Assignment Instructions:

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 (https://www.kaggle.com/gilsousa/habermans-survival-data-set)) or you can also run the below cell and load the data directly.
2. Perform a similar anlaysis as done in the reference notebook on this dataset.

1.1 Analyze high level statistics of the dataset: number of points, numer of features, number of classes, data-points per class.

- You have to write all of your observations in Markdown cell with proper formatting.You can go through the following blog to understand formatting in markdown cells - https://www.markdownguide.org/basic-syntax/ (https://www.markdownguide.org/basic-syntax/)
- Do not write your observations as comments in code cells.
- Write comments in your code cells in order to explain the code that you are writing. Proper use of commenting can make code maintenance much easier, as well as helping make finding bugs faster.
- You can add extra cells using **Insert cell below command** in Insert tab. You can also use the shortcut Alt+Enter
- It is a good programming practise to define all the libraries that you would be using in a single cell

In [1]:

```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
from statsmodels import robust
import warnings
warnings.filterwarnings("ignore")
```

In [2]:

```
Data = pd.read_csv('/content/haberman.csv')
```

In [3]:

```
Data.head()
```

Out[3]:

	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

Explanation of Data

##1. **age** : Age is time in patient operation was done ##2 **year**: year is operation year in which patient operation was done ##3. **nodes** : nodes is if patient lymph got effection by operation or not ##4. **status** : status is 0 or 1 if patient got survived then status is 1 if not then survival status is 0

#Statistical Analysis

In [4]:

```
print(Data.shape)
print(Data.shape[0])
```

```
(306, 4)
306
```

In [5]:

```
print(Data['status'].nunique())
print(Data['status'].unique())
```

```
2
[1 2]
```

In [6]:

```
print(Data['status'].value_counts())
```

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

In [7]:

```
Data_1 = Data.loc[Data["status"] == 1]
Data_2 = Data.loc[Data["status"] == 2]
```

1.2 - Explain the objective of the problem.

(The objective for a problem can be defined as a brief explanation of problem that you are trying to solve using the given dataset)

Data observations

##1. Data is imbalanced dataset ##2. Data is consist of 3 independent variables **year , nodes ,age** and 1 dependent variable **status** ##3. survival status is defined by value 0 and 1

#Objective of Data : we have to check whether patient was survived for more than 5 years or not

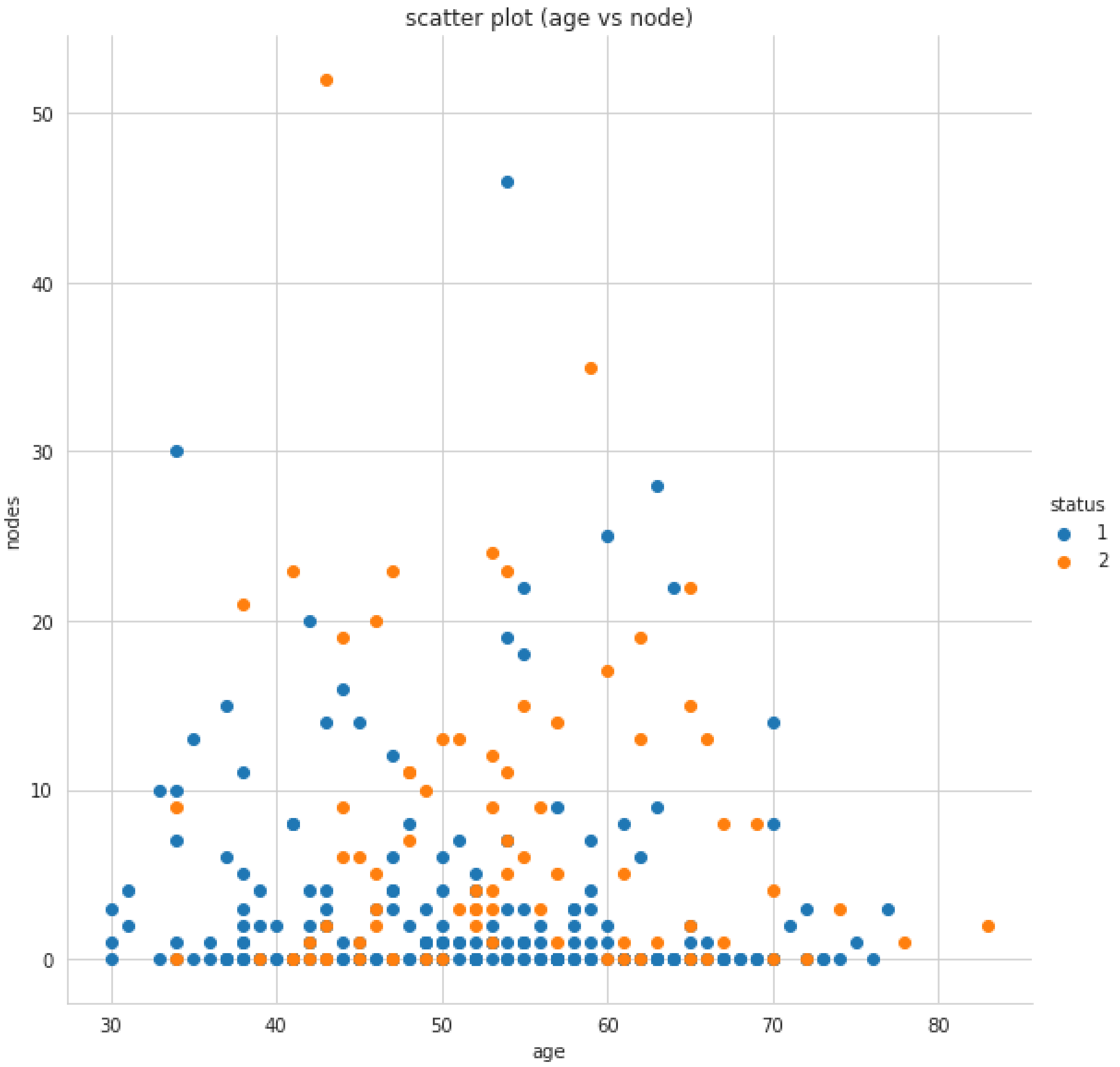
#Bi-Variate Analysis 2D Scatter Plot

In [8]:

```
plt.figure()
sns.set_style("whitegrid")
g=sns.FacetGrid(Data,hue="status",size=8)
g.map(plt.scatter,'age','nodes')
plt.title("scatter plot (age vs node)")
g.add_legend()
```

Out[8]:

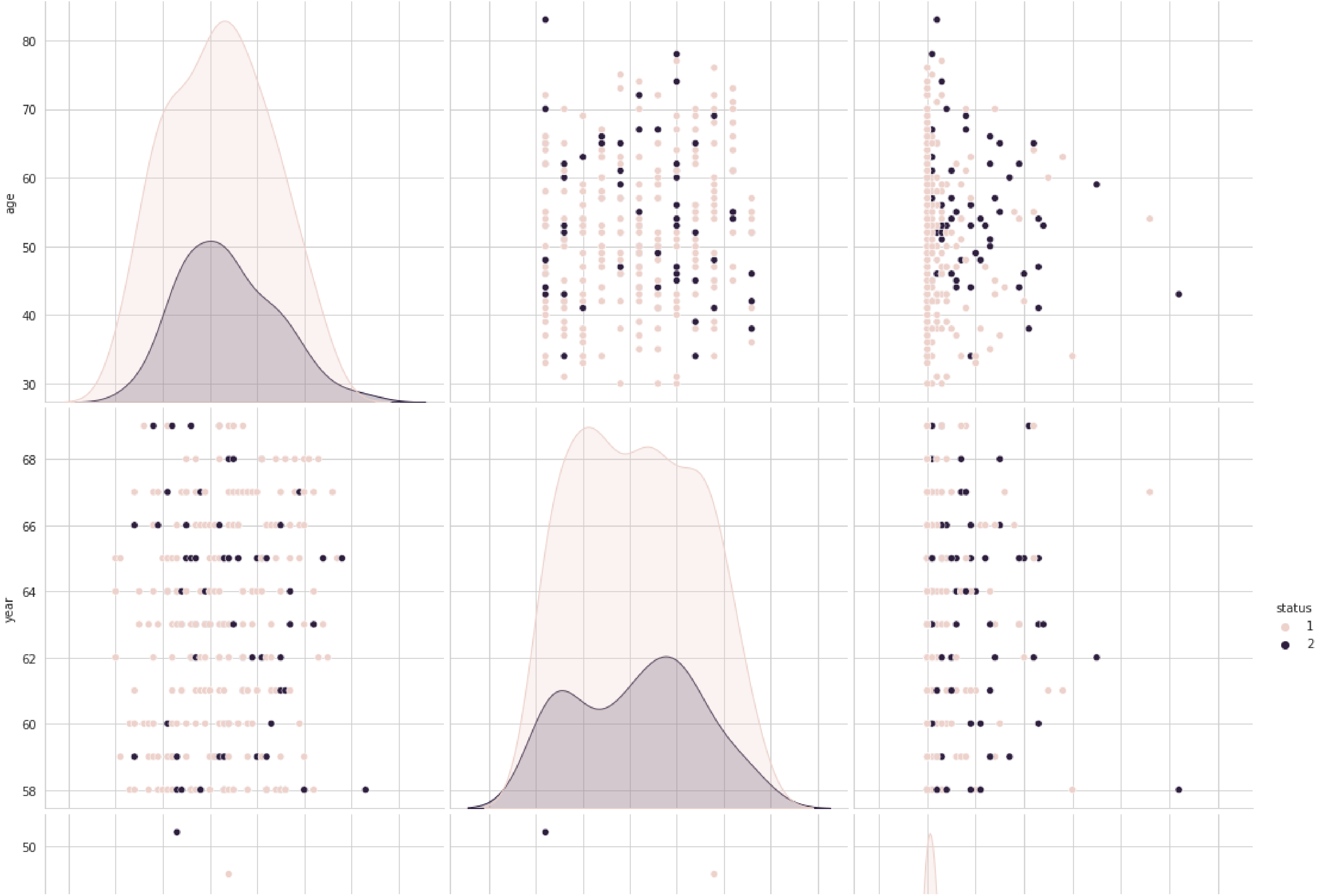
```
<seaborn.axisgrid.FacetGrid at 0x7f02fb5df250>

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

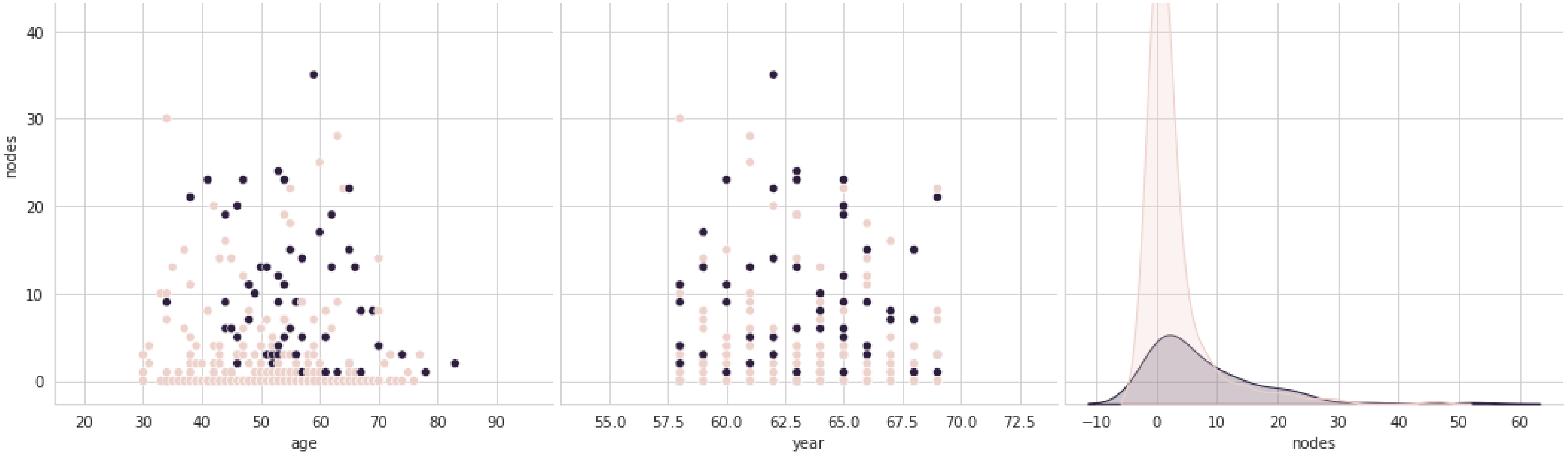

scatter plot (age vs node)
nodes
age
0
10
20
30
40
50
30
40
50
60
70
80
status
● 1
● 2

#Pair Plot

```
In [9]: sns.pairplot(Data,hue="status",vars=["age","year","nodes"],size=5)
```

```
Out[9]: <seaborn.axisgrid.PairGrid at 0x7f02fb5d1090>
```





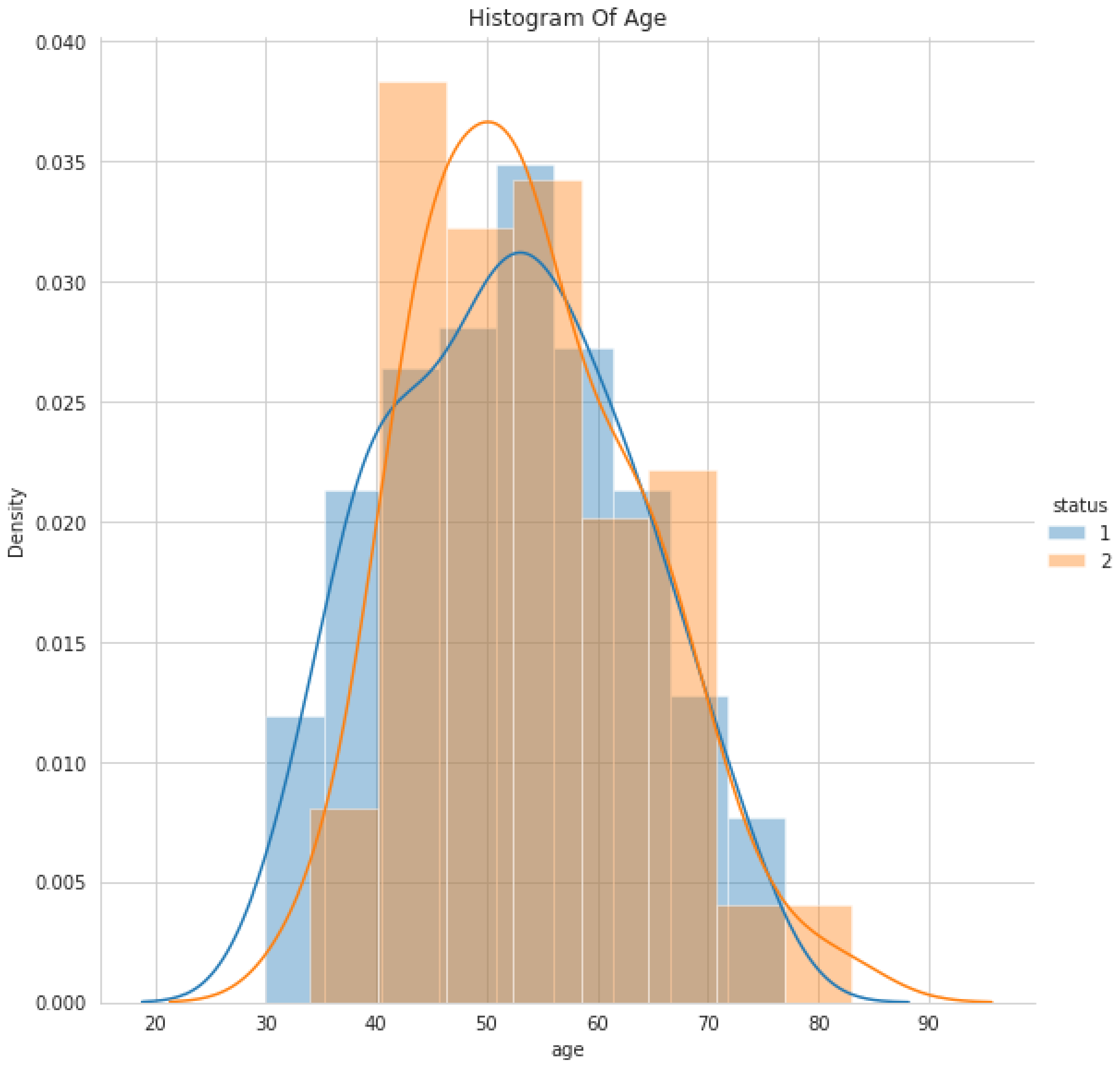
#Uni-Variate Analysis Histogram

In [10]:

```
plt.figure()
g=sns.FacetGrid(Data,hue="status",size=8)
g.map(sns.distplot,"age")
g.add_legend()
plt.title("Histogram Of Age")
```

Out[10]:

```
Text(0.5, 1.0, 'Histogram Of Age')

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

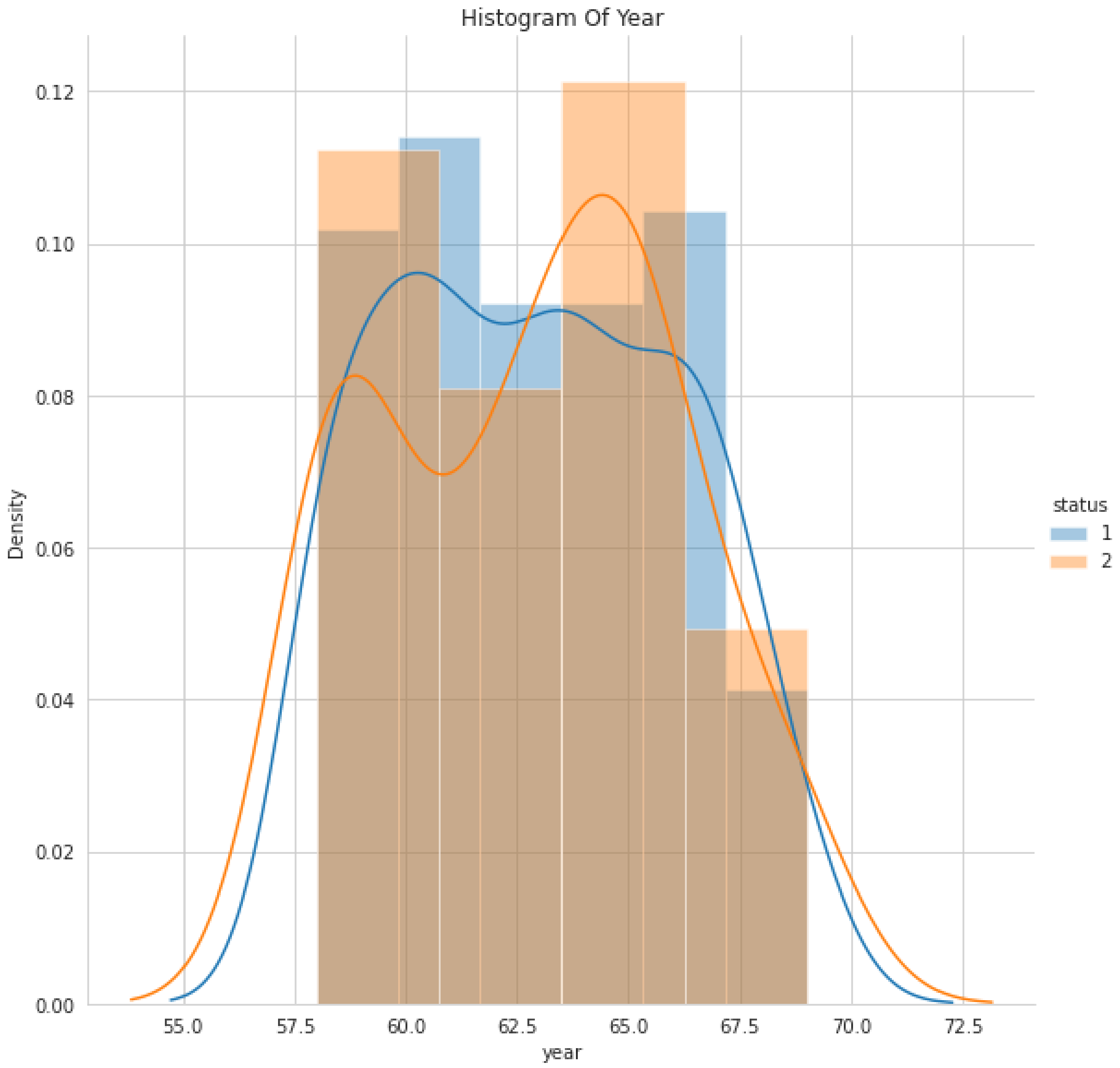

Histogram Of Age
Density
0.040
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
20
30
40
50
60
70
80
90
age
status
1
2

In [11]:

```
plt.figure()
g=sns.FacetGrid(Data,hue="status",size=8)
g.map(sns.distplot,"year")
plt.title("Histogram Of Year")
g.add_legend()
```

Out[11]:

```
<seaborn.axisgrid.FacetGrid at 0x7f02f8325ad0>

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


Histogram Of Year
Density
0.00
0.02
0.04
0.06
0.08
0.10
0.12
55.0
57.5
60.0
62.5
65.0
67.5
70.0
72.5
year
status
1
2

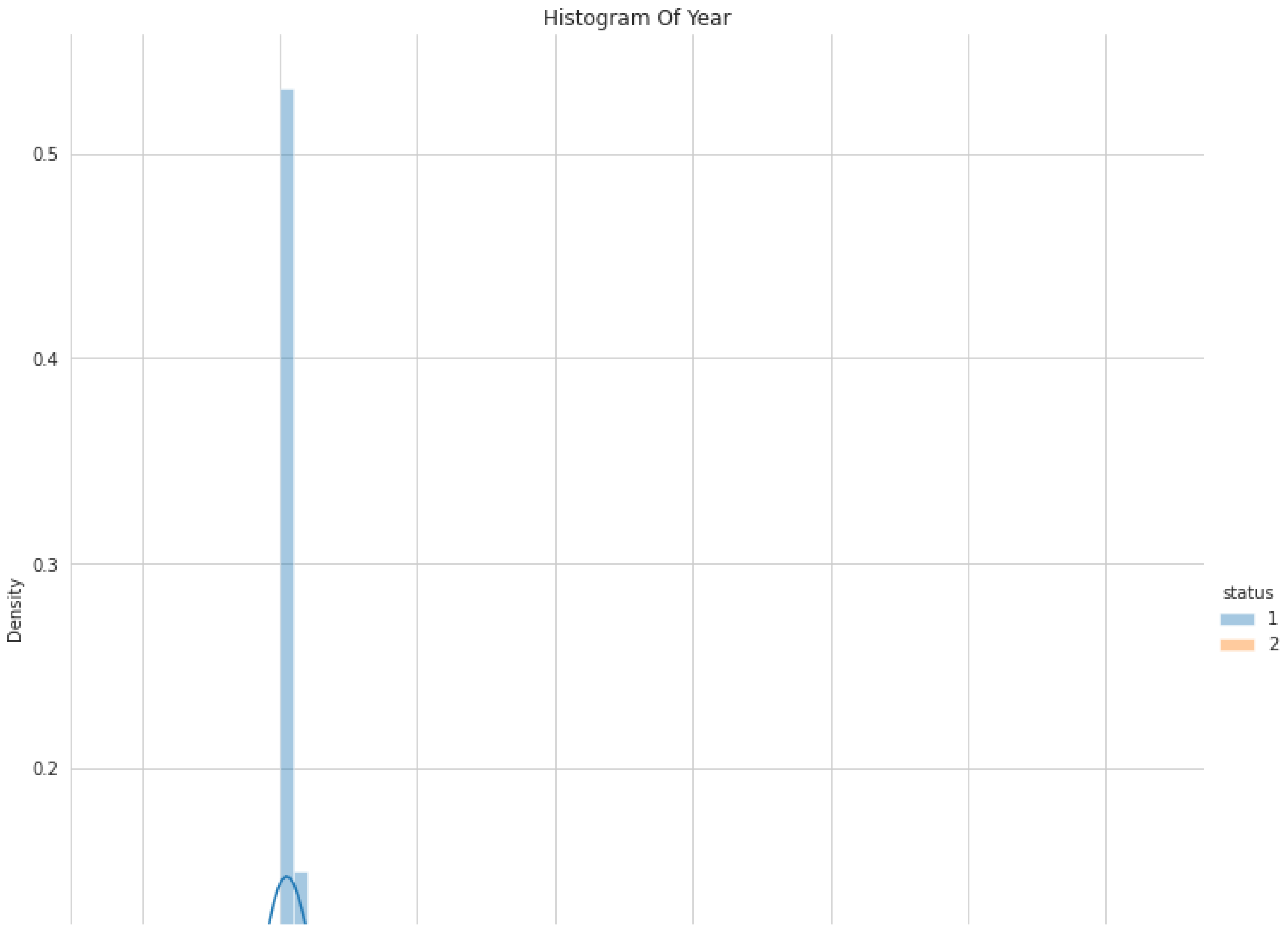
In [12]:

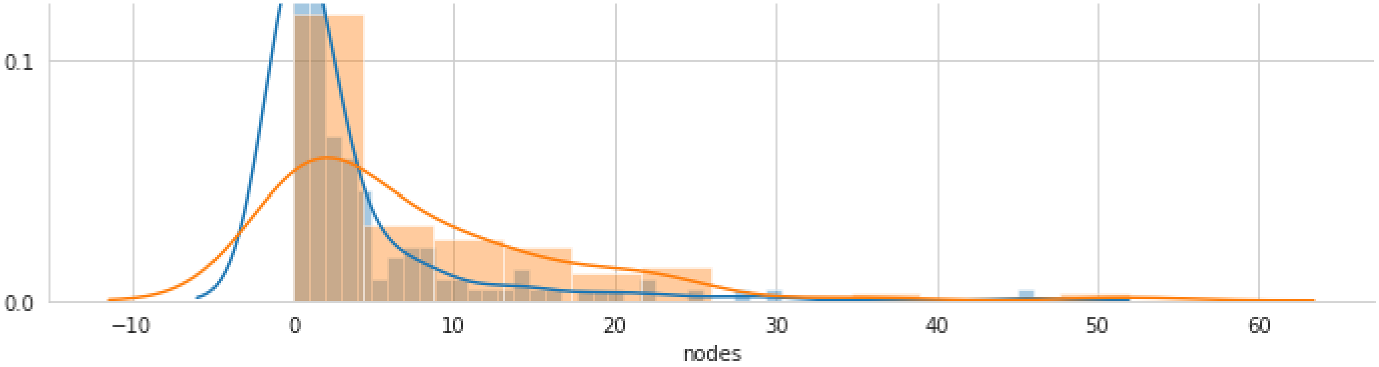
```
plt.figure()
g=sns.FacetGrid(Data,hue="status",size=10)
g.map(sns.distplot,"nodes")
plt.title("Histogram Of Year")
g.add_legend()
```

Out[12]:

```
<seaborn.axisgrid.FacetGrid at 0x7f02f6a3a8d0>
```

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





OBSERVATION

##1 . I DONT THINK WE HAVE GOT ANY CLEAR PICTURE FROM THIS HISTOGRAM . ##2. FEATURE AGE AND YEAR IS HIGHLY OVRLAPPING ##3. WE HAVE TO GO FOR FURTHER ANALYSIS LIKE BIVARIATE ANALYSIS

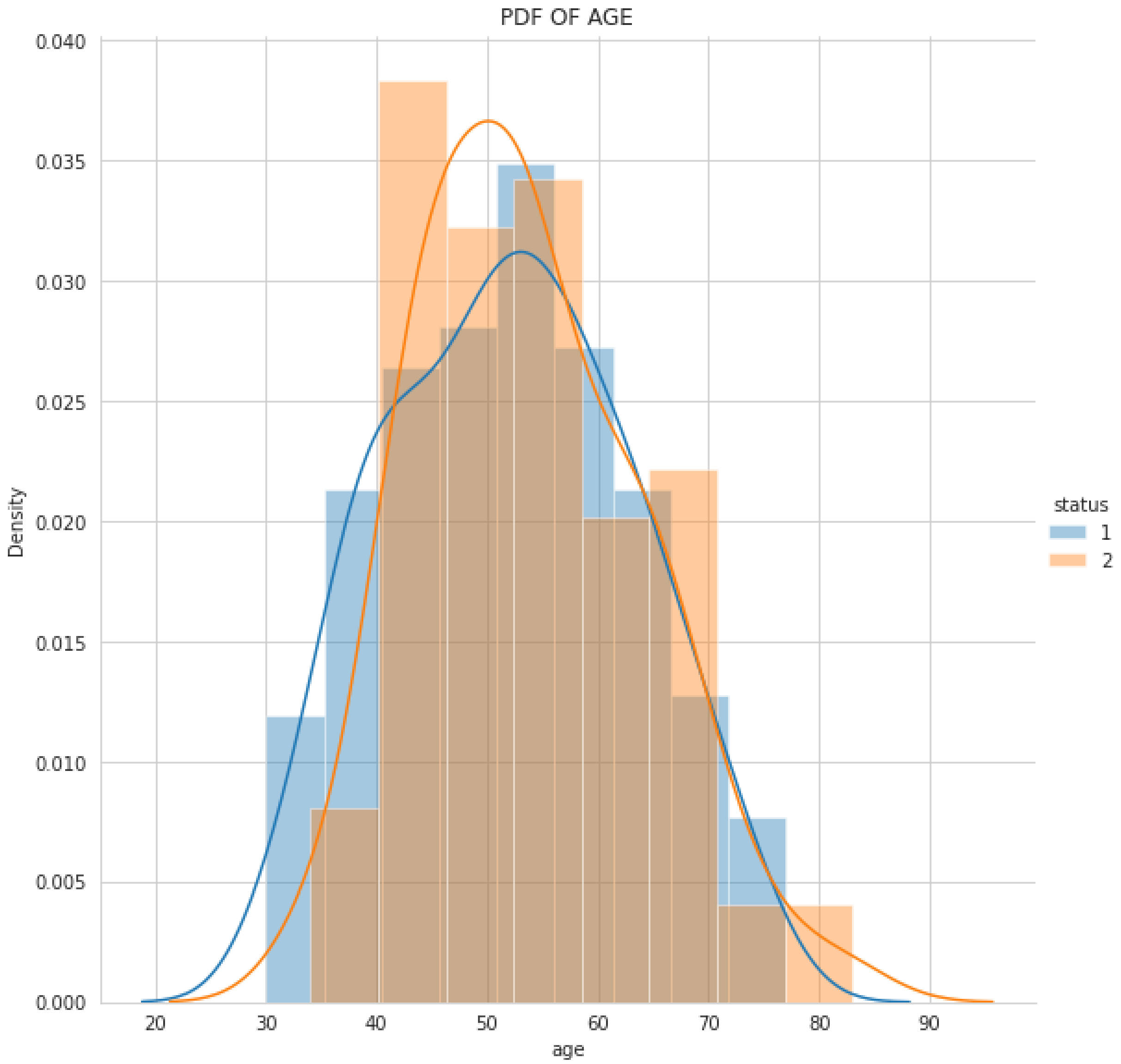
1.3 Perform Univariate analysis - Plot PDF, CDF, Boxplot, Voilin plots

- Plot the required charts to understand which feature are important for classification.
- Make sure that you add titles, legends and labels for each and every plots.
- Suppress the warnings you get in python, in that way it makes your notebook more presentable.
- Do write observations/inference for each plot.

PDF AND CDF

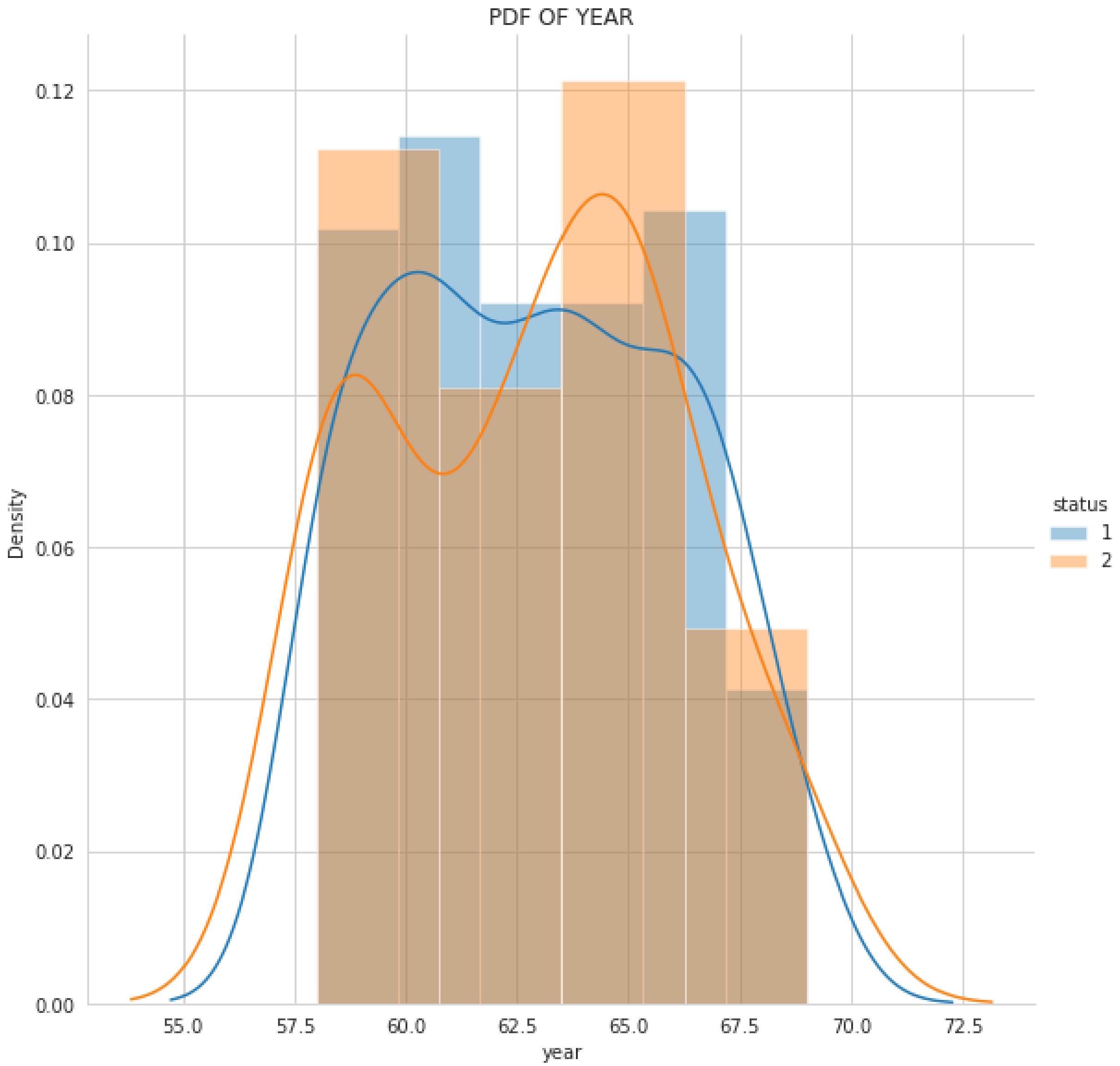
In [13]:

```
sns.FacetGrid(Data,hue="status",height = 8)\
.map(sns.distplot,"age").set(title='PDF OF AGE')\
. add_legend();
plt.show()
```



we cannot conclude more from this plot its highly overlapping

In [14]:
```
sns.FacetGrid(Data,hue="status",height = 8)\
.map(sns.distplot,"year").set(title='PDF OF YEAR')\
. add_legend();
plt.show()
```

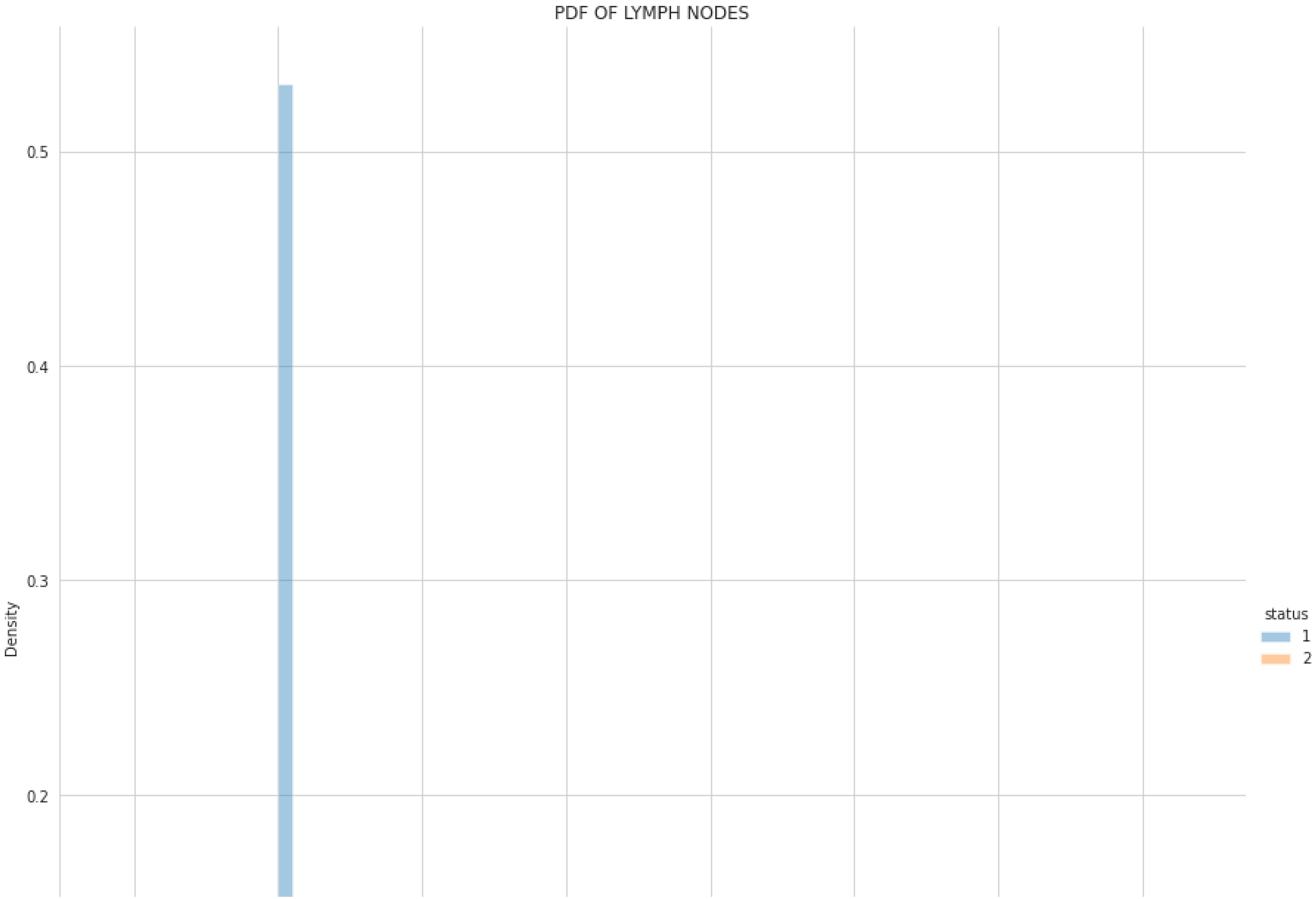


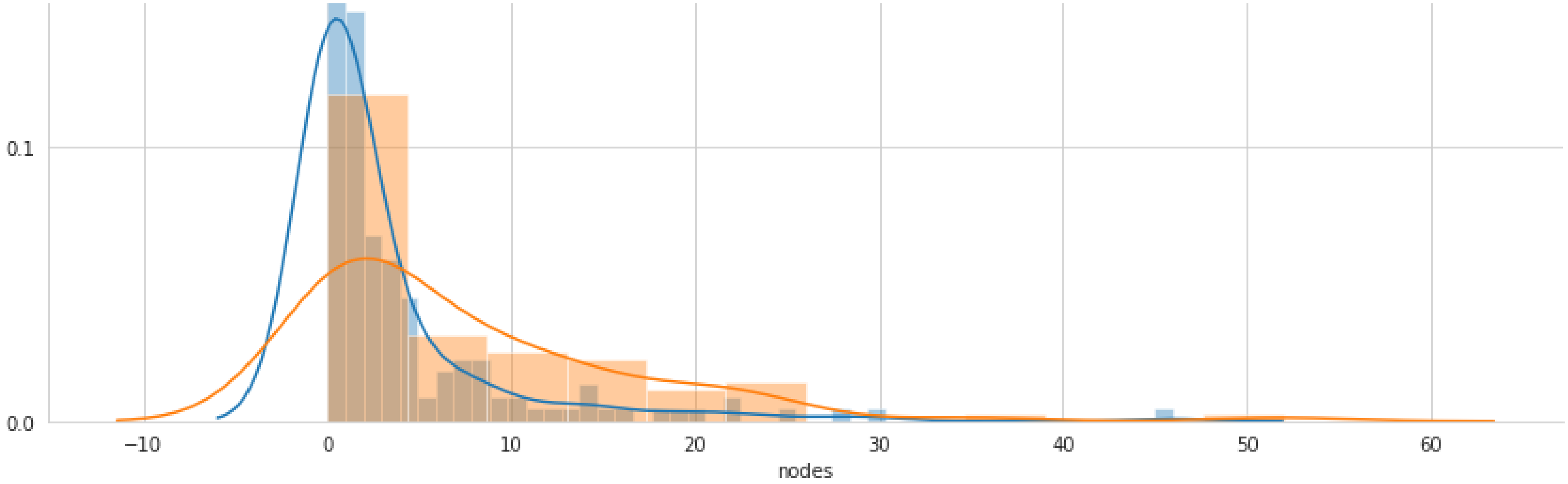
the patient who has done the operation their age is between 58 to 68 years

but how many patient survived or not survived cannot conclude more because of overlapping

In [15]:

```
sns.FacetGrid(Data,hue="status",height = 12)\
.map(sns.distplot,"nodes").set(title='PDF OF LYMPH NODES')\
. add_legend();
plt.show()
```

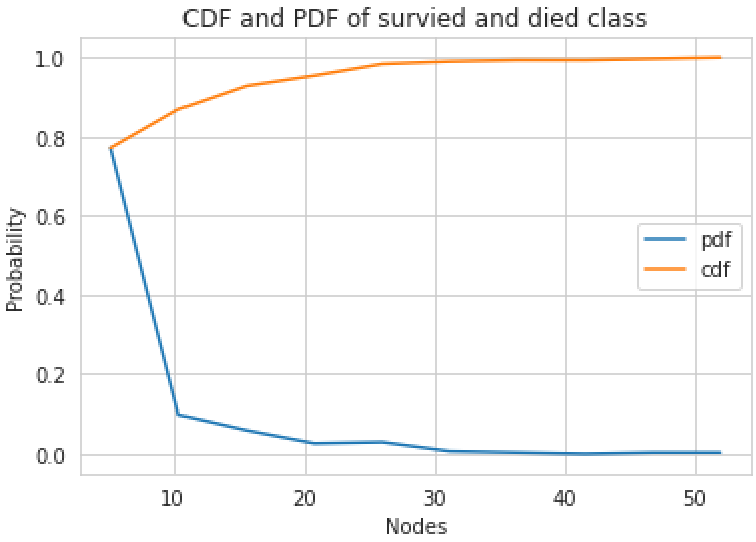




majority of patient who has survived they have less number of nodes

In [16]:

```
#Plot CDF of nodes for survied and died
counts, bin_edges = np.histogram(Data['nodes'], bins=10, density = True)
pdf = counts/(sum(counts))
#print("pdf for nodes", pdf);

cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf, label='pdf');
plt.plot(bin_edges[1:], cdf, label='cdf')
plt.title('CDF and PDF of survied and died class')
plt.xlabel('Nodes')
plt.ylabel('Probability')
plt.legend()
plt.show();
```

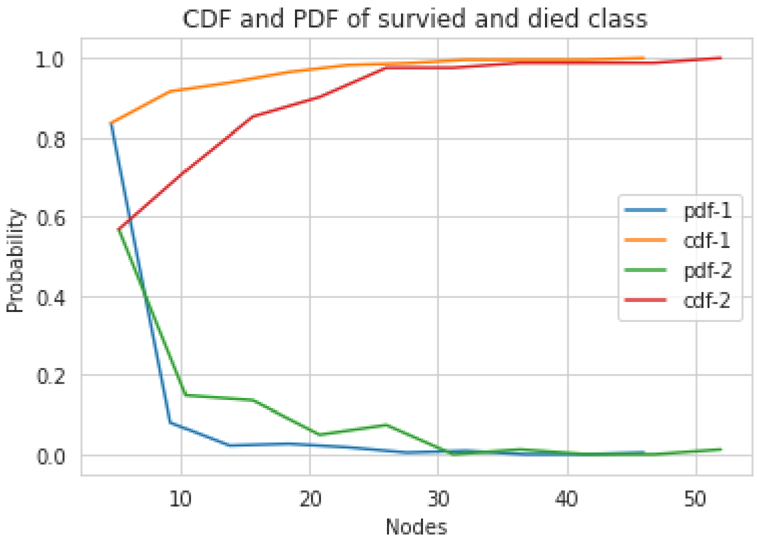


observation

1. around 78-80% patient has probability of surviving if patient has less than 10 lymph nodes

In [17]:

```
#Plot CDF of nodes for survied and died
counts, bin_edges = np.histogram(Data_1['nodes'], bins=10, density = True)
pdf = counts/(sum(counts))
#print("pdf for nodes", pdf);

cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf, label='pdf-1');
plt.plot(bin_edges[1:], cdf, label='cdf-1')

#Plot CDF of nodes for survied and died
counts, bin_edges = np.histogram(Data_2['nodes'], bins=10, density = True)
pdf = counts/(sum(counts))
#print("pdf for nodes", pdf);

cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf, label='pdf-2');
plt.plot(bin_edges[1:], cdf, label='cdf-2')
plt.title('CDF and PDF of survied and died class')
plt.xlabel('Nodes')
plt.ylabel('Probability')
plt.legend()
plt.show();
```



OBSERVATION

1. IT seems that from above pdf 1 that if patient has less than 10 nodes then patient has 82% chances of surviving

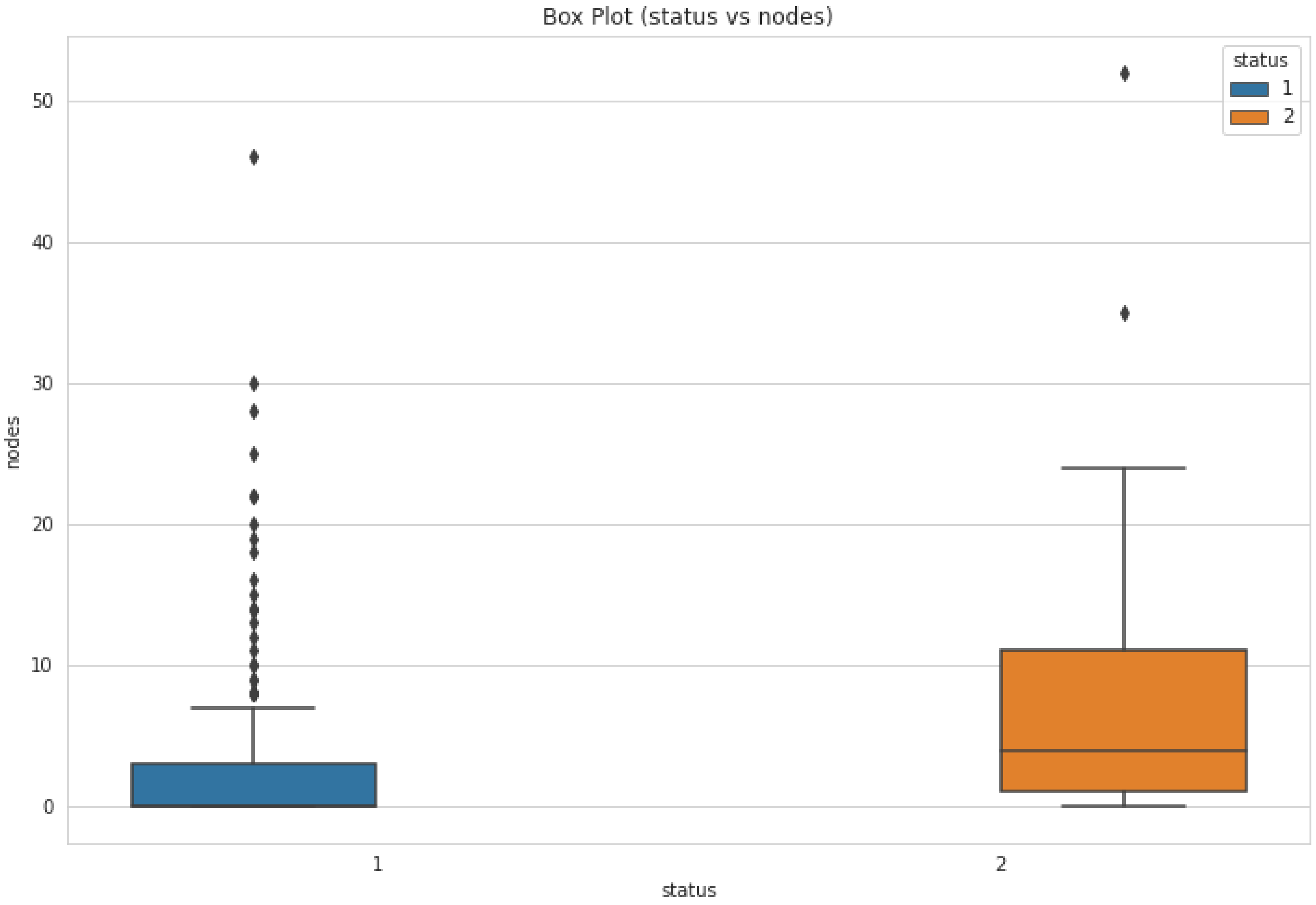
2. we can see that patient has both probability of surviving and dieing.

3. from pdf2 we can see that around 58% patient died who as 10 or less than 10 lymoh nodes

#Box Plot

In [18]:
```
plt.figure(figsize=(12,8))
plt.title("Box Plot (status vs nodes)")
sns.boxplot(data=Data,x='status',y='nodes',hue='status')
```

Out[18]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7f02f65d0f10>
```



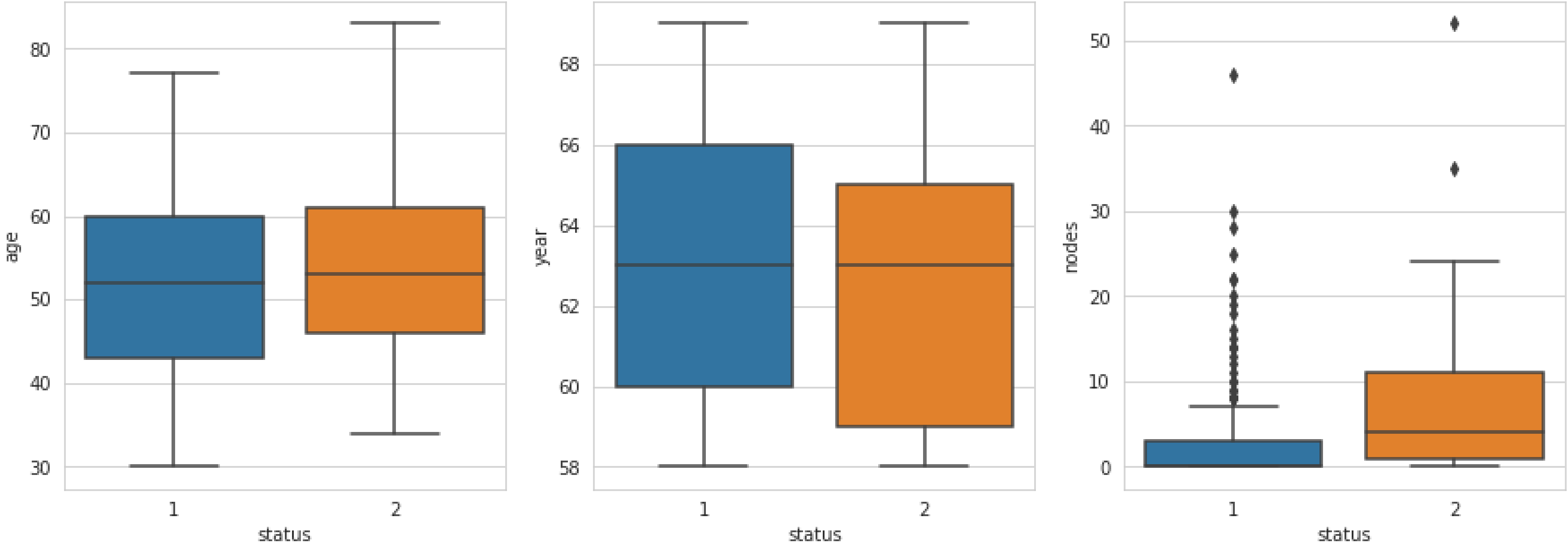
In [18]:

obervation

1. most number of patient survived who has less number of nodes and patient who has not survived has more number of nodes

In [19]:

```
fig, axes = plt.subplots(1,3,figsize=(15,5))
for idx, feature in enumerate(list(Data.columns)[:-1]):
  sns.boxplot(x="status", y=feature,data=Data, ax=axes[idx])
plt.show()
```



observation

patient who has survived more than five year their age lies between 42 to 60

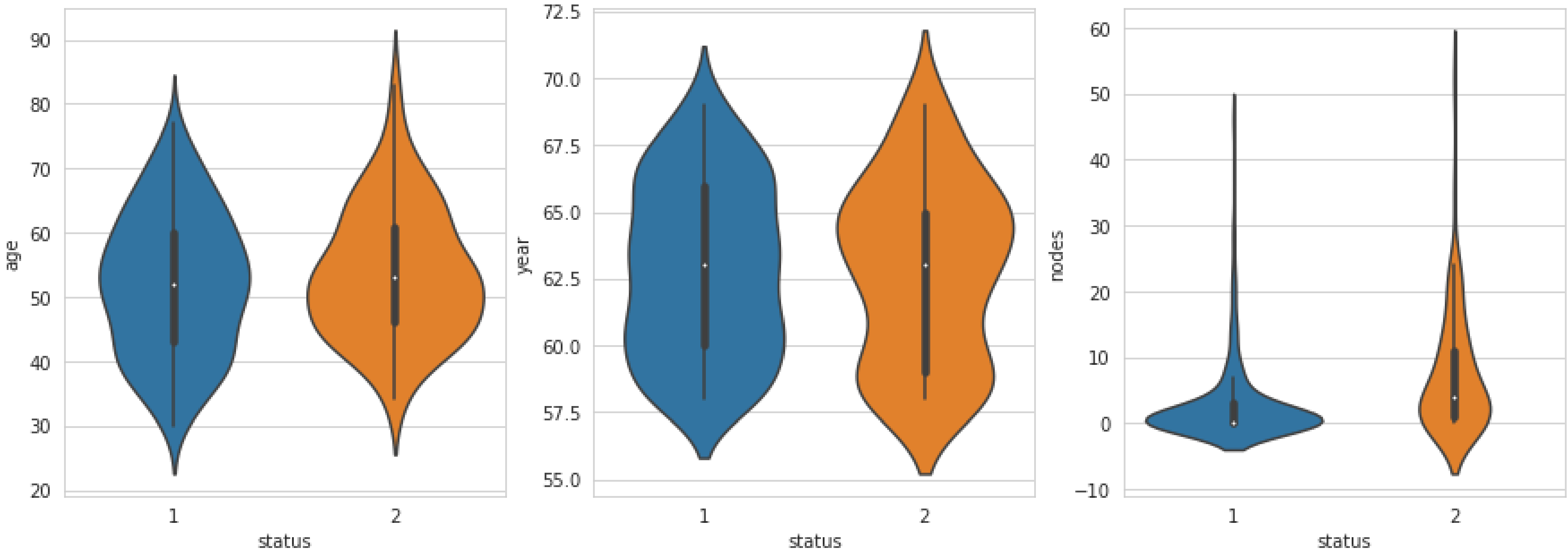
patient who has not survived more than five years their age group 45 to 62

patient has survived of them 80% has less than 10 nodes and patient who dies most they have more than 10 nodes

#Violin Plot

In [20]:

```
fig, axes = plt.subplots(1,3,figsize=(15,5))
for idx, feature in enumerate(list(Data.columns)[:-1]):
  sns.violinplot(x="status", y=feature,data=Data, ax=axes[idx])
plt.show()
```



observation : Voilin plot

Most patient who survived age lis between 42 to 65 and patient most of patient who has not survived their age is between 45 to 55

patient who survived more than 5 years they lies between 60 to 67 and patient who did not survived more than 5 year their age lies between 62 to 68 its overlapping here

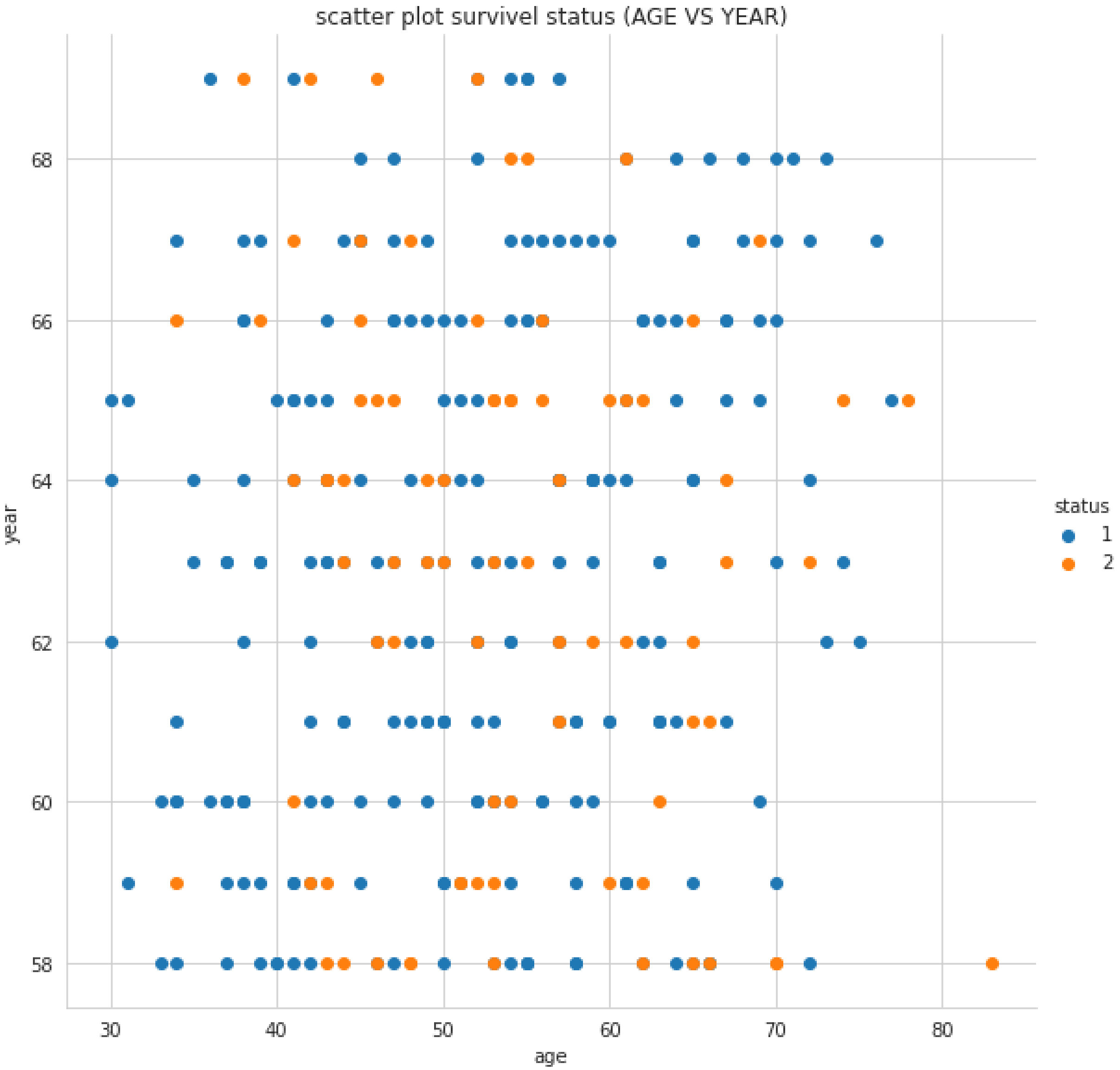
almost patient who has survived their nodes lies in less than 10 nodes , And patient who not survived they more number of nodes or can say more than 10 nodes

1.4 Perform Bivariate analysis - Plot 2D Scatter plots and Pair plots

- Plot the required Scatter plots and Pair plots of different features to see which combination of features are useful for clasification task
- Make sure that you add titles, legends and labels for each and every plots.
- Suppress the warnings you get in python, in that way it makes your notebook more presentable.
- Do write observations/inference for each plot.

scatter plot

```
In [21]: sns.set_style("whitegrid")
         sns.FacetGrid(Data, hue = "status" , height = 8)\
         .map(plt.scatter,"age","year").set(title='scatter plot survivel status (AGE VS YEAR)')\
         .add_legend()
         plt.show()
```



observation : scatter plot

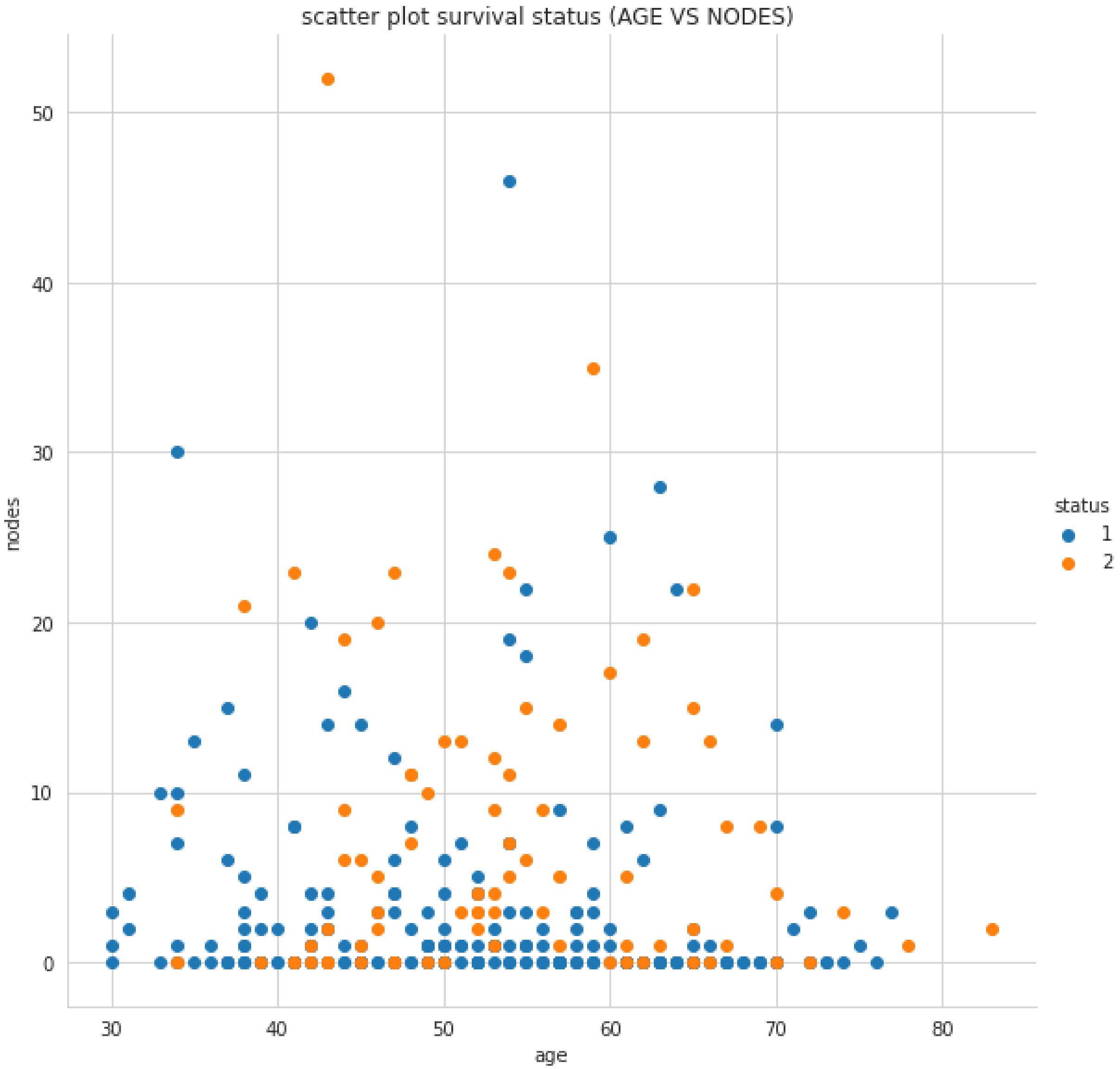
you can see high overlap between patient age who has survived or not survived so cannot conclude more from this plot

observation

This plot year vs age is highly overlapping we cannot conclude more from this

In [22]:

```
sns.set_style("whitegrid")
sns.FacetGrid(Data, hue = "status" , height = 8)\
.map(plt.scatter,"age","nodes").set(title='scatter plot survival status (AGE VS NODES) ')\
.add_legend()
plt.show()
```

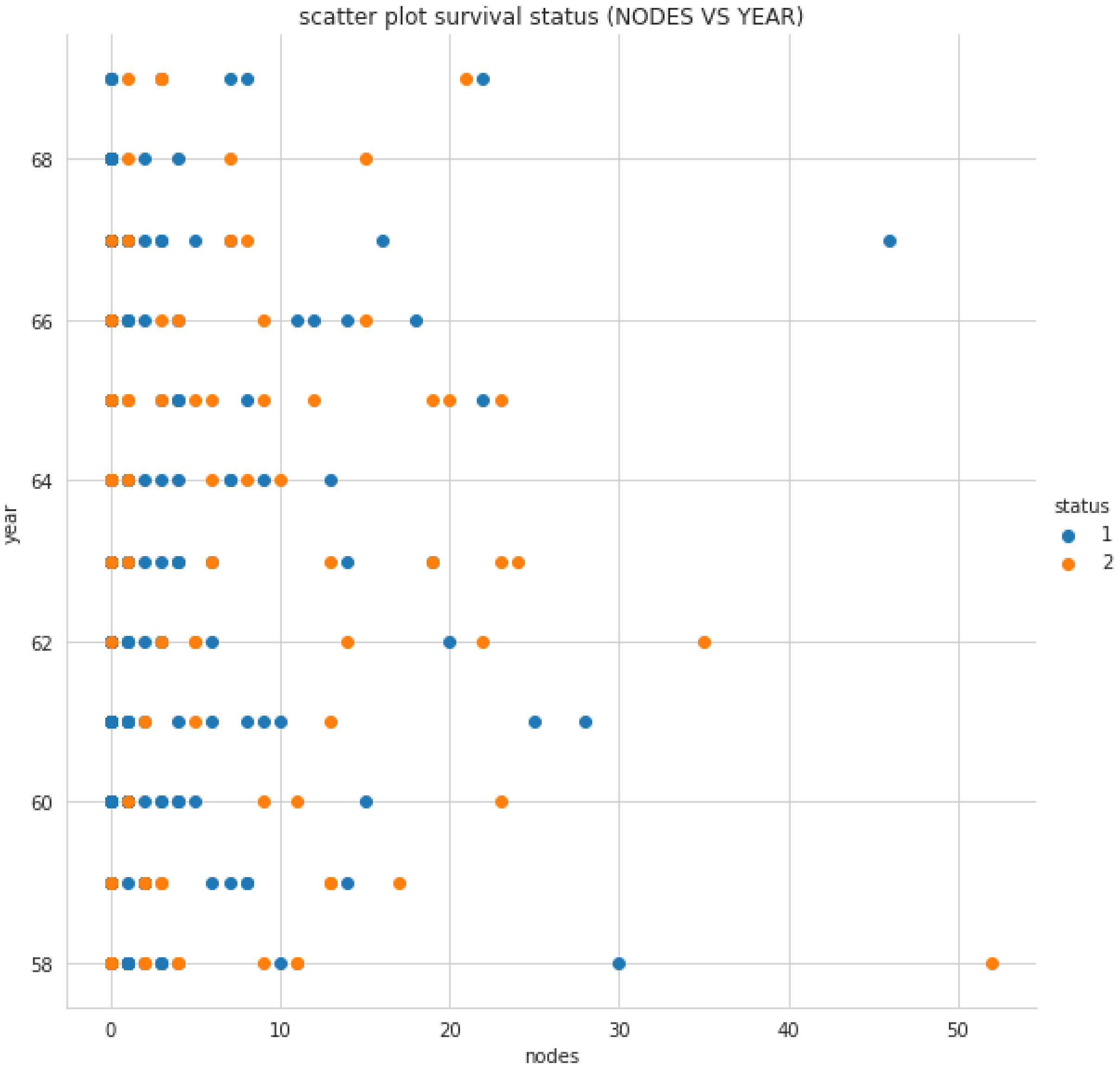


#OBERVATION : **NODEX VS AGE**

##1. patient has less number of nodes their chances of survival are high. ##2. more than 80-90% patient got survived who has less than 10 nodes . ##3. yess their is some ouliter situation where patient survied and some dies

In [23]:

```
sns.set_style("whitegrid")
sns.FacetGrid(Data, hue = "status" , height = 8)\
.map(plt.scatter,"nodes","year").set(title='scatter plot survival status (NODES VS YEAR)')\
.add_legend()
plt.show()
```



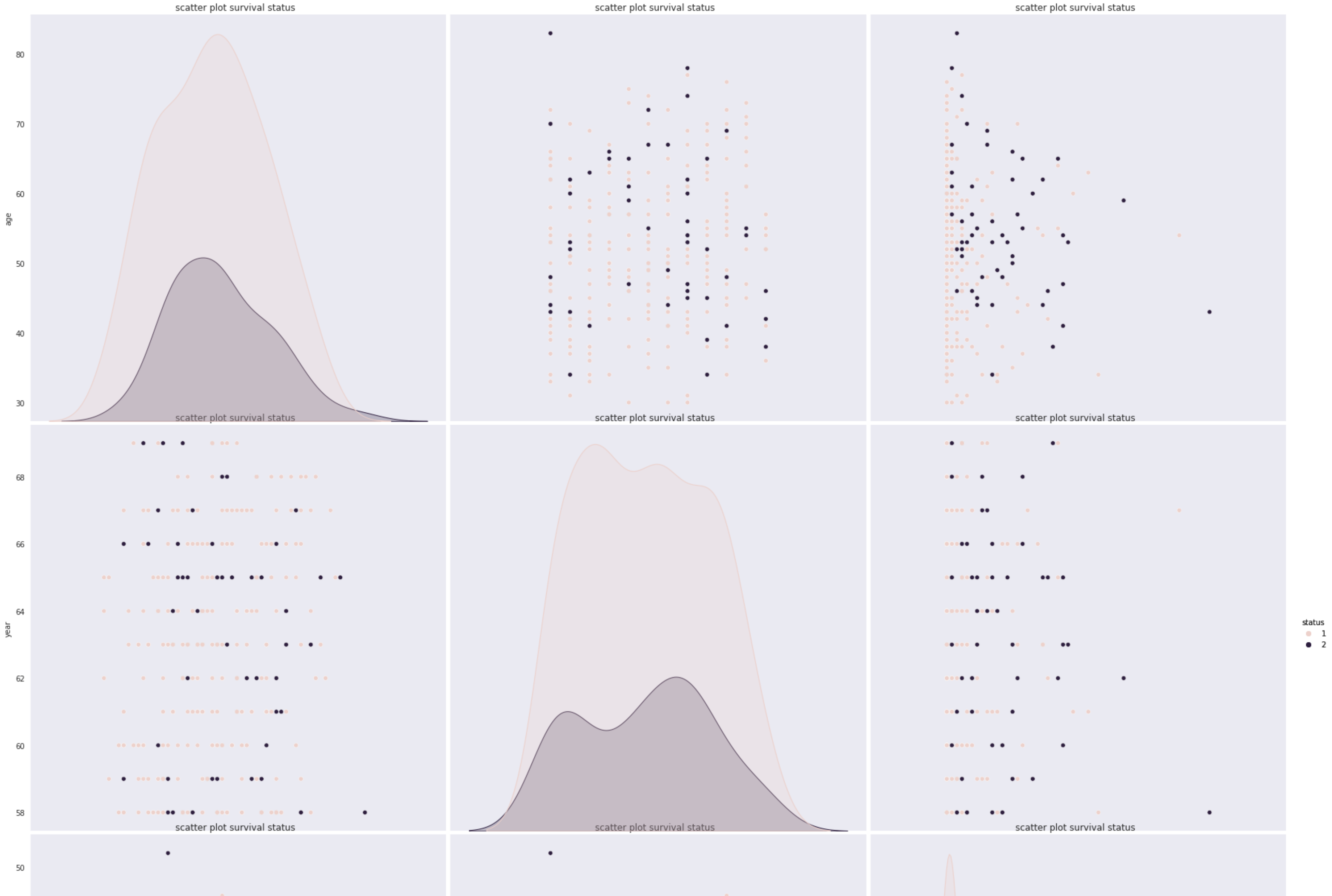
#Observation **year vs nodes**

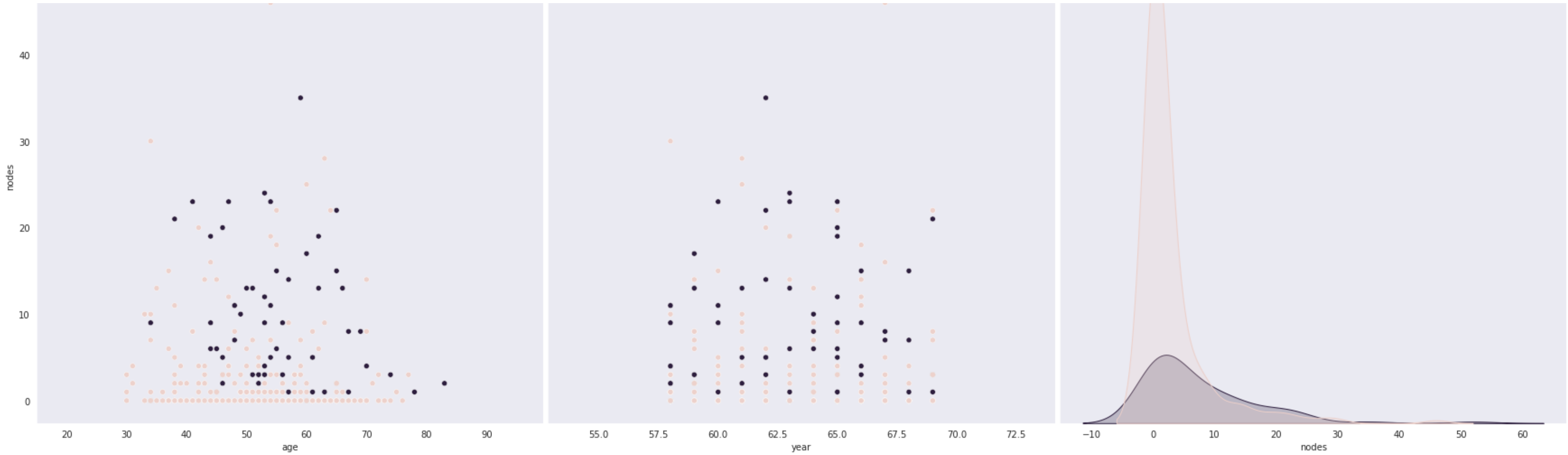
##1. patient who has more than 10 nodes their chances of living very less ##2. patient who has age between 60 to 65 they have done more number of operations

3. high overlapping in plot

Pair plot

In [24]:
```
sns.set_style("dark")
sns.pairplot(Data, hue="status", height = 8).set(title='scatter plot survival status  ')\
.add_legend()
plt.show()
```





observation : pair plot

##**ignore the digonal plot first for better understanding** ##plot no 2 : **high overlapping between data points cannot conclude more** ##plot no 3 : **yes in this plot we can see much better sepration between datapoints** ##plot no 4 : **again highoverlapping between datapoints** #3plot no 6 : **litte bit overlap but betwen than plot 4** #3plot no 7 : **yes this plot looks some sensibe both the patient who has survived or not survived seprated well** ##plot 8: **not looking too sensible**

1.5 Summarize your final conclusions of the Exploration

- You can desrcibe the key features that are important for the Classification task.
- Try to quantify your results i.e. while writing observations include numbers,percentages, fractions etc.
- Write a brief of your exploratory analysis in 3-5 points
- Write your observations in english as crisply and unambigously as possible.

stastical analysis

patient who survived

```
In [25]: Data_1.describe()
```

```
Out[25]:
                age          year        nodes   status
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
```

patient who not survived

```
In [26]: Data_2.describe()
```

```
Out[26]:
               age        year       nodes   status
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
```

observation : Statistical analysis

nodes mean for patient who **survived is : 2.79**

nodes mean for patient who **not survived : 7.456**

nodes standard_devi for patient who **survived :5.870**

nodes standard_devi for patient who **not survived : 9.185**

conclusion

Feature node is most imp in term of chances of survival of patient but not sufficient

feature age and year is not imporatant like nodes

80 % of patient survived more than 5 years who has less than 5 or having no nodes

Dataset highly overlap and imbalanced dataset

between the age_group of 45 to 60 patient has survived more

we have to do more featurization for more better analysis and insights

```
In [26]:
```