Exploratory_assignment

October 7, 2018

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

In [2]:
```
#Reading the data
df = pd.read_csv("haberman.csv")
df.describe()
```

Out[2]:

	Age	op_year	axil_nodes_det	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

In [7]:
```
#Number of data points
df.shape
```

Out[7]: (305, 4)

In [10]:
```
#number of features
print(df.columns)
```

```
Index(['Age', 'op_year', 'axil_nodes_det', 'Surv_status'], dtype='object')
```

In [16]:
```
#number of classes
df['Surv_status'].unique()
```

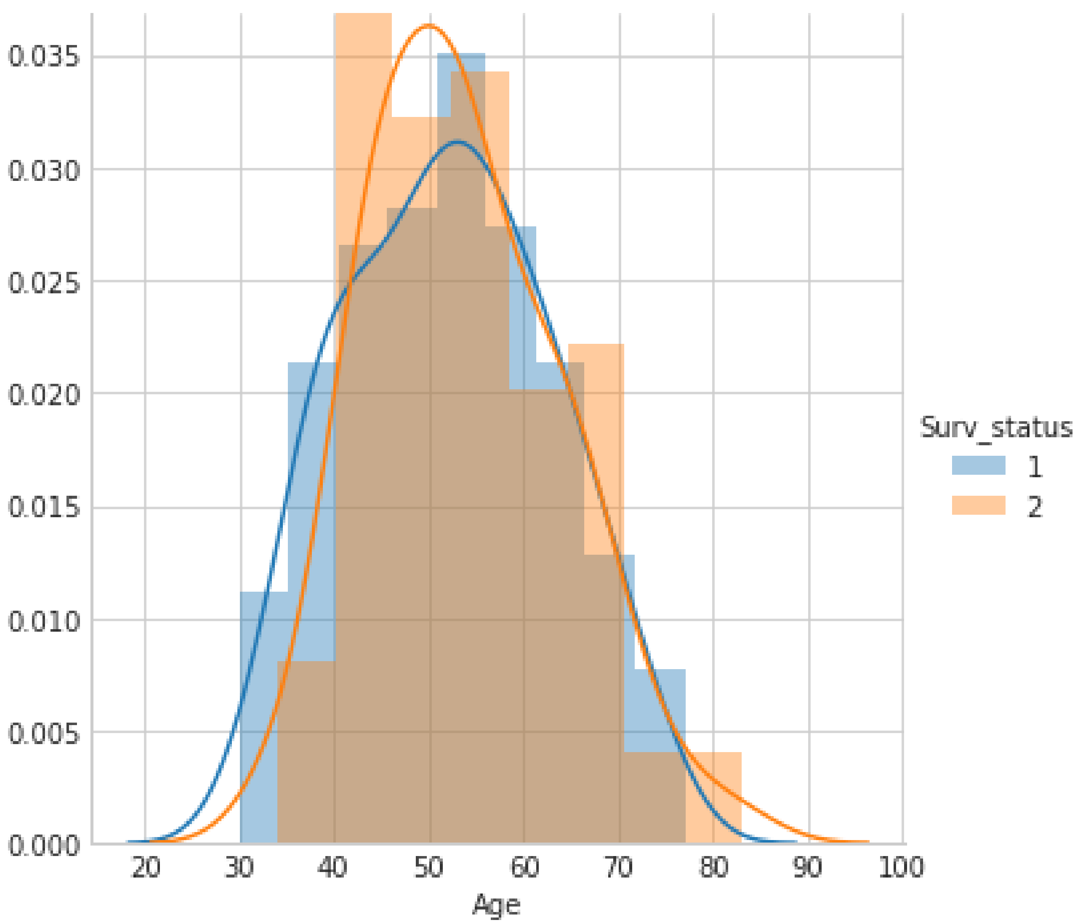
Out[16]: array([1, 2])

In [17]:
```
#Number of datapoints for each class

df['Surv_status'].value_counts()
```

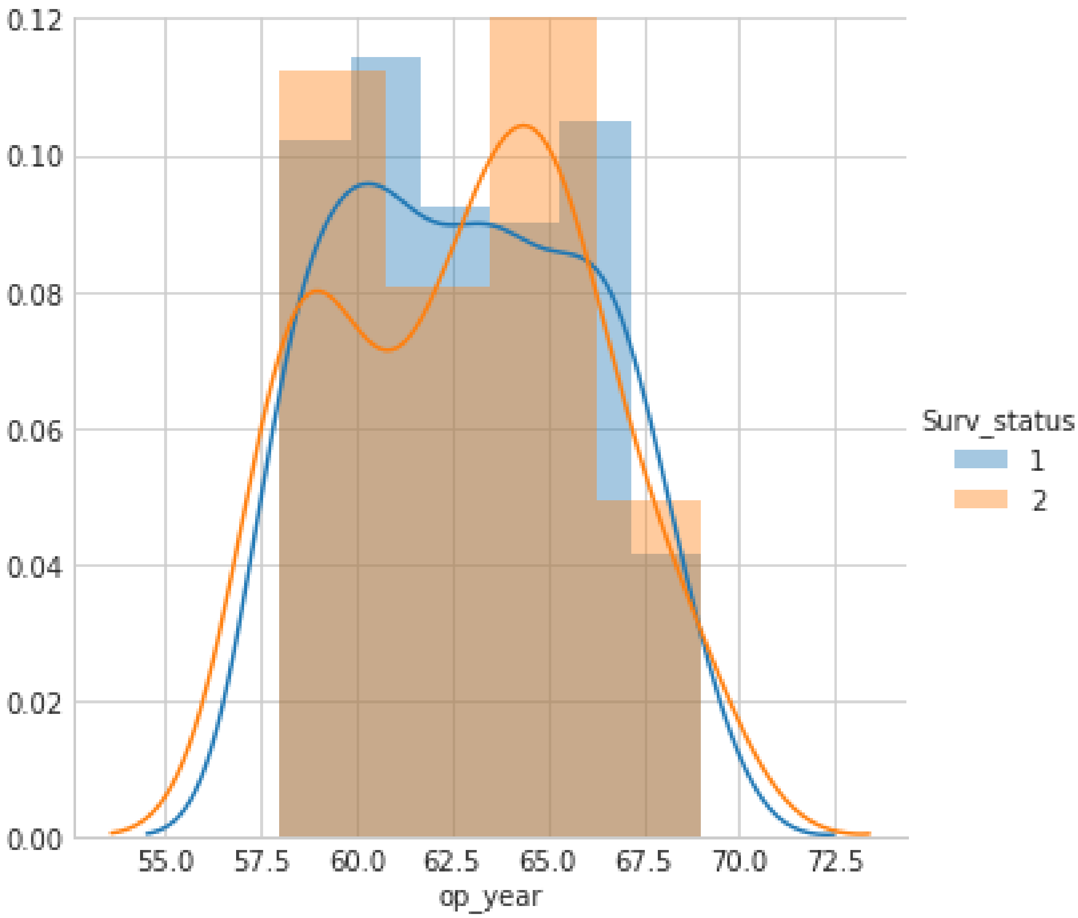
```
Out[17]: 1    224
         2     81
         Name: Surv_status, dtype: int64
```

```
In [ ]: #Our objective is to identify the whether the patient survived in a 5 years
        #span or not after getting operated for Breast cancer.
```

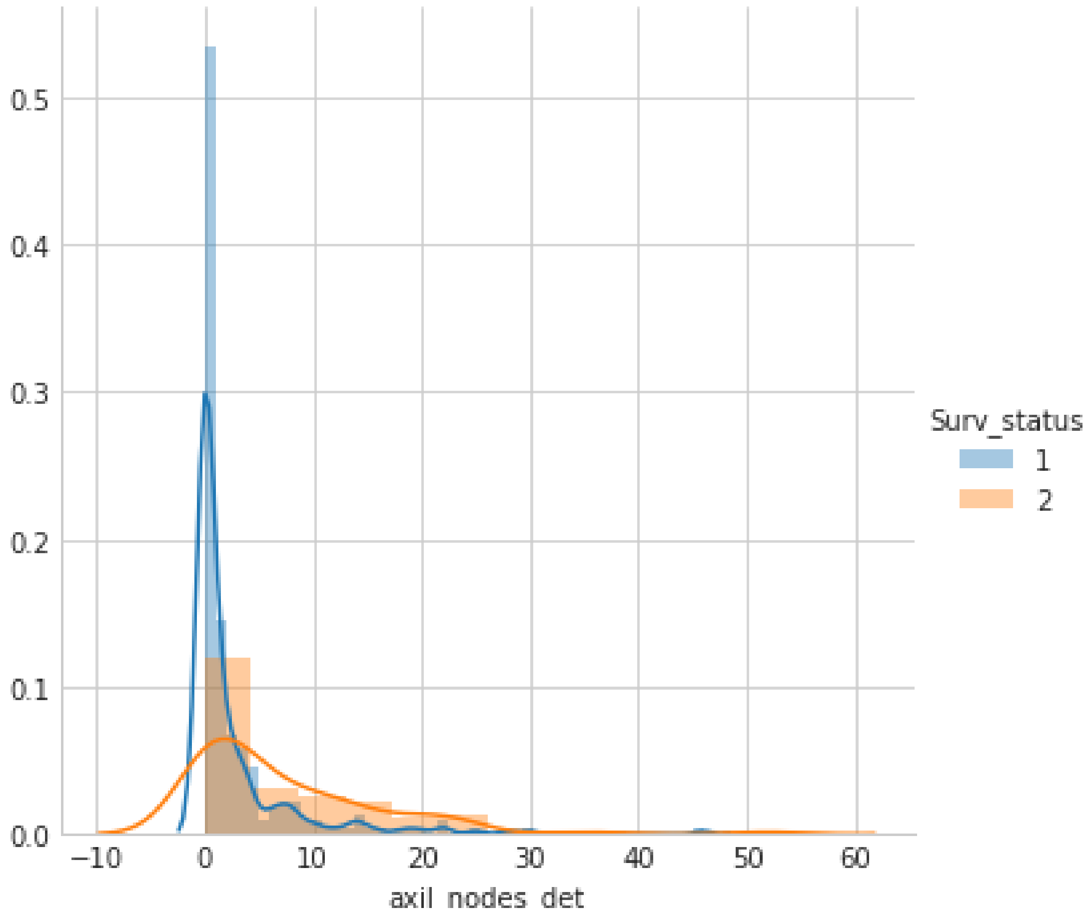
```
In [7]: #PDF for each feature(Age, op_year, axil_nodes_det)
        sns.set_style("whitegrid");
        sns.FacetGrid(df, hue="Surv_status", size=5) \
           .map(sns.distplot, "Age") \
           .add_legend();
        plt.show();

        #The graph actually quite complex and it is really hard to conclude
        #that what are results in output 1 or 2 ( being survived or not)
        #but for not survived(2)graph follows a bell curve or normal distribution.
        #One thing I infer from this is that density for patient survived is more where Age is
        #And when Age is > 75 it's quite visible in the graph that the patient didn't survived
```



In [8]:
```
sns.FacetGrid(df, hue="Surv_status", size=5) \
   .map(sns.distplot, "op_year") \
   .add_legend();
plt.show();

#The graph shows that the feature op_year doesn't really provide any good evidence to f
#Neither of the graph follows normal distribution.
```



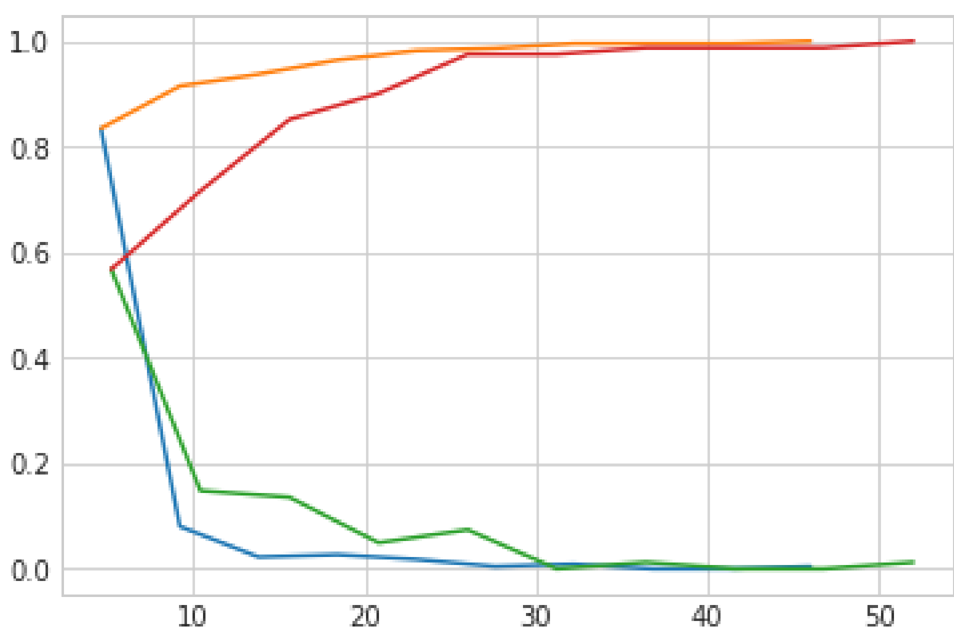
In [9]:
```
sns.set_style("whitegrid");
sns.FacetGrid(df, hue="Surv_status", size=5) \
   .map(sns.distplot, "axil_nodes_det") \
   .add_legend();
plt.show();

#This is rather a better graph that may just seperates the results whether the patient
#The graph really depicts that the probability of a patient survived is much higher wh
#The height of the graph for blue line(1) says that axil_nodes_det has most of the val
#Also the density for the patient survived is more where axil_nodes_det is between 0 a
```




```
In [14]: #plot CDF of axil_nodes_det
         df_survived = df.loc[df["Surv_status"] == 1];
         df_not_survived = df.loc[df["Surv_status"] == 2];

         #Survived
         counts, bin_edges = np.histogram(df_survived['axil_nodes_det'], 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)


         # Not Survived
         counts, bin_edges = np.histogram(df_not_survived['axil_nodes_det'], 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();

#There are 92% people who survived when axil_nodes_det < 15.
#For the same case patients not survived was approx 85% as we have seen in the above g
#Although it does not make much sense because CDF for Survived patients is kind of res
#We will see try and analyse both Age and axil_nodes_det feature together in Bi-varia
```

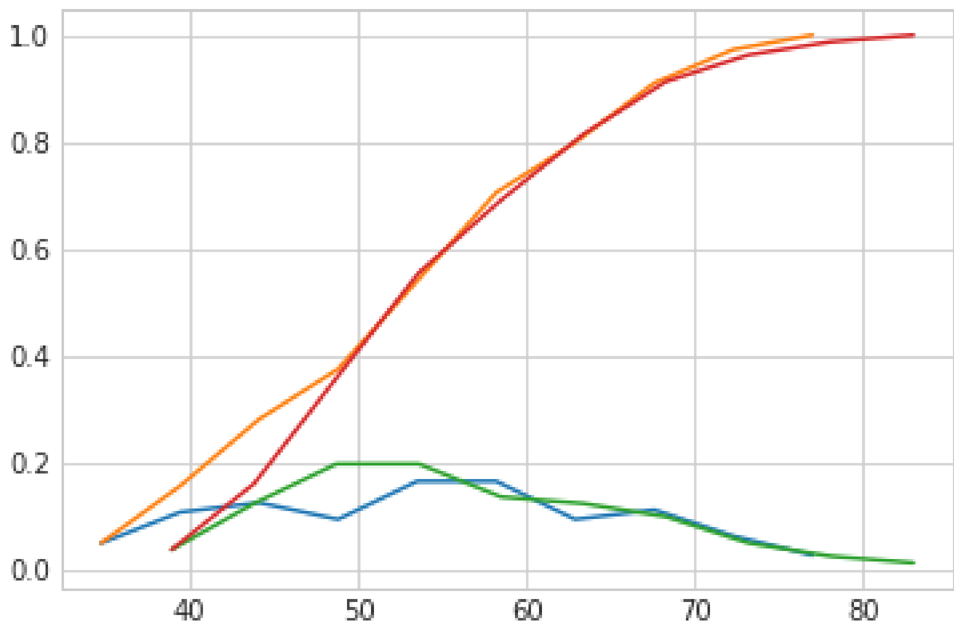
```
[ 0.83482143  0.08035714  0.02232143  0.02678571  0.01785714  0.00446429
  0.00892857  0.          0.          0.00446429]
[  0.    4.6   9.2  13.8  18.4  23.   27.6  32.2  36.8  41.4  46. ]
[ 0.56790123  0.14814815  0.13580247  0.04938272  0.07407407  0.
  0.01234568  0.          0.          0.01234568]
[  0.    5.2  10.4  15.6  20.8  26.   31.2  36.4  41.6  46.8  52. ]
```



In [15]:
```
#plot CDF of Age
#Survived
counts, bin_edges = np.histogram(df_survived['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)


# Not Survived
counts, bin_edges = np.histogram(df_not_survived['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();

#It's really hard to predict the results with Age feature as seen in the below graph.
#What's infered is that there is approx to 100% chance that patients did not survived
#We can better quantify results in Bi-variate analyses
```

```
[ 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. ]
[ 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. ]
```

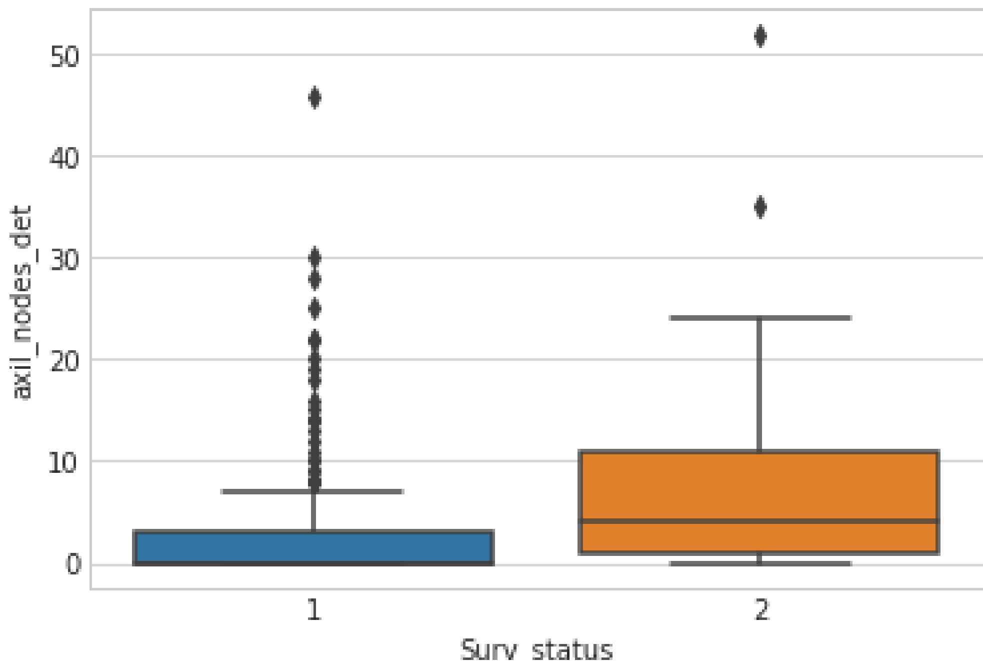



```
In [24]: #Before plotting the Box plots and Voilin plots, we start with computing mean, median
         print("Means :")
         print("Mean for axil nodes for survived  is :",  np.mean(df_survived['axil_nodes_det']
         print("Mean for axil nodes for not survived  is :", np.mean(df_not_survived['axil_node

         print("Mean for Age for survived  is :", np.mean(df_survived['Age']))
         print("Mean for Age for not survived  is :", np.mean(df_not_survived['Age']))

         print("Standard Deviation :")
         print("Standard deviation for axil nodes for survived  is :", np.std(df_survived['axil
         print("Standard deviation for axil nodes for not survived  is :", np.std(df_not_survi

         print("Standard deviation for Age for survived  is :", np.std(df_survived['Age']))
         print("Standard deviation for Age for not survived  is :", np.std(df_not_survived['Age

         #From the below values. The mean of survived and not survived for Age is almost simil
         #But the mean for axil_nodes_det says something, that patients that survived have ave
         #value of axil_nodes_det approx 3 in comparison to those who not survived having aver
         #Also the spread of axil nodes for survived is slightly lower than those who did not
```

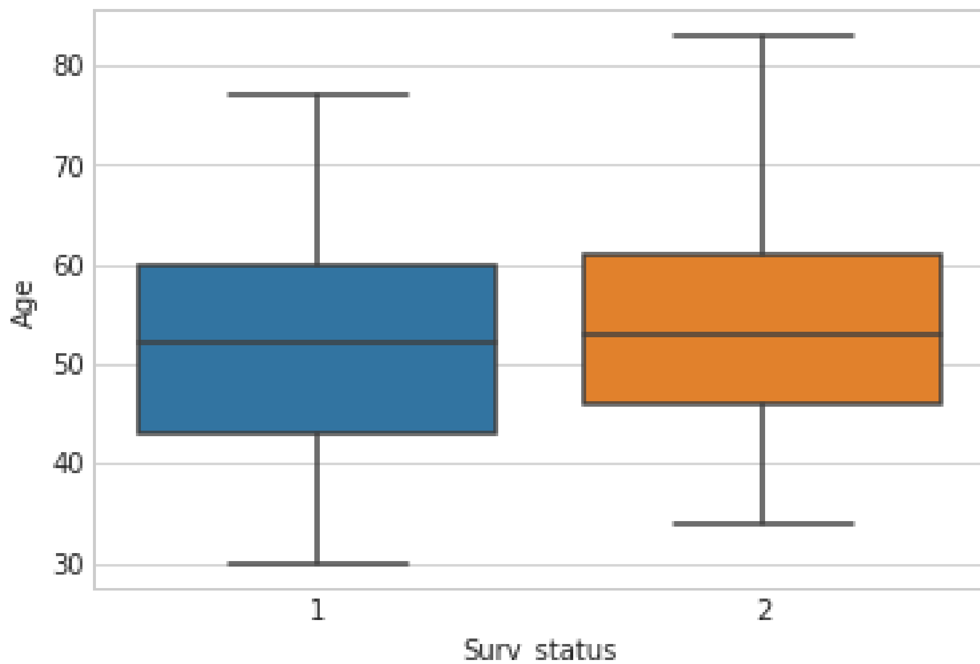
```
Means :
Mean for axil nodes for survived  is : 2.799107142857143
Mean for axil nodes for not survived  is : 7.45679012345679
Mean for Age for survived  is : 52.11607142857143
Mean for Age for not survived  is : 53.67901234567901
Standard Deviation :
```

```
Standard deviation for axil nodes for survived  is : 5.869092706952767
Standard deviation for axil nodes for not survived  is : 9.128776076761632
Standard deviation for Age for survived  is : 10.913004640364269
Standard deviation for Age for not survived  is : 10.10418219303131
```

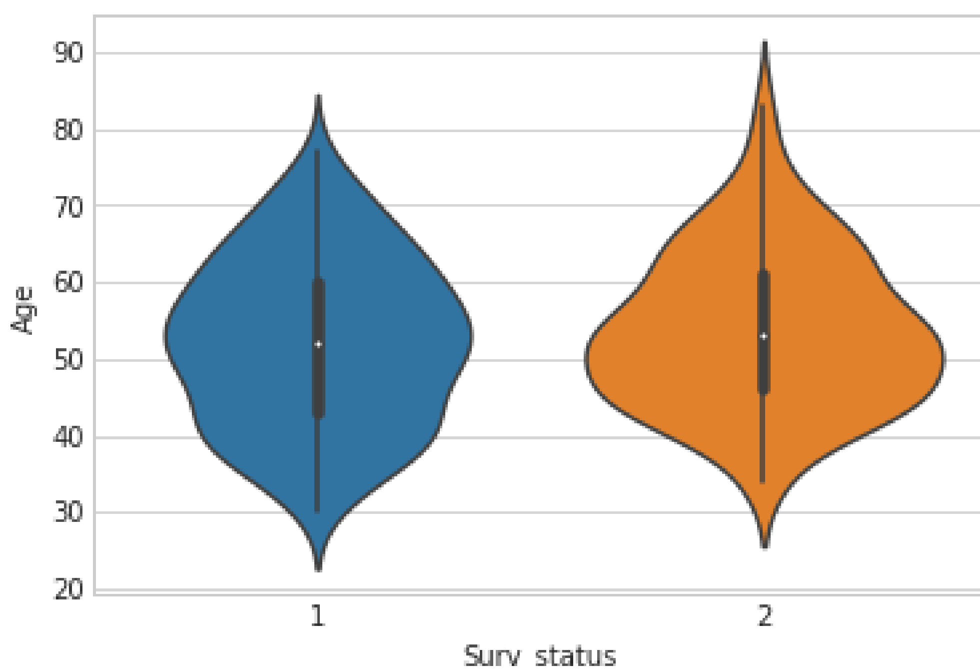
In [25]:
```python
#Box plot for axil nodes det

sns.boxplot(x = 'Surv_status', y = 'axil_nodes_det', data = df)
plt.show()

#We can say that when ax >= 2 and ax < 11, then patient is not survived.
#But by making the above assumption we also concluded that there are roughly 50 perce
#classified as not survived i.e 50% error.
```



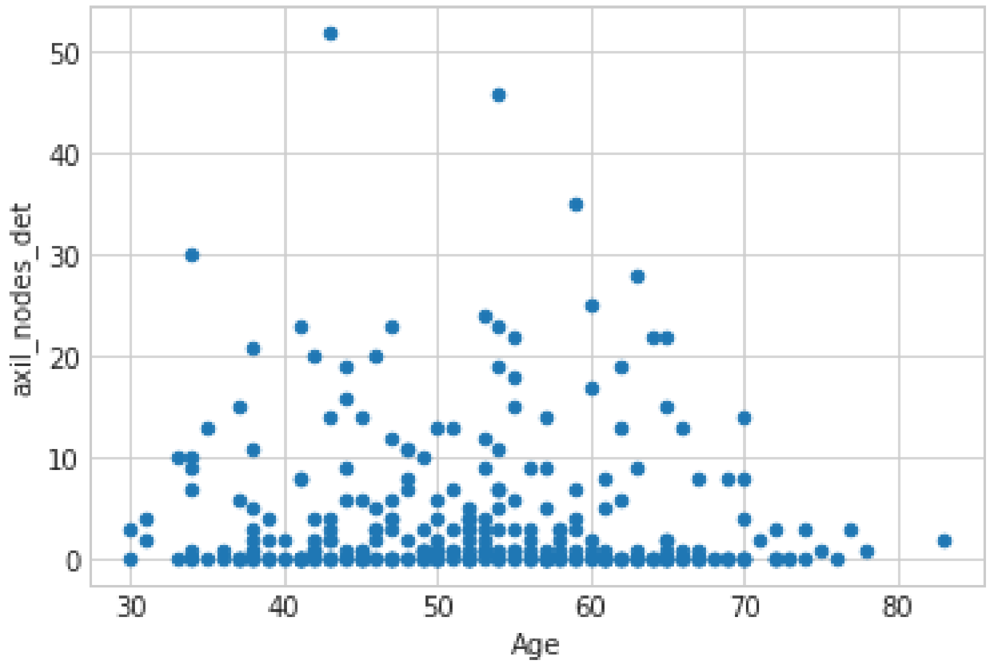
In [26]:
```python
#Box plot for Age

sns.boxplot(x = 'Surv_status', y = 'Age', data = df)
plt.show()

#It's hard to make any assumptions by looking at the below graph because it will lead
#The only assumptions I can make is that for patients who survived most of them aged
#While those who did not survived have aged >=35 and <85.
```




```
In [29]: #Violin plots for axil_nodes_det
         sns.violinplot(x = 'Surv_status', y = 'Age', data = df, size = 5)
         plt.show()
```



In [30]:
```
df.plot(kind= 'scatter', x = 'Age', y = 'axil_nodes_det')
plt.show()

#The scatter plot between features Age and axil nodes tells that Age varies typically
#Whereas the axil nodes vary from 0 to 52 approx.
```



In [7]:
```
# pairwise scatter plot: Pair-Plot
df['Surv_status'] = df['Surv_status'].map(lambda x : 'Y' if x == 1 else 'N')# Y being

plt.close();
sns.set_style("whitegrid");
sns.pairplot(df, hue="Surv_status", size=3);
plt.show()
```


```
In [ ]: #The overall conclusion on which I came to is that op_year feature does not support in
        #predict the objective which is to classify whether the patient has survived or not as
        #overlapping and quite hard to infer anything from that.
        #Moreover Age feature shows almost same tendency except the fact that at extreme data
        #whether the patient survived or not.
        #Axil nodes is the best among all three features as it helps further to classify based
        #patient survived or not.
```