Objective :

To analyse :
1.If patient lives for 5 years or longer
2.If patient dies within 5 years

In [117]:
```
import seaborn as sns
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
```

There are three features:

1.Age of the patient at the time of operation.
2.Year in which the operation took place(1900).
3.number of positive axillary nodes.(A positive axillary lymph node is a lymph node in the area to which cancer has spread.)

Output variable : Survival status of the patient

In [118]:
```
#reading the haberman.csv file
#naming columns as['age','year','node','survival']
value=pd.read_csv("haberman.csv",names=['age','op_year','ax_node','survival_stat'

#knowing the shape i.e number of rows and columns
print(value.shape)
```

```
(306, 4)
```

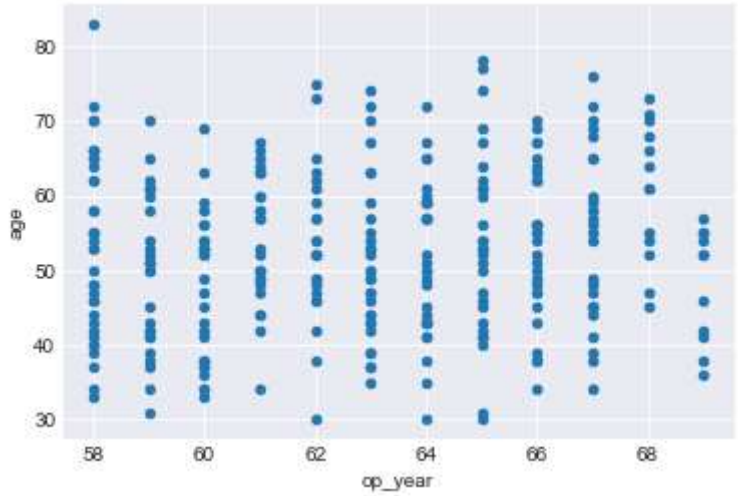
The file has 306 rows and 4 columns.

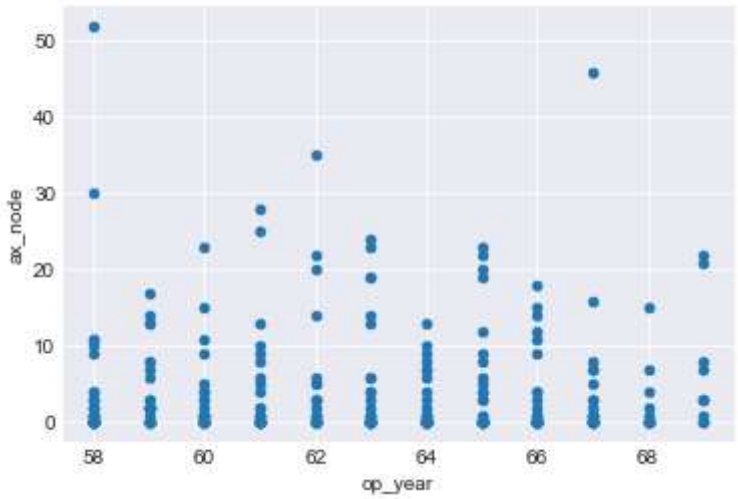
In [119]:
```
print(value.survival_stat.value_counts())  #this to check the total number of sur
```

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

1 are patient who have lived for 5 years and more
2 are patient who died in 5 years

In [120]:
```
value.plot(kind="scatter",x="op_year",y="age")       #plot of age vs operation yea
value.plot(kind="scatter",x="op_year",y="ax_node")   #plot of axilliary node vs op
plt.show()
```



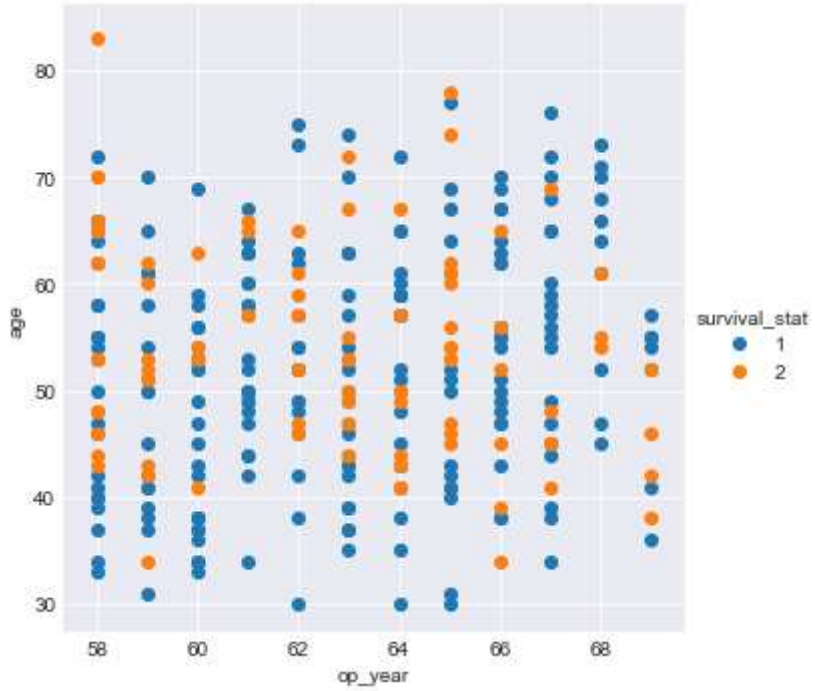


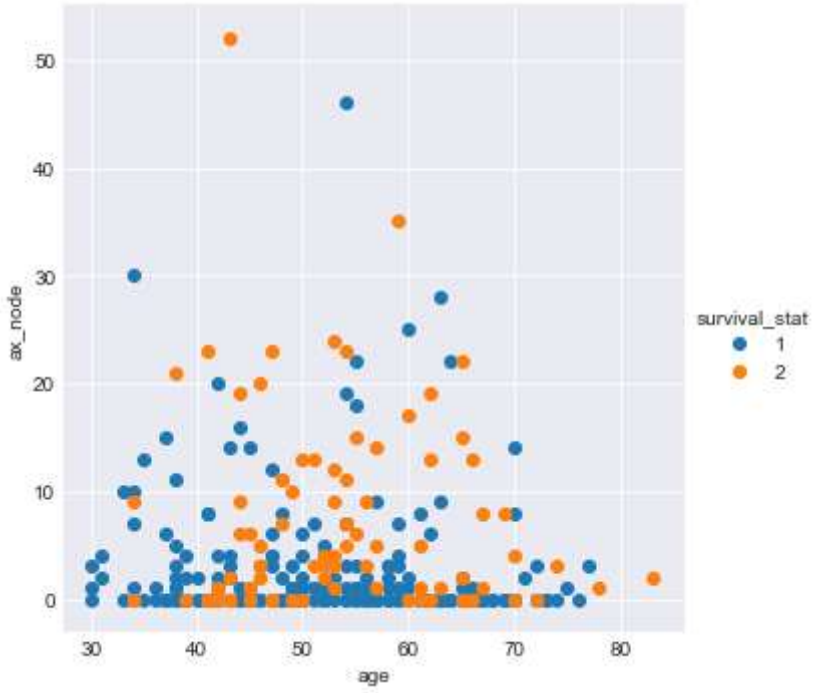
Observation :

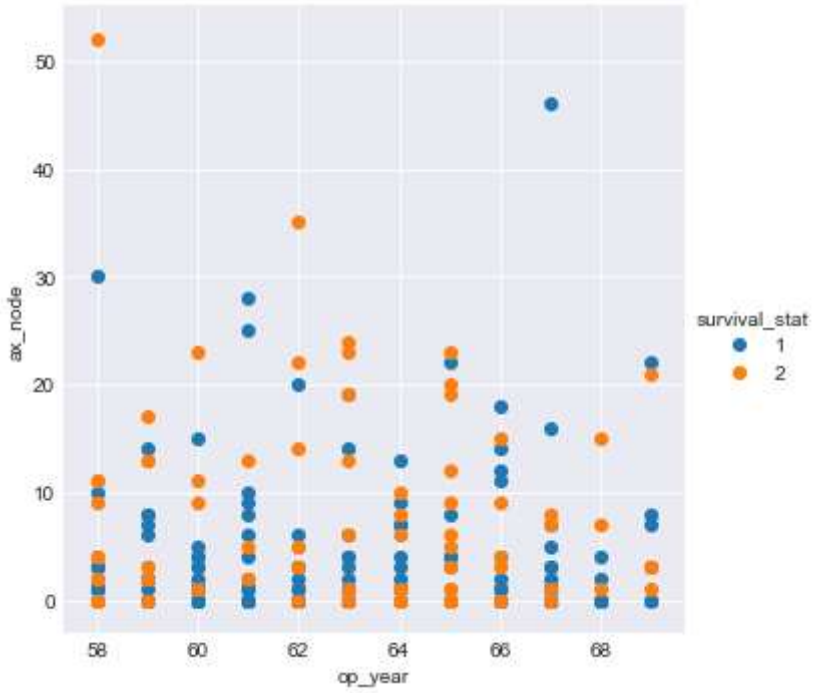
In the above plots we are not able to find anything useful,as we are not able to differentiate. Let us try other types of plot and try to extract useful information.

we have to colour the output value to understand the difference.

In [121]:
```
sns.set_style("darkgrid")
#plot of age vs operation year
sns.FacetGrid(value,hue='survival_stat',size=5).map(plt.scatter,'op_year','age').
#plot of axilliary node vs age
sns.FacetGrid(value,hue='survival_stat',size=5).map(plt.scatter,'age','ax_node').
#plot of axilliary node vs operation year
sns.FacetGrid(value,hue='survival_stat',size=5).map(plt.scatter,'op_year','ax_nod
plt.show()
```







Let us use pair plotting to see other possibilities and try to extract some useful data.

pair plotting comes under multi variate, it gives all possibilites of graph(it is useful only when we have less features)

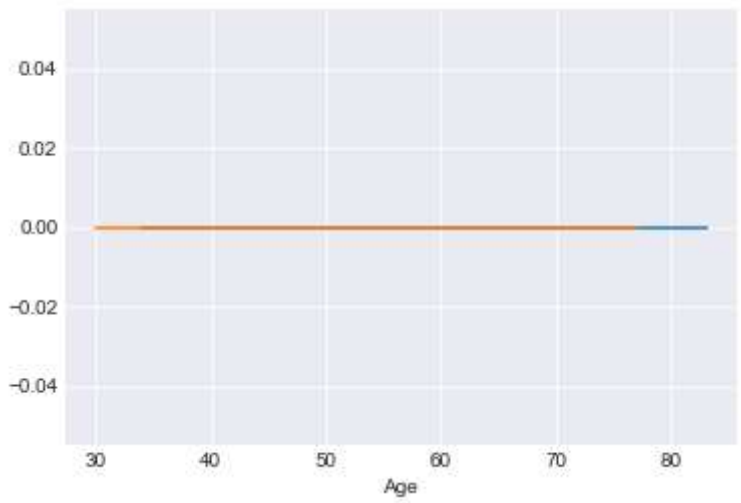
In [122]:
```
sns.set_style("darkgrid")
#hue : Variable in "value" which is to be differentiated.
#vars : It makes combinations of all the plots in vars,otherwise it takes all col
sns.pairplot(value,hue="survival_stat",vars=['age','op_year','ax_node'],size=6)
plt.show()
```

Observation :

All these plots are not able to produce different pattern to predict survival status.

So we have to try other methods (univariate) like pdf ,cdf ,boxplot ,violinplot.

In [123]:
```
under_5=value.loc[value.survival_stat==2] #patient died within 5 years
over_5=value.loc[value.survival_stat==1]  #patient lived 5 years or more
plt.plot(under_5.age,np.zeros_like(under_5.age))
plt.plot(over_5.age,np.zeros_like(over_5.age))
plt.xlabel("Age")
plt.show()
```



observation :

This 1D plot is not at all useful as both lines are overlapping, making no useful information extraction

In [124]:
```
sns.FacetGrid(value,hue="survival_stat",size=5).map(sns.distplot,'age').add_legen
sns.FacetGrid(value,hue="survival_stat",size=5).map(sns.distplot,'op_year').add_l
sns.FacetGrid(value,hue="survival_stat",size=5).map(sns.distplot,'ax_node').add_l
plt.show()
```

```
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erWarning: The 'normed' kwarg is deprecated, and has been replaced by the 'dens
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  warnings.warn("The 'normed' kwarg is deprecated, and has been "
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  warnings.warn("The 'normed' kwarg is deprecated, and has been "
```
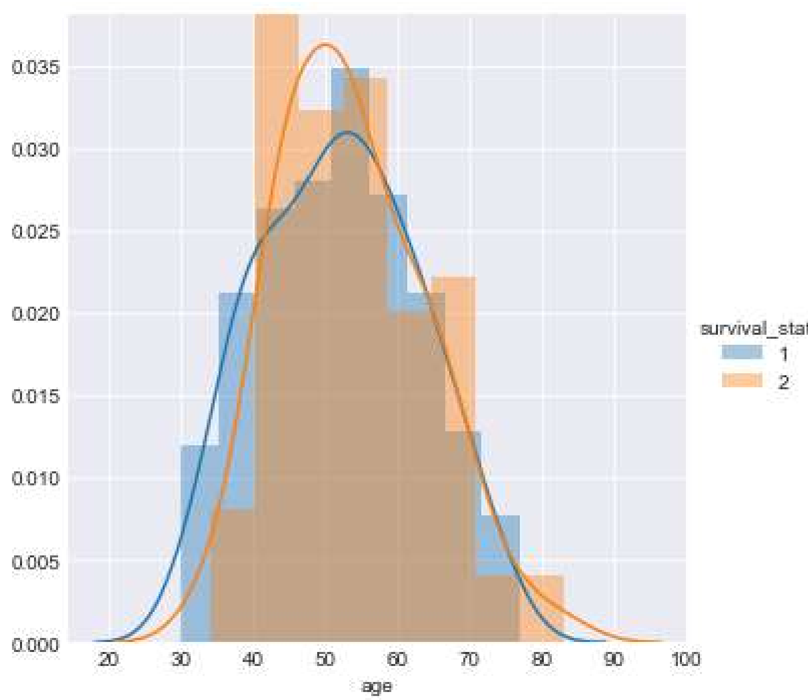
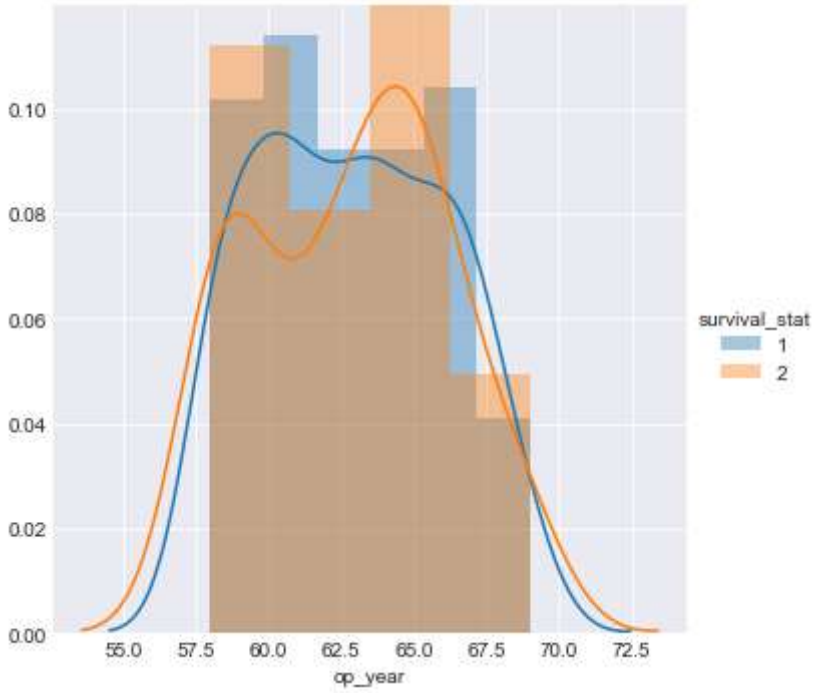
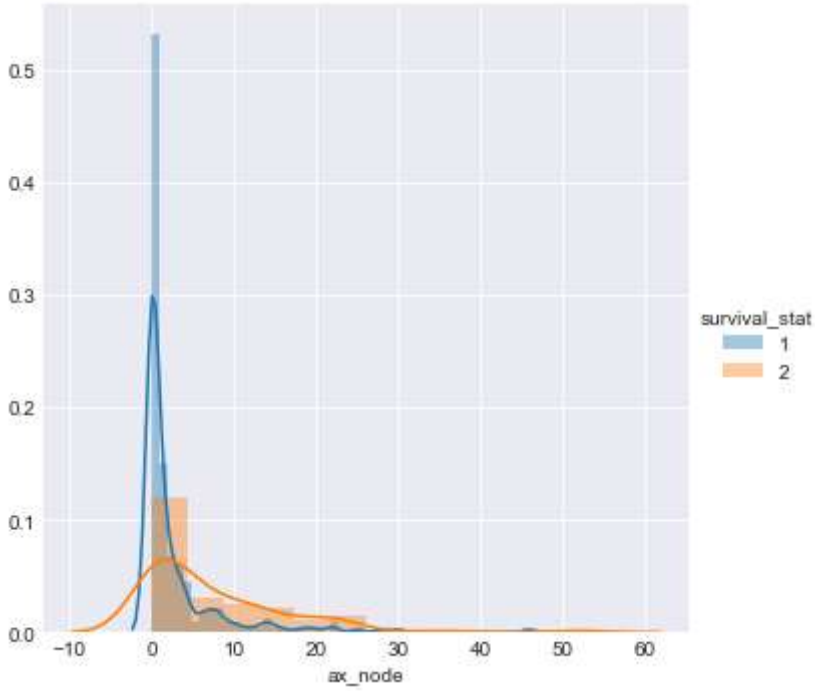



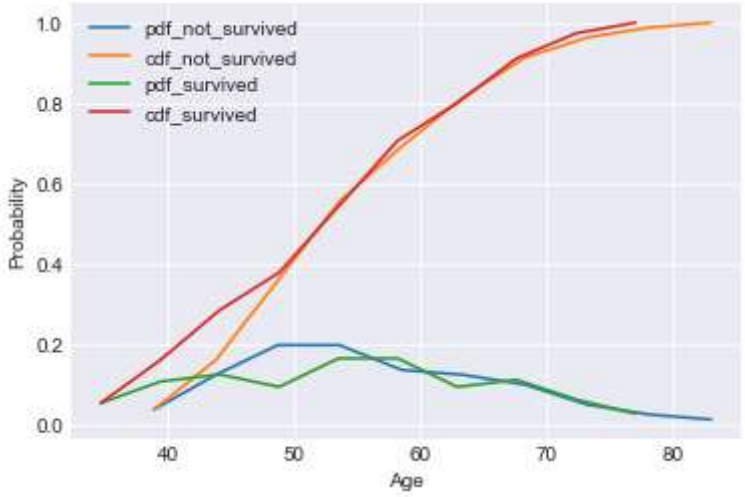




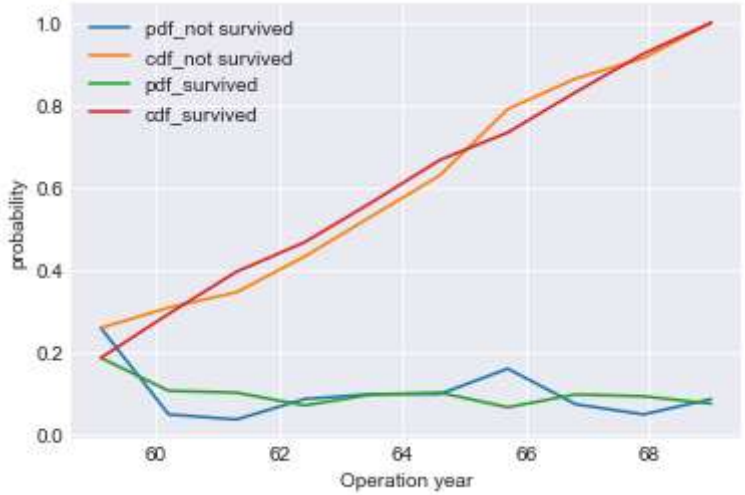
Observation :

According to the plots , histogram and pdf are not useful for extracting information.
As they both are overlapped for respective survival status.

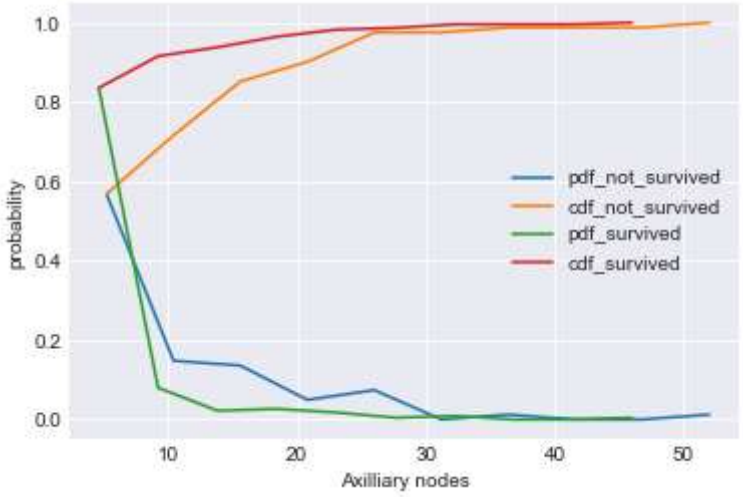
In [125]:
```
#plotting both survival status
c_age,b_age=np.histogram(under_5.age,bins=10,density=True)
c_age_s,b_age_s=np.histogram(over_5.age,bins=10,density=True)

pdf_ns=c_age/sum(c_age)
cdf_ns=np.cumsum(pdf_ns)
pdf_s=c_age_s/sum(c_age_s)
cdf_s=np.cumsum(pdf_s)

plt.plot(b_age[1:],pdf_ns)
plt.plot(b_age[1:],cdf_ns)
plt.plot(b_age_s[1:],pdf_s)
plt.plot(b_age_s[1:],cdf_s)

plt.xlabel("Age")
plt.ylabel("Probability")
plt.legend(['pdf_not_survived','cdf_not_survived','pdf_survived','cdf_survived'])
plt.show()
```



In [126]:
```
c_op,b_op=np.histogram(under_5.op_year,bins=10,density=True)
c_op_s,b_op_s=np.histogram(over_5.op_year,bins=10,density=True)

pdf_ns=c_op/sum(c_op)
cdf_ns=np.cumsum(pdf_ns)
pdf_s=c_op_s/sum(c_op_s)
cdf_s=np.cumsum(pdf_s)

plt.plot(b_op[1:],pdf_ns)
plt.plot(b_op[1:],cdf_ns)
plt.plot(b_op_s[1:],pdf_s)
plt.plot(b_op_s[1:],cdf_s)

plt.xlabel("Operation year")
plt.ylabel("probability")
plt.legend(['pdf_not survived','cdf_not survived','pdf_survived','cdf_survived'])
plt.show()
```



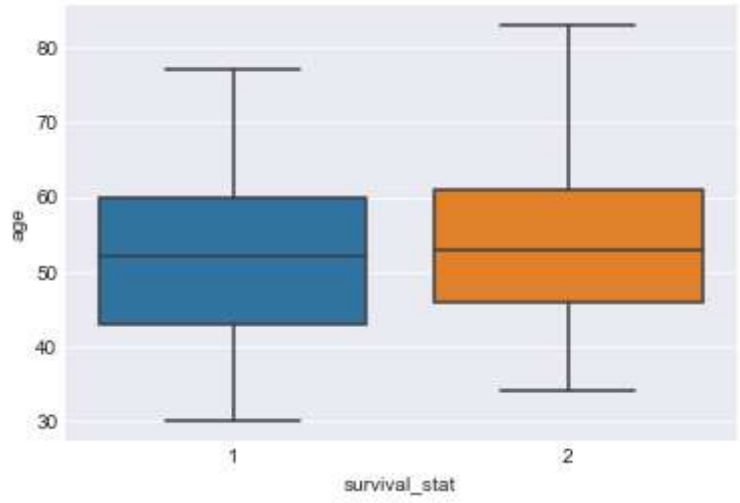
In [127]:
```
c_ax,b_ax=np.histogram(under_5.ax_node,bins=10,density=True)
c_ax_s,b_ax_s=np.histogram(over_5.ax_node,bins=10,density=True)


pdf_ns=c_ax/sum(c_ax)
cdf_ns=np.cumsum(pdf_ns)
pdf_s=c_ax_s/sum(c_ax_s)
cdf_s=np.cumsum(pdf_s)

plt.plot(b_ax[1:],pdf_ns)
plt.plot(b_ax[1:],cdf_ns)
plt.plot(b_ax_s[1:],pdf_s)
plt.plot(b_ax_s[1:],cdf_s)

plt.xlabel("Axilliary nodes")
plt.ylabel("probability")
plt.legend(['pdf_not_survived','cdf_not_survived','pdf_survived','cdf_survived'])
plt.show()
```

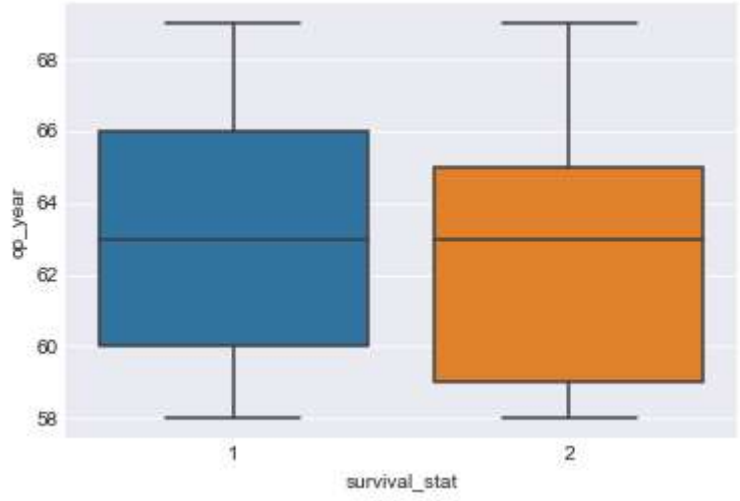


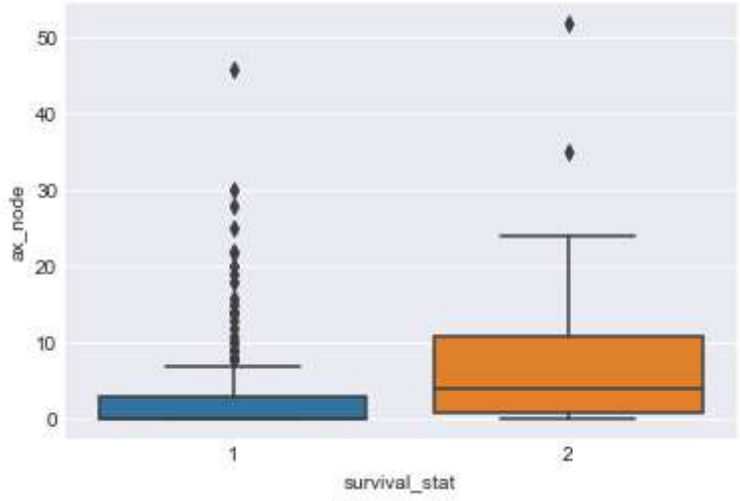
Observation :

As we can see pdf are also overlapping a lot it is difficult to differentiate with pdf.
Lets try boxplot and violinplot.

In [128]:
```
sns.boxplot(x="survival_stat",y="age",data=value)
plt.show()
sns.boxplot(x="survival_stat",y="op_year",data=value)
plt.show()
sns.boxplot(x="survival_stat",y="ax_node",data=value)
plt.show()
```







Observation:

Boxplot is also not helpful as 25th,50th,75th percentile have approximately same values.
lets once check for mean ,median ,std.

In [143]:
```
print(over_5.describe())
print("*"*57)
print(under_5.describe())
```

```
              age     op_year     ax_node  survival_stat
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
*********************************************************
             age    op_year    ax_node  survival_stat
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
```

In [140]:
```
print(under_5.median())
print("*")
print(over_5.median())
```

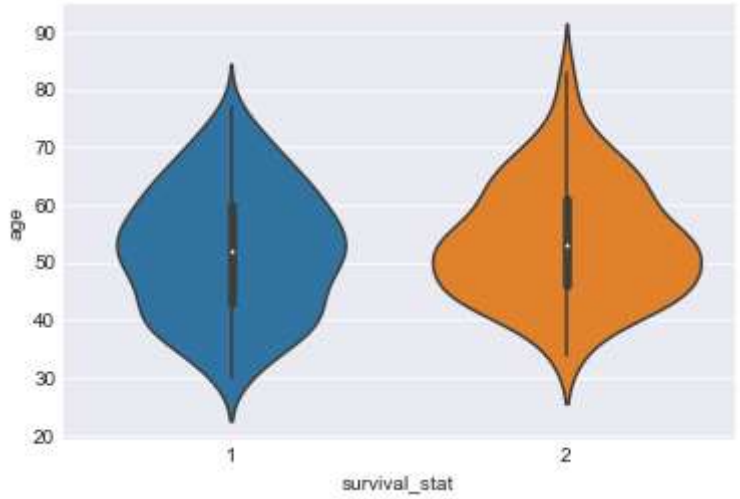
```
age              53.0
op_year          63.0
ax_node           4.0
survival_stat     2.0
dtype: float64
**********
age              52.0
op_year          63.0
ax_node           0.0
survival_stat     1.0
dtype: float64
```

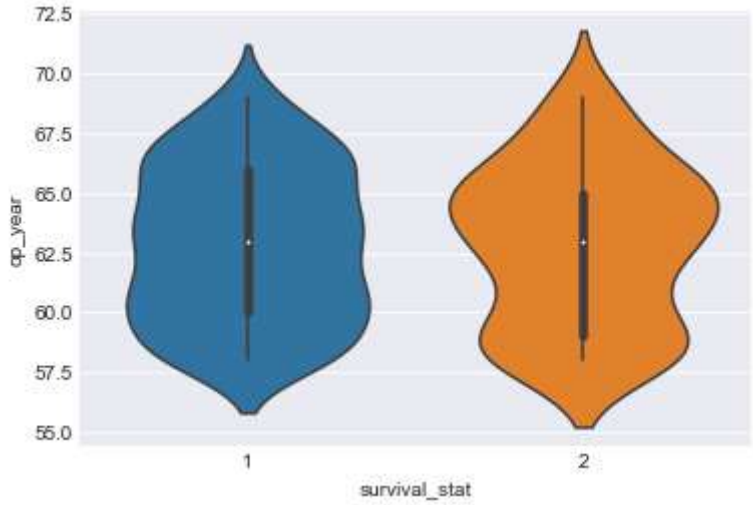
Observation:

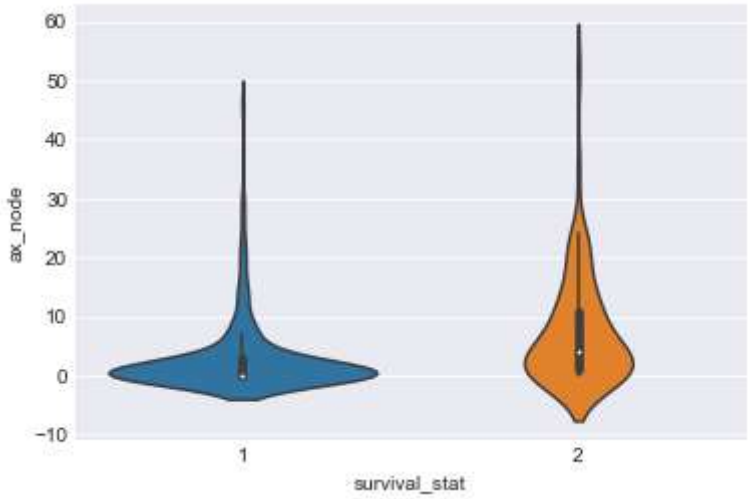
1.The median of axilliary node of patient living for 5 years and more is LESS than the median patient died within 5years
2.The mean of axilliary node of patient living for 5 years and more is LESS than the mean of patient died within 5years

lets even checkout violinplot.

In [131]:
```
sns.violinplot(x="survival_stat",y="age",data=value)
plt.show()
sns.violinplot(x="survival_stat",y="op_year",data=value)
plt.show()
sns.violinplot(x="survival_stat",y="ax_node",data=value)
plt.show()
```







Observation :

The violin plots are also very similar to the each other ,so the violin plots are not able to provide the information.

Conclusion :

1.Scatter plots were unable to provide required information.
2.1-D plots are overlapping,so the required information was not acquired.
3.Pair plotting didn't have the required graph.
4.Histogram was also a failure as both survival status were overlapping.
5.pdf and cdf were also overlapping.
6.Boxplot and violin plot had similar values for both survival status.
7.Mean and median are helpful.longliving have less mean and median than shortliving.