Assignment1_Haberman's_Survival_Data_Set

1.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.

2.In this assignment I am trying to show different plotting techniques and their observations

Brief about Dataset

1.Dataset has four features a)age b)year c)nodes d)status

2.age feature shows age of pateint,Year shows at which year operation is performed,nodes shows number of lymph nodes removed during surgery,status shows the patient survived 5 years or longer

Domain knowledge

1. lymph node.

Ans: Lymph nodes are major sites of B and T lymphocytes, and other white blood cells. Lymph nodes are important for the proper functioning of the immune system, acting as filters for foreign particles and cancer cells. Lymph nodes do not have a detoxification function, which is primarily dealt with by the liver and kidneys[1]

2. Why to remove lymph node

Ans: If breast cancer spreads, it typically goes first to nearby lymph nodes. Knowing whether the cancer has spread to your lymph nodes helps medical providers find the best way to treat your cancer. If you have been diagnosed with breast cancer, it’s important to find out how far the cancer has spread. To help find out if the cancer has spread beyond the breast, one or more of the lymph nodes under the arm (axillary lymph nodes) are removed[2]

Basic statistics on dataset

In [3]:

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

'''downlaod haberman.csv from https://www.kaggle.com/gilsousa/habermans
-survival-data-set/version/1'''

#Load .csv into a pandas dataFrame.

hdata = pd.read_csv("haberman.csv")
print("first 3 rows data of dataset")
print("="*100)
hdata.head(3)
```

```
first 3 rows data of dataset
=======================================================================
=============================
```

Out[3]:

	age	year	nodes	status
0	30	64	1	1
1	30	62	3	1
2	30	65	0	1

In [4]:

```
# finding number of rows and coumns in dataset with shape
print("Shape of dataset")
print("="*100)
print(hdata.shape)
```

```
Shape of dataset
=======================================================================
=============================
(306, 4)
```

In [4]:

```
#(Q) What are the column names in our dataset?
print("columns of dataset")
print("="*100)
print(hdata.columns)
```

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

In [5]:

```
#survival and death count  1 = the patient survived 5 years or longer 2
 = the patient died within 5 year
print("1 = the patient survived 5 years or longer 2 = the patient died
 within 5 year")
print("="*100)
print("75% of data shows survival patents and 25% of data shows usurviv
al of pateints ")
print("It is imbalanced dataset for predicting next case")
hdata.status.value_counts()
```

```
1 = the patient survived 5 years or longer 2 = the patient died within
5 year
=======================================================================
=============================
75% of data shows survival patents and 25% of data shows usurvival of p
ateints
It is imbalanced dataset for predicting next case
```

Out[5]:

```
1    225
```

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

In [5]:

```
hdata['status']=hdata.status.map({1:'yes',2:'no'}).astype('category')
print("first three columns of dataset after map")
print("="*100)
hdata.head(3)
```

```
first three columns of dataset after map
======================================================================
==============================
```

Out[5]:

	age	year	nodes	status
0	30	64	1	yes
1	30	62	3	yes
2	30	65	0	yes

In [7]:

```
#summary of data
print("summary of dataset")
print("="*100)
hdata.describe()
```

```
summary of dataset
======================================================================
==============================
```

Out[7]:

	age	year	nodes
count	306.000000	306.000000	306.000000
mean	52.457516	62.852941	4.026144
std	10.803452	3.249405	7.189654
min	30.000000	58.000000	0.000000
25%	44.000000	60.000000	0.000000

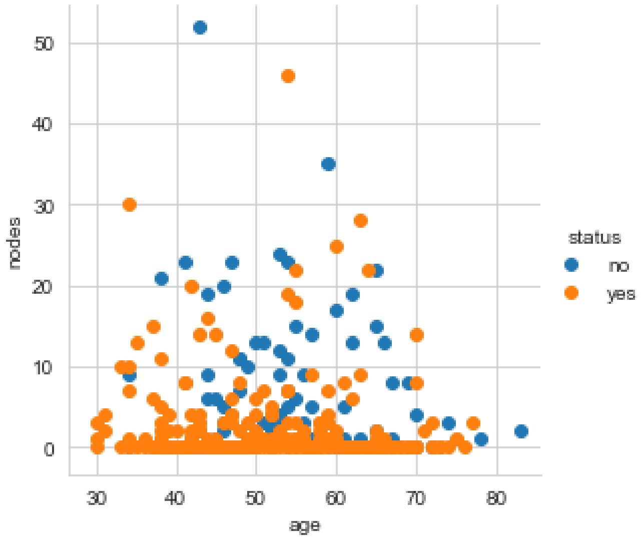
	age	year	nodes
50%	52.000000	63.000000	1.000000
75%	60.750000	65.750000	4.000000
max	83.000000	69.000000	52.000000

2-D Scatter Plot

In [8]:

```
#2 D scatter plot of eatures age and nodes
sns.set_style("whitegrid");
sns.FacetGrid(hdata, hue="status", height=4) \
   .map(plt.scatter, "age", "nodes") \
   .add_legend();
print("2D scatter plot ")
print("="*100)
plt.show();
```

```
2D scatter plot
=======================================================================
=============================
```



Observations from 2D scatter plot of age and nodes

1.There is considerable overlap .From plot we say that pateint having age less than 40 has equal chances of survival and unsurvival.

2.pateints who under gone for surgery but there were no lymph node removed from breast has high rate of survival.

Model 1.

if age<40 and nodes<=8 then survival after 5 and more

Model 2 (no limit for age)

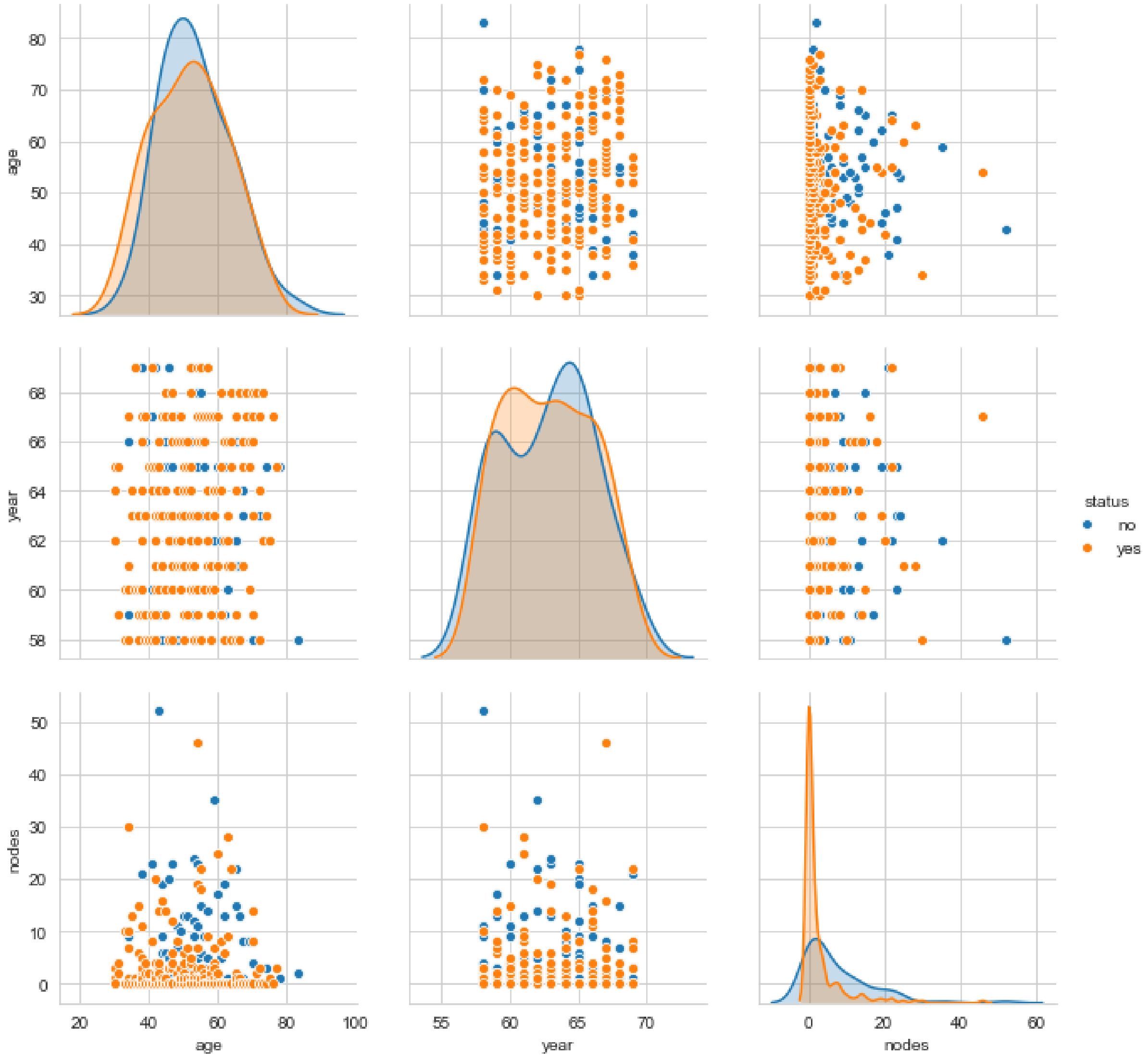
if nodes<=1 then survival after 5 and more

Pair-plot

In [42]:

```
plt.close();
sns.set_style("whitegrid");
sns.pairplot(hdata, hue="status", height=3);

print("2D scatter plot ")

print("="*100)

plt.show()
# NOTE: the diagnol elements are PDFs for each feature
```

```
2D scatter plot 
======================================================================
==============================
```



Observations from pair plot

1.There are considerable overlap in almost all plots.

2.From pair plot of year and nodes :we can find maximum survival of pateints with no or very less number of nodes

3.From pair plot of age and nodes :we can find maximum survival of pateints with no or very less number of nodes

4.We can find "if-else" conditions to build a simple model to classify based on number of nodes

5.From above pair plot we can say that "nodes" is important feature of dataset

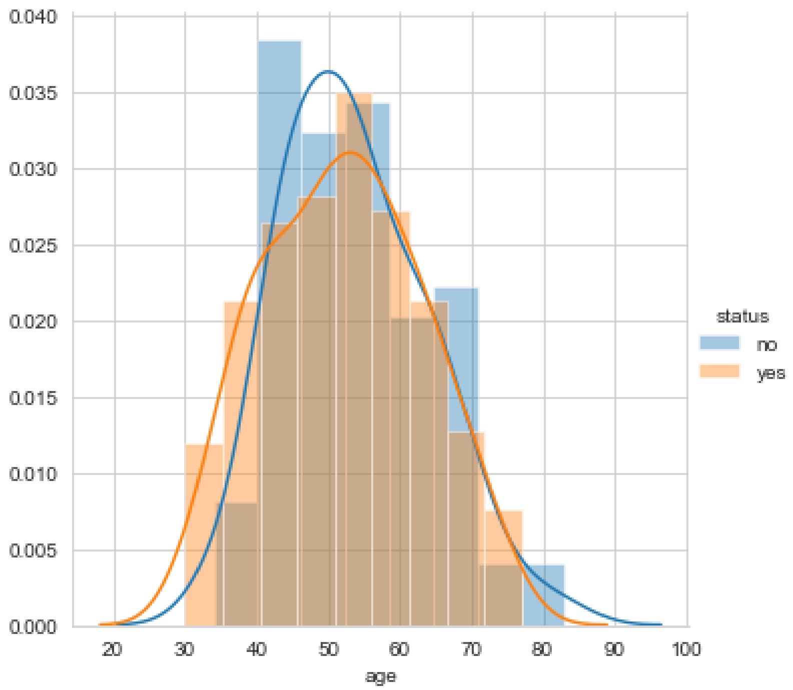
model 1 from pair plot of nodes and year

if nodes<=2 then survival after 5 and more

Univariant analysis,PDF

In [10]:

```
sns.FacetGrid(hdata, hue="status",height=5) \
   .map(sns.distplot, "age") \
   .add_legend();
plt.show();
```



Observations

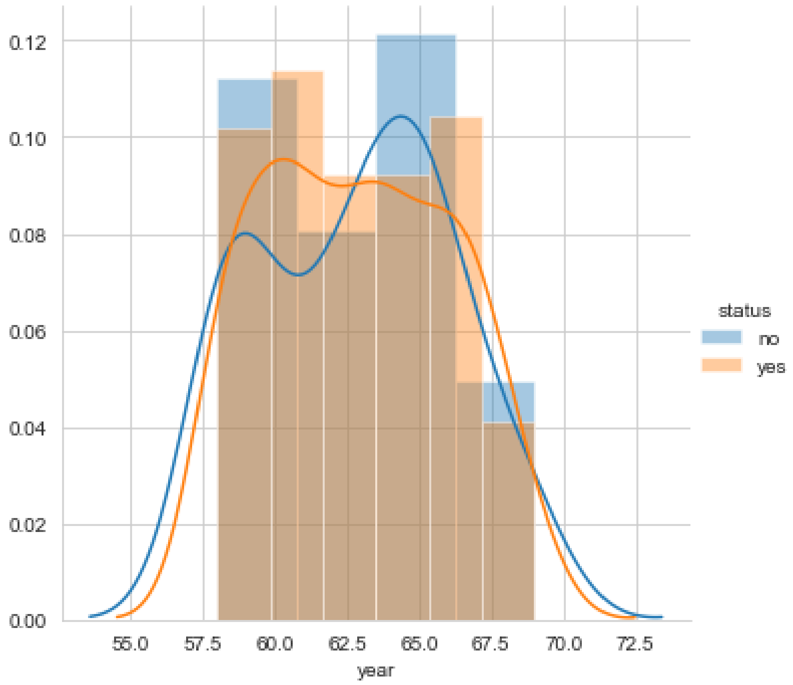
y axis shows count ,x axis shows the interested variable age

1.patents of age betwen 40 to 45 shows high number of patents who were not survived after 5 years.

2.patents of age betwen 50 to 55 shows high number of patents who were survived after 5 years.

3.There is massive overlap from approximetly age 35 to 75

In [11]:
```
sns.FacetGrid(hdata, hue="status",height=5) \
    .map(sns.distplot, "year") \
    .add_legend();
plt.show();
```



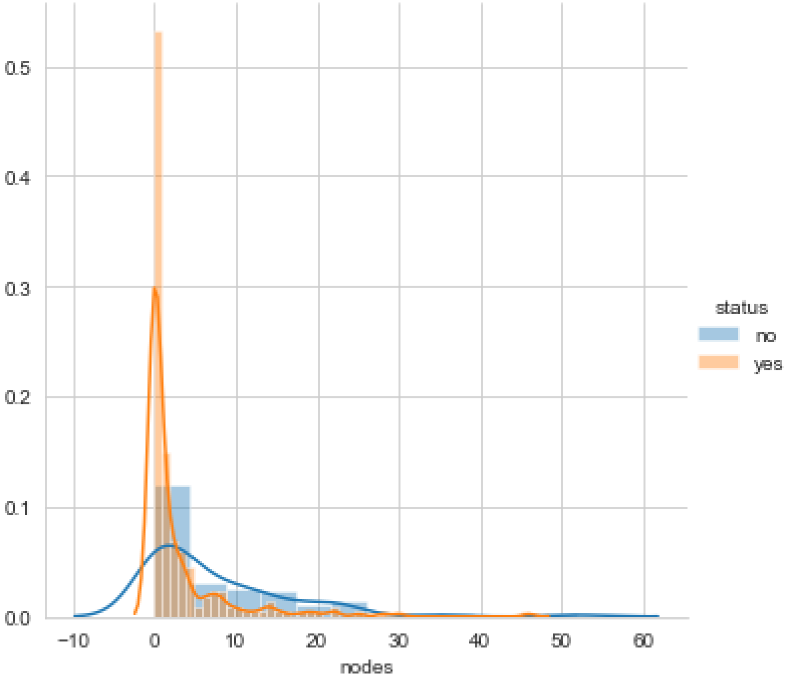
Observations

y axis shows count ,x axis shows the interested variable year

1. year approximately from 1964 to 1966 performed highest number of operations for patients who not survived after 5 years

1. year approximately from 1960 to 1963 performed highest number of operations for patients who survived after 5 years

```
In [12]: sns.FacetGrid(hdata, hue="status",height=5) \
            .map(sns.distplot, "nodes") \
            .add_legend();
         plt.show();
```



Observations

y axis shows count,x axis shows the interested variable nodes

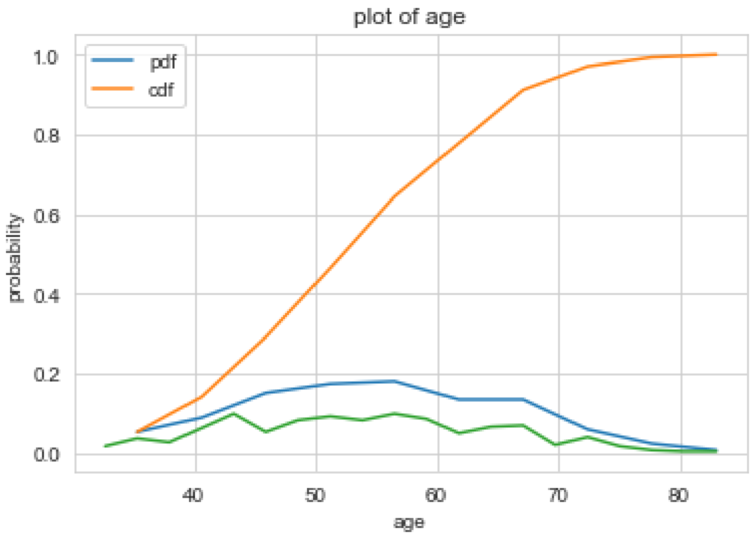
1. histogram bucket from 0 to 3 shows highest number of nodes found in survival patients.

Cumulative Distribution Function

In [51]:

```
#Plot CDF of age

counts, bin_edges = np.histogram(hdata['age'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges);
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)


counts, bin_edges = np.histogram(hdata['age'], bins=20,
                                 density = True)

pdf = counts/(sum(counts))
plt.plot(bin_edges[1:],pdf);
plt.title("plot of age")
plt.xlabel('age')
plt.ylabel('probability')
plt.legend(["pdf","cdf"])
plt.xlabel('age')
plt.ylabel('probability')
print("\nCDF and PDF of age:")
print("="*100)
plt.show();
```

```
[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. ]

CDF and PDF of age and status:
========================================================================
=============================
```



Observations

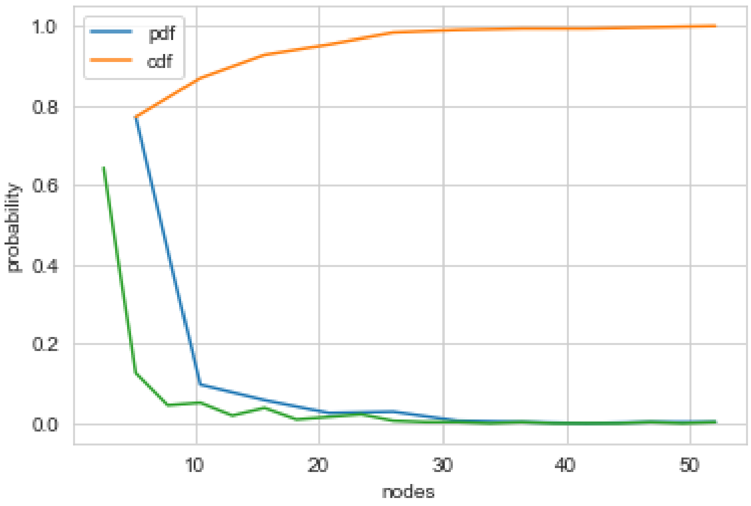
1.There are 19% of pateints having age in range of 50 to 60

2.There are 100% of pateints below age of 85

In [14]:
```
counts, bin_edges = np.histogram(hdata['nodes'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges);
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)


counts, bin_edges = np.histogram(hdata['nodes'], bins=20,
                                 density = True)
pdf = counts/(sum(counts))
```

```
plt.plot(bin_edges[1:],pdf);
plt.legend(["pdf","cdf"])
plt.xlabel('nodes')
plt.ylabel('probability')
print("\nCDF and PDF of nodes:")
print("="*100)

plt.show();
```

```
[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. ]
```



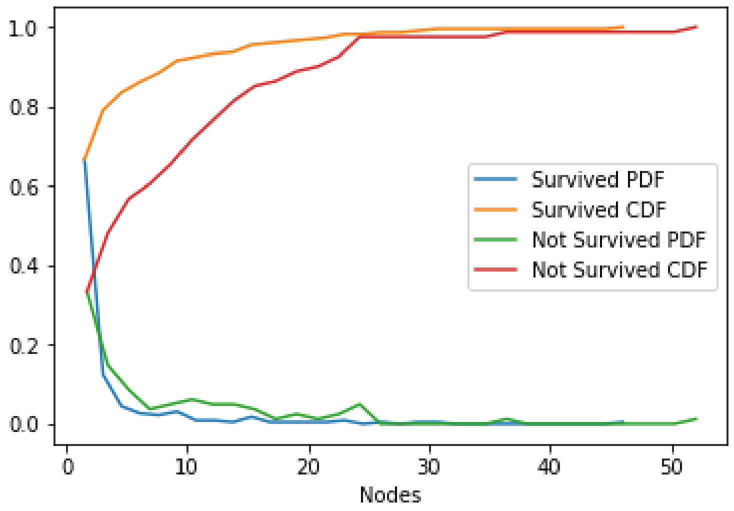
Observation

1.There are 98% of pateints having nodes less than 30

In [14]:
```
counts_Non, bin_edges_Non = np.histogram(Non_Survived["nodes"], bins=30
, density=True)
```

```
#PDF and CDF of survived
pdf_survived = counts/sum(counts)
cdf_survived = np.cumsum(pdf_survived)

#PDFand CDF of non survived
pdf_Non_survived = counts_Non/sum(counts_Non)
cdf_Non_survived = np.cumsum(pdf_Non_survived)

# Plot survived and non survived PDF, CDF in a single plot
plt.plot(bin_edges[1:], pdf_survived)
plt.plot(bin_edges[1:], cdf_survived)
plt.plot(bin_edges_Non[1:], pdf_Non_survived)
plt.plot(bin_edges_Non[1:], cdf_Non_survived)
#plt.xticks(np.linspace(0,50,13))
print("\nSurvived and unsurvived CDF and PDF based on  nodes:")

print("="*100)



plt.xlabel("Nodes")

plt.legend(["Survived PDF", "Survived CDF", "Not Survived PDF", "Not Su
rvived CDF" ])
plt.show()
```

```
Survived and unsurvived CDF and PDF based on  nodes:
=======================================================================
=============================
```



Observations

1.If nodes are greater than 46 then pateint wont survived

2.If nodes are less than 46 then there are same chances of survived and not survived

3.If nodes are less than 3 then chances of survived is more.

Mean, Variance and Std-dev

In [26]:

```
#Mean, Variance, Std-deviation,
print("Means:")
print("="*100)
print("age",np.mean(hdata["age"]))
print("year",np.mean(hdata["year"]))
print("nodes",np.mean(hdata["nodes"]))
#Mean with an outlier.
```

```
print("\nStd-dev:");
print("="*100)
print("age",np.std(hdata["age"]))
print("year",np.std(hdata["year"]))
print("nodes",np.std(hdata["nodes"]))
```

```
Means:
=======================================================================
=============================
age 52.45751633986928
year 62.85294117647059
nodes 4.026143790849673

Std-dev:
=======================================================================
=============================
age 10.78578520363183
year 3.244090833563246
nodes 7.177896092811152
```

Median, Percentile, Quantile, IQR, MAD

In [27]:

```
print("Median:")
print("="*100)
print("age",np.median(hdata["age"]))
print("year",np.median(hdata["year"]))
print("nodes",np.median(hdata["nodes"]))

print("\nPercentile:")
print("="*100)
print("age",np.percentile(hdata["age"],np.arange(0, 100, 25)))
print("year",np.percentile(hdata["year"],np.arange(0, 100, 25)))
print("nodes",np.percentile(hdata["nodes"],np.arange(0, 100, 25)))

from statsmodels import robust
print ("\nMedian Absolute Deviation")
```

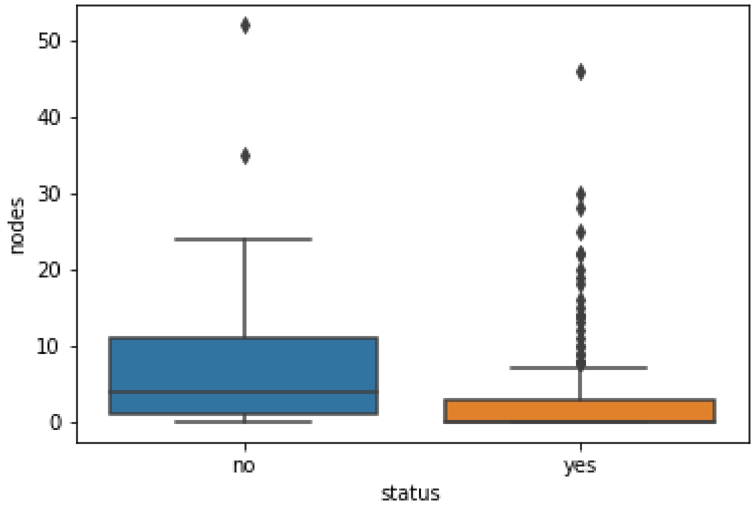
```
print("="*100)
print("age",robust.mad(hdata["age"]))
print("year",robust.mad(hdata["year"]))
print("nodes",robust.mad(hdata["nodes"]))
```

```
Median:
=======================================================================
=============================
age 52.0
year 63.0
nodes 1.0

Percentile:
=======================================================================
=============================
age [30.   44.   52.   60.75]
year [58.   60.   63.   65.75]
nodes [0. 0. 1. 4.]

Median Absolute Deviation
=======================================================================
=============================
age 11.860817748044816
year 4.447806655516806
nodes 1.482602218505602
```

Box plot and Whiskers

In [10]:

```
sns.boxplot(x='status',y='nodes', data=hdata)

plt.show()
```

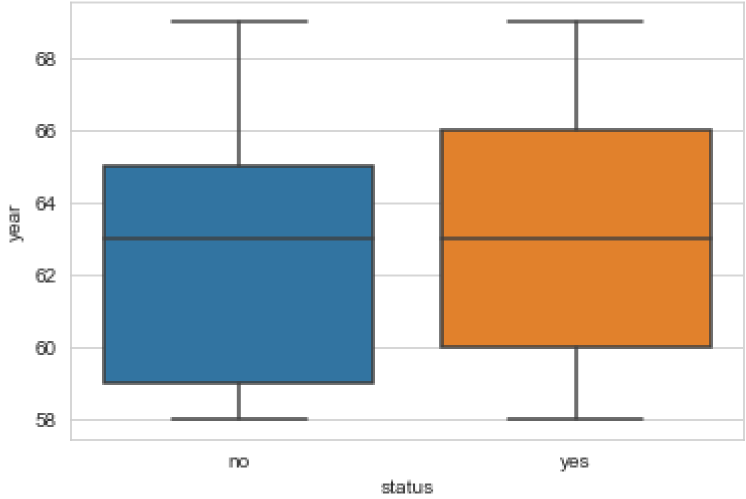


Observations

1.Pateints who survived after 5 years having nodes less than ~4 but there are cases of unsurvived too.

```
In [44]: sns.boxplot(x='status',y='year', data=hdata)
         print("\nBox plot of year and status:")
         print("="*100)
         plt.show()
```

```
Box plot of year and status:
=======================================================================
=============================
```



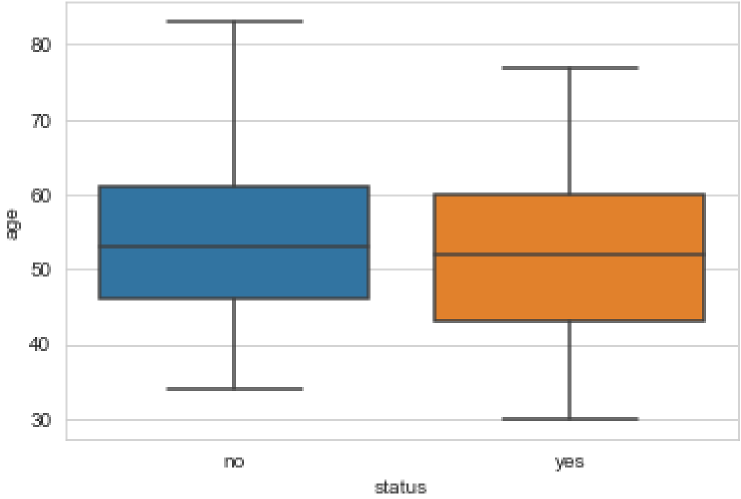
Observations

1.75% of operations carried before 1966.From which there are cases of survived pateints and unsurvived pateints.

In [46]:

```
sns.boxplot(x='status',y='age', data=hdata)
print("\nBox plot of age and status:")
print("="*100)
plt.show()
```

```
Box plot of age and status:
=======================================================================
=============================
```



Observation

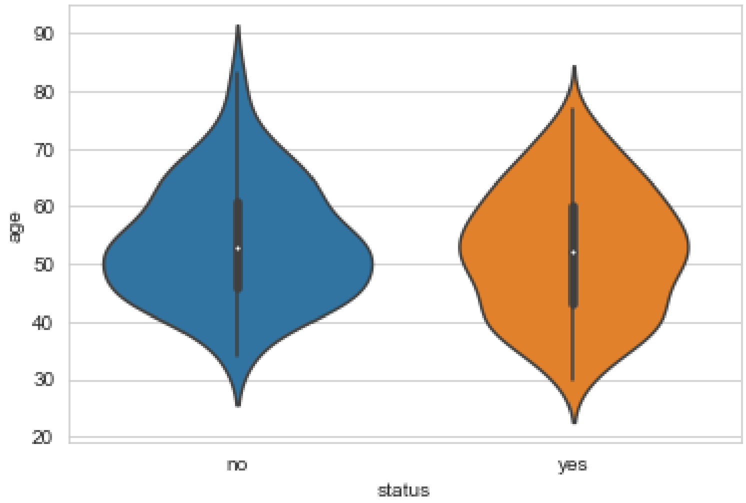
1.75 % of pateints who survived and unsurvived having age less than 63

2.minimum age of survived pateints is less than minimum age of unsurvived pateints.

Violin plots (Violin plot is combination of pdf and boxplot.)

In [47]:
```
sns.violinplot(x="status", y="age", data=hdata, height=8)
print("\nViolin plot of age and status:")
print("="*100)
plt.show()
```

```
Violin plot of age and status:
=======================================================================
=============================
```



Observations

1.Highest number of pateints who survived after 5 year lie in age value between 50 to 60

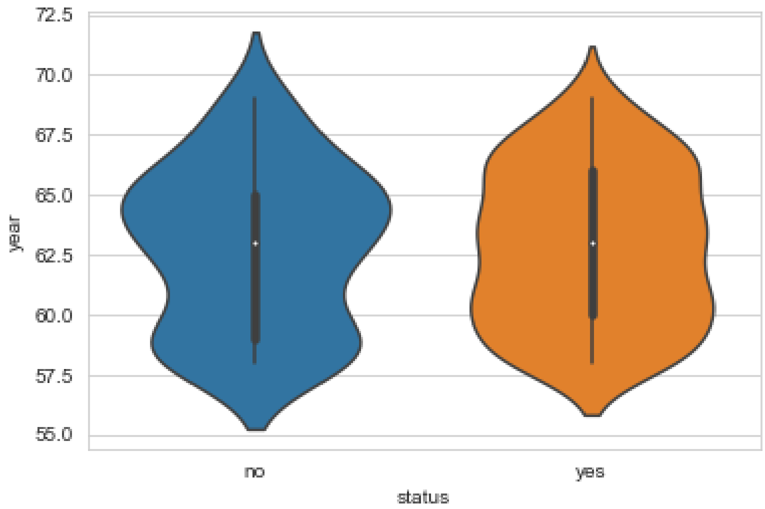
2.Highest number of pateints who not survived after 5 year lie in age value between 45 to 55

3.If age is more there are chances of unsurvived.

In [48]:

```
sns.violinplot(x="status", y="year", data=hdata, height=8)
print("\nViolin plot of year and status:")
print("="*100)
plt.show()
```

```
Violin plot of year and status:
========================================================================
=============================
```



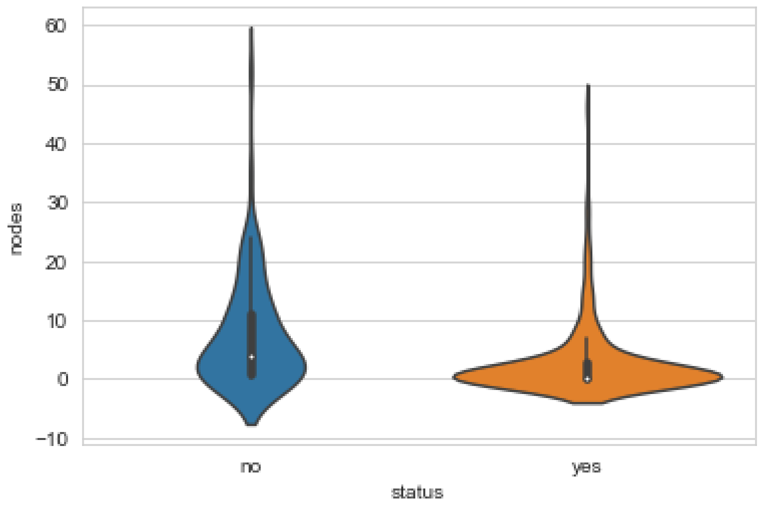
Observation

1.Maximum number of operations takes place in year 1963 to 1966.I which count of unsurvived pateints are more than survived.

In [49]:

```
sns.violinplot(x="status", y="nodes", data=hdata, height=8)
print("\nViolin plot of nodes and status:")
print("="*100)
plt.show()
```

```
Violin plot of nodes and status:
=======================================================================
=============================
```



Observation

1.Pateits having more than 50 nodes shows unsurvived status.

References

[1]https://en.wikipedia.org/wiki/Lymph_node

[2] https://www.cancer.org/cancer/breast-cancer/treatment/surgery-for-breast-cancer/lymph-node-surgery-for-breast-cancer.html