Haberman_Survival_Data_Analysis_Model_1

July 3, 2018

1 Haberman's Survival Data Assignment

The Haberman's dataset contains cases from a study that was conducted between 1958 and 1970 at the University of Chicago's Billings Hospital on the survival of patients who had undergone surgery for breast cancer.

1.0.1 Attribute Information:

```
Age of patient at time of operation (numerical)
Patient's year of operation (year - 1900, numerical)
Number of positive axillary nodes detected (numerical)
Survival status (class attribute) 1 = the patient survived 5 years or longer 2 = the patient di
```

1.0.2 Objective :-

```
Find the model to classify the Patient Survival from the given attributes
```

```
In [1]: import pandas as pd
        import seaborn as sns
        import matplotlib.pyplot as plt
        import numpy as np
        '''Reading the Haberman's Data'''
        #Load haberman.csv into a pandas dataFrame.
        #To read the data from the specified convert the data file path from normal string to r
        Haber = pd.read_csv(r"C:\Users\TEJA\Desktop\DATA SCi\my work\habermans-survival-data-se
```

View the dataframe shape and colums details

```
In [2]: print (Haber.shape)
        print (Haber.columns)
```

```
(305, 4)
Index(['30', '64', '1', '1.1'], dtype='object')
```

```
In [3]: ### Adding headder to the Haber dataframe
        Haber.columns=["Age","Operation_year","axil_nodes","Surv_Status"]
```

```
In [4]: print (Haber.columns)
```

```
Index(['Age', 'Operation_year', 'axil_nodes', 'Surv_Status'], dtype='object')
```

```
In [5]: Haber.head(5)
```

```
Out[5]:    Age  Operation_year  axil_nodes  Surv_Status
        0   30              62           3            1
        1   30              65           0            1
        2   31              59           2            1
        3   31              65           4            1
        4   33              58          10            1
```

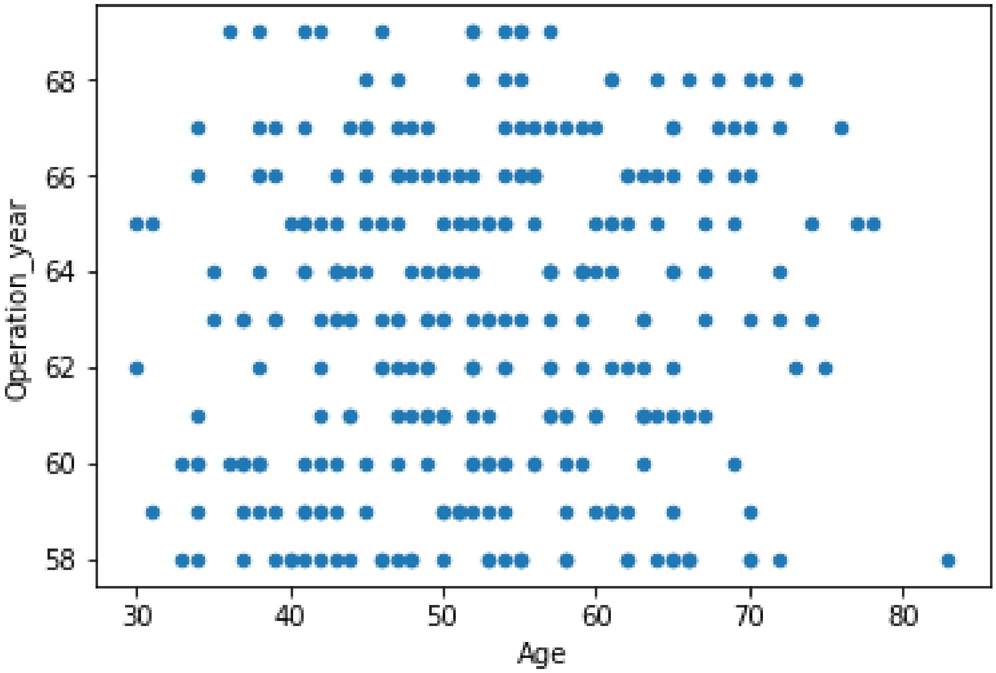
```
In [6]: Haber.describe()
```

```
Out[6]:               Age  Operation_year  axil_nodes  Surv_Status
        count  305.000000      305.000000  305.000000   305.000000
        mean    52.531148       62.849180    4.036066     1.265574
        std     10.744024        3.254078    7.199370     0.442364
        min     30.000000       58.000000    0.000000     1.000000
        25%     44.000000       60.000000    0.000000     1.000000
        50%     52.000000       63.000000    1.000000     1.000000
        75%     61.000000       66.000000    4.000000     2.000000
        max     83.000000       69.000000   52.000000     2.000000
```

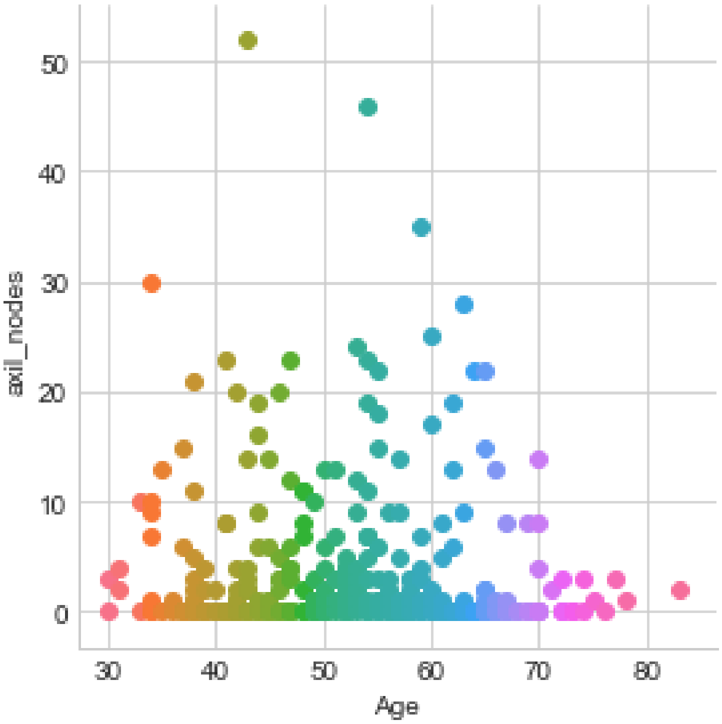
1.0.3 Observation :-

1.The Age tells us the Dataset is between the Age the age group (30-83) with an average age of
2.The Data set has been collected during the time priod (58-69) 12 years of data
3.The positive axillary nodes are ranging from (0-52) looking at the 75% value and the Max ther
data currepted
4.The survival status has only two values 1 and 2

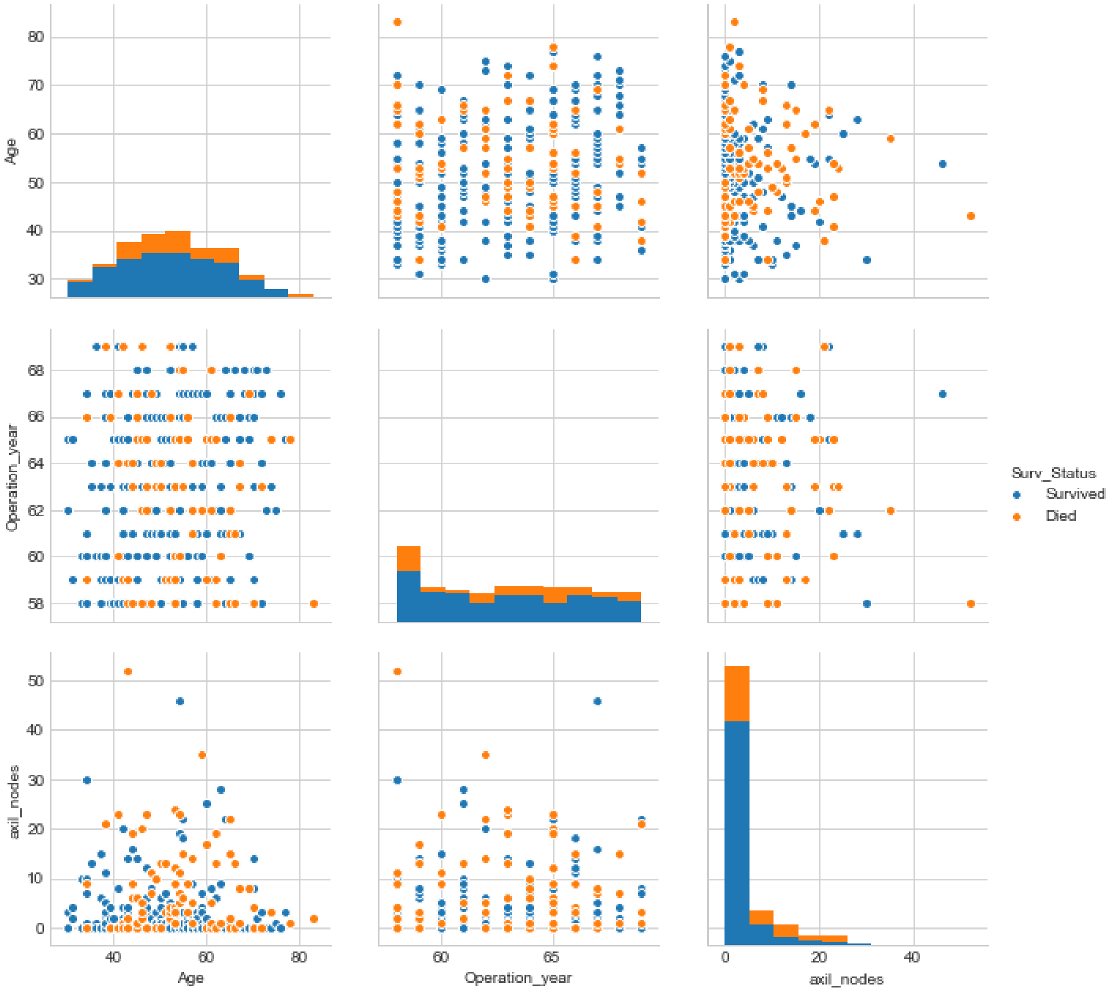
```
In [7]: Haber.plot(kind='Scatter',x='Age',y='Operation_year')
        plt.show()
```



```
In [8]: sns.set_style("whitegrid")
        sns.FacetGrid(Haber,hue='Age',size=4)\
          .map(plt.scatter,"Age","axil_nodes")
        plt.show()
```



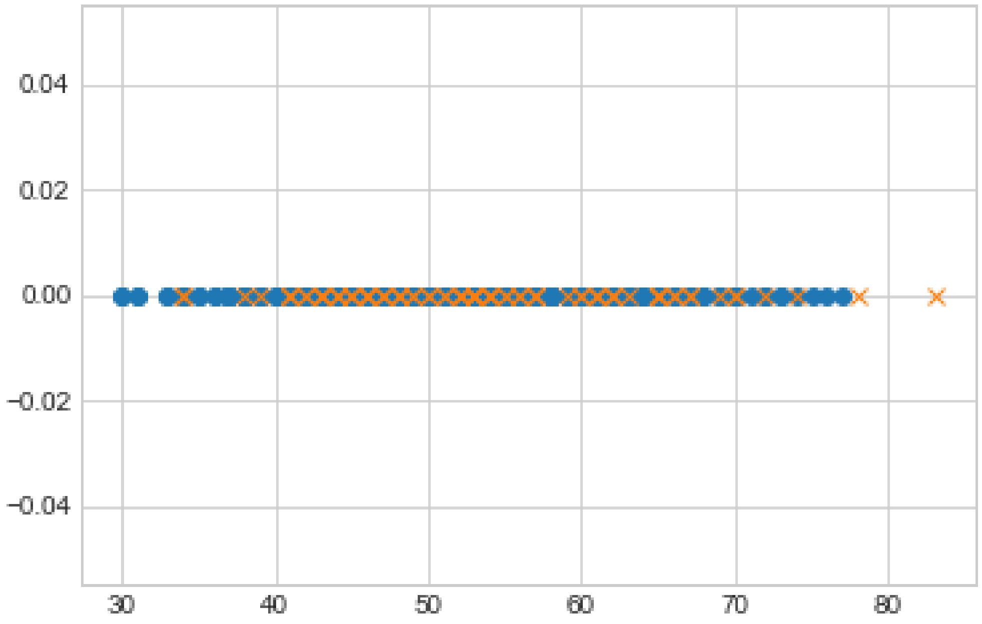
In [20]:
```
plt.close()
sns.set_style("whitegrid")
sns.pairplot(Haber,hue='Surv_Status',size=3)
Haber["Surv_Status"] = Haber["Surv_Status"].apply(lambda y: "Survived" if y == 1 else
plt.show()
```



1.0.4 Observation:

We are not able to clearly seperate the Survival catagory but looking at the axillary nodes plot graph it is showing some better classification

```
In [10]: import numpy as np
         Survive_long=Haber.loc[Haber["Surv_Status"] == "Survived"]
         Survive_short=Haber.loc[Haber["Surv_Status"] == "Died"]
         plt.plot(Survive_long["Age"],np.zeros_like(Survive_long['axil_nodes']),'o')
         plt.plot(Survive_short["Age"],np.zeros_like(Survive_short['axil_nodes']),'x')
         plt.show()
```



```
In [11]: Survive_long.describe()
```

```
Out[11]:              Age  Operation_year  axil_nodes
         count  224.000000      224.000000  224.000000
         mean    52.116071       62.857143    2.799107
         std     10.937446        3.229231    5.882237
         min     30.000000       58.000000    0.000000
         25%     43.000000       60.000000    0.000000
         50%     52.000000       63.000000    0.000000
         75%     60.000000       66.000000    3.000000
         max     77.000000       69.000000   46.000000
```

```
In [12]: Survive_short.describe()
```

```
Out[12]:             Age  Operation_year  axil_nodes
         count  81.000000       81.000000   81.000000
         mean   53.679012       62.827160    7.456790
         std    10.167137        3.342118    9.185654
         min    34.000000       58.000000    0.000000
         25%    46.000000       59.000000    1.000000
         50%    53.000000       63.000000    4.000000
         75%    61.000000       65.000000   11.000000
         max    83.000000       69.000000   52.000000
```

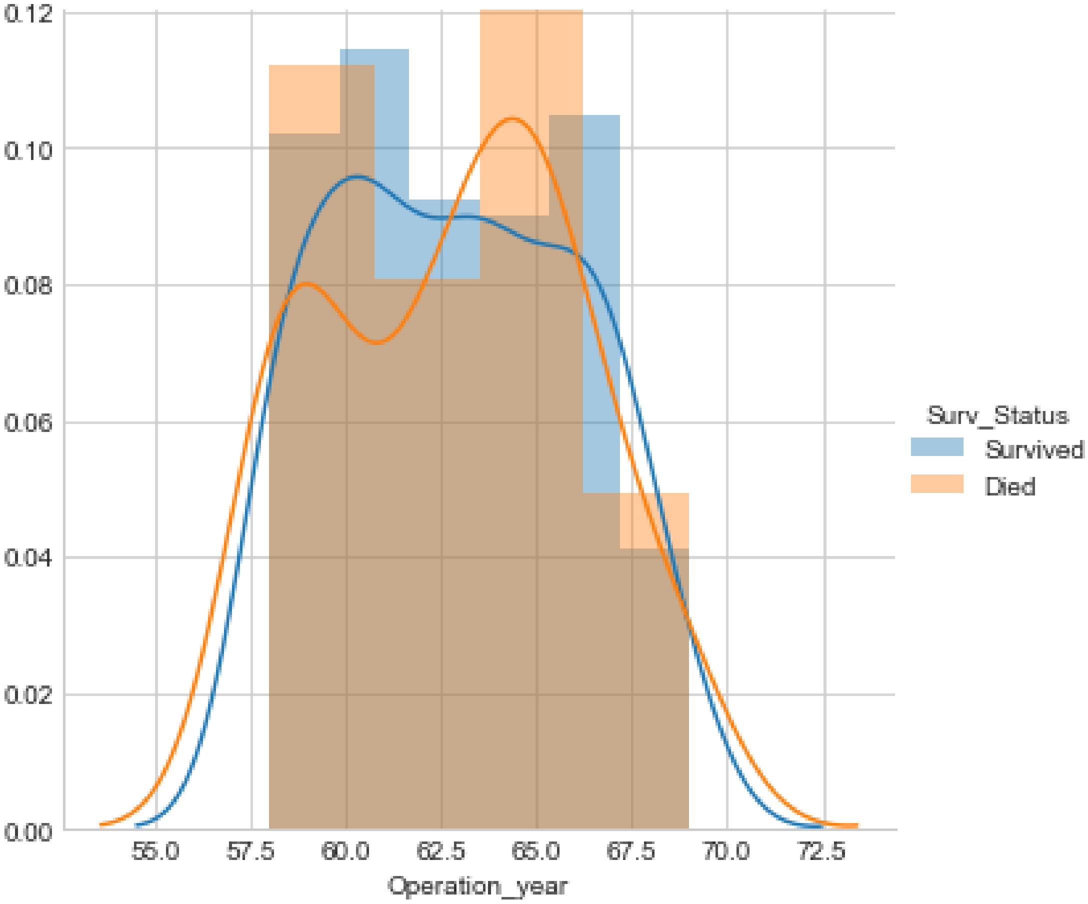
1.0.5 Observation :-

Looking at the data above we can clearly say that axillary nodes is much differed between the two catagories

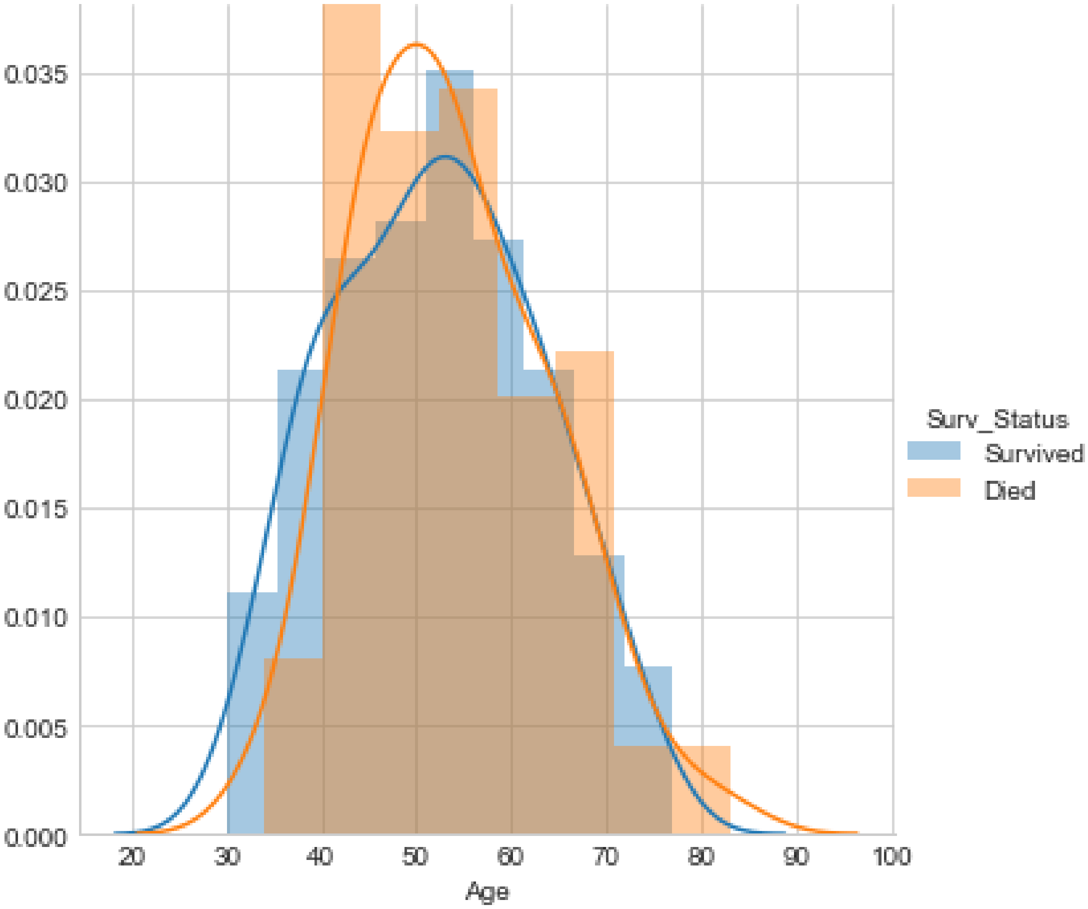
```
1.Though the Pactients survived long has the axillary nodes max as 46 25%-75% of the pactients
   rage of [0-3]   axillary nodes
2.The Pactients Survived short has the axillary nodes rage  [0-11] observing the the 25%-75%
```

We can Build a simple model on the axillary nodes to by if else codition to say all the patients with less than the 3 can Survive more than 5 years further we can look at the other attribute combinations to improvise our model

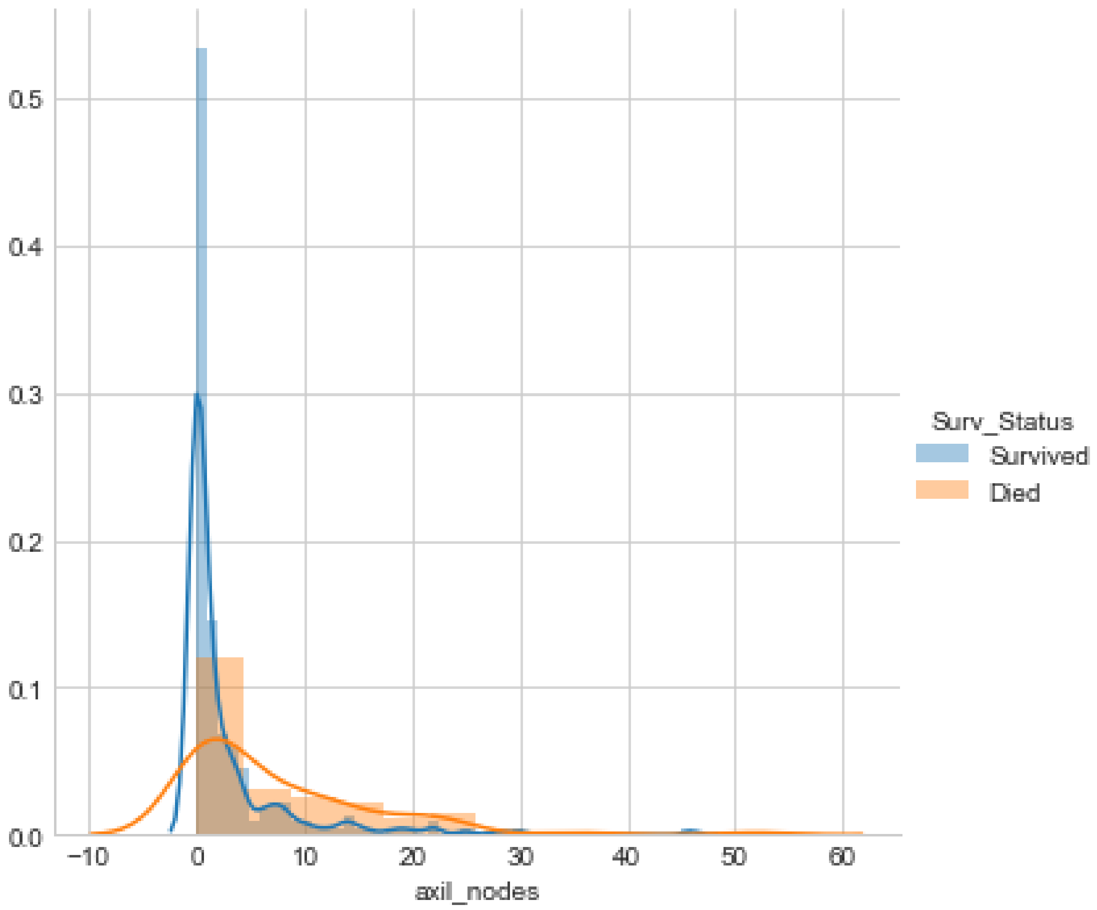
```
In [13]: sns.FacetGrid(Haber,hue="Surv_Status",size=5)\
             .map(sns.distplot,"Operation_year")\
             .add_legend()
         plt.show()
```



```
In [14]: sns.FacetGrid(Haber,hue="Surv_Status",size=5)\
             .map(sns.distplot,"Age")\
             .add_legend()
         plt.show()
```



```
In [15]: sns.FacetGrid(Haber,hue="Surv_Status",size=5)\
             .map(sns.distplot,"axil_nodes")\
             .add_legend()
         plt.show()
```

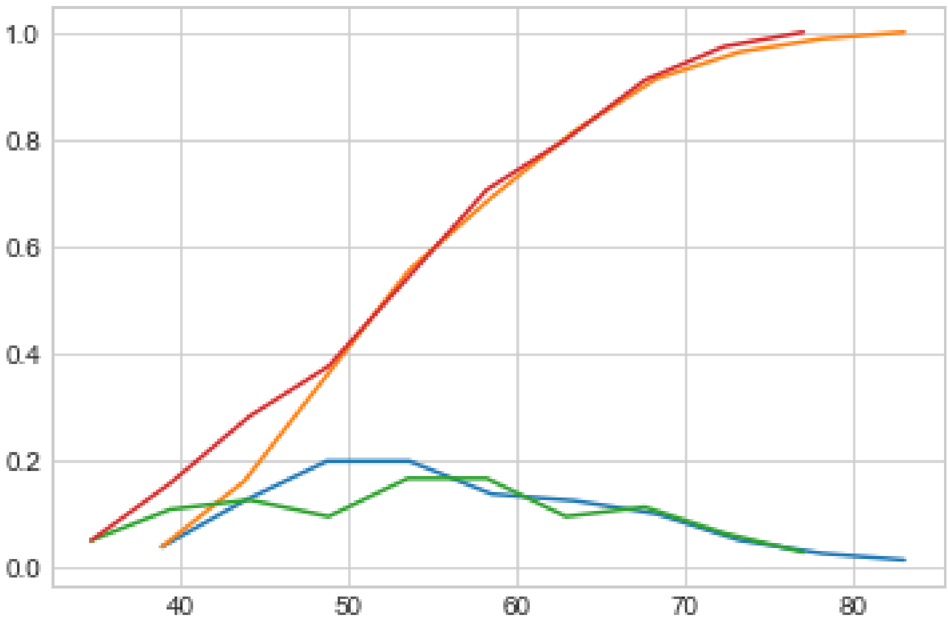


1.0.6 Observation:-

FacetGrid dosen't provide much information on the age and the operation year but by looking at the Axil nodes we can clearly say that the Survived percentage is high when the axil node value is some were between 0-5

```
In [16]: #Plot CDF of Survive_Status

         # Survive_short
         counts, bin_edges = np.histogram(Survive_short['Age'], 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)
         #Survive_long
         counts, bin_edges = np.histogram(Survive_long['Age'], 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();
```

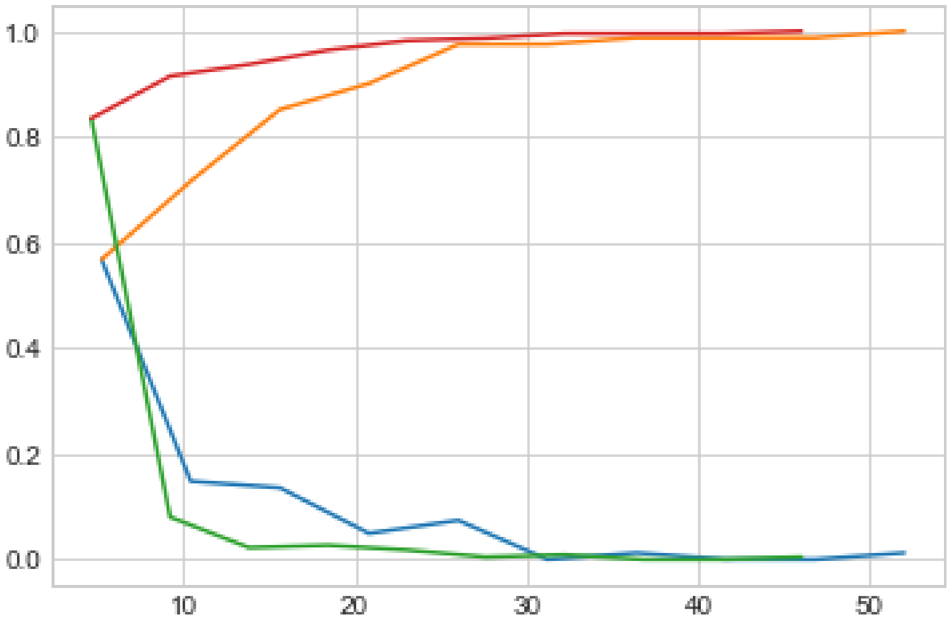
```
[0.03703704 0.12345679 0.19753086 0.19753086 0.13580247 0.12345679
 0.09876543 0.04938272 0.02469136 0.01234568]
[34.  38.9 43.8 48.7 53.6 58.5 63.4 68.3 73.2 78.1 83. ]
[0.04910714 0.10714286 0.125      0.09375    0.16517857 0.16517857
 0.09375    0.11160714 0.0625     0.02678571]
[30.  34.7 39.4 44.1 48.8 53.5 58.2 62.9 67.6 72.3 77. ]
```



```
In [17]: #Plot CDF of Survive_Status

         # Survive_short
         counts, bin_edges = np.histogram(Survive_short['axil_nodes'], bins=10,
                                          density = True)
         pdf = counts/(sum(counts))
```

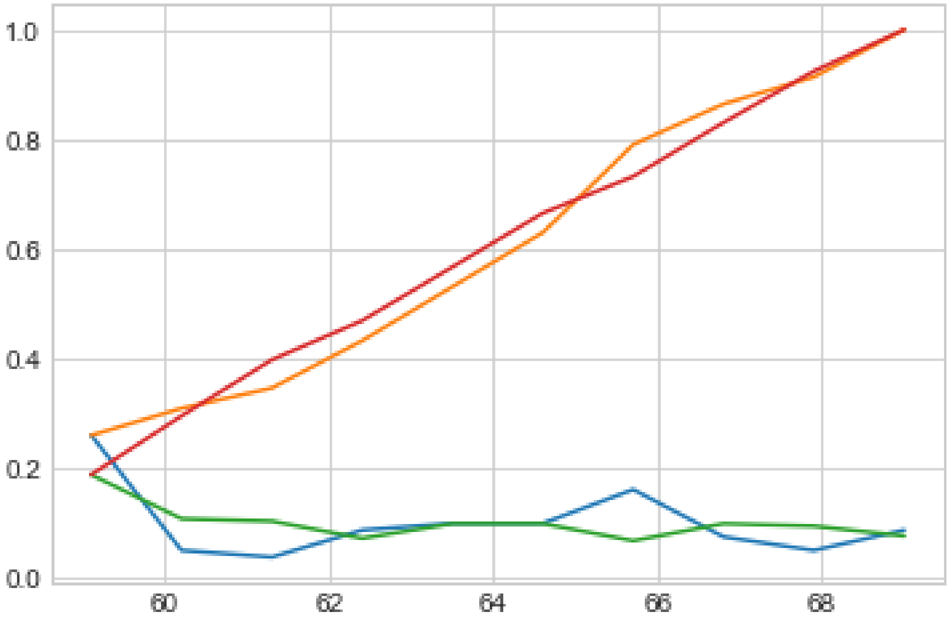
```
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


#Survive_long
counts, bin_edges = np.histogram(Survive_long['axil_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();
```

```
[0.56790123 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. ]
[0.83482143 0.08035714 0.02232143 0.02678571 0.01785714 0.00446429
 0.00892857 0.         0.         0.00446429]
[ 0.   4.6  9.2 13.8 18.4 23.  27.6 32.2 36.8 41.4 46. ]
```

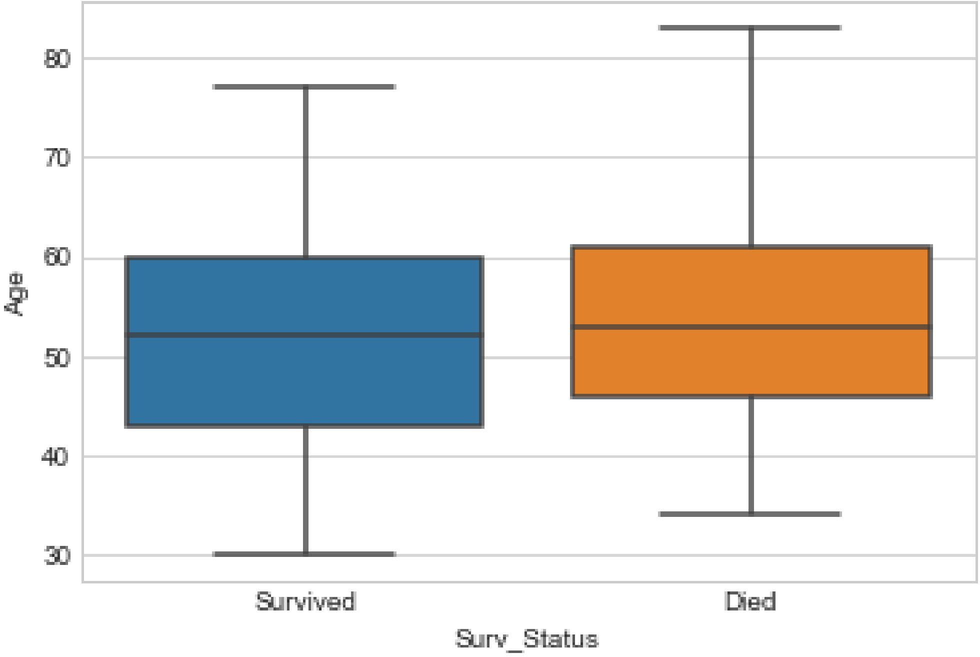


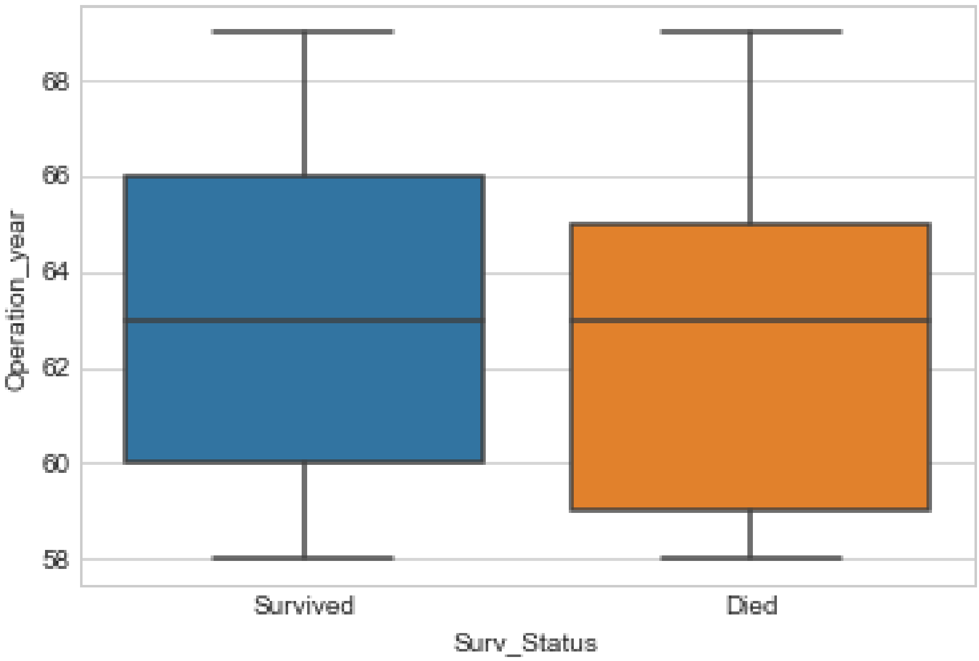
```
In [18]: # virginica
         counts, bin_edges = np.histogram(Survive_short['Operation_year'], bins=10,
                                          density = True)
         pdf = counts/(sum(counts))
         print(pdf);
         print(bin_edges)
         cdf = np.cumsum(pdf)
         plt.plot(bin_edges[1:],pdf)
         plt.plot(bin_edges[1:], cdf)


         #versicolor
         counts, bin_edges = np.histogram(Survive_long['Operation_year'], 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();
```

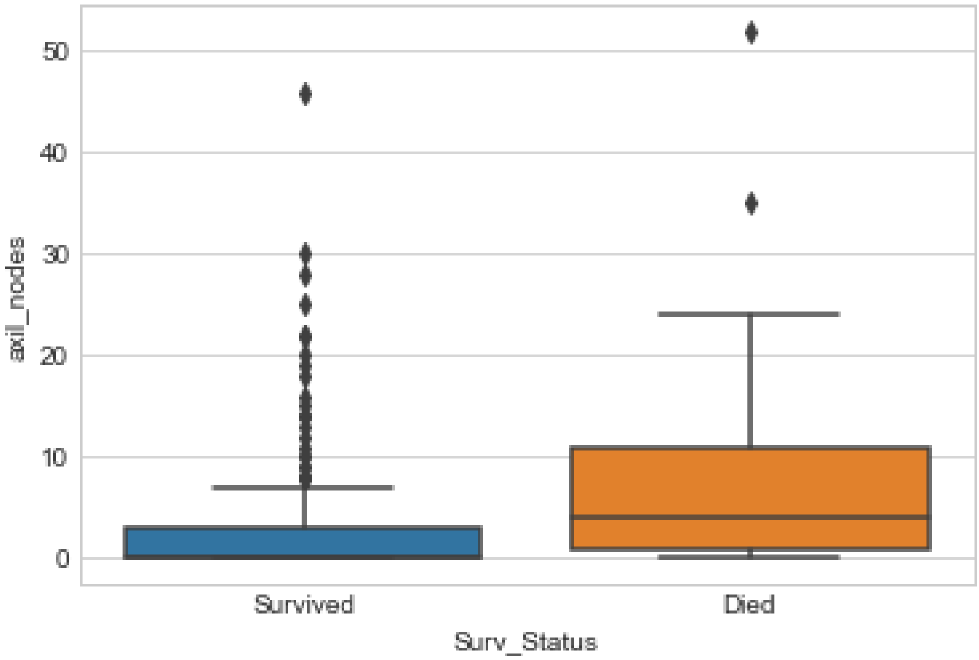
```
[0.25925926 0.04938272 0.03703704 0.08641975 0.09876543 0.09876543
 0.16049383 0.07407407 0.04938272 0.08641975]
[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
[0.1875     0.10714286 0.10267857 0.07142857 0.09821429 0.09821429
 0.06696429 0.09821429 0.09375    0.07589286]
[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
```



```
In [19]: sns.boxplot(x='Surv_Status',y='Age', data=Haber)
         plt.show()
         sns.boxplot(x='Surv_Status',y='Operation_year', data=Haber)
         plt.show()
         sns.boxplot(x='Surv_Status',y='axil_nodes', data=Haber)
         plt.show()
```







1.0.7 Observation:-

1.The patients treated after 1966 have higher chance to surive than the rest

```
2. Age group of 30 -34 are in the survived region
3.Age group of the 78-83 are in dead reagion
```

1.0.8 Final Thoughts:-

The Dataset is an imbalanced dataset and based on the observations we can build a model with the below conditions for chances of Survival and Non Survival

Survival :-

```
1.Axillary nodes value less than 3 Can  survive
2.Axillary nodes value less than 3 and treated after 1966 has higher chance to Survive
3.Axillary nodes value less than 3 and treated after 1966 and patient's with in the age less th
Can definitely Survive
```

Non Survival:-

```
1.Axillary nodes value grater than 3 chances of surviving  is less
2.Axillary nodes value grater than 3 and treated before 1966 has veryless chances of surviving
3.Axillary nodes value grater than 3 and treated before 1966 and patient's with age gretar than
definitely Can't Survive
```