EDA on Haberman's Survival Data Set

(Survival of patients who had undergone surgery for breast cancer)

About the Dataset

Haberman's data set

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.

Reference : https://www.kaggle.com/gilsousa/habermans-survival-data-set (https://www.kaggle.com/gilsousa/habermans-survival-data-set)

Feature/Variable/Input-variable/Independent-varibale

> There are 4 attributes: 'Age', 'Op_Year', 'axil_nodes', 'Surv_status'
>
> - Feature Information:
> - 'Age'-----------Age of patient at time of operation (numerical)
> - 'Op_Year'-----Patient's year of operation (year - 1900, numerical)
> - 'axil_nodes'--Number of positive axillary nodes detected (numerical)

Label/Depdendent-variable

> - Survival status (class attribute)
>   --------------1 = the patient survived 5 years or longer
>   --------------2 = the patient died within 5 years

In [18]:
```
import pandas as pd
import seaborn as sbn
import matplotlib.pyplot as plt
import numpy as np
```

In [50]:
```
import warnings
warnings.filterwarnings("ignore")
```

In [4]:
```
#Load haberman.csv into a pandas dataFrame.
df = pd.read_csv("haberman.csv")
df.head()
```

Out[4]:

	30	64	1	1.1
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]:
```
#Rename the column name
df = df.rename(columns={'30': 'Age', '64': 'Op_Year', '1': 'axil_nodes', '1.1'
:  'Surv_status'})
df.columns
```

Out[6]:
```
Index(['Age', 'Op_Year', 'axil_nodes', 'Surv_status'], dtype='object')
```

In [8]:
```
#Data-point
print(df.shape)

print("=="*10)
print("Data points per each class: ")
df['Surv_status'].value_counts()
```

```
(305, 4)
====================
Data points per each class:
```

Out[8]:
```
1    224
2     81
Name: Surv_status, dtype: int64
```

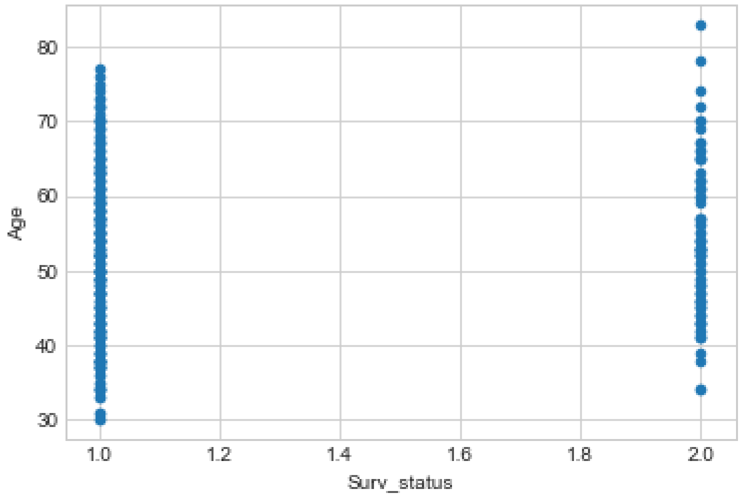
Observation:

- There are two classes 1 and 2, class 1 denotes patients who survived 5 years or longer after the operation and class 2 denotes to patients who died within 5 years of operation.
- class 1 contains 224 values and class 2 contain 81 values
- It is being clear that 224 patients survived 5 years or longer after the operation and 81 patients died within 5 years of operation.

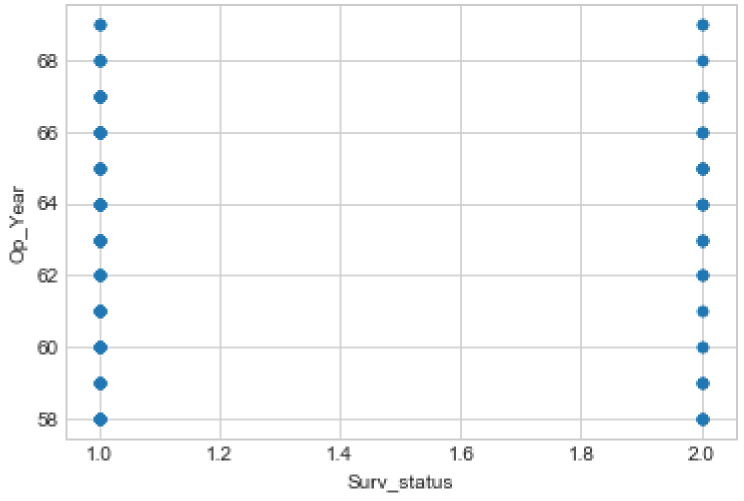
Bi-variate analysis

1) 2-D Scatter Plot

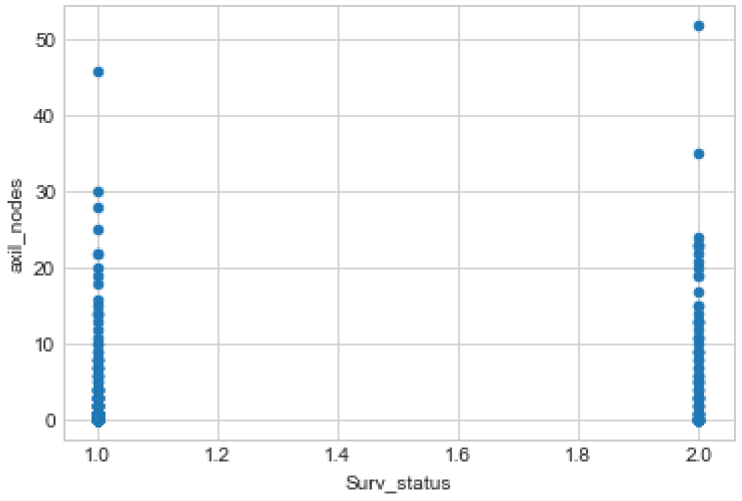
In [21]:
```
#Age
df.plot(kind="scatter", x ="Surv_status", y="Age")
plt.show()
```



In [22]:
```
#Op_Year
df.plot(kind="scatter", x ="Surv_status", y="Op_Year")
plt.show()
```



In [23]:
```
#axil_nodes
df.plot(kind="scatter", x ="Surv_status", y="axil_nodes")
plt.show()
```

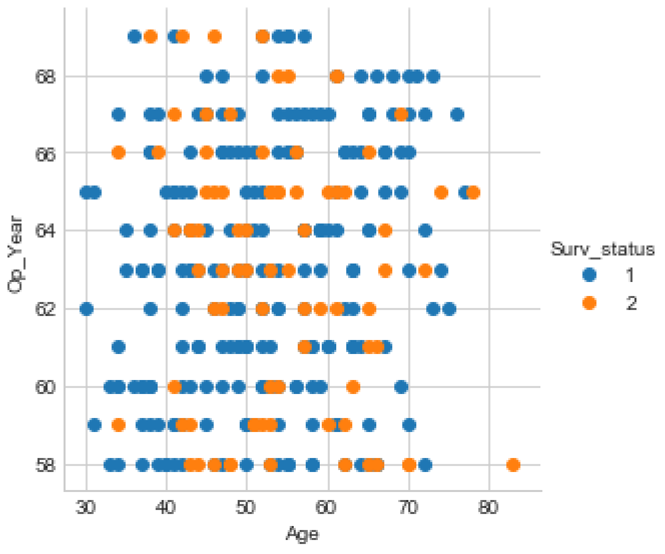


Observation

- This cann't make much sense out it.
- we can color the points by thier Feature/Survival Status.

2-D Scatter plot with color-coding

In [17]:
```
sbn.set_style("whitegrid");
sbn.FacetGrid(df, hue="Surv_status", size=4) \
   .map(plt.scatter, "Age", "Op_Year") \
   .add_legend();
plt.show();
```



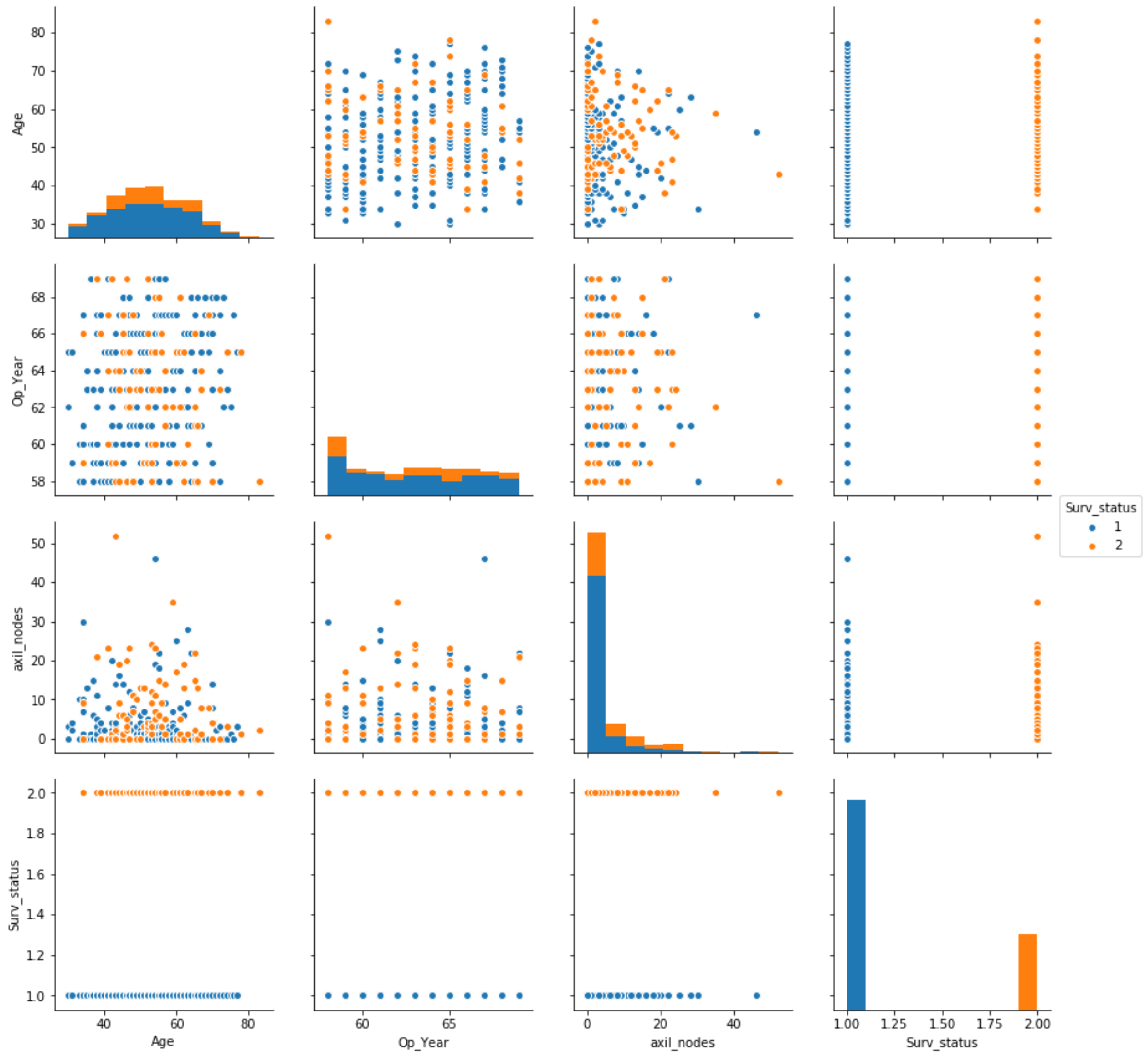
Observation

- We can plot 2-D Scatter plot with color-coding for each Feature/Survival Status
- It's a little bit difficult to identify the plots one by one.

2) Pair-plot

- We can draw multiple 2-D scatter plots for each combination of features.

In [14]:
```
sbn.pairplot(df, hue="Surv_status", size=3)
plt.show()
```



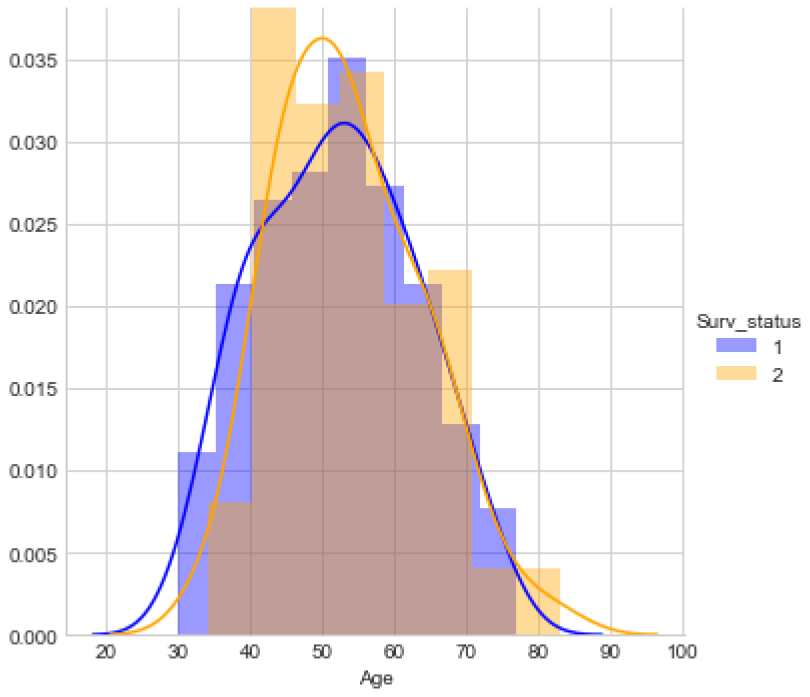
Observations

- axil_nodes and Surv_status are the most useful features to identify Survival status of the patitents.
- We can use "line: between both" and "if-else" conditions to build a simple model to classify patients status.

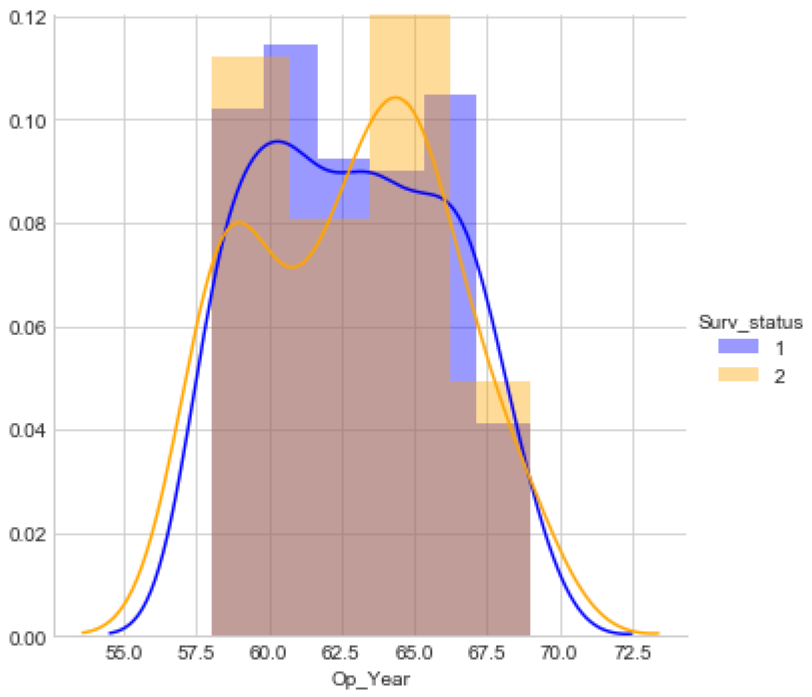
Histogram

- 1-D scatter plot

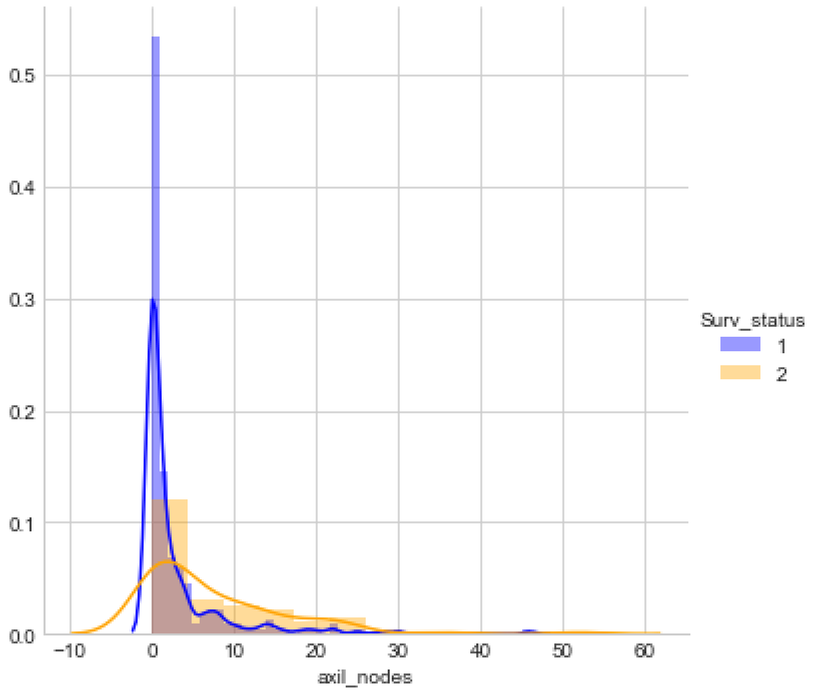
In [59]:
```
#Age
sbn.set_style("whitegrid")
pal = ["blue","orange"]
sbn.FacetGrid(df, hue="Surv_status", palette= pal,size = 5)\
    .map(sbn.distplot, "Age")\
    .add_legend()
plt.show()
```



In [61]:
```
#Op_Year
sbn.set_style("whitegrid")
sbn.FacetGrid(df, hue= "Surv_status", palette= pal, size= 5)\
    .map(sbn.distplot, "Op_Year")\
    .add_legend()
plt.show()
```



In [62]:
```
#axil_nodes
sbn.set_style("whitegrid")
sbn.FacetGrid(df, hue= "Surv_status", palette= pal, size= 5)\
    .map(sbn.distplot, "axil_nodes")\
    .add_legend()
plt.show()
```



Univariate Analysis using PDF

- one variable analysis

In [10]:
```
df_survived = df.loc[df["Surv_status"] == 1]
df_died = df.loc[df["Surv_status"] == 2]
```

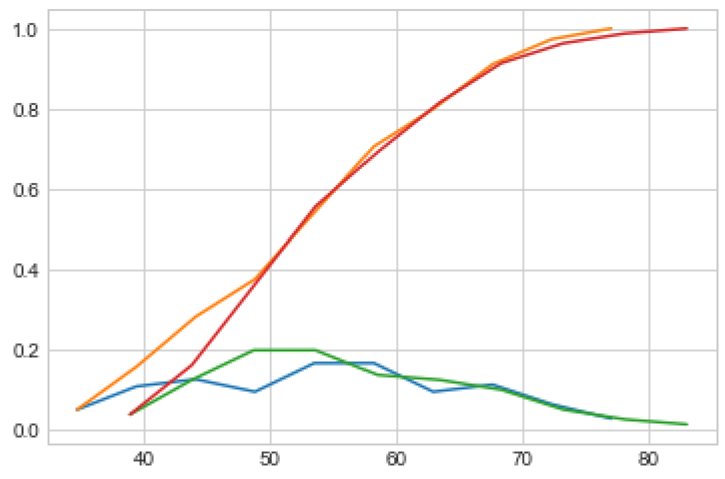
In [66]:
```
#Age
counts, bin_edges = np.histogram(df_survived['Age'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


counts, bin_edges = np.histogram(df_died['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()
```

```
[0.04910714 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. ]
```



Observation:

- Univariate analysis based on Age gives a slightly different plot for both classes with some overlap of data points.
- it is difficult to set a threshold to distinguish the two classes.
- Age is not a very important feature for determining the survival of a patient.

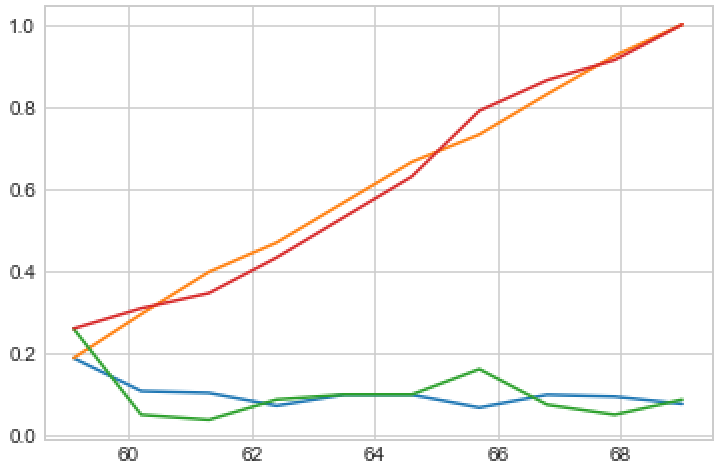
In [67]:
```
#Op_Year
counts, bin_edges = np.histogram(df_survived['Op_Year'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


counts, bin_edges = np.histogram(df_died['Op_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()
```

```
[0.1875     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. ]
[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. ]
```



Observation:

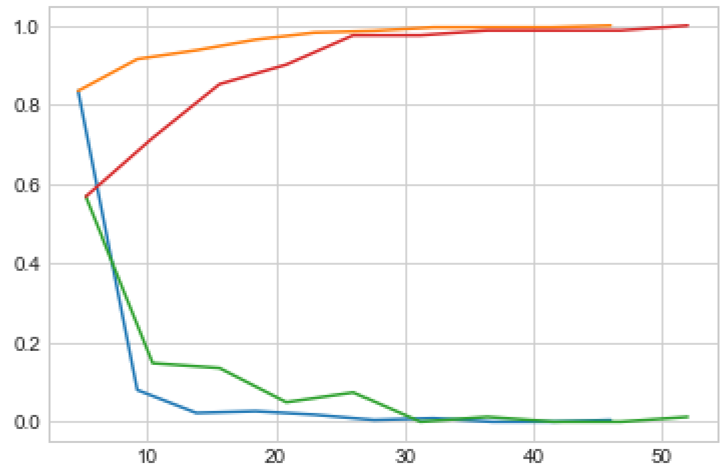
- Univariate analysis based on Year_of_operation(Op_Year) gives similar plots for both classes with a huge overlap rate of data points.
- Year_of_operation(Op_Year) is not an important feature for determining the survival of a patient.
- it's also difficult to set a threshold to distinguish the two classes.

In [65]:
```
#axil_nodes
counts, bin_edges = np.histogram(df_survived['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)


counts, bin_edges = np.histogram(df_died['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()
```

```
[0.83482143 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. ]
```



Observation:

- Univariate analysis based on axil_nodes gives less overlap of data points as compared to other features.
- It's also difficult to set a threshold for axillary nodes which will differentiate both classes of patients.
- axil_nodes can be an important feature for determining the survival of a patient.

Mean, Variance and Std-dev

In [83]:
```
print(df_survived.describe())
```

```
              Age     Op_Year  axil_nodes  Surv_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 [86]:
```
#Median is equvalent to Mean
print("Median from df_survived")
print(np.median(df_survived["Age"]))
print(np.median(df_survived["Op_Year"]))
print(np.median(df_survived["axil_nodes"]))
print("=="*30)
print("Median from df_died")
print(np.median(df_died["Age"]))
print(np.median(df_died["Op_Year"]))
print(np.median(df_died["axil_nodes"]))
```

```
Median from df_survived
52.0
63.0
0.0
============================================================
Median from df_died
53.0
63.0
4.0
```

In [82]:
```
print("\n90th Percentiles:")
print(np.percentile(df_survived["Age"],90))
print(np.percentile(df_survived["Op_Year"],90))
print(np.percentile(df_survived["axil_nodes"],90))
print("=="*30)
print(np.percentile(df_died["Age"],90))
print(np.percentile(df_died["Op_Year"],90))
print(np.percentile(df_died["axil_nodes"],90))
```

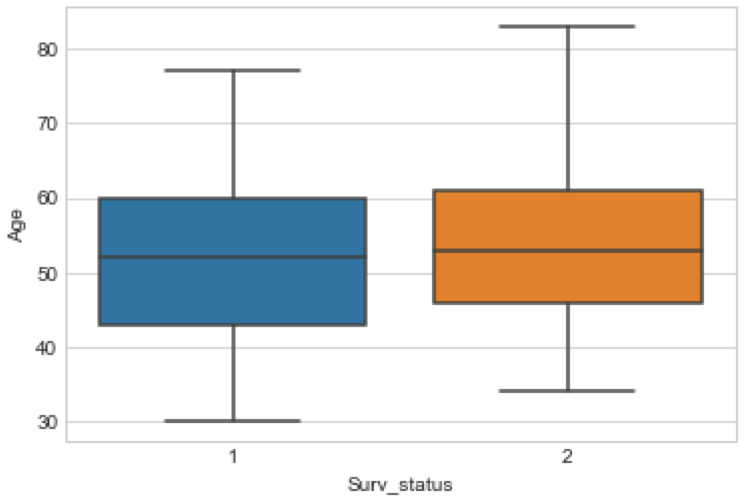
```
90th Percentiles:
67.0
67.0
8.0
============================================================
67.0
67.0
20.0
```

In [92]:
```
#MAD is equevalent to std-dev
print ("\nMedian Absolute Deviation")
from statsmodels import robust
print(robust.mad(df_survived["Age"]))
print(robust.mad(df_survived["Op_Year"]))
print(robust.mad(df_survived["axil_nodes"]))
print("=="*30)
print(robust.mad(df_died["Age"]))
print(robust.mad(df_died["Op_Year"]))
print(robust.mad(df_died["axil_nodes"]))
```

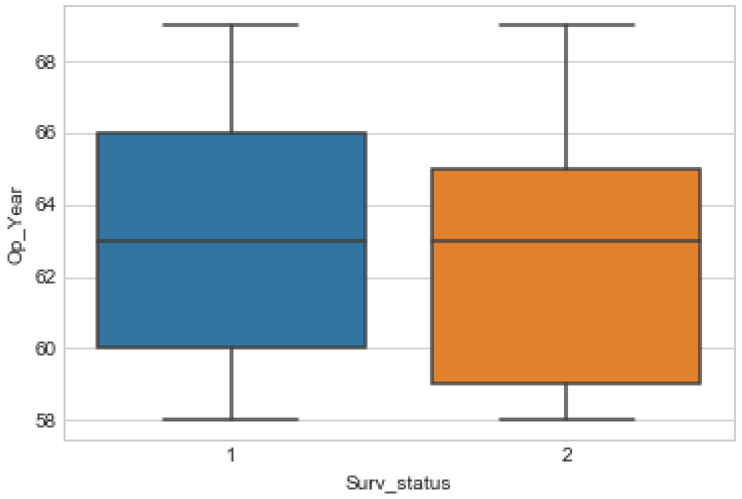
```
Median Absolute Deviation
13.343419966550417
4.447806655516806
0.0
============================================================
11.860817748044816
4.447806655516806
5.930408874022408
```

Box plot and Whiskers

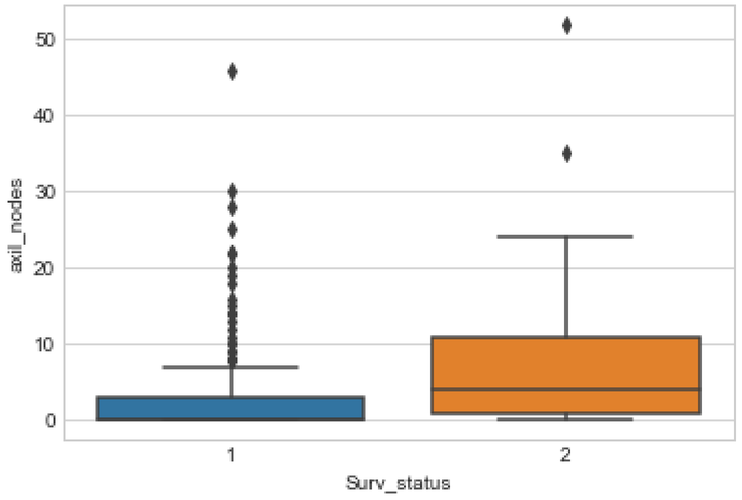
In [94]:
```
sbn.boxplot(x="Surv_status", y="Age", data=df)
plt.show()
```



In [95]:
```
sbn.boxplot(x="Surv_status", y="Op_Year", data=df)
plt.show()
```



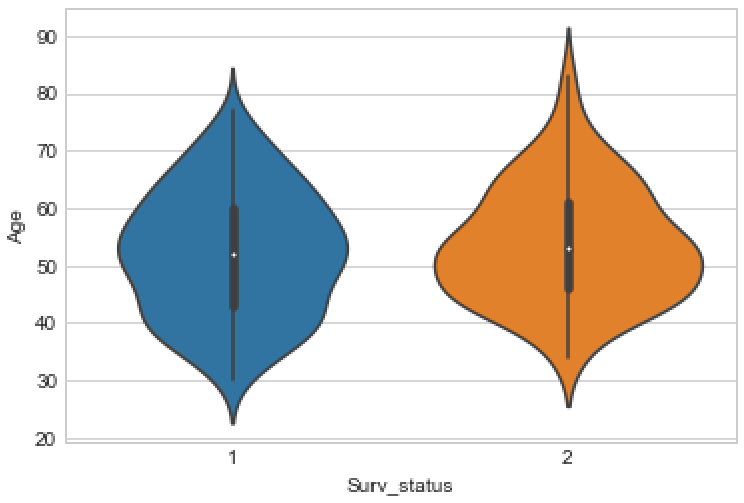
In [96]:
```
sbn.boxplot(x="Surv_status", y="axil_nodes", data=df)
plt.show()
```



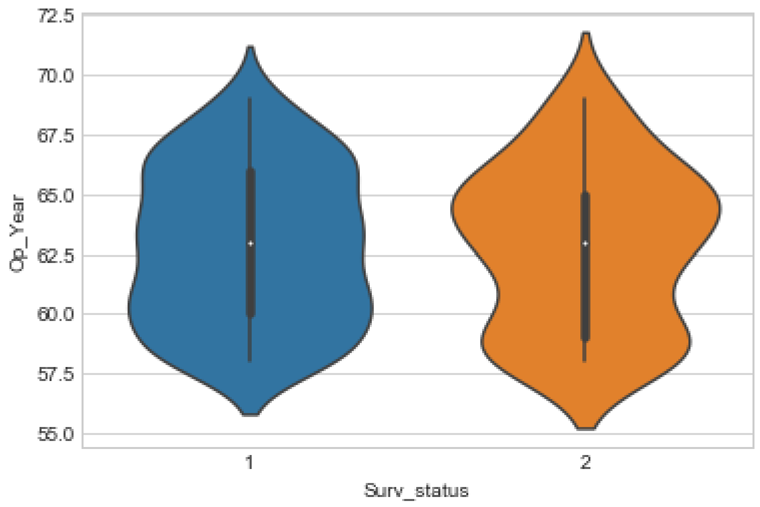
Violin plots

Boxplot + PDF

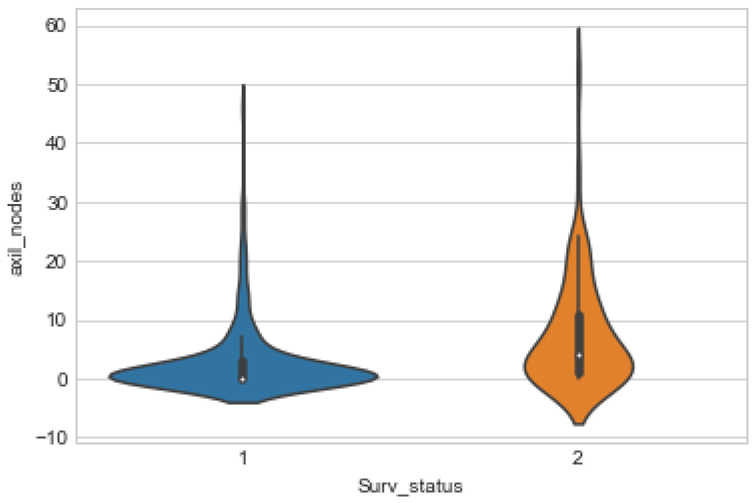
In [97]:
```
sbn.violinplot(x= "Surv_status", y ="Age", data=df, size= 8)
plt.show()
```



In [98]:
```
sbn.violinplot(x= "Surv_status", y ="Op_Year", data=df, size= 8)
plt.show()
```



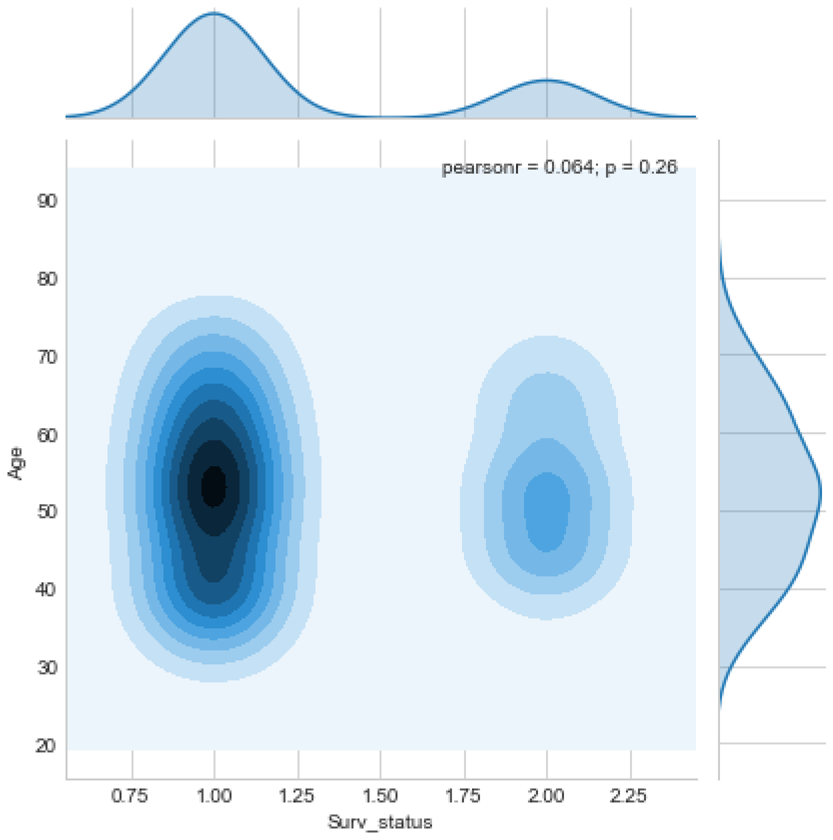
In [99]:
```
sbn.violinplot(x= "Surv_status", y ="axil_nodes", data=df, size= 8)
plt.show()
```



Multivariate probability density, contour plot.

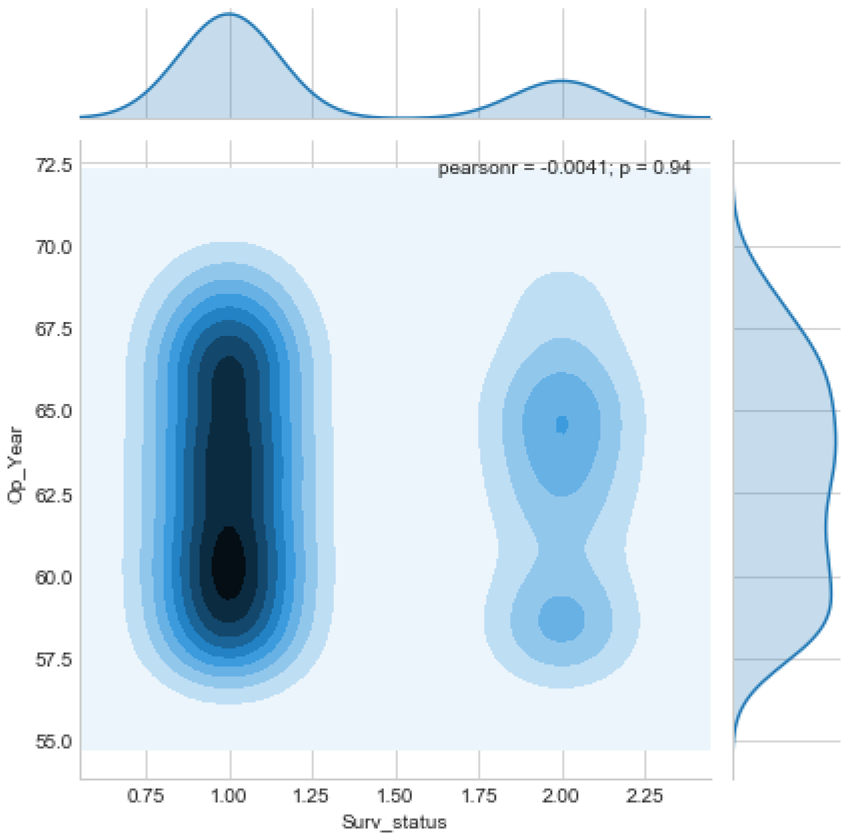
In [104]:
```
sbn.jointplot(x= "Surv_status", y="Age", data= df, kind= "kde")
plt.plot()
```

Out[104]:
```
[]
```



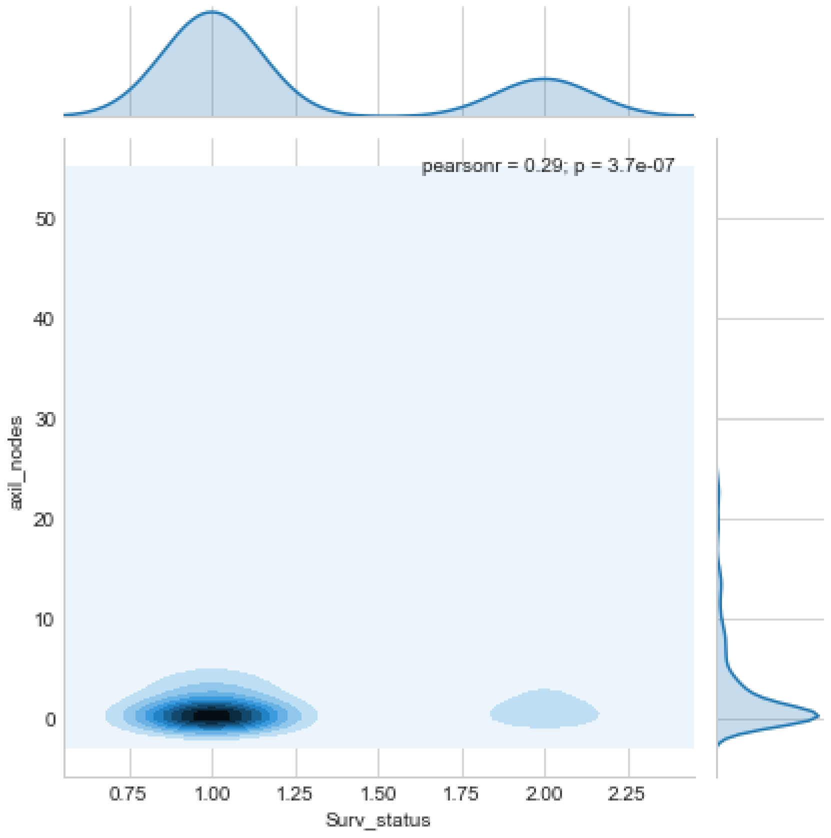
```
In [103]: sbn.jointplot(x= "Surv_status", y="Op_Year", data= df, kind= "kde")
          plt.plot()
```

```
Out[103]: []
```



In [105]:
```
sbn.jointplot(x= "Surv_status", y="axil_nodes", data= df, kind= "kde")
plt.plot()
```

Out[105]:
```
[]
```



Conclusions:

- Patient's age(Age) and year of operation(Op_Year) only can not define the survival status that, the patient survived 5 years or longer or died within 5 years. it is difficult to predict.
- axillary(axil_nodes) node plays important role to perform EDA on Haberman's Data Set.