Haberman_EDA

October 18, 2018

1 Exploratory Data Analysis on Haberman Dataset

1.1 About Dataset

The 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.

1.2 Load Dataset

```
In [43]: import pandas as pd
         import numpy as np
         import matplotlib.pyplot as plt
         import seaborn as sns

         import warnings
         warnings.filterwarnings("ignore")


         #load "Haberman" dataset into pandas dataframe
         haberman = pd.read_csv("haberman.csv")

         # no. of datapoints
         print("Number of datapoints are : ", haberman.shape[0])

         # no. of features
         print("Number of features are : ", haberman.shape[1])

         # column names in dataset
         print("The column names are : ", haberman.columns)
```

```
Number of datapoints are :  306
Number of features are :  4
The column names are :  Index(['Age', 'Year of operation', 'axillary nodes', 'Survival status']
```

Observations : 1. There are total 306 number of instances 2. There are 3 features with one class label 3. The different features are - 'age', 'axillary nodes' and 'year of operation' 4. The class label is 'survival status'

```
In [44]: # top 5 dataset
         print("Top 5 data points in the dataset")
         print("-------------------------------------------------")
         print(haberman.head(5))
```

```
Top 5 data points in the dataset
-------------------------------------------------
   Age  Year of operation  axillary nodes  Survival 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 [45]: # datapoints for each class
         haberman["Survival status"].value_counts()
```

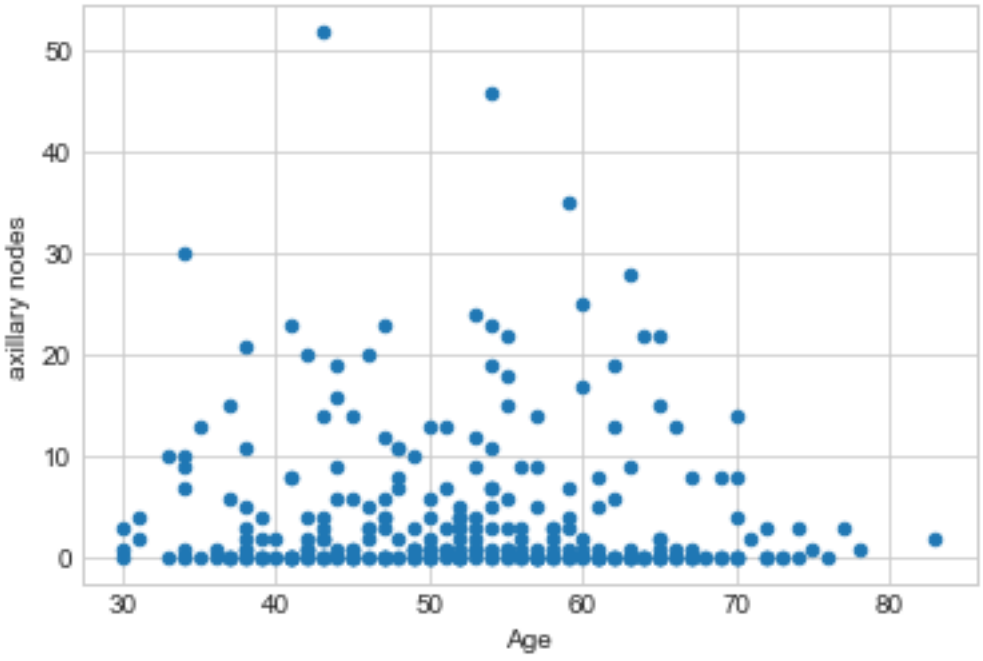
```
Out[45]: 1    225
         2     81
         Name: Survival status, dtype: int64
```

Observations : 1. All 3 features are numerical 2. Class label is also numerical 3. Dataset has imbalanced data

1.2.1 2D Scatter Plot

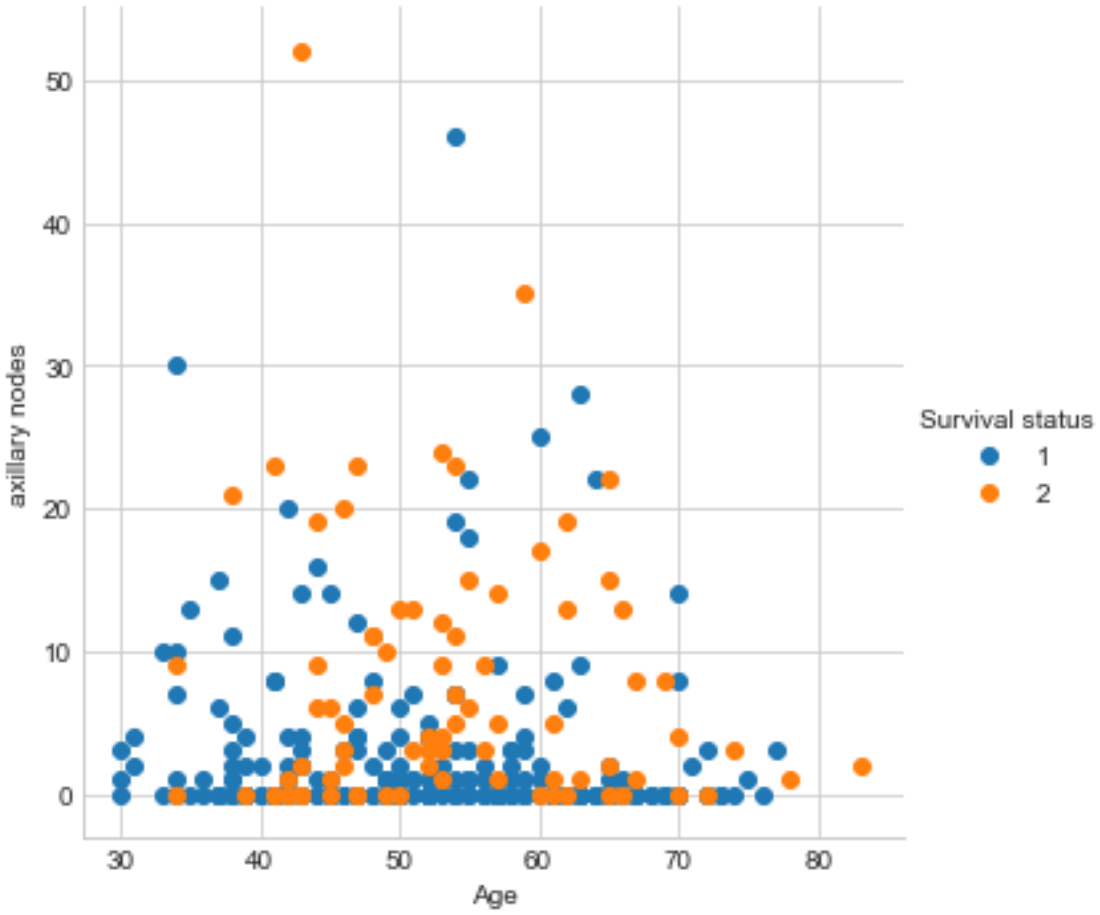
```
In [46]: # 2D Scatter Plot
         haberman.plot(kind='scatter', x='Age', y='axillary nodes')
```

```
Out[46]: <matplotlib.axes._subplots.AxesSubplot at 0x2068815fcc0>
```



Observation : Cannot observe clearly in this plot

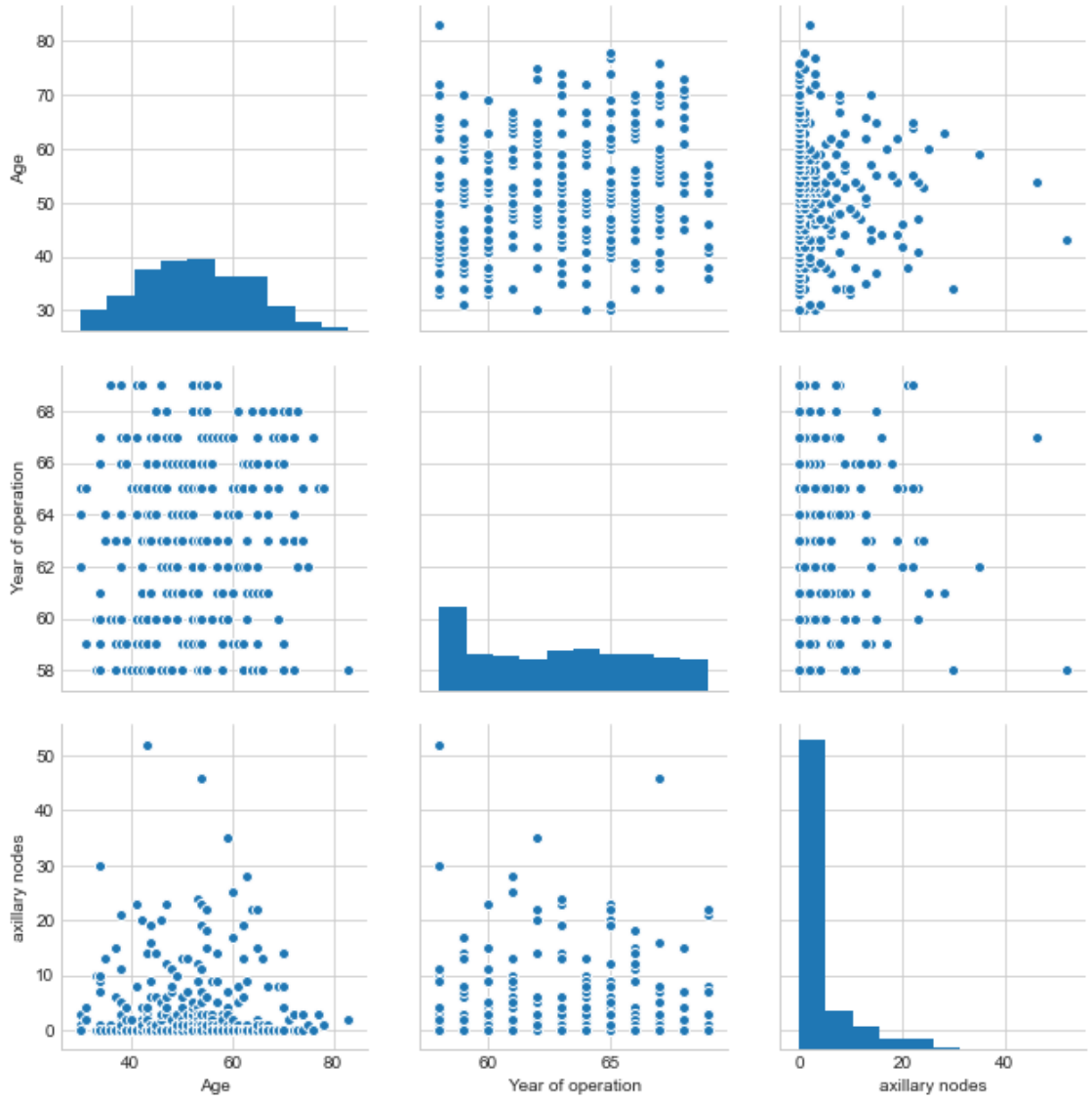
```
In [47]: # Scatter plot with coloring
         sns.set_style("whitegrid")
         sns.FacetGrid(haberman, hue="Survival status", size=5)  \
            .map(plt.scatter, "Age", "axillary nodes") \
            .add_legend();
         plt.show()
```



Observation : Even colored scatter plot also not much informative

1.2.2 3D Scatter Plot

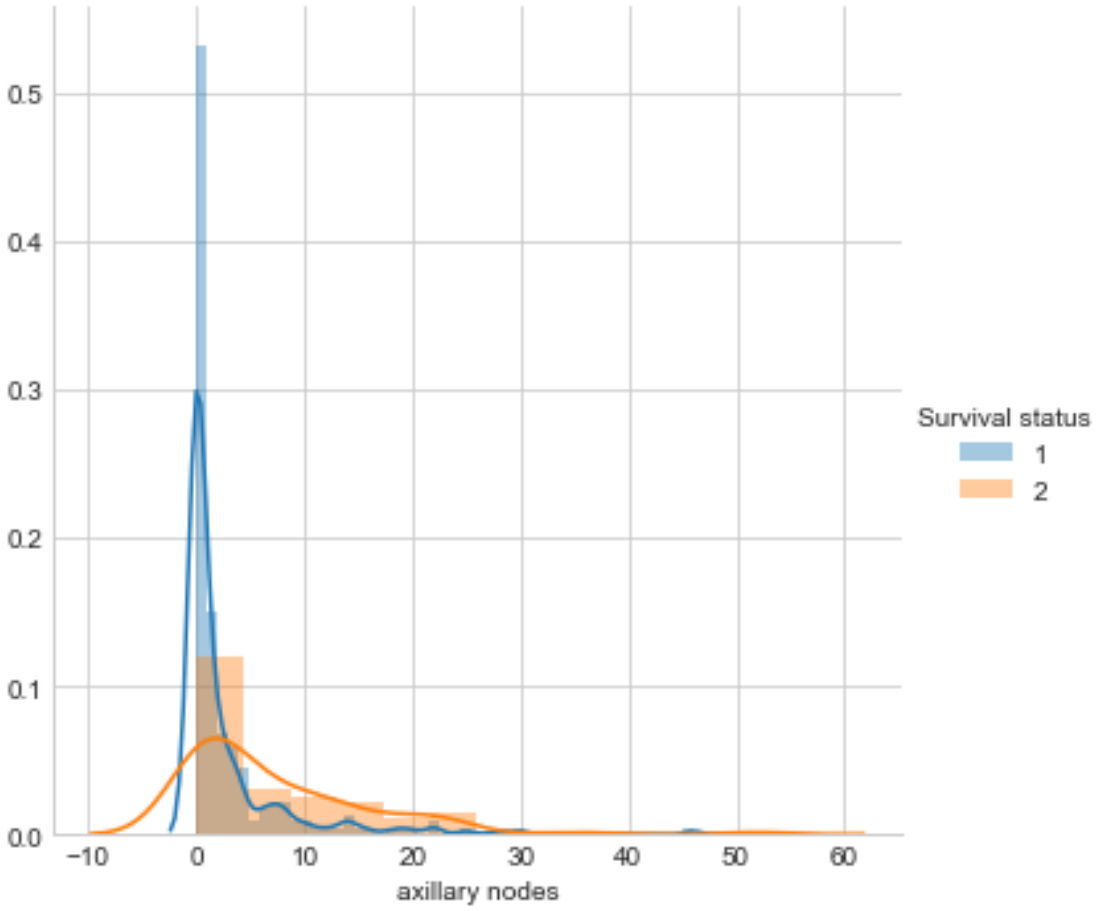
```
In [48]: haberman_features = haberman[haberman.columns[0:3]]
         plt.close()
         sns.set_style("whitegrid")
         sns.pairplot(haberman_features, size=3);
         plt.show()
```



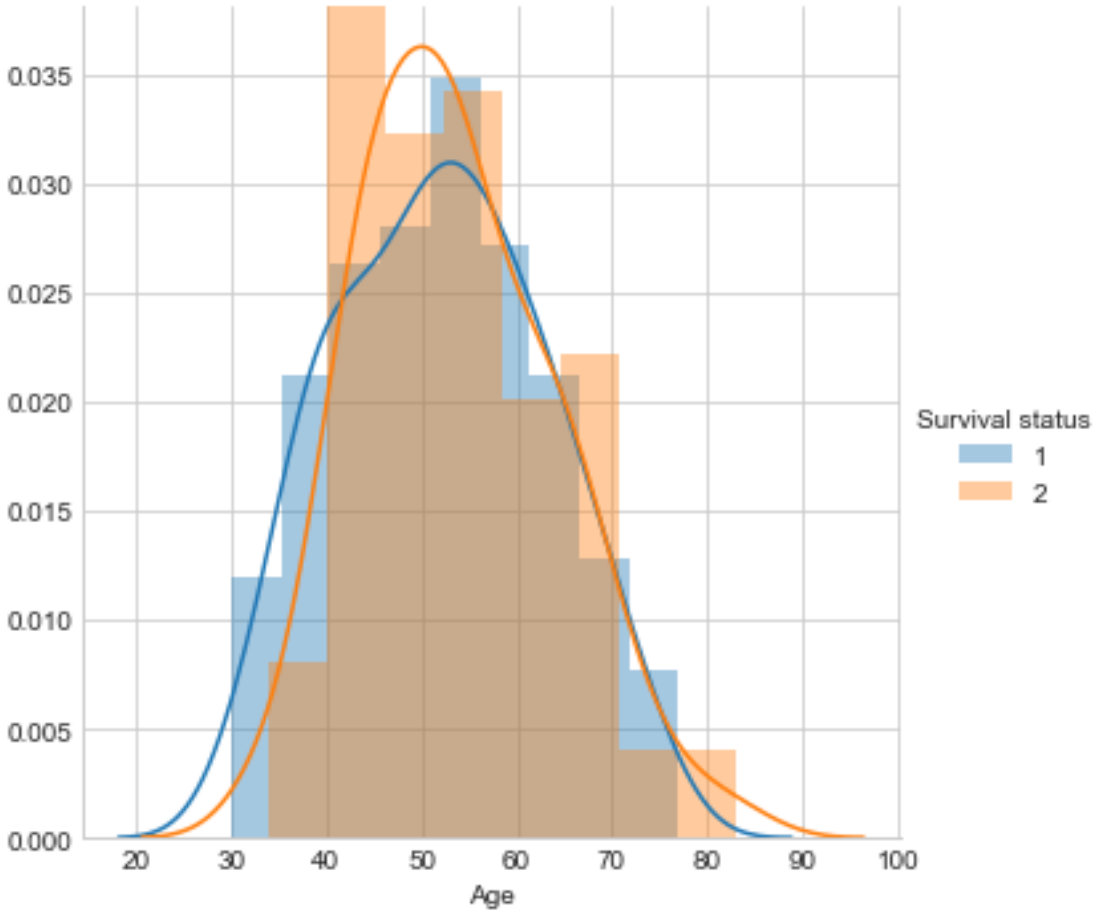
Observations : 1. Not able to identify useful features by 2D scatter and 3D pair plots 2. The features are overlapped

1.2.3 Histogram and Univariate Analysis

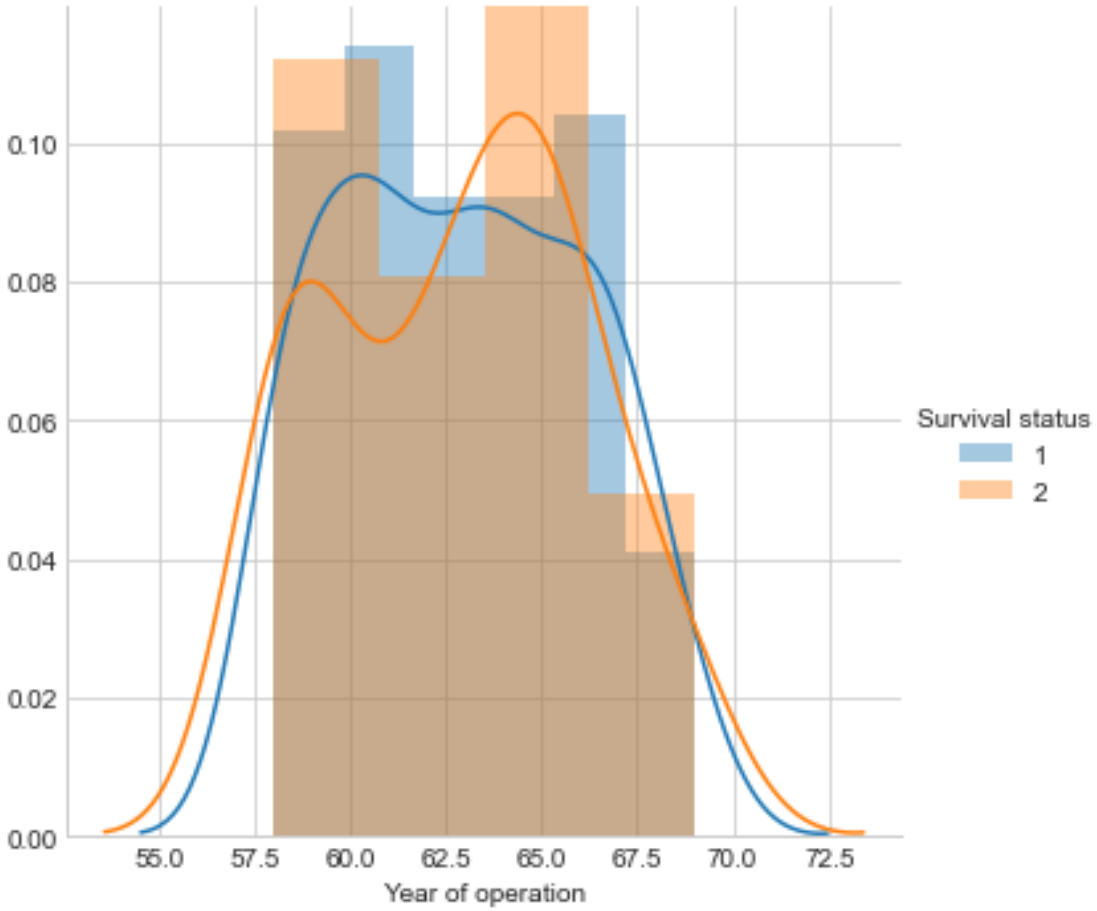
```
In [49]: sns.FacetGrid(haberman, hue="Survival status", size=5) \
            .map(sns.distplot, "axillary nodes") \
            .add_legend();
         plt.show()
```




```
In [50]: sns.FacetGrid(haberman, hue="Survival status", size=5) \
             .map(sns.distplot, "Age") \
             .add_legend()
         plt.show()
```




```
In [51]: sns.FacetGrid(haberman, hue="Survival status", size=5) \
             .map(sns.distplot, "Year of operation") \
             .add_legend()
         plt.show()
```



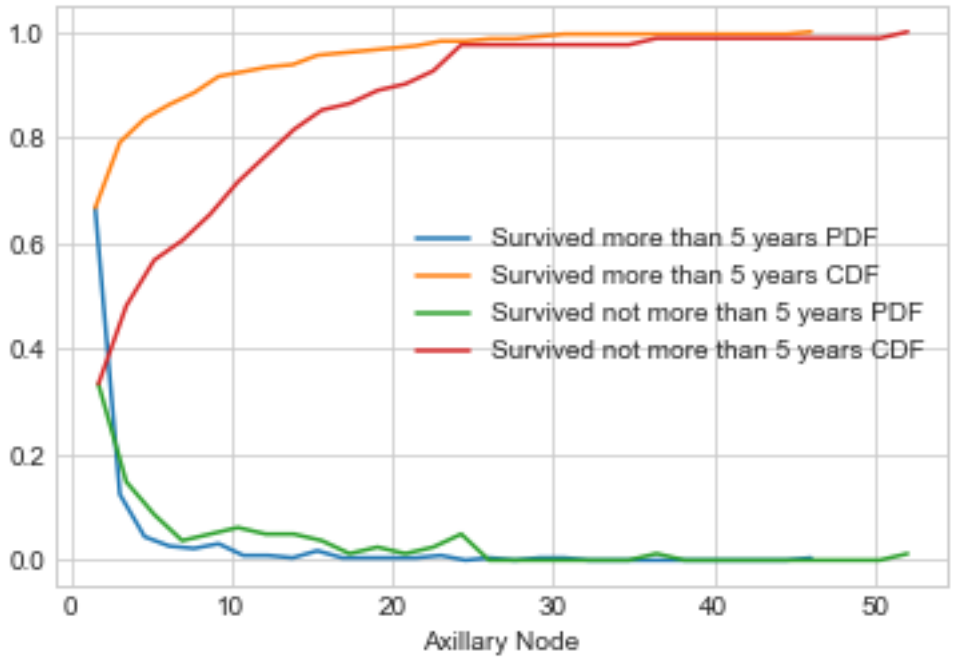
Observations : 1. "Axillary nodes" feature has distribution different than other two features. 2. "Age" and "Year of operation" have almost same distribution and are not helpful for analysis. 3. Many survival patients fall into zero axillary nodes

1.2.4 PDF and CDF

```
In [52]: haberman_survived = haberman[haberman["Survival status"] == 1]
         haberman_non_survived = haberman[haberman["Survival status"] == 2]

         counts_survived, bin_edges_survived = np.histogram(haberman_survived["axillary nodes"]
         print (" counts ---------------- \n",counts_survived)
         print ("\n Bin Edges --------------\n",bin_edges_survived)

         counts_non_survived, bin_edges_non_survived = np.histogram(haberman_non_survived["axi
         print (" counts ---------------- \n",counts_non_survived)
         print ("\n Bin Edges --------------\n",bin_edges_non_survived)

         #compute PDF and CDF for survived
         pdf_survived = counts_survived/sum(counts_survived)
```

```
        cdf_survived = np.cumsum(pdf_survived)

        #compute PDF and CDF for non-survived
        pdf_non_survived = counts_non_survived/sum(counts_non_survived)
        cdf_non_survived = np.cumsum(pdf_non_survived)

        plt.plot(bin_edges_survived[1:], pdf_survived)
        plt.plot(bin_edges_survived[1:], cdf_survived)
        plt.plot(bin_edges_non_survived[1:], pdf_non_survived)
        plt.plot(bin_edges_non_survived[1:], cdf_non_survived)

        plt.xlabel("Axillary Node")

        plt.legend(["Survived more than 5 years PDF", "Survived more than 5 years CDF", "Surv

        plt.show();
```

```
counts ----------------
[0.43478261 0.08115942 0.02898551 0.0173913  0.01449275 0.02028986
0.0057971  0.0057971  0.00289855 0.0115942  0.00289855 0.00289855
0.00289855 0.00289855 0.0057971  0.         0.00289855 0.
0.00289855 0.00289855 0.         0.         0.         0.
0.         0.         0.         0.         0.         0.00289855]

Bin Edges --------------
[ 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.        ]
counts ----------------
[0.19230769 0.08547009 0.04985755 0.02136752 0.02849003 0.03561254
0.02849003 0.02849003 0.02136752 0.00712251 0.01424501 0.00712251
0.01424501 0.02849003 0.         0.         0.         0.
0.         0.         0.00712251 0.         0.         0.
0.         0.         0.         0.         0.         0.00712251]

Bin Edges --------------
[ 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.        ]
```



Observations : 1. If Axillary nodes < 46 is => Survived 2. If Axillary nodes > 46 is => Non Survived

```
In [53]: print("Statistics about survived more than 5 years")
         haberman_survived.describe()
```

```
Statistics about survived more than 5 years
```

Out[53]:

	Age	Year of operation	axillary nodes	Survival 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 [54]: print("Statistics about not survived more than 5 years")
         haberman_non_survived.describe()
```

```
Statistics about not survived more than 5 years
```

Out[54]:

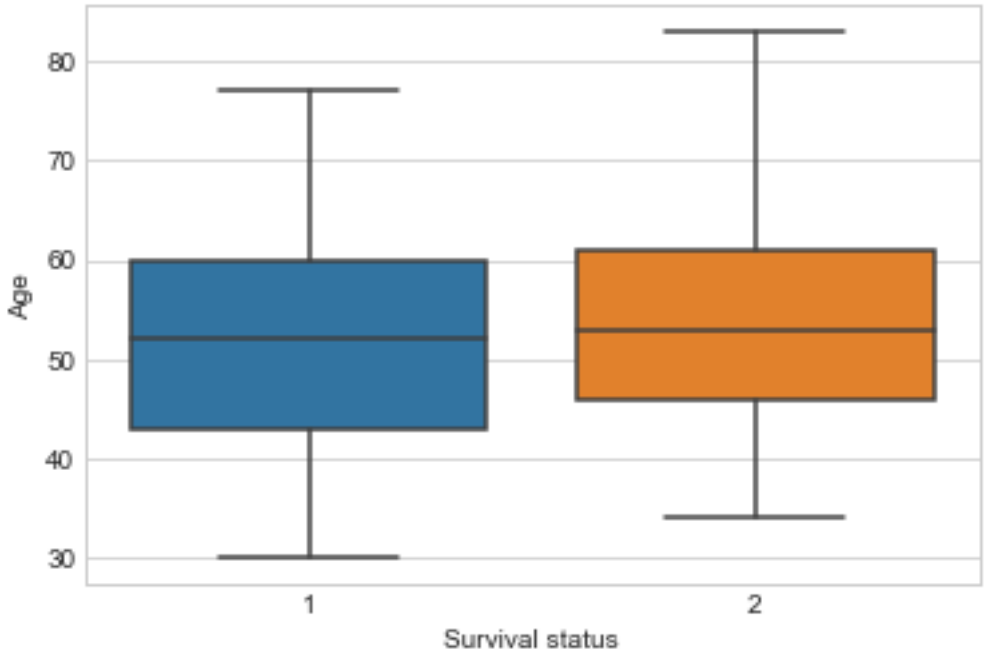
	Age	Year of operation	axillary nodes	Survival status
count	81.000000	81.000000	81.000000	81.0

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

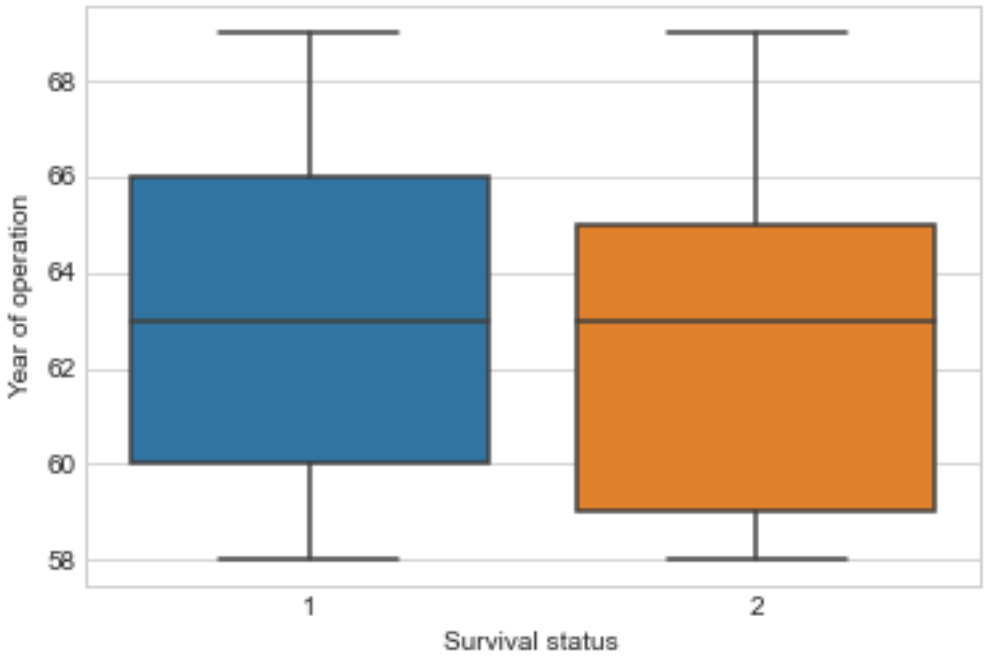
Observations : 1. Mean of axillary nodes is greater for the patients who are non survived

1.2.5 Box Plot

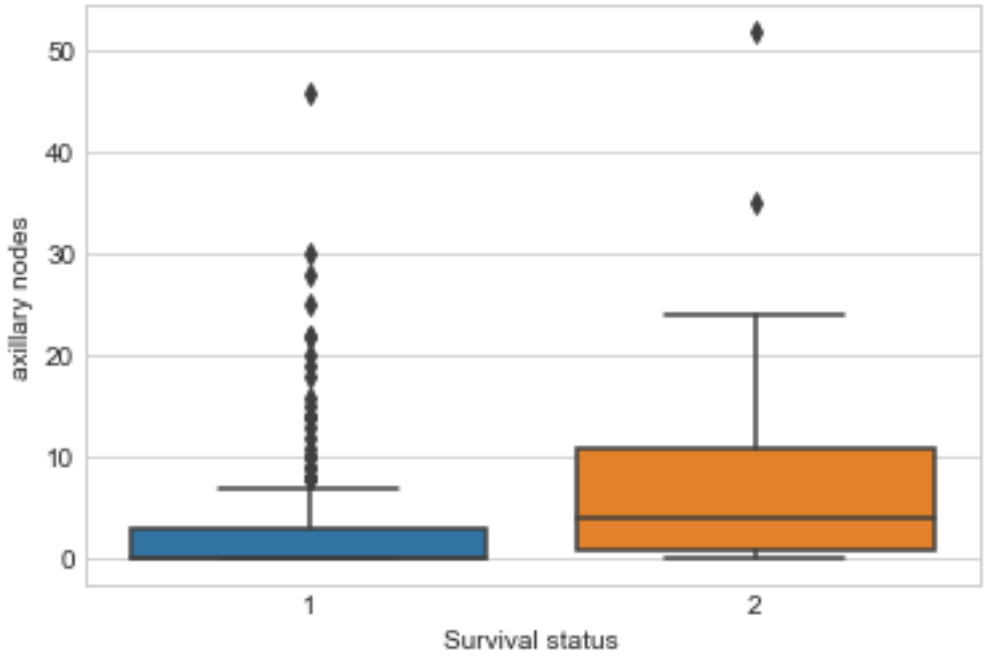
In [57]:
```
sns.boxplot(x='Survival status',y='Age', data=haberman)
plt.show()
```



In [58]:
```
sns.boxplot(x='Survival status',y='Year of operation', data=haberman)
plt.show()
```

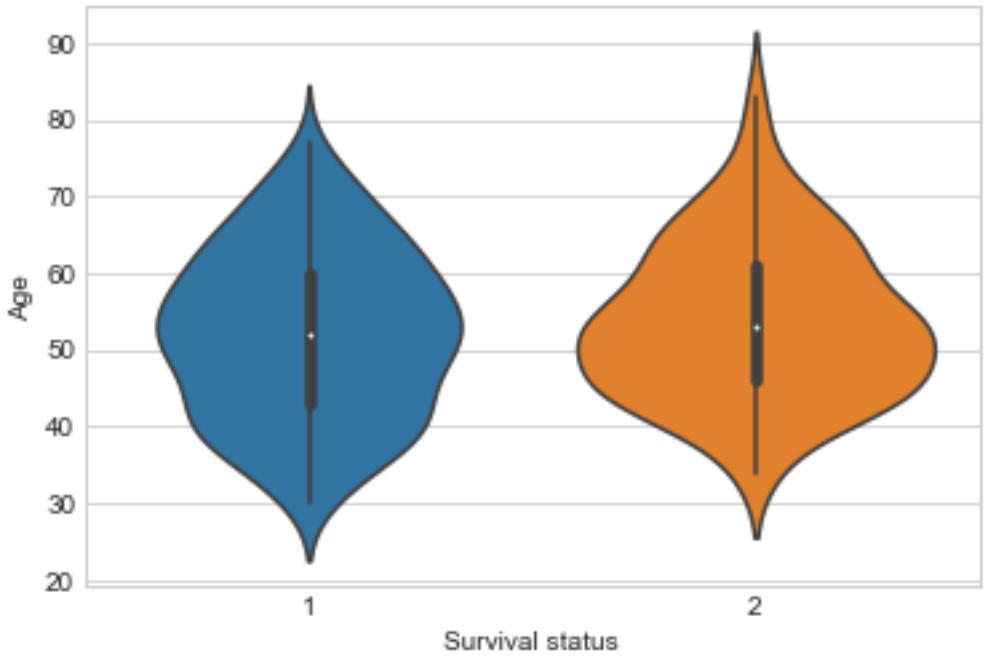


In [59]:
```
sns.boxplot(x='Survival status',y='axillary nodes', data=haberman)
plt.show()
```

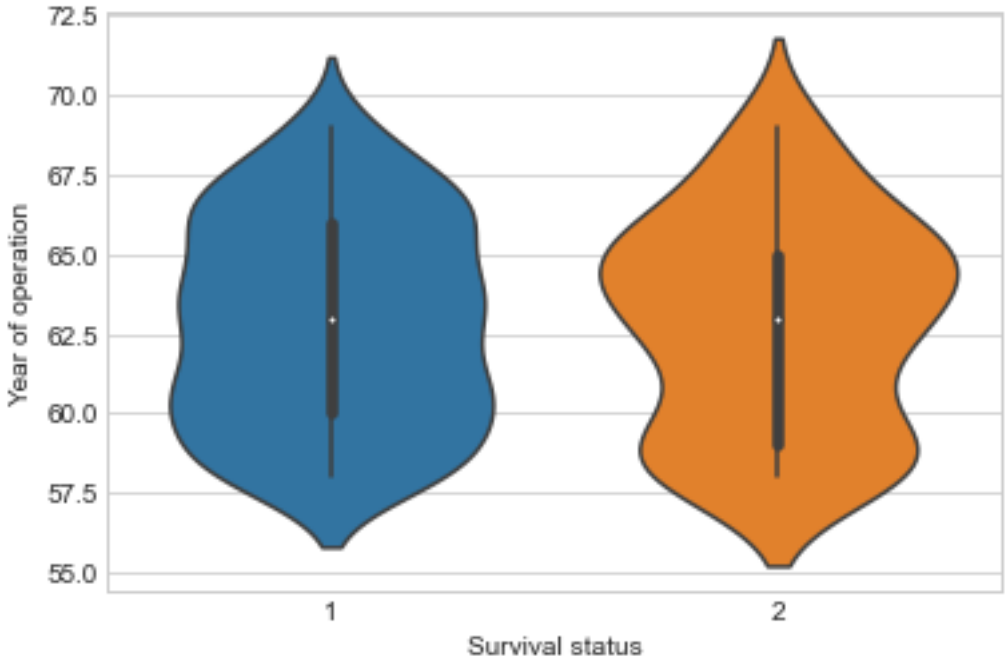


1.2.6 Violin Plots

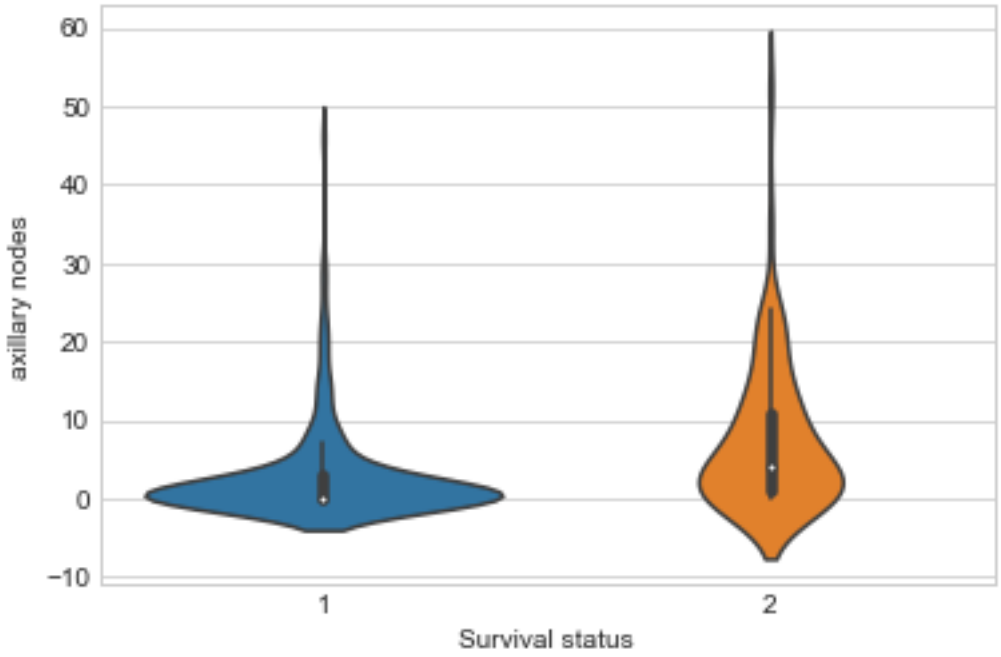
```
In [37]: sns.violinplot(x='Survival status',y='Age', data=haberman)
         plt.show()
```




```
In [38]: sns.violinplot(x='Survival status',y='Year of operation', data=haberman)
         plt.show()
```



```
In [39]: sns.violinplot(x='Survival status',y='axillary nodes', data=haberman)
         plt.show()
```

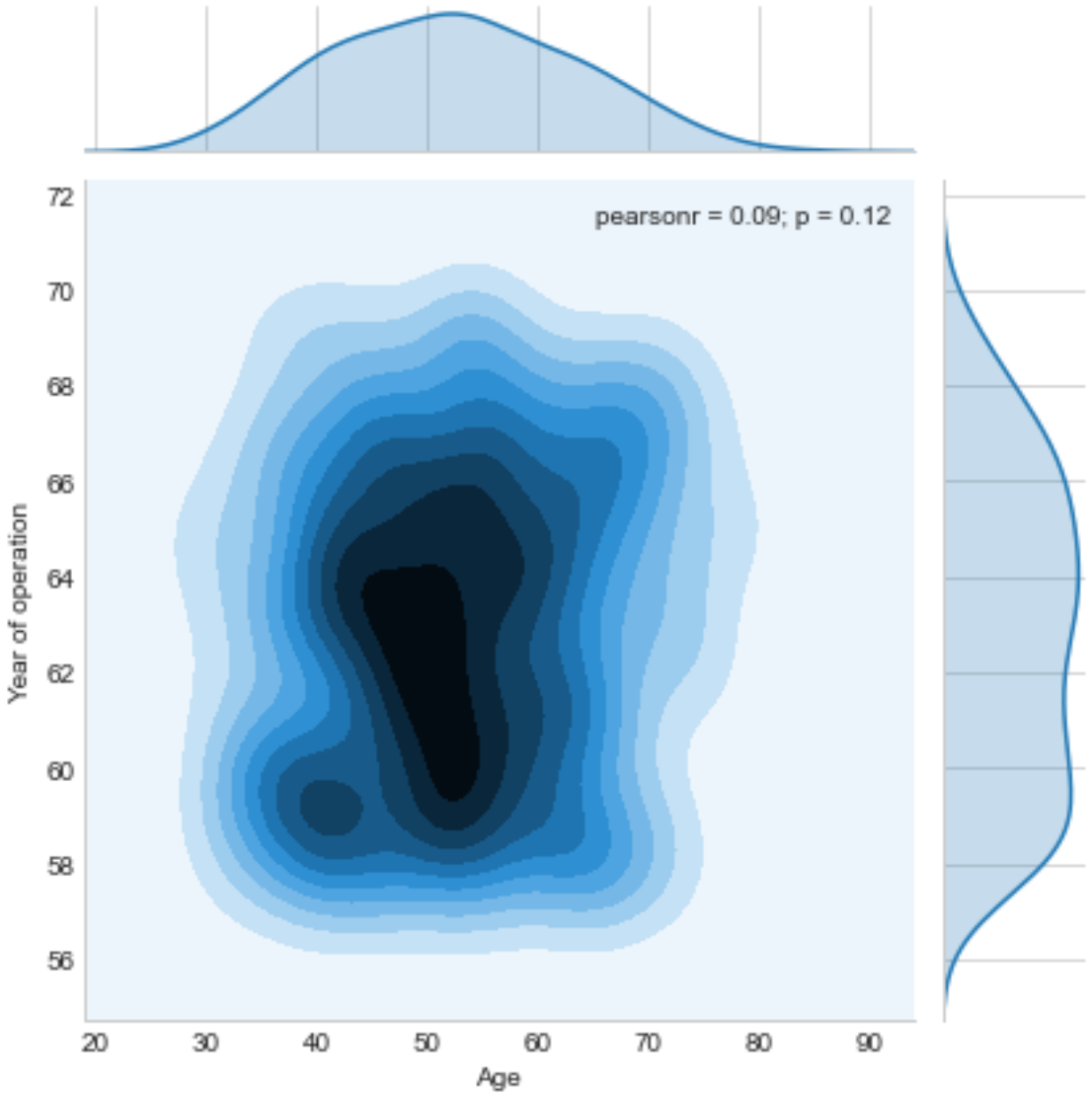


Observation (Univariate Analysis) :

The patients who undergone treatment after 1966 have higher chance to surive. The patients who undergone treatment before 1959 have the lower chance to surive.

1.2.7 Joint Plot

```
In [40]: sns.jointplot(data=haberman, x="Age", y="Year of operation", kind="kde")
         plt.show()
```



Observations : 1. There are more patients operation year between 59 and 63 2. And Age of them is between 43 to 55

Conclusion : 1. The Haberman dataset is imbalanced dataset with very few features 2. The features are non-linearly separable and most of them are overlapped. 3. Axillary node feature was helpful compared to other features, a) If Axillary nodes < 46 is => Survived b) If Axillary nodes > 46 is => Non Survived 4. The patients who undergone treatment after 1966 have higher chance to surive. The patients who undergone treatment before 1959 have the lower chance to surive. 5. This dataset doesnot easily modelled by if-else need complex models.