In [16]:
```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
import os
os.chdir("/users/sujis/Downloads/Applied AI")
#Load Haberman.csv into a pandas dataFrame.
haberman=pd.read_csv('haberman.csv')
```

In [17]:
```
# (Q) how many data-points and features?
print (haberman.shape)
```

```
(306, 4)
```

In [18]:
```
# (Q) What are the column names present in the Haberman Data Set?
print (haberman.columns)
```

```
Index([u'Age', u'Operation Year', u'Axil Node', u'Survival Status'], dtype='o
bject')
```

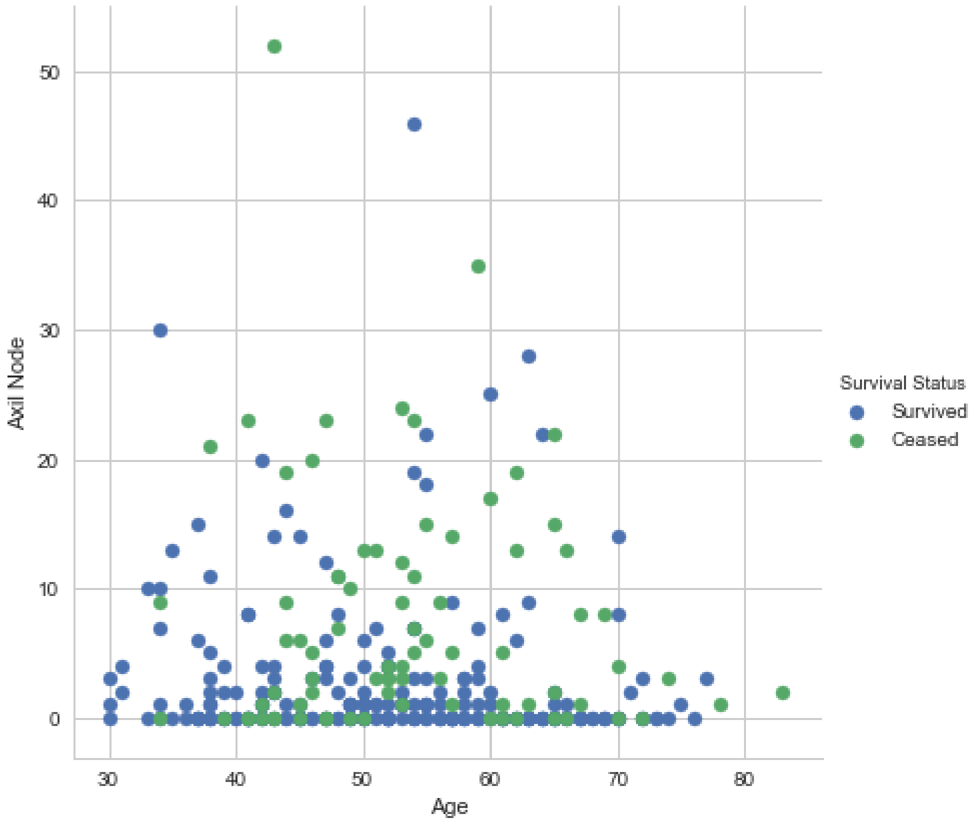
In [19]:
```
# (Q) How many patients have will survive the cancer present in the dataset ?
# 1 in Suv_status represents 1 = the patient survived 5 years or longer (Yes)
 2 = the patient died within 5 year (No)
# Replaced the values of Survival Status with the strings for the better under
standing.

haberman['Survival Status'] = haberman['Survival Status'].map({1: 'Survived',
2: 'Ceased'})
haberman['Survival Status'].value_counts()

#haberman is an unbalanced dataset as patients survival percentages are 73.5%
 & 26.4%
```

Out[19]:
```
Survived    225
Ceased       81
Name: Survival Status, dtype: int64
```

Observations

1. The Haberman Dataset is an unbalanced dataset.
2. The patients survival ratio is approximately 3:1

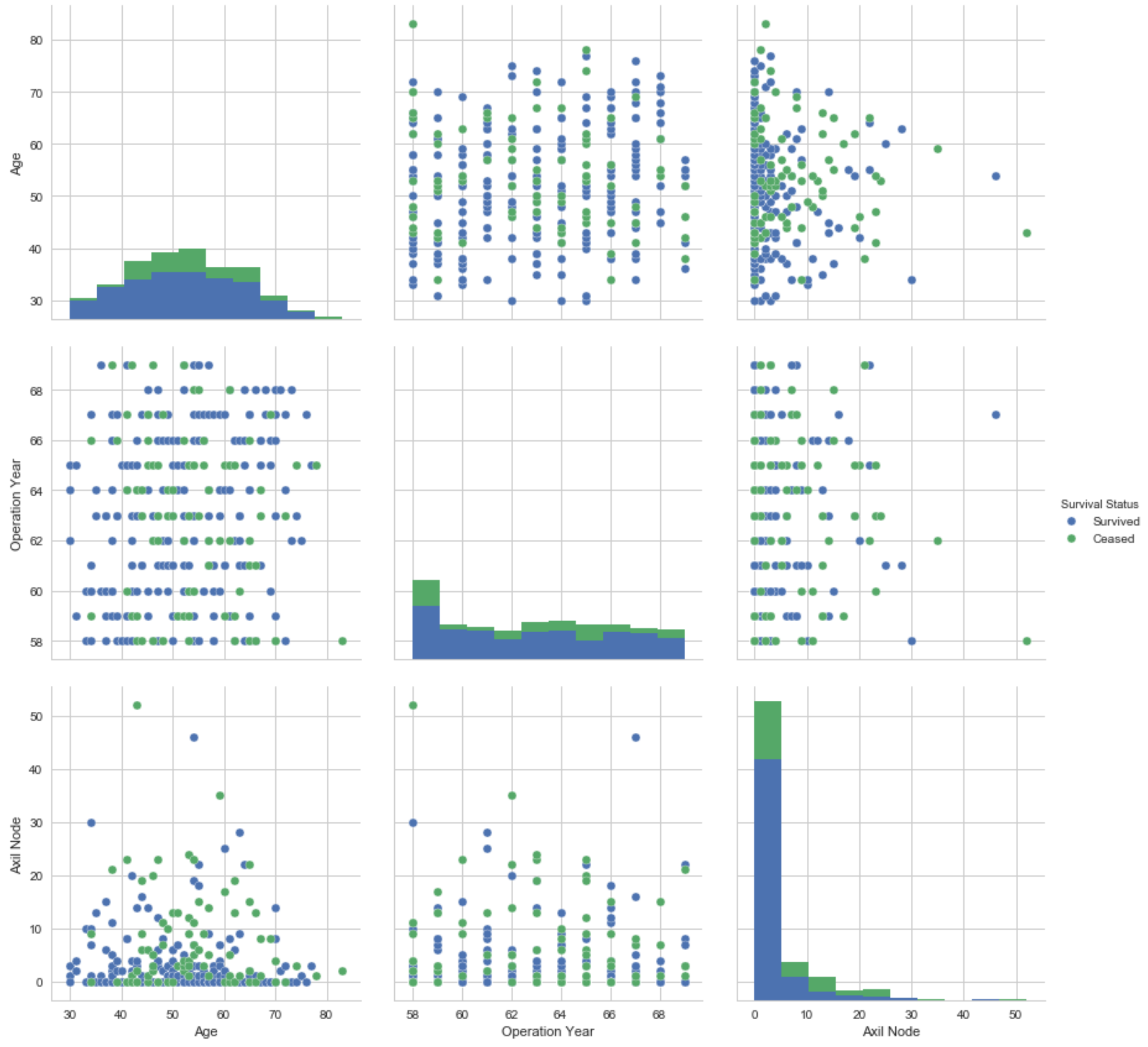
```
In [28]: #2D Scatterplot with color coding for survival status
         sns.set_style("whitegrid");
         sns.FacetGrid(haberman, hue="Survival Status", size=6) \
            .map(plt.scatter, "Age", "Axil Node") \
            .add_legend();
         plt.show();
```



Observation(s):

1. Seperating Survived patients from Ceased patients is much harder as the data points are very clumsy

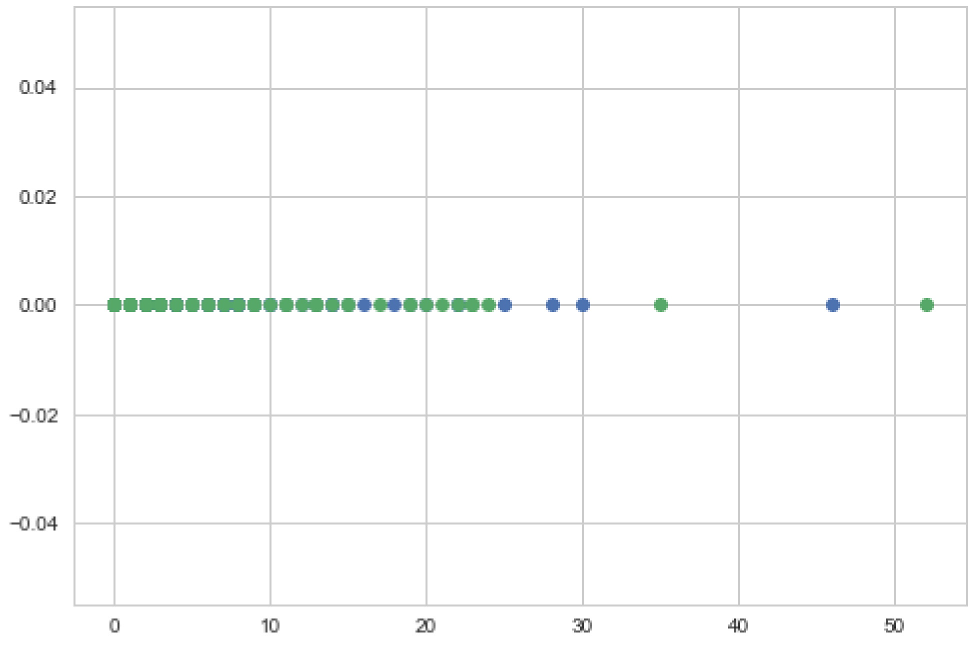
In [22]:
```
#Pair Plot
plt.close();
sns.set_style("whitegrid");
sns.pairplot(haberman, hue="Survival Status", size=4);
plt.show()
```



Oberservatons

1. It is very dificult to define any conditions to classify patients survival status since both are overlapping extensively.

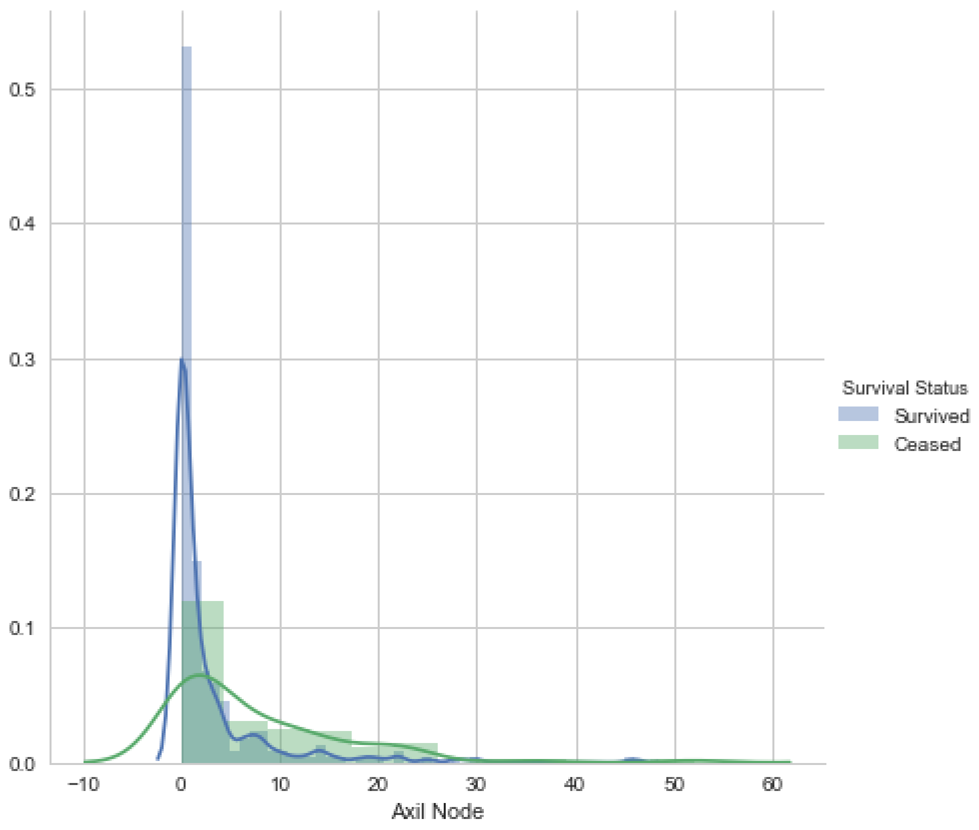
```
In [29]: # What about 1-D scatter plot using just one feature?
         import numpy as np
         Survived= haberman.loc[haberman["Survival Status"] == "Survived"];
         Ceased= haberman.loc[haberman["Survival Status"] == "Ceased"];

         plt.plot(Survived["Axil Node"], np.zeros_like(Survived['Axil Node']), 'o')
         plt.plot(Ceased["Axil Node"], np.zeros_like(Ceased['Axil Node']), 'o')

         plt.show()
```

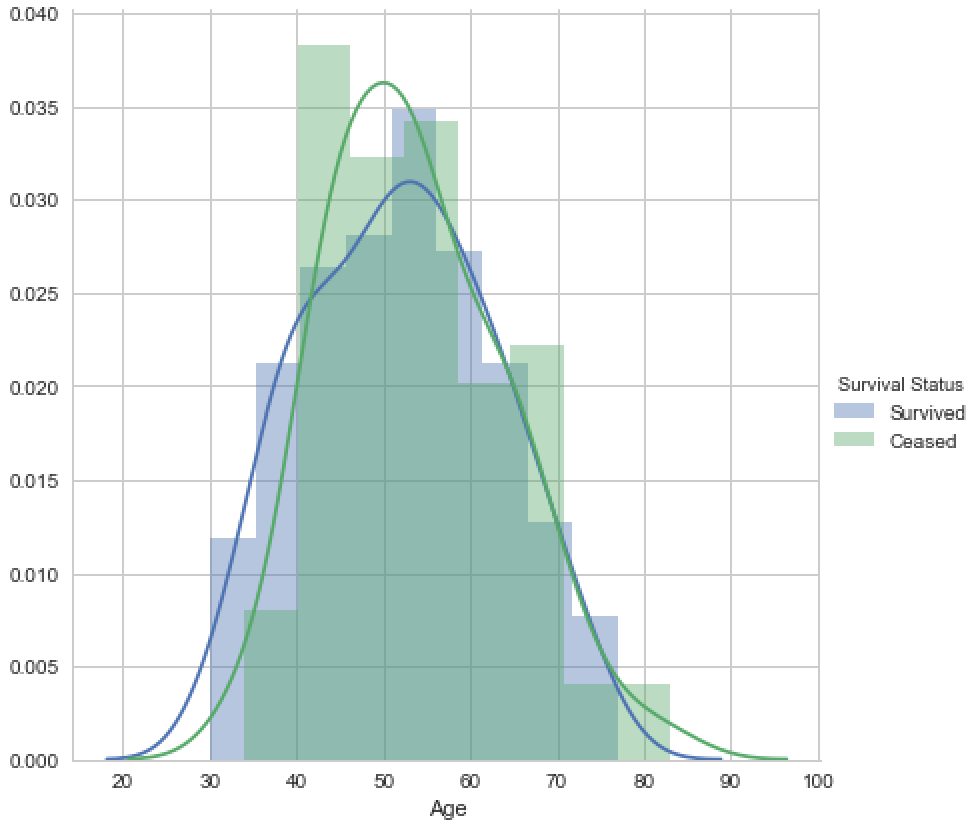


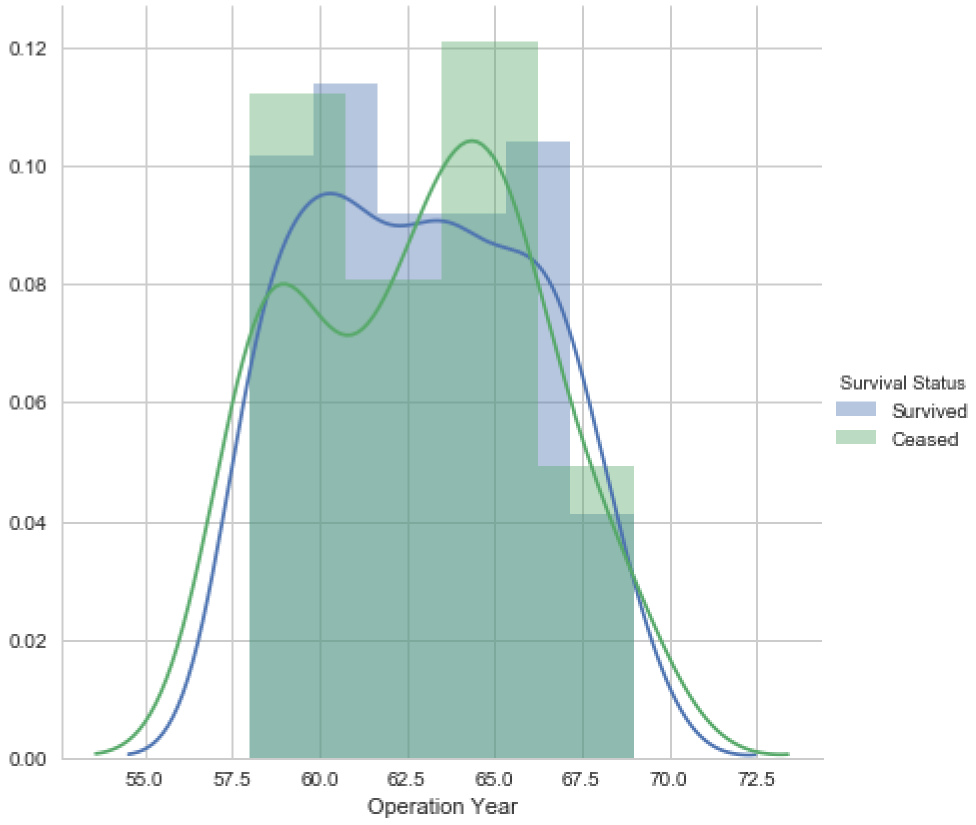
Obersvations

1. The 1D scatterplot won't give any understanding as they are overlapping a lot.

In [23]:
```
#Hisogram & PDF for each and every variable
sns.FacetGrid(haberman, hue="Survival Status", size=6) \
   .map(sns.distplot, "Axil Node") \
   .add_legend();
sns.FacetGrid(haberman, hue="Survival Status", size=6) \
   .map(sns.distplot, "Age") \
   .add_legend();
sns.FacetGrid(haberman, hue="Survival Status", size=6) \
   .map(sns.distplot, "Operation Year") \
   .add_legend();

plt.show();
```


0.5
0.4
0.3
0.2
0.1
0.0
−10
0
10
20
30
40
50
60
Axil Node
Survival Status
Survived
Ceased


0.040
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
20
30
40
50
60
70
80
90
100
Age
Survival Status
Survived
Ceased

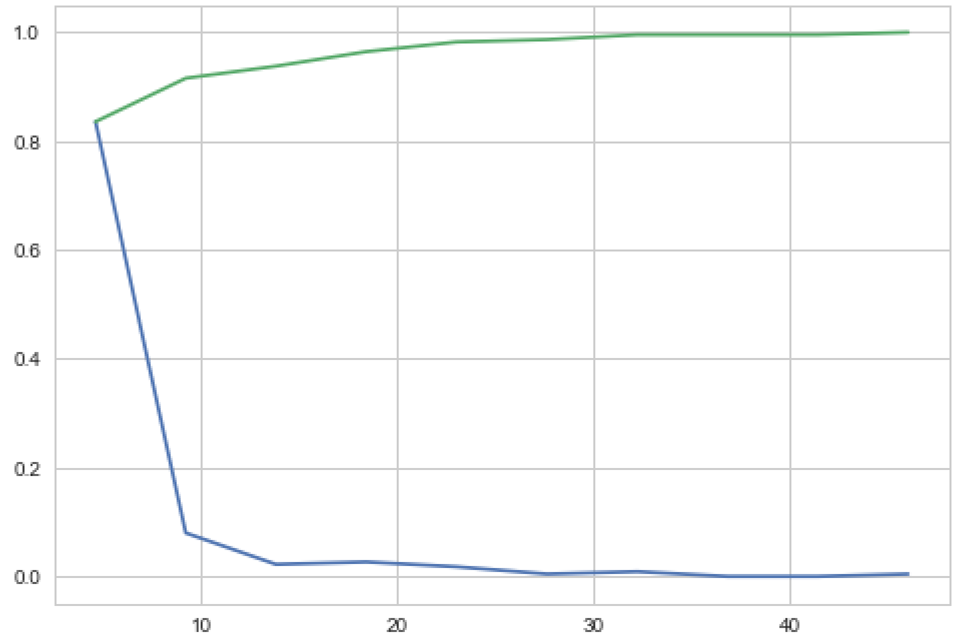


Observations

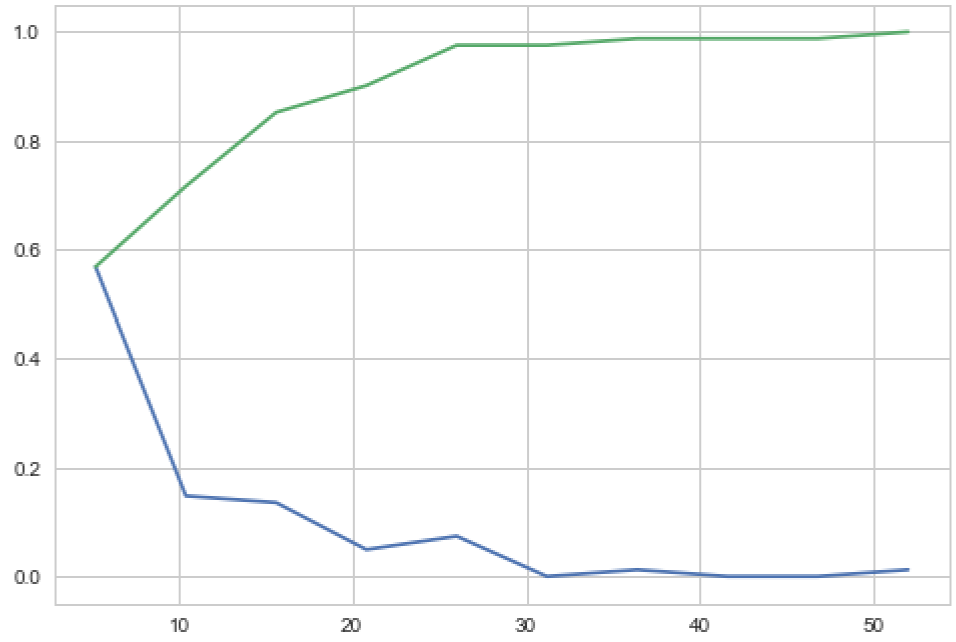
1. By the historams of all variables in the dataset, Distribution of data points Axil Node is very narrow. On the other hand for Age & Operation Year, the disribution of data points is broad yet very hard to frame a logic to classify due to overlap.
2. Axil Node is the bes variable compared to Age & Operation year.

In [50]:
```
#Survived
counts, bin_edges = np.histogram(Survived['Axil Node'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)

#compute CDF of Survived Patients
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)

plt.show();

#Ceased
counts, bin_edges = np.histogram(Ceased['Axil Node'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)

#compute CDF of Ceased Patients
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


plt.show();
```

```
[ 0.83555556  0.08        0.02222222  0.02666667  0.01777778  0.00444444
  0.00888889  0.          0.          0.00444444]
[  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. ]
```



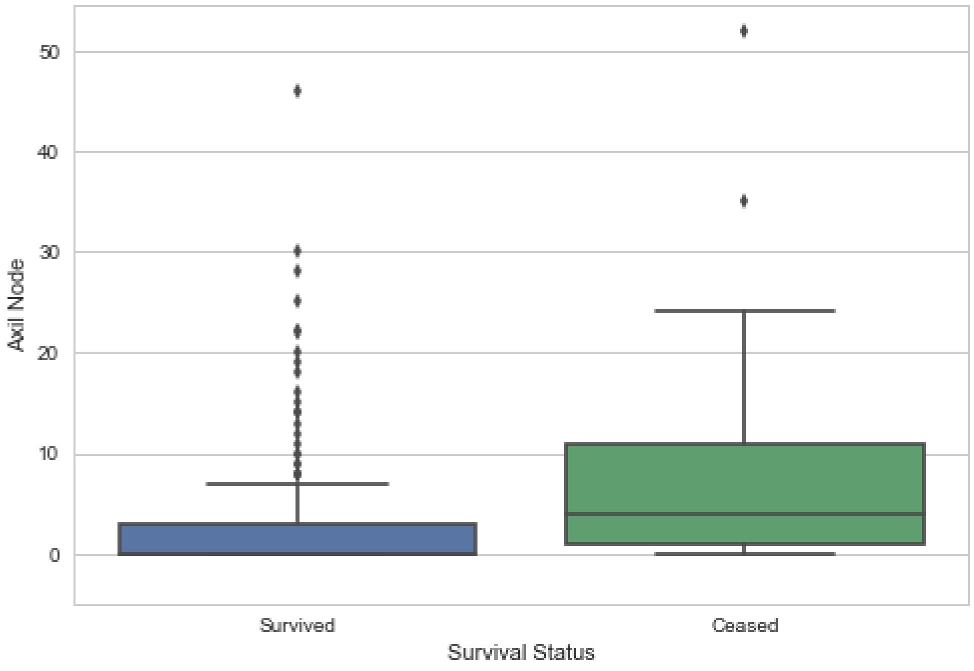
In [43]:
```
#Univariate Analysis of "Axil Node"
#Mean, Variance, Std-deviation,
print("Means:")
print('Survived',np.mean(Survived["Axil Node"]))
print('Ceased',np.mean(Ceased["Axil Node"]))

print("\nStd-dev:");
print('Survived',np.std(Survived["Axil Node"]))
print('Ceased',np.std(Ceased["Axil Node"]))

print("\nMedian:")
print('Survived',np.median(Survived["Axil Node"]))
print('Ceased',np.median(Ceased["Axil Node"]))

from statsmodels import robust
print("\nMad:");
print('Survived',robust.mad(Survived["Axil Node"]))
print('Ceased',robust.mad(Ceased["Axil Node"]))

print("\nPercentiles:25% 50% 75% 100% ")
print('Survived',np.percentile(Survived["Axil Node"],np.arange(25, 125, 25)))
print('Ceased',np.percentile(Ceased["Axil Node"],np.arange(25, 125, 25)))

print("\nQuantiles:")
print('Survived',np.percentile(Survived["Axil Node"],90))
print('Ceased',np.percentile(Ceased["Axil Node"],90))
```

```
Means:
('Survived', 2.7911111111111113)
('Ceased', 7.45679012345679)

Std-dev:
('Survived', 5.857258449412131)
('Ceased', 9.128776076761632)

Median:
('Survived', 0.0)
('Ceased', 4.0)

Mad:
('Survived', 0.0)
('Ceased', 5.9304088740224081)

Percentiles:25% 50% 75% 100%
('Survived', array([  0.,   0.,   3.,  46.]))
('Ceased', array([  1.,   4.,  11.,  52.]))

Quantiles:
('Survived', 8.0)
('Ceased', 20.0)
```

Observations

1. By seeing the output we can say that most of the data points in the "survived" class are 0, infact approximately 50% data points are less than "Zero(0)"
2. For "Ceased" class 50% data points are less than "4".

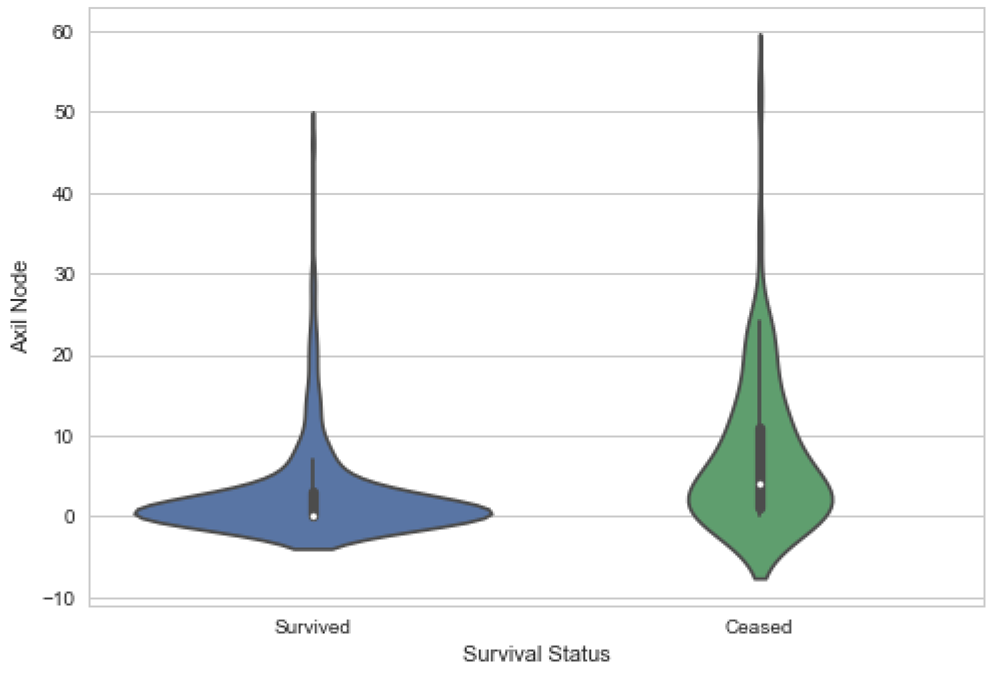
```
In [48]: #Box Plot
         sns.boxplot(x='Survival Status',y='Axil Node', data=haberman)
         sns.plt.ylim(-5, None)
         plt.show()
```



Observations

1. The Lower whisker, 25% and 50% are combined since the 50% data points are 0 and min data point is also 0.
2. The 75% Survived class quartile & 50% Ceased class has same number of Axil Nodes.

In [33]:
```
#Violin Plot
sns.violinplot(x="Survival Status", y="Axil Node", data=haberman, size=8)
plt.show()
```


Axil Node
Survived
Ceased
Survival Status