EDA-HabermanDataset

January 6, 2018

1 Exploratory Data analysis on HabermanDataset

1.1 Dataset Information:

```
Number of Instances: 306
Number of Attributes: 4 (including the class attribute)
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 died within 5 year
```

```
In [1]: import pandas as pd
        import seaborn as sns
        import matplotlib.pyplot as plt
        import numpy as np
```

```
In [2]: #download the data set from
        #https://www.kaggle.com/gilsousa/habermans-survival-data-set/data
        # load the data set
        haberman=pd.read_csv("haberman.csv")
```

```
In [3]: #  data-points and features
        print (haberman.shape)
```

```
(305, 4)
```

```
In [4]: #no column names mentioned in the data set. so will add headers to the columns.
        haberman.columns = ["Age","Year","Axillary nodes","Survival status"]
        print (haberman.columns)
```

```
Index(['Age', 'Year', 'Axillary nodes', 'Survival status'], dtype='object')
```

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

```
Out[5]:    Age  Year  Axillary nodes  Survival 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]: #how many patients are survived 5 years and more and how many died within 5years
        haberman["Survival status"].value_counts()
```

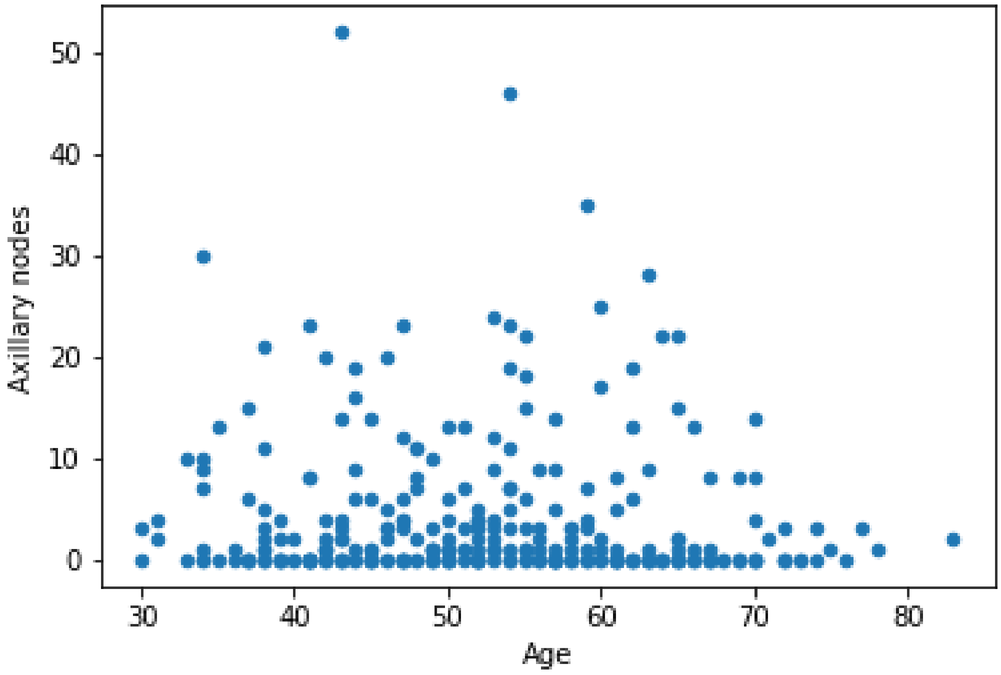
```
Out[6]: 1    224
        2     81
        Name: Survival status, dtype: int64
```

1.1.1 Obervation:

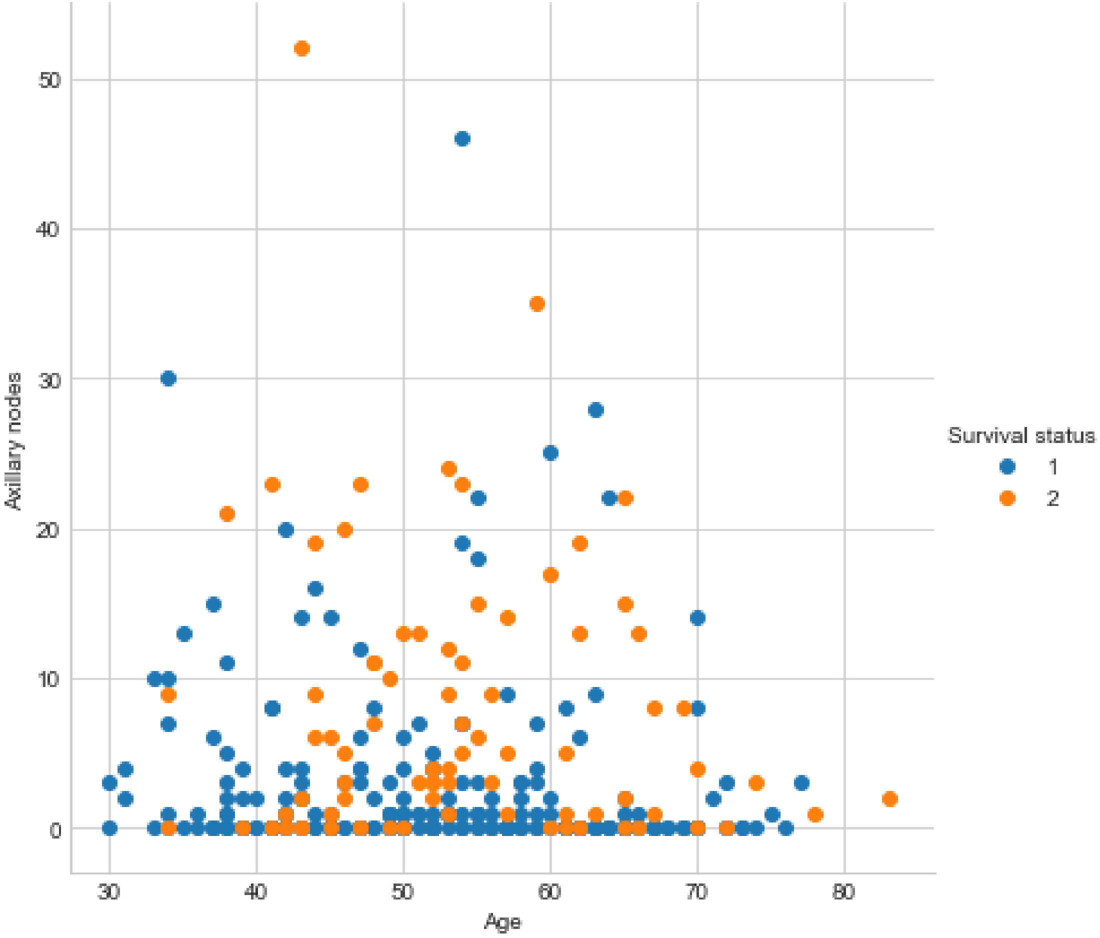
1. **Imbalanced** data set.
2. Clearly the data is not balanced as we have **224 patients survived more than 5 years and 81 patients died within 5 years**.

1.2 2-D ScatterPlot

```
In [7]: # lets plot plain scatter plot considering age and axillary nodes
        haberman.plot(kind='scatter', x='Age', y='Axillary nodes') ;
        plt.show()
```



```
In [8]: sns.set_style("whitegrid");
        sns.FacetGrid(haberman, hue="Survival status", size=6) \
           .map(plt.scatter, "Age", "Axillary nodes") \
           .add_legend();
        plt.show();
```

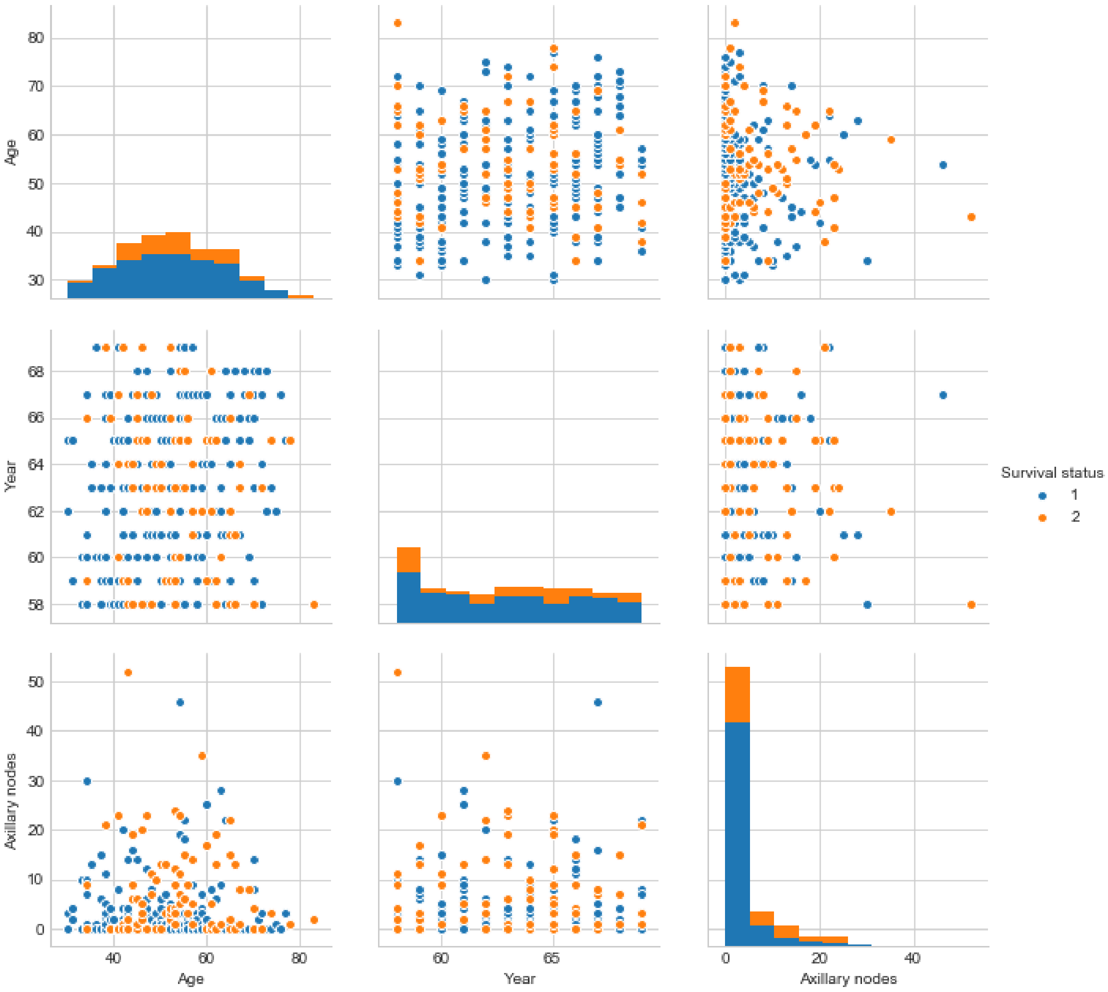


1.2.1 Observation:

1. It seems most of the patients have 0 Auxillary nodes detected.

1.3 Pair Plot

```
In [9]: plt.close();
        sns.set_style("whitegrid");
        sns.pairplot(haberman, hue="Survival status",
                     vars=['Age','Year','Axillary nodes'], size=3)
        plt.show()
        # The diagnol elements are PDFs for each feature.
```

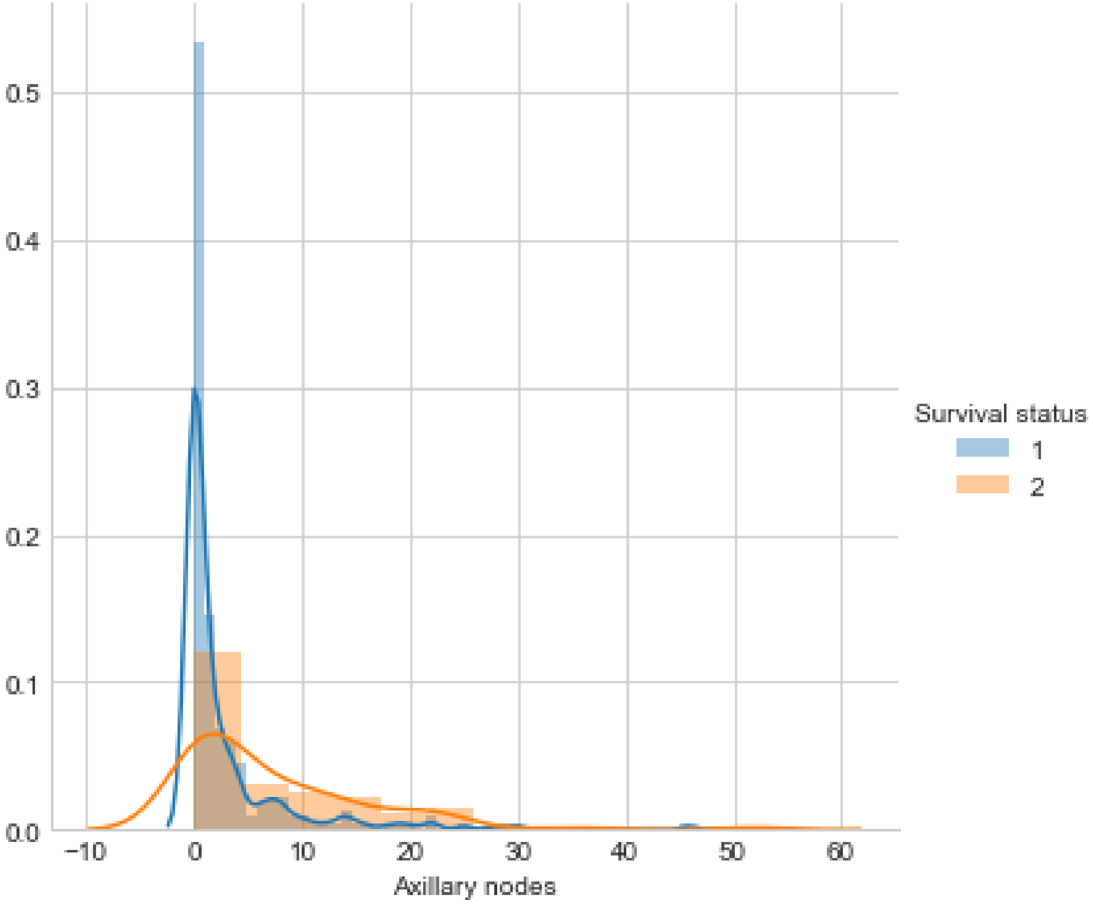


1.3.1 Observation:

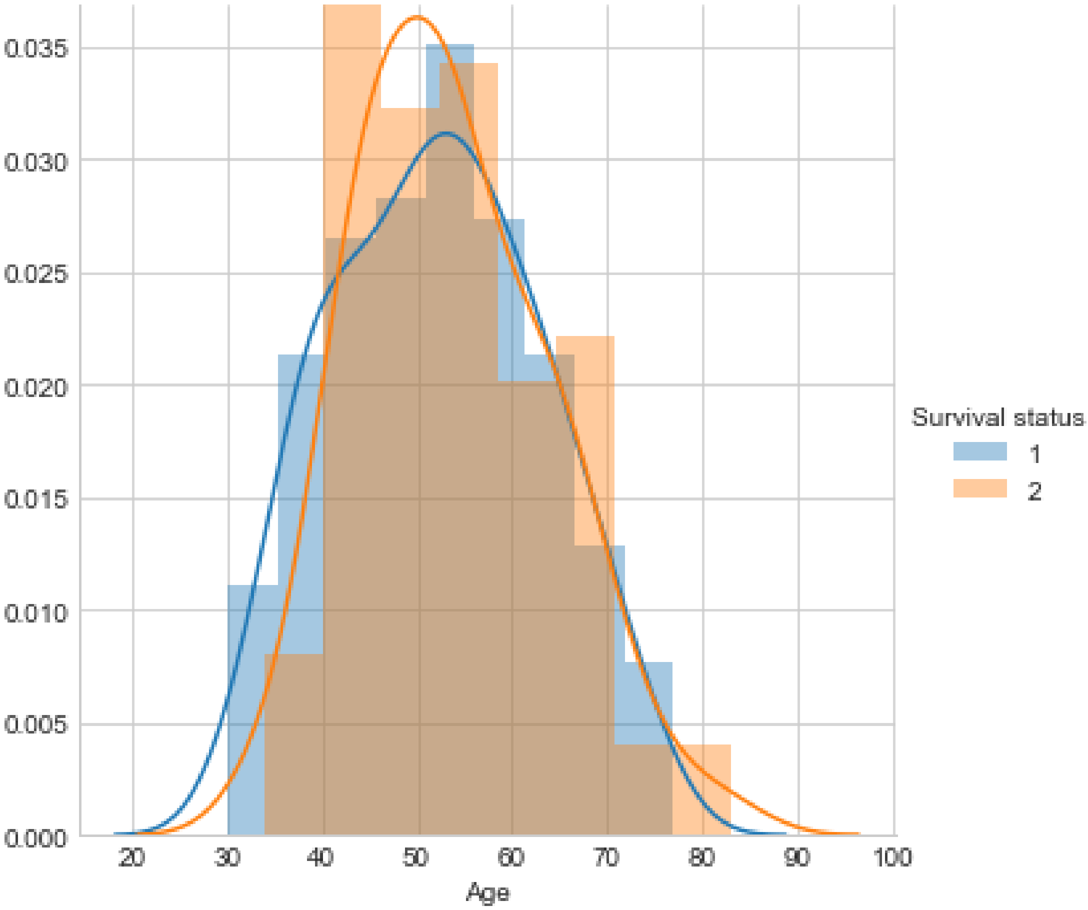
1. ***Auxillary nodes versus Age*** is the useful plot to atleast get the insight that most people who survived have 0 Auxillary nodes detected.
2. It looks like we cannot distinguish the data easily with the help of above scalar plots as most of them are ***overlapping***.

1.4 Histogram, PDF

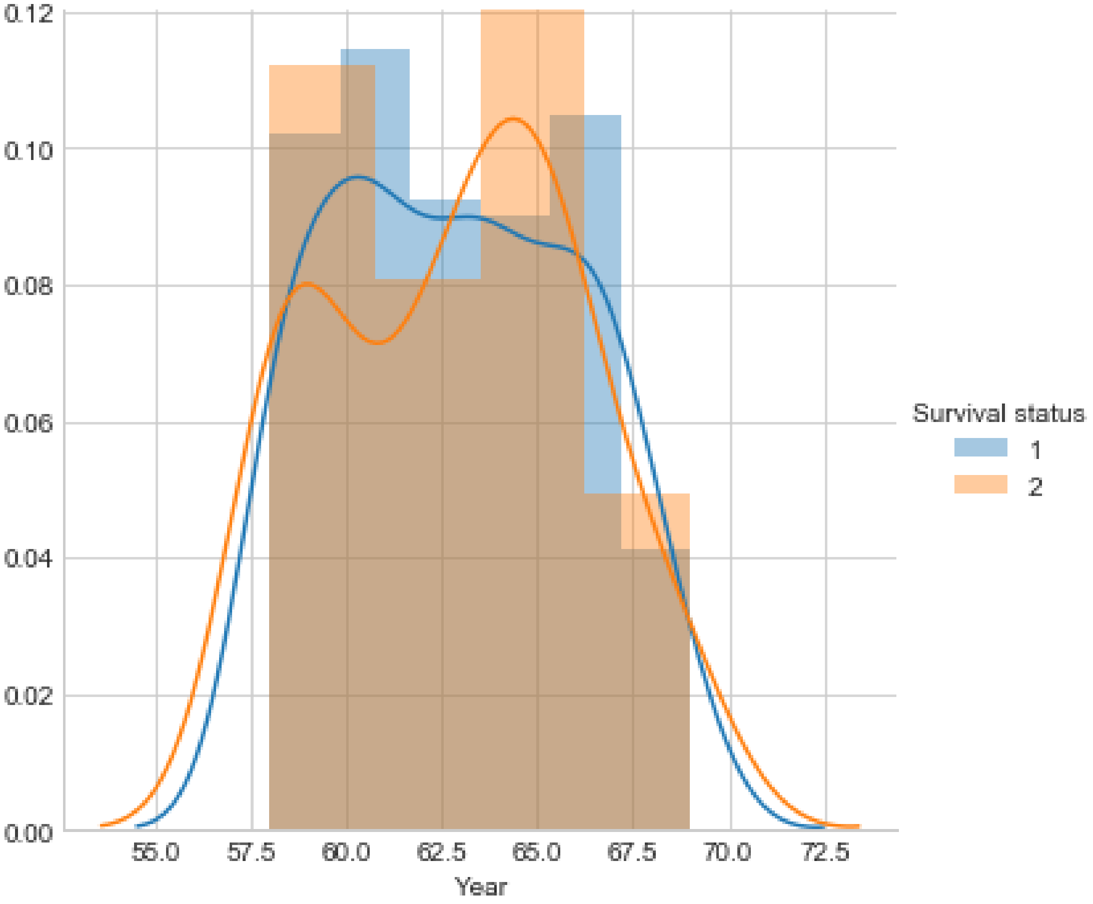
```
In [10]: sns.FacetGrid(haberman, hue="Survival status", size=5) \
             .map(sns.distplot, "Axillary nodes") \
             .add_legend();
         plt.show();
```



```
In [11]: sns.FacetGrid(haberman, hue="Survival status", size=5) \
            .map(sns.distplot, "Age") \
            .add_legend();
         plt.show();
```



```
In [12]: sns.FacetGrid(haberman, hue="Survival status", size=5) \
            .map(sns.distplot, "Year") \
            .add_legend();
         plt.show();
```



1.4.1 Observation:

1. From the above PDFS(Univariate analysis) both Age and Year are not good features for useful insights as the **distibution is more similar for both people who survived and also dead**.

2. **axillary nodes** is the only feature that is useful to know the survival status of patients as there is difference between the distributions for both classes(labels). From that distibution we can infer that **most survival patients have fall in to zero axillary nodes**.

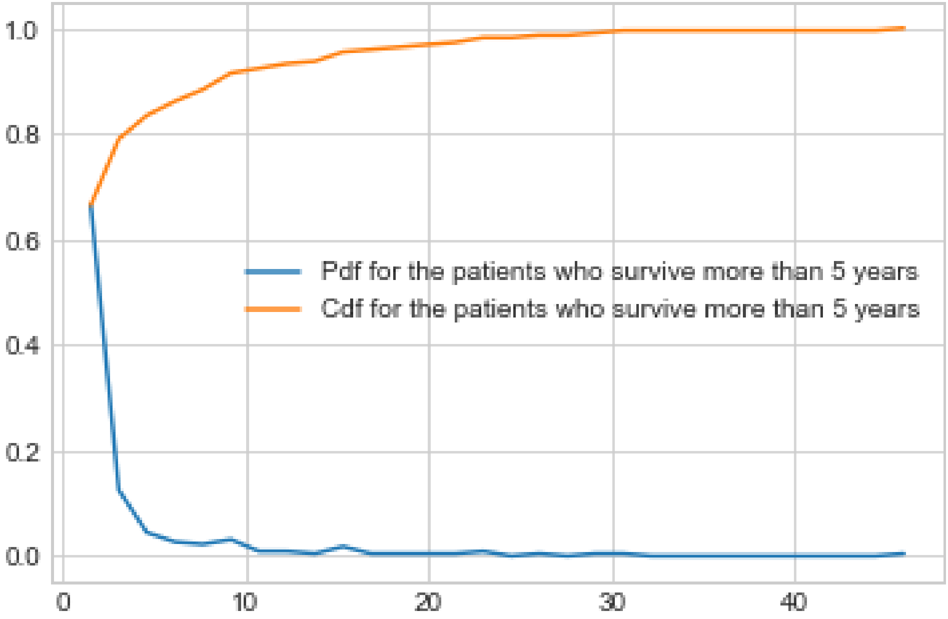
3. From the year distribution, we can observe that people who didnt survive suddenly fall and rise in between 1958 and 1960. lets check the summary statistics to get more insights.

2 CDF

```
In [13]: #divide the data set in two according to the label Survival status
         # alive means status=1 and dead means status =2
         alive=haberman.loc[haberman["Survival status"]==1]
         dead=haberman.loc[haberman["Survival status"]==2]
```

```
In [14]: counts, bin_edges = np.histogram(alive['Axillary nodes'], bins=30,
                                          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.legend(['Pdf for the patients who survive more than 5 years',
                     'Cdf for the patients who survive more than 5 years'])
         plt.show()
```

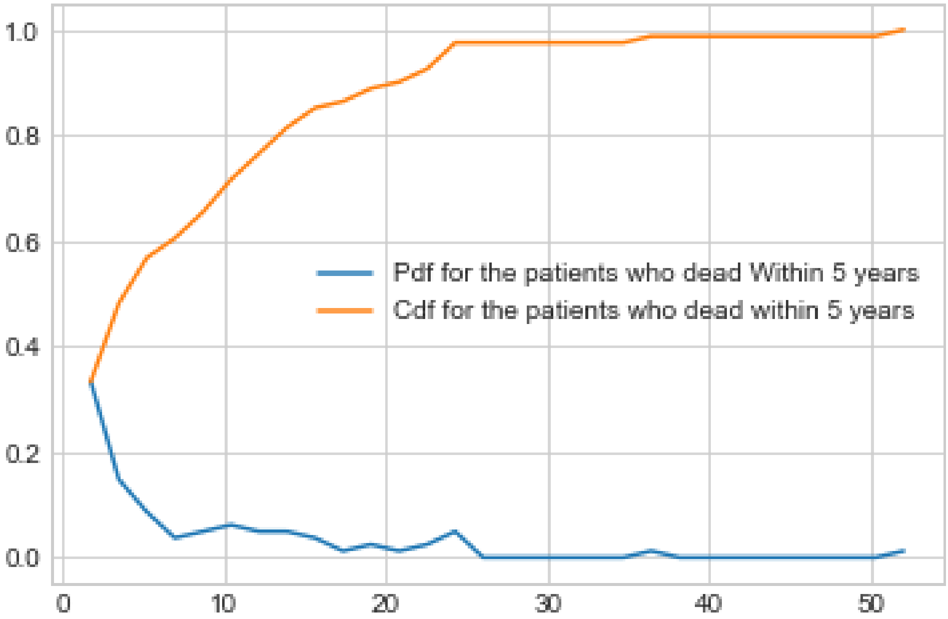
```
[ 0.66517857  0.125       0.04464286  0.02678571  0.02232143  0.03125
  0.00892857  0.00892857  0.00446429  0.01785714  0.00446429  0.00446429
  0.00446429  0.00446429  0.00892857  0.          0.00446429  0.
  0.00446429  0.00446429  0.          0.          0.          0.          0.
  0.          0.          0.          0.          0.00446429]
[  0.           1.53333333   3.06666667   4.6          6.13333333
   7.66666667   9.2         10.73333333  12.26666667  13.8         15.33333333
  16.86666667  18.4         19.93333333  21.46666667  23.         24.53333333
  26.06666667  27.6         29.13333333  30.66666667  32.2        33.73333333
  35.26666667  36.8         38.33333333  39.86666667  41.4        42.93333333
  44.46666667  46.        ]
```



```
In [15]: counts, bin_edges = np.histogram(dead['Axillary nodes'], bins=30, 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.legend(['Pdf for the patients who dead Within 5 years',
                     'Cdf for the patients who dead within 5 years'])
         plt.show()
```

```
[ 0.33333333  0.14814815  0.08641975  0.03703704  0.04938272  0.0617284
  0.04938272  0.04938272  0.03703704  0.01234568  0.02469136  0.01234568
  0.02469136  0.04938272  0.          0.          0.          0.          0.
  0.          0.01234568  0.          0.          0.          0.          0.
  0.          0.          0.          0.01234568]
[  0.           1.73333333   3.46666667   5.2          6.93333333
   8.66666667  10.4         12.13333333  13.86666667  15.6         17.33333333
  19.06666667  20.8         22.53333333  24.26666667  26.          27.73333333
  29.46666667  31.2         32.93333333  34.66666667  36.4         38.13333333
  39.86666667  41.6         43.33333333  45.06666667  46.8         48.53333333
  50.26666667  52.        ]
```



```
In [16]: # check also summary statistics below to get an idea to distinguish the
         #survival and not survival
```

3 Mean, Variance and Std-dev

```
In [17]: print("Summary Statistics of Patients who are alive for more than 5 years:")
         alive.describe()
```

```
Summary Statistics of Patients who are alive for more than 5 years:
```

```
Out[17]:              Age        Year  Axillary nodes  Survival status
         count  224.000000  224.000000      224.000000            224.0
         mean    52.116071   62.857143        2.799107              1.0
         std     10.937446    3.229231        5.882237              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 [18]: print("Summary Statistics of Patients who are dead within 5 years:")
         dead.describe()
```

```
Summary Statistics of Patients who are dead within 5 years:
```

```
Out[18]:             Age       Year  Axillary nodes  Survival 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
         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
```

3.0.1 Observations:

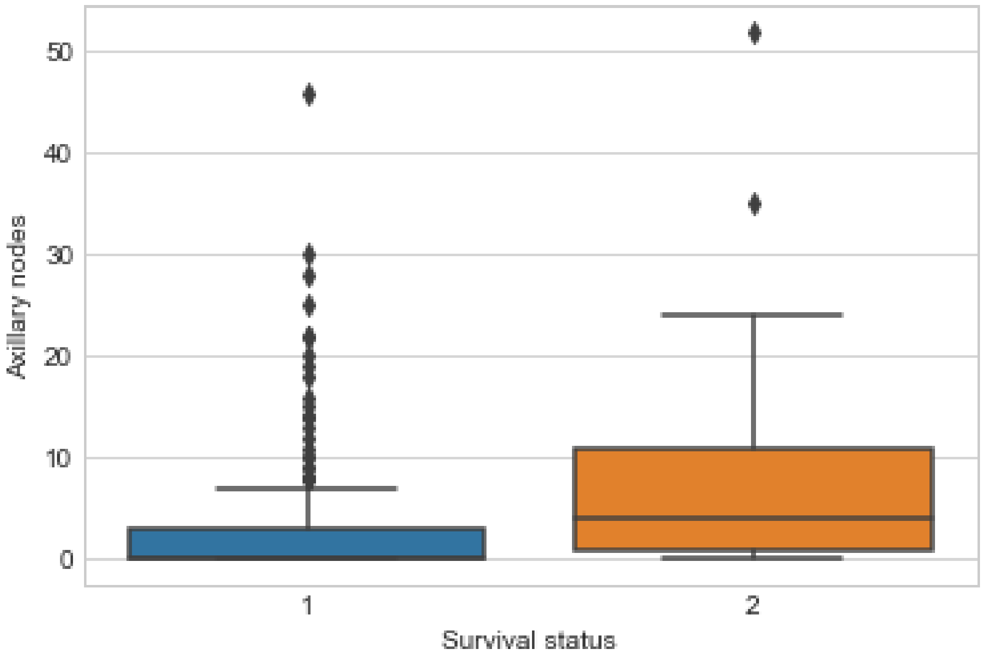
1. From both the tables we can observe that almost for all the features the statistics are **similar except for Axillary nodes**.

2. The **auxillary nodes mean(average) is more** for people who died within 5 years than people who live more than 5 years

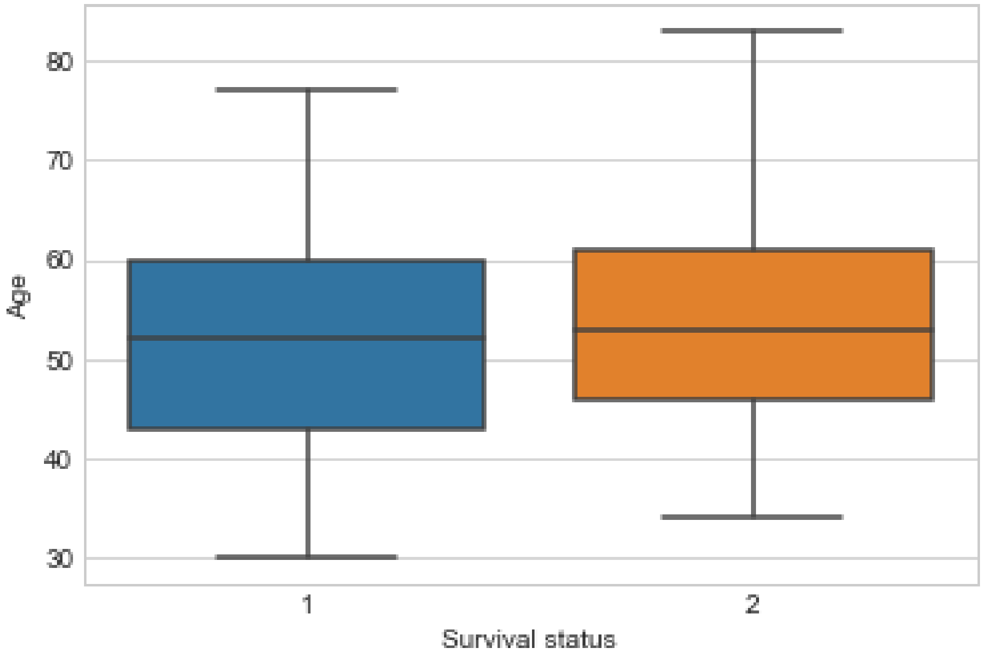
3. From the observation of Cdfs, we can infer that patients **above 46 axillary nodes detected** can be considered as dead within 5 years.

4 Box plot and Whiskers

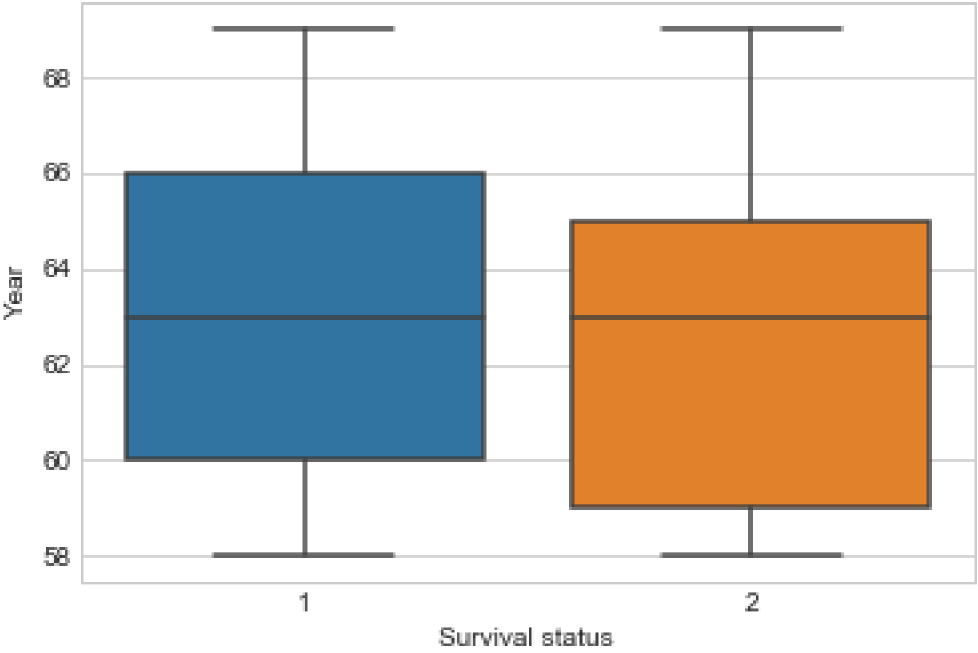
```
In [19]: sns.boxplot(x='Survival status',y='Axillary nodes', data=haberman)
         plt.show()
```



```
In [20]: sns.boxplot(x='Survival status',y='Age', data=haberman)
         plt.show()
```

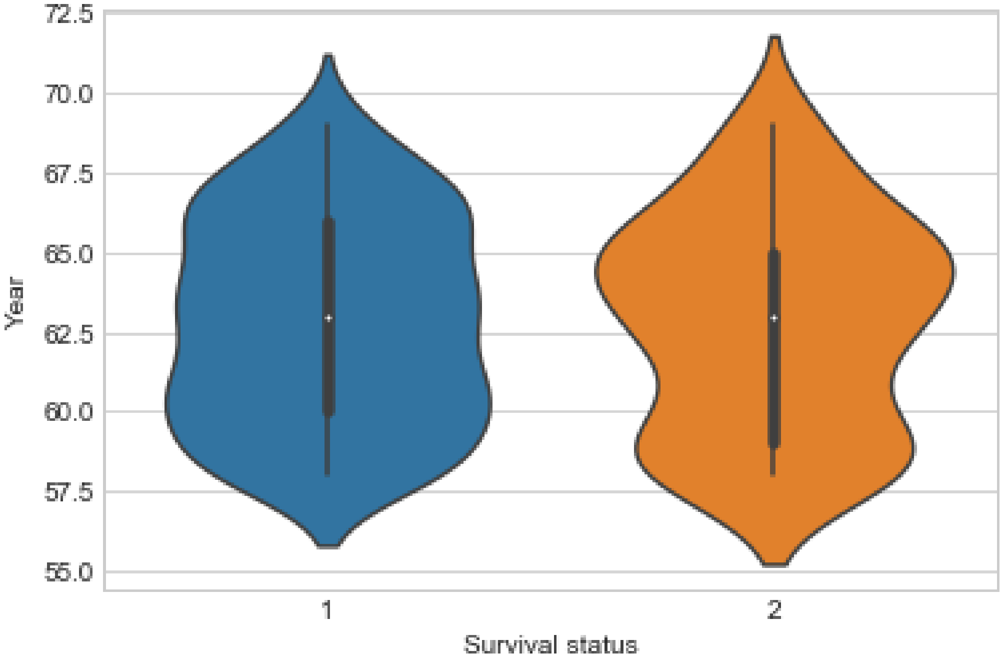


```
In [21]: sns.boxplot(x='Survival status',y='Year', data=haberman)
         plt.show()
```

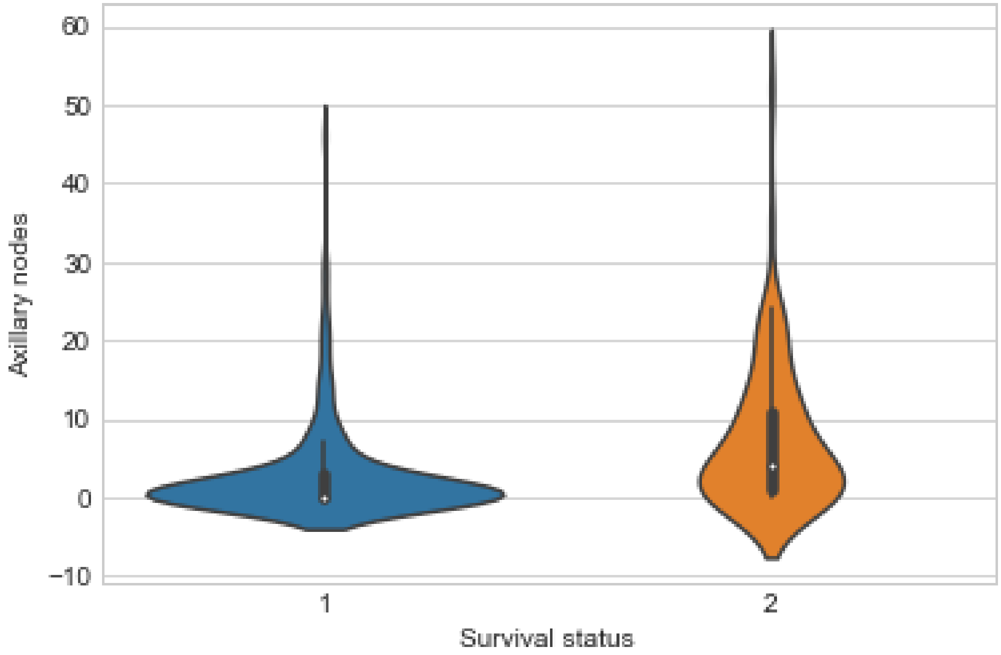


4.1 Violin plots

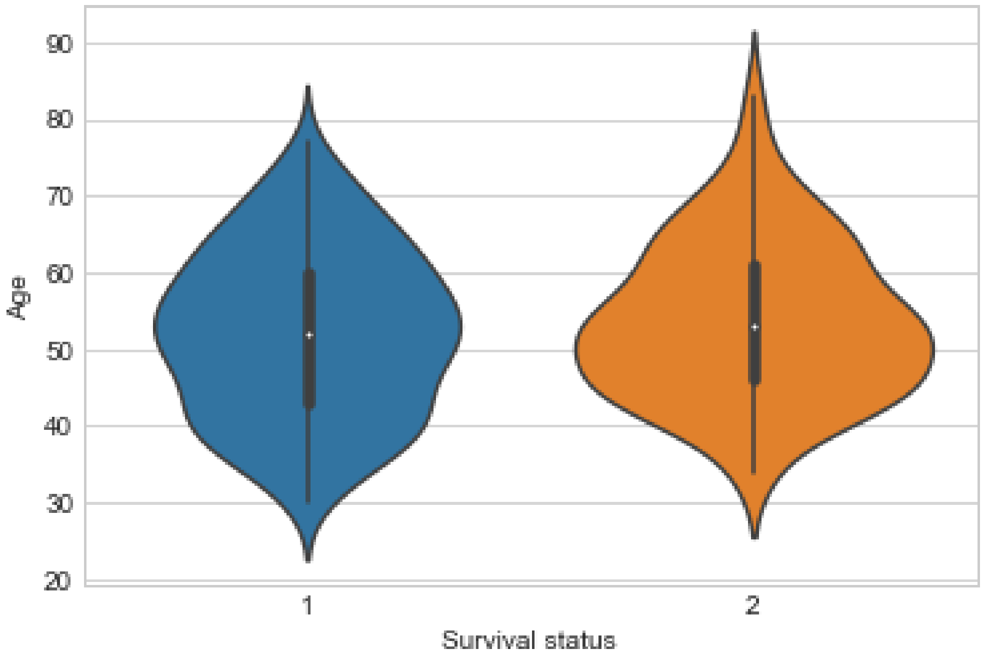
```
In [22]: # Denser regions of the data are fatter, and sparser ones thinner
         #in a violin plot

         sns.violinplot(x='Survival status',y='Year', data=haberman,size=8)
         plt.show()
```



```
In [23]: sns.violinplot(x='Survival status',y='Axillary nodes', data=haberman,size=8)
         plt.show()
```



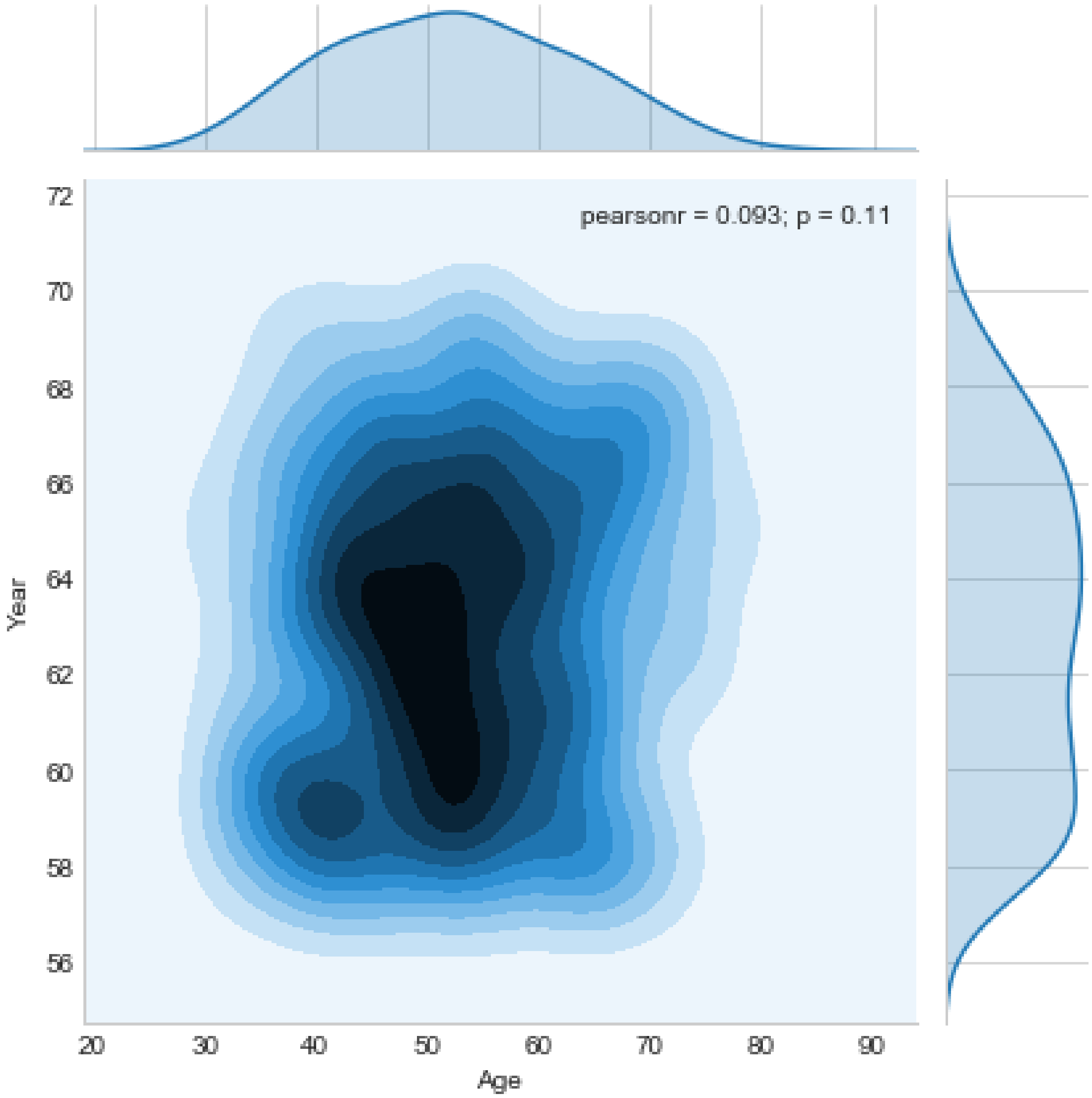
```
In [24]: sns.violinplot(x='Survival status',y='Age', data=haberman,size=8)
         plt.show()
```



4.1.1 Observation:

1. From box,violin plots we can say that more no of patients who are dead have **age between 46-62,year between 59-65** and the patients who survived have **age between 42-60, year between 60-66**.

```
In [25]: # contors-plot
         sns.jointplot(x="Age", y="Year", data=haberman, kind="kde");
         plt.show();
```


pearsonr = 0.093; p = 0.11
72
70
68
66
64
62
60
58
56
Year
20
30
40
50
60
70
80
90
Age