EDA_assignment_updated

April 4, 2020

[1]:
```
import warnings
warnings.filterwarnings("ignore")
```

[2]:
```
import pandas as pd
import seaborn as sb
import matplotlib.pyplot as plt
import numpy as np

haber=pd.read_csv("haberman.csv")#loading datset
```

[3]:
```
print (haber.shape)
```

```
(306, 4)
```

the dataset contains data of 306 patients stored in rows and 4 columns describes the feautres of dataset

[4]:
```
print (haber.columns)#columns names in dataset
```

```
Index(['age', 'year', 'nodes', 'status'], dtype='object')
```

[5]:
```
print(haber[:8])#first 8 rows of the dataset
```

```
   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
5   33    58     10       1
6   33    60      0       1
7   34    59      0       2
```

here class attribute is status which means survial status. status=1 means patient survied 5 or more than 5 years. status=2 means died with in 5 years.

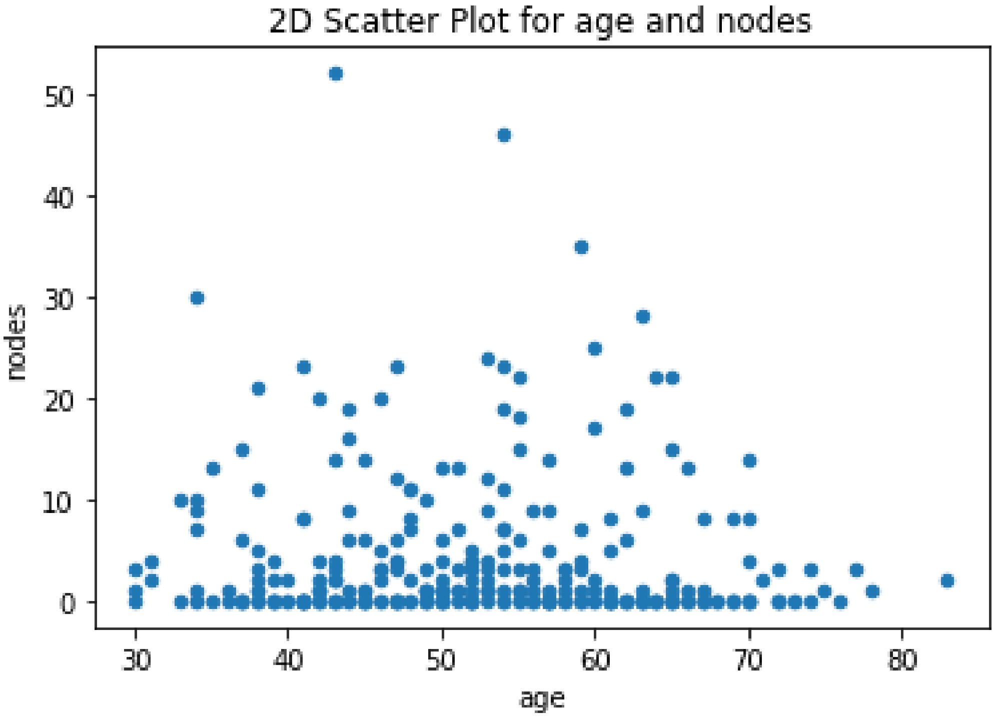
[6]:
```
haber["status"].value_counts()
```

```
[6]: 1    225
     2     81
     Name: status, dtype: int64
```

Data set is imbalanced. out of 306 patients: 225 survied 5 or more than 5 years and 81 died with in 5 years i.e not survied beyond 5 years.

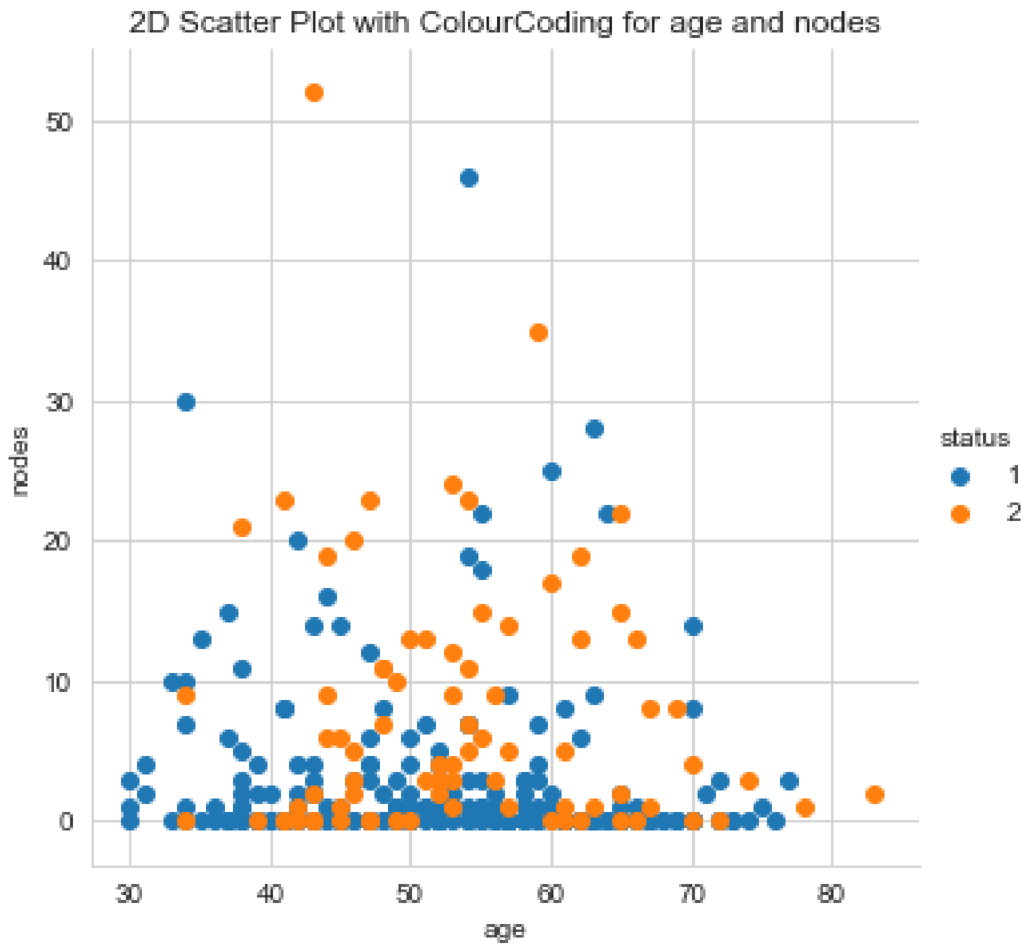
1 2D SCATTER PLOT

```
[7]: haber.plot(kind="scatter", x="age", y="nodes");
     plt.title("2D Scatter Plot for age and nodes")
     plt.show()
```



In the above 2D scatter plot we can say that patients with more than 30 nodes are difficult to survive i.e Patients having more number of nodes are difficult to survive

```
[8]: #2D Scatter plot with Colourcoding
     sb.set_style("whitegrid")
     sb.FacetGrid(haber,hue="status",height=5)\
         .map(plt.scatter,"age","nodes")\
         .add_legend();
     plt.title("2D Scatter Plot with ColourCoding for age and nodes")
     plt.show();
```

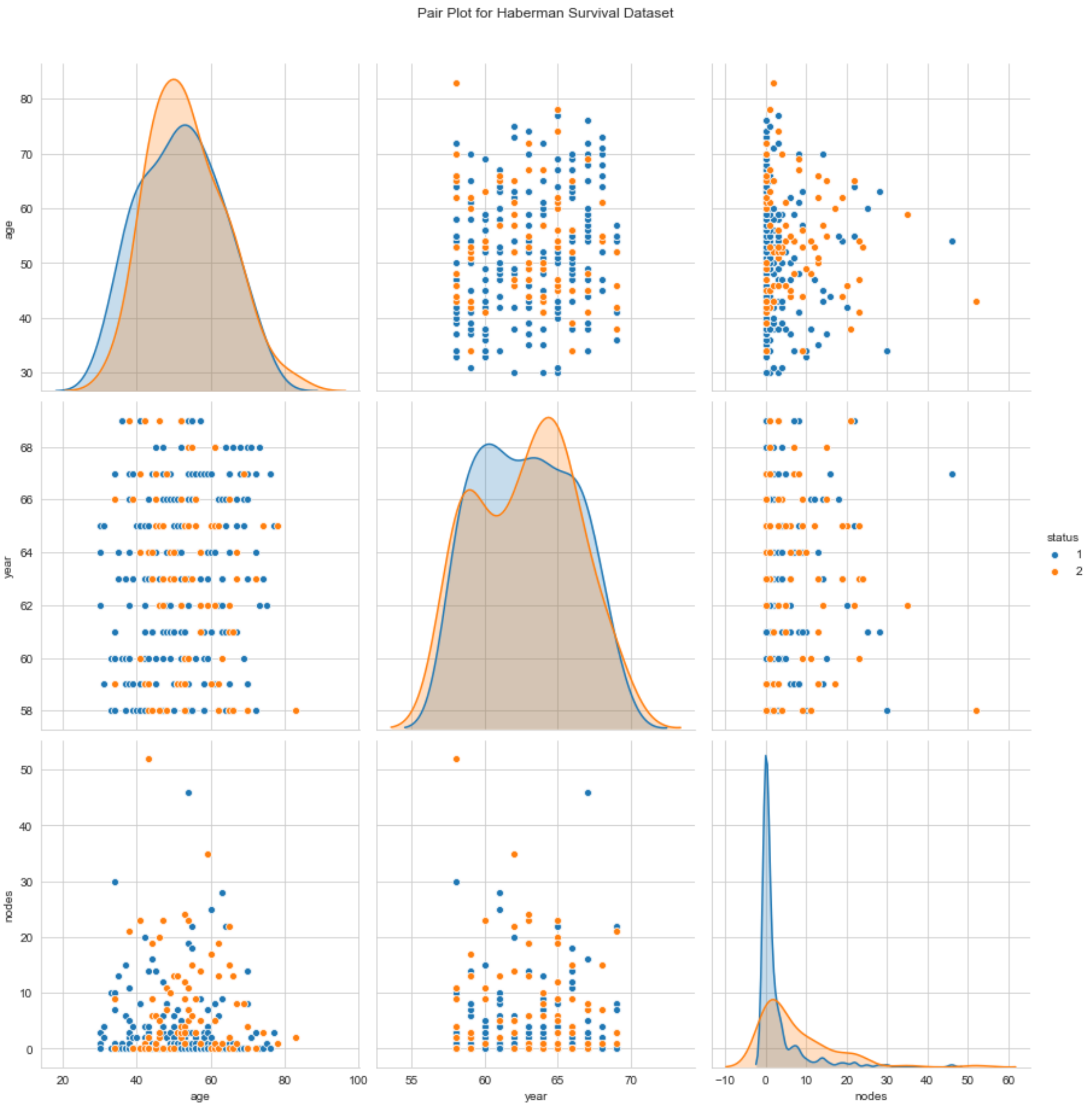


Observations: 1.Almost all the Patients whose age is between 30 and 40 are survived beyond 5 years. 2.Many Patients with more than 20 and 30 nodes are difficult to survive beyond 5 years.

2 Pair Plot

[9]:
```
#pairplot for Haberman Survival

plt.close();
sb.set_style("whitegrid");
sb.pairplot(haber, hue='status', height=4).fig.suptitle("Pair Plot for Haberman␣
 ↪Survival Dataset",y=1.05);
plt.show()
```

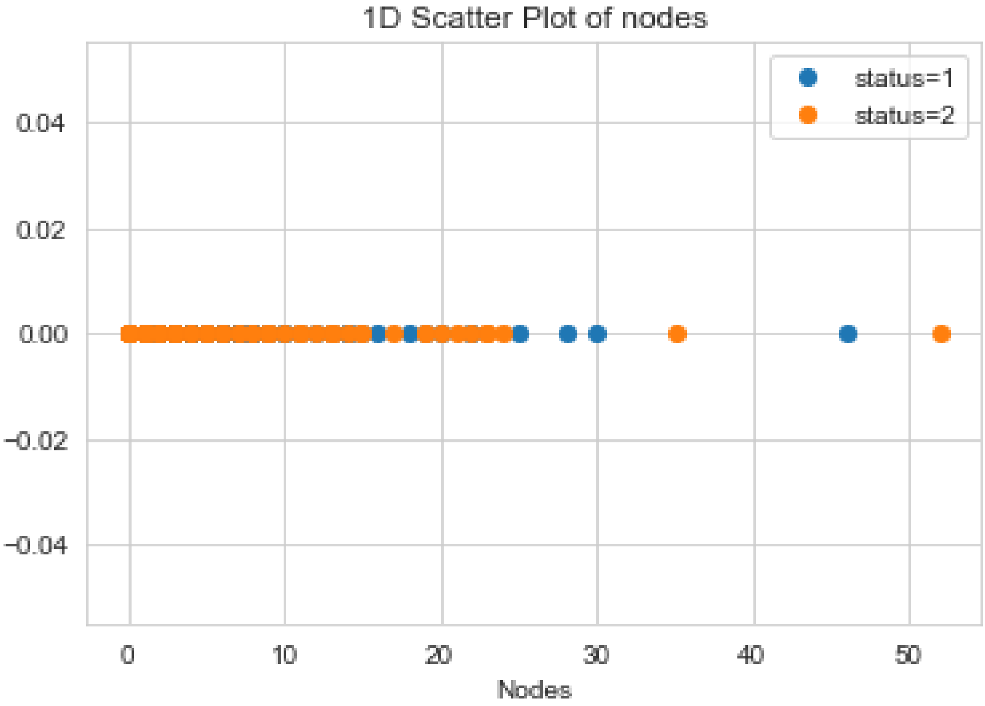


Observations 1.Almost all Patients whose age is less than 38 are survived beyond 5 years. 2.Patients whose age is above 77 are not survived beyond 5 years. 3.Patients with more than 30 nodes are difficult to survive beyond 5 years.

3 Histogram, PDF , CDF

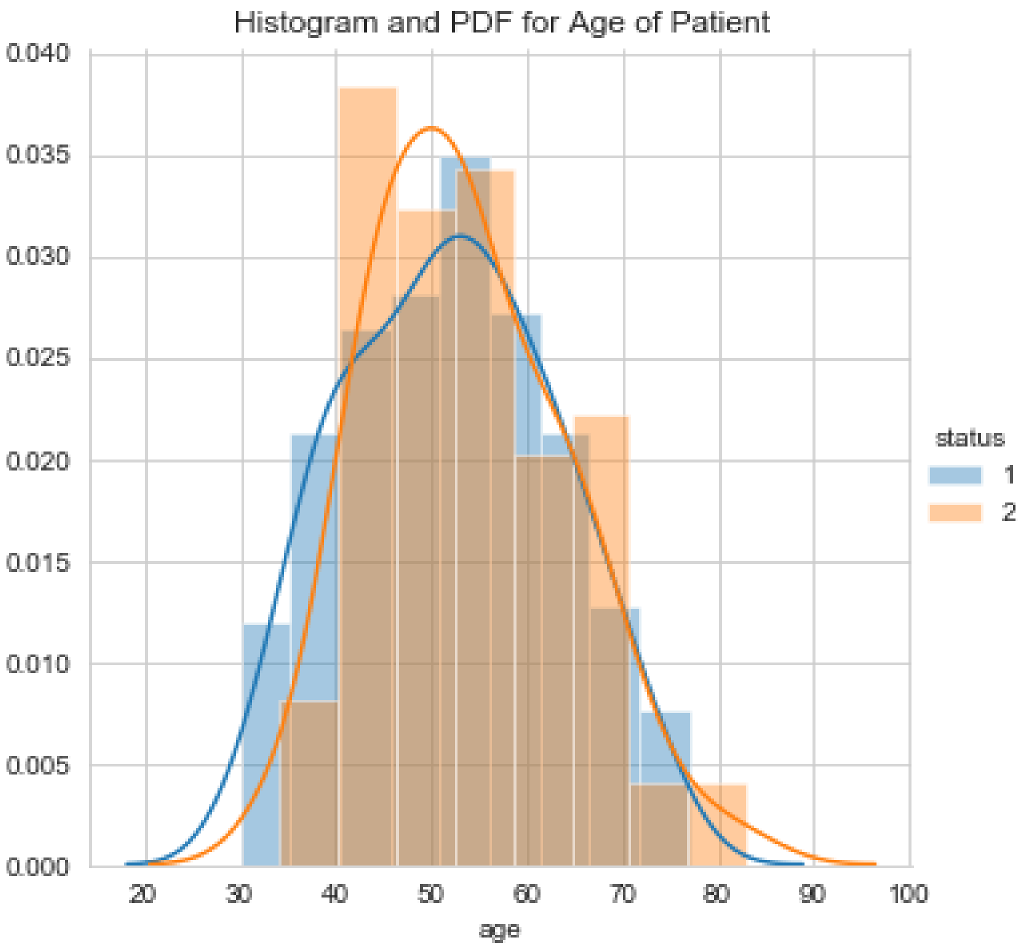
```
[10]: #1D scatter plot of nodes

haber_1=haber.loc[haber["status"]==1];
haber_2=haber.loc[haber["status"]==2];
plt.plot(haber_1["nodes"],np.zeros_like(haber_1["nodes"]),"o",label="status=1");
plt.plot(haber_2["nodes"],np.zeros_like(haber_2["nodes"]),"o",label="status=2");
plt.title("1D Scatter Plot of nodes")
plt.xlabel("Nodes")
plt.legend()
plt.show()
```



[11]:

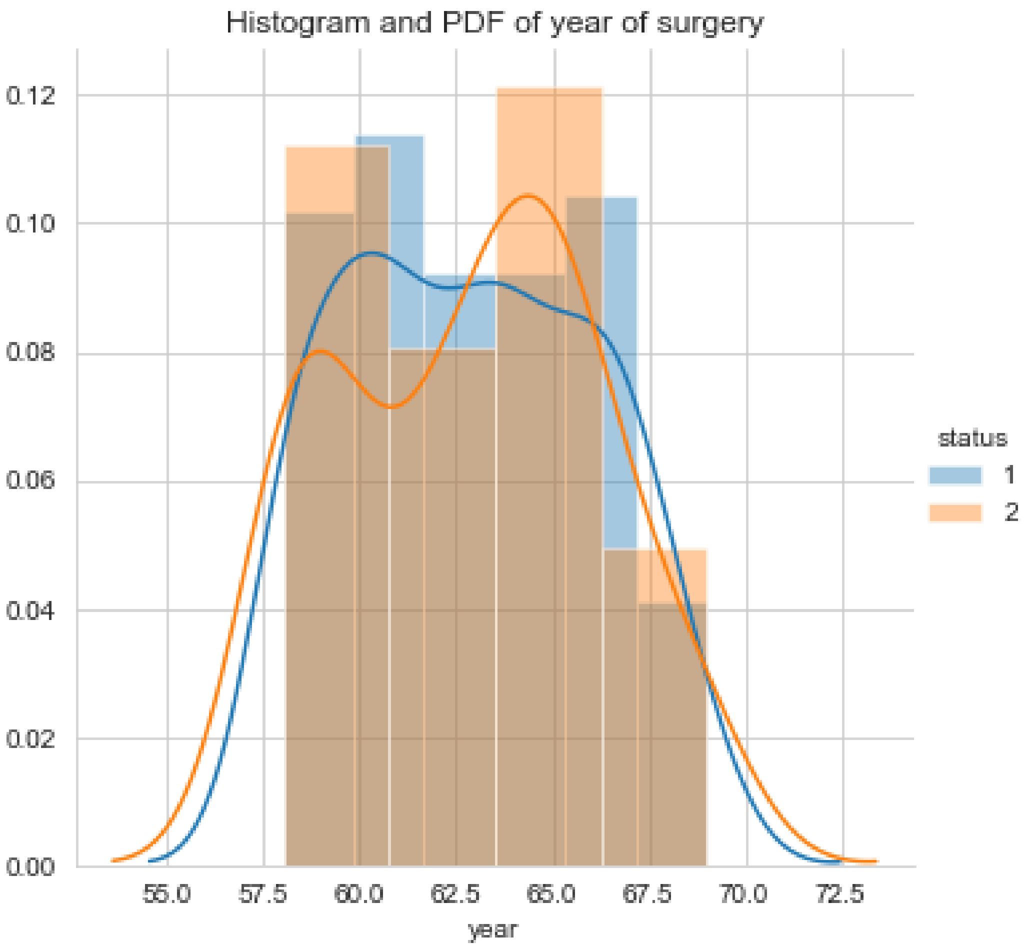
```
sb.FacetGrid(haber, hue="status",height=5)\
   .map(sb.distplot,"age")\
   .add_legend();
plt.title("Histogram and PDF for Age of Patient")
plt.show();
```



Observations 1.more overlappings occured. 2.patients ages between 30 and 40 have higher chance of survival beyond 5 years. 3.Chances for survival and non-survival is equal between ages 65 and 78.

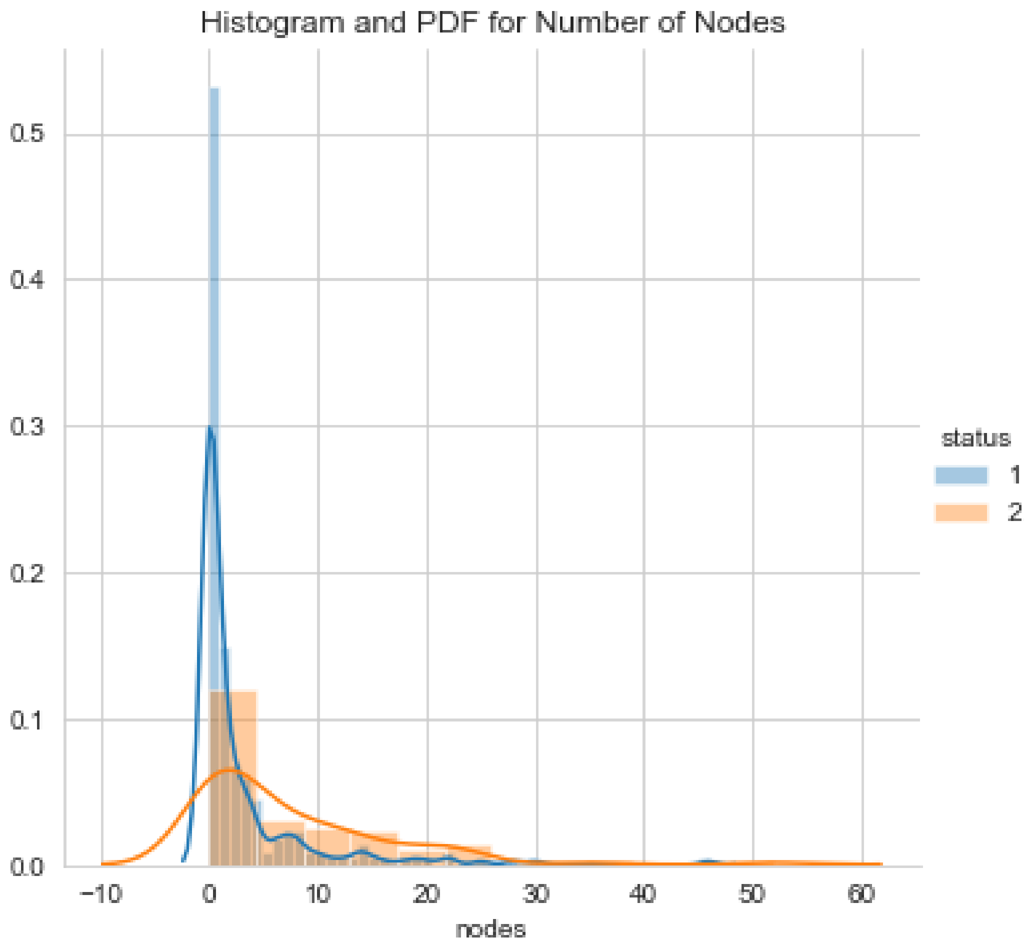
[12]:

```
sb.FacetGrid(haber, hue="status", height=5)\
   .map(sb.distplot,"year")\
   .add_legend();
plt.title("Histogram and PDF of year of surgery")
plt.show();
```



observations: 1.more overlappings occured. year of surgery doesnot effect the chance of patient survial. 2.patients survial is high in between 1960 and 1962. 3.in 1965 there was high chance for non survival i.e survial less than 5 years.

[13]:
```
sb.FacetGrid(haber, hue="status", height=5)\
    .map(sb.distplot,"nodes")\
    .add_legend();
plt.title("Histogram and PDF for Number of Nodes")
plt.show();
```



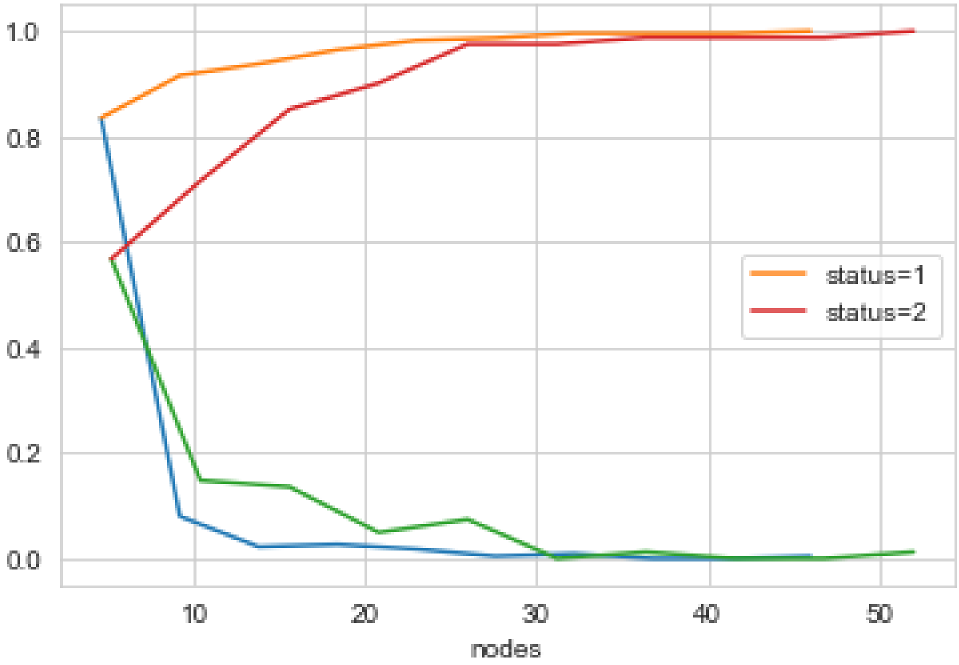
obeservations: 1.From the above plot,we can say number of nodes affects the survival rate more than age and year. 2.Patients with 0 and 1 nodes have high chance for survival. 3.non survival increases after patient having more than 5 nodes.

[14]:
```
#pdf and cdf of number of nodes

counts,bin_edges=np.histogram(haber_1["nodes"],bins=10,density=True)
pdf=counts/sum(counts)
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.xlabel("nodes")
plt.title("PDF and CDF for Number of Nodes and when status=1")
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. ]
```

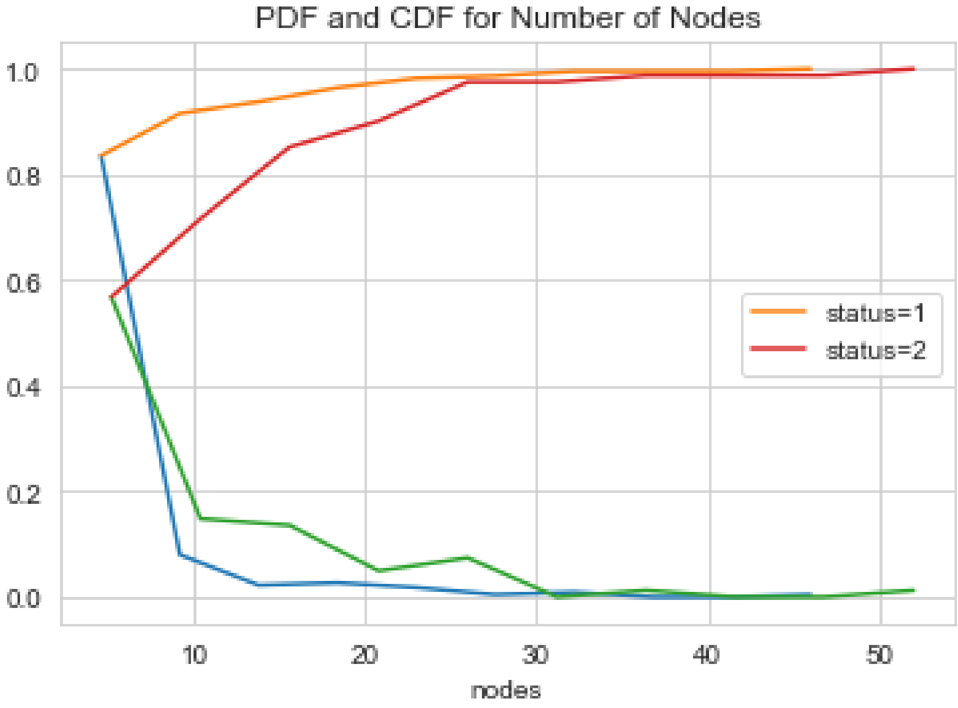


[15]:

```
#pdf and cdf of number of nodes when status=1
counts,bin_edges=np.histogram(haber_1["nodes"],bins=10,density=True)
pdf=counts/sum(counts)
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf,label="status=1")

#pdf and cdf of number of nodes when status=2
counts,bin_edges=np.histogram(haber_2["nodes"],bins=10,density=True)
pdf=counts/sum(counts)
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf,label="status=2")
plt.xlabel("nodes")
plt.title("PDF and CDF for Number of Nodes")
plt.legend()
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. ]
```



observations: 83.5% of patients who survived are having nodes between 0 and 4.6 56.8% of patients who non survived are having nodes between 0 and 5.2

4 Mean , Variance and Standard Deviation

[16]:
```
#means of number of nodes when status=1 and status=2
print("Means:")
print(np.mean(haber_1["nodes"]))
print(np.mean(haber_2["nodes"]))

#standard Deviation of number of nodes when status=1 and status=2
print("\nStandard Deviation:")
print(np.std(haber_1["nodes"]))
print(np.std(haber_2["nodes"]))
```

```
Means:
2.7911111111111113
```

```
7.45679012345679

Standard Deviation:
5.857258449412131
9.128776076761632
```

observation There is increase in mean of number of nodes of non survival patients when compared to survival patients similarlly there is increase in standard deviation also. so, number of nodes increases there is less chance for survival.

5 Median, Percentile, Quantile, IQR ,MAD

[17]:

```python
#median of number of nodes when status=1 and status=2

print("\nMedians:")
print(np.median(haber_1["nodes"]))
print(np.median(haber_2["nodes"]))

#90th percentile of number of nodes when status=1 and status=2

print("\n90th Percentile:")
print(np.percentile(haber_1["nodes"],90))
print(np.percentile(haber_2["nodes"],90))

#quantile of number of nodes when status=1 and status=2

print("\nQuantile:")
print(np.percentile(haber_1["nodes"],np.arange(0,100,25)))
print(np.percentile(haber_2["nodes"],np.arange(0,100,25)))

#median absolute deviation of number of nodes when status=1 and status=2

from statsmodels import robust
print("\nMedian Absolute Deviation:")
print(robust.mad(haber_1["nodes"]))
print(robust.mad(haber_2["nodes"]))
```

```
Medians:
0.0
4.0

90th Percentile:
8.0
20.0

Quantile:
```

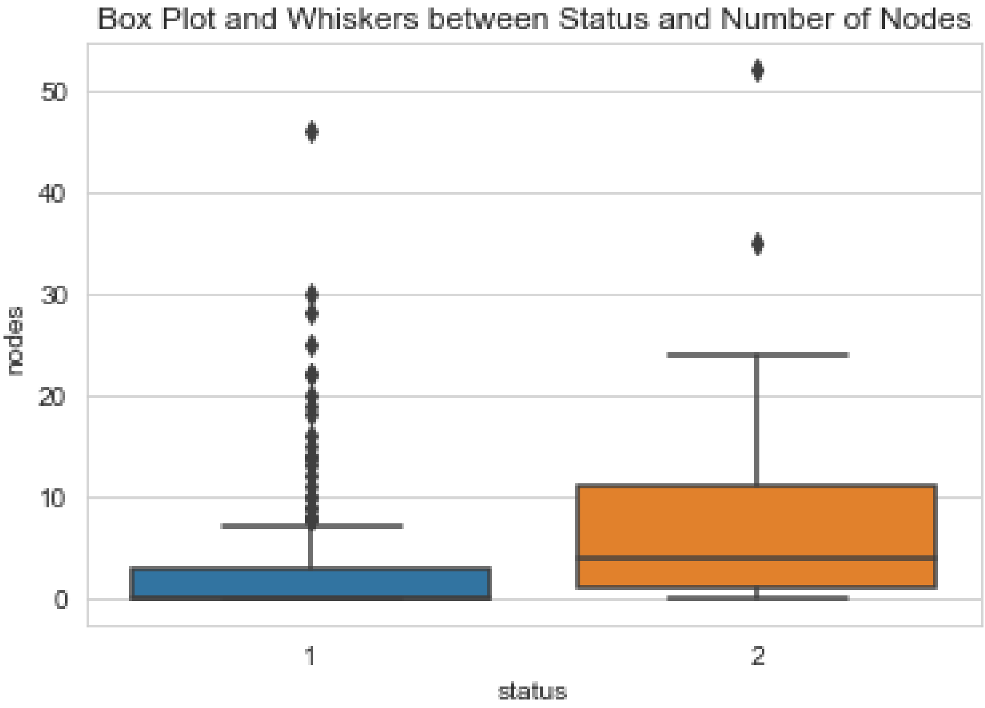
```
[0. 0. 0. 3.]
[ 0.  1.  4. 11.]

Median Absolute Deviation:
0.0
5.930408874022408
```

observations 1.Median of nodes is high for non survival dataset compared to survival dataset. 2.similarlly,The percentile quartile is high for non survival dataset than survival dataset. 3.75% of non survival patients have 11 or more nodes where as 75% of survied patients have only 3 nodes.

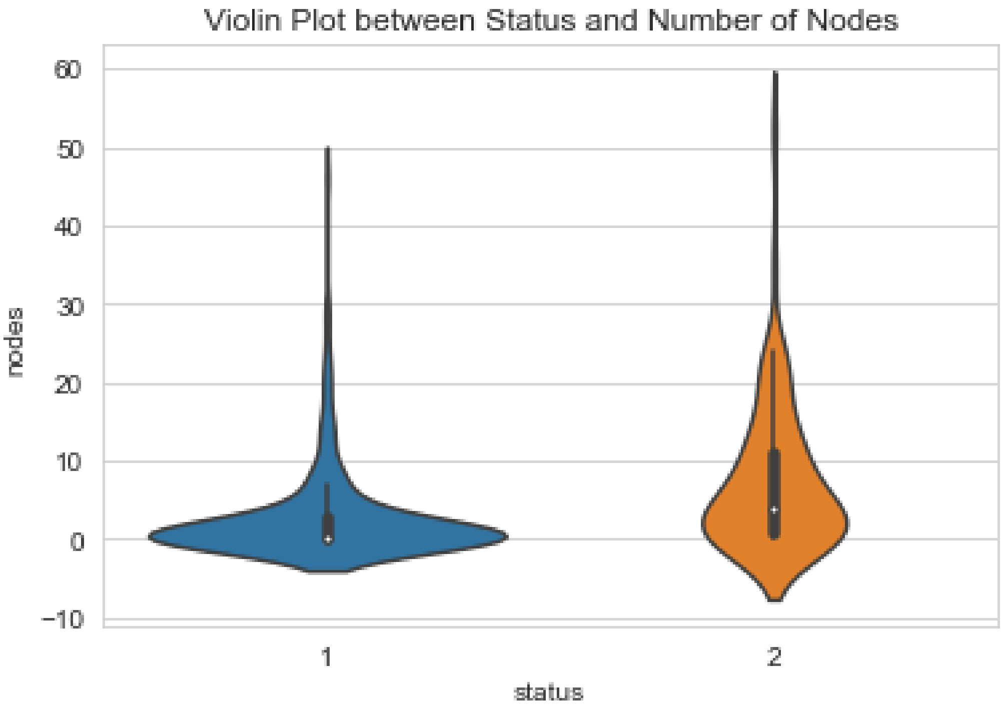
6 BoxPlot and Whiskers

[18]:
```
sb.boxplot(x="status", y="nodes", data=haber)
plt.title("Box Plot and Whiskers between Status and Number of Nodes")
plt.show()
```



7 Violin Plots

[19]:
```
sb.violinplot(x="status", y="nodes", data=haber)
plt.title("Violin Plot between Status and Number of Nodes")
plt.show()
```

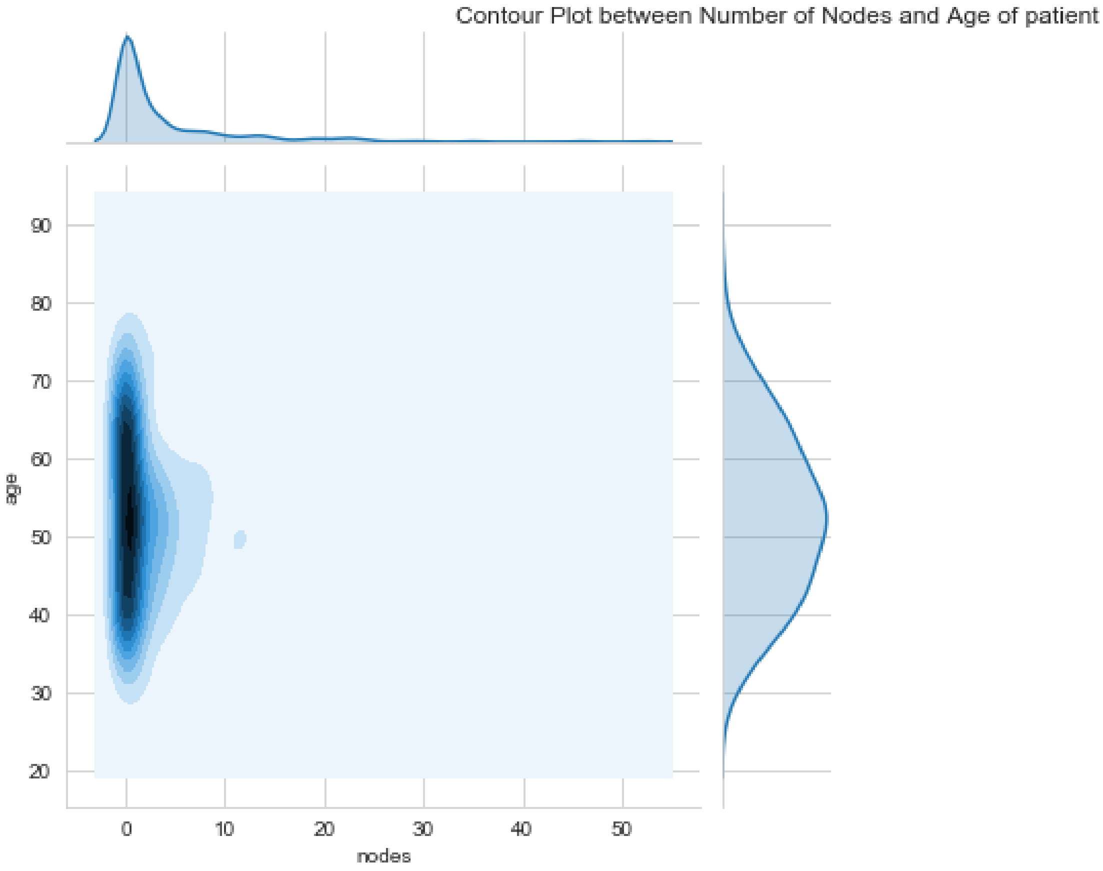


observations: 1.There are many patients who survived having 0 nodes and at the same time there are some patients having 0 nodes survived less than 5 years 2.The increase in nodes number there is decrease in survival rate i.e patients with more than 1 node have less chance of survival

8 Multivariate Analysis and Contour Plot

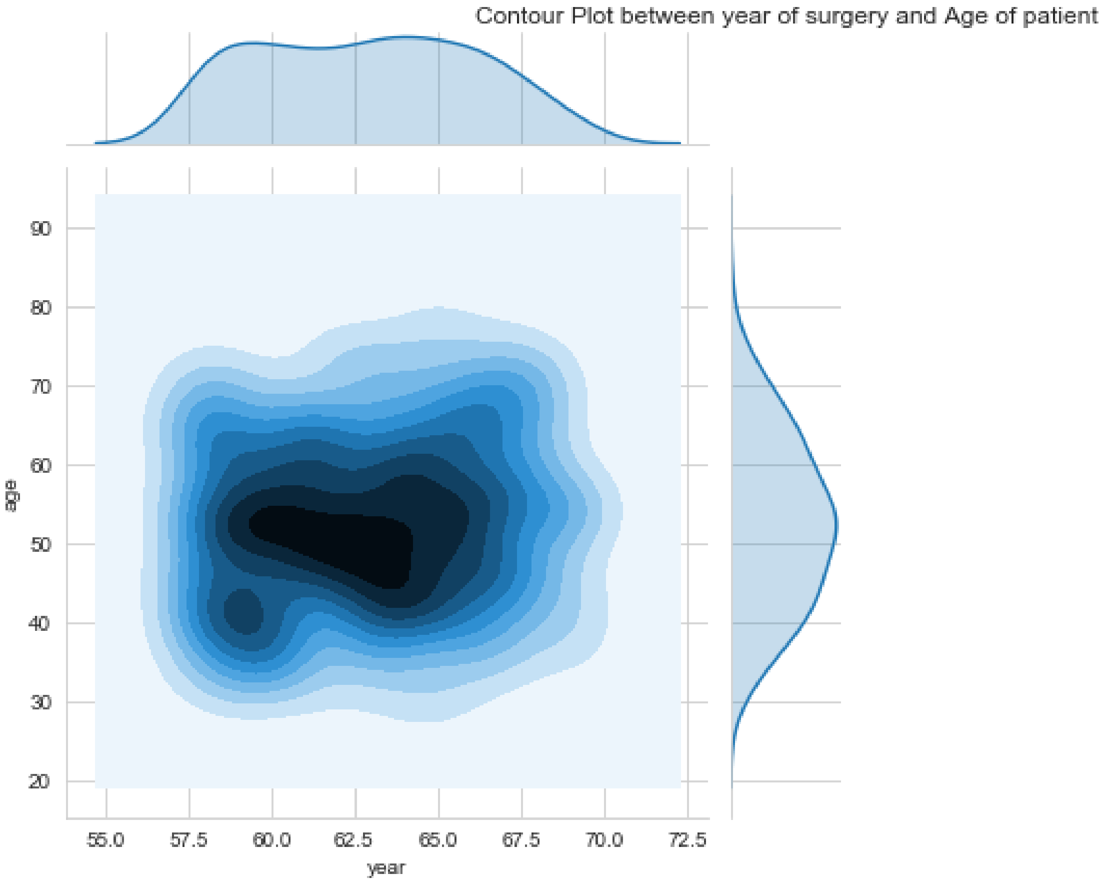
[20]:

```
sb.jointplot(x="nodes", y="age", data=haber, kind="kde")
plt.title("Contour Plot between Number of Nodes and Age of patient",y=1.2)
plt.show()
```



observations Most patients with 0 and 1 nodes are in between ages 45 and 55.

[21]:
```
sb.jointplot(x="year", y="age", data=haber,kind="kde")
plt.title("Contour Plot between year of surgery and Age of patient",y=1.2)
plt.show()
```



observations From 1960-1964 ,more surgeries done on patients between ages 45 and 55.

Conclusions: 1.Patient's Age and Year of surgeory are not the deciding features for their survival but a patients whose age is less than 35 have high chance of survival. 2.Chance of survival depends on number of nodes in a patient. patient with less number of nodes have higher chance for survival. 3.Absence of nodes in patients doesn't guarantee the survival of the Patient.

[ ]: