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1 Data Visualization with Haberman Dataset

```
In [138]: #import statements
          import numpy as np
          import pandas as pd
          import seaborn as sns
          import matplotlib.pyplot as plt
```

1.1 Haberman Survival Dataset

Sources: (a) Donor: Tjen-Sien Lim (limt@stat.wisc.edu) (b) Date: March 4, 1999 Past Usage:

Haberman, S. J. (1976). Generalized Residuals for Log-Linear Models, Proceedings of the 9th International Biometrics Conference, Boston, pp. 104-122. Landwehr, J. M., Pregibon, D., and Shoemaker, A. C. (1984), Graphical Models for Assessing Logistic Regression Models (with discussion), Journal of the American Statistical Association 79: 61-83. Lo, W.-D. (1993). Logistic Regression Trees, PhD thesis, Department of Statistics, University of Wisconsin, Madison, WI. Relevant Information: 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.

1.1.1 More information about Haberman Survival Dataset

Number of Instances: 306 Number of Attributes: 4 (including the class attribute)

Attribute Information: Age of patient at time of operation (numerical) Patient's year of operation (year - 1900, numerical) Number of positive axillary nodes detected (numerical) Survival status (class attribute) 1 = the patient survived 5 years or longer 2 = the patient died within 5 year

Missing Attribute Values: None

```
In [139]: df=pd.read_csv("haberman.csv",header=None)
          df.columns=['age','operation_at_age','number_auxilary_nodes','survival_status']
          df.shape
```

```
Out[139]: (306, 4)
```

```
In [140]: df.columns
```

Out[140]: Index(['age', 'operation_at_age', 'number_auxilary_nodes', 'survival_status'], dtype=

```
In [141]: print("Number of points is %d" %(df.shape[0]))
```

Number of points is 306

```
In [142]: print("Number of features is %d" %(df.shape[1]-1))
```

Number of features is 3

```
In [143]: len(df['survival_status'].unique())
```

Out[143]: 2

```
In [144]: #chnage level 2 to 0
          def change_2_to_0(x):
              if x==2:
                  return 0
              else:
                  return 1
          #print(df['survival_status'][7])
          df['survival_status']=df['survival_status'].apply(change_2_to_0)
          #print(df['survival_status'][7])
```

```
In [145]: print("This is a imbalance data set as the ratio of positive to negative points is %
```

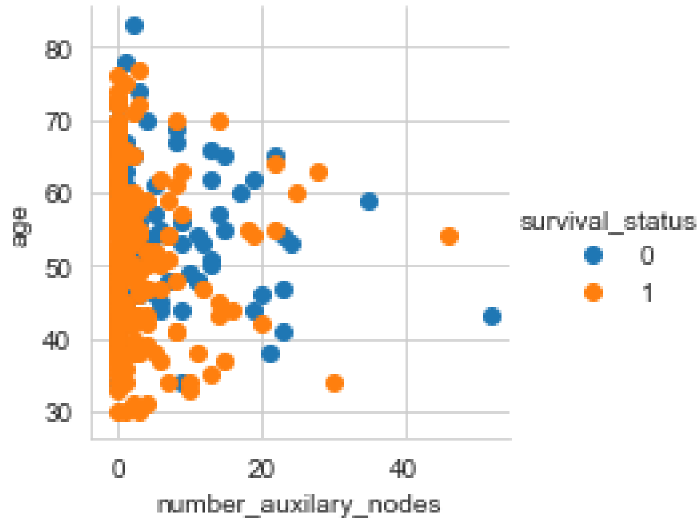
This is a imbalance data set as the ratio of positive to negative points is 225 : 81

```
In [146]: df['survival_status'].value_counts()
```

```
Out[146]: 1    225
          0     81
          Name: survival_status, dtype: int64
```

1.1.2 Observation 1: This might require a upsampling of data

```
In [147]: sns.set_style("whitegrid")
          sns.FacetGrid(df,hue='survival_status').map(plt.scatter,'number_auxilary_nodes','age
          plt.show()
```




```
In [148]: sns.pairplot(df,hue='survival_status',vars=['age', 'operation_at_age', 'number_auxila
```

```
Out[148]: <seaborn.axisgrid.PairGrid at 0x1fc13161978>
```

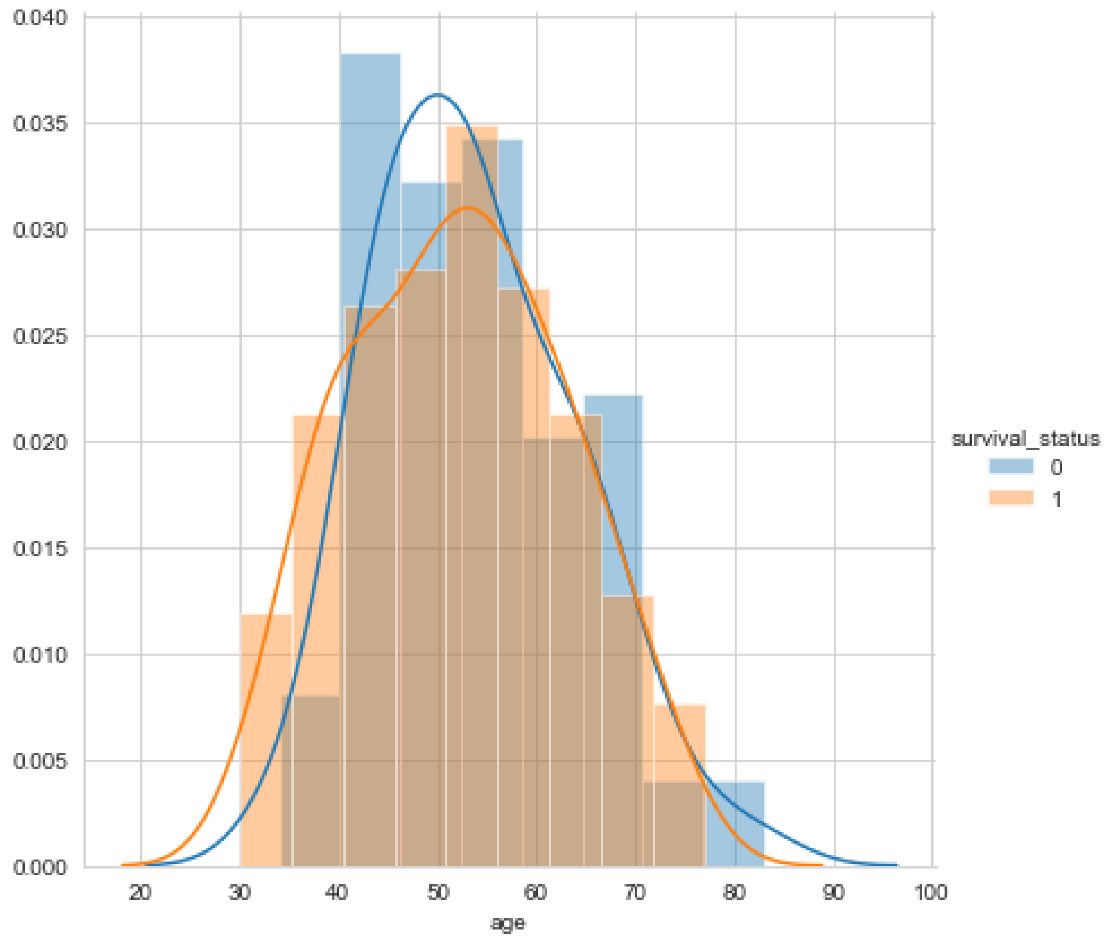
1.1.3 Observation 2:

- if given condition to choose two features I will prefer 'number of auxilary nodes' and 'operation at age'
- survival status is maximum if the patient has 0

1.2 Distribution plots of paired features

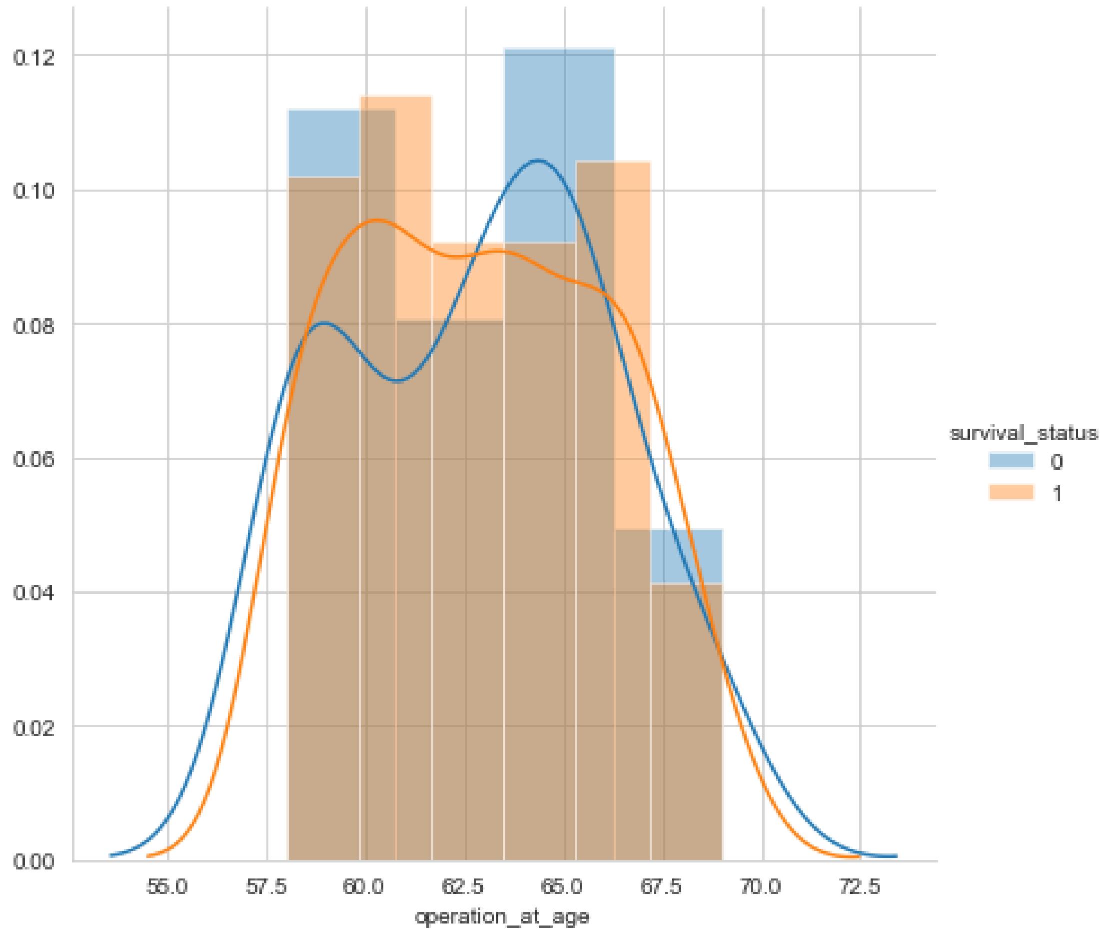
```
In [149]: sns.FacetGrid(df,hue='survival_status',height=6).map(sns.distplot,'age').add_legend(
```

```
Out[149]: <seaborn.axisgrid.FacetGrid at 0x1fc14591358>
```



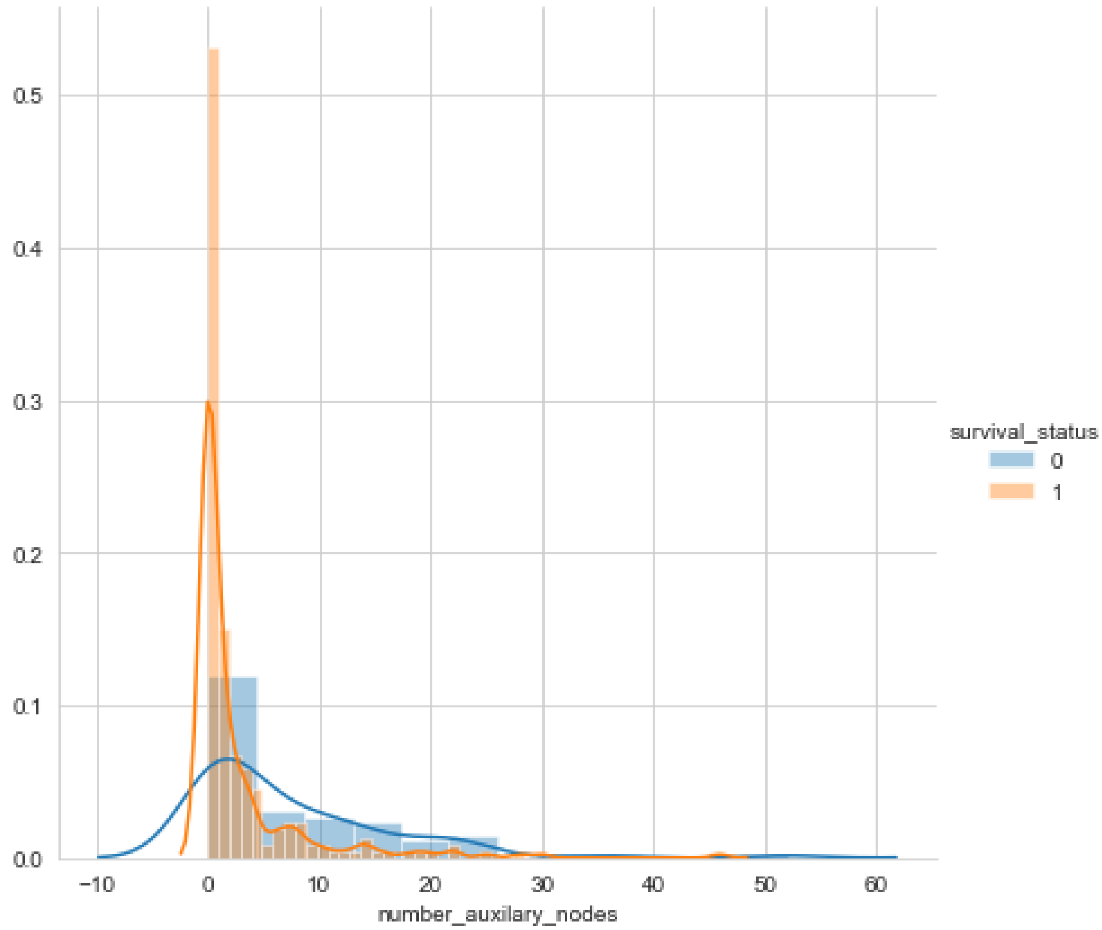

```
In [150]: sns.FacetGrid(df,hue='survival_status',height=6).map(sns.distplot,'operation_at_age'
```

```
Out[150]: <seaborn.axisgrid.FacetGrid at 0x1fc148fcf28>
```




```
In [151]: sns.FacetGrid(df,hue='survival_status',height=6).map(sns.distplot,'number_auxilary_no
```

```
Out[151]: <seaborn.axisgrid.FacetGrid at 0x1fc1499c1d0>
```



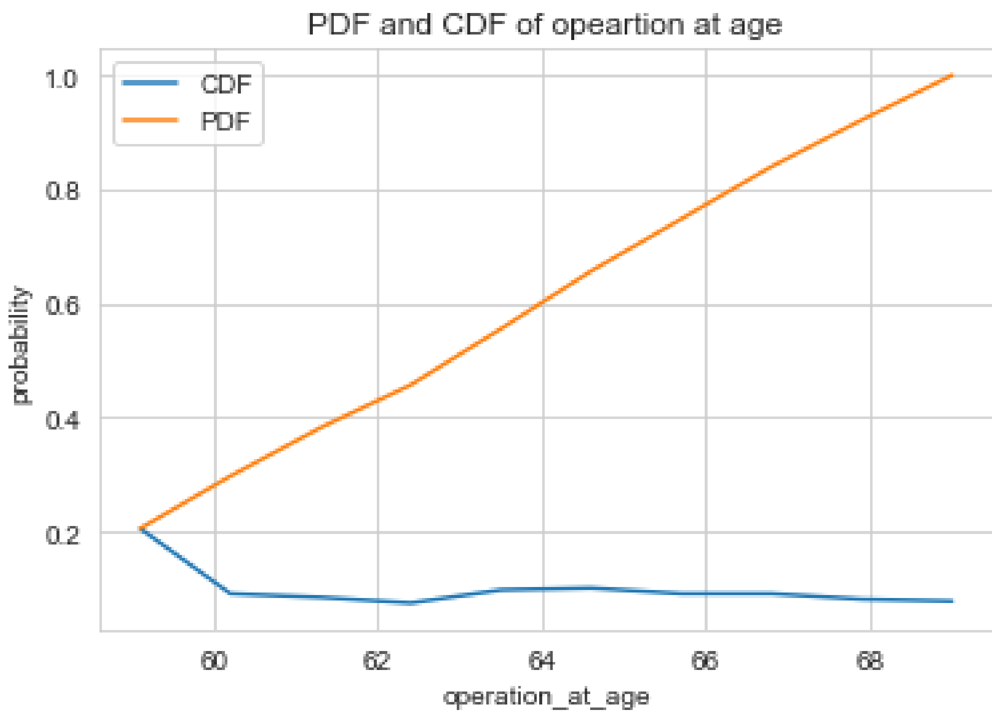
1.2.1 Observation 3

- plot of auxilary nodes and survival status seems reasonable, but it has a lot of over lapping too. The model can not be concrete on this feature.

In [161]:
```
import numpy as np
count,bin_edges=np.histogram(df['operation_at_age'],density=True,bins=10)
pdf=count/sum(count)
#print(pdf)
cdf=np.cumsum(pdf)
print(cdf)
print(bin_edges)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.legend({'PDF','CDF'})
plt.xlabel('operation_at_age')
plt.ylabel('probability')
plt.title('PDF and CDF of opeartion at age')
```

```
[0.20588235 0.29738562 0.38235294 0.45751634 0.55555556 0.65686275
 0.74836601 0.83986928 0.92156863 1.        ]
[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
```

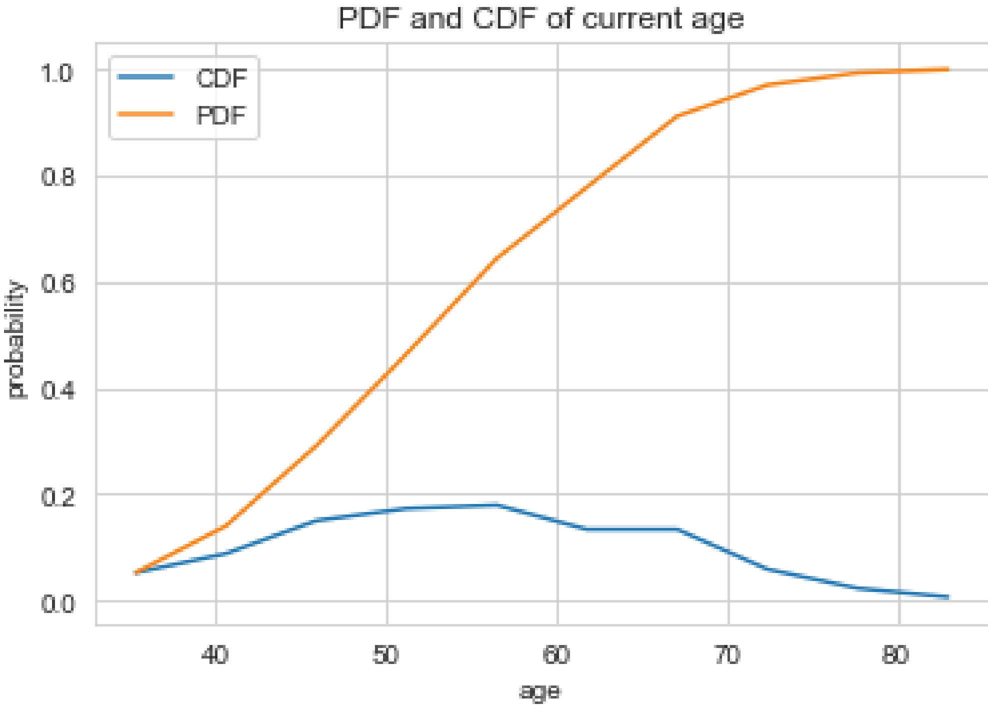
Out[161]: Text(0.5,1,'PDF and CDF of opeartion at age')



In [162]:
```python
import numpy as np
count,bin_edges=np.histogram(df['age'],density=True,bins=10)
pdf=count/sum(count)
#print(pdf)
cdf=np.cumsum(pdf)
print(cdf)
print(bin_edges)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.legend({'PDF','CDF'})
plt.xlabel('age')
plt.ylabel('probability')
plt.title('PDF and CDF of current age')
```

```
[0.05228758 0.14052288 0.29084967 0.46405229 0.64379085 0.77777778
 0.91176471 0.97058824 0.99346405 1.        ]
[30.  35.3 40.6 45.9 51.2 56.5 61.8 67.1 72.4 77.7 83. ]
```

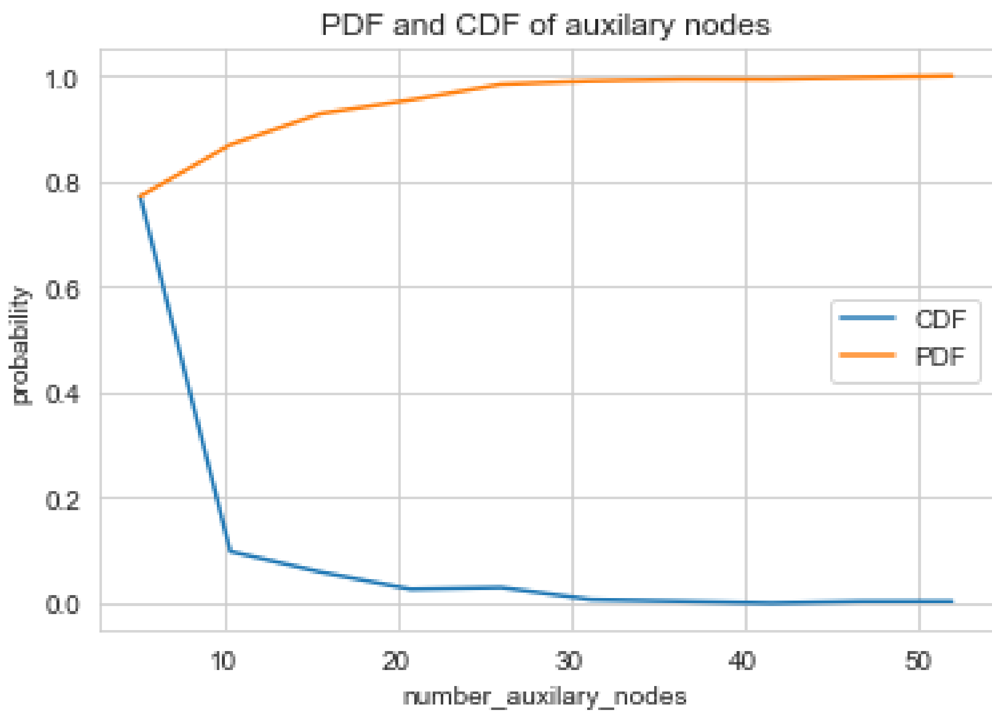
Out[162]: Text(0.5,1,'PDF and CDF of current age')




```
In [163]: import numpy as np
          count,bin_edges=np.histogram(df['number_auxilary_nodes'],density=True,bins=10)
          pdf=count/sum(count)
          #print(pdf)
          cdf=np.cumsum(pdf)
          print(cdf)
          print(bin_edges)
          plt.plot(bin_edges[1:],pdf)
          plt.plot(bin_edges[1:],cdf)
          plt.legend({'PDF','CDF'})
          plt.xlabel('number_auxilary_nodes')
          plt.ylabel('probability')
          plt.title('PDF and CDF of auxilary nodes')
```

```
[0.77124183 0.86928105 0.92810458 0.95424837 0.98366013 0.99019608
 0.99346405 0.99346405 0.99673203 1.        ]
[ 0.   5.2 10.4 15.6 20.8 26.  31.2 36.4 41.6 46.8 52. ]
```

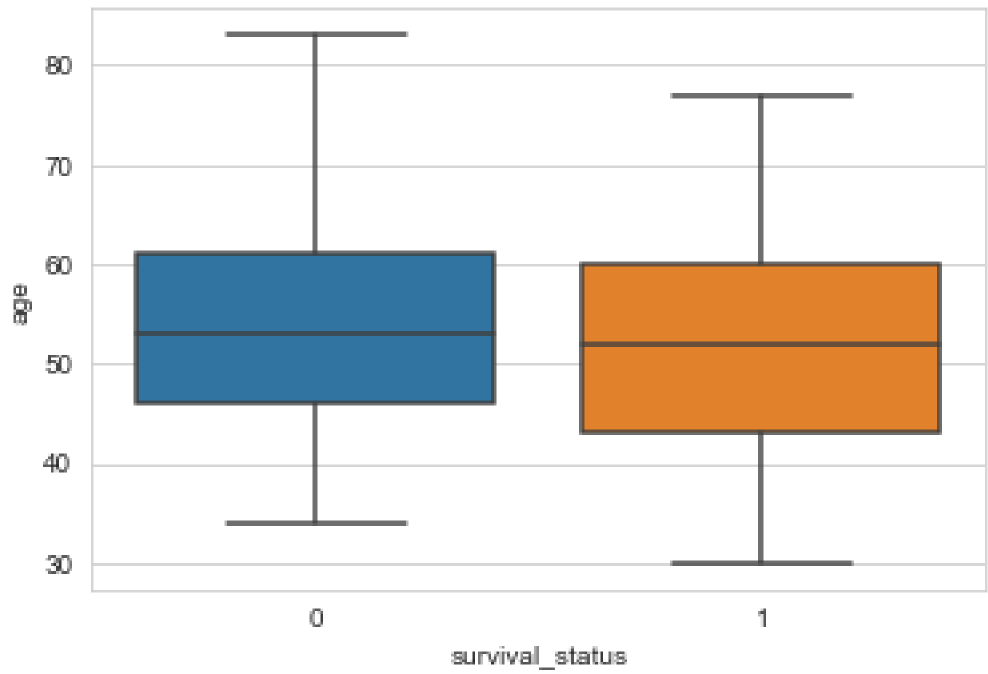
Out[163]: Text(0.5,1,'PDF and CDF of auxilary nodes')



1.2.2 Plotting box plot will let us know more about the quantiles

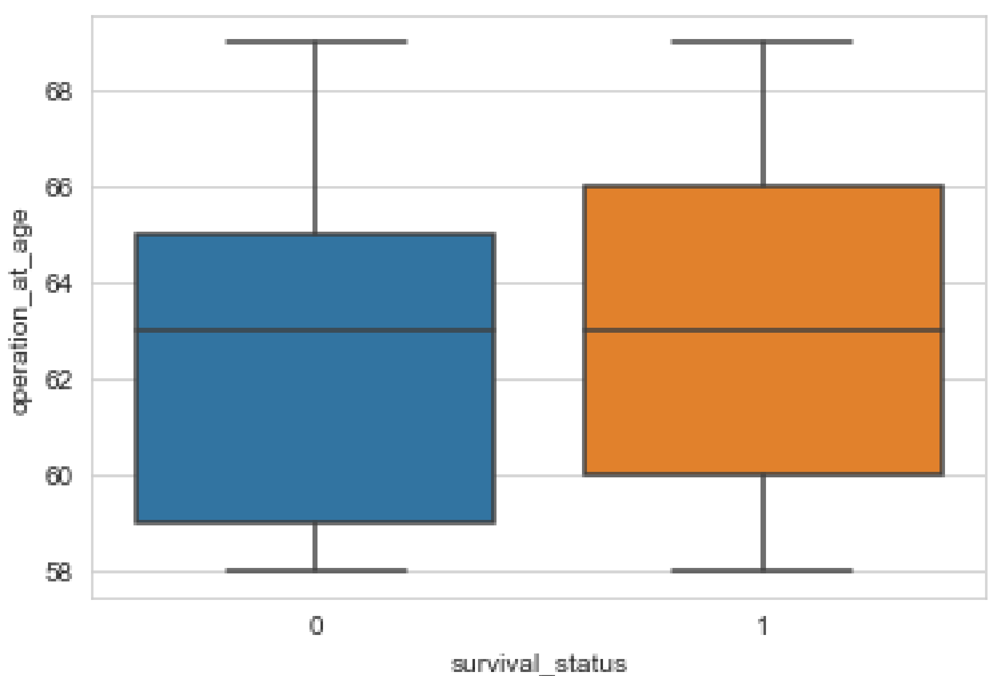
```
In [164]: sns.boxplot(data=df,x='survival_status',y='age')
```

```
Out[164]: <matplotlib.axes._subplots.AxesSubplot at 0x1fc0d521b00>
```



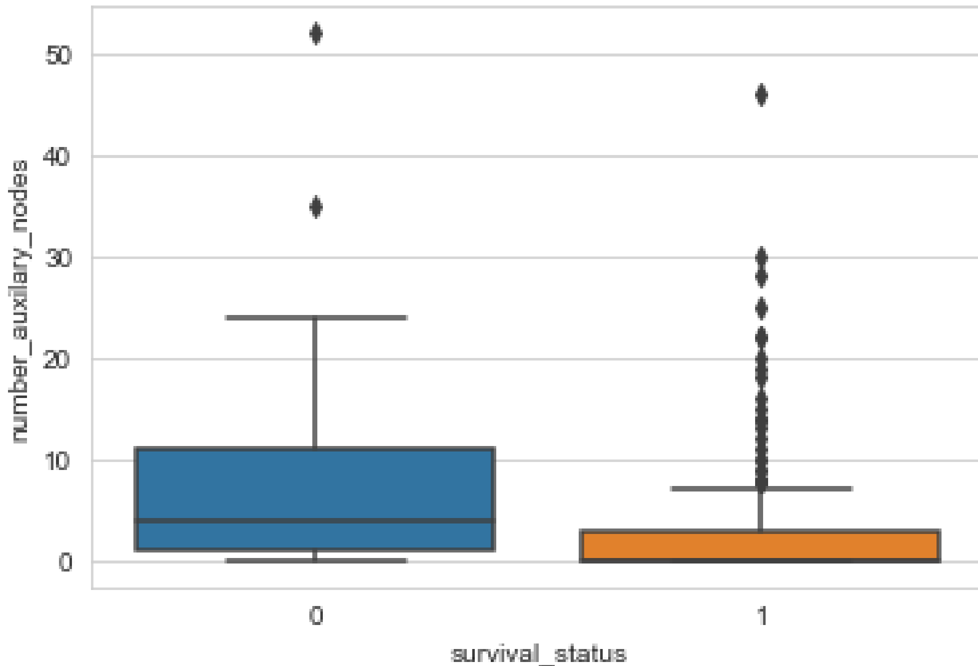

```
In [165]: sns.boxplot(data=df,x='survival_status',y='operation_at_age')

Out[165]: <matplotlib.axes._subplots.AxesSubplot at 0x1fc14c66470>
```



```
In [166]: sns.boxplot(data=df,x='survival_status',y='number_auxilary_nodes')
```

```
Out[166]: <matplotlib.axes._subplots.AxesSubplot at 0x1fc14cd0a58>
```

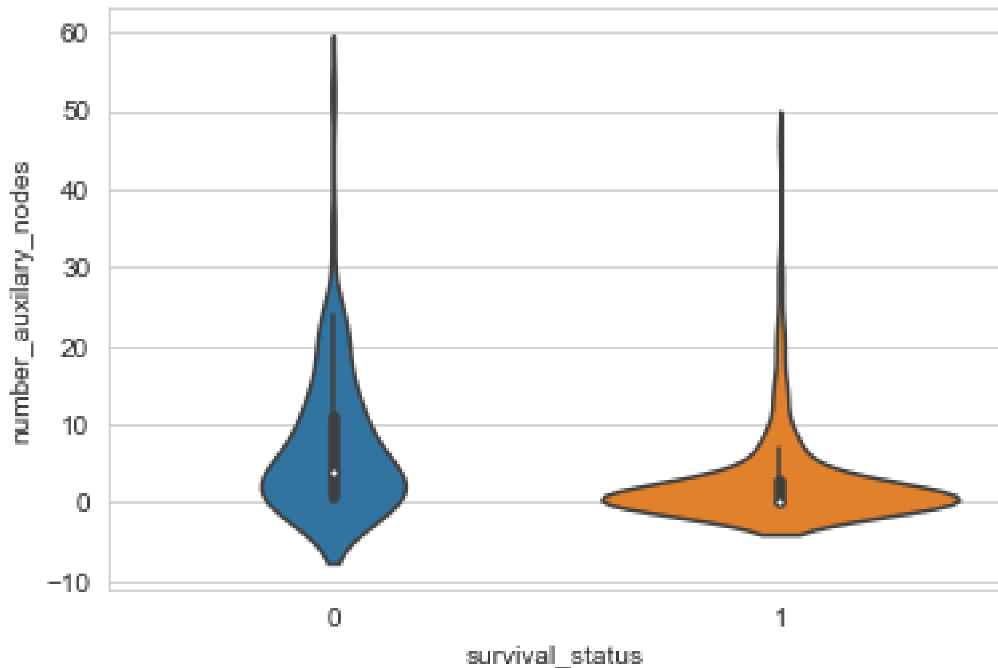


1.2.3 Observation 4

- From the above plot of auxilary nodes and survival status -- there are a lot of outlier points who survived. At this point of time I believe the dataset is in separable using linear models.
- From other two box plots, the data is very less likely to be separable

```
In [167]: sns.violinplot(data=df,x='survival_status',y='number_auxilary_nodes')
```

```
Out[167]: <matplotlib.axes._subplots.AxesSubplot at 0x1fc14d335c0>
```



1.2.4 Observation 5

- The distribution of data is slightly skewed

1.2.5 Conclusion

1.2.6 Data seems in separable using linear models. Some more complex models which can capture curves in might be helpful here.

```
In [ ]:
```

```
In [ ]:
```