EDA_haberman_cancer_survival

July 28, 2018

1 HABERMAN CANCER SURVIVAL

2 (3.12) Exercise:

1. Download Haberman Cancer Survival dataset from Kaggle. You may have to create a Kaggle account to donwload data. (https://www.kaggle.com/gilsousa/habermans-survival-data-set)
2. Perform a similar alanlaysis as above on this dataset with the following sections:

- High level statistics of the dataset: number of points, numer of features, number of classes, data-points per class.
- Explain our objective.
- Perform Univaraite analysis(PDF, CDF, Boxplot, Voilin plots) to understand which features are useful towards classification.
- Perform Bi-variate analysis (scatter plots, pair-plots) to see if combinations of features are useful in classfication.
- Write your observations in english as crisply and unambigously as possible. Always quantify your results.

```
In [1]: #importing libraries
        import numpy as np
        import pandas as pd
        import matplotlib.pyplot as plt
        import seaborn as sns
```

```
In [2]: 1. #read data
        cancer = pd.read_csv('haberman.csv')
        cancer.columns = 'age' , 'year' , 'nodes' , 'survival'
        cancer.head()
```

```
Out[2]:    age  year  nodes  survival
        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 [3]: 2. #how many patients data and features we have

        cancer.shape

        #305 patients and 4 features

Out[3]: (305, 4)

In [4]: 3. #is it a balanced or Imbalnced dataset

        cancer['survival'].value_counts()

        #Imbalanced

Out[4]: 1    224
        2     81
        Name: survival, dtype: int64
```

3 Objective: To see if a patient survived 5 years after cancer treatment

survival = 1 - yes, survived 5 or more years
survival = 2 - no
Questions:
in data we know some of them died before 5 years and some were good enough to live past five years so what was the reason that some were able to live past 5 years
is it age?? or is it no. of auxillary node??
lets see if we can interpret data to find answers

4 Insights From Data

```
In [5]: #what was the minimum and maximum age that didnot survive 5years
        cancer.age[cancer['survival'] == 2].describe()

        #min = 34 years
        #max = 83 years
        #total of 81 patients didnt survive 5years

Out[5]: count    81.000000
        mean     53.679012
        std      10.167137
        min      34.000000
        25%      46.000000
        50%      53.000000
        75%      61.000000
        max      83.000000
        Name: age, dtype: float64
```

```
In [6]: #what was the minimum and maximum age that survived 5years or more

        cancer.age[cancer['survival'] == 1].describe()

        #min = 30
        #max = 77
```

```
Out[6]: count    224.000000
        mean      52.116071
        std       10.937446
        min       30.000000
        25%       43.000000
        50%       52.000000
        75%       60.000000
        max       77.000000
        Name: age, dtype: float64
```

```
In [7]: #number of nodes in minimum and maximum year patients that did not survive 5years

        cancer.nodes[(cancer['age']==83) & (cancer['survival']==2)]

        #node in max age = 2
```

```
Out[7]: 304    2
        Name: nodes, dtype: int64
```

```
In [8]: cancer.nodes[(cancer['age']== 34) & (cancer['survival']==2)]
        #number of nodes in min age patients = 0, 9.
```

```
Out[8]: 6    0
        7    9
        Name: nodes, dtype: int64
```

```
In [9]: #number of nodes in minimum and maximum year patients that survived 5years

        cancer.nodes[(cancer['age']==77) & (cancer['survival']==1)]

        #node in max age = 3
```

```
Out[9]: 302    3
        Name: nodes, dtype: int64
```

```
In [10]: cancer.nodes[(cancer['age']==30) & (cancer['survival']==1)]
         #number of nodes in min age patients = 0, 3.
```

```
Out[10]: 0    3
         1    0
         Name: nodes, dtype: int64
```

```
In [11]: #number of nodes in patients not survived
         cancer.nodes[cancer['survival']==2].value_counts()

         #max num of patients had zero nodes but still they died before 5 years
```

```
Out[11]: 0     19
         1      8
         3      7
         2      5
         9      4
         5      4
         13     4
         23     3
         4      3
         6      3
         11     3
         19     2
         15     2
         7      2
         8      2
         52     1
         10     1
         35     1
         14     1
         17     1
         20     1
         21     1
         22     1
         24     1
         12     1
         Name: nodes, dtype: int64
```

```
In [12]: #patients who have zero auxillary nodes

         cancer[cancer['nodes'] == 0].describe()

         #136 patients out of 305. (roughly 35% of patients had zero nodes)
```

```
Out[12]:               age        year  nodes    survival
         count  136.000000  136.000000  136.0  136.000000
         mean    53.705882   63.102941    0.0    1.139706
         std     11.247464    3.181612    0.0    0.347963
         min     30.000000   58.000000    0.0    1.000000
         25%     44.000000   60.000000    0.0    1.000000
         50%     54.000000   63.000000    0.0    1.000000
         75%     63.000000   66.000000    0.0    1.000000
         max     76.000000   69.000000    0.0    2.000000
```

```
In [13]: cancer[(cancer['nodes'] == 0) & (cancer['survival'] == 2)].describe()
```

```
        #19 patients didnot survive despite have 0 auxillary nodes
```

```
Out[13]:              age       year  nodes  survival
         count  19.000000  19.000000   19.0      19.0
         mean   51.421053  62.526316    0.0       2.0
         std    11.634794   3.151162    0.0       0.0
         min    34.000000  58.000000    0.0       2.0
         25%    42.500000  59.000000    0.0       2.0
         50%    47.000000  64.000000    0.0       2.0
         75%    61.500000  65.000000    0.0       2.0
         max    72.000000  67.000000    0.0       2.0
```

5 Observations From dataset:

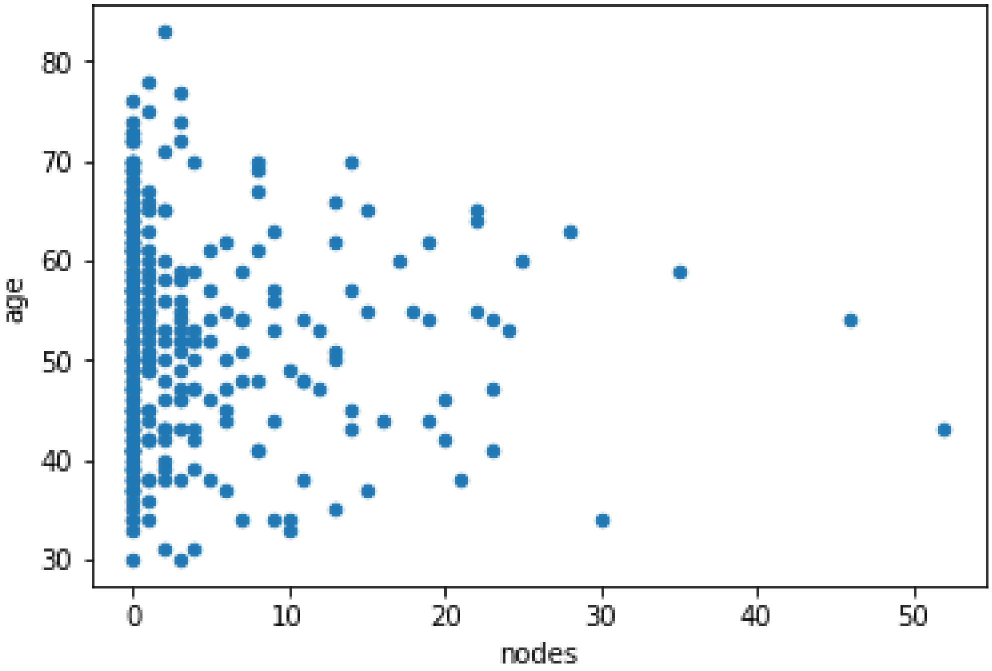
1. its an unbalanced dataset.
2. patients range in age of 30 to 83. Max age is 83 and didnt survive 5 years and min age is 30 and has two persons, both survived 5 years or more.
3. out of 305 members 136 members have zero auxillary nodes with max age = 76 and min age = 30 and 19 members did not survive 5 years
4. any person who did not survive minimum 5 years have an age max 72 and age min of 34

6 Graphical Understanding of Data

lets have graphical understanding of datas to get some insights

```
In [14]: cancer.plot(kind= 'scatter', x='nodes', y='age')

         #cant understand data since all data are in same colour
```

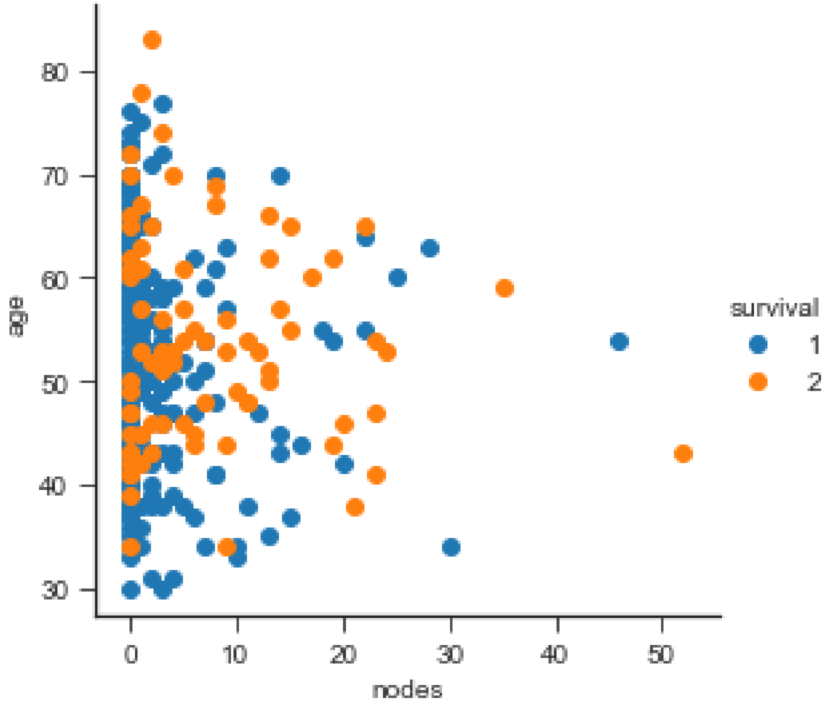
```
Out[14]: <matplotlib.axes._subplots.AxesSubplot at 0x19e2ec75e10>
```



7 BI-variate Analysis (scatterplot, pairplots)

8 scatter plots

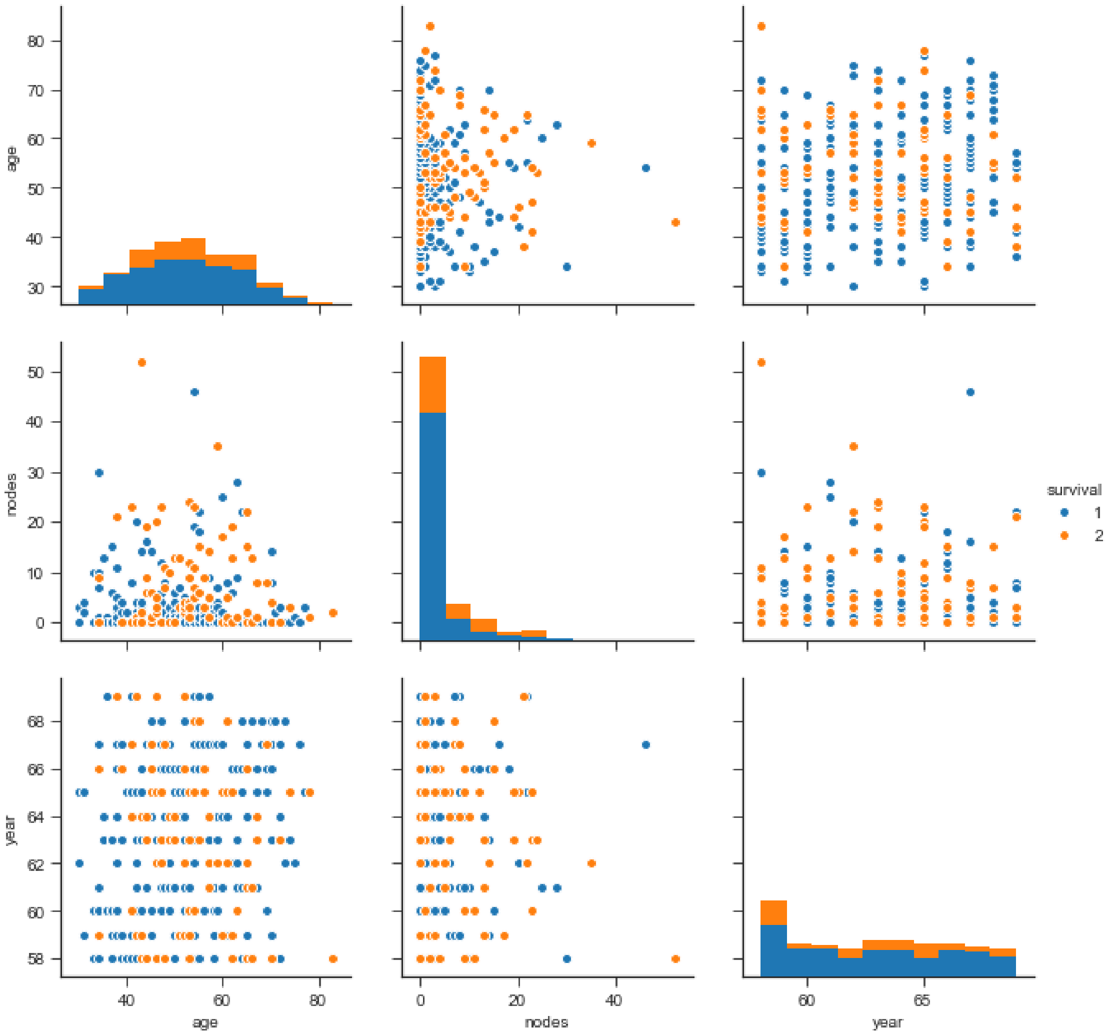
```
In [15]: #scatter plot with different colour based on survival
         sns.set_style('ticks')
         sns.FacetGrid(cancer, hue=('survival') , size=4) \
         .map(plt.scatter, 'nodes' , 'age') \
         .add_legend()
         #not much of information could be understood even from scatterplot. so lets try other

Out[15]: <seaborn.axisgrid.FacetGrid at 0x19e2efca4a8>
```



observations 1. seems patients with age between 40 to 70 has equi-probable survival

9 Pair plots

```
In [16]: sns.set_style('ticks')
         sns.pairplot(cancer, hue='survival', vars = ('age', 'nodes', 'year'), size=3)
         #vars = ('Columns must be given or it'll calculate pairplots for all columns)

Out[16]: <seaborn.axisgrid.PairGrid at 0x19e300183c8>
```

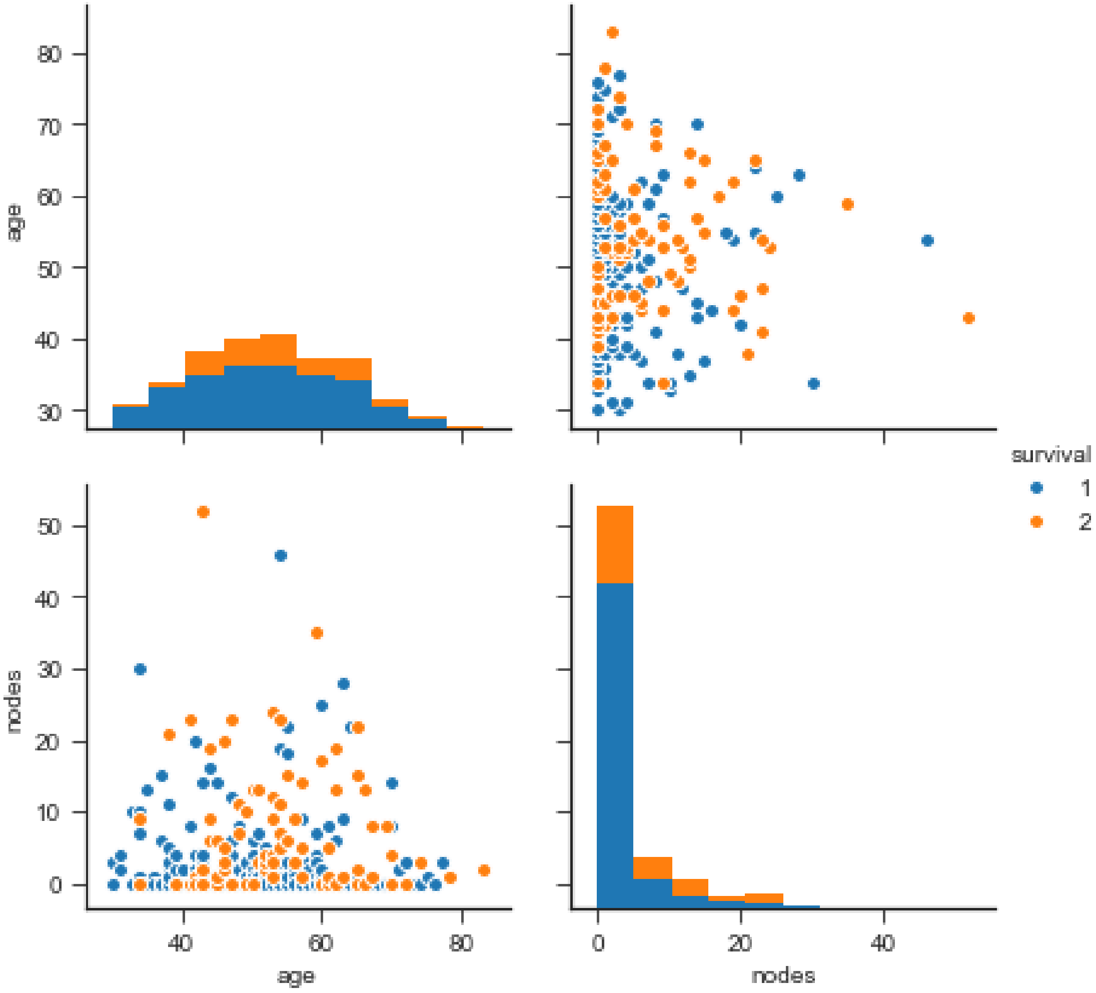


observations

1. From the data and information we have, irrespective of operating year, we want the patient to survive 5 years. so, the year of operation is not a good varible to say if a patient will survive 5years or more.(so it is not considered)
2. age and number of auxillary nodes are the important features.

```
In [17]: sns.set_style('ticks')
         sns.pairplot(cancer, hue='survival', vars = ('age', 'nodes'), size=3)
         #vars = ('Columns must be given or it'll calculate pairplots for all columns since it
```

```
Out[17]: <seaborn.axisgrid.PairGrid at 0x19e304be6a0>
```

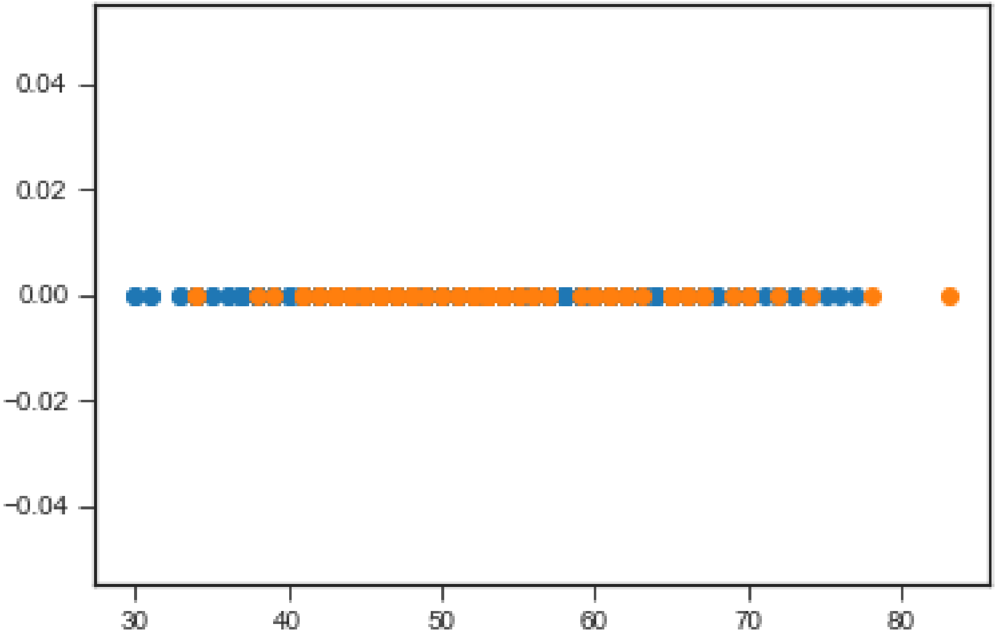


observations 1. for any person between age 40 to 70 their chance of surviving is 50:50 (lets cross verify it with other plots)

10 Histogram, PDF, CDF

```
In [18]: #1d scatter plot
         #divide cancer dataset into two based on survival status 1 & 2 using .loc
         cancer_1 = cancer.loc[cancer['survival'] == 1]
         cancer_2 = cancer.loc[cancer['survival'] == 2]
         #now plot new dataset w.r.t age and nodes of patients in one dimension
         plt.plot(cancer_1['age'], np.zeros_like(cancer_1['age']), 'o' , Label="1")
         plt.plot(cancer_2['age'], np.zeros_like(cancer_2['age']), 'o' , label="2")
```

```
Out[18]: [<matplotlib.lines.Line2D at 0x19e30c1b978>]
```

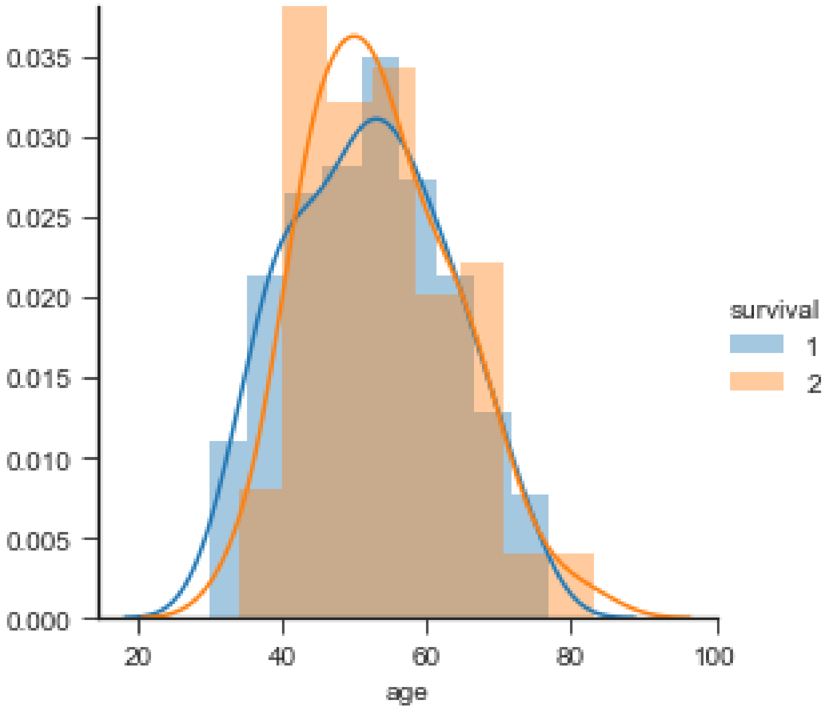


observation 1. from 1D plot we can see that most of the people that didnt survive five years range from age 40 to age70(90%)

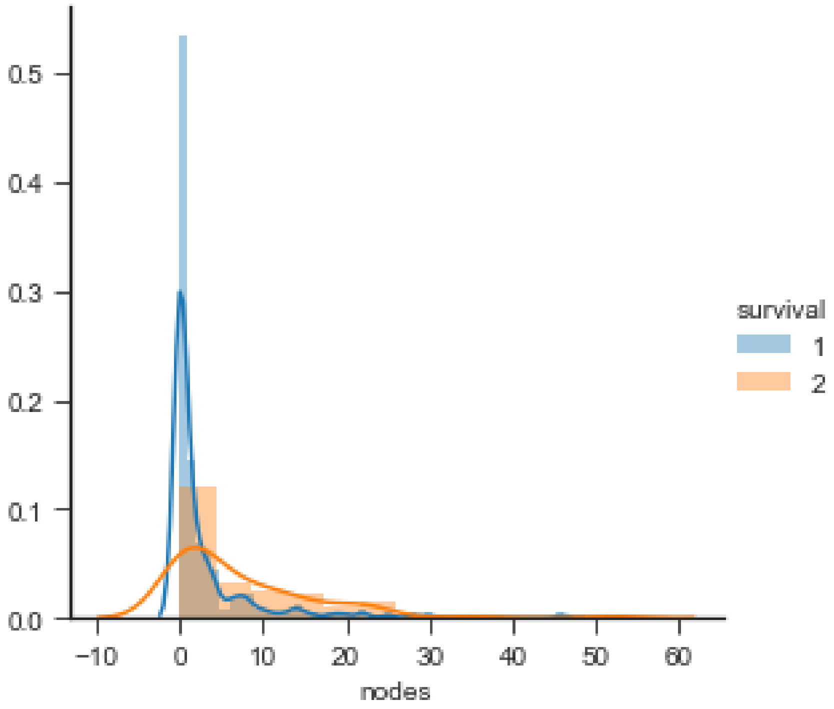
```
In [19]: sns.FacetGrid(cancer, hue='survival', size=4) \
         .map(sns.distplot, 'age') \
         .add_legend()
```

```
C:\Users\Aravindh\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: UserWarning: The
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\Aravindh\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: UserWarning: The
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
```

```
Out[19]: <seaborn.axisgrid.FacetGrid at 0x19e30c44da0>
```



```
In [20]: sns.FacetGrid(cancer, hue='survival', size=4) \
            .map(sns.distplot, 'nodes') \
            .add_legend()

C:\Users\Aravindh\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: UserWarning: The
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\Aravindh\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: UserWarning: The
  warnings.warn("The 'normed' kwarg is deprecated, and has been "


Out[20]: <seaborn.axisgrid.FacetGrid at 0x19e30d3e7f0>
```



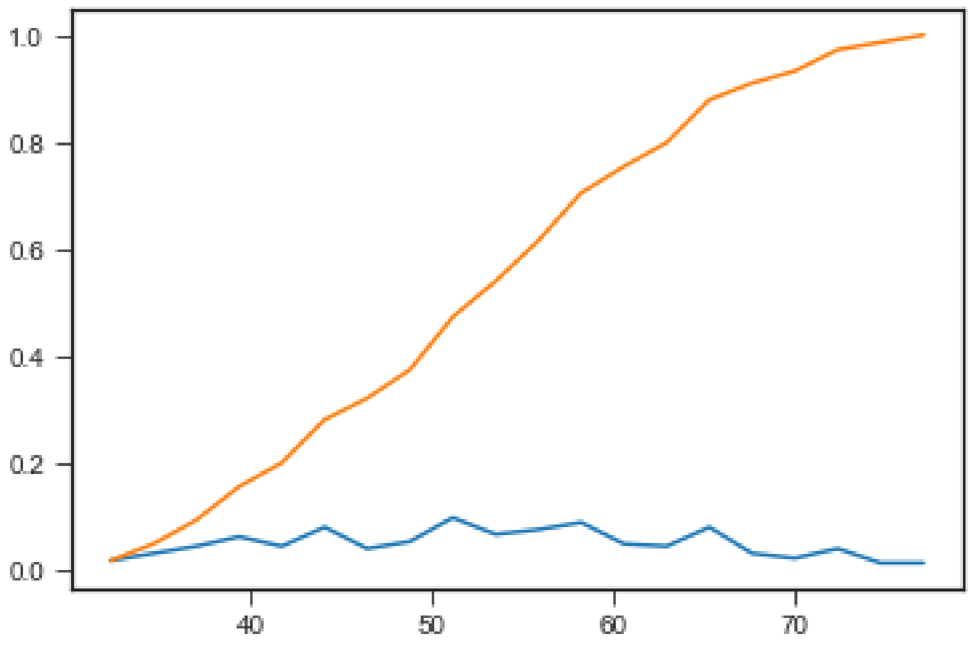
11 CDF

```
In [21]: #CDF
         #counts = number of patients survived
         #bin_edges = no. of sub-points where total no.of points act Ex: @age=65 80% of data p
         counts, bin_edges = np.histogram(cancer_1['age'], bins=20, density=True,)

         #calculate PDF & Bin_edges
         pdf = counts/sum(counts)
         print(pdf)
         print(bin_edges)

         #plot CDF
         cdf=np.cumsum(pdf)
         plt.plot(bin_edges[1:],pdf)
         plt.plot(bin_edges[1:],cdf)
```

```
[0.01785714 0.03125    0.04464286 0.0625     0.04464286 0.08035714
 0.04017857 0.05357143 0.09821429 0.06696429 0.07589286 0.08928571
 0.04910714 0.04464286 0.08035714 0.03125    0.02232143 0.04017857
 0.01339286 0.01339286]
[30.   32.35 34.7  37.05 39.4  41.75 44.1  46.45 48.8  51.15 53.5  55.85
```

```
 58.2   60.55 62.9   65.25 67.6   69.95 72.3   74.65 77.   ]
```

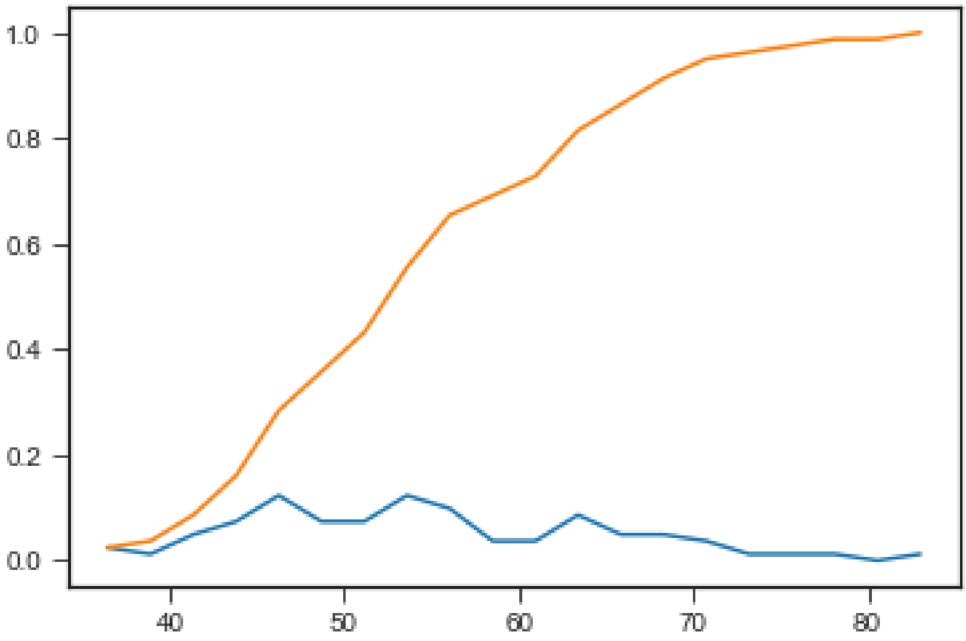
```
Out[21]: [<matplotlib.lines.Line2D at 0x19e30ddd8d0>]
```



```
In [22]: #CDF
         counts, bin_edges = np.histogram(cancer_2['age'], bins=20, density=True,)

         #calculate PDF & Bin_edges
         pdf = counts/sum(counts)
         print(pdf)
         print(bin_edges)

         #plot CDF
         cdf=np.cumsum(pdf)
         plt.plot(bin_edges[1:],pdf)
         plt.plot(bin_edges[1:],cdf)
```

```
[0.02469136 0.01234568 0.04938272 0.07407407 0.12345679 0.07407407
 0.07407407 0.12345679 0.09876543 0.03703704 0.03703704 0.08641975
 0.04938272 0.04938272 0.03703704 0.01234568 0.01234568 0.01234568
 0.         0.01234568]
[34.   36.45 38.9  41.35 43.8  46.25 48.7  51.15 53.6  56.05 58.5  60.95
 63.4  65.85 68.3  70.75 73.2  75.65 78.1  80.55 83.  ]
```

```
Out[22]: [<matplotlib.lines.Line2D at 0x19e30eabcc0>]
```

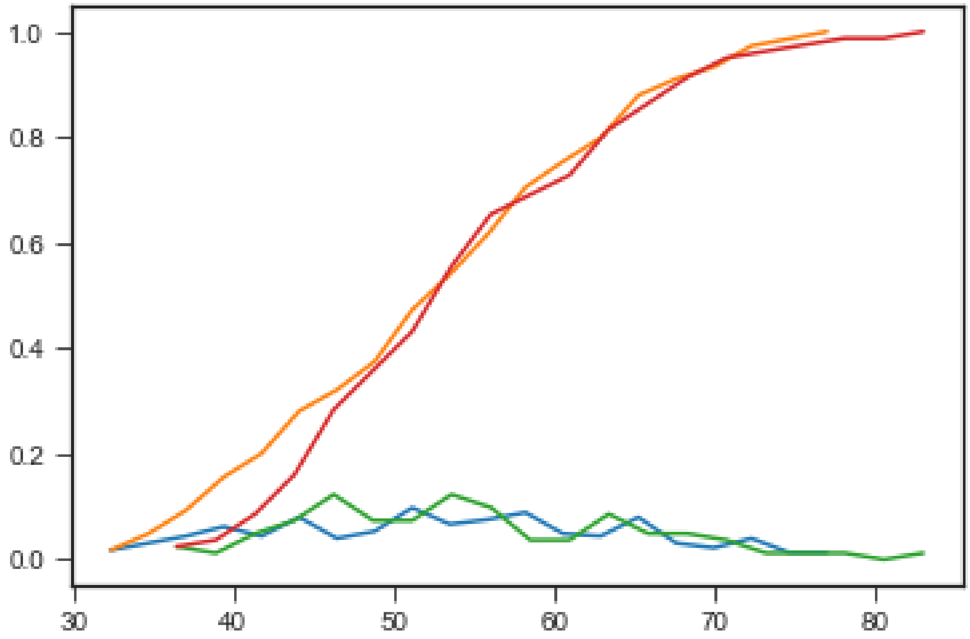


```
In [23]: #combined cdf on age with peoples survived and those didnt
         #CDF
         counts, bin_edges = np.histogram(cancer_1['age'], bins=20, density=True,)

         #calculate PDF & Bin_edges
         pdf = counts/sum(counts)
         print(pdf)
         print(bin_edges)

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

         #CDF
         counts, bin_edges = np.histogram(cancer_2['age'], bins=20, density=True,)

         #calculate PDF & Bin_edges
         pdf = counts/sum(counts)
         print(pdf)
         print(bin_edges)

         #plot CDF
```

```
        cdf=np.cumsum(pdf)
        plt.plot(bin_edges[1:],pdf)
        plt.plot(bin_edges[1:],cdf)
```

```
[0.01785714 0.03125    0.04464286 0.0625     0.04464286 0.08035714
 0.04017857 0.05357143 0.09821429 0.06696429 0.07589286 0.08928571
 0.04910714 0.04464286 0.08035714 0.03125    0.02232143 0.04017857
 0.01339286 0.01339286]
[30.   32.35 34.7  37.05 39.4  41.75 44.1  46.45 48.8  51.15 53.5  55.85
 58.2  60.55 62.9  65.25 67.6  69.95 72.3  74.65 77.  ]
[0.02469136 0.01234568 0.04938272 0.07407407 0.12345679 0.07407407
 0.07407407 0.12345679 0.09876543 0.03703704 0.03703704 0.08641975
 0.04938272 0.04938272 0.03703704 0.01234568 0.01234568 0.01234568
 0.         0.01234568]
[34.   36.45 38.9  41.35 43.8  46.25 48.7  51.15 53.6  56.05 58.5  60.95
 63.4  65.85 68.3  70.75 73.2  75.65 78.1  80.55 83.  ]
```

```
Out[23]: [<matplotlib.lines.Line2D at 0x19e30f5cf28>]
```



observtions on CDF with age (all values in approximate from above graph)

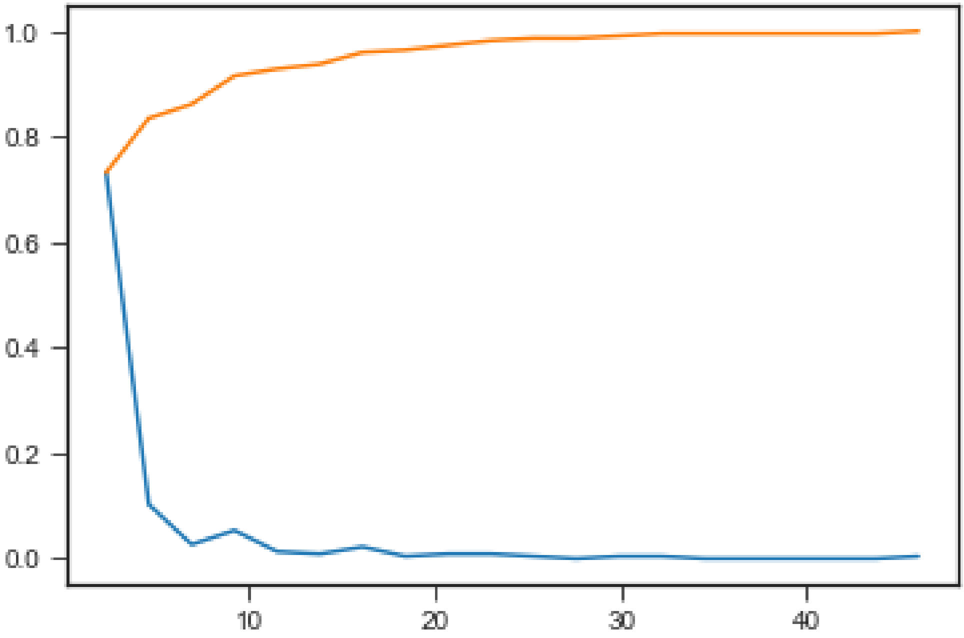
1. 80% of patients have age ranging from 30 to 65.
2. lowest age that didnt survive 5 years is approx. 35 and highest is 83
3. lowest age that survived 5 years is approx. 32 and highest is 76

4. **patients from age 48 to age 75 have almost equal probability of surviving or not surviving.**

```
In [24]: #cdf on auxillary nodes with peoples survived and those didnt
         #CDF
         counts, bin_edges = np.histogram(cancer_1['nodes'], bins=20, density=True,)

         #calculate PDF & Bin_edges
         pdf = counts/sum(counts)
         print(pdf)
         print(bin_edges)

         #plot CDF
         cdf=np.cumsum(pdf)
         plt.plot(bin_edges[1:],pdf)
         plt.plot(bin_edges[1:],cdf)
```

```
[0.73214286 0.10267857 0.02678571 0.05357143 0.01339286 0.00892857
 0.02232143 0.00446429 0.00892857 0.00892857 0.00446429 0.
 0.00446429 0.00446429 0.         0.         0.         0.
 0.         0.00446429]
[ 0.   2.3  4.6  6.9  9.2 11.5 13.8 16.1 18.4 20.7 23.  25.3 27.6 29.9
 32.2 34.5 36.8 39.1 41.4 43.7 46. ]
```

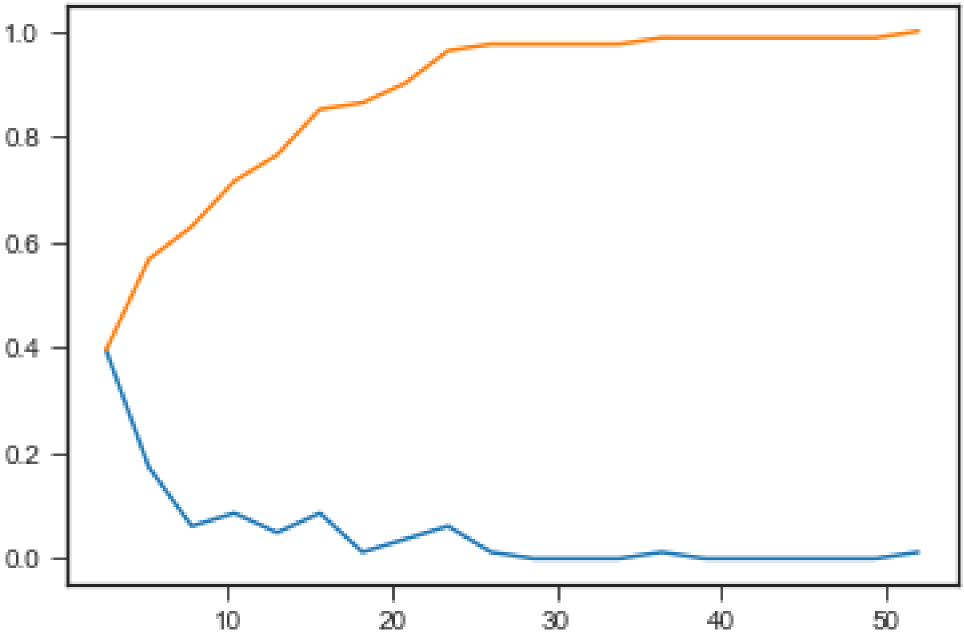
```
Out[24]: [<matplotlib.lines.Line2D at 0x19e30f9f0b8>]
```



```
In [25]: #cdf on auxillary nodes with peoples those didnt survive
         counts, bin_edges = np.histogram(cancer_2['nodes'], bins=20, density=True,)

         #calculate PDF & Bin_edges
         pdf = counts/sum(counts)
         print(pdf)
         print(bin_edges)

         #plot CDF
         cdf=np.cumsum(pdf)
         plt.plot(bin_edges[1:],pdf)
         plt.plot(bin_edges[1:],cdf)
```

```
[0.39506173 0.17283951 0.0617284  0.08641975 0.04938272 0.08641975
 0.01234568 0.03703704 0.0617284  0.01234568 0.         0.
 0.         0.01234568 0.         0.         0.         0.
 0.         0.01234568]
[ 0.   2.6  5.2  7.8 10.4 13.  15.6 18.2 20.8 23.4 26.  28.6 31.2 33.8
 36.4 39.  41.6 44.2 46.8 49.4 52. ]
```

```
Out[25]: [<matplotlib.lines.Line2D at 0x19e30fe4ef0>]
```

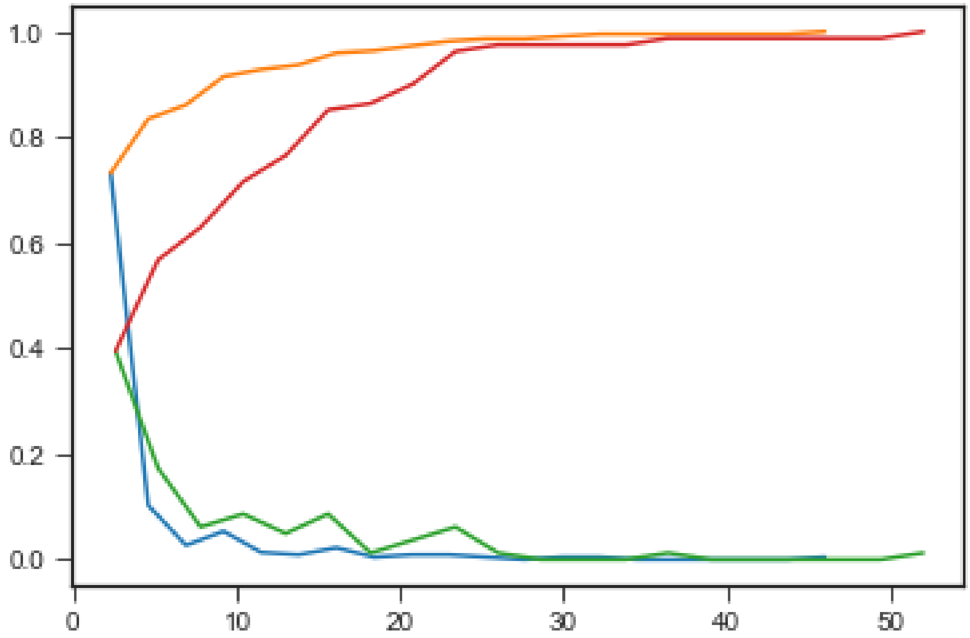


```
In [26]: #Combined cdf on nodes with peoples survived and those didnt
         #CDF
         counts, bin_edges = np.histogram(cancer_1['nodes'], bins=20, density=True,)
```

```
#calculate PDF & Bin_edges
pdf = counts/sum(counts)
print(pdf)
print(bin_edges)

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

#CDF
counts, bin_edges = np.histogram(cancer_2['nodes'], bins=20, density=True,)

#calculate PDF & Bin_edges
pdf = counts/sum(counts)
print(pdf)
print(bin_edges)

#plot CDF
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
```

```
[0.73214286 0.10267857 0.02678571 0.05357143 0.01339286 0.00892857
 0.02232143 0.00446429 0.00892857 0.00892857 0.00446429 0.
 0.00446429 0.00446429 0.         0.         0.         0.
 0.         0.00446429]
[ 0.   2.3  4.6  6.9  9.2 11.5 13.8 16.1 18.4 20.7 23.  25.3 27.6 29.9
 32.2 34.5 36.8 39.1 41.4 43.7 46. ]
[0.39506173 0.17283951 0.0617284  0.08641975 0.04938272 0.08641975
 0.01234568 0.03703704 0.0617284  0.01234568 0.         0.
 0.         0.01234568 0.         0.         0.         0.
 0.         0.01234568]
[ 0.   2.6  5.2  7.8 10.4 13.  15.6 18.2 20.8 23.4 26.  28.6 31.2 33.8
 36.4 39.  41.6 44.2 46.8 49.4 52. ]
```

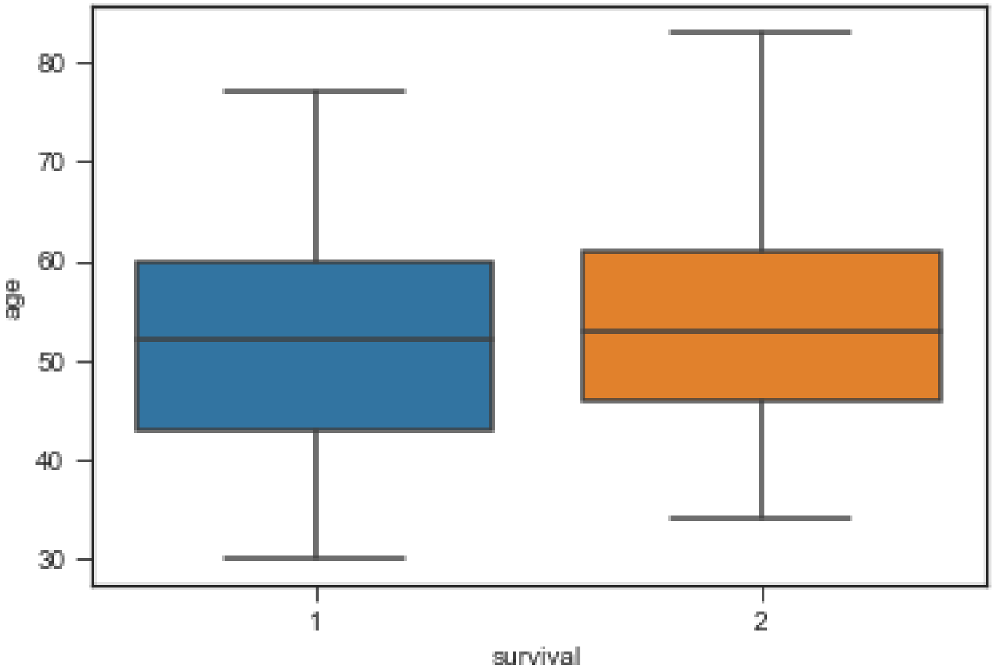
```
Out[26]: [<matplotlib.lines.Line2D at 0x19e32045470>]
```



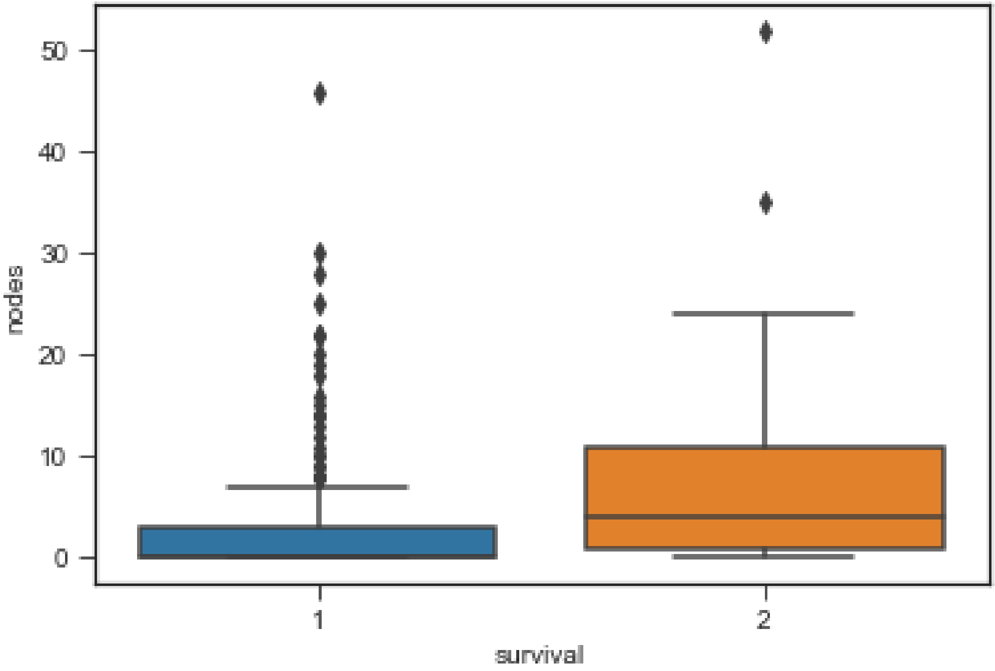
observation from CDF plot with auxillary nodes 1. number of auxillary nodes range from 0 to 53 2. 75% of patients that survived 5 years had zero nodes out of 224 patients 3. 40% of patients that didnt survive even they had zero nodes out of 81 patients 4. for any age person if they have nodes ranging from 25 to 43 their chance of surviving is 50:50

12 Box plot

```
In [27]: #boxplot
         sns.boxplot(x='survival', y='age', data=cancer)

Out[27]: <matplotlib.axes._subplots.AxesSubplot at 0x19e320701d0>
```



```
In [28]: sns.boxplot(data=cancer, x='survival', y='nodes')

Out[28]: <matplotlib.axes._subplots.AxesSubplot at 0x19e320e6400>
```



observation

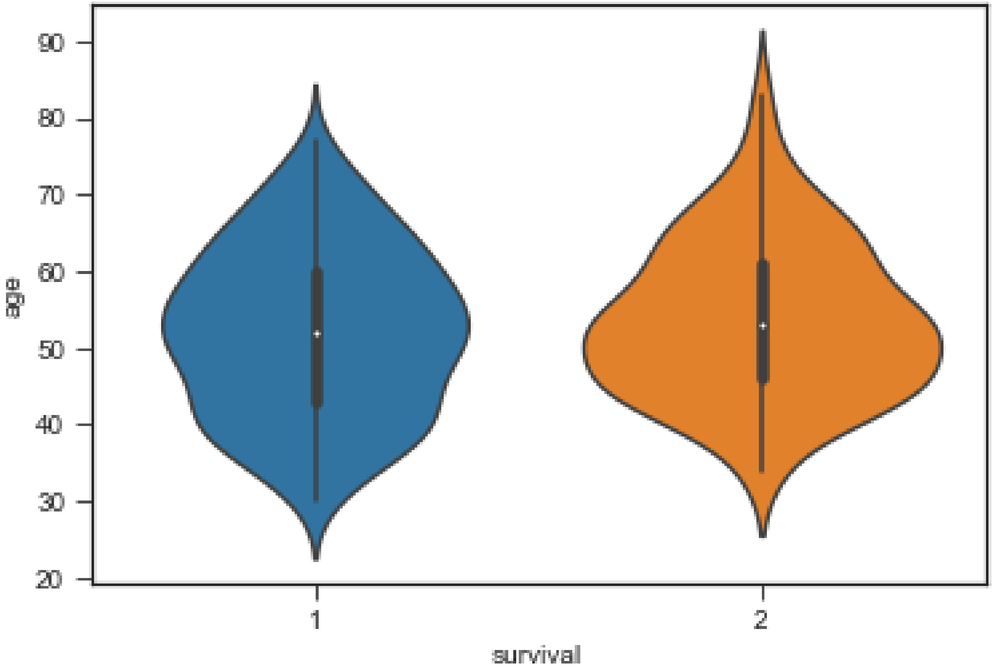
1. from boxplot we can see that age was not the factor in decicing survival. they play close as mean age of survival is ~52 and mean age of not survival patients is ~54.

2. in box plots of nodes we can see that for patients that didnot survive the nodes were considerably high than those survived.

13 violin plots

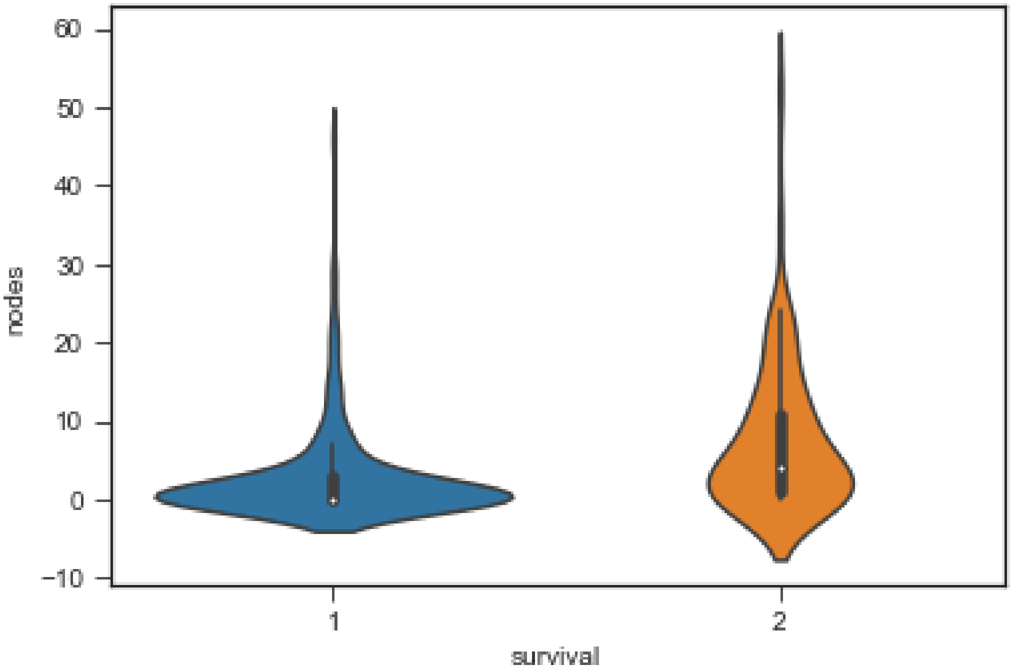
```
In [29]: sns.violinplot(x='survival', y='age', data=cancer)
```

```
Out[29]: <matplotlib.axes._subplots.AxesSubplot at 0x19e321464e0>
```



```
In [30]: sns.violinplot(x='survival', y='nodes', data=cancer)
```

```
Out[30]: <matplotlib.axes._subplots.AxesSubplot at 0x19e321a47b8>
```



Conclusive Observation

1. Age of patients range from 30 to 83
2. Number of auxillary nodes range from 0 to 53. with roughly 35% of patients having Zero auxillary nodes.
3. patients with age ranging from 40 to 75, despite of number of Auxillary nodes their chance of survival is 50%
4. may be we need much more data to completly understand why certaon patients survived while others didn't. it may be due to other health conditions associated like obesity or physical conditions.
5. From the data we have for any age patients their chance of survival is 50:50. because minimum age a patient survived 5years is 30. while, patient that didn't survive is 34. & maximum age that survived is 77 and maximum age that didnt survive is 83. so, for any patient it is a 50:50 as per our given data.