Data Description :

The Haberman's survival 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.

Attribute Information :

*Age of patient at time of operation (numerical)

*Patient's year of operation (year - 1900, numerical)

*Number of positive axillary nodes detected (numerical)

*Survival status (class attribute) 1 = the patient survived 5 years or longer 2 = the patient died within 5 years

NOTE : Copied this description from https://www.kaggle.com/kundnjha/detailed-eda-on-haberman-s-survival-dataset (https://www.kaggle.com/kundnjha/detailed-eda-on-haberman-s-survival-dataset)

In [1]:

```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np

#Load haberman.csv into a pandas dataFrame.
hbman = pd.read_csv("haberman.csv")
```

In [7]:

```
print(hbman.shape)
```

```
(306, 4)
```

Observation

- There are 4 columns and 306 entries

In [4]:

```
print(hbman.columns)
```

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

Observation

- Name of the columns in dataset

```
In [5]: print(hbman.info())
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 306 entries, 0 to 305
Data columns (total 4 columns):
age       306 non-null int64
year      306 non-null int64
nodes     306 non-null int64
status    306 non-null int64
dtypes: int64(4)
memory usage: 9.6 KB
None
```

Observation:

- Datatype, null or non-null, and size of all the columns

```
In [6]: hbman['year'].value_counts()
```

```
Out[6]: 58    36
        64    31
        63    30
        66    28
        65    28
        60    28
        59    27
        61    26
        67    25
        62    23
        68    13
        69    11
        Name: year, dtype: int64
```

Observation:

- Count of each year value in dataset

```
In [29]: hbman['status'] = hbman['status'].map({1:"yes", 2:"no"})
         hbman['status'].value_counts()
```

```
Out[29]: yes    225
         no      81
         Name: status, dtype: int64
```

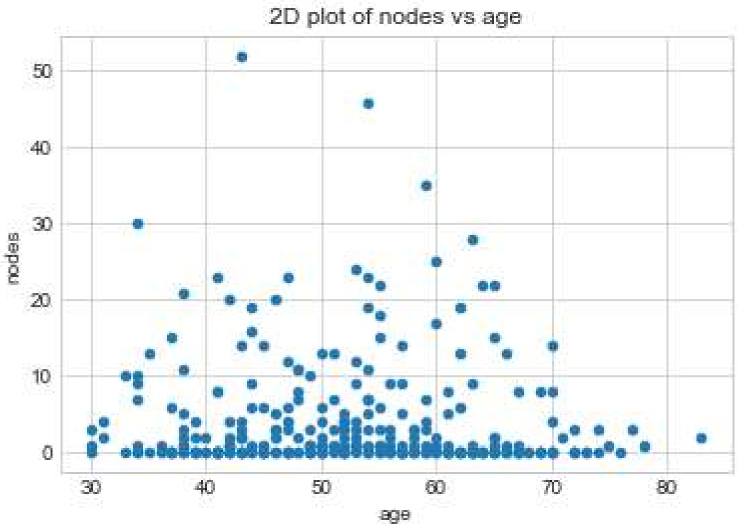
Observation:

- mapped status value from 1 to yes and 2 to no for better readability
- 225 patients survived 5 years or longer
- 81 patients could not survive 5 years or longer

2-D Scatter Plot

In [130]:

```
hbman.plot(kind='scatter', x='age', y='nodes')
plt.title('2D plot of nodes vs age')
plt.show()
```

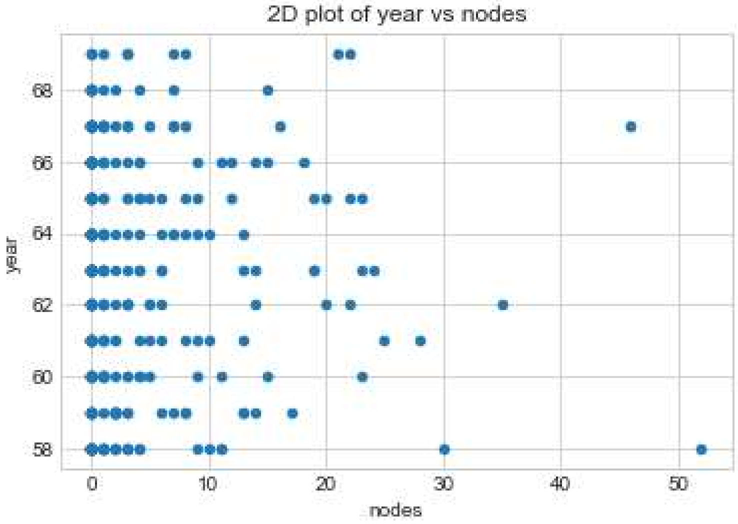


Observation:

- Cannot say anything from this plot as all ages of patients with similar axillary nodes detected survived 5 years or longer as well as died before 5 years

In [131]:

```
## pending
hbman.plot(kind='scatter', x='nodes', y='year')
plt.title('2D plot of year vs nodes')
plt.show()
```

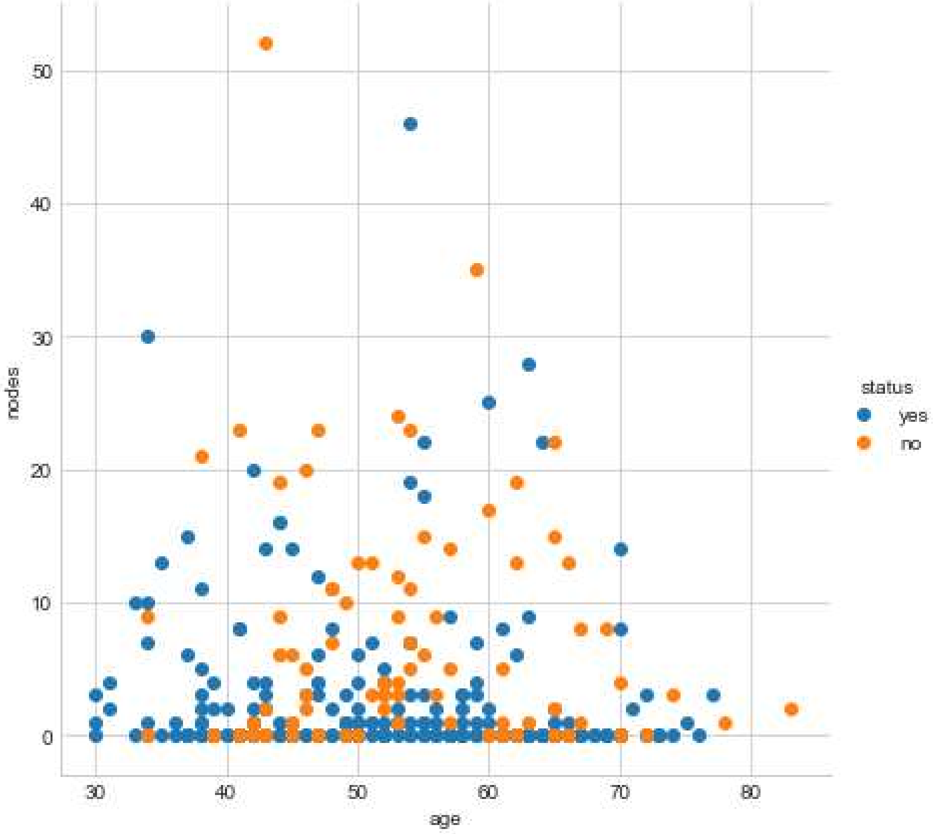


Observation:

- Cannot say much as patients with similar positive axillary nodes detected in all years, were able to survive 5 years or longer as well as almost half of them died before 5 years

In [137]:

```
sns.set_style("whitegrid");
sns.FacetGrid(hbman, hue="status", size=6) \
   .map(plt.scatter, "age", "nodes") \
   .add_legend();
plt.title('')
plt.show();
```

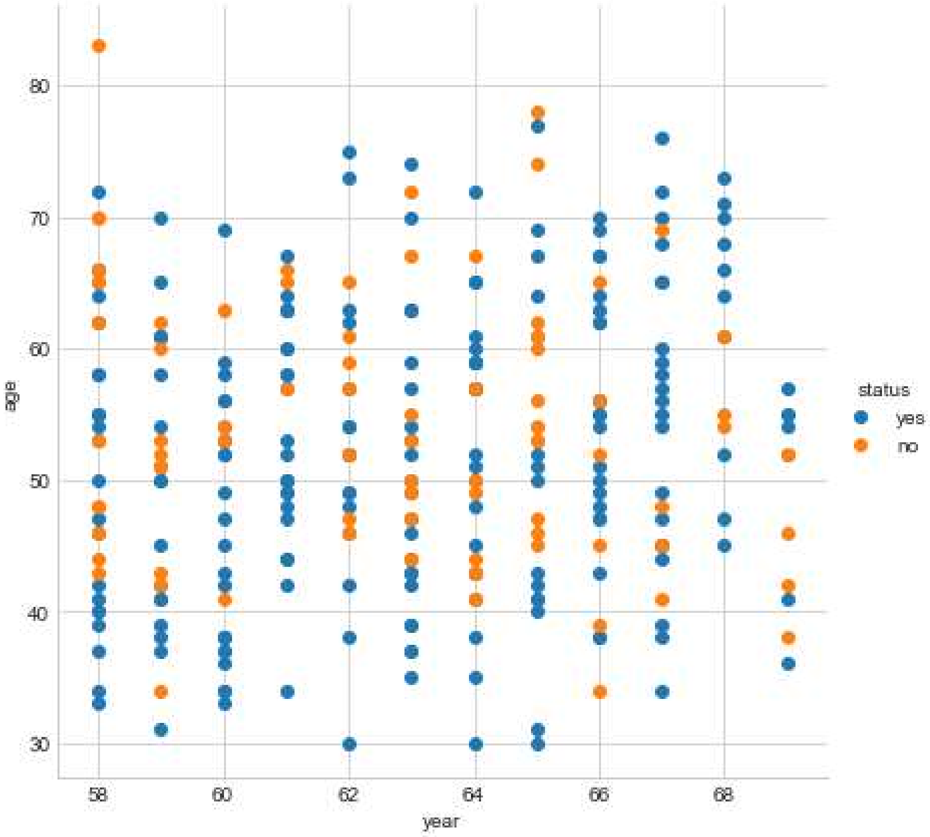


Observation:

- Using age and number of nodes detected features, we are able to differentiate between survival status based on colors but we are not able to separate the data points
- From scatterplot, we can see more blue points which is of survival status in range of age < 40 and nodes < 10. It can be said survival rate is higher in this region.

In [136]:

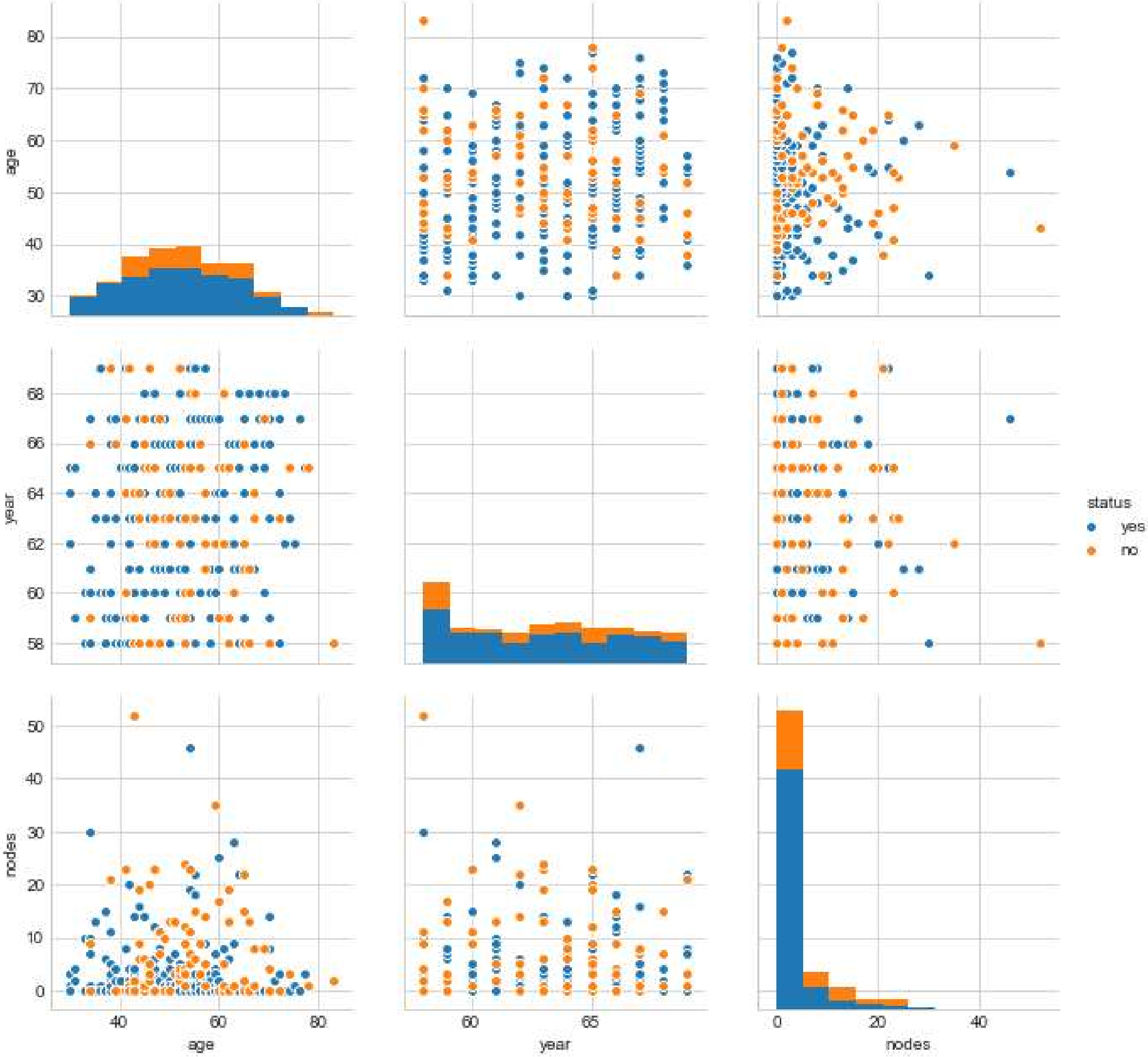
```
sns.set_style("whitegrid");
sns.FacetGrid(hbman, hue="status", size=6) \
   .map(plt.scatter, "year", "age") \
   .add_legend();
plt.title('')
plt.show();
```



Observation:

- It can be inferred that there are more blue points than orange points in year 60, 61, 67, and 68. It can be said that survival rate is higher in these years

In [139]:
```
plt.close();
sns.set_style("whitegrid");
sns.pairplot(hbman, hue="status", size=3);
plt.show()
```

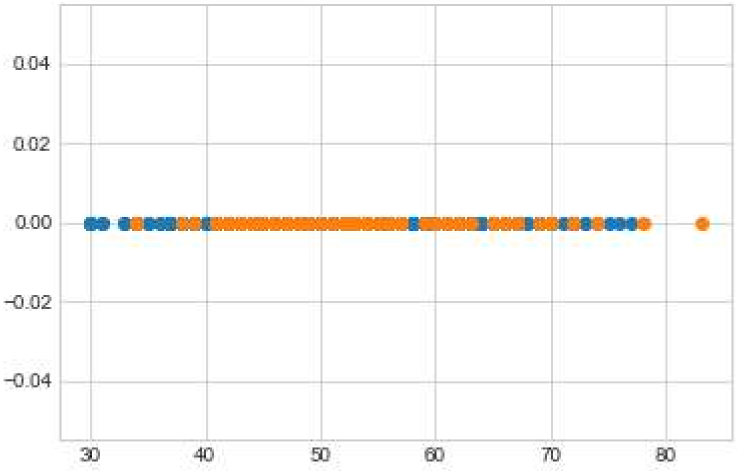


Observation:

- In none of the plots, we could separate survival patient's data points
- The diagonal plots are PDFs for each feature

Histogram, PDF, CDF

```
In [49]: import numpy as np
         status_yes = hbman.loc[hbman["status"] == "yes"];
         status_no = hbman.loc[hbman["status"] == "no"];
         #print(iris_setosa["petal_length"])
         plt.plot(status_yes["age"], np.zeros_like(status_yes['age']), 'o')
         plt.plot(status_no["age"], np.zeros_like(status_no['age']), 'o')
         plt.show()
```

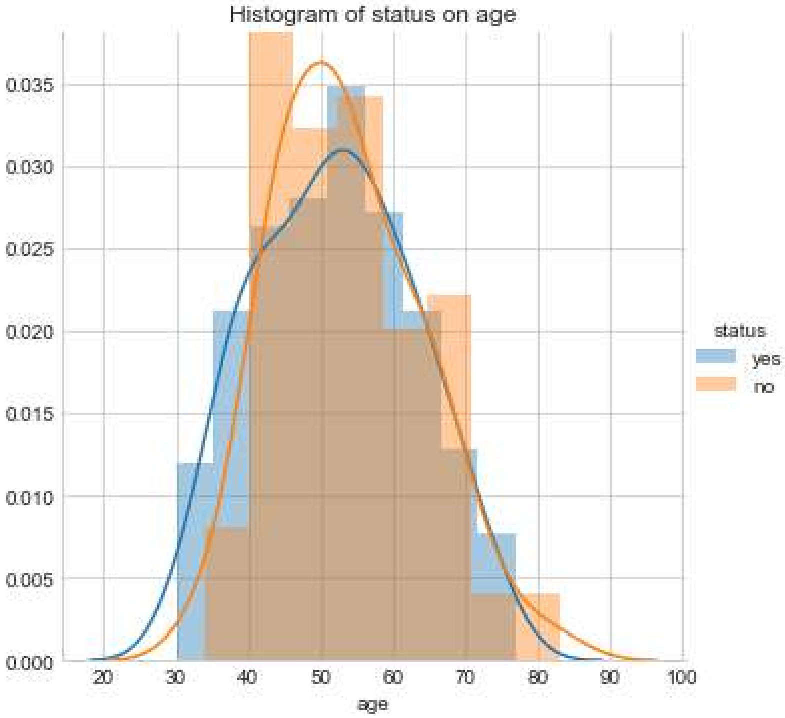


Observation:

- All the data points are scaled on the zero horizontal axis
- We can see few orange points on the line, but we are not sure if there are blue points beneath. Hence, we are not able to separate the data points based on this plot.

In [140]:
```
sns.FacetGrid(hbman, hue="status", size=5) \
   .map(sns.distplot, "age") \
   .add_legend();
plt.title('Histogram of status on age')
plt.show();
```

```
C:\Users\Pooja\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: Use
rWarning: The 'normed' kwarg is deprecated, and has been replaced by the 'den
sity' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\Pooja\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: Use
rWarning: The 'normed' kwarg is deprecated, and has been replaced by the 'den
sity' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
```



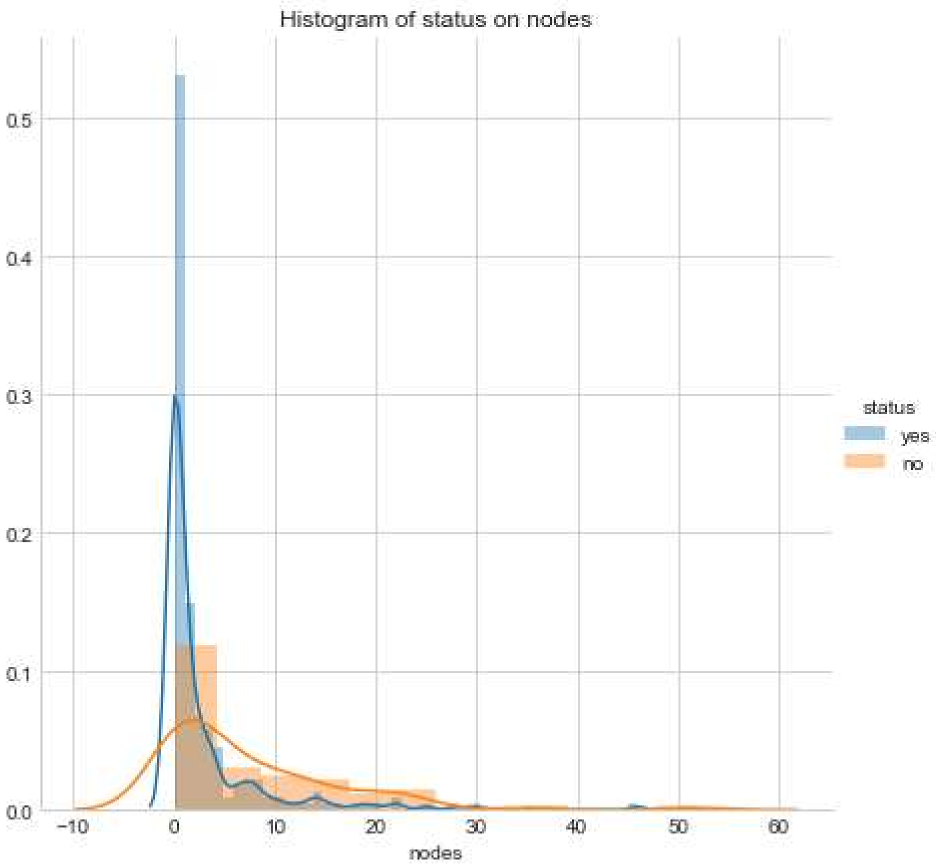
Observation:

- Based on age, it can be seen that patients between age of 40 and 60 have survived the most.

In [142]:

```
sns.FacetGrid(hbman, hue="status", size=6) \
   .map(sns.distplot, "nodes") \
   .add_legend();
plt.title('Histogram of status on nodes')
plt.show();
```

```
C:\Users\Pooja\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: Use
rWarning: The 'normed' kwarg is deprecated, and has been replaced by the 'den
sity' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\Pooja\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: Use
rWarning: The 'normed' kwarg is deprecated, and has been replaced by the 'den
sity' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
```



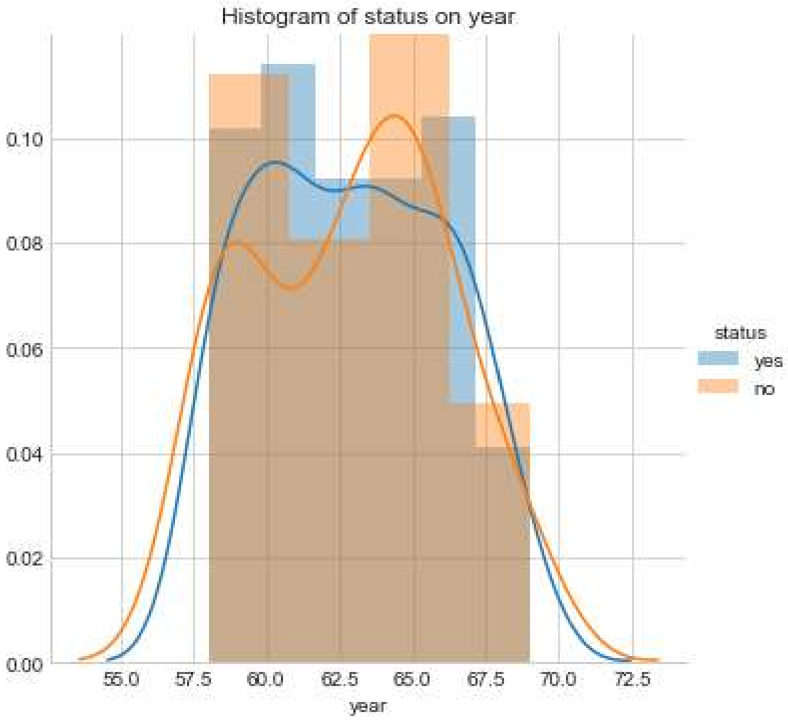
Observation:

- Based on nodes, it can be seen that patients that were detected with 0 positive axillary nodes have highest survival rate.

In [141]:

```
sns.FacetGrid(hbman, hue="status", size=5) \
   .map(sns.distplot, "year") \
   .add_legend();
plt.title('Histogram of status on year')
plt.show();
```

```
C:\Users\Pooja\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: Use
rWarning: The 'normed' kwarg is deprecated, and has been replaced by the 'den
sity' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\Pooja\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: Use
rWarning: The 'normed' kwarg is deprecated, and has been replaced by the 'den
sity' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
```



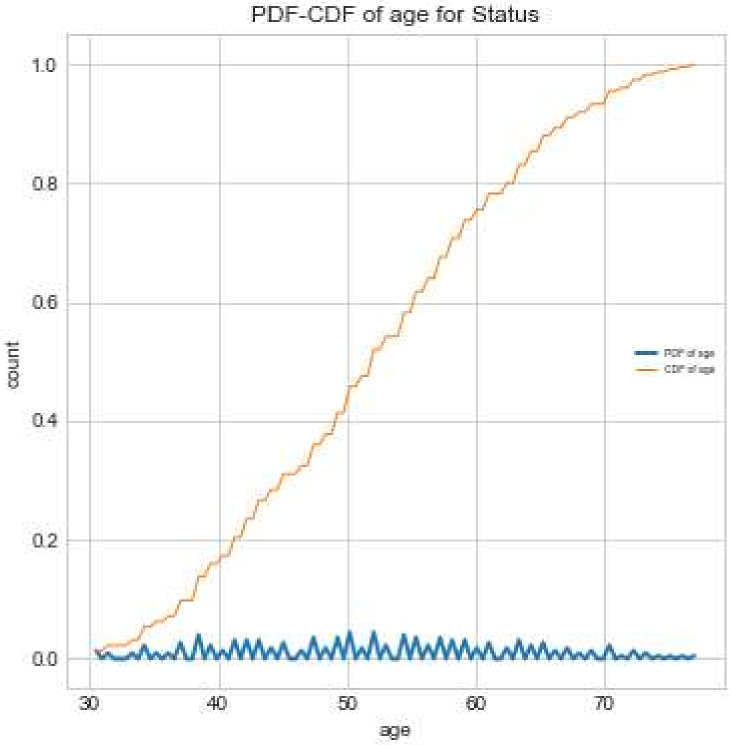
Observation:

- Based on year, it can be seen that patients survived the most in year 60
- The patients survived the least in year 63 to 66

PDF and CDF

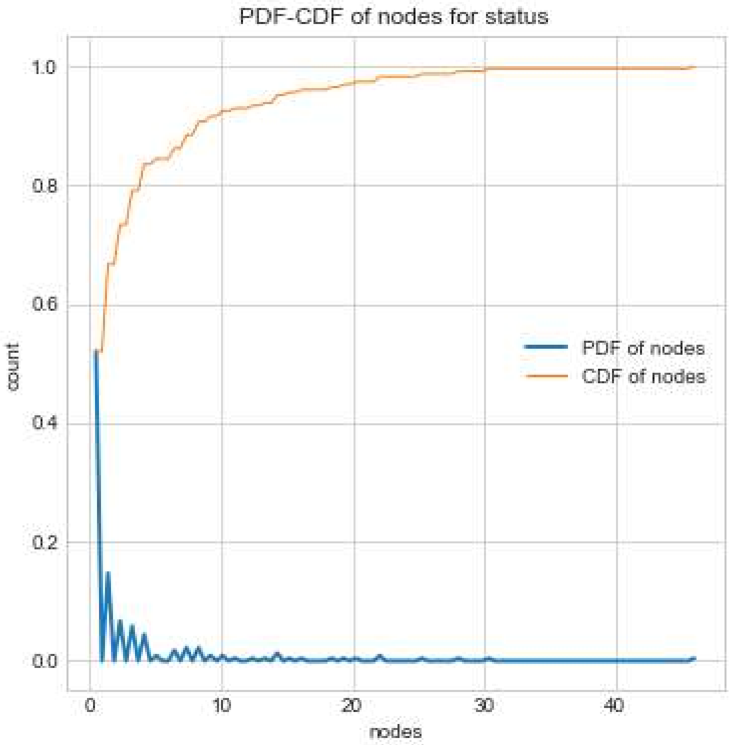
In [143]:

```
plt.figure(figsize=(20,6))
plt.subplot(131)
counts,bin_edges=np.histogram(status_yes["age"],bins=100,density=True)
pdf=counts/sum(counts)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,linewidth=2.0)
plt.plot(bin_edges[1:],cdf,linewidth=1.0)
plt.xlabel('age')
plt.ylabel("count")
plt.title('PDF-CDF of age for Status')
plt.legend(['PDF of age', 'CDF of age'], loc = 5,prop={'size': 5})
plt.show()
```



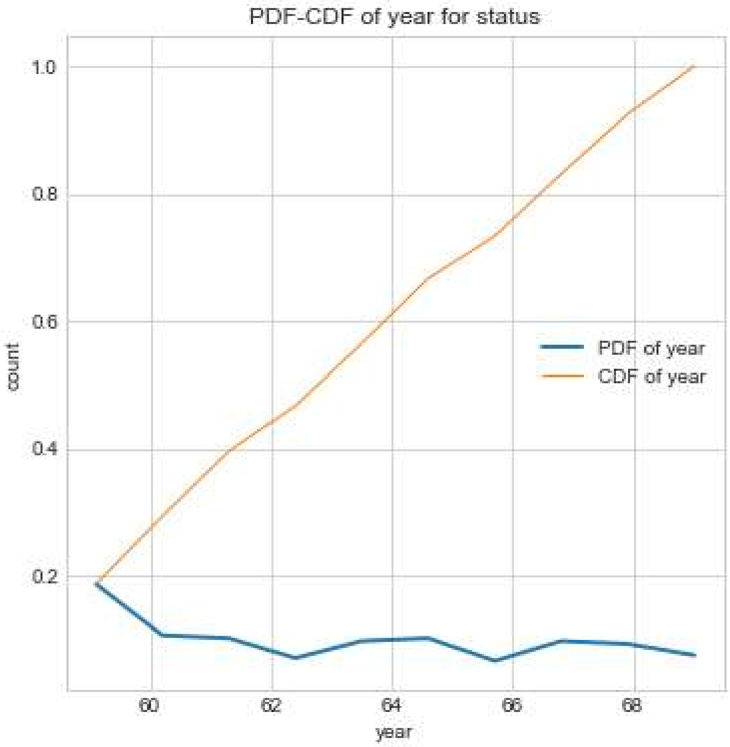
In [144]:

```
plt.figure(figsize=(20,6))
plt.subplot(131)
counts,bin_edges=np.histogram(status_yes['nodes'], bins=100, density=True)
pdf=counts/sum(counts)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,linewidth=2.0)
plt.plot(bin_edges[1:],cdf,linewidth=1.0)
plt.xlabel('nodes')
plt.ylabel('count')
plt.title('PDF-CDF of nodes for status')
plt.legend(['PDF of nodes','CDF of nodes'], loc=5, prop={'size':10})
plt.show()
```



In [145]:

```
plt.figure(figsize=(20,6))
plt.subplot(131)
counts,bin_edges=np.histogram(status_yes['year'], bins=10, density=True)
pdf=counts/sum(counts)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,linewidth=2.0)
plt.plot(bin_edges[1:],cdf,linewidth=1.0)
plt.xlabel('year')
plt.ylabel('count')
plt.title('PDF-CDF of year for status')
plt.legend(['PDF of year','CDF of year'], loc=5, prop={'size':10})
plt.show()
```



Observation:

- There are majority of patients with number of detected nodes are <= 10

Mean, Variance and Std-dev

In [103]:

```
print("Means:")
print(np.mean(status_yes["age"]))
print(np.mean(status_yes["nodes"]))
#Mean with an outlier.
print(np.mean(np.append(status_yes["age"],2)));
print(np.mean(status_no["age"]))
print(np.mean(status_no["nodes"]))

print("\nStd-dev:");
print(np.std(status_yes["age"]))
print(np.std(status_yes["nodes"]))
print(np.std(status_no["age"]))
print(np.std(status_no["nodes"]))
```

```
Means:
52.01777777777778
2.7911111111111113
51.796460176991154
53.67901234567901
7.45679012345679

Std-dev:
10.98765547510051
5.857258449412131
10.10418219303131
9.128776076761632
```

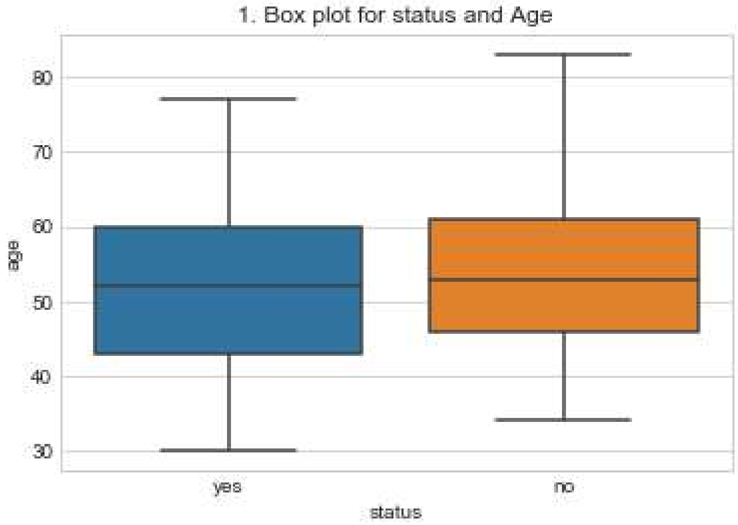
Median, Percentile, Quantile, IQR, MAD

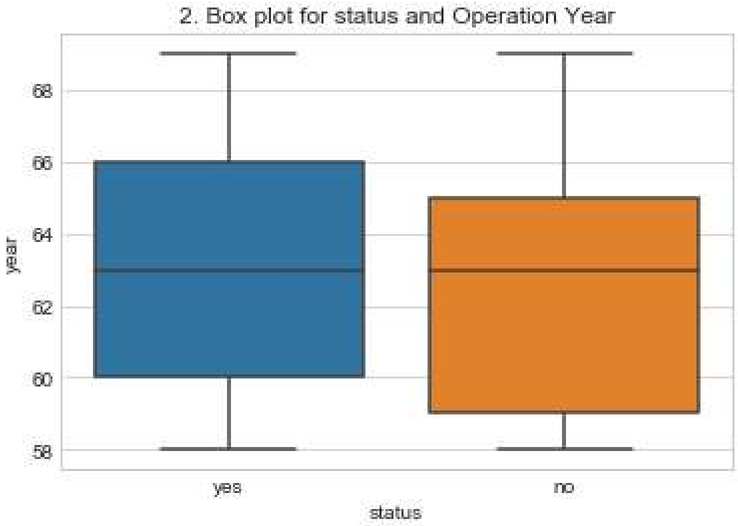
In [108]:

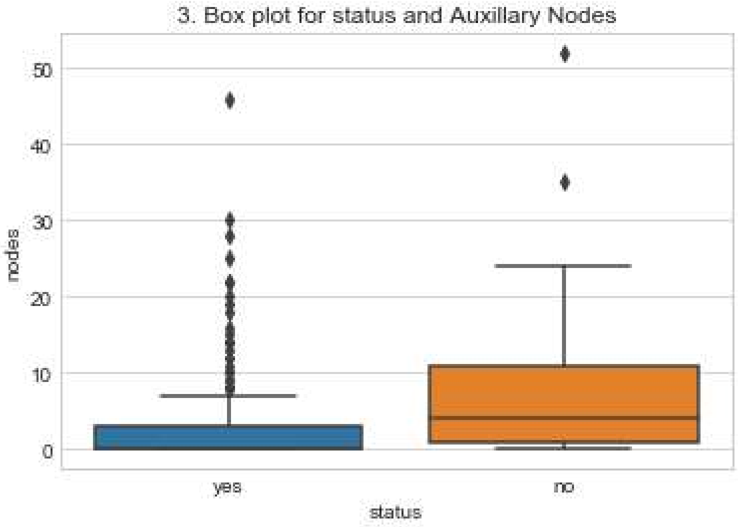
```
print("\nMedians:")
print(np.median(status_yes["age"]))
#Median with an outlier
print(np.median(np.append(status_yes["age"],50)));
print(np.median(status_no["age"]))


print("\nQuantiles:")
print(np.percentile(status_yes["age"],np.arange(0, 100, 25)))
print(np.percentile(status_no["age"],np.arange(0, 100, 25)))

print("\n90th Percentiles:")
print(np.percentile(status_yes["age"],90))
print(np.percentile(status_no["age"],92))

from statsmodels import robust
print ("\nMedian Absolute Deviation")
print(robust.mad(status_yes["age"]))
print(robust.mad(status_no["age"]))
```

```
Medians:
52.0
52.0
53.0

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

90th Percentiles:
67.0
68.20000000000002

Median Absolute Deviation
13.343419966550417
11.860817748044816
```

```
In [128]: sns.boxplot(x = "status" , y = "age", data = hbman )
          plt.title("1. Box plot for status and Age")
          plt.show()

          sns.boxplot(x = "status" , y = "year", data = hbman )
          plt.title("\n2. Box plot for status and Operation Year")
          plt.show()

          sns.boxplot(x = 'status', y = 'nodes', data = hbman)
          plt.title("\n3. Box plot for status and Auxillary Nodes")
          plt.show()
```


1. Box plot for status and Age
80
70
60
50
40
30
age
yes
no
status


2. Box plot for status and Operation Year
68
66
64
62
60
58
year
yes
no
status

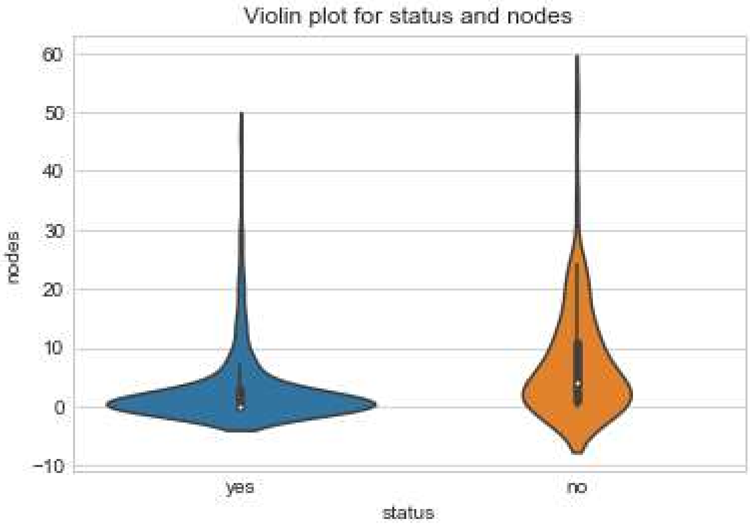

3. Box plot for status and Auxillary Nodes
50
40
30
20
10
0
nodes
yes
no
status

Observation:

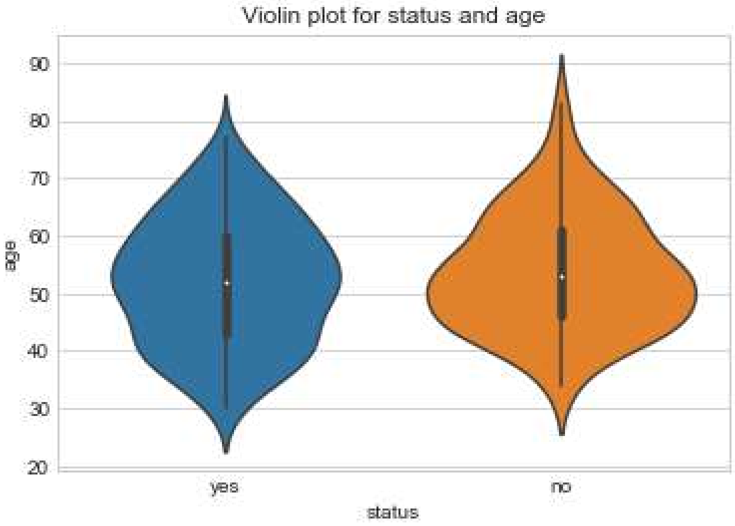
- In boxplot 3, it can be seen that as the number of nodes increases, the chances of dying increases.
- In boxplot 1, it can be said that there is a chance of death only for the patients of age more than 35 and there is no chance of survival for the patients with age more than 77.
- In boxplot 1, it can be inferred that the patients of age between 40 and 60 have survived the most as interquantile range exists in this range.

Violin plots

In [115]:
```
sns.violinplot(x="status", y="nodes", data=hbman)
plt.title('Violin plot for status and nodes')
plt.show()
```



```
In [116]: sns.violinplot(x='status', y='age', data=hbman)
          plt.title('Violin plot for status and age')
          plt.show()
```

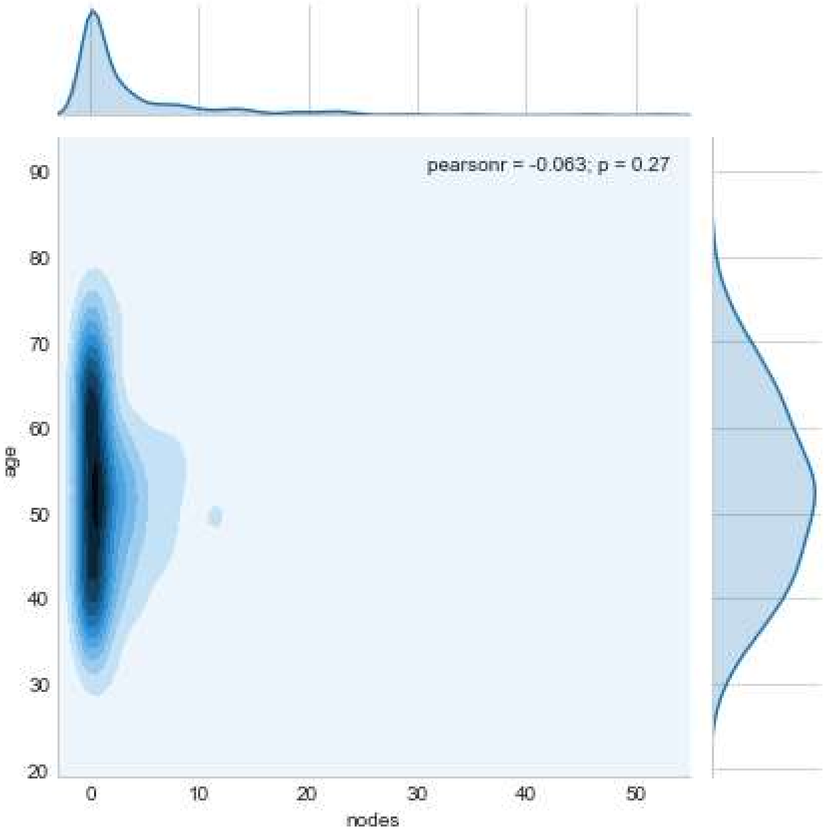


Observation:

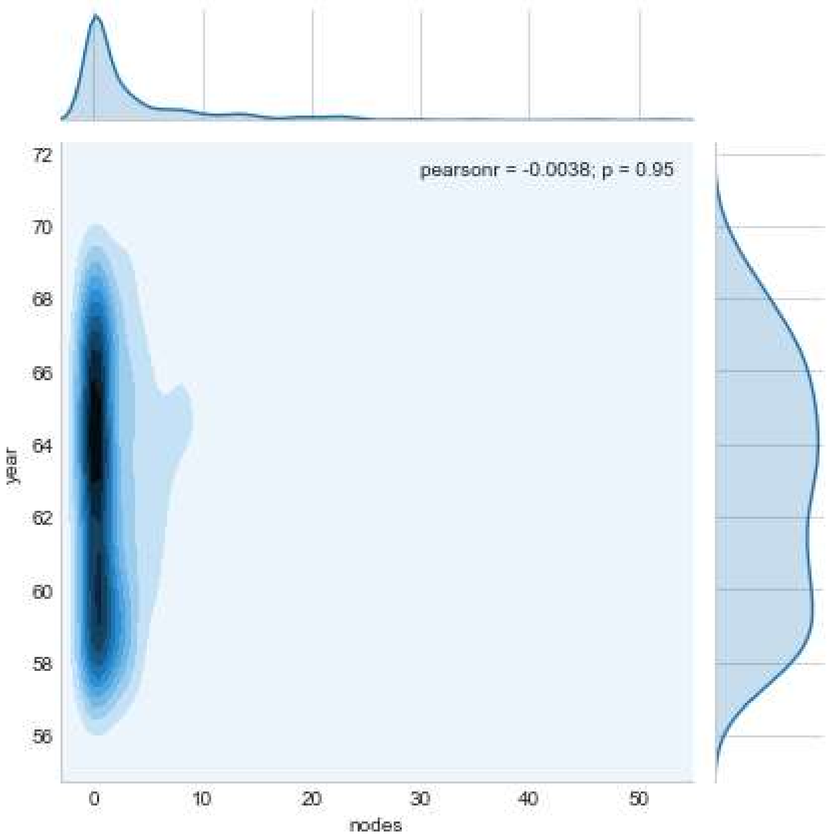
- The violin plots are similar as box plot, just has a smooth curve at the interquantile range.

Contour Plot

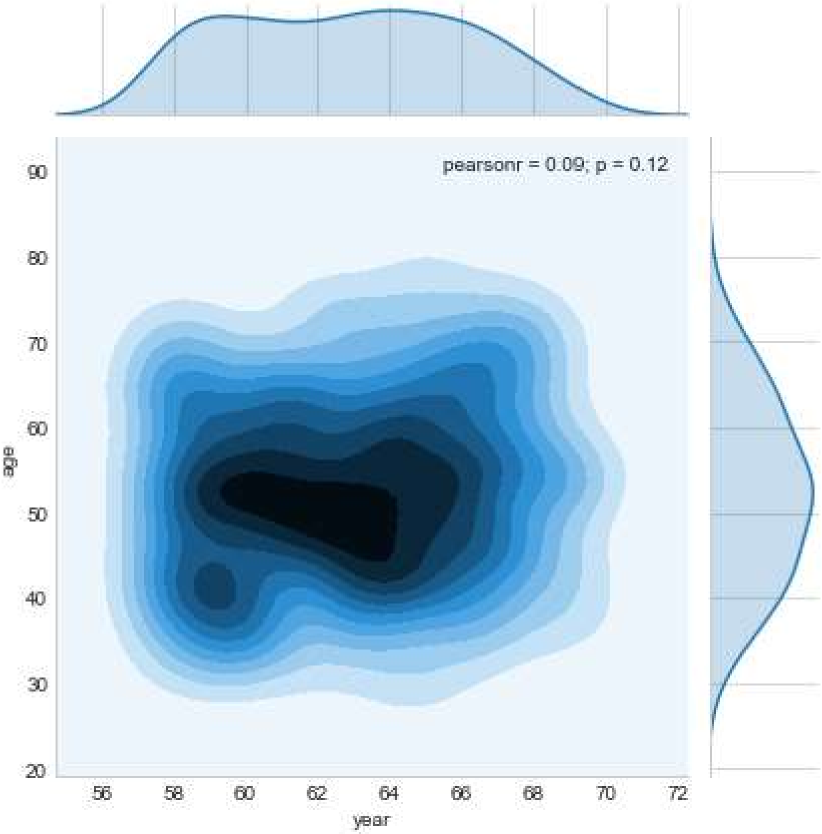
In [146]:
```
sns.jointplot(x='nodes', y='age', data=hbman, kind='kde')
plt.show()
```



In [147]:
```
sns.jointplot(x='nodes', y='year', data=hbman, kind='kde')
plt.show()
```



```
In [148]: sns.jointplot(x='year', y='age', data=hbman, kind='kde')
          plt.show()
```



FINAL OBSERVATIONS :

- Dataset is not balanced but there are no missing values, and hence, it is a complete dataset
- Class label 'status' is in integer form and needs to be converted into categorical values for better readability and understanding.
- Values in status are now labelled as yes & no, saying "yes" as survived and "no" as Not Survived.
- Survival rate is higher in range between age < 40 and nodes < 10
- Operation year 60, 61, 67, and 68 have more survival rate.
- Patients with age in between 40 and 60 have survived the most.
- Based on year, it can be seen that patients survived the most in year 60
- The patients survived the least in year 63 to 66
- Based on nodes, it can be seen that patients that were detected with 0 positive axillary nodes have highest survival rate.
- There are majority of patients with number of detected nodes are <= 10
- It can be said that there is a chance of death only for the patients of age more than 35 and there is no chance of survival for the patients with age more than 77.
- As the number of nodes increases, the chances of dying increases.
- We can conclude from the pairplots that data points of survival status are not separable by simply drawing a line.