In [9]:

```
import warnings
warnings.filterwarnings("ignore")
```

In [2]:

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
ds=pd.read_csv("haberman.csv")
print(ds.shape)
print(ds.columns)
```

```
(306, 4)
Index(['age', 'year', 'nodes', 'status'], dtype='object')
```

It has 306 rows with 4 features(age, year, node, status)

In [3]:

```
ds['status'].value_counts()
```

Out[3]:

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

The dataset has 225 data points where te survival status is 1 & 81 data points where the status was 2.
225- survived for more than 5 years
81 - survived less than 5 years

In [4]:

```
print(ds.describe())
print(np.percentile(ds['status'],70))
```

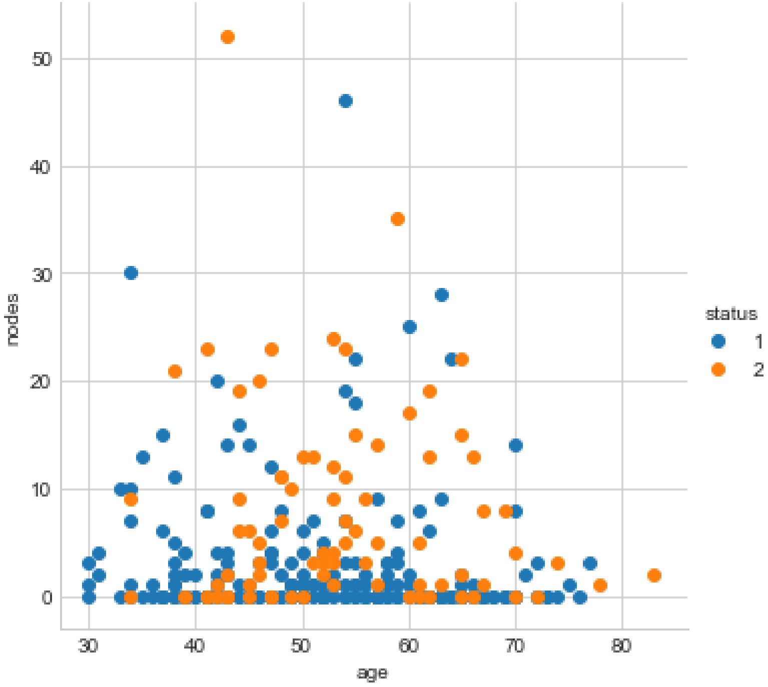
```
              age        year       nodes      status
count  306.000000  306.000000  306.000000  306.000000
mean    52.457516   62.852941    4.026144    1.264706
std     10.803452    3.249405    7.189654    0.441899
min     30.000000   58.000000    0.000000    1.000000
25%     44.000000   60.000000    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
1.0
```

Avg age of patient is 52.4 years, Avg num of nodes is 4.
From Percentile values, it can be said that more than 70 % of patients survived for > 5 years

2D Scatter plot

In [5]:

```
sns.set_style("whitegrid")
sns.FacetGrid(ds,hue="status",size=5)\
   .map(plt.scatter,"age","nodes")\
    .add_legend();
plt.show()
```

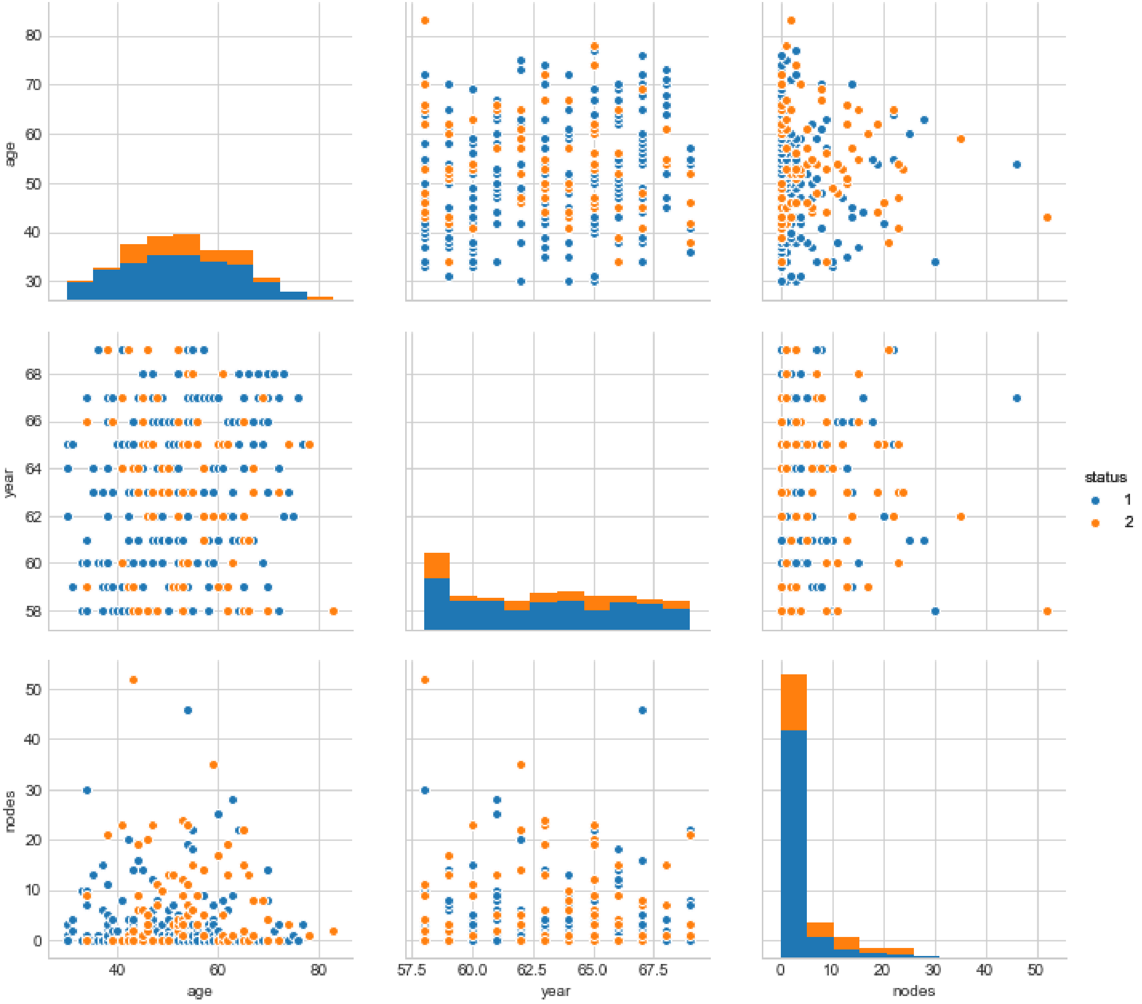


- The graph for both categories(status=1 and status=2) are spread across
- Its is difficult to distinguish or form a separation for two categories
- One more observation is that category STATUS=1 (survival > 5 years) are concentrated towards lesser number of nodes when compared to category STATUS=2 (survival < 5 years) which are spread from 0-35 nodes

Pair-plotting

In [6]:

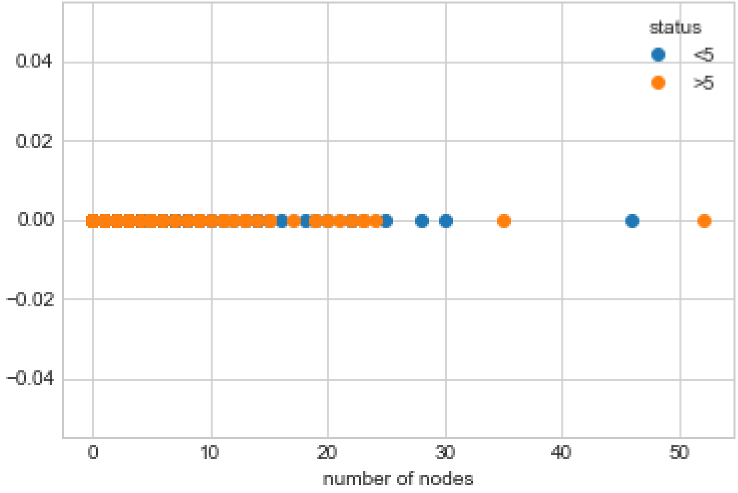
```
plt.close()
sns.set_style("whitegrid")
sns.pairplot(ds,hue="status",size=3,vars=['age','year','nodes']).add_legend()
plt.show()
```



- Plot - Age vs Year
  The data is very scattered and the spread is overlapping. Difficult to make further analysis with these features.
- Plot - Age vs Nodes
  The data is overlapping with these feaures too but helps to distinguish slightly better than previous features.
- Plot - Year vs Nodes
  It is difficult to distinguish or make any classification with this plot

In [7]:

```
ds_status1=ds.loc[ds["status"]==1]
ds_status2=ds.loc[ds["status"]==2]
plt.plot(ds_status1["nodes"],np.zeros_like(ds_status1["nodes"]),'o',label="<5")
plt.plot(ds_status2["nodes"],np.zeros_like(ds_status2["nodes"]),'o',label=">5")
plt.legend(title="status")
plt.xlabel("number of nodes")
plt.show()
```

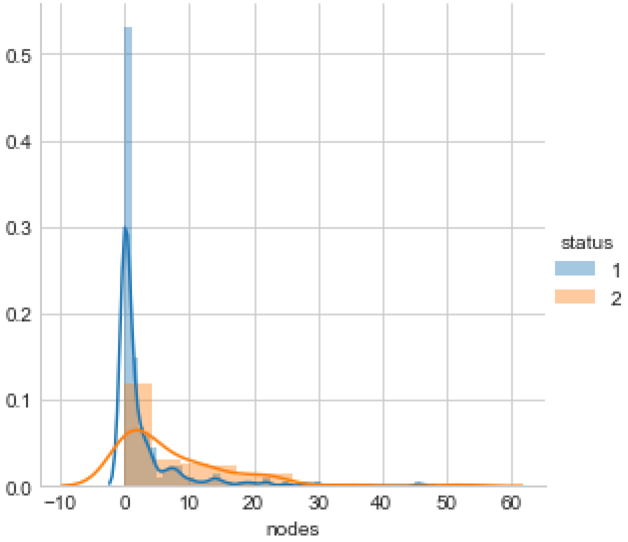


this graph has overlapping, hence not very helpful to draw conclusion

Histogram, PDF, CDF

In [10]:

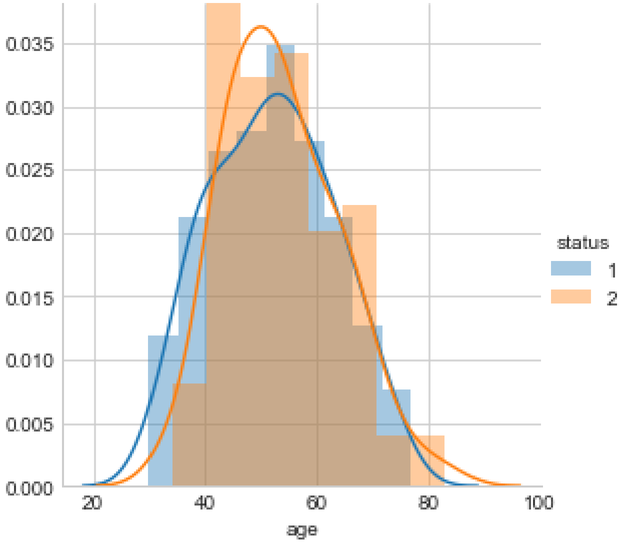
```
sns.FacetGrid(ds,hue="status",size=4)\
   .map(sns.distplot,"nodes")\
   .add_legend();
plt.show();
```



this graph tells us that the probability of patient to survive more than 5 years is greater, if patients has less number of nodes(~2-3)
and patients having more number of nodes, are likely to survive less than 5 years.

In [11]:

```
sns.FacetGrid(ds,hue="status",size=4)\
   .map(sns.distplot,"age")\
   .add_legend();
plt.show();
```

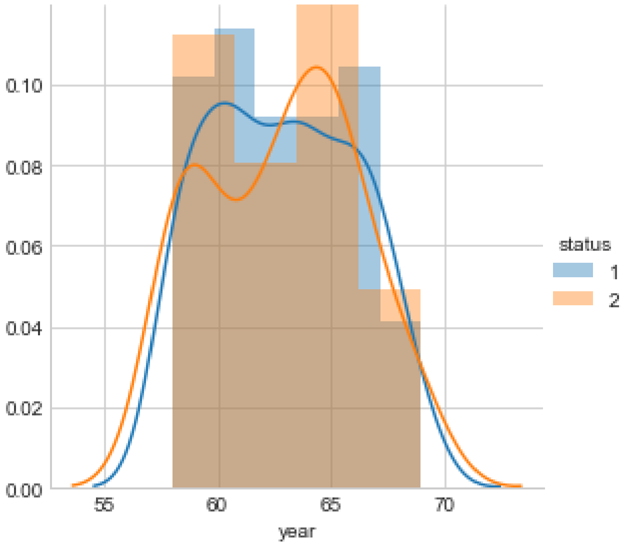


A major part of graph is overlapped.
Some of the conclusions can be

- Patients betwen the age group 25-40 are morelikely to survive more than 5 years and between 40-60 are more likey to survive lss than 5 years
- for age group beyound 60, this plotting does not help much to draw conclusion on status of patient

In [12]:

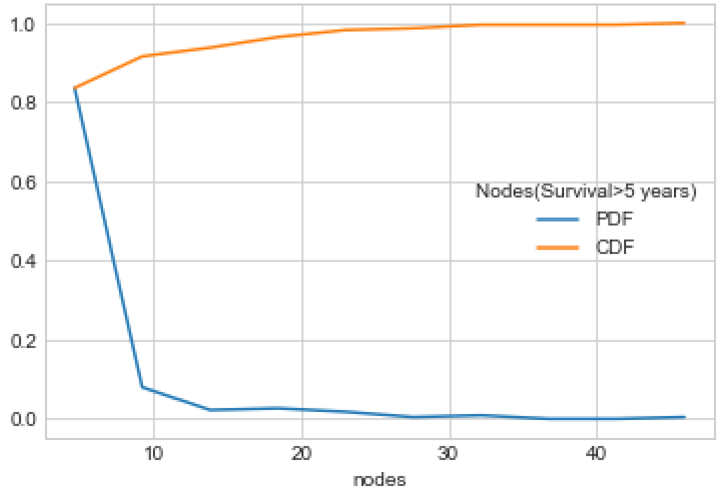
```
sns.FacetGrid(ds,hue="status",size=4)\
   .map(sns.distplot,"year")\
   .add_legend();
plt.show();
```



This data also has overlapping. However it shows there were significantly more successfull operations than unsuccessfull during years 62-63 & 67-68. But information is not very helpful to make further analysis.

In [13]:

```
counts,bin_edges=np.histogram(ds_status1["nodes"],bins=10,density=True)
pdf=counts/(sum(counts))
#print(pdf)
#print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,label="PDF")
plt.plot(bin_edges[1:],cdf,label="CDF")
plt.xlabel('nodes')
plt.legend(title="Nodes(Survival>5 years)")
plt.show()
```

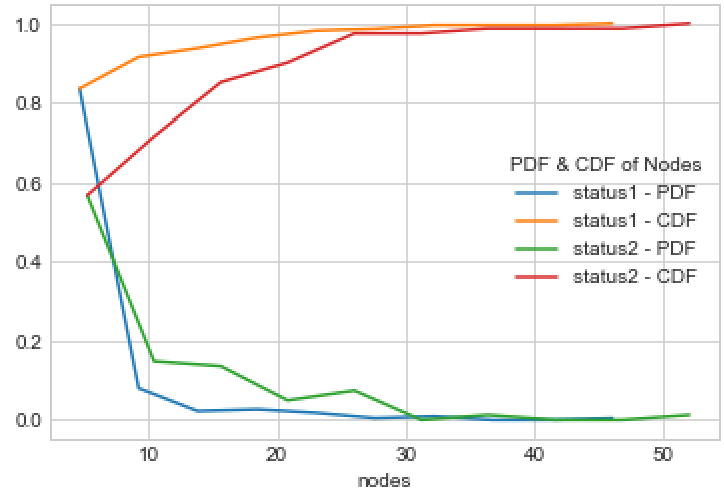


- ~82 % of people who had survived >5 years had nodes between ~0-5. So if a patient has less number of nodes,there are chances are that patients will survive >5 years when compared to a patient with more nodes

In [15]:

```
counts,bin_edges=np.histogram(ds_status1["nodes"],bins=10,density=True)
pdf=counts/(sum(counts))
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,label="status1 - PDF")
plt.plot(bin_edges[1:],cdf,label="status1 - CDF")
#plt.show()
counts,bin_edges=np.histogram(ds_status2["nodes"],bins=10,density=True)
pdf=counts/(sum(counts))
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,label="status2 - PDF")
plt.plot(bin_edges[1:],cdf,label="status2 - CDF")
plt.legend(title="PDF & CDF of Nodes")
plt.xlabel('nodes')
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. ]
```



- 83.55 % Patients who survived more than 5 years,had less than 5(4.6) nodes
- 56.79 % patients who survived less than 5 years had less than 5(5.2)nodes

Mean, Variance and Std-dev, Median, Percentile, Quantile, IQR, MAD

In [16]:

```
print("Mean: (age)")
print(np.mean(ds_status1["age"]))
print(np.mean(ds_status2["age"]))
print("\nMean:(nodes)")
print(np.mean(ds_status1["nodes"]))
print(np.mean(ds_status2["nodes"]))
print("\nStd Dev: (age)")
print(np.std(ds_status1["age"]))
print(np.std(ds_status2["age"]))
print("\nStd Dev:(nodes)")
print(np.std(ds_status1["nodes"]))
print(np.std(ds_status2["nodes"]))
print("\n Quantiles- age")
print(np.percentile(ds_status1["age"],np.arange(0,100,25)))
print(np.percentile(ds_status2["age"],np.arange(0,100,25)))

print("\n Quantiles- nodes")
print(np.percentile(ds_status1["nodes"],np.arange(0,100,25)))
print(np.percentile(ds_status2["nodes"],np.arange(0,100,25)))

print("\n Quantiles- age")
print(np.percentile(ds_status1["age"],90))
print(np.percentile(ds_status2["age"],90))

print("\n Quantiles- nodes")
print(np.percentile(ds_status1["nodes"],90))
print(np.percentile(ds_status2["nodes"],90))

from statsmodels import robust
print("\nMedian ABsolute Deviation- nodes")
print(robust.mad(ds_status1["nodes"]))
print(robust.mad(ds_status2["nodes"]))

print("\nMedian ABsolute Deviation- age")
print(robust.mad(ds_status1["age"]))
print(robust.mad(ds_status2["age"]))
```

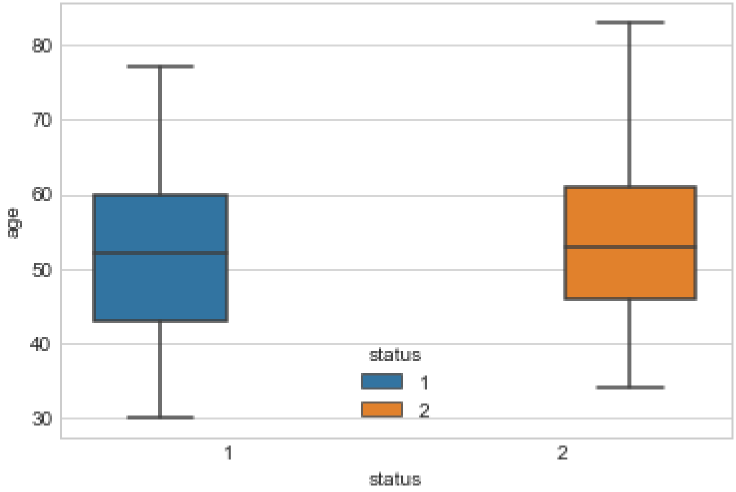
```
Mean: (age)
52.017777777777778
53.67901234567901

Mean:(nodes)
2.7911111111111113
7.45679012345679

Std Dev: (age)
10.98765547510051
10.10418219303131

Std Dev:(nodes)
5.857258449412131
9.128776076761632

 Quantiles- age
[30. 43. 52. 60.]
[34. 46. 53. 61.]

 Quantiles- nodes
[0. 0. 0. 3.]
[ 0.  1.  4. 11.]

 Quantiles- age
67.0
67.0

 Quantiles- nodes
8.0
20.0

Median ABsolute Deviation- nodes
0.0
5.930408874022408

Median ABsolute Deviation- age
13.343419966550417
11.860817748044816
```

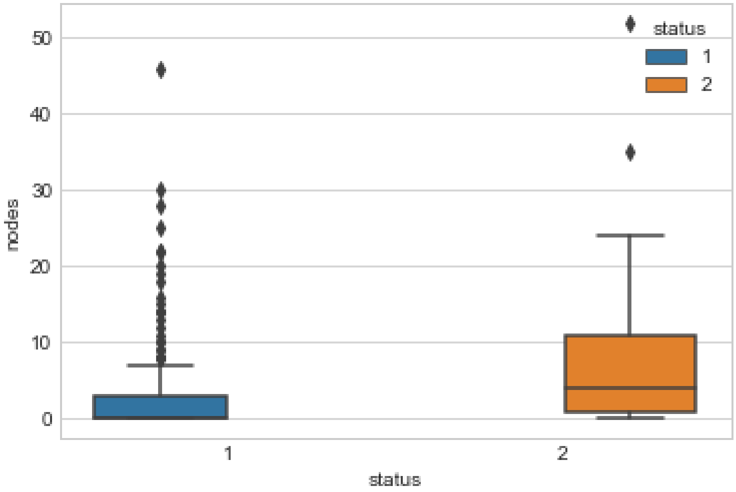
- The above statistics are comparison of features between patients who >5 years & < 5years respectively.

Box plot and Whiskers

In [17]:

```
ax=sns.boxplot(x='status',y='age',data=ds,hue="status")
plt.show()
sns.boxplot(x='status',y='nodes',data=ds,hue="status")
plt.show()
```



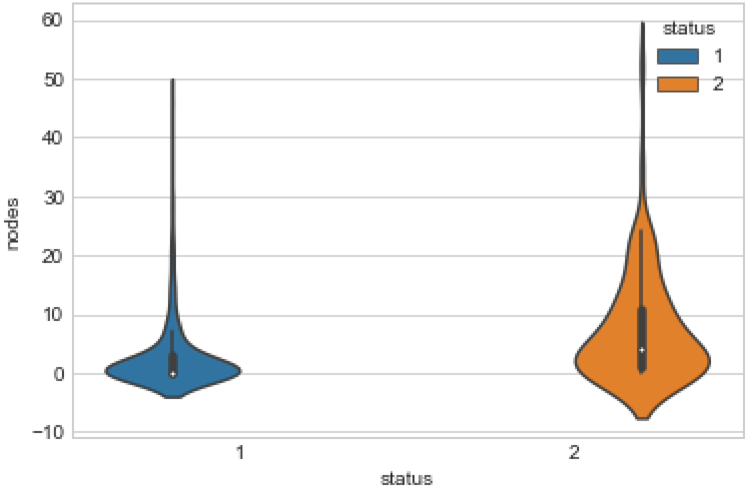


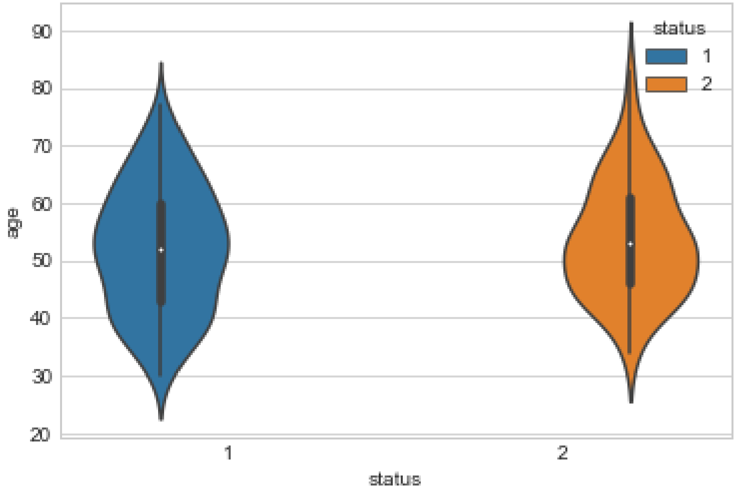
- 25% & 50% line is almost same for nodes for patients (surviving more than 5 years)
- Percentiles of age for both sets of patients(survival >5 years & survival<5 years) is very close

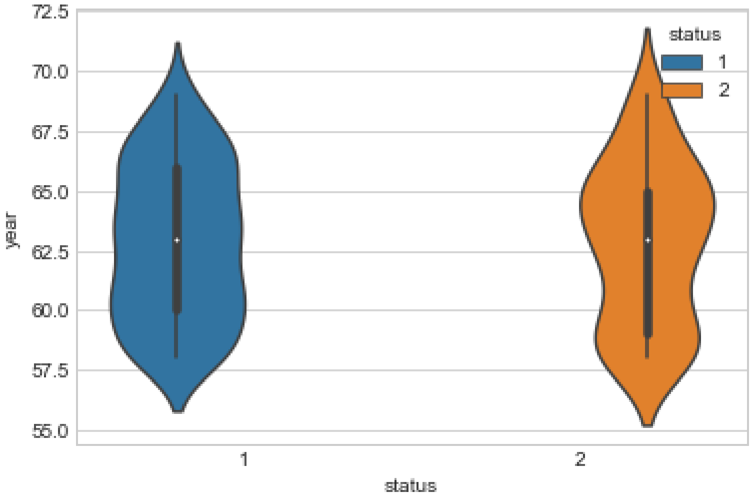
Violin plots

In [18]:

```
ax=sns.violinplot(x='status',y='nodes',data=ds,size=5,hue="status")
handles, labels = ax.get_legend_handles_labels()
plt.show()
sns.violinplot(x='status',y='age',data=ds,size=5,hue="status")
plt.show()
sns.violinplot(x='status',y='year',data=ds,size=5,hue="status")
plt.show()
```





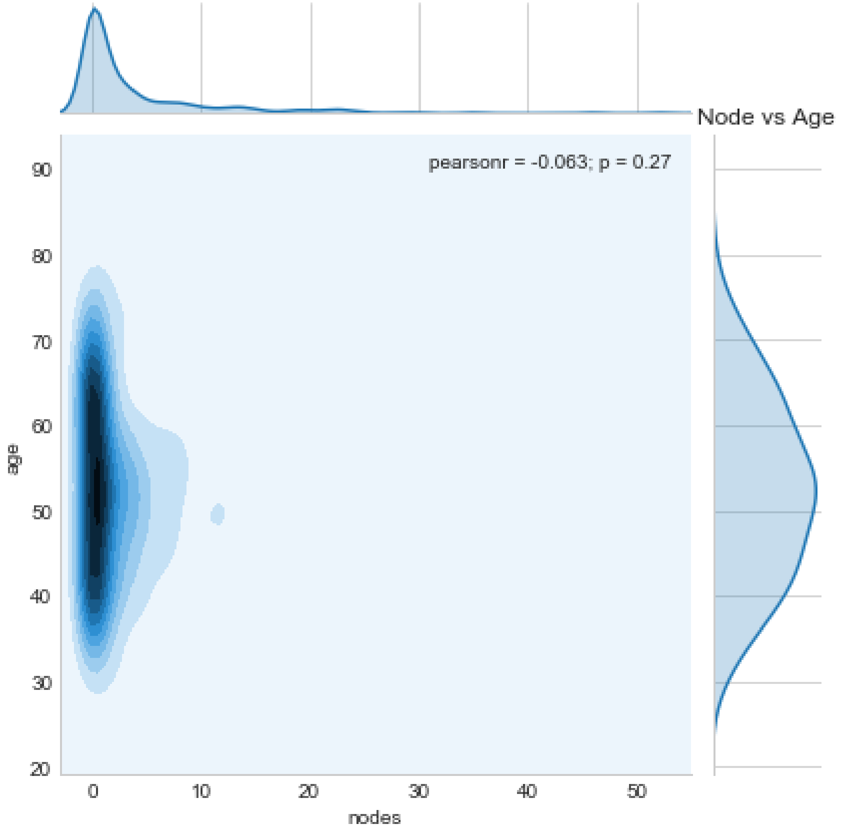


- the plot of node vs status gives more clear information, that lesser the number of nodes, more are the chances of survival.
- age, year plot gives information which is more overlappping i.e density across the spread is very similar, not very distinctive which makes it difficult to rely on feature

Multivariate probability density, contour plot

In [26]:

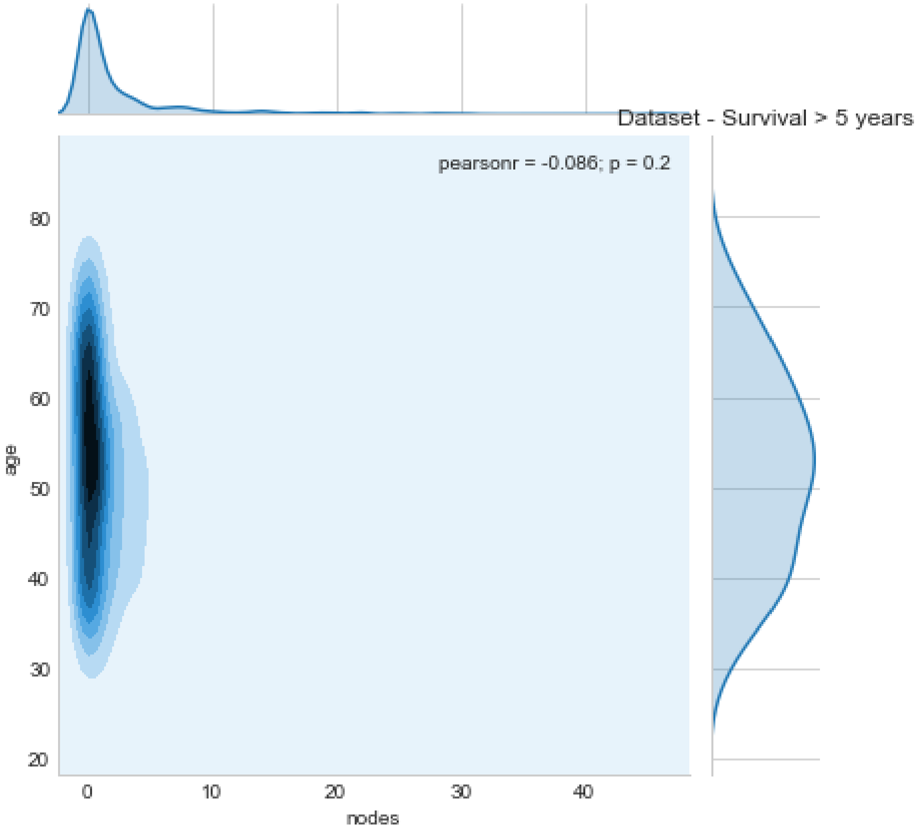
```
sns.jointplot(x="nodes", y="age", data=ds, kind="kde");
plt.title("Node vs Age")
plt.show();
```



- Through this plot we can say that number of nodes is bbetween 0-5 majorly in cancer patients and it is majorly in agegroup 40-65 as the density in the graph shows

In [27]:

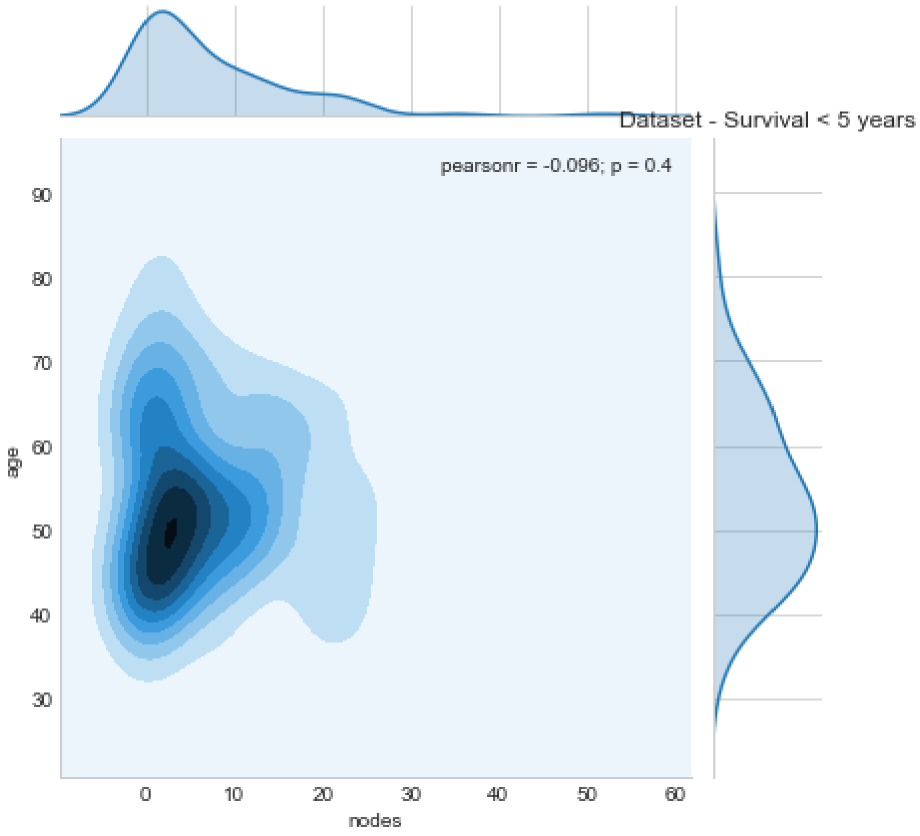
```
patients_survival_1 = ds[ds['status'] == 1];
patients_survival_2 = ds[ds['status'] == 2];
sns.jointplot(x="nodes", y="age", data=patients_survival_1, kind="kde");
plt.title("Dataset - Survival > 5 years")
plt.show();
```



- The first graph shows data of patients who **survived more than 5 years**, majorly belonged to age group 40-50 & had nodes in range ~0-3

In [28]:

```
sns.jointplot(x="nodes", y="age", data=patients_survival_2, kind="kde");
plt.title("Dataset - Survival < 5 years")
plt.show();
```



- The above plotting shows that patients who **survived less than 5 years**, had more number of nodes and density shows their age group between 45-55 years & had nodes in range ~5-8

Conclusion

- The data is skewed. It has more records of patients who survived >5years than <5years.
- Survival chances are majorly in relation(inversely proportional) with number of nodes. Lesser the number of nodes, greater the chances of survival.
- Age is also a factor contributing towards patients survival. Cancer patients of age group(25-40) tend to live longer than age group of (>50 years)
- Though the dataset set gives information about these patterns, it is difficult to **clearly distinguish** patients with different survival statuses.

References-

- https://seaborn.pydata.org/generated/seaborn.pairplot.html (https://seaborn.pydata.org/generated/seaborn.pairplot.html)
- https://stackoverflow.com/questions/19125722/adding-a-legend-to-pyplot-in-matplotlib-in-the-most-simple-manner-possible (https://stackoverflow.com/questions/19125722/adding-a-legend-to-pyplot-in-matplotlib-in-the-most-simple-manner-possible)