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) 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.

In [5]:
```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings('ignore')

# we can read the data directly from raw github link
# we are also defining the name of the columns.
#make sure that your csv file and ipynb notebook are in the same folder. If they are in diff
erent folder then you have to define the complete path
df=pd.read_csv('/content/drive/MyDrive/Dataset/haberman.csv')
df.head()
```

Out[5]:

	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

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/
- 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

(Q) how many data-points and features?

In [6]:
```
df.shape
```

Out[6]:
```
(306, 4)
```

(Q) What are the column names in our dataset?

In [7]:
```
df.columns
```

Out[7]:
```
Index(['age', 'year', 'nodes', 'status'], dtype='object')
```

Q) How many data points for each class are present? (or) How many flowers for each species are present?

In [8]:
```
df['status'].value_counts()
```

Out[8]:
```
1    225
2     81
Name: status, dtype: int64
```

The data is unbalanced with ratio of 70:30

In [9]:
```
df.groupby('status').describe()
```

Out[9]:

	age								year		...			nodes		
	count	mean	std	min	25%	50%	75%	max	count	mean	...	75%	max	count	mean	std
status																
1	225.0	52.017778	11.012154	30.0	43.0	52.0	60.0	77.0	225.0	62.862222	...	66.0	69.0	225.0	2.791111	5.870318
2	81.0	53.679012	10.167137	34.0	46.0	53.0	61.0	83.0	81.0	62.827160	...	65.0	69.0	81.0	7.456790	9.185654

2 rows × 24 columns

Patients who survived have mean nodes of 2.8 and 75% of nodes are 3

patients who did not survived have a mean node of 7.5 and 75% nodes are 11

- More the number of nodes less chances of survival

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)

We are working on dataset for cancer prediction

The output is binary varibale with values

- **1: If the patient survives treatment 5 year or longer**
- **2: if the patient dies within 5 years.**

We have feature like

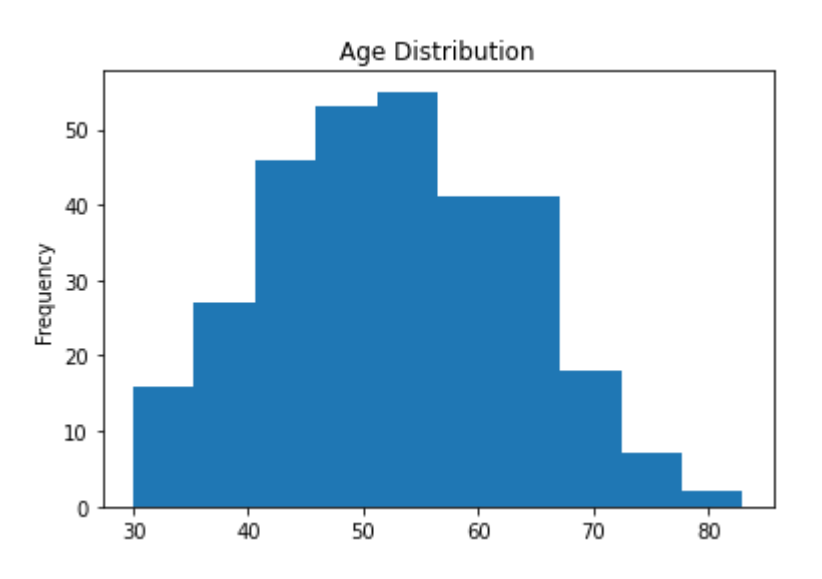
- **age : The age of patient**
- **year: year in which patient was operate data is from 1958 to 1970**
- **nodes: number of nodes detected (domain term)**

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.

In [11]:
```
df['age'].plot(kind='hist')
plt.title('Age Distribution')
```

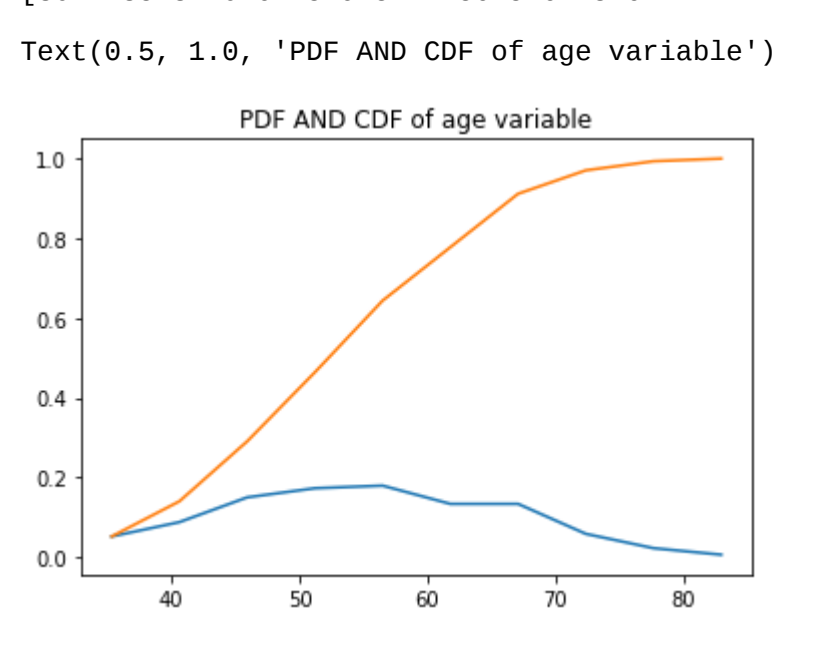
Out[11]:
```
Text(0.5, 1.0, 'Age Distribution')
```



In [12]:
```
counts,bins  = np.histogram(df['age'])
pdf = counts/(sum(counts))
print(pdf);
print(bins);
cdf = np.cumsum(pdf)
plt.plot(bins[1:],pdf);
plt.plot(bins[1:], cdf)
plt.title('PDF AND CDF of age variable')
```

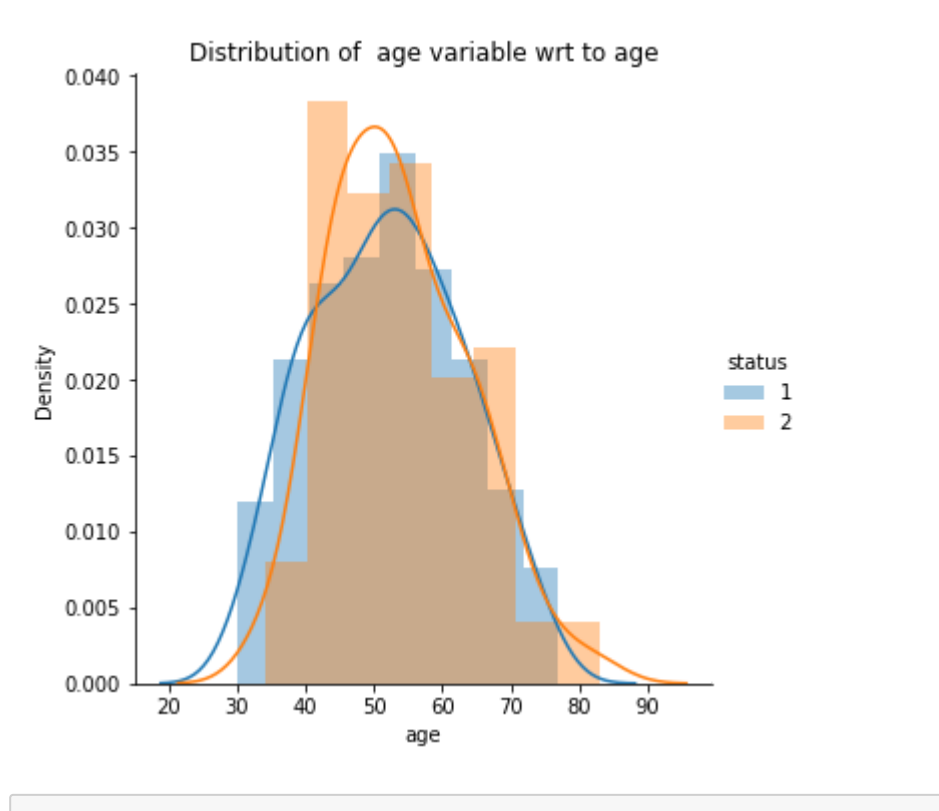
```
[0.05228758 0.08823529 0.1503268  0.17320261 0.17973856 0.13398693
 0.13398693 0.05882353 0.02287582 0.00653595]
[30.  35.3 40.6 45.9 51.2 56.5 61.8 67.1 72.4 77.7 83. ]
```

Out[12]:
```
Text(0.5, 1.0, 'PDF AND CDF of age variable')
```



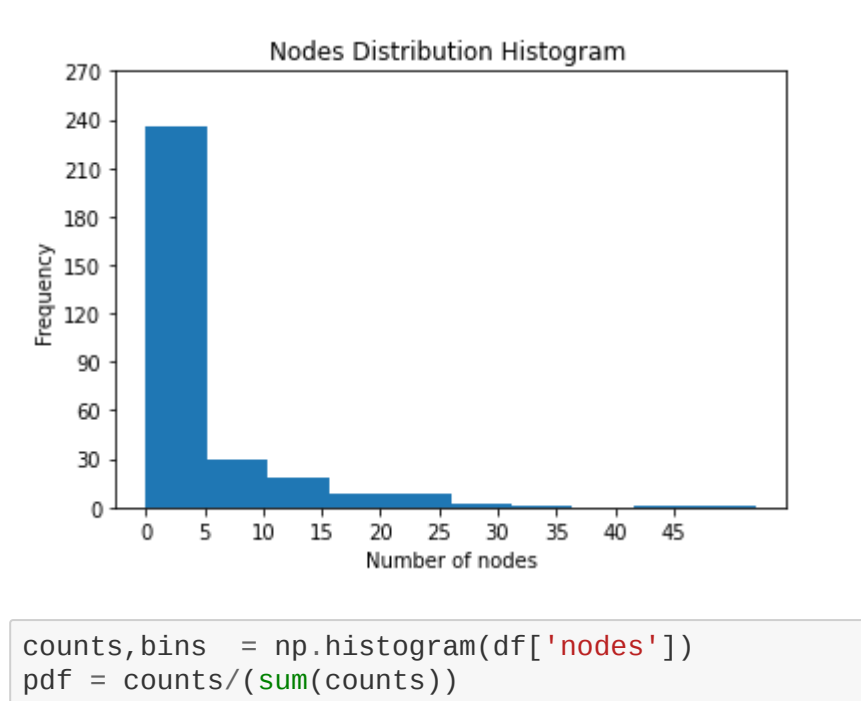
In [13]:
```
sns.FacetGrid(df, hue = 'status',size = 5).map(sns.distplot, 'age').add_legend()
plt.title('Distribution of  age variable wrt to age')
```

Out[13]:
```
Text(0.5, 1.0, 'Distribution of  age variable wrt to age')
```



In [14]:
```
df['nodes'].plot(kind='hist')
plt.xticks(np.arange(0,50,step = 5))
plt.yticks(np.arange(0,300,step = 30))
plt.xlabel('Number of nodes')
plt.title('Nodes Distribution Histogram ')
```

Out[14]:
```
Text(0.5, 1.0, 'Nodes Distribution Histogram ')
```

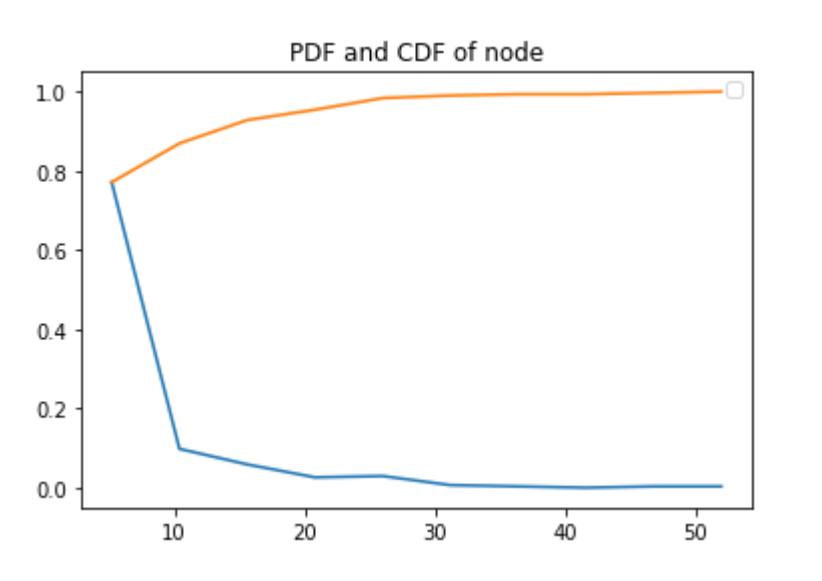


In [15]:
```
counts,bins  = np.histogram(df['nodes'])
pdf = counts/(sum(counts))
print(pdf);
print(bins);
cdf = np.cumsum(pdf)
plt.plot(bins[1:],pdf);
plt.plot(bins[1:], cdf)
plt.title('PDF and CDF of node')
plt.legend()
```

```
No handles with labels found to put in legend.
```

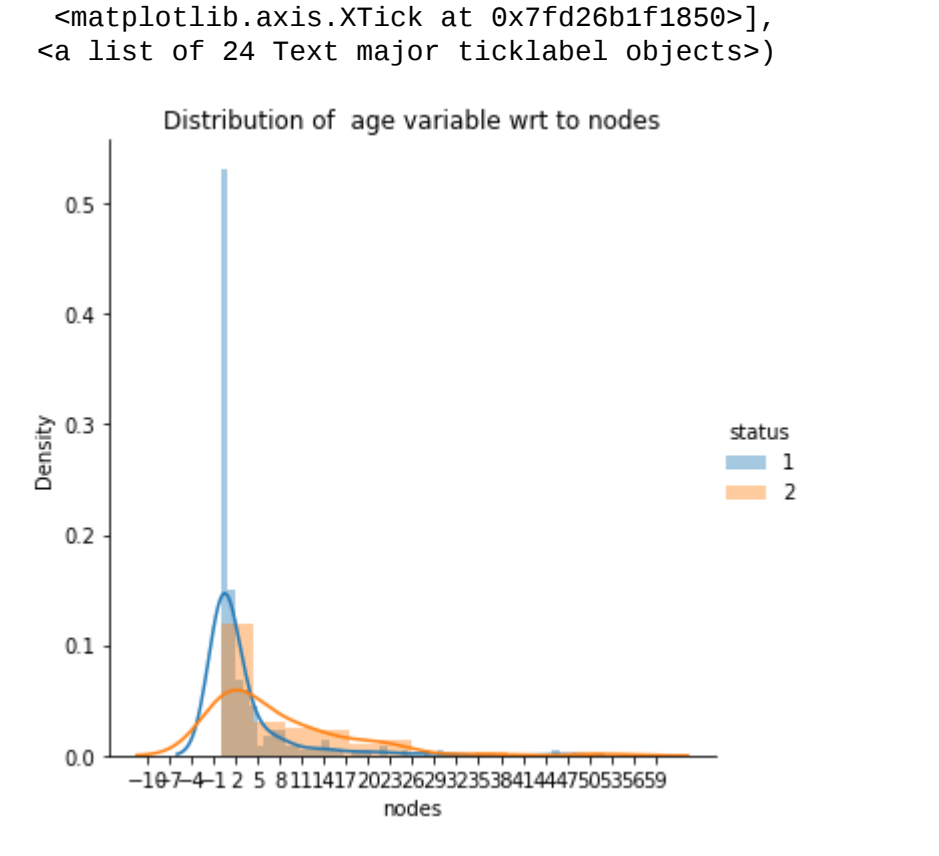
```
[0.77124183 0.09803922 0.05882353 0.02614379 0.02941176 0.00653595
 0.00326797 0.         0.00326797 0.00326797]
[ 0.   5.2 10.4 15.6 20.8 26.  31.2 36.4 41.6 46.8 52. ]
```

Out[15]:
```
<matplotlib.legend.Legend at 0x7fd26ddaea50>
```



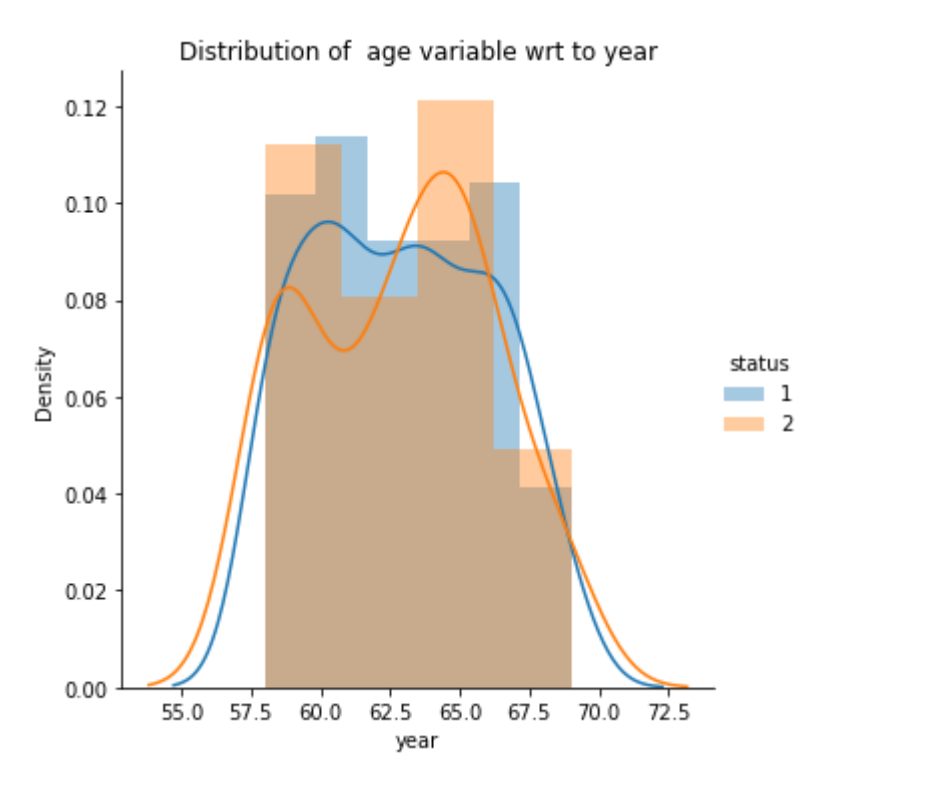
In [16]:
```
sns.FacetGrid(df, hue = 'status',size = 5).map(sns.distplot, 'nodes').add_legend()
plt.title('Distribution of  age variable wrt to nodes')
plt.xticks(np.arange(-10 ,60,step = 3))
```

Out[16]:
```
([<matplotlib.axis.XTick at 0x7fd26b340690>,
  <matplotlib.axis.XTick at 0x7fd26b340650>,
  <matplotlib.axis.XTick at 0x7fd26b3474d0>,
  <matplotlib.axis.XTick at 0x7fd26b363410>,
  <matplotlib.axis.XTick at 0x7fd26b363e10>,
  <matplotlib.axis.XTick at 0x7fd26b2eb5d0>,
  <matplotlib.axis.XTick at 0x7fd26b27add0>,
  <matplotlib.axis.XTick at 0x7fd26b28f410>,
  <matplotlib.axis.XTick at 0x7fd26b304a10>,
  <matplotlib.axis.XTick at 0x7fd26b23d990>,
  <matplotlib.axis.XTick at 0x7fd26b340290>,
  <matplotlib.axis.XTick at 0x7fd26b1e5710>,
  <matplotlib.axis.XTick at 0x7fd26b1e7710>,
  <matplotlib.axis.XTick at 0x7fd26b1e5d90>,
  <matplotlib.axis.XTick at 0x7fd26b25eed0>,
  <matplotlib.axis.XTick at 0x7fd26b25ea50>,
  <matplotlib.axis.XTick at 0x7fd26b248410>,
  <matplotlib.axis.XTick at 0x7fd26b1e78d0>,
  <matplotlib.axis.XTick at 0x7fd26b1e7150>,
  <matplotlib.axis.XTick at 0x7fd26b1ec310>,
  <matplotlib.axis.XTick at 0x7fd26b1ec850>,
  <matplotlib.axis.XTick at 0x7fd26b1ecd90>,
  <matplotlib.axis.XTick at 0x7fd26b1f1310>,
  <matplotlib.axis.XTick at 0x7fd26b1f1850>],
 <a list of 24 Text major ticklabel objects>)
```



In [17]:
```
sns.FacetGrid(df, hue = 'status',size = 5).map(sns.distplot, 'year').add_legend()
plt.title('Distribution of  age variable wrt to year')
```

Out[17]:
```
Text(0.5, 1.0, 'Distribution of  age variable wrt to year')
```



Conclusion

Age:

- **variable is not usefull as the plots are overlapping**

Nodes:

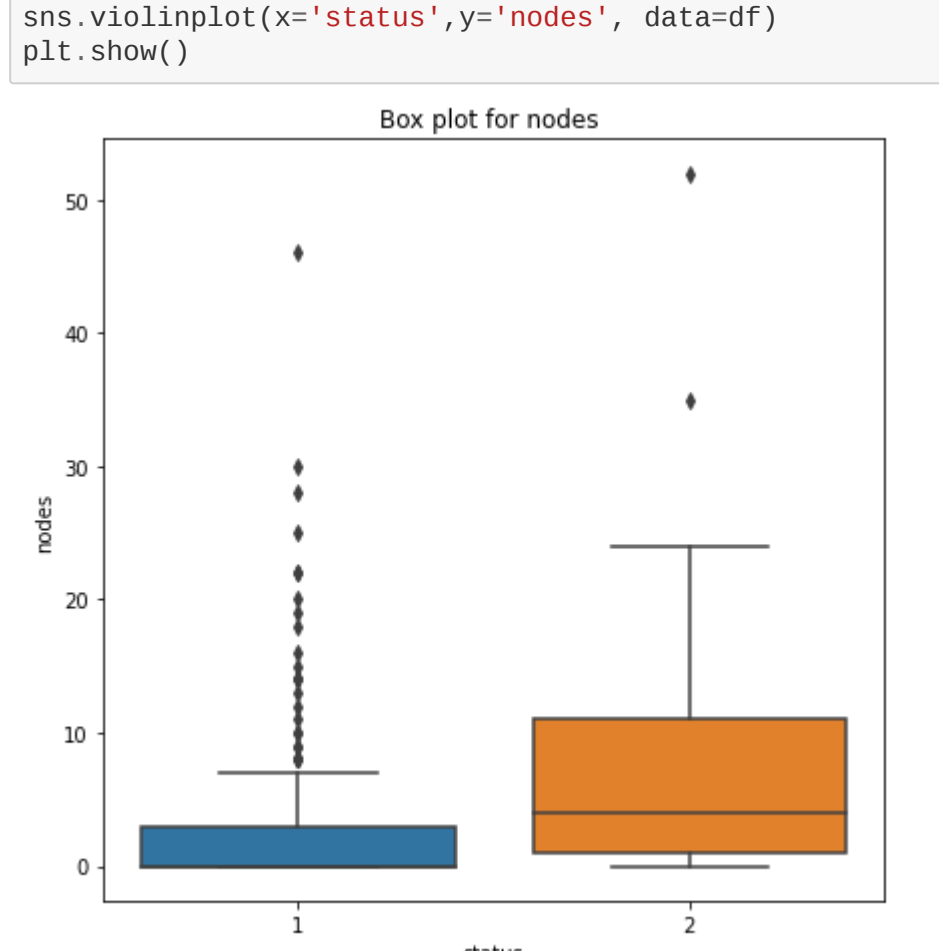
- **We can use this feature to separate data at value of approx 2 nodes to make a decision surface**
- **patients who had 2 nodes have more chances of success than patients having more than 2 nodes**

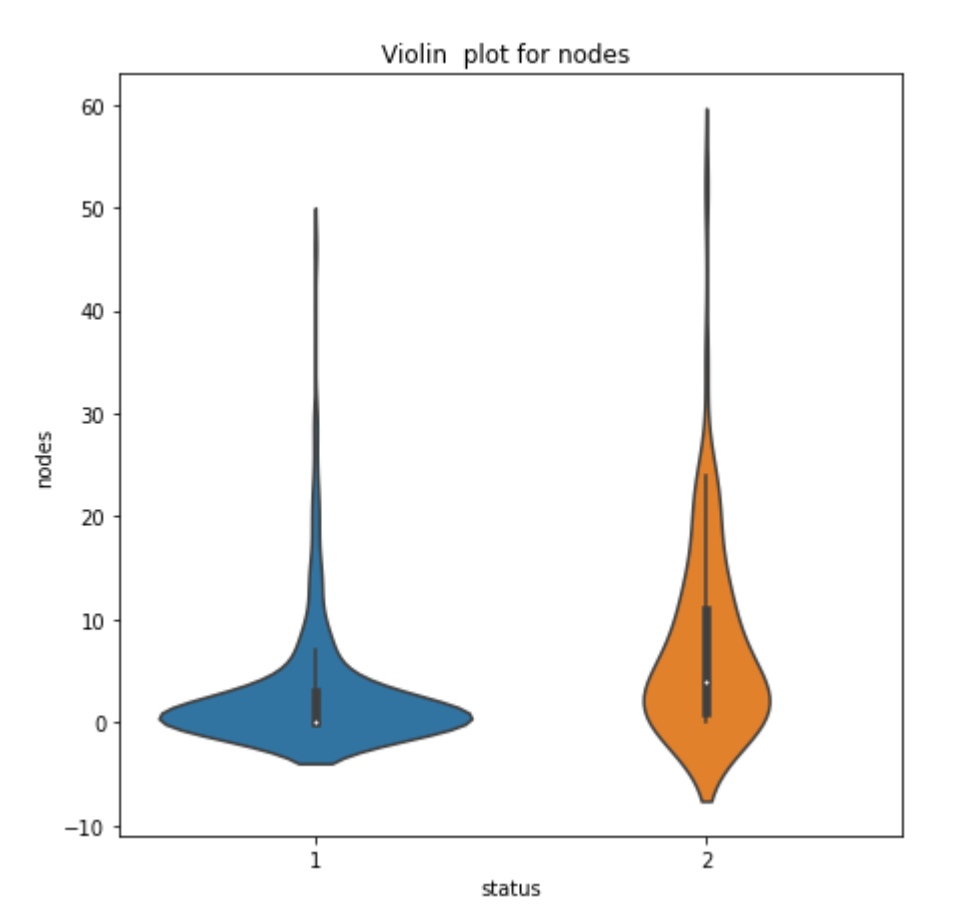
Year:

- **This is also not usefull feature**

In [18]:
```
# Understanding the node variable more
plt.figure(figsize = (7,7))
plt.title('Box plot for nodes ')
sns.boxplot(x='status',y='nodes', data=df)
plt.show()


plt.figure(figsize = (7,7))
plt.title('Violin  plot for nodes ')
sns.violinplot(x='status',y='nodes', data=df)
plt.show()
```



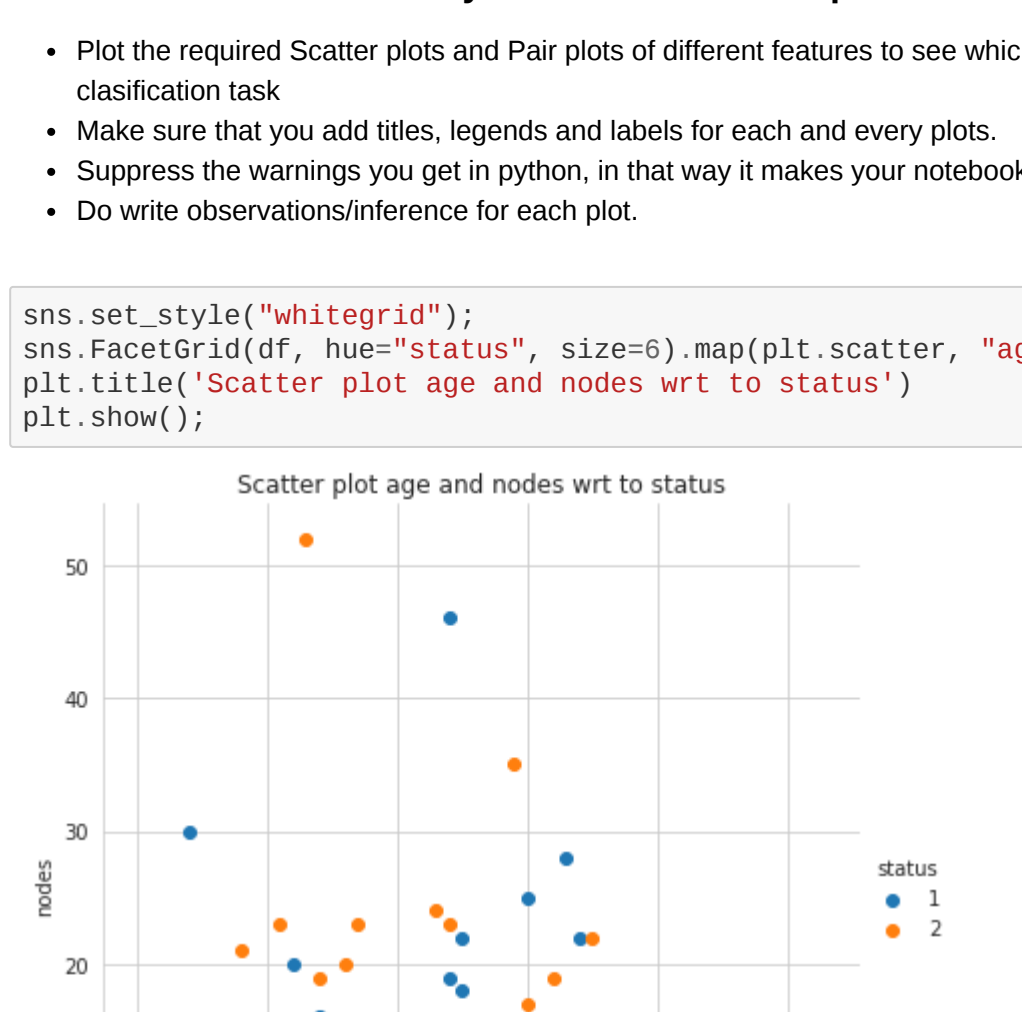


- For otput var = 1 Data is less spread and has more outliers
- For otput var = 2 Data is more spread and has less outliers

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

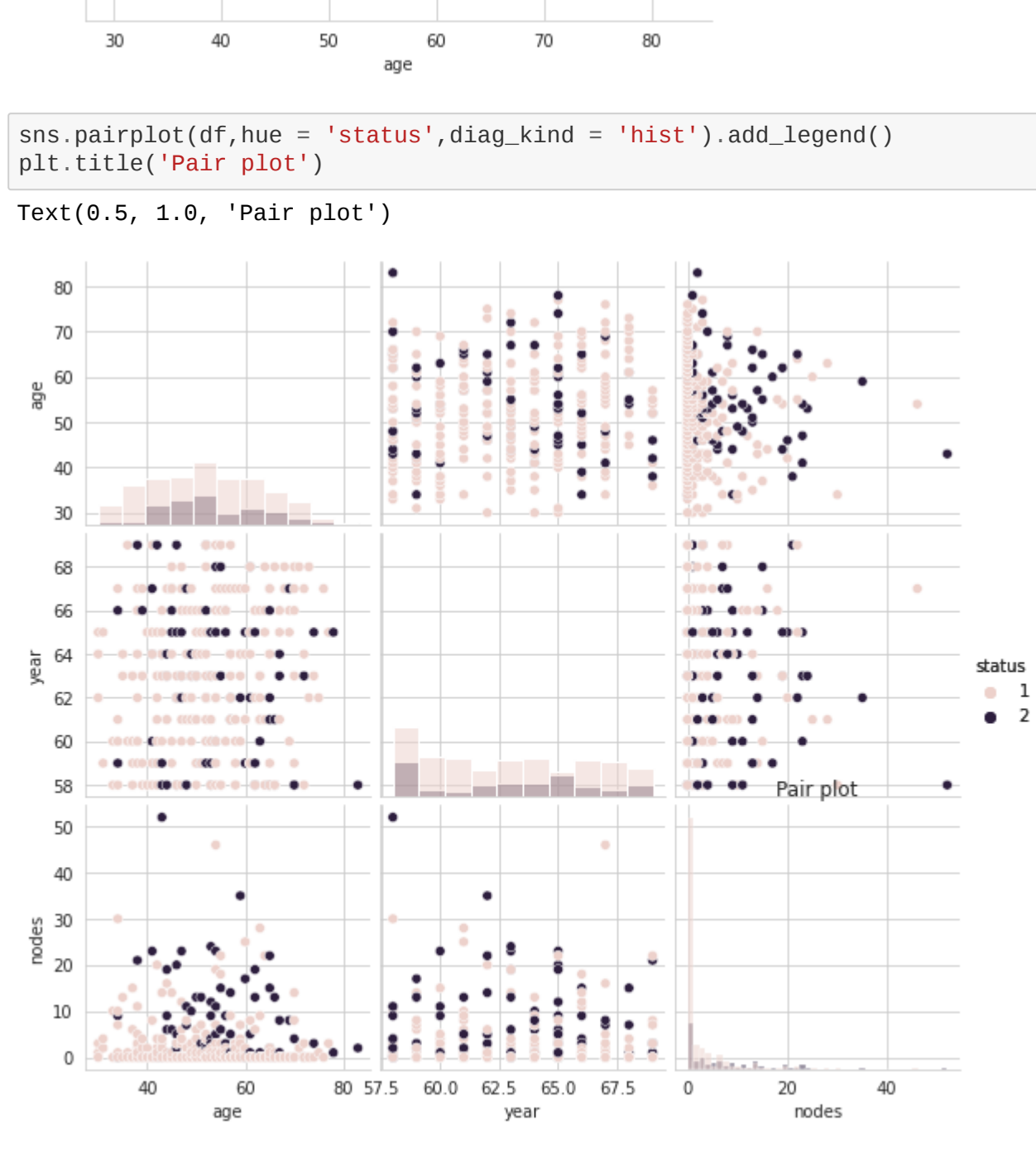
- Plot the required Scatter plots and Pair plots of different features to see which combination of features are useful for clasification task
- Make sure that you add titles, legends and labels for each and every plots.
- Suppress the warnings you get in python, in that way it makes your notebook more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

In [21]:
```
sns.set_style("whitegrid");
sns.FacetGrid(df, hue="status", size=6).map(plt.scatter, "age", "nodes").add_legend()
plt.title('Scatter plot age and nodes wrt to status')
plt.show();
```



In [20]:
```
sns.pairplot(df,hue = 'status',diag_kind = 'hist').add_legend()
plt.title('Pair plot')
```

Out[20]:
```
Text(0.5, 1.0, 'Pair plot')
```



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.

Summary

The most important feature is number of nodes

- Patients who survived have mean nodes of 2.8 and 75% of nodes are 3

- patients who did not survived have a mean node of 7.5 and 75% nodes are 11

The other feature age and year are overlapping hence not usefull

There is also a data imbalance of 70:30

- from the violin plot the number of outliers in label = 1 are more and variance is less
- When we will balance data more points will be in outlier in label 2 varience will be more

More the number of nodes less chances of survival