In [1]:

```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import seaborn as sns
```

In [2]:

```
haberman=pd.read_csv('haberman.csv',names=['Age','Op_date','axil_nodes','Survsts
haberman.head()
```

Out[2]:

	Age	Op_date	axil_nodes	Survsts
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

Number of Datapoints

In [3]:

```
print(haberman.shape)
```

```
(306, 4)
```

Columns

In [4]:

```
print(haberman.columns)
```

```
Index(['Age', 'Op_date', 'axil_nodes', 'Survsts'], dtype='object')
```

In [5]:

```
haberman['Survsts'].value_counts()
```

Out[5]:

```
1    225
2     81
Name: Survsts, dtype: int64
```

In [6]:

```
haberman['Survsts'].value_counts()
```

Out[6]:

```
1    225
2     81
Name: Survsts, dtype: int64
```

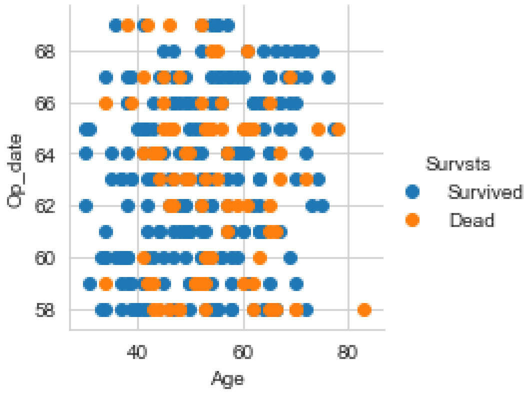
Note:

The survival status is represented in 1's and 2's which is a bit confusing. So i have taken "Survived" for those who survived above 5 years after surgery and "Dead" for those who did not, for convenience

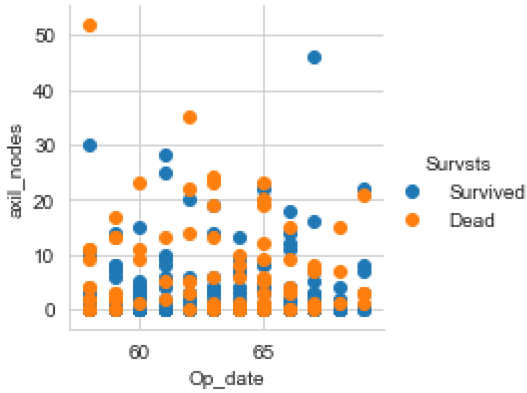
In [7]:
```
haberman['Survsts'].replace({1:'Survived',2:'Dead'},inplace=True)
```

2D Scatter Plot

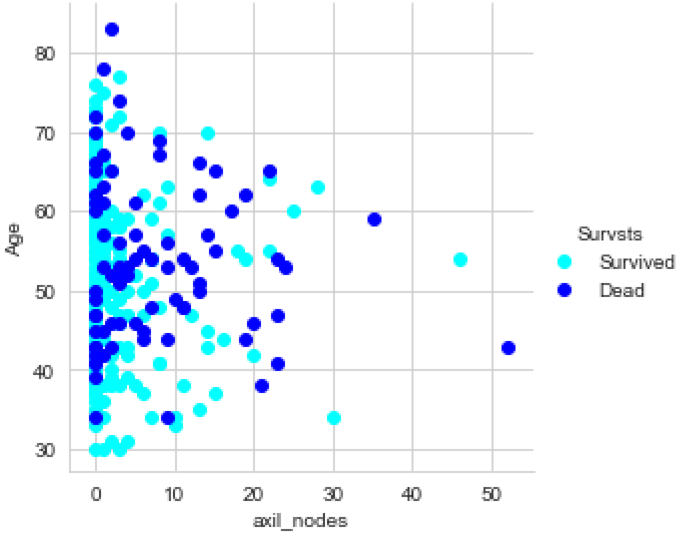
In [9]:
```
sns.set_style('whitegrid')
sns.FacetGrid(haberman, hue="Survsts", height=3) \
    .map(plt.scatter, 'Age', 'Op_date') \
    .add_legend()
plt.show()
```



In [10]:
```
sns.set_style("whitegrid")
sns.FacetGrid(haberman, hue="Survsts",height=3).map(plt.scatter,'Op_date','axil_
plt.show()
```



In [11]:
```
sns.set_style("whitegrid")
sns.FacetGrid(haberman,hue='Survsts',palette=['cyan','blue'],height=4).map(plt.s
plt.show()
```

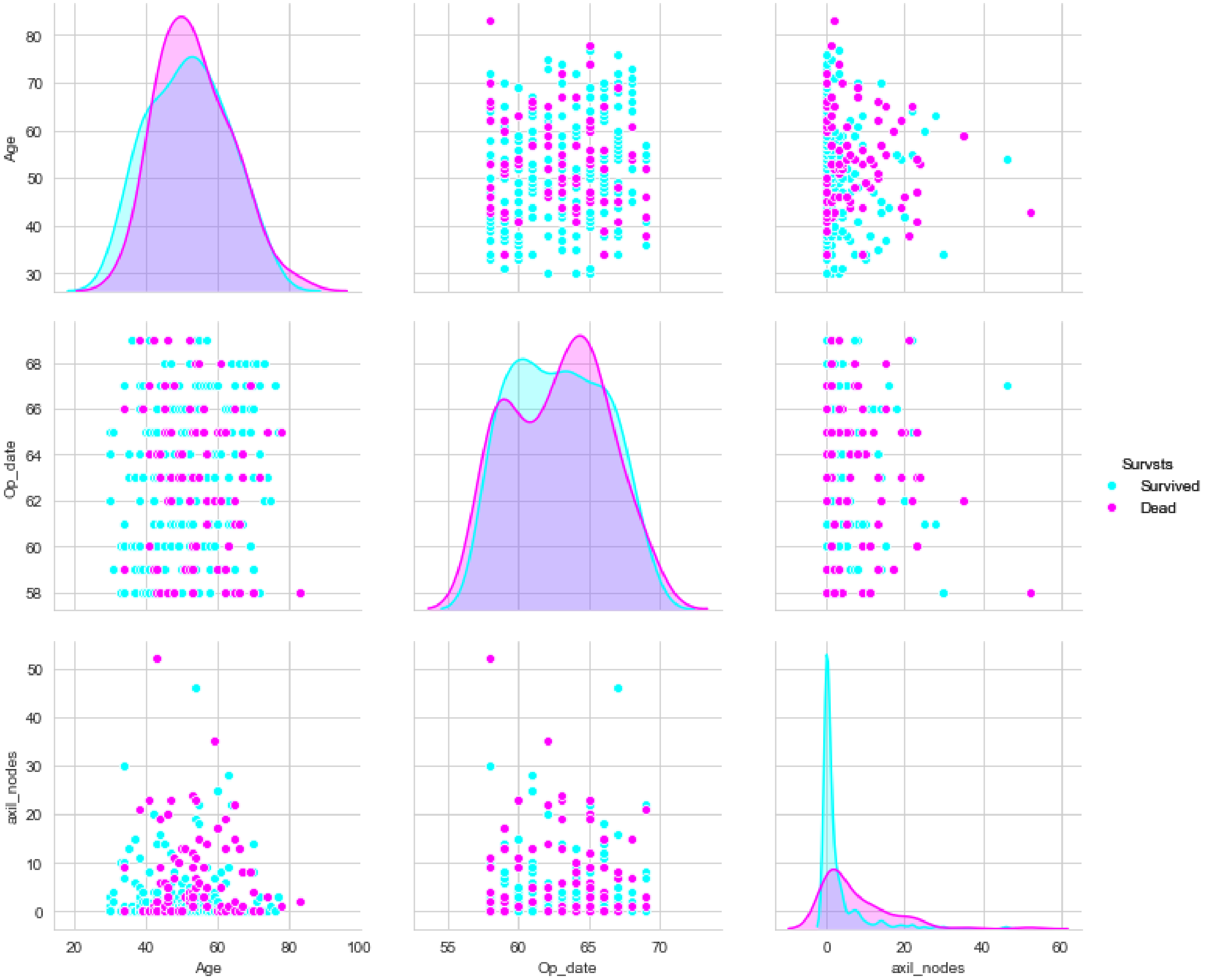


OBSERVATION:

From the above 3 Scatter plots, we cannot obtain any conclusions due to overlapping

Pair Plots

In [12]:
```
plt.close()
sns.set_style("whitegrid")
sns.pairplot(haberman,hue='Survsts',palette=['cyan','magenta'],height=3).add_leg
plt.show()
```



In [13]:
```
type(haberman.columns)
```

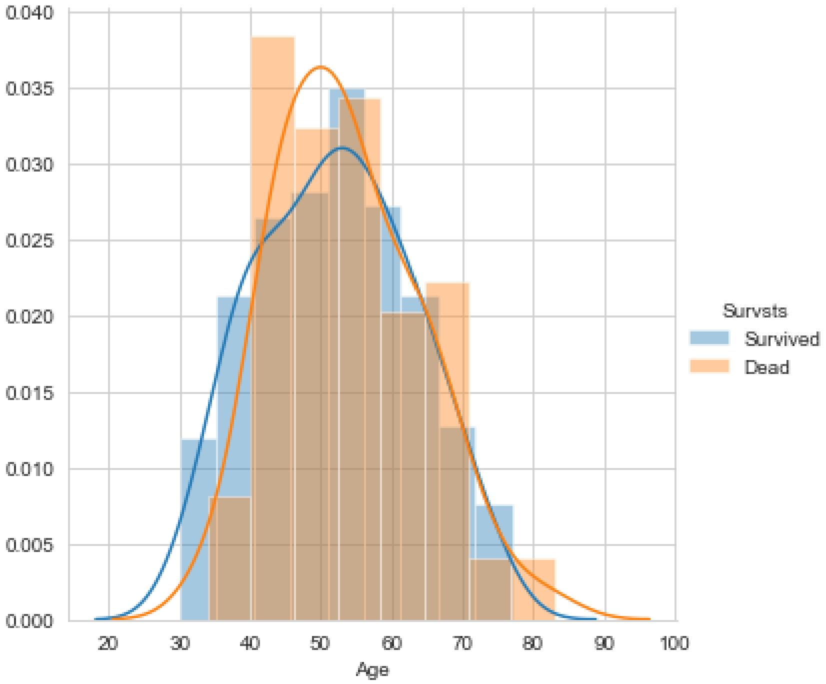
Out[13]:
```
pandas.core.indexes.base.Index
```

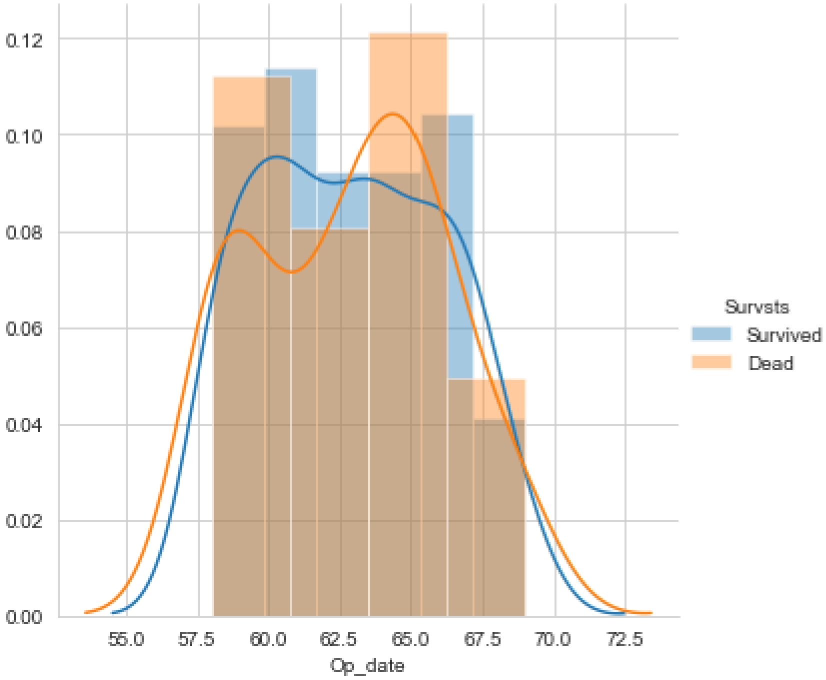
In [14]:
```
list(enumerate(haberman.columns))
```

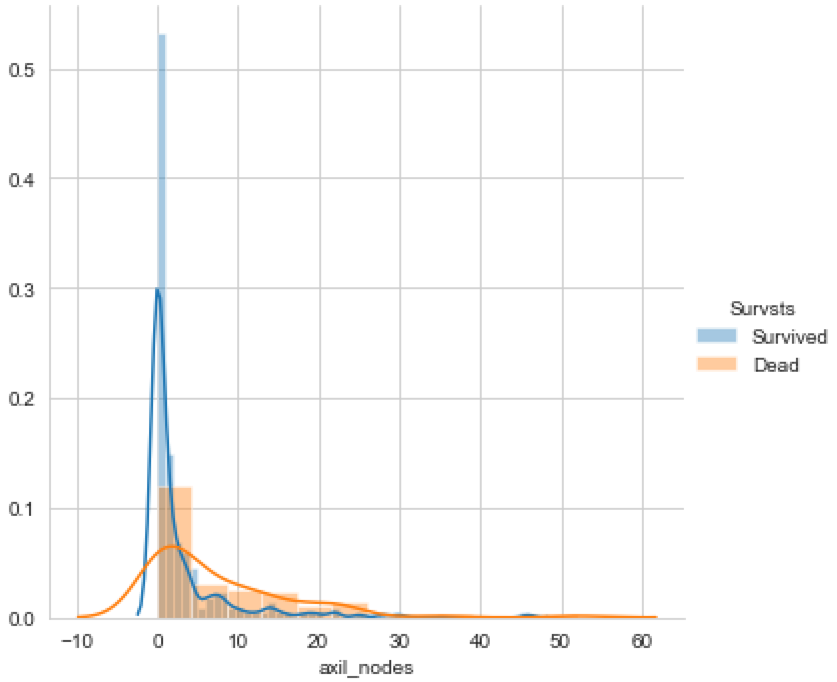
Out[14]:
```
[(0, 'Age'), (1, 'Op_date'), (2, 'axil_nodes'), (3, 'Survsts')]
```

Histogram

In [15]:
```
for index,feat in enumerate(list(haberman.columns)[:-1]):
    sns.set_style("whitegrid")
    sns.FacetGrid(haberman,hue='Survsts',height=5).map(sns.distplot,feat).add_leg
    plt.plot()
```







OBSERVATION

1.From the above figures only axil_nodes figure is somewhat distinguishable

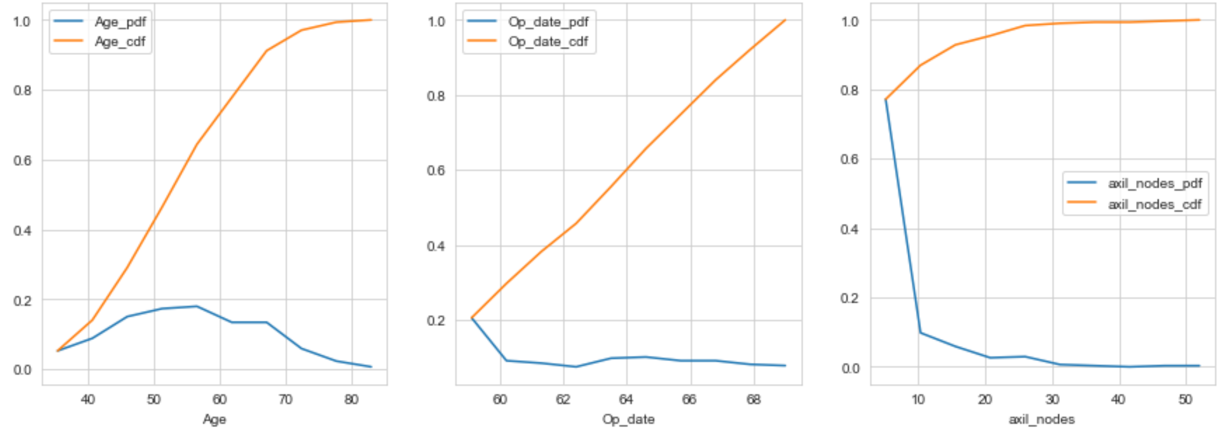
2.The density people survived is more in the range 0-3 axil nodes

PDF , CDF

In [18]:

```
plt.figure(figsize=(15,5))
for index,feat in enumerate(list(haberman.columns)[:-1]):
    plt.subplot(1,3,index+1)
    counts,bin_edges=np.histogram(haberman[feat],bins=10)
    pdf = counts/(sum(counts))

    cdf = np.cumsum(pdf)
    plt.plot(bin_edges[1:],pdf);
    plt.plot(bin_edges[1:], cdf)
    plt.xlabel(feat)
    plt.legend([feat+'_pdf',feat+'_cdf'])
```



OBSERVATION:

1.Here almost 78% of the people have axil nodes less than 5 axil nodes. Other pdfs doesnt help much.

2.For more clarity,lets divide the people who survived 5 years or more after surgery and those who did not survive above 5 years

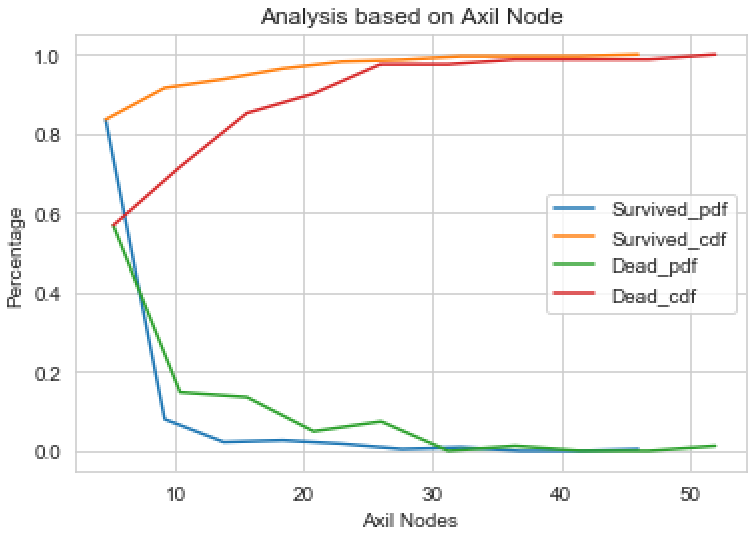
In [20]:

```
haberman_surv=haberman[haberman.Survsts=='Survived']
haberman_dead=haberman[haberman.Survsts=='Dead']
```

In [22]:

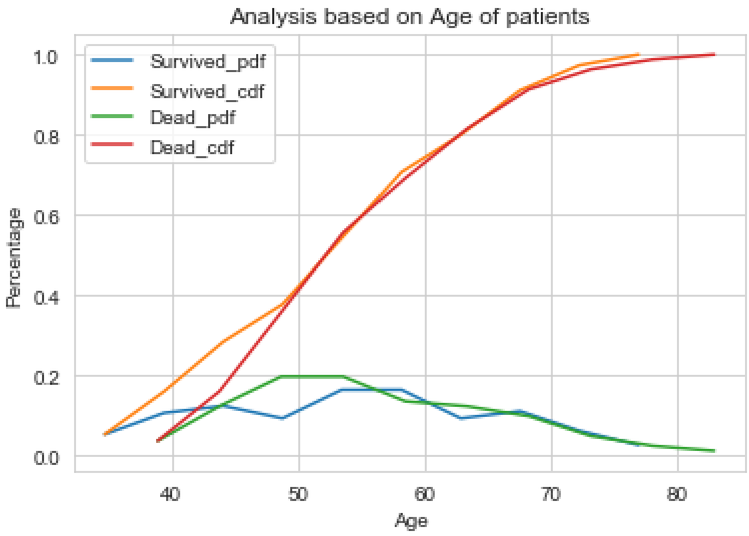
```
counts,bin_edges=np.histogram(haberman_surv['axil_nodes'],bins=10)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)

counts,bin_edges=np.histogram(haberman_dead['axil_nodes'],bins=10)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)
plt.legend(['Survived_pdf','Survived_cdf','Dead_pdf','Dead_cdf'])
plt.xlabel("Axil Nodes")
plt.ylabel("Percentage")
plt.title('Analysis based on Axil Node')
plt.show()
```



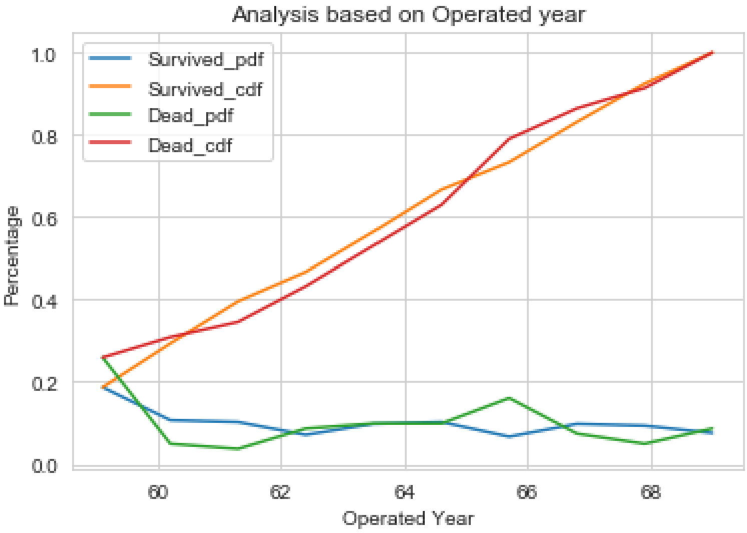
In [23]:
```
counts,bin_edges=np.histogram(haberman_surv['Age'],bins=10)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)

counts,bin_edges=np.histogram(haberman_dead['Age'],bins=10)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)
plt.legend(['Survived_pdf','Survived_cdf','Dead_pdf','Dead_cdf'])
plt.xlabel("Age")
plt.ylabel("Percentage")
plt.title('Analysis based on Age of patients')
plt.show()
```



In [24]:
```
counts,bin_edges=np.histogram(haberman_surv['Op_date'],bins=10)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)

counts,bin_edges=np.histogram(haberman_dead['Op_date'],bins=10)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)
plt.legend(['Survived_pdf','Survived_cdf','Dead_pdf','Dead_cdf'])
plt.xlabel("Operated Year")
plt.ylabel("Percentage")
plt.title('Analysis based on Operated year')
plt.show()
```



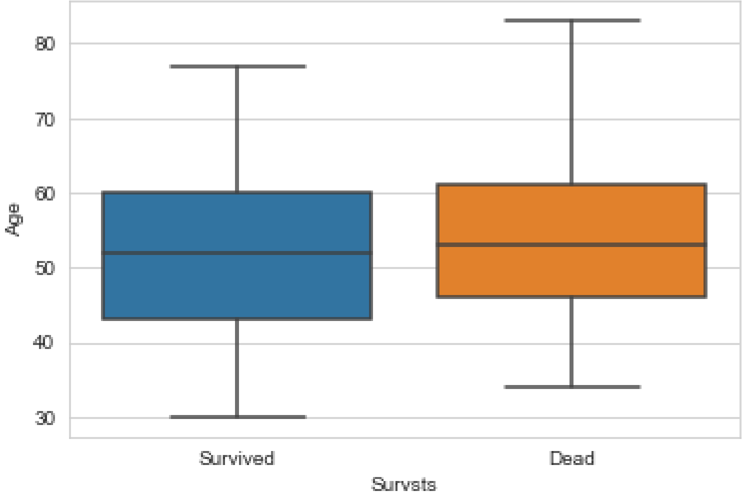
OBSERVATIONS:

1.83% of the people survived has less than 5 axil nodes which means only 17% of people survived has more than 5 axil nodes. Similarly, 42-44% of the people dead has more than 5 axil nodes. People having above 46 nodes obviously died.

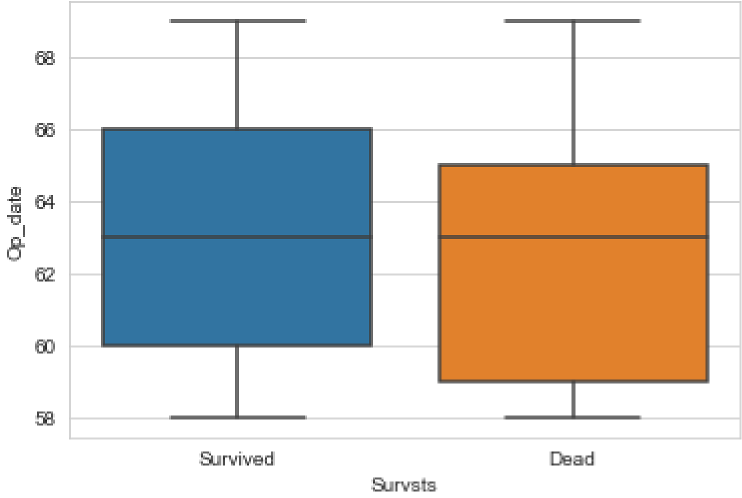
2.People less than 38 years survived. People with cancer symptoms lived maximum upto 77 years.

Box Plot

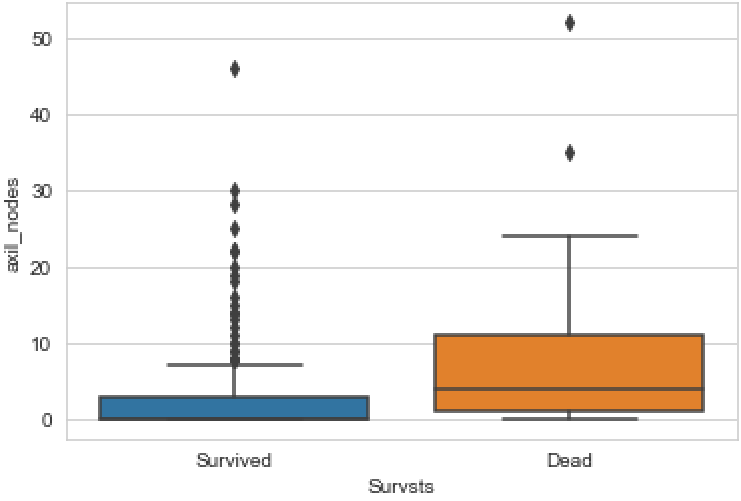
In [25]:
```
sns.boxplot(x='Survsts',y='Age',data=haberman)
plt.show()
```



In [26]:
```
sns.boxplot(x='Survsts',y='Op_date',data=haberman)
plt.show()
```

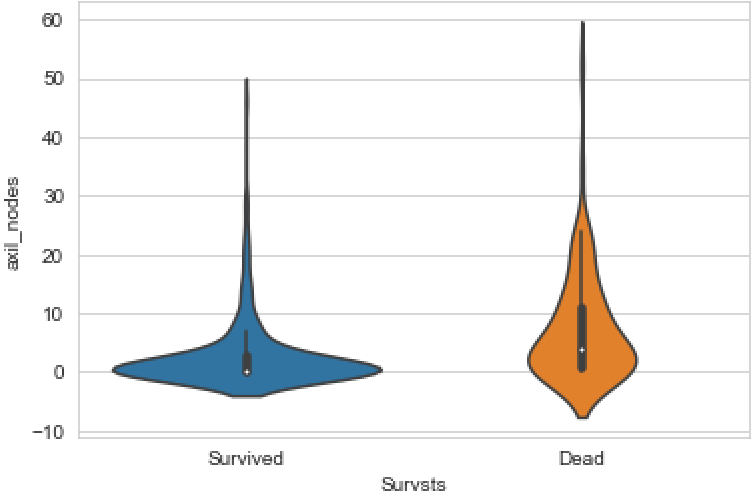


```
In [183]: sns.boxplot(x='Survsts',y='axil_nodes',data=haberman)
          plt.show()
```

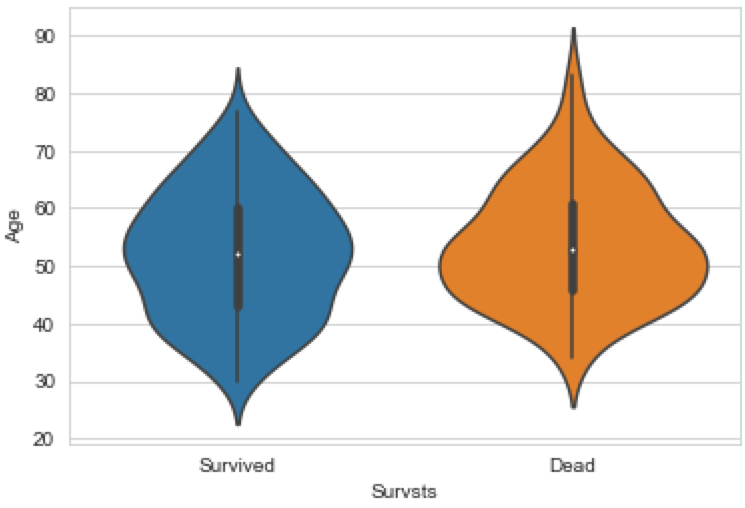


Violin Plot

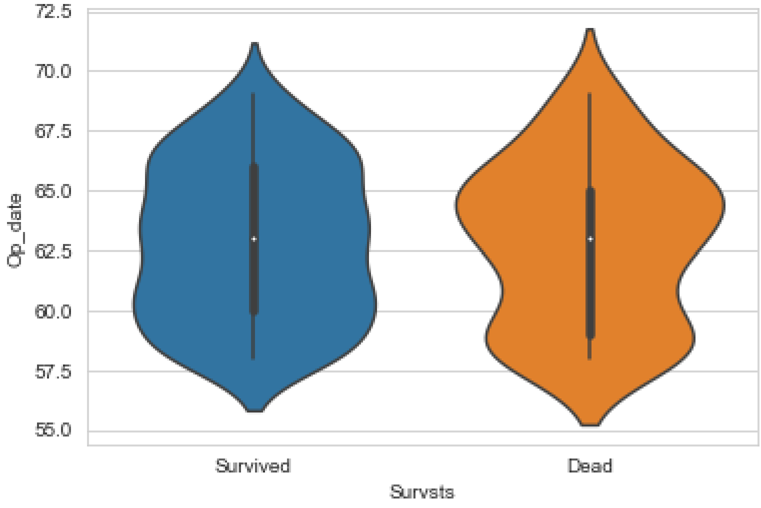
```
In [184]: sns.violinplot(x='Survsts',y='axil_nodes',data=haberman,size=5)
          plt.show()
```



In [29]:
```
sns.violinplot(x='Survsts',y='Age',data=haberman,size=5)
plt.show()
```



In [28]:
```
sns.violinplot(x='Survsts',y='Op_date',data=haberman,size=5)
plt.show()
```

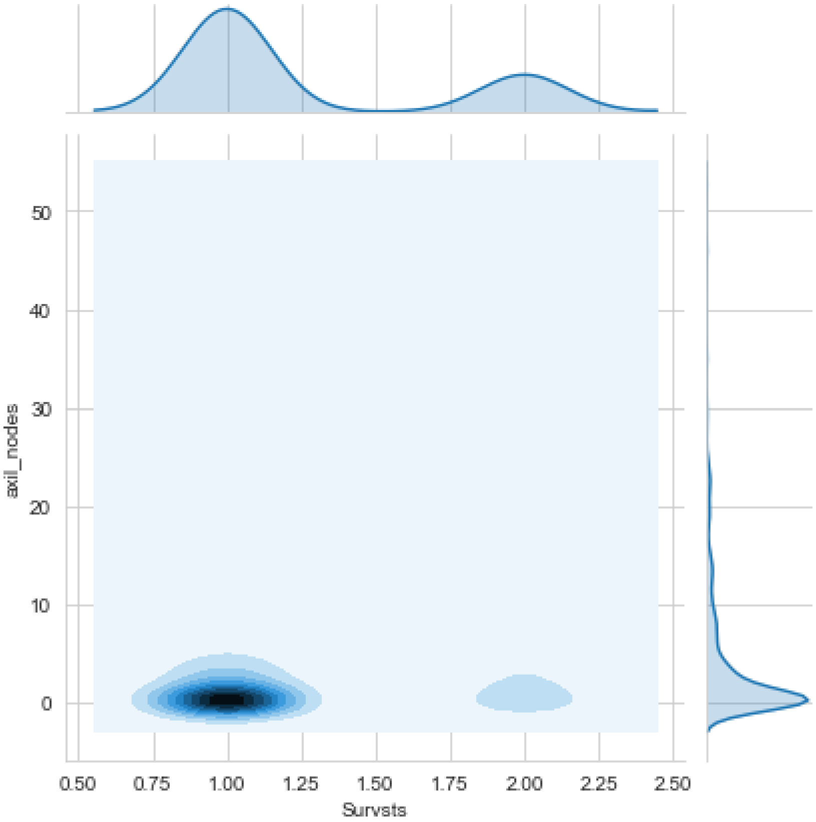


Observations

```
1.50th percentile of survivors have 0 nodes, 75th percentie of survivors have
less than 3 axil nodes

2.25th percentile of dead have 1 axil node, 50th percentile of dead have axil
nodes below 4,75th percentile of dead have axil nodes below 11.
```

```
In [48]: sns.jointplot(x="Survsts", y="axil_nodes", data=haberman, kind="kde");
         plt.show();
```



CONCLUSION

1.From the 3 Scatter plots, we cannot obtain any conclusions due to overlapping

2.From the Histogram, only axil_nodes figure is somewhat distinguishable

3.And, the density people survived is more in the range 0-3 axil nodes

4.From pdfs,cdfs 83% of the people survived has less than 5 axil nodes which means only 17% of people survived has more than 5 axil nodes. Similarly, 42-44% of the people dead has more than 5 axil nodes. People having above 46 nodes obviously died.

5.People less than 38 years survived. People with cancer symptoms lived maximum upto 77 years.

6.From boxplots, 50th percentile of survivors have 0 nodes, 75th percentie of survivors have less than 3 axil nodes & 25th percentile of dead have 1 axil node, 50th percentile of dead have axil nodes below 4,75th percentile of dead have axil nodes below 11.

7.Finally we get only one conclusion :if number of axillary node is less,than survival of patients is more. We need more features to comes on very good conlusion

```
In [ ]:
```