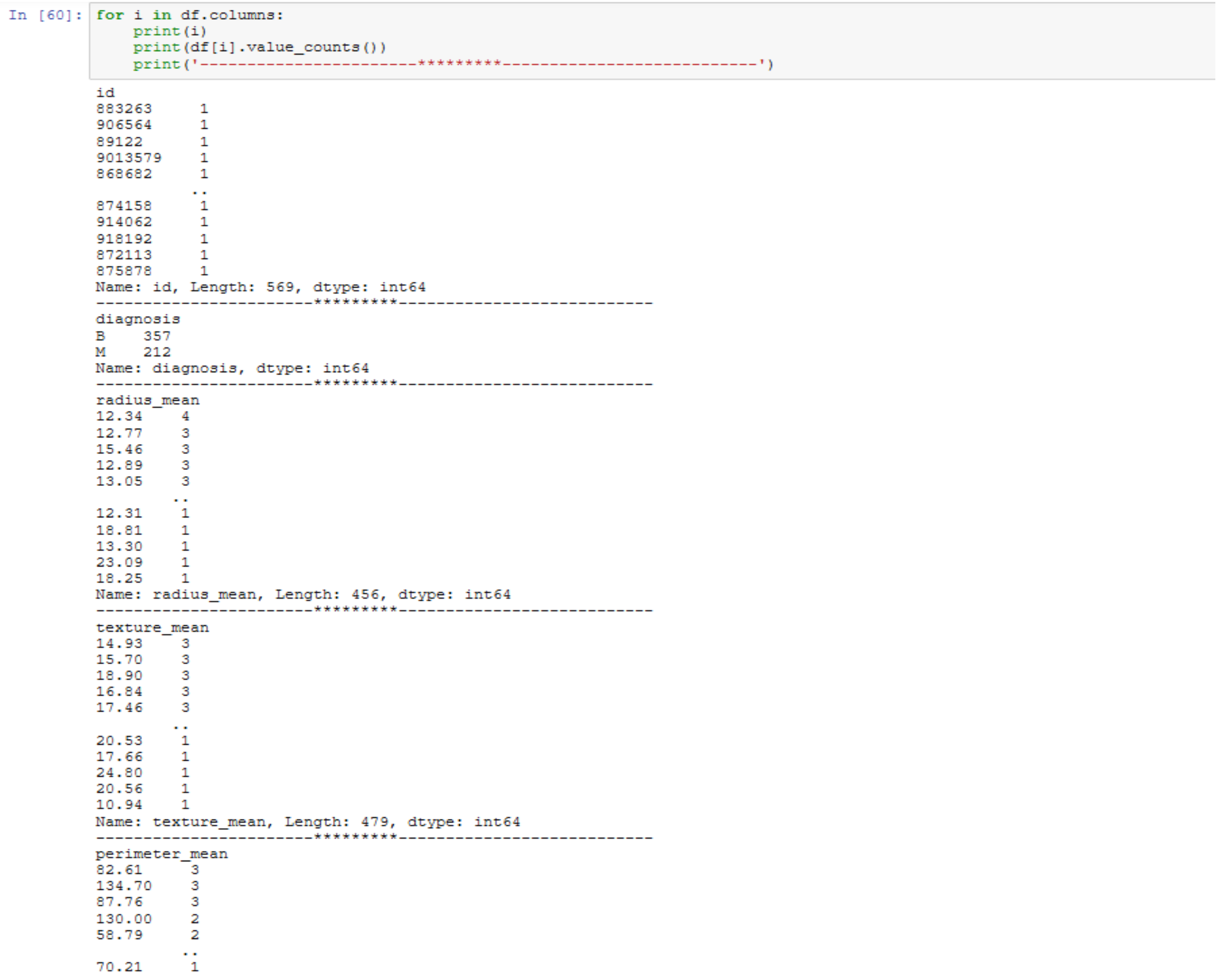
```
In [53]: df.head(10)
```

Out[53]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concav points_mea
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.147
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.070
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.127
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.105
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.104
5	843786	M	12.45	15.70	82.57	477.1	0.12780	0.17000	0.15780	0.080
6	844359	M	18.25	19.98	119.60	1040.0	0.09463	0.10900	0.11270	0.074
7	84458202	M	13.71	20.83	90.20	577.9	0.11890	0.16450	0.09366	0.059
8	844981	M	13.00	21.82	87.50	519.8	0.12730	0.19320	0.18590	0.093
9	84501001	M	12.46	24.04	83.97	475.9	0.11860	0.23960	0.22730	0.085

10 rows × 33 columns

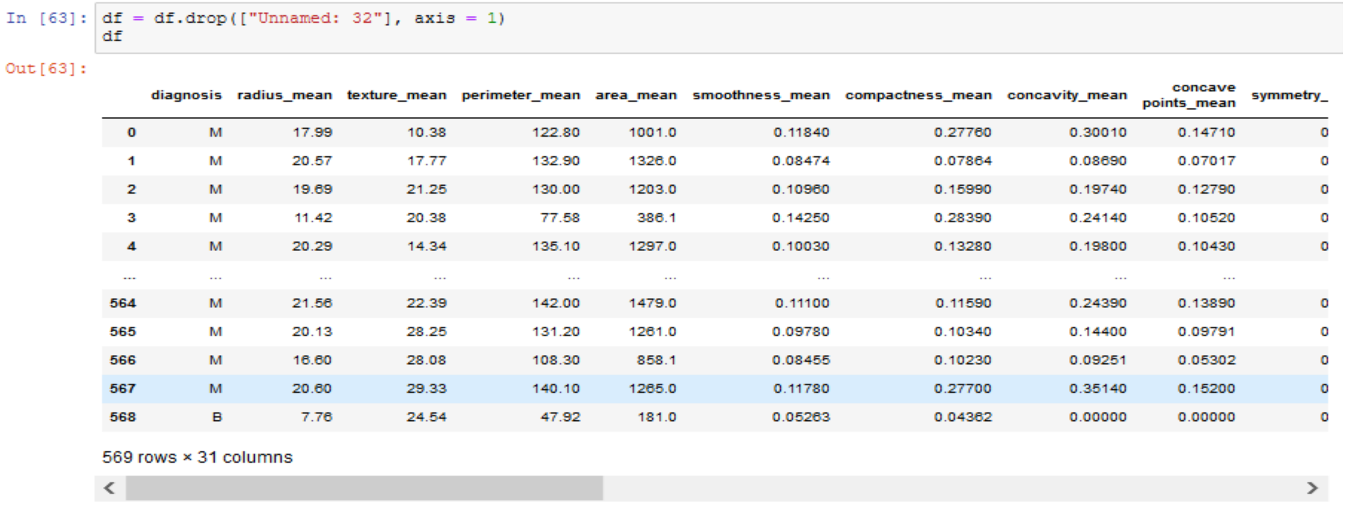
Preprocessing/Cleaning of dataset



In [60]:

```
for i in df.columns:
    print(i)
    print(df[i].value_counts())
    print('-----------------------*********---------------------------')
```

```
id
883263     1
906564     1
89122      1
9013579    1
868682     1
          ..
874158     1
914062     1
918192     1
872113     1
875878     1
Name: id, Length: 569, dtype: int64
-----------------------*********---------------------------
diagnosis
B    357
M    212
Name: diagnosis, dtype: int64
-----------------------*********---------------------------
radius_mean
12.34    4
12.77    3
15.46    3
12.89    3
13.05    3
        ..
12.31    1
18.81    1
13.30    1
23.09    1
18.25    1
Name: radius_mean, Length: 456, dtype: int64
-----------------------*********---------------------------
texture_mean
14.93    3
15.70    3
18.90    3
16.84    3
17.46    3
        ..
20.53    1
17.66    1
24.80    1
20.56    1
10.94    1
Name: texture_mean, Length: 479, dtype: int64
-----------------------*********---------------------------
perimeter_mean
82.61     3
134.70    3
87.76     3
130.00    2
58.79     2
         ..
70.21     1
```



In [63]:

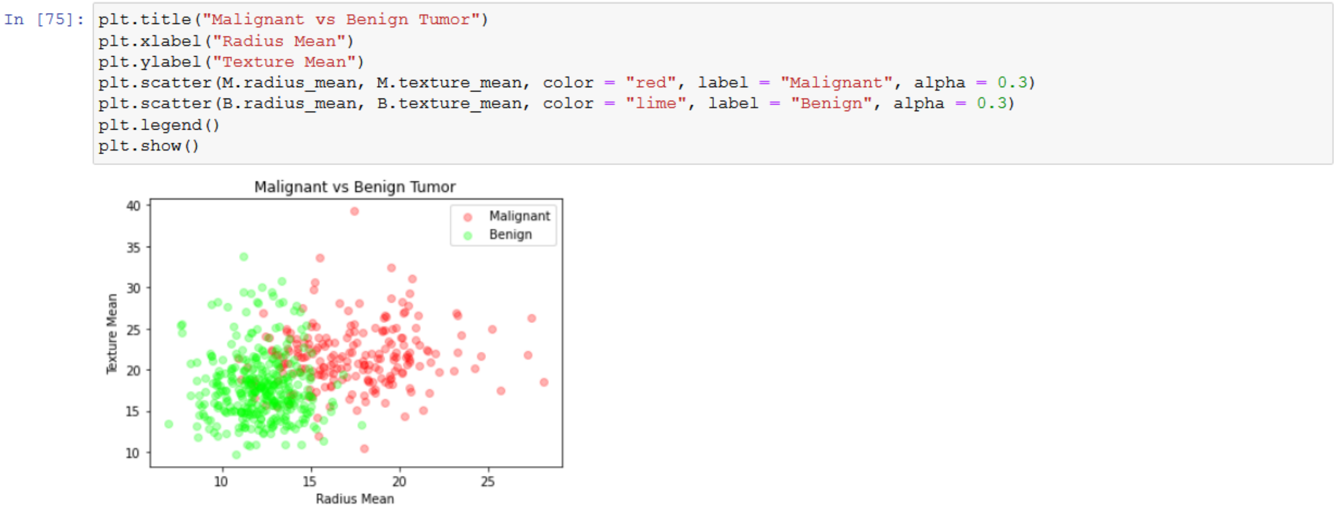
```
df = df.drop(["Unnamed: 32"], axis = 1)
df
```

Out[63]:

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_
0	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.14710	0
1	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.07017	0
2	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.12790	0
3	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.10520	0
4	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.10430	0
...	...	...	...	...	...	...	...	...	...	
564	M	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	0
565	M	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	0
566	M	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	0
567	M	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	0
568	B	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	0

569 rows × 31 columns

Visualization

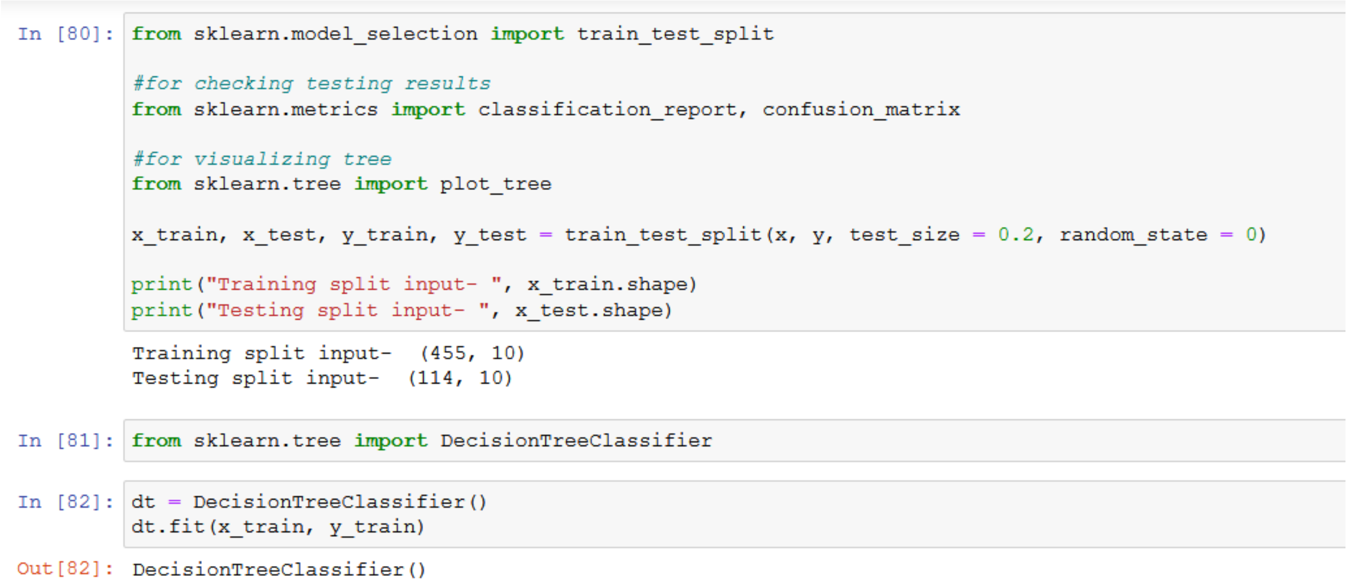


```
In [75]: plt.title("Malignant vs Benign Tumor")
         plt.xlabel("Radius Mean")
         plt.ylabel("Texture Mean")
         plt.scatter(M.radius_mean, M.texture_mean, color = "red", label = "Malignant", alpha = 0.3)
         plt.scatter(B.radius_mean, B.texture_mean, color = "lime", label = "Benign", alpha = 0.3)
         plt.legend()
         plt.show()
```

ML algorithm implementation of prediction or comparison

Decision tree models where the target variable uses a discrete set of values are classified as Classification Trees. In these trees, each node, or leaf, represent class labels while the branches represent conjunctions of features leading to class labels.

A decision tree where the target variable takes a continuous value, usually numbers, are called Regression Trees. The two types are commonly referred to together at CART (Classification and Regression Tree).



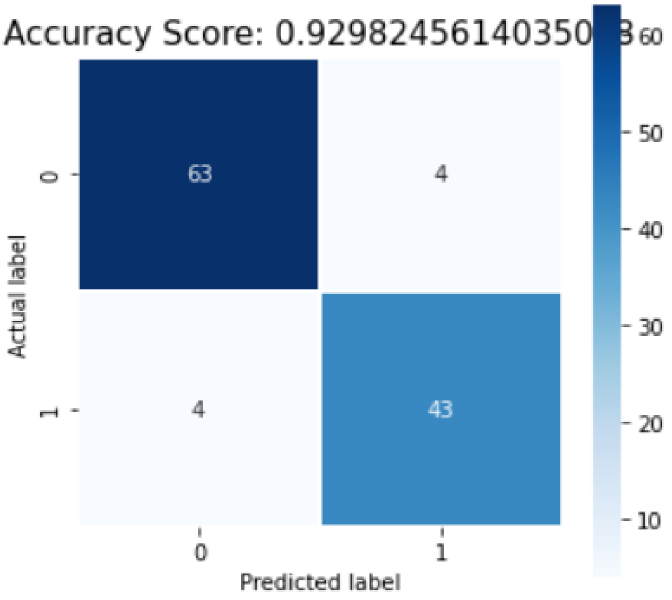
```
In [80]: from sklearn.model_selection import train_test_split

         #for checking testing results
         from sklearn.metrics import classification_report, confusion_matrix

         #for visualizing tree
         from sklearn.tree import plot_tree

         x_train, x_test, y_train, y_test = train_test_split(x, y, test_size = 0.2, random_state = 0)

         print("Training split input- ", x_train.shape)
         print("Testing split input- ", x_test.shape)

         Training split input-  (455, 10)
         Testing split input-  (114, 10)

In [81]: from sklearn.tree import DecisionTreeClassifier

In [82]: dt = DecisionTreeClassifier()
         dt.fit(x_train, y_train)

Out[82]: DecisionTreeClassifier()
```

ROC/AUC/Confusion matrix

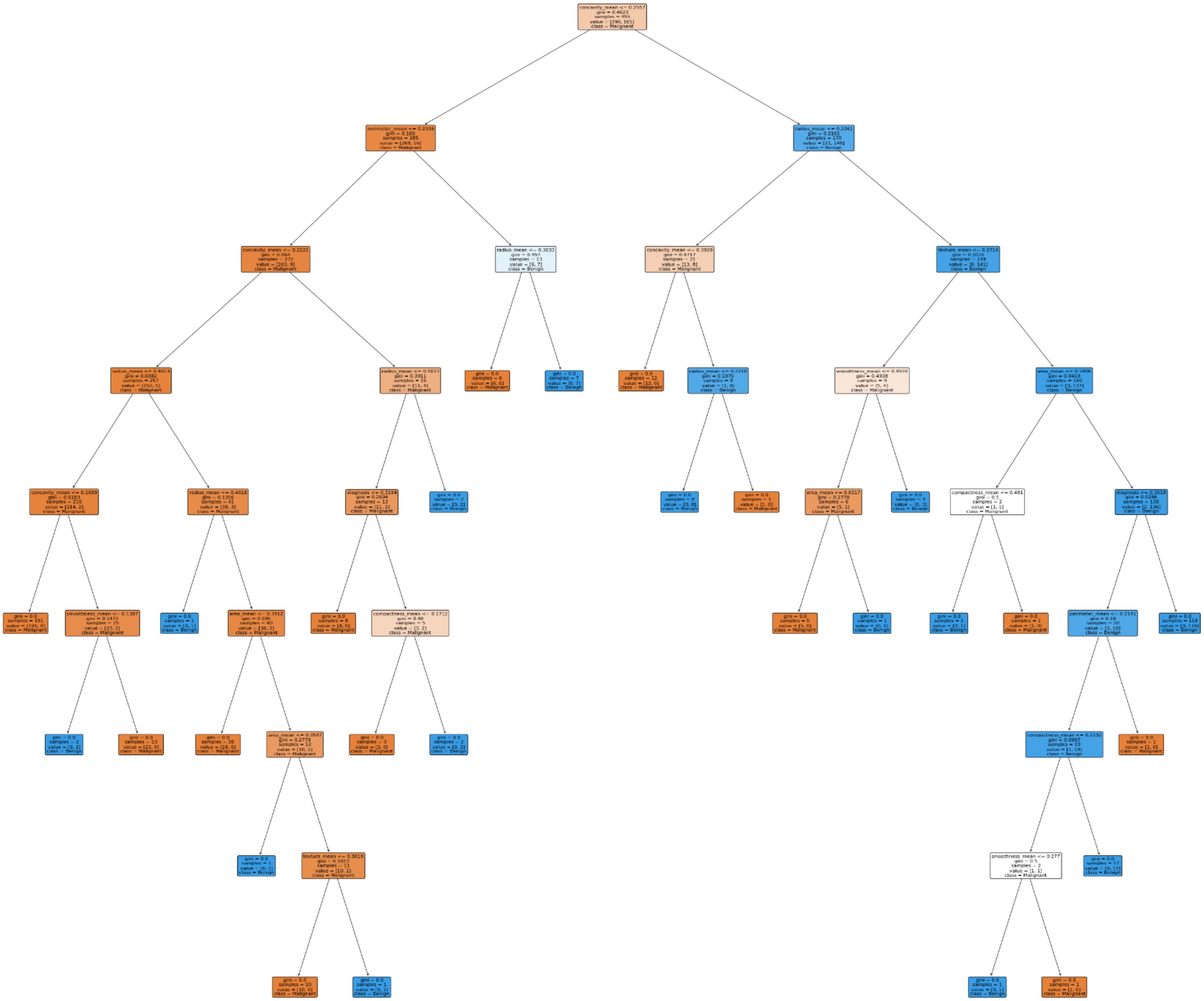
```
In [83]: y_pred = dt.predict(x_test)
         print("Classification report - \n", classification_report(y_test,y_pred))

         Classification report -
                       precision    recall  f1-score   support

                   B       0.94      0.94      0.94        67
                   M       0.91      0.91      0.91        47

            accuracy                           0.93       114
           macro avg       0.93      0.93      0.93       114
        weighted avg       0.93      0.93      0.93       114
```

```
In [84]: cm=confusion_matrix(y_test,y_pred)
         cm

Out[84]: array([[63,  4],
                [ 4, 43]], dtype=int64)
```

```
In [85]: plt.figure(figsize=(5,5))

         sns.heatmap(data=cm,linewidths=1.0, annot=True,square = True,  cmap = 'Blues')

         plt.ylabel('Actual label')
         plt.xlabel('Predicted label')

         all_sample_title = 'Accuracy Score: {0}'.format(dt.score(x_test, y_test))
         plt.title(all_sample_title, size = 15)

         plt.savefig("D:/accu.png")
```



Final graph


concavity_mean <= 0.2557
gini = 0.4623
samples = 455
value = [290, 165]
class = Malignant
perimeter_mean <= 0.2336
gini = 0.106
samples = 285
value = [269, 16]
class = Malignant
radius_mean <= 0.2261
gini = 0.2165
samples = 170
value = [21, 149]
class = Benign
concavity_mean <= 0.2222
gini = 0.064
samples = 272
value = [263, 9]
class = Malignant
radius_mean <= 0.3033
gini = 0.497
samples = 13
value = [6, 7]
class = Benign
concavity_mean <= 0.3929
gini = 0.4717
samples = 21
value = [13, 8]
class = Malignant
texture_mean <= 0.2714
gini = 0.1016
samples = 149
value = [8, 141]
class = Benign
radius_mean <= 0.4013
gini = 0.0382
samples = 257
value = [252, 5]
class = Malignant
radius_mean <= 0.5073
gini = 0.3911
samples = 15
value = [11, 4]
class = Malignant
gini = 0.0
samples = 6
value = [6, 0]
class = Malignant
gini = 0.0
samples = 7
value = [0, 7]
class = Benign
gini = 0.0
samples = 12
value = [12, 0]
class = Malignant
radius_mean <= 0.2218
gini = 0.1975
samples = 9
value = [1, 8]
class = Benign
smoothness_mean <= 0.4559
gini = 0.4938
samples = 9
value = [5, 4]
class = Malignant
area_mean <= 0.2406
gini = 0.0419
samples = 140
value = [3, 137]
class = Benign
concavity_mean <= 0.1699
gini = 0.0183
samples = 216
value = [214, 2]
class = Malignant
radius_mean <= 0.4018
gini = 0.1356
samples = 41
value = [38, 3]
class = Malignant
diagnosis <= 0.3194
gini = 0.2604
samples = 13
value = [11, 2]
class = Malignant
gini = 0.0
samples = 2
value = [0, 2]
class = Benign
gini = 0.0
samples = 8
value = [0, 8]
class = Benign
gini = 0.0
samples = 1
value = [1, 0]
class = Malignant
area_mean <= 0.6317
gini = 0.2778
samples = 6
value = [5, 1]
class = Malignant
gini = 0.0
samples = 3
value = [0, 3]
class = Benign
compactness_mean <= 0.481
gini = 0.5
samples = 2
value = [1, 1]
class = Malignant
diagnosis <= 0.3518
gini = 0.0286
samples = 138
value = [2, 136]
class = Benign
gini = 0.0
samples = 191
value = [191, 0]
class = Malignant
smoothness_mean <= 0.1387
gini = 0.1472
samples = 25
value = [23, 2]
class = Malignant
gini = 0.0
samples = 1
value = [0, 1]
class = Benign
area_mean <= 0.3412
gini = 0.095
samples = 40
value = [38, 2]
class = Malignant
gini = 0.0
samples = 8
value = [8, 0]
class = Malignant
compactness_mean <= 0.1712
gini = 0.48
samples = 5
value = [3, 2]
class = Malignant
gini = 0.0
samples = 5
value = [5, 0]
class = Malignant
gini = 0.0
samples = 1
value = [0, 1]
class = Benign
gini = 0.0
samples = 1
value = [0, 1]
class = Benign
gini = 0.0
samples = 1
value = [1, 0]
class = Malignant
perimeter_mean <= 0.2141
gini = 0.18
samples = 20
value = [2, 18]
class = Benign
gini = 0.0
samples = 118
value = [0, 118]
class = Benign
gini = 0.0
samples = 2
value = [0, 2]
class = Benign
gini = 0.0
samples = 23
value = [23, 0]
class = Malignant
gini = 0.0
samples = 28
value = [28, 0]
class = Malignant
area_mean <= 0.3507
gini = 0.2778
samples = 12
value = [10, 2]
class = Malignant
gini = 0.0
samples = 3
value = [3, 0]
class = Malignant
gini = 0.0
samples = 2
value = [0, 2]
class = Benign
compactness_mean <= 0.2102
gini = 0.0997
samples = 19
value = [1, 18]
class = Benign
gini = 0.0
samples = 1
value = [1, 0]
class = Malignant
gini = 0.0
samples = 1
value = [0, 1]
class = Benign
texture_mean <= 0.3019
gini = 0.1653
samples = 11
value = [10, 1]
class = Malignant
smoothness_mean <= 0.277
gini = 0.5
samples = 2
value = [1, 1]
class = Malignant
gini = 0.0
samples = 17
value = [0, 17]
class = Benign
gini = 0.0
samples = 10
value = [10, 0]
class = Malignant
gini = 0.0
samples = 1
value = [0, 1]
class = Benign
gini = 0.0
samples = 1
value = [0, 1]
class = Benign
gini = 0.0
samples = 1
value = [1, 0]
class = Malignant