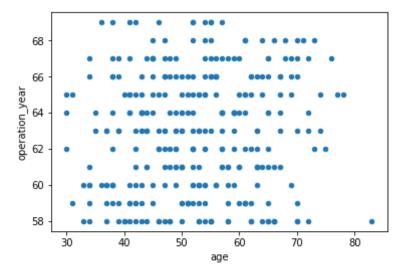
EXPLORATORY DATA ANALYSIS ON HABERMAN DATASET

Loading the dataset

```
In [9]: import pandas as pd
         import warnings
         warnings.filterwarnings("ignore")
         import seaborn as sns
         import numpy as np
         import matplotlib.pyplot as plt
In [10]: haberman = pd.read csv("haberman.csv")
In [12]: labels = [ 'age' , 'operation year' , 'axil nodes' , 'survive status']
         Adding labels to dataset
In [13]: haberman = pd.read csv("haberman.csv" , names = labels)
In [14]: haberman.head()
Out[14]:
            age operation_year axil_nodes survive status
                          64
                                    1
             30
             30
                          62
          2 30
                          65
```

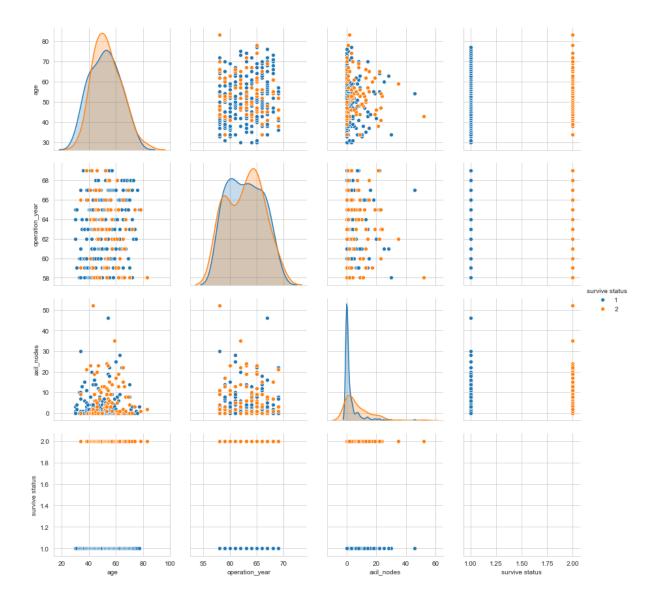
```
age operation_year axil_nodes survive status
          3 31
                         59
            31
In [16]: #Print data points and features
         print (haberman.shape)
         (306, 4)
In [17]: #column names
         print(haberman.columns)
         Index(['age', 'operation_year', 'axil_nodes', 'survive status'], dtype
         ='object')
In [18]: #How many data points
         haberman["survive status"].value_counts()
Out[18]: 1
              225
               81
         Name: survive status, dtype: int64
         SCATTER PLOT
In [19]: haberman.plot(kind = "scatter" , x= 'age' , y = 'operation year')
         plt.show()
```



The scatterplot seems very mixed and we cannot deduce anything from it.

PAIR PLOTS

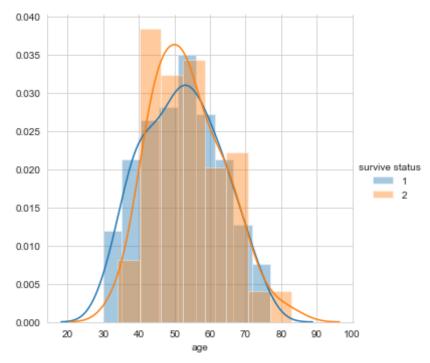
```
In [20]: plt.close();
    sns.set_style("whitegrid");
    sns.pairplot (haberman , hue = "survive status" , size =3)
    plt.show()
```



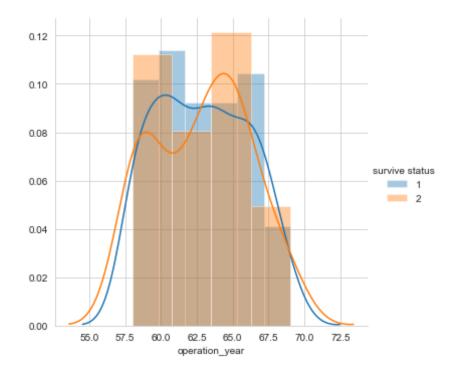
- 1. Age and operation year has effect on survival status
- 2. Axil node has effect on survival status.
- 3. There is also too much overlapping to understand the features.

UNIVARIATE ANALYSIS USING PDF

```
In [21]: sns.FacetGrid( haberman, hue= "survive status" , size = 5) \
    .map (sns.distplot , "age") \
    .add_legend();
plt.show()
```

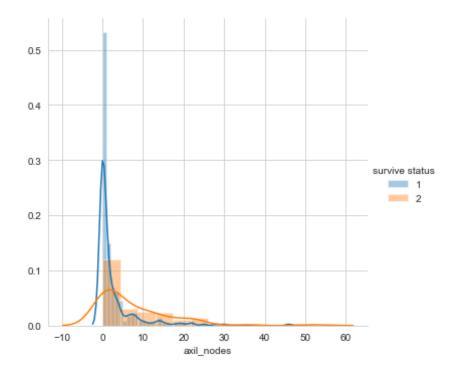


```
In [22]: sns.FacetGrid( haberman, hue= "survive status" , size = 5) \
    .map (sns.distplot , "operation_year") \
    .add_legend();
plt.show()
```



1. There is too much overlapping and it seems year of operations is not a useful feauture to determine status of patients.

```
In [23]: sns.FacetGrid( haberman, hue= "survive status" , size = 5) \
    .map (sns.distplot , "axil_nodes") \
    .add_legend();
plt.show()
```

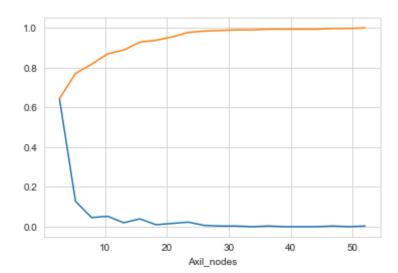


1. The PDF of all axil nodes for patients who survived more than 5 years is less than 0.

CDF PLOT

```
plt.plot(bin_edges[1:], cdf)
plt.xlabel('Axil_nodes')
plt.show()

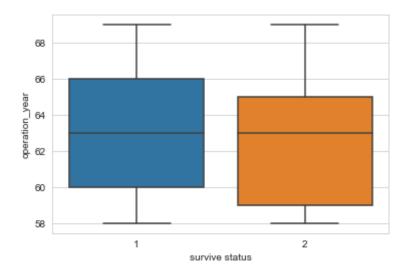
[0.64379085 0.12745098 0.04575163 0.05228758 0.01960784 0.03921569
```



- 1. Orange line determines the cdf of patients who survived for more than 5 years.
- 2. Blue line determine the pdf of pattients who survived for more than 5 years.
- 3. The patients above 46 axil nodes can be considered dead within 5 years.
- 4. People having less number of lymph node survived.

BOXPLOT

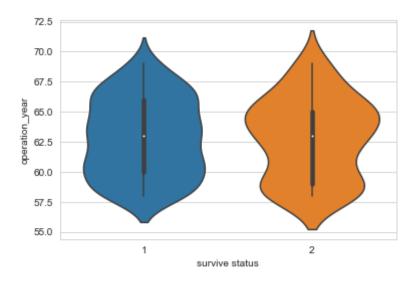
```
In [25]: sns.boxplot( x = 'survive status' , y ='operation_year', data = haberma
n)
plt.show()
```



VIOLIN PLOT

It is combination of boxplot and PDF

```
In [26]: sns.violinplot ( x = "survive status" , y = "operation_year", data =hab
    erman , size = 8)
    plt.show()
```



CONCLUSION

1. From BoxPlot and Violin Plot it is determined that number of patients have died between 46-62 and between 59-65. The patients who have survived have gae between 60-66.

FINAL CONCLUSION

- 1. Axil node is a major feauture to determine survival statud of patients.
- 2. The pair and scatter plots does not help in the distinguishing between the survial staus of patients.
- 3. People having less number of lymph nodes have survived for more than 5 years.