Necessary imports

```
In [72]: import pandas as pd
         import numpy as np
         import seaborn as sns
         import matplotlib.pyplot as plt
```

Understanding data

```
In [73]: data = pd.read_csv('haberman.csv')
         print(data.head())
```

```
   age  year  nodes  status
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
```

```
In [74]: data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 306 entries, 0 to 305
Data columns (total 4 columns):
age       306 non-null int64
year      306 non-null int64
nodes     306 non-null int64
status    306 non-null int64
dtypes: int64(4)
memory usage: 9.6 KB
```

```
In [75]: data.columns
Out[75]: Index(['age', 'year', 'nodes', 'status'], dtype='object')
```

```
In [76]: print (data.head())
```

```
   age  year  nodes  status
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
```

```
In [77]: """A manual inspection of data seems to give only two class labels. Either 1 or 2 but we would confirm"""
         print(data['status'].unique())
```

```
[1 2]
```

```
In [78]: data.describe()
```

Out[78]:

	age	year	nodes	status
count	306.000000	306.000000	306.000000	306.000000
mean	52.457516	62.852941	4.026144	1.264706
std	10.803452	3.249405	7.189654	0.441899
min	30.000000	58.000000	0.000000	1.000000
25%	44.000000	60.000000	0.000000	1.000000
50%	52.000000	63.000000	1.000000	1.000000
75%	60.750000	65.750000	4.000000	2.000000
max	83.000000	69.000000	52.000000	2.000000

Before plotting, we also can find how many of the people treated survived and how many didn't

```
In [71]: print ('count of people who survived and who didn\'t')
         print (data['status'].value_counts())
         print ('ratio of people who survived and who didn\'t')
         print (data['status'].value_counts(normalize = True))
```

```
count of people who survived and who didn't
1    225
2     81
Name: status, dtype: int64
ratio of people who survived and who didn't
1    0.735294
2    0.264706
Name: status, dtype: float64
```

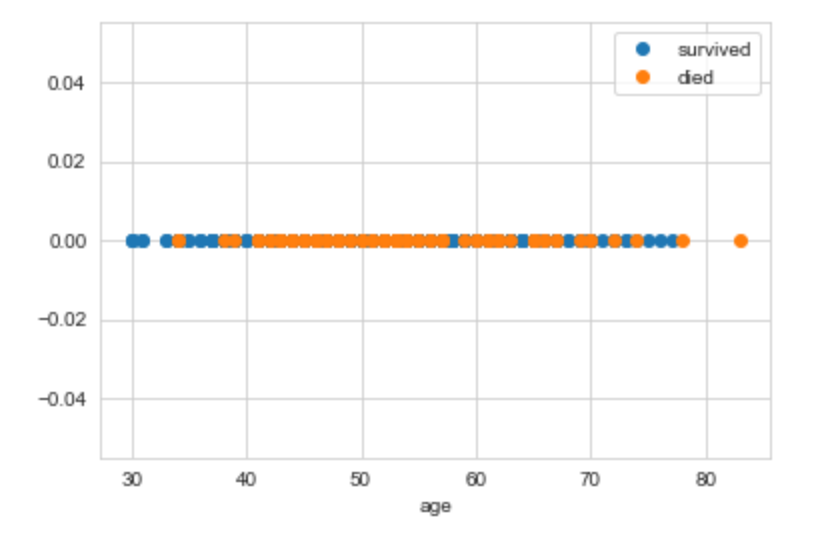
OBSERVATIONS

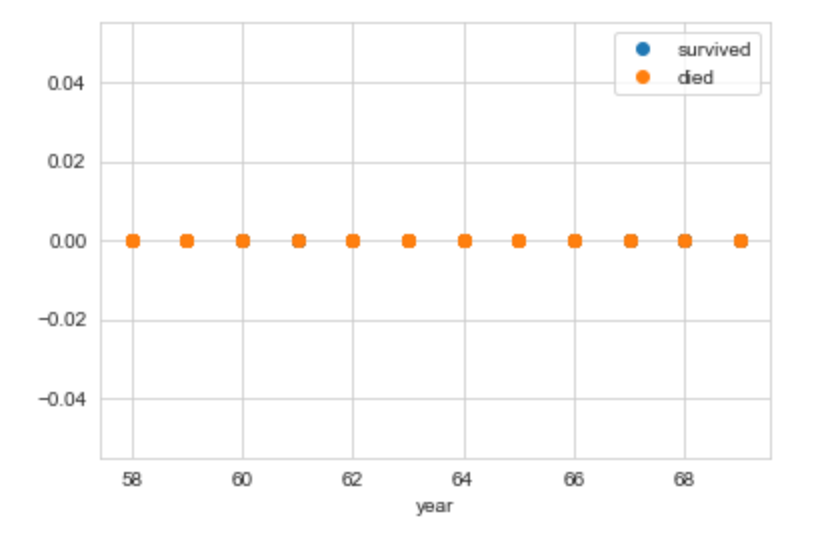
- The dataset is complete with no null values
- The mean age is approx 52
- The nodes has most of the data in 75th percentile with an absurdly huge outlier of 52 nodes
- approximately 73% people survived after the treatment

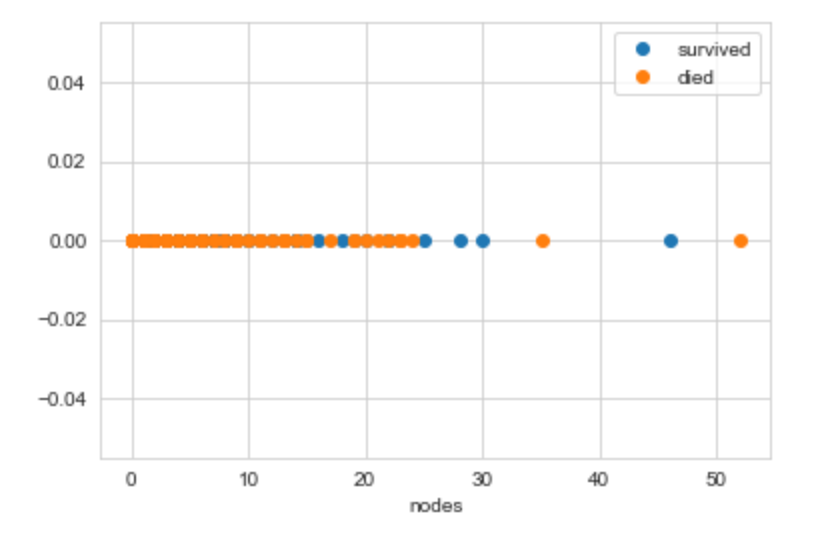
Plotting data and inferencing from it

```
In [97]: # 1 d scatter plot
         index = 1
         print (list(data.columns))
         for feature in list(data.columns[:-1]):
             plt.figure(index)
             data_status1 = data.loc[data['status'] == 1]
             data_status2 = data.loc[data['status'] == 2]
             plt.plot(data_status1[feature],np.zeros_like(data_status1[feature]),'o',label = 'survived')
             plt.plot(data_status2[feature],np.zeros_like(data_status2[feature]),'o', label = 'died')
             plt.xlabel(feature)
             plt.legend()
             index += 1
```

```
['age', 'year', 'nodes', 'status']
```



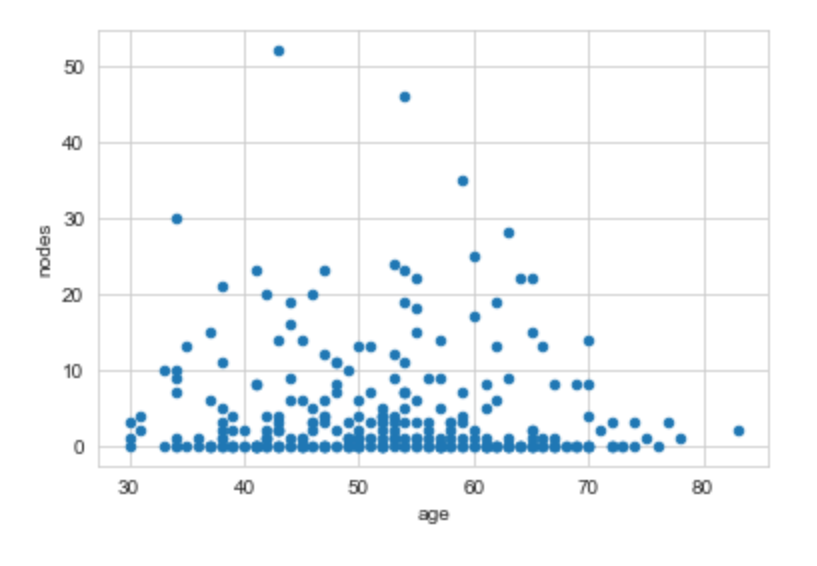




Observations

- Nothing useful can be observed/inferenced from the data

```
In [126]: # 2d scatter plot
          data.plot(kind = 'scatter', x = 'age', y = 'nodes')
          plt.show()
```

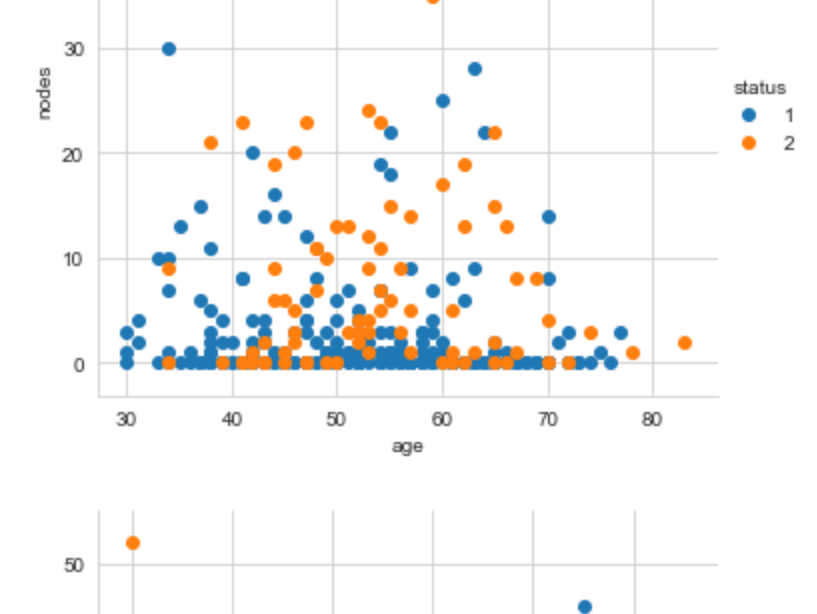


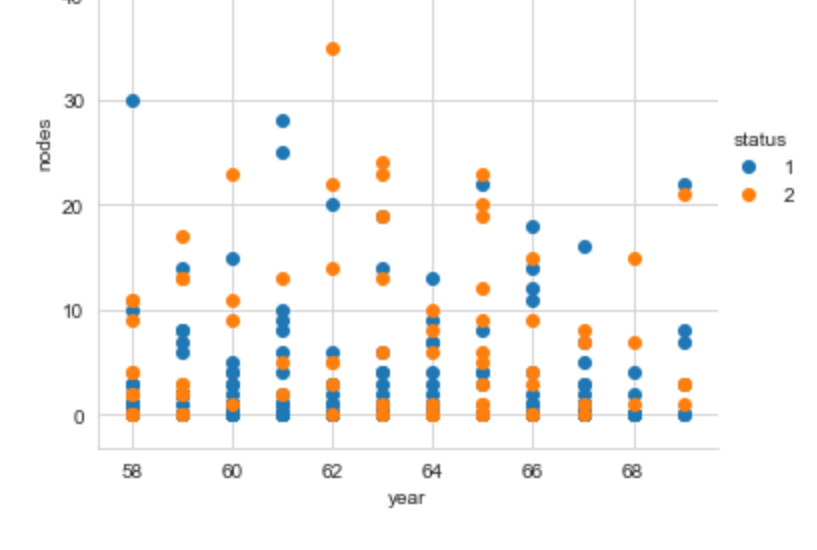
Observations:

- Nothing can be deduced from the above graph (we need to color the nodes)

```
In [128]: # using seaborn for plotting
          plt.close()
          plt.figure(1)
          sns.set_style('whitegrid');
          sns.FacetGrid(data, hue='status', height = 5) \
              .map(plt.scatter,'age','nodes') \
              .add_legend();
          plt.figure(2)
          sns.set_style('whitegrid');
          sns.FacetGrid(data, hue='status', height = 5) \
              .map(plt.scatter,'year','nodes') \
              .add_legend();
          plt.figure(3)
          sns.set_style('whitegrid');
          sns.FacetGrid(data, hue='status', height = 5) \
              .map(plt.scatter,'age','year') \
              .add_legend();
          plt.show()
```

```
<Figure size 432x288 with 0 Axes>
```



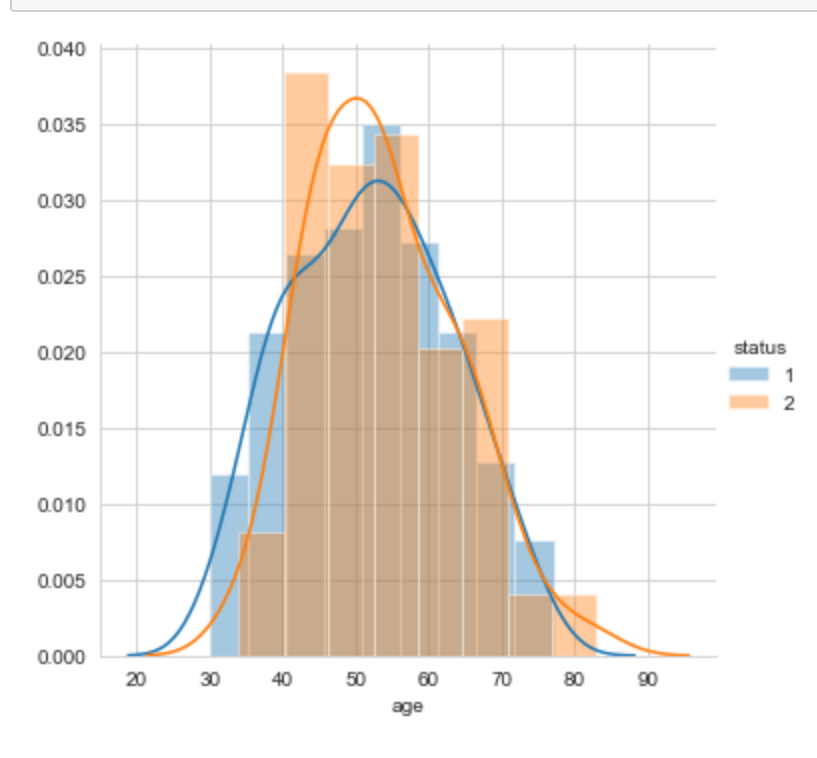


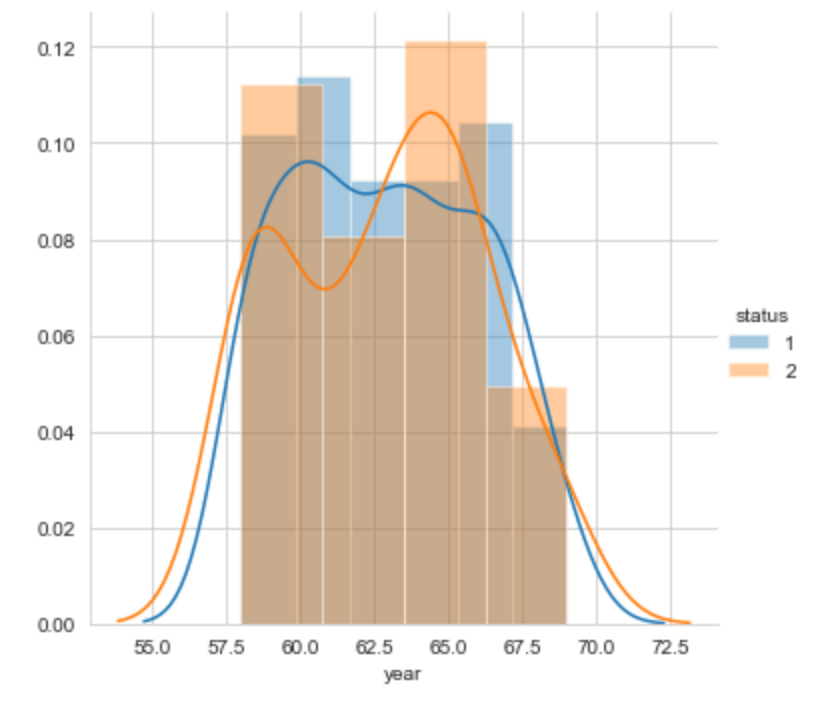
Observations:

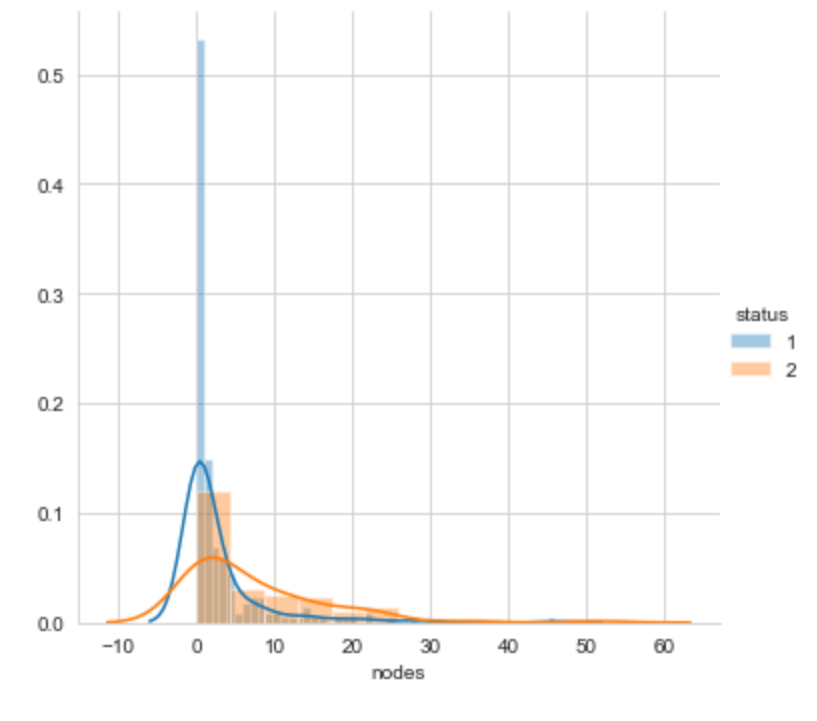
- No correlation between age, year and number of nodes can be observed

Trying univariate analysis

```
In [101]: for feature in list(data.columns[:-1]):
              fig = sns.FacetGrid(data,hue='status',height = 5)
              fig.map(sns.distplot, feature).add_legend()
              plt.show()
```







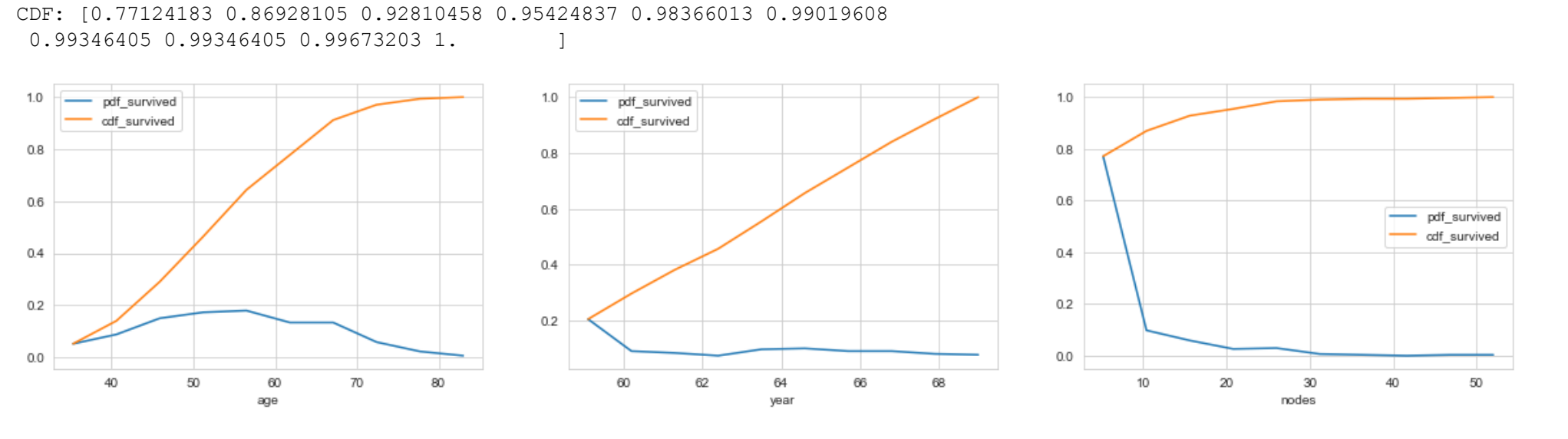

```
In [108]: plt.figure(figsize=(20,4))
          for idx,feature in enumerate(list(data.columns[:-1])):
              plt.subplot(1, 3, idx+1)
              print("{} \n\n",format(feature))
              counts, bin_edges = np.histogram(data[feature], bins=10, density=True)
              print("Bin Edges: {}".format(bin_edges))
              pdf = counts/sum(counts)
              print("PDF: {}".format(pdf))
              cdf = np.cumsum(pdf)
              print("CDF: {}".format(cdf))
              plt.plot(bin_edges[1:], pdf, bin_edges[1:], cdf)
              plt.legend(['pdf_survived','cdf_survived'])
              plt.xlabel(feature)
```

```
{}

 age
Bin Edges: [30.   35.3 40.6 45.9 51.2 56.5 61.8 67.1 72.4 77.7 83. ]
PDF: [0.05228758 0.08823529 0.1503268  0.17320261 0.17973856 0.13398693
 0.13398693 0.05882353 0.02287582 0.00653595]
CDF: [0.05228758 0.14052288 0.29084967 0.46405229 0.64379085 0.77777778
 0.91176471 0.97058824 0.99346405 1.        ]
{}

 year
Bin Edges: [58.   59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
PDF: [0.20588235 0.09150327 0.08496732 0.0751634  0.09803922 0.10130719
 0.09150327 0.09150327 0.08169935 0.07843137]
CDF: [0.20588235 0.29738562 0.38235294 0.45751634 0.55555556 0.65686275
 0.74836601 0.83986928 0.92156863 1.        ]
{}

 nodes
Bin Edges: [ 0.   5.2 10.4 15.6 20.8 26.  31.2 36.4 41.6 46.8 52. ]
PDF: [0.77124183 0.09803922 0.05882353 0.02614379 0.02941176 0.00653595
 0.00326797 0.         0.00326797 0.00326797]
CDF: [0.77124183 0.86928105 0.92810458 0.95424837 0.98366013 0.99019608
 0.99346405 0.99346405 0.99673203 1.        ]
```



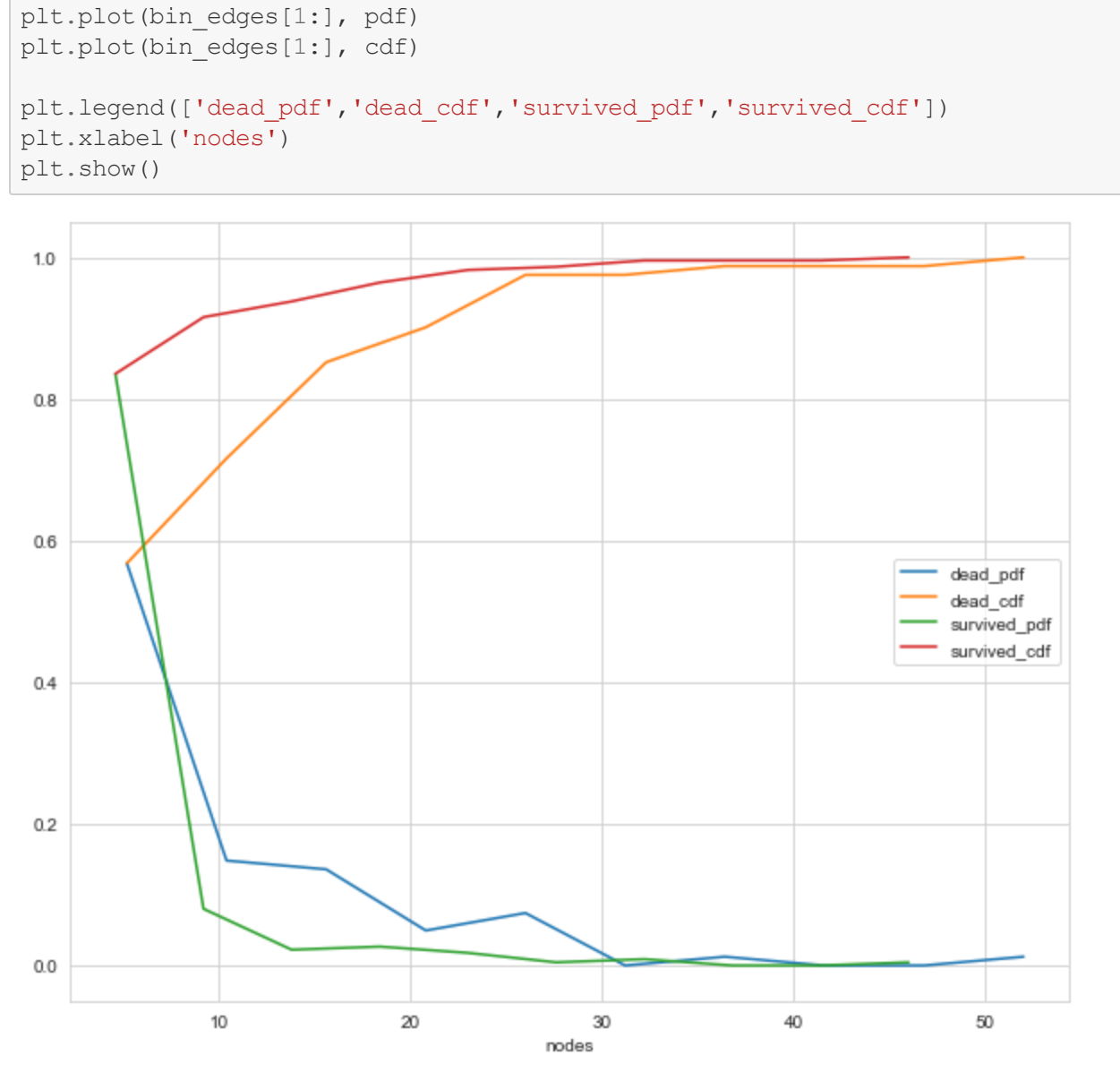

```
In [129]: # The node count is a feature that has reasonably visible affects hence plotting the node count values
          # and it's affect on survial status
          plt.figure(figsize = (10,8))

          data_died = data.loc[data['status'] == 2]
          data_sur = data.loc[data['status'] == 1]

          counts, bin_edges = np.histogram(data_died['nodes'],bins = 10, density = True)
          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(data_sur['nodes'], bins=10, density=True)
          pdf = counts/sum(counts)
          cdf = np.cumsum(pdf)
          plt.plot(bin_edges[1:], pdf)
          plt.plot(bin_edges[1:], cdf)

          plt.legend(['dead_pdf','dead_cdf','survived_pdf','survived_cdf'])
          plt.xlabel('nodes')
          plt.show()
```

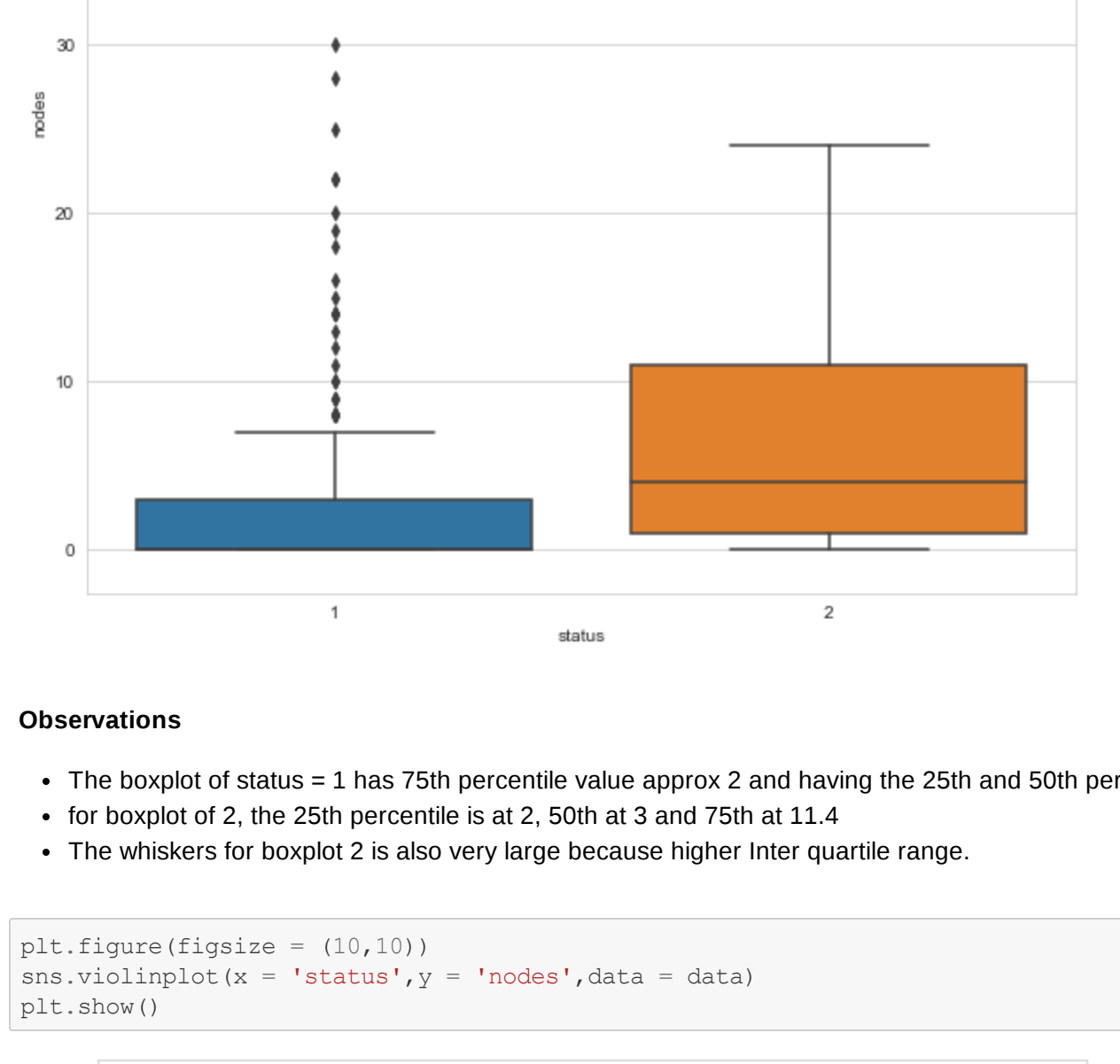


Observation

- for now it can be observed that the number of nodes is a key factor in determining whether a patient lives or not.
- the probability that the patient with less than equal to 4 nodes survives is very high.

making box plots and violin plots for better visualization

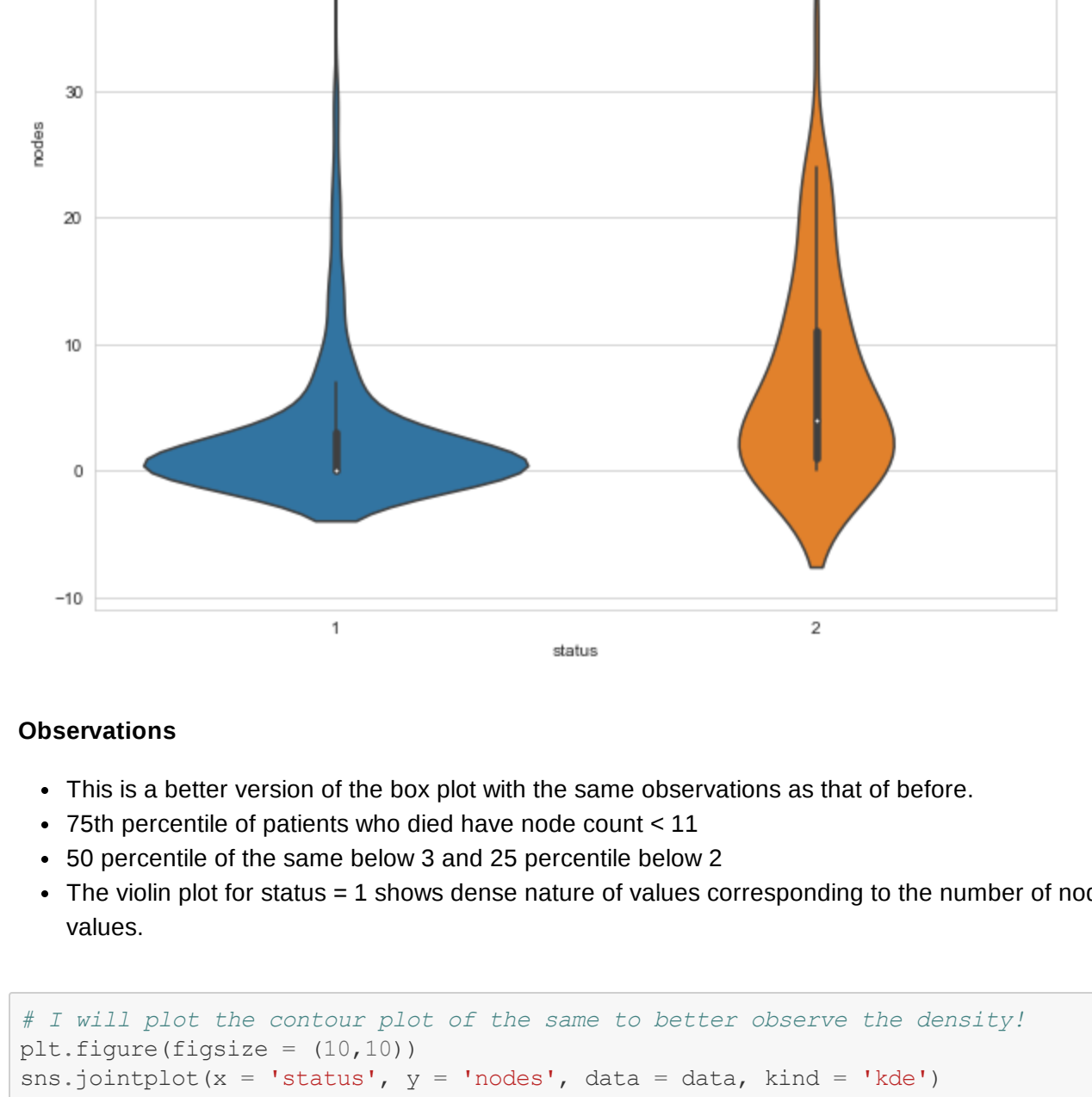
```
In [119]: plt.figure(figsize = (10,10))
          sns.boxplot(x = 'status',y = 'nodes',data = data)
          plt.show()
```



Observations

- The boxplot of status = 1 has 75th percentile value approx 2 and having the 25th and 50th percentlie overlaped
- for boxplot of 2, the 25th percentile is at 2, 50th at 3 and 75th at 11.4
- The whiskers for boxplot 2 is also very large because higher Inter quartile range.

```
In [123]: plt.figure(figsize = (10,10))
          sns.violinplot(x = 'status',y = 'nodes',data = data)
          plt.show()
```

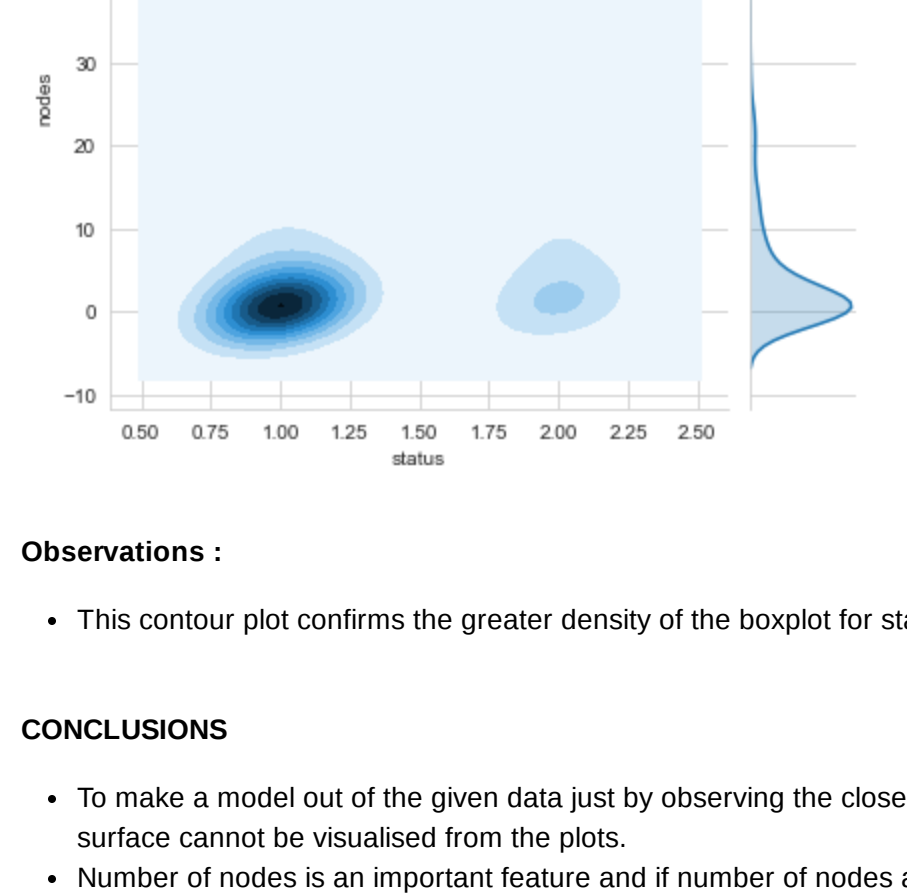


Observations

- This is a better version of the box plot with the same observations as that of before.
- 75th percentile of patients who died have node count < 11
- 50 percentile of the same below 3 and 25 percentile below 2
- The violin plot for status = 1 shows dense nature of values corresponding to the number of nodes which can be observed from the distplot and the mean values.

```
In [125]: # I will plot the contour plot of the same to better observe the density!
          plt.figure(figsize = (10,10))
          sns.jointplot(x = 'status', y = 'nodes', data = data, kind = 'kde')
          plt.show()
```

```
<Figure size 720x720 with 0 Axes>
```



Observations :

- This contour plot confirms the greater density of the boxplot for status 1 corresponding to the number of nodes

CONCLUSIONS

- To make a model out of the given data just by observing the closeness of the data is not possible because a visible boundary/plane/any n-dimensional surface cannot be visualised from the plots.
- Number of nodes is an important feature and if number of nodes are less, the patient is likely to survive.
- We need to add additional features to better fit the data, features incorporating nodes and age can work(polynomial features)