Haberman's survival-data-set EDA

The dataset contains cases from a study that was conducted between 1958 and 1970 at the University of Chicago's Billings Hospital on the survival of patients who had undergone surgery for breast cancer.

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

%matplotlib inline
```

To predict whether the patient will survive after 5 years or not based upon the patient's age, year of treatment and the number of positive lymph nodes

In [3]:
```
# let us prepare the data and get some initial insights on the dataset.
```

In [5]:
```
df = pd.read_csv("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

- The age feature is the age of the patient.
- the year feature describes year in which the patient was undergone a surgery.
- the nodes are basically the number of positive axillary nodes detected.
- If patients survived 5 years or more is represented as 1 in status and patients who survived less than 5 years is represented as 2 under status.

- There are four attributes in this dataset out of which 3 of them are taken as features and 1 as a class attrinute.
- we have taken age, year, nodes as features and "status" as aour class label.

In [7]:
```
# how many data points do we have?
df.shape
```

Out[7]:
```
(306, 4)
```

In [8]:
```
# getting the column names in the dataset

df.columns
```

Out[8]:
```
Index(['age', 'year', 'nodes', 'status'], dtype='object')
```

In [14]:
```
# what all type of status do we have?
print(df['status'].value_counts())
```

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

In [15]:
```
# we can conclude that the dataset is not balanced.
```

In [17]:
```
df.info()
```

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

In [73]:
```
print("Number of rows: " + str(df.shape[0]))
print("Number of columns: " + str(df.shape[1]))
print("Columns: " + ", ".join(df.columns))

print("Target variable distribution")
print(df.iloc[:,-1].value_counts())
print("*"*50)
print(df.iloc[:,-1].value_counts(normalize = True))
```

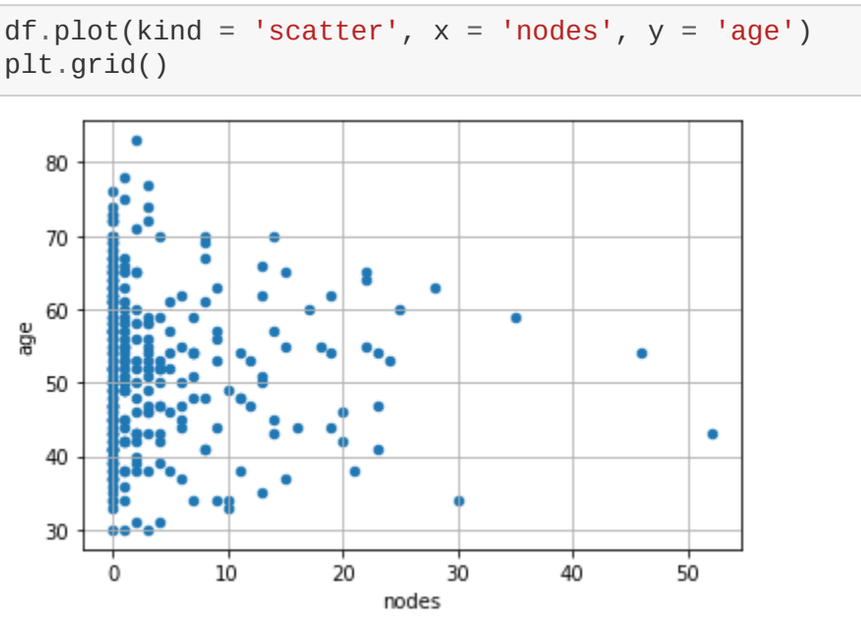
```
Number of rows: 306
Number of columns: 4
Columns: age, year, nodes, status
Target variable distribution
1    225
2     81
Name: status, dtype: int64
**************************************************
1    0.735294
2    0.264706
Name: status, dtype: float64
```

Observations:

- The age of the patients vary from 30 to 83 with the median of 52.
- Although the maximum number of positive lymph nodes observed is 52, nearly 75% of the patients have less than 5 positive lymph nodes and nearly 25% of the patients have no positive lymph nodes
- The dataset contains only a small number of records (306). and have no missing values
- The target column is imbalanced with 73% of values are 'yes'

2-D Scatter Plot

In [19]:
```
df.plot(kind = 'scatter', x = 'nodes', y = 'age')
plt.grid()
```

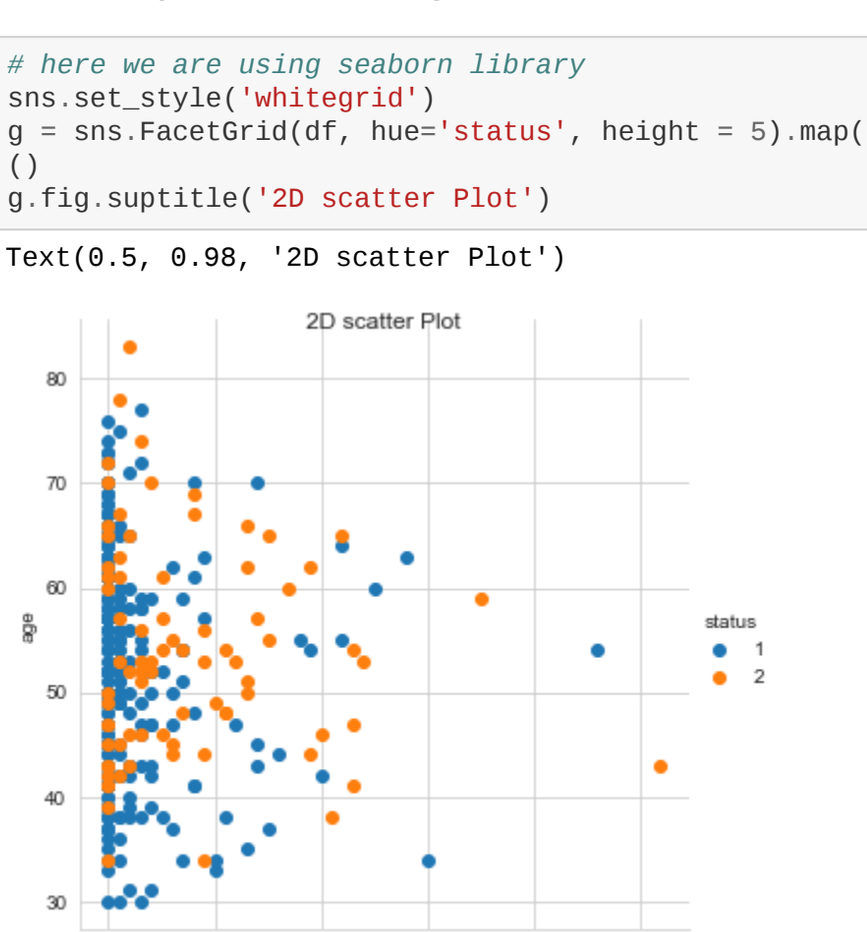


In [20]:
```
# to distinguish between the data
# we can use seaborn packages function which simply to distinguish data visually by allocati
ng different colours to every
#classification feature.
```

2-D Scatter plot with color-coding for each status class.

In [25]:
```
# here we are using seaborn library
sns.set_style('whitegrid')
g = sns.FacetGrid(df, hue='status', height = 5).map(plt.scatter, 'nodes', 'age').add_legend
()
g.fig.suptitle('2D scatter Plot')
```

Out[25]:
```
Text(0.5, 0.98, '2D scatter Plot')
```



In [26]:
```
# here the blue dots (status 1) represents
# the survival rate more than 5 years
# and orange dots(status 2) represents survival rate less than 5 years.
```

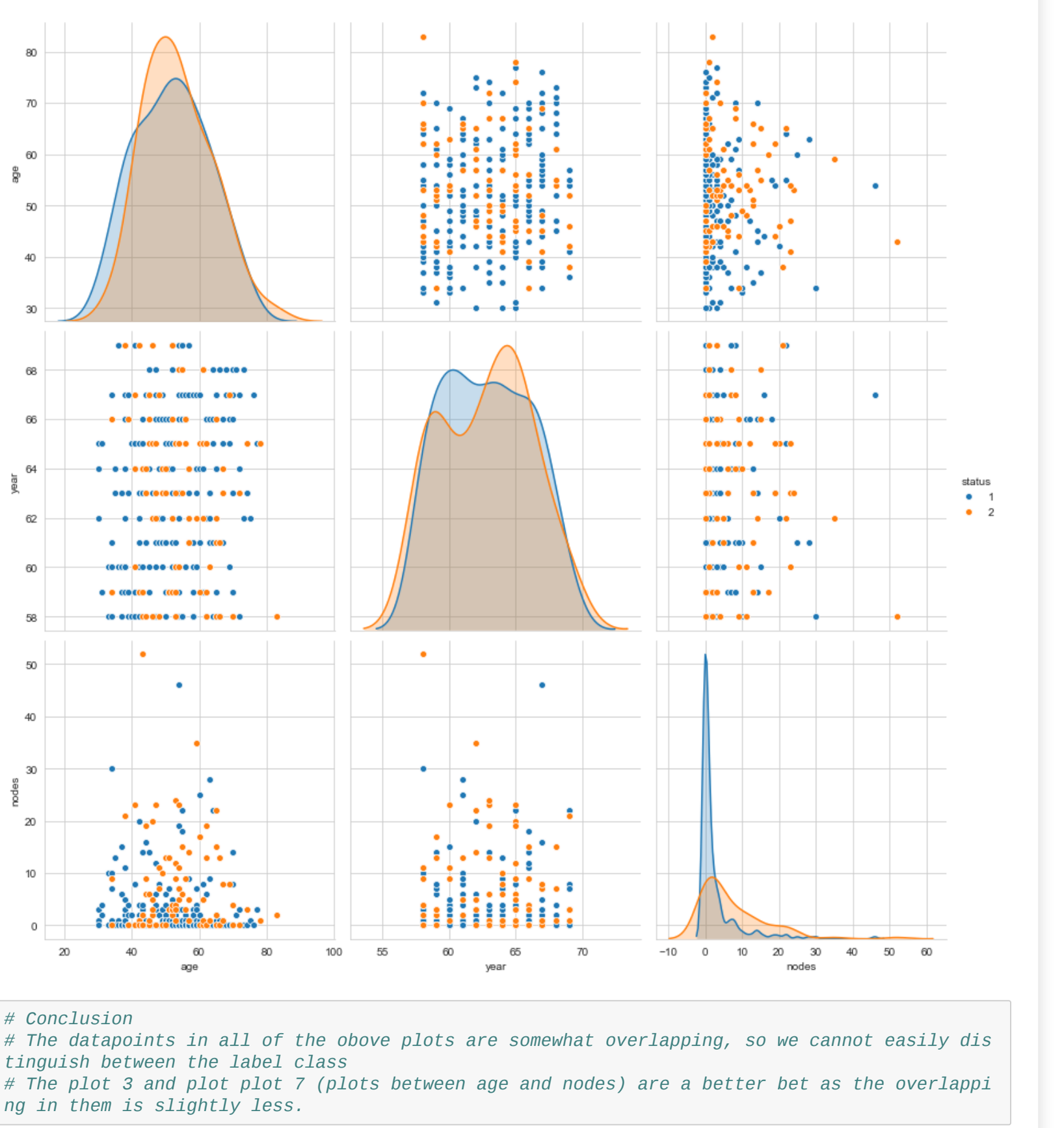
In [27]:
```
# but we cannot easily distinguish/ classify between the statuses with this plot.
```

Pairplots

let us draw pairplots to get a much more clear understanding of how are features are able to classify among the statuses.

In [30]:
```
sns.set_style('whitegrid')
sns.pairplot(df, hue="status", height = 4)
```

Out[30]:
```
<seaborn.axisgrid.PairGrid at 0x253899e8>
```

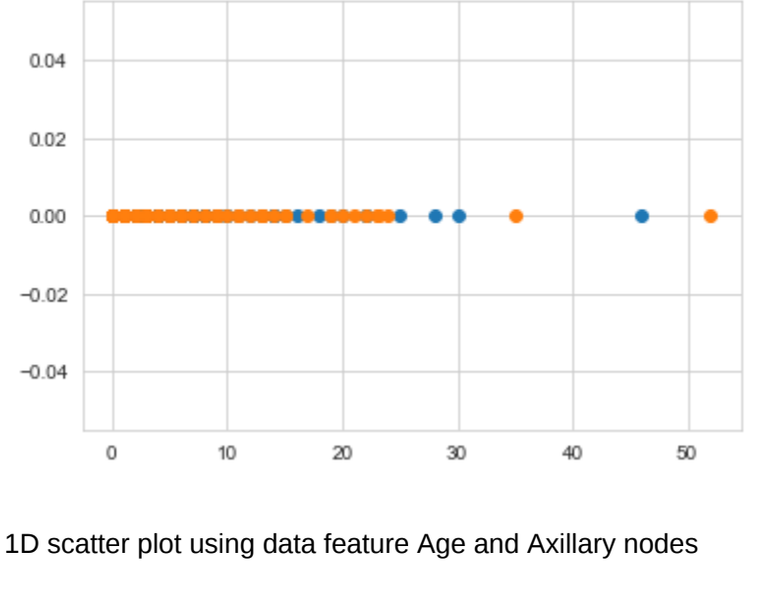


In [32]:
```
# Conclusion
# The datapoints in all of the obove plots are somewhat overlapping, so we cannot easily dis
tinguish between the label class
# The plot 3 and plot plot 7 (plots between age and nodes) are a better bet as the overlappi
ng in them is slightly less.
```

In [36]:
```
# Let's plot a 1D scatter plot
```

1D scatter plot

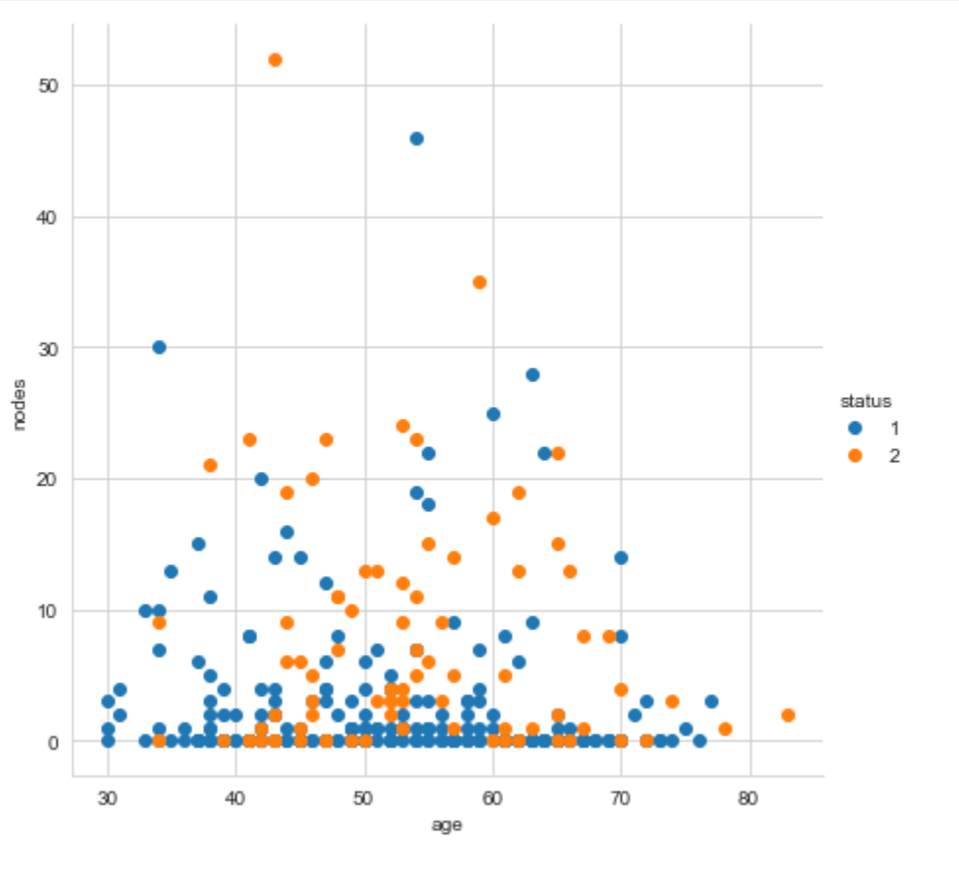
In [42]:
```
import numpy as np
status_long_survival = df.loc[df["status"] == 1]
status_short_survival = df.loc[df["status"] == 2]
plt.plot(status_long_survival["nodes"], np.zeros_like(status_long_survival["nodes"]), 'o')
plt.plot(status_short_survival["nodes"], np.zeros_like(status_short_survival["nodes"]), 'o')
plt.show()
```



1D scatter plot using data feature Age and Axillary nodes

2D scatter plot

In [92]:
```
# AGE VS AUXILLARY NODES
sns.FacetGrid(df, hue="status", height=6).map(plt.scatter, "age", "nodes").add_legend();
plt.show();
```



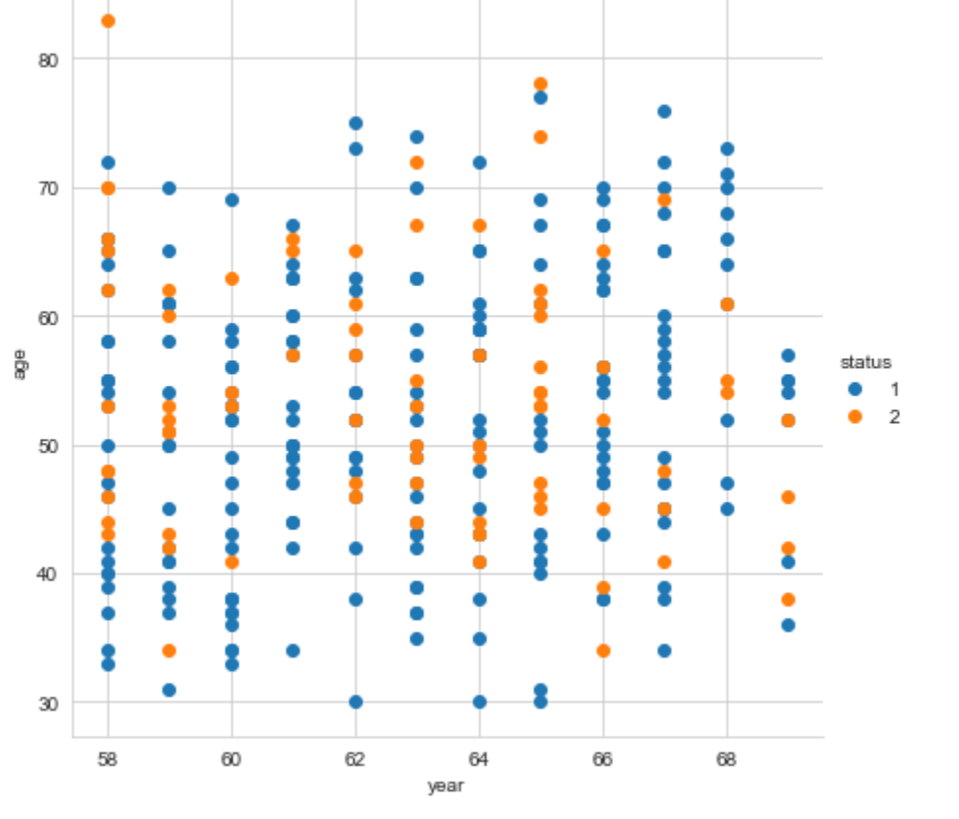
Observations :

- Patients with Age < 40 and Auxillary nodes < 30 have higher chances of survival.
- Patients with Age > 50 and Auxillary nodes > 10 has less chances of survival.

In [93]:
```
#AUXILLARY NODES VS OPERATION YEAR
sns.FacetGrid(df, hue="status", height=6).map(plt.scatter, "nodes", "year").add_legend();
plt.show();
```

In [94]:
```
# no conclusions can be drawn from above plot
```

In [95]:
```
#AGE VS OPERATION YEAR
sns.FacetGrid(df, hue="status", height=6).map(plt.scatter, "year", "age").add_legend();
plt.show();
```

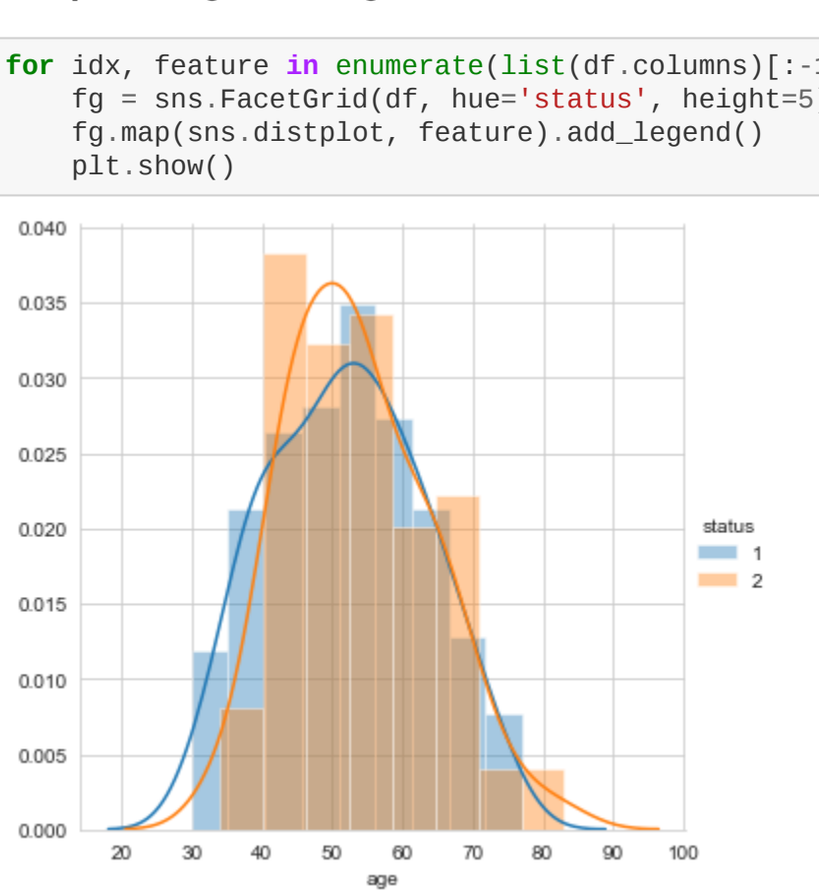


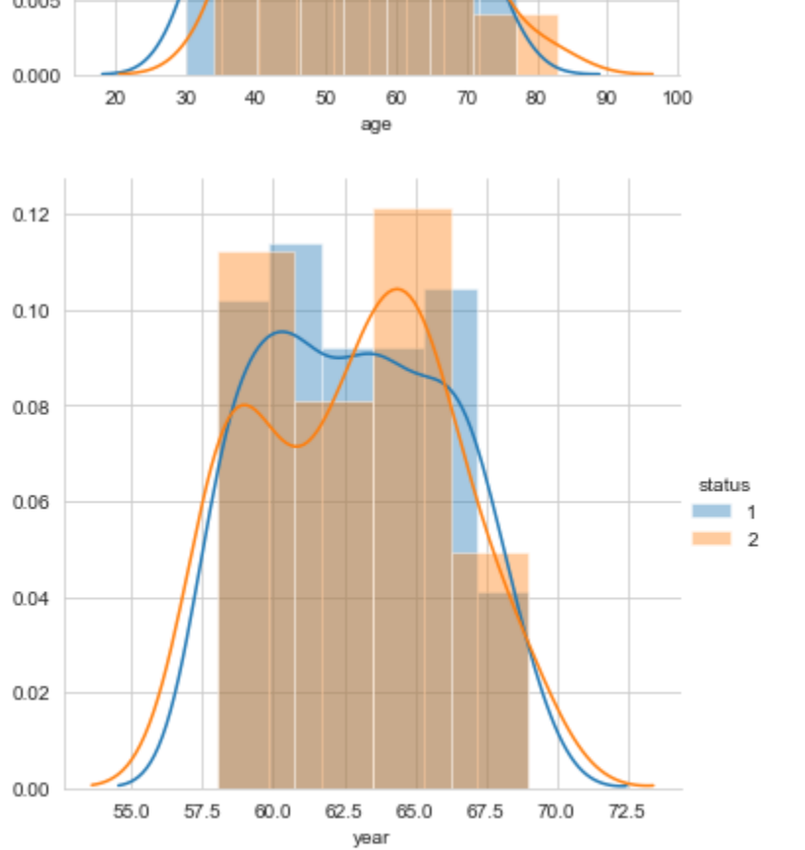
Observation :

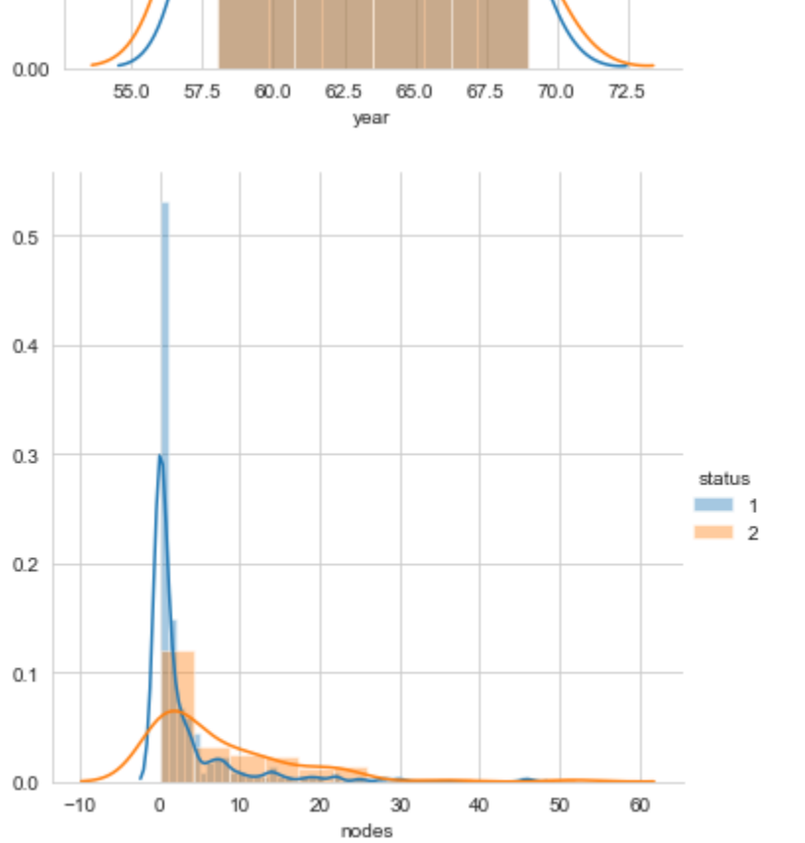
- One interesting observation can be drawn as for the operation year 60, 61 and 68 the survival rate is significantly more.

Distplot for generating PDFs

In [96]:
```
for idx, feature in enumerate(list(df.columns)[:-1]):
    fg = sns.FacetGrid(df, hue='status', height=5)
    fg.map(sns.distplot, feature).add_legend()
    plt.show()
```







Conclusions from the above PDFs and histogram

- In the first and second plot (pdfs of age and year) we cannot clearly classify and seperate the datapoints.
- In the third plot of PDF of nodes, we can observe that more number of people survive if they have less axillary nodes.

With the help of a simple if else statement, we can come to a conclusion that is->

if (nodes <= 0) -> patient = long_survival
elif (nodes in between 0 and 3.5) -> patient = long_survival
elif (nodes>= 3.5) -> patient = short_survival

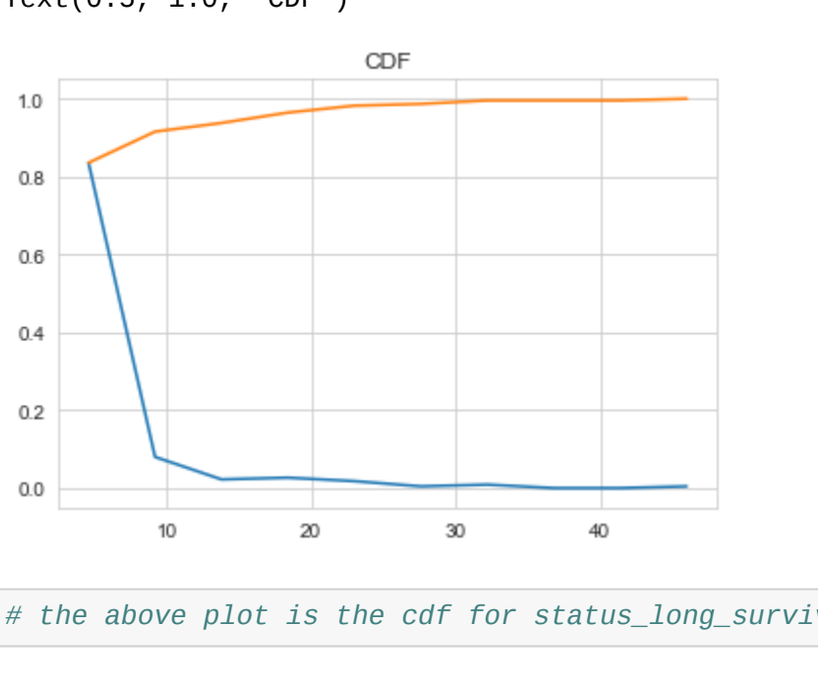
In [97]:
```
# let's plot cdf for the selected plot
```

CDF

In [98]:
```
counts, bin_edges = np.histogram(status_long_survival["nodes"], bins=10,
 density = True)
pdf = counts/(sum(counts))
print("pdf = ",pdf)
print("bin_edges =", bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)
plt.title("CDF")
```

```
pdf =  [0.83555556 0.08       0.02222222 0.02666667 0.01777778 0.00444444
 0.00888889 0.         0.         0.00444444]
bin_edges = [ 0.   4.6  9.2 13.8 18.4 23.  27.6 32.2 36.8 41.4 46. ]
```

Out[98]:
```
Text(0.5, 1.0, 'CDF')
```



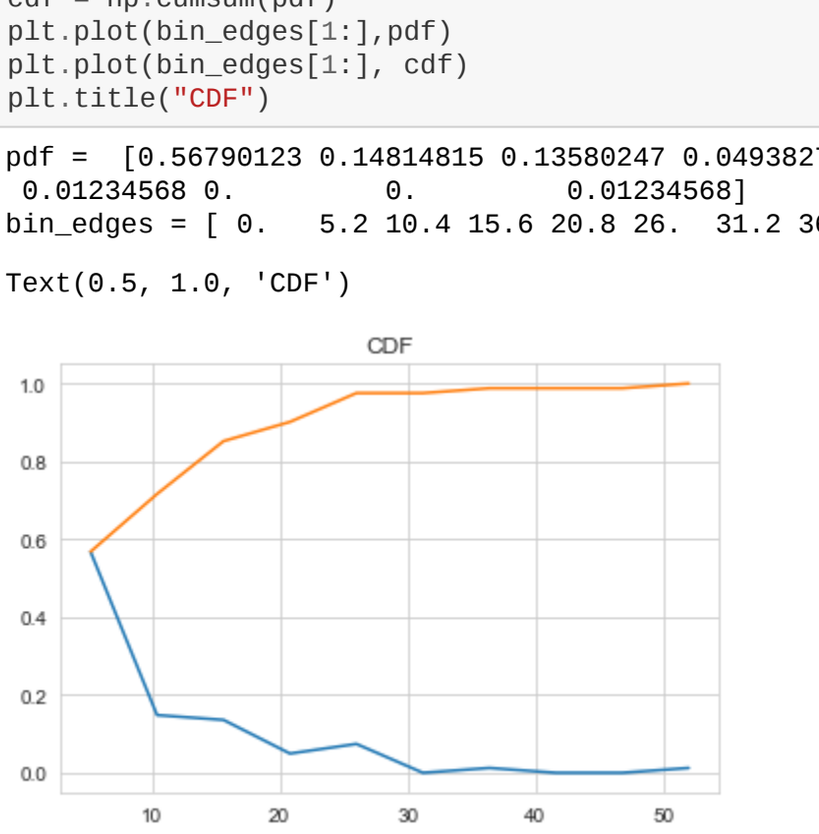
In [99]:
```
# the above plot is the cdf for status_long_survival (status = 1)
```

From above CDF we can observe that orange line shows there is around 85% chance of long survival if number of axillary nodes detected are < 5. Also we can see as number of axillary nodes increases survival chances also reduces means it is clearly observed that 80% — 85% of people have good chances of survival if they have less no of auxillary nodes detected and as nodes increases the survival status also decreases as a result 100% of people have less chances of survival if nodes increases >40

In [100]:
```
counts, bin_edges = np.histogram(status_short_survival["nodes"], bins=10,
 density = True)
pdf = counts/(sum(counts))
print("pdf = ",pdf)
print("bin_edges =", bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)
plt.title("CDF")
```

```
pdf =  [0.56790123 0.14814815 0.13580247 0.04938272 0.07407407 0.
 0.01234568 0.         0.         0.01234568]
bin_edges = [ 0.   5.2 10.4 15.6 20.8 26.  31.2 36.4 41.6 46.8 52. ]
```

Out[100]:
```
Text(0.5, 1.0, 'CDF')
```



In [101]:
```
# the above plot is the cdf for status_short_survival (status = 2)
```

From the above two plots we can conclude that: nearly 55% of people who have nodes less than 5 and there are nearly 100% of people in short survival if nodes are > 40

In [102]:
```
# let us predict the status and get the insights on data through statistical analyses
```

Mean, Variance and Std-dev

In [103]:
```
print("Mean")
print (np.mean(status_long_survival["nodes"]))
print (np.mean(status_short_survival["nodes"]))
print("\nStandard-deviation")
print(np.std(status_long_survival["nodes"]))
print(np.std(status_short_survival["nodes"]))
```

```
Mean
2.7911111111111113
7.45679012345679

Standard-deviation
5.857258449412138
9.128776076761635
```

we can draw the conclusions like

- long survival (status 1) have mean value of nodes as 2.79 whereas the short survival of (status 2) have mean value of nodes as 7.45 which is quite high.
- also the standard deviation (spread of data-points) is huge with respect to the short survival category.

Median, Quantiles and Percentile

In [104]:
```
print("medians")
print("status 1 :",np.median(status_long_survival["nodes"]))
print("status 2 :",np.median(status_short_survival["nodes"]))
print("\n Quantiles")
print("status 1 :",np.percentile(status_long_survival["nodes"],np.arange(0,100,25)))
print("status 2 :",np.percentile(status_short_survival["nodes"],np.arange(0,100,25)))

print("\n 90th percentile")
print("status 1 :",np.percentile(status_long_survival["nodes"],90))
print("status 2 :",np.percentile(status_short_survival["nodes"],90))
```

```
medians
status 1 : 0.0
status 2 : 4.0

 Quantiles
status 1 : [0. 0. 0. 3.]
status 2 : [ 0.  1.  4. 11.]

 90th percentile
status 1 : 8.0
status 2 : 20.0
```

Conclusions

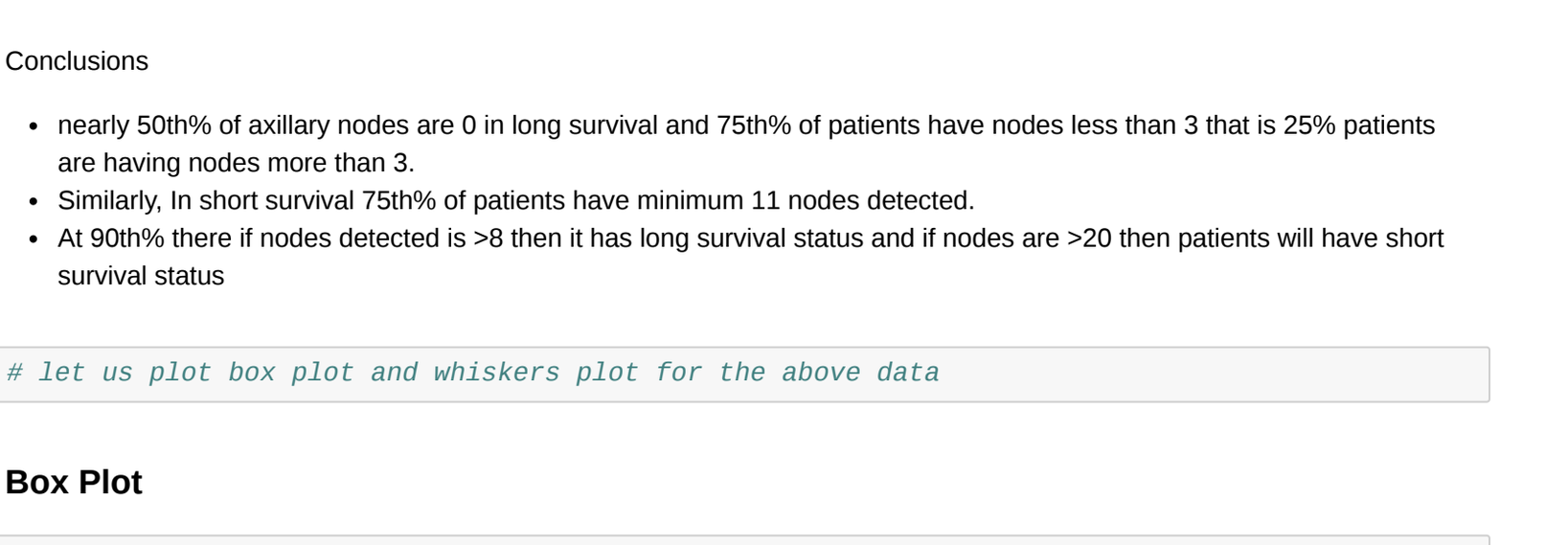
- nearly 50th% of axillary nodes are 0 in long survival and 75th% of patients have nodes less than 3 that is 25% patients are having nodes more than 3.
- Similarly, In short survival 75th% of patients have minimum 11 nodes detected.
- At 90th% there if nodes detected is >8 then it has long survival status and if nodes are >20 then patients will have short survival status

In [105]:
```
# let us plot box plot and whiskers plot for the above data
```

Box Plot

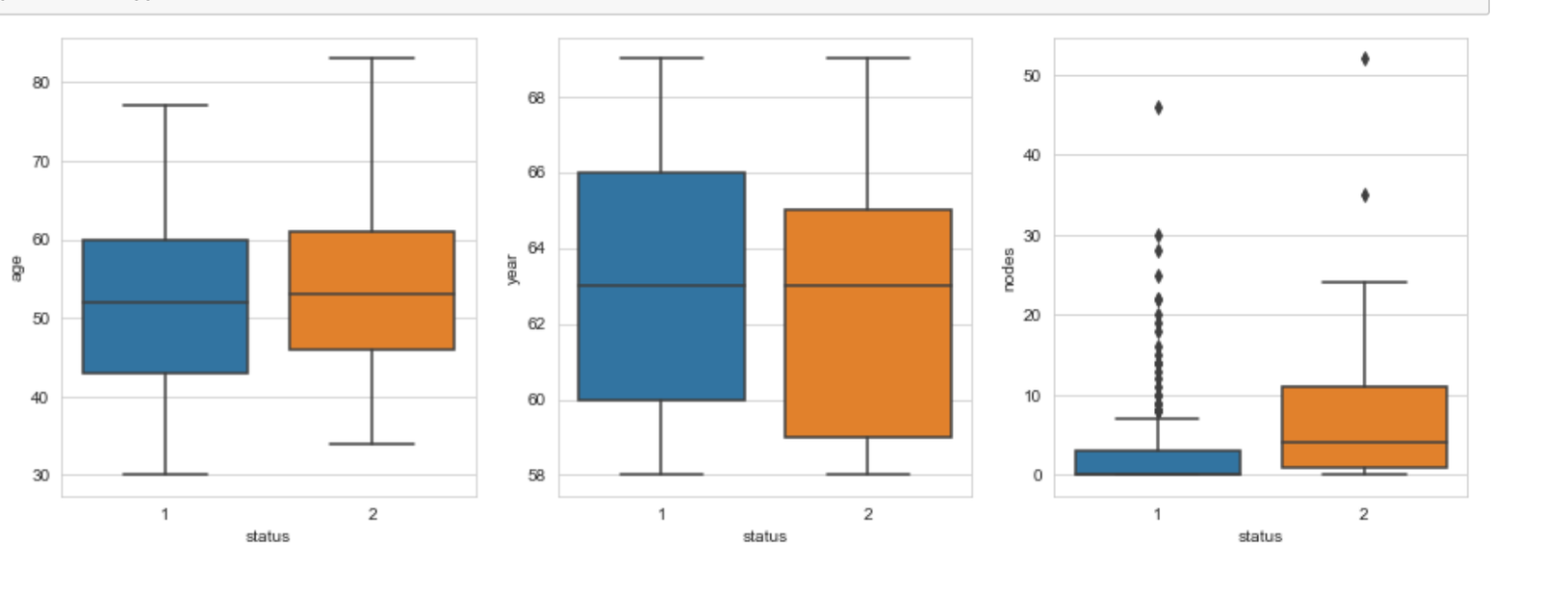
In [106]:
```
# let's take all the features and plot a box plot
```

In [107]:
```
fig, axes = plt.subplots(1, 3, figsize=(15, 5))
for idx, feature in enumerate(list(df.columns)[:-1]):
    sns.boxplot( x='status', y=feature, data=df, ax=axes[idx])
plt.show()
```



Violoin plot

In [108]:
```
fig, axes = plt.subplots(1, 3, figsize=(15, 5))
for idx, feature in enumerate(list(df.columns)[:-1]):
    sns.violinplot( x='status', y=feature, data=df, ax=axes[idx])
plt.show()
```

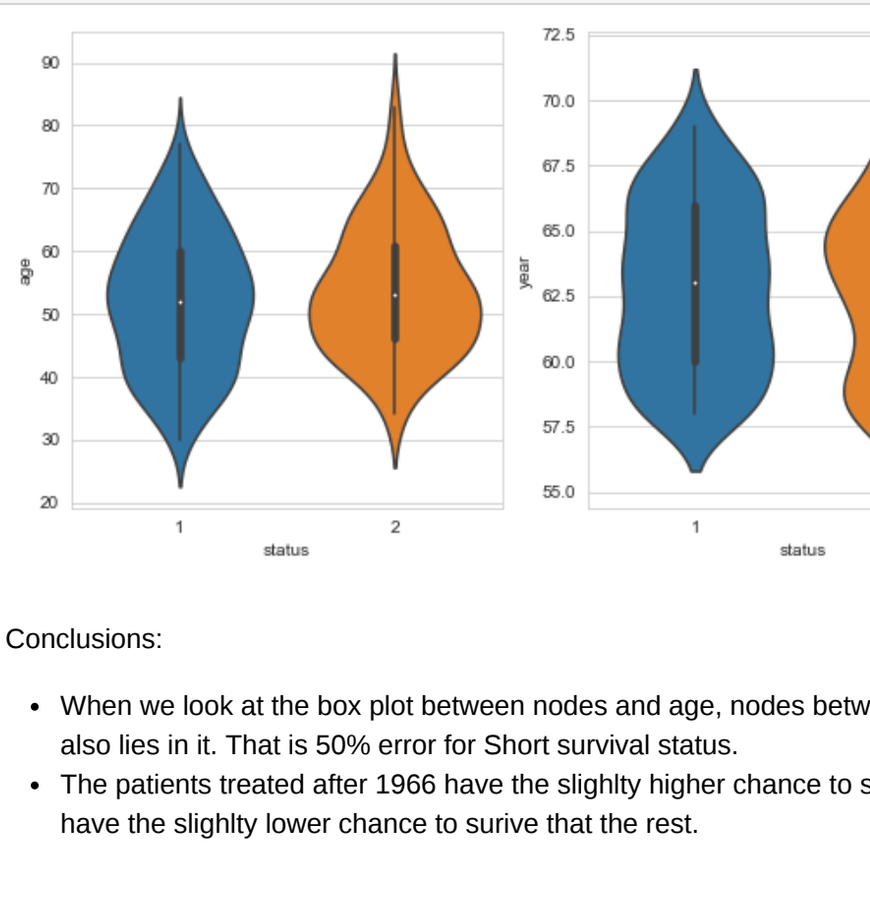


Conclusions:

- When we look at the box plot between nodes and age, nodes between 0–7 have chances of error as short survival plot also lies in it. That is 50% error for Short survival status.
- The patients treated after 1966 have the slighlty higher chance to surive that the rest. The patients treated before 1959 have the slighlty lower chance to surive that the rest.

Contour Plot

In [109]:
```
sns.jointplot(x="age",y="nodes",data=status_long_survival,kind="kde")
plt.grid()
plt.show()
```



Obseravations:

- For nodes less than 5 and age range between 47-60 the chances of survival are more

In [110]:
```
# this concludes EDA
```

Conclusion

The Exploratory data analysis for Haberman's dataset is concluded and with the help pf various python libraries and statistical medthods we can classify the different status patients.