Exploratory Data Analysis on Haberman's Dataset

About Haberman's dataset

References:

https://www.kaggle.com/gilsousa/habermans-survival-data-set

https://github.com/Kurian-lalan/EDA-on-haberman-survival-dataset/blob/master/EDA_Assignment.ipynb

Information about dataset :

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.

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 year

In [1]:

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

In [2]:

```
# Import data as csv file and put it into dataframe
```

```
haberman = pd.read_csv('haberman.csv')
```

In [3]:

```
print('Column names:')
print(haberman.columns)
```

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

In [4]:

```
print('Some of the datapoints are:')
print(haberman.head(10))
print(haberman.tail(10))
```

```
Some of the datapoints are:
   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
5   33    58     10       1
6   33    60      0       1
7   34    59      0       2
8   34    66      9       2
9   34    58     30       1
     age  year  nodes  status
296   72    67      3       1
297   73    62      0       1
298   73    68      0       1
299   74    65      3       2
300   74    63      0       1
301   75    62      1       1
302   76    67      0       1
303   77    65      3       1
304   78    65      1       2
305   83    58      2       2
```

In [5]:

```
print("The number of data points and features respectievely:" , haberma
n.shape)
```

```
print("\n")
print("Data points per class:")
print(haberman['status'].value_counts())
```

```
The number of data points and features respectievely: (306, 4)


Data points per class:
1    225
2     81
Name: status, dtype: int64
```

Observations:

1. As per the dataset, 'status' is the class label which can take 2 values; 1 and 2. Status 1 represents the patients who survived more than 5 years after the surgery and status 2 represents the patients who survived less than 5 years after the surgery.
2. There are 225 datapoints for class 1 and 81 datapoints for class 2. Since there is substantial difference in the count, we can infer that it is an imbalanced dataset.

Objective:

The objective of Haberman's dataset analysis is to predict whether the patient will survive more than 5 years or not given the patient’s age, year of treatment and the number of positive auxillary lymph nodes.

In [6]:

```
hb_survived = haberman.loc[haberman['status'] == 1]
hb_died = haberman.loc[haberman['status'] == 2]

print('Basic statistics about patients who survived 5 years or longer a
fter operation:\n')
print(hb_survived.describe())

print('\n\nBasic statistics about patients who died within 5 years afte
r operation:\n')
print(hb_died.describe())
```

```
Basic statistics about patients who survived 5 years or longer after op
eration:

              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


Basic statistics about patients who died within 5 years after operatio
n:

             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
```

Observations based on the basic statistics:

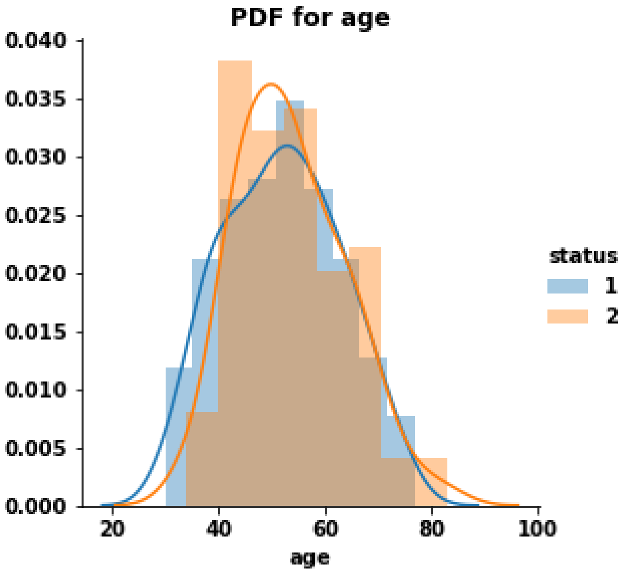
1. The statistics for age and year are more or less similar for both the survival statuses. But we can see notable difference in number of nodes for status 1 and 2.
2. For the patients who survived more than 5 years, 75% patients are having nodes less than or equal to 3. On the other hand, 25% of the patients of class 2 have number of nodes less than or equal to 1 but still they didn't survive more than 5 years.

Univariate Analysis

(1) Based on age of the patient

1. Histogram with PDF

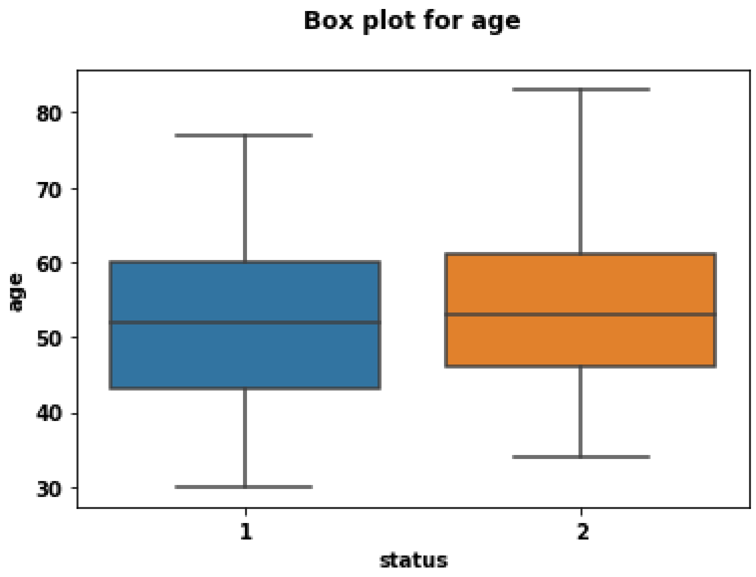
```
In [7]: plt.close()
        sns.FacetGrid(haberman, hue = 'status', height = 4).map(sns.distplot,
        'age').add_legend()
        plt.title('PDF for age')
        plt.show()
```



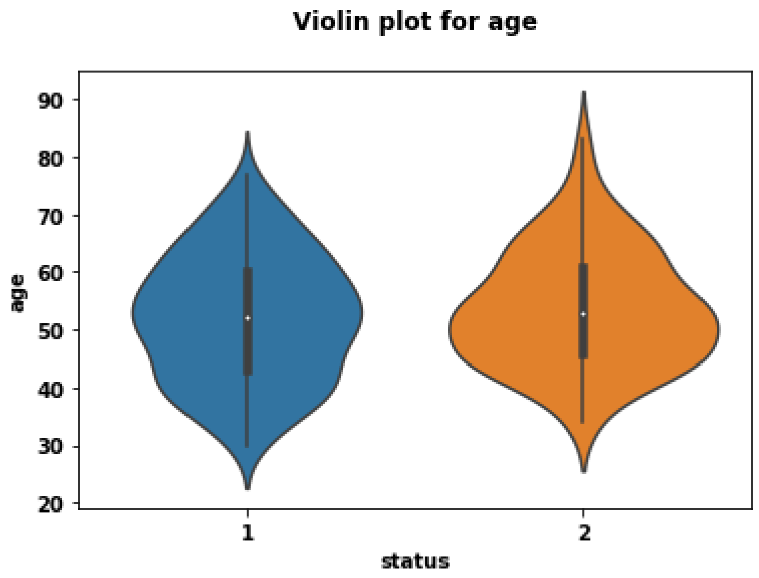
2. Boxplot and Violin plot

```
In [8]: sns.boxplot(x='status', y='age', data= haberman)
```

```
plt.title('Box plot for age\n')
plt.show()
```



In [9]:
```
sns.violinplot(x='status', y='age', data= haberman)
plt.title('Violin plot for age\n')
plt.show()
```



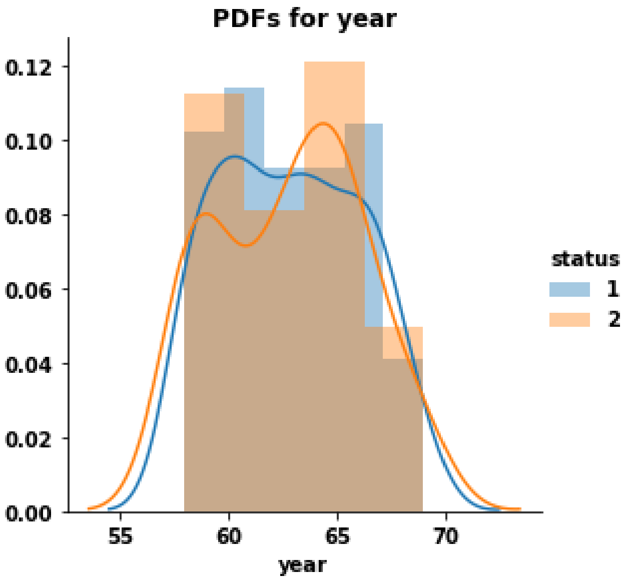
Observations:

1. There is a huge overlap between pdfs of class 1 and 2 considering age as the parameter.
2. The plots are very similar for both the classes.
3. Thus, age alone can't decide the survival status.

(2) Based on year of operation

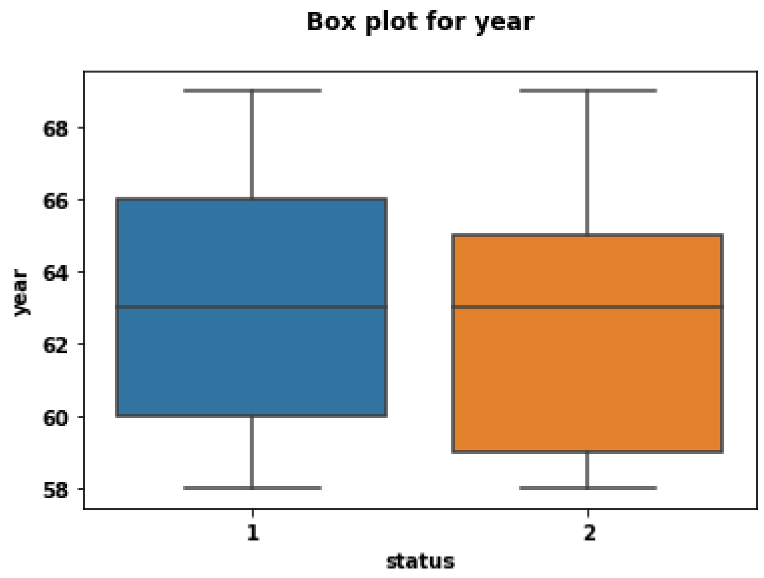
1. Histogram with PDF

In [10]:
```
plt.close()
sns.FacetGrid(haberman, hue = 'status', height = 4).map(sns.distplot,
'year').add_legend()
plt.title('PDFs for year')
plt.show()
```

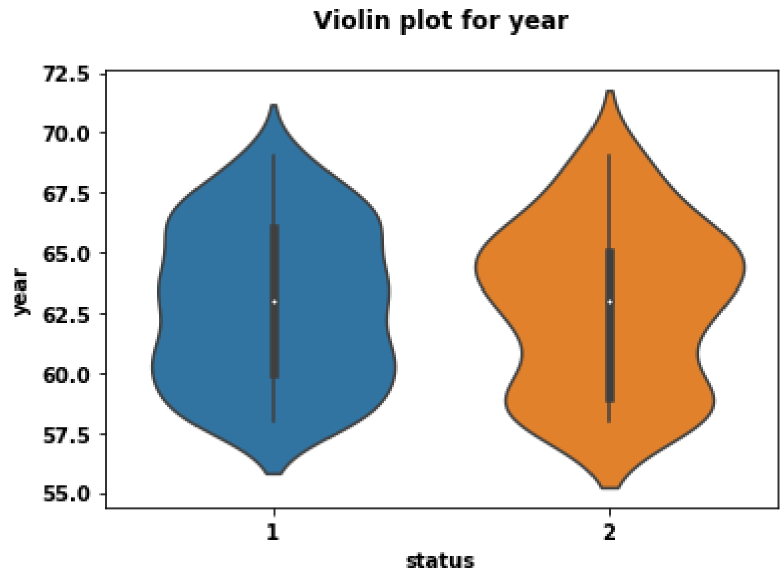


2. Boxplot and Violin plot

```
In [11]: sns.boxplot(x='status', y='year', data= haberman)
         plt.title('Box plot for year\n')
         plt.show()
```



In [12]:
```
sns.violinplot(x='status', y='year', data= haberman)
plt.title('Violin plot for year\n')
plt.show()
```



Observations:

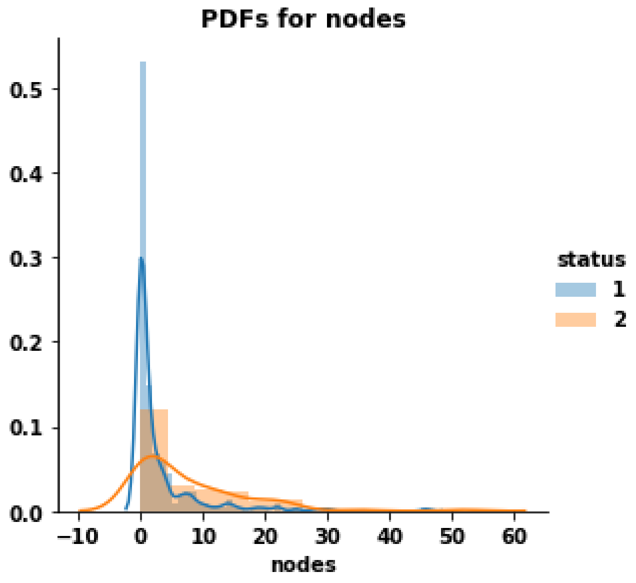
1. There is a huge overlap between pdfs of class 1 and 2 considering year as the parameter.
2. Thus, year alone can't decide the survival status.

(3) Based on number of positive lymph nodes

1. Histogram with PDF

In [13]:

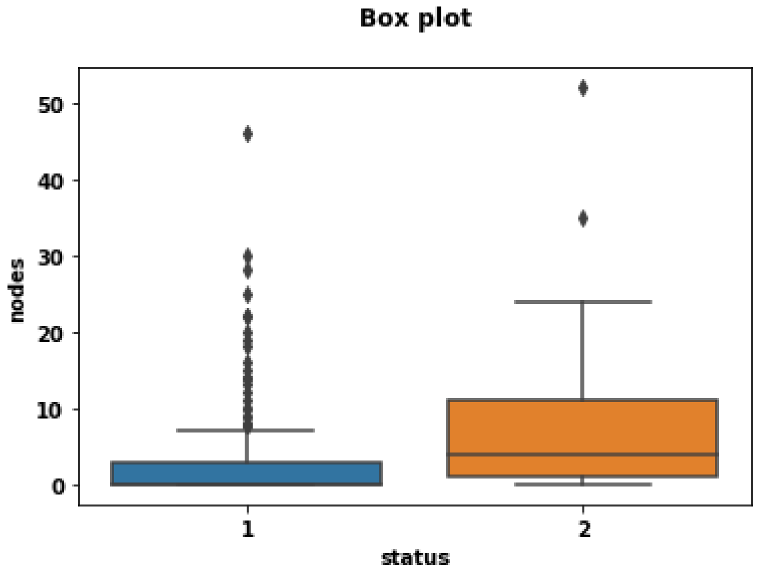
```
plt.close()
sns.FacetGrid(haberman, hue = 'status', height = 4).map(sns.distplot,
'nodes').add_legend()
plt.title('PDFs for nodes')
plt.show()
```



2. Boxplot and Violin plot

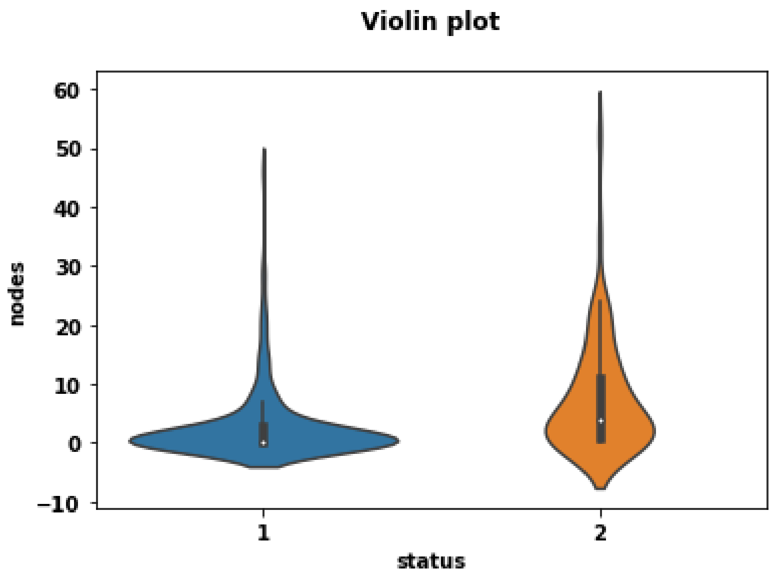
In [14]:

```
sns.boxplot(x='status', y='nodes', data= haberman)
plt.title('Box plot\n')
plt.show()
```



In [15]:

```
sns.violinplot(x='status', y='nodes', data= haberman)
plt.title('Violin plot\n')
plt.show()
```



Observations:

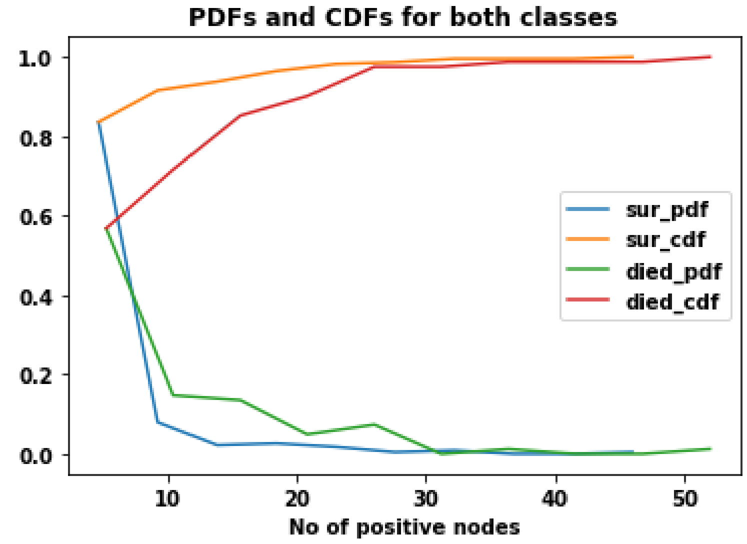
1. Even though there is overlap between 2 classes while ploting based on nodes, the overlap is less compared to other features.
2. Large number of patients with 0 nodes have survived more than 5 years
3. As number of positive axillary nodes increase the chance of survival decreases

Plotting cdf and pdf considering nodes as the parameter for more quantitative analysis

In [16]:

```
counts, bin_edges = np.histogram(hb_survived['nodes'], bins=10, density = True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
```

```
counts, bin_edges = np.histogram(hb_died['nodes'], bins=10, density = True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:] ,cdf)
plt.legend(['sur_pdf', 'sur_cdf','died_pdf', 'died_cdf'])
plt.xlabel('No of positive nodes')
plt.title('PDFs and CDFs for both classes')
plt.show()
```



Observations:

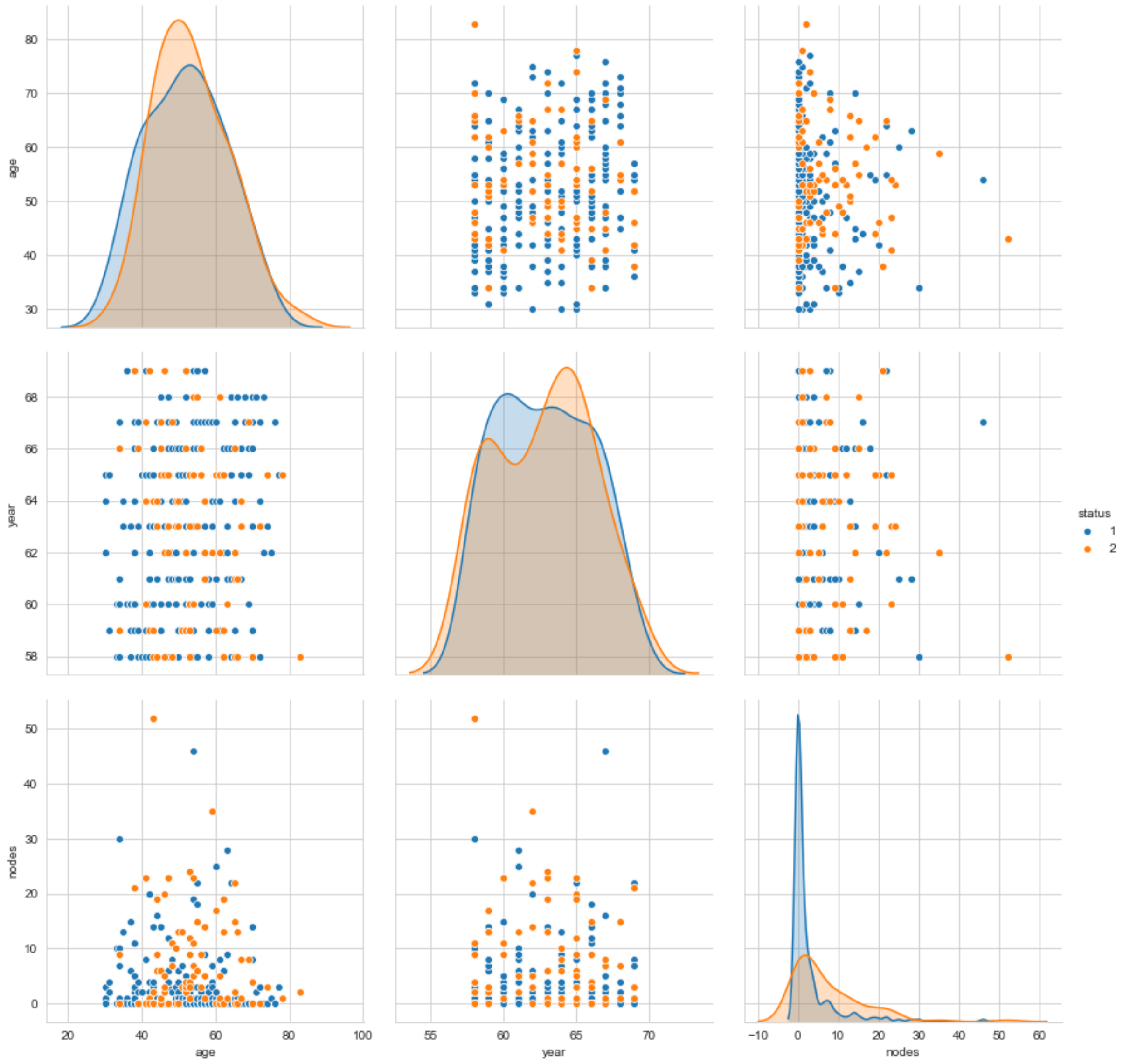
1. 83% of survived patients have 0 positive nodes. But 55% of died patients also have 0 positive nodes.
2. Thus, thus absence of positive axillary nodes cannot always guarente survival.

Bivariate analysis

Pair plot

In [17]:

```
plt.close()
sns.set_style('whitegrid')
sns.pairplot(haberman, hue = 'status', height = 4, vars = ['age', 'year', 'nodes'])
plt.show()
```



Observations:

1. We can say that the chances of survival for a patient are more in case age is less than 40 years and number of positive nodes are less than 20.
2. In general, it is difficult to classify a patient considering only the given features

Conclusions:

1. As the number of positive auxillary nodes increase the chance of survival of patient decreases; but at the same time, having zero postivie axillary nodes does not guarentee survival as there are cases where patients with zero positive axillary nodes could not survive 5 years from the time of operation.
2. Even if we could come up with a simple model which could predict the survival of a patient based on the insights we got, the chance of misclassification is high.
3. The objective of classifying the survival status of a new patient based on given features is a difficult task.