

# HABERMANS DATASET ASSIGNMENT

Description of dataset:-

1. AGE - Age of patient
2. YOP - Year of operation
3. POS\_NODES - No. of positive auxillary nodes found
4. STATUS:- 1= Patient survived for 5 or more years, 2= Patient died within 5 years.

```
In [4]: import pandas as p
x=['AGE', 'YOP', 'POS_NODES', 'STATUS']
a=p.read_csv('haberman.csv', names=x)
print(a.head())
```

	AGE	YOP	POS_NODES	STATUS
0	30	64	1	1
1	30	62	3	1
2	30	65	0	1
3	31	59	2	1
4	31	65	4	1

```
In [7]: print(a.shape)
```

(306, 4)

-> There are 306 datapoints and 4 features.

```
In [8]: print(a.columns)
```

Index(['AGE', 'YOP', 'POS\_NODES', 'STATUS'], dtype='object')

-> These are the column name in the dataset.

```
In [9]: print(a['STATUS'].value_counts())
```

```
1    225
2     81
Name: STATUS, dtype: int64
```

-> There are 2 classes:'1' and '2' -> Datapoints present for class '1' : 225 -> Datapoints present for class '2' : 81

## OBSERVATION

1. The dataset is classified into two classes i.e 225 patients of class 1, those who survived for more than 5 years,81 patients of class 2, those who not survived for more than 5 years.
2. This dataset is an imbalanced dataset as there is huge margin between the datapoints of class-1 and class-2.

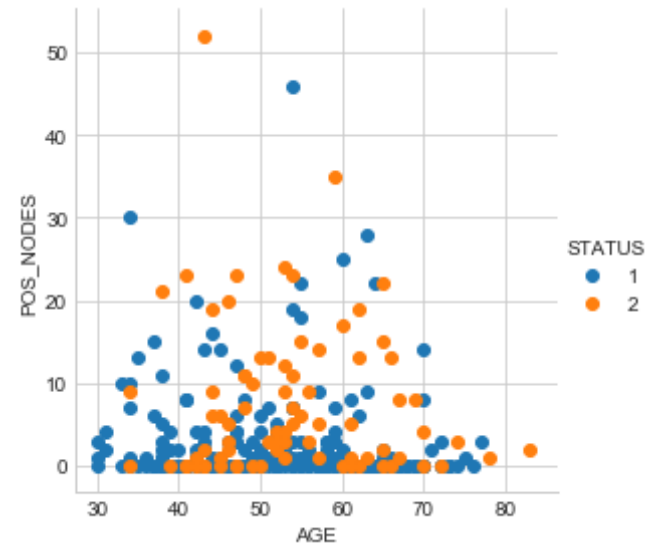
## OBJECTIVE

Given a persons age,positive nodes and year of operation we have to find whether that person lies in class-1 or class-2.

## 2-D SCATTER PLOT

```
In [14]: import seaborn as sea
import matplotlib.pyplot as plt
sea.set_style("whitegrid")
sea.FacetGrid(a,hue="STATUS",size=4) \
    .map(plt.scatter,'AGE','POS_NODES') \
```

```
.add_legend()  
plt.show()
```

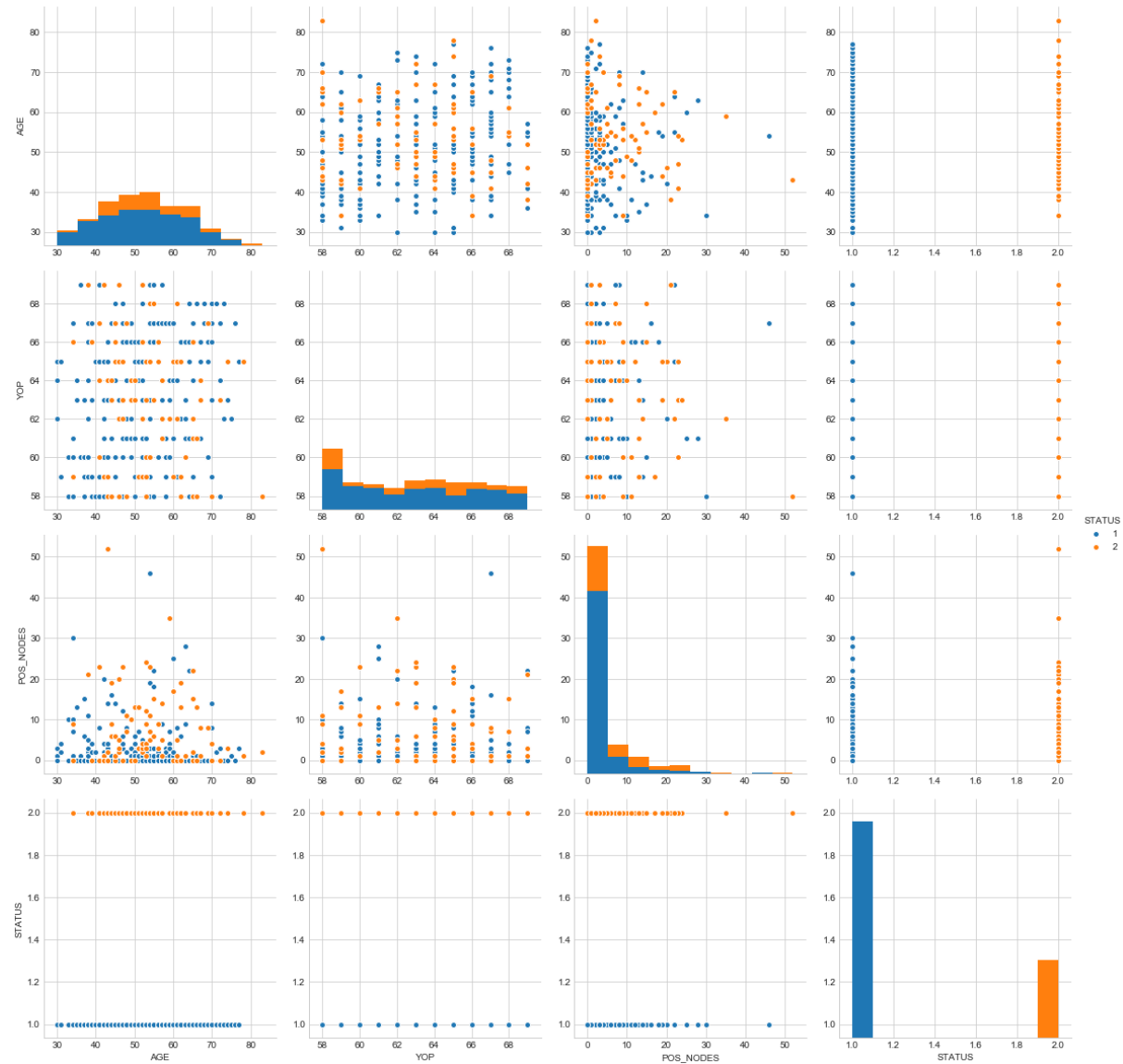


OBSERVATIONS:-

1. Using age and no. of positive axillary nodes as features, we cannot make any difference since both are overlapping each other.
2. Most of the people have 0 positive axillary node.

## PAIR-PLOT

```
In [23]: plt.close()  
          sea.set_style("whitegrid")  
          sea.pairplot(a, hue="STATUS", size=4)  
          plt.show()
```



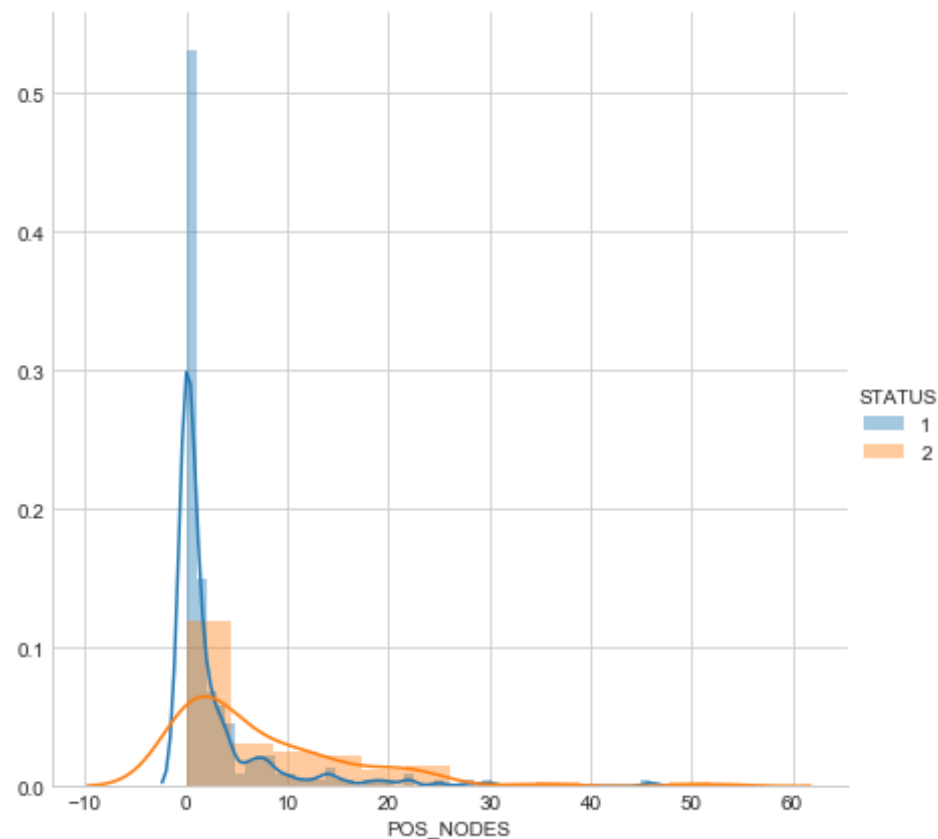
OBSERVATION:-

1. There are no two features through which we can easily distinguish between class-1 and

class-2.

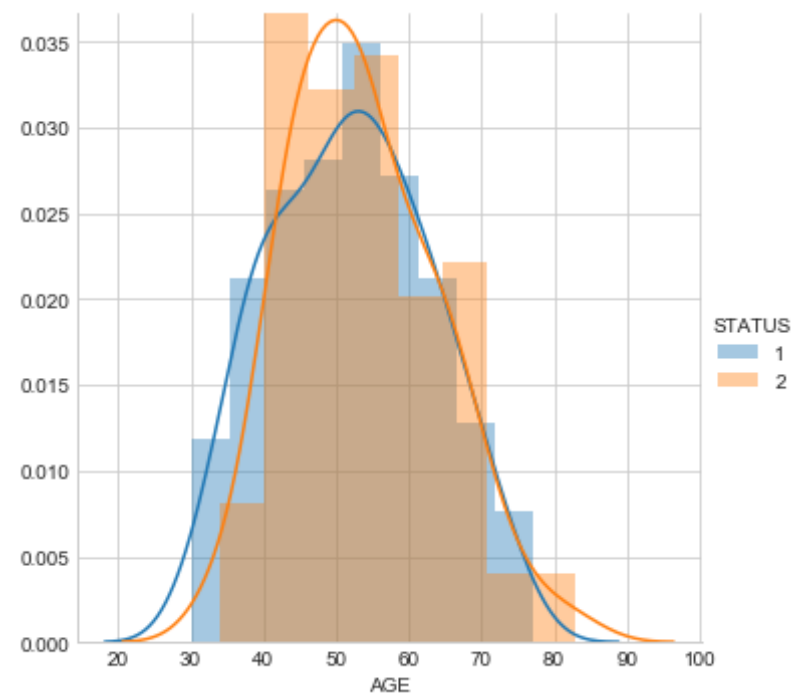
## HISTOGRAM AND PDF

```
In [25]: sea.FacetGrid(a,hue='STATUS',size=6) \
        .map(sea.distplot,'POS_NODES') \
        .add_legend()
plt.show()
```

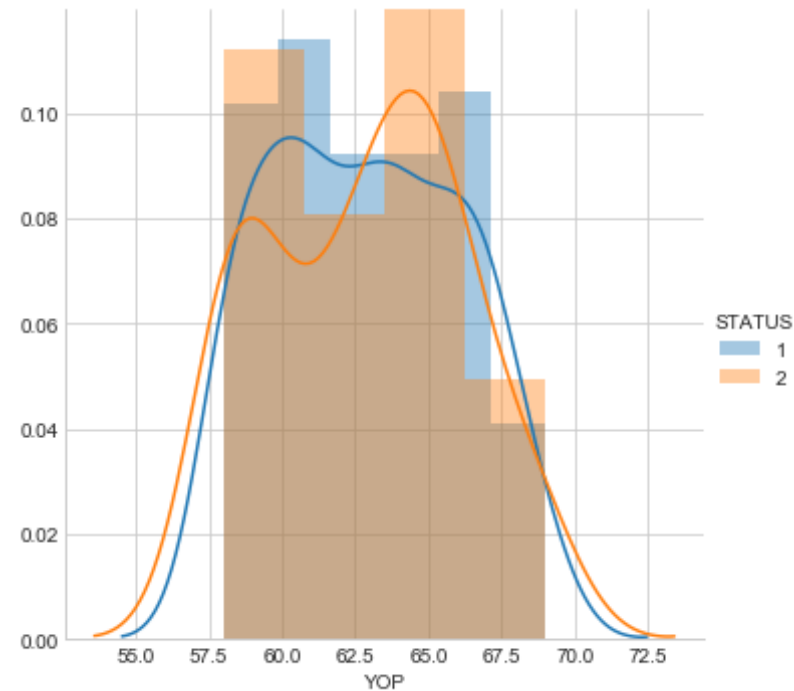


```
In [26]: sea.FacetGrid(a,hue='STATUS',size=5) \
        .map(sea.distplot,'AGE') \
```

```
.add_legend()  
plt.show()
```



```
In [27]: sea.FacetGrid(a,hue='STATUS',size=5) \  
         .map(sea.distplot,'YOP') \  
         .add_legend()  
         plt.show()
```



As the distribution for class-1 and class-2 overlaps in huge amount, so we will go for the mean.

```
In [43]: import numpy as np
a1= a.loc[a['STATUS']==1];
a2= a.loc[a["STATUS"]==2];
print("MEANS-:")
print(".FOR AGE")
print(round(np.mean(a1["AGE"])))
print(round(np.mean(a2["AGE"])))
print("-----")
print(".FOR POS_NODES")
print(round(np.mean(a1["POS_NODES"])))
print(round(np.mean(a2["POS_NODES"])))
print("-----")
print(".FOR YOP")
print(round(np.mean(a1["YOP"])))
print(round(np.mean(a2["YOP"])))
```

```
MEANS - :  
.FOR AGE  
52  
54  
-----  
.FOR POS_NODES  
3  
7  
-----  
.FOR YOP  
63  
63
```

OBSERVATION-:

1. Of the three features POS\_NODES is a very important feature in identifying the class as the difference between the means are more as compared to others.
2. Most of the people that have 0 POS\_NODES have survived.
3. The mean positive auxiliary nodes for the person that survived are 3 as compared to 7 which have not survived.
4. The mean age of the patients which survived is 52 years and not survived is 54 years.

## CDF

```
In [75]: counts, bin_edges = np.histogram(a1['POS_NODES'], bins=10,  
                                         density = True)  
pdf = counts/(sum(counts))  
print(pdf);  
print(bin_edges)  
cdf = np.cumsum(pdf)  
plt.plot(bin_edges[1:],pdf)  
plt.plot(bin_edges[1:], cdf)  
#plt.show()  
counts, bin_edges = np.histogram(a2['POS_NODES'], bins=10,
```



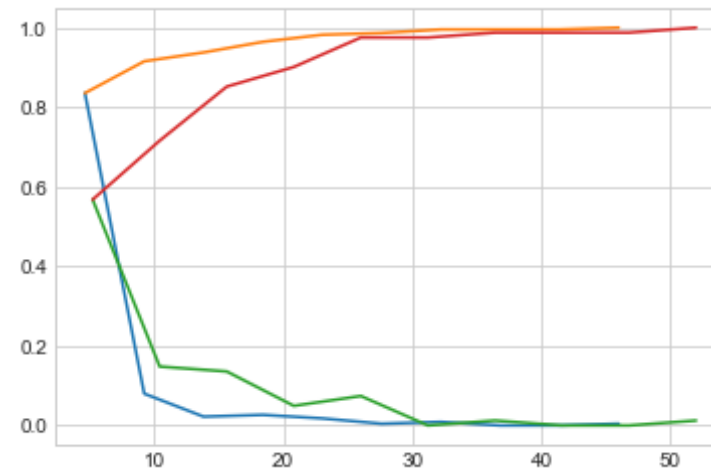
```

density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)

plt.show()

```

[ 0.83555556	0.08	0.02222222	0.02666667	0.01777778	0.00444444
4					
0.00888889	0.	0.	0.00444444]		
[ 0.	4.6	9.2	13.8	18.4	23.
[ 0.56790123	0.14814815	0.13580247	0.04938272	0.07407407	0.
0.01234568	0.	0.	0.01234568]		
[ 0.	5.2	10.4	15.6	20.8	26.
				31.2	36.4
				41.6	46.8
				52.	



OBSERVATION:-

1. If the positive auxillary nodes are more than 46 then the person definately comes under the class-2.

2. If the no. of positive auxillary nodes lies between 0-24 then there are 82%-98% chances of survival whereas the non-survival ranges from 59% to 84%.

## STATISTICAL DESCRIPTION

In [76]: `a1.describe()`

Out[76]:

	AGE	YOP	POS_NODES	STATUS
count	225.000000	225.000000	225.000000	225.0
mean	52.017778	62.862222	2.791111	1.0
std	11.012154	3.222915	5.870318	0.0
min	30.000000	58.000000	0.000000	1.0
25%	43.000000	60.000000	0.000000	1.0
50%	52.000000	63.000000	0.000000	1.0
75%	60.000000	66.000000	3.000000	1.0
max	77.000000	69.000000	46.000000	1.0

In [77]: `a2.describe()`

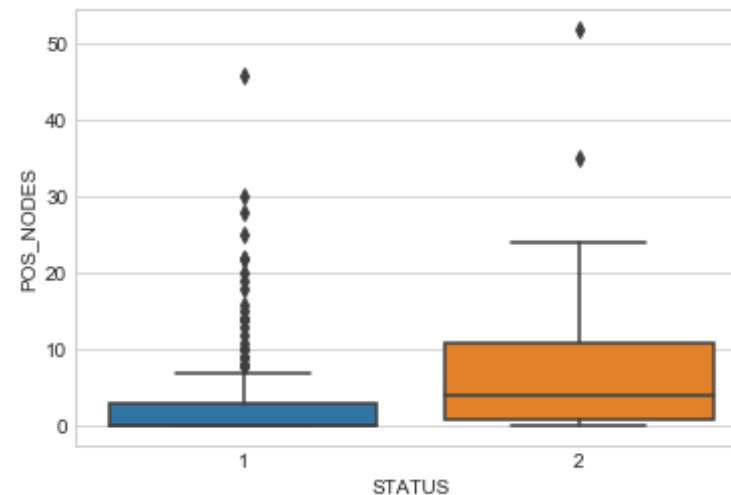
Out[77]:

	AGE	YOP	POS_NODES	STATUS
count	81.000000	81.000000	81.000000	81.0
mean	53.679012	62.827160	7.456790	2.0
std	10.167137	3.342118	9.185654	0.0
min	34.000000	58.000000	0.000000	2.0
25%	46.000000	59.000000	1.000000	2.0

	AGE	YOP	POS_NODES	STATUS
50%	53.000000	63.000000	4.000000	2.0
75%	61.000000	65.000000	11.000000	2.0
max	83.000000	69.000000	52.000000	2.0

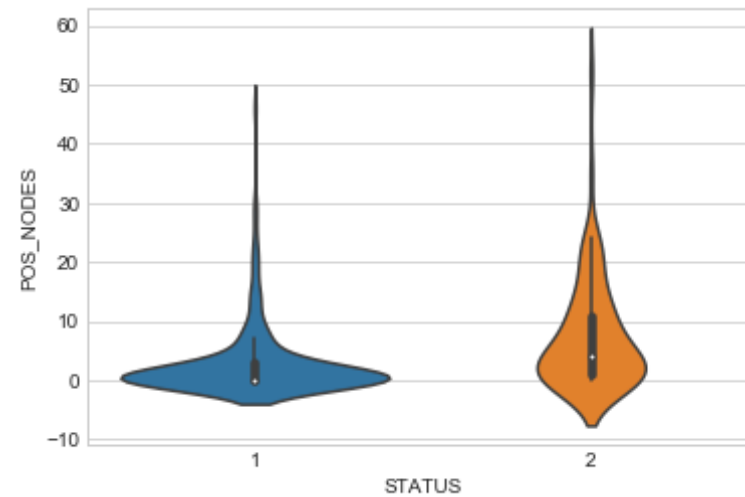
## BOX PLOT

```
In [81]: sea.boxplot(y='POS_NODES',x='STATUS',data=a)
plt.show()
```



## VIOLIN PLOT

```
In [82]: sea.violinplot(x='STATUS',y='POS_NODES',data=a,size=8)
plt.show()
```



OBSERVATION:-

1. The Plots tells us that 50% of points in class-2 are having auxillary nodes less than 5.
2. 75% of points in class-1 are having auxillary nodes less than 5.
3. The plot also tells us that if the value of positive auxillary nodes are greater than 7 then the patient will not survive.