habermandataset_phanindrakumar

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1 Haberman's Survival: Exploratory Data Analysis

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.

2 Attribute Information:

Age of patient at the 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

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

[3]:
```
#reading the csv file
haberman_dataset= pd.read_csv(r'/home/user/Downloads/haberman.csv')
```

[4]:
```
##Prints the first 5 entries from the csv file
haberman_dataset.head()
```

[4]:

	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]:
```
#shape of the dataset
haberman_dataset.shape
```

[5]: (306, 4)

[6]:
```
#priniting the columns
haberman_dataset.columns
```

[6]:
```
Index(['age', 'year', 'nodes', 'status'], dtype='object')
```

[7]:
```
#brief info of the dataset
haberman_dataset.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
```

[8]:
```
#haberman_dataset['status'] = ['True' if var == 1 else 'False' for var in␣
 ↪haberman_dataset['status']]

for index, var1 in enumerate(haberman_dataset['status']):
    if var1 == 1 :
        haberman_dataset.loc[index,'status']= True
    else:
        haberman_dataset.loc[index,'status']= False
```

observation:
1.There is no missing data in this dataset.
2.All the columns are of integer data type.
3.The datatype of the status is an integer, it has to be converted to a categorical datatype

[9]:
```
haberman_dataset.describe()
#describes the dataset
```

[9]:

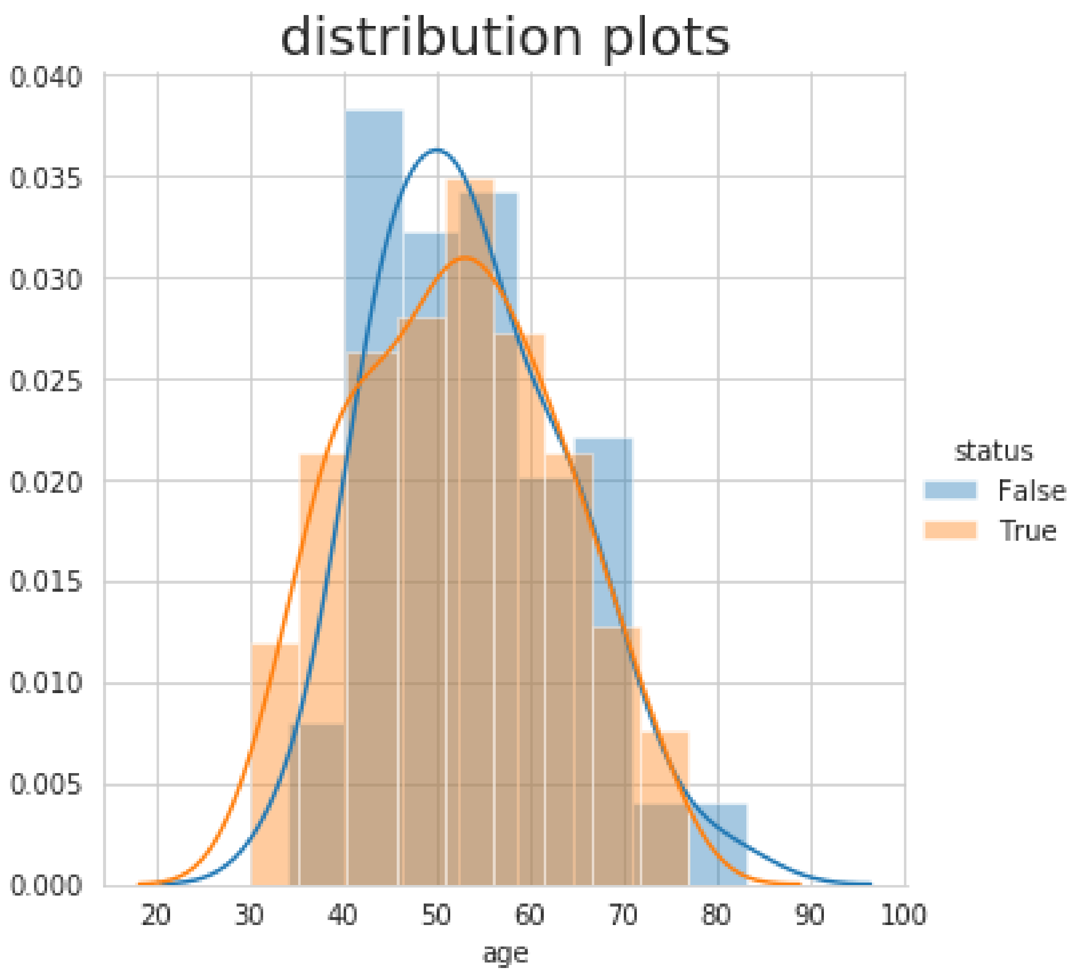
	age	year	nodes
count	306.000000	306.000000	306.000000
mean	52.457516	62.852941	4.026144
std	10.803452	3.249405	7.189654
min	30.000000	58.000000	0.000000
25%	44.000000	60.000000	0.000000
50%	52.000000	63.000000	1.000000
75%	60.750000	65.750000	4.000000
max	83.000000	69.000000	52.000000

[10]:
```
haberman_dataset['status'].value_counts()
#gives each count of the status type
```

[10]:
```
True     225
False     81
Name: status, dtype: int64
```

univariant analysis

[48]:
```
sns.FacetGrid(haberman_dataset,hue="status",height = 5)\
    .map(sns.distplot,"age")\
    .add_legend()
plt.title("distribution plots",fontsize=20)
plt.show()
```



observations:

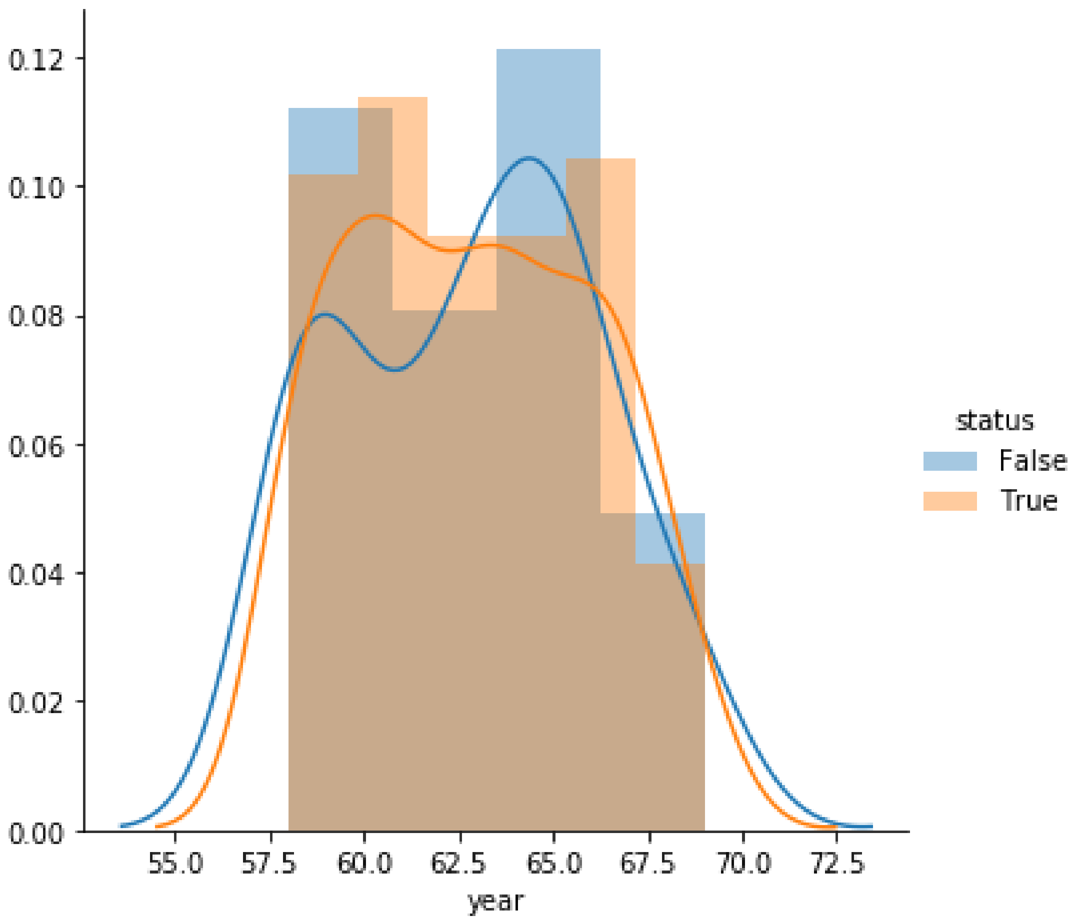
1.Major overlapping is observed, which tells us that survival chances are irrespective of a person's age.

2.Although there is overlapping we can vaguely tell that people whose age is in the range 30–40 are more likely to survive, and 40–60 are less likely to survive. While people whose age is in the range 60–75 have equal chances of surviving and not surviving

3.Yet, this cannot be our final conclusion.

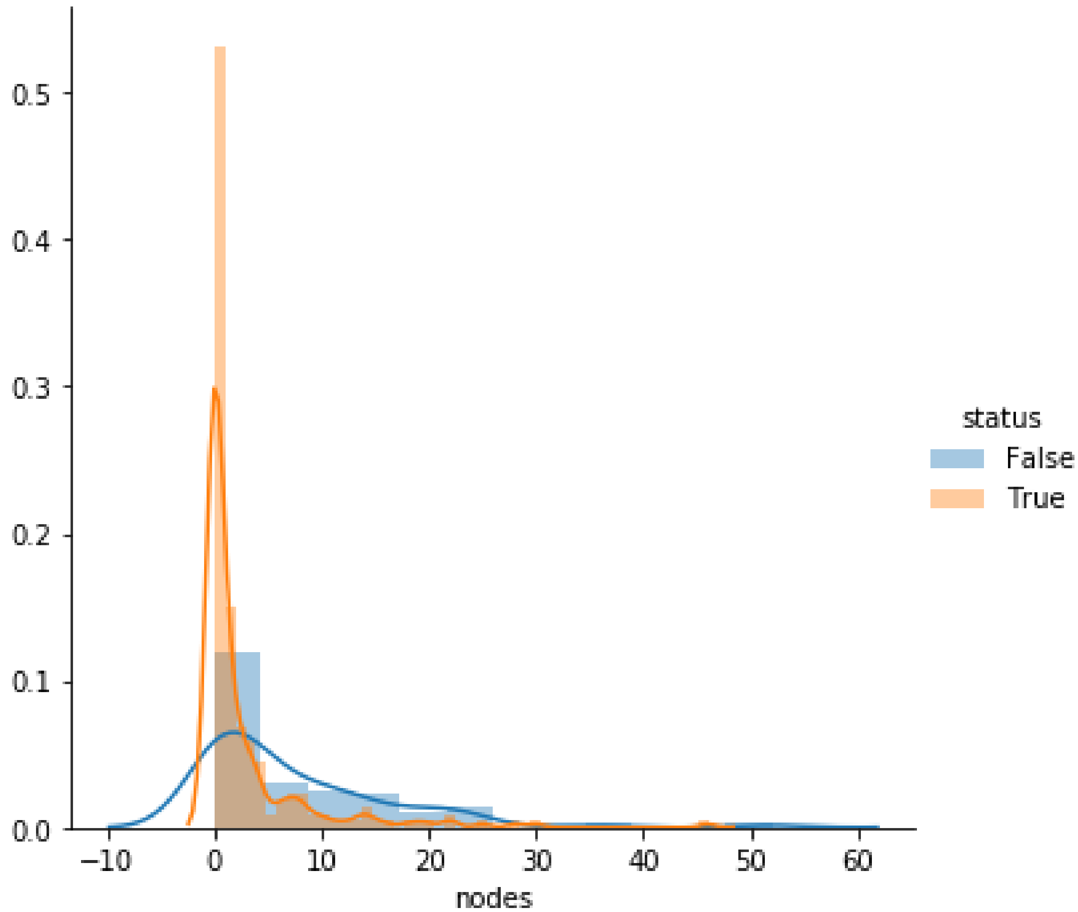
[12]:
```
sns.FacetGrid(haberman_dataset,hue="status",height = 5)\
  .map(sns.distplot,"year")\
  .add_legend();
```

```
plt.show()
```



observations:
1.There is major overlapping observed.
2.This graph only tells how many of the operations were successful and how many weren't. This cannot be a parameter to decide the patient's survival chances.

[13]:
```
sns.FacetGrid(haberman_dataset,hue="status",height = 5)\
 .map(sns.distplot,"nodes")\
 .add_legend()
plt.show()
```

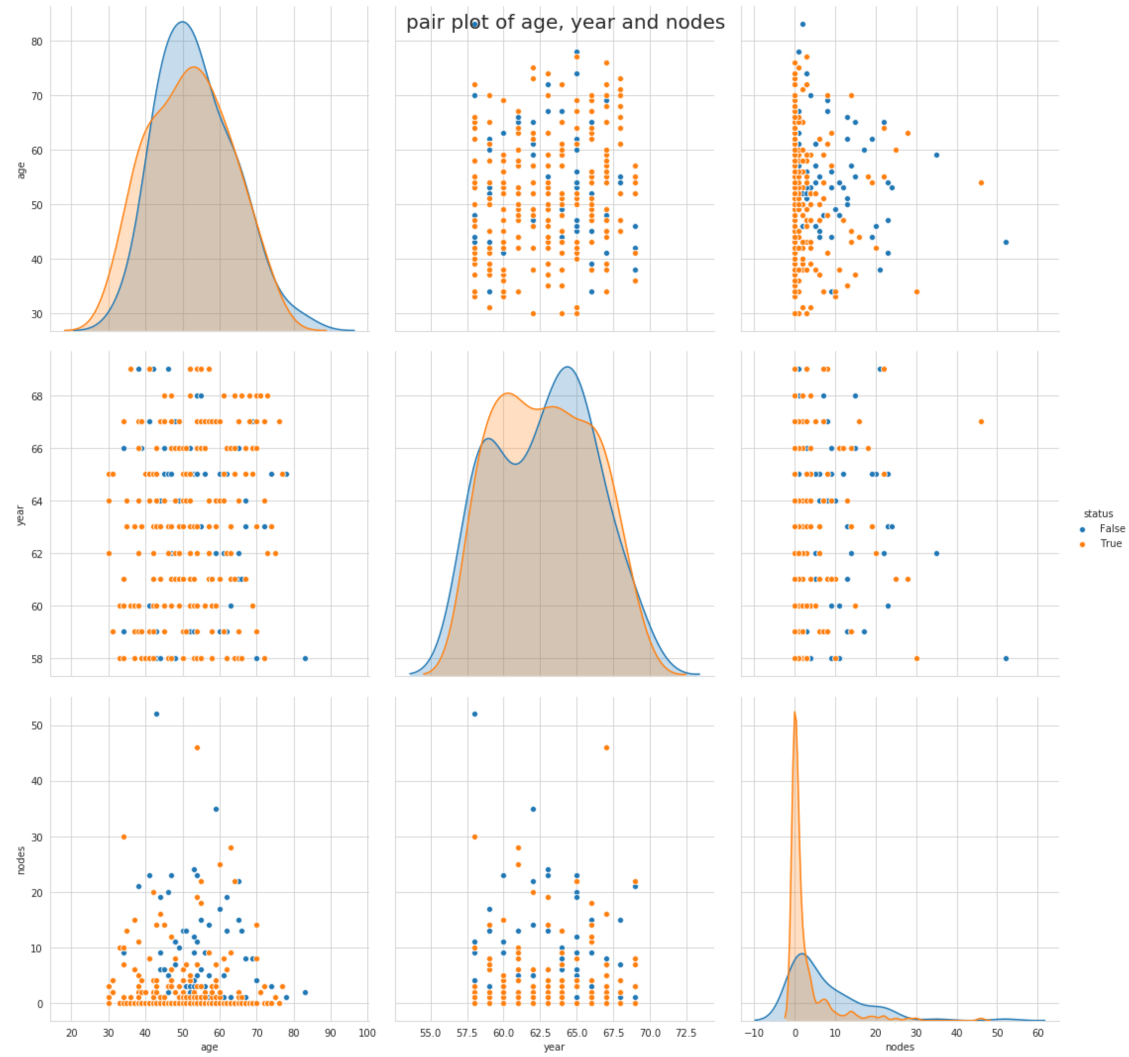


observations

1.Patients with no nodes or 1 node are more likely to survive. There are very few chances of surviving if there are 25 or more nodes.

Bi-variant analysis

[31]:
```
sns.set_style("whitegrid")
sns.pairplot(haberman_dataset, hue="status",vars=["age","year","nodes"],height␣
↪= 5)
plt.suptitle("pair plot of age, year and nodes",fontsize=20)
plt.show()
```

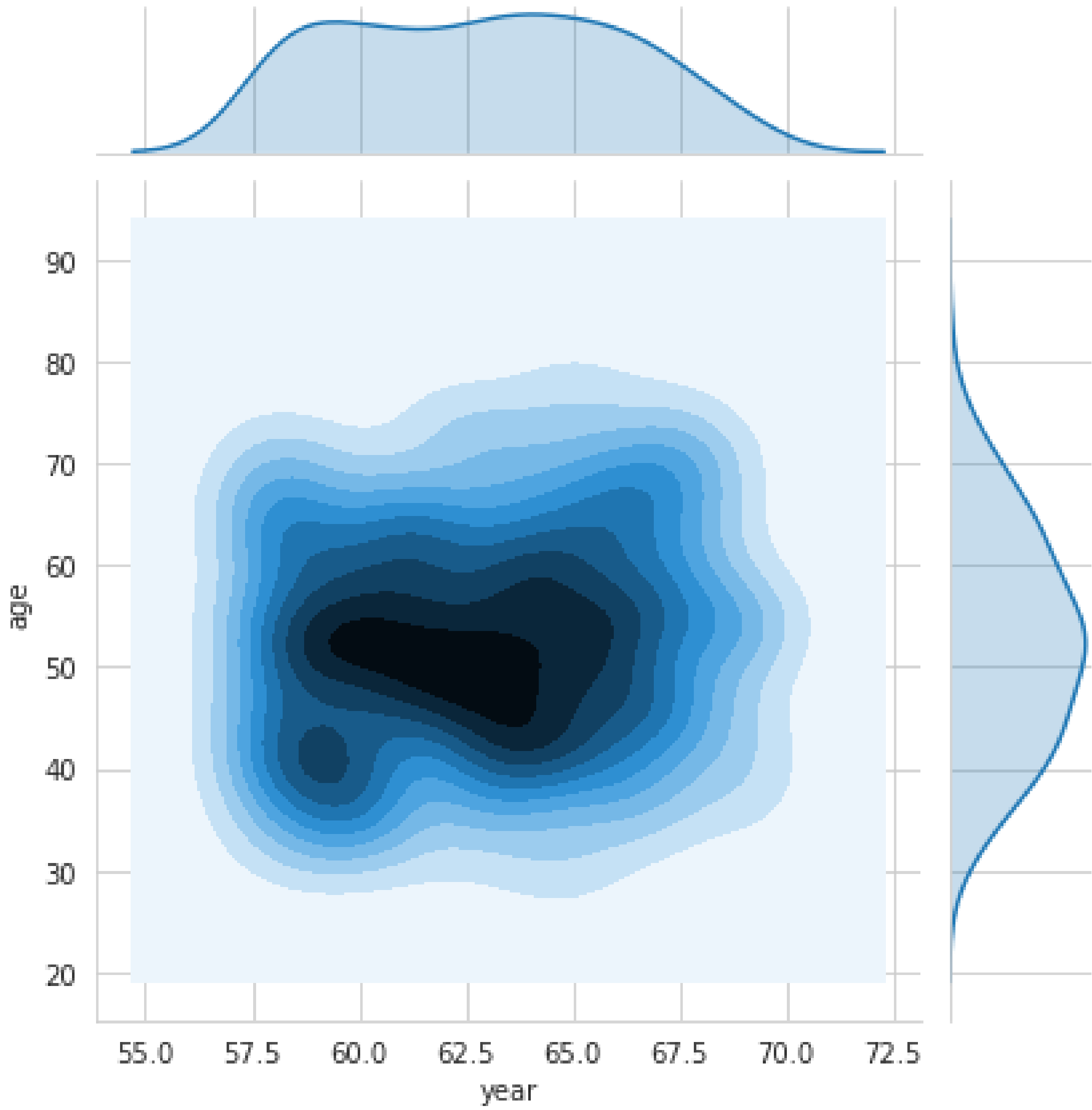


observation:
plot between year and nodes is comparitvely better.

multivariant analysis

contour plot

[43]:
```
sns.jointplot(x = 'year', y = 'age', data = haberman_dataset, kind = "kde")
plt.show()
```

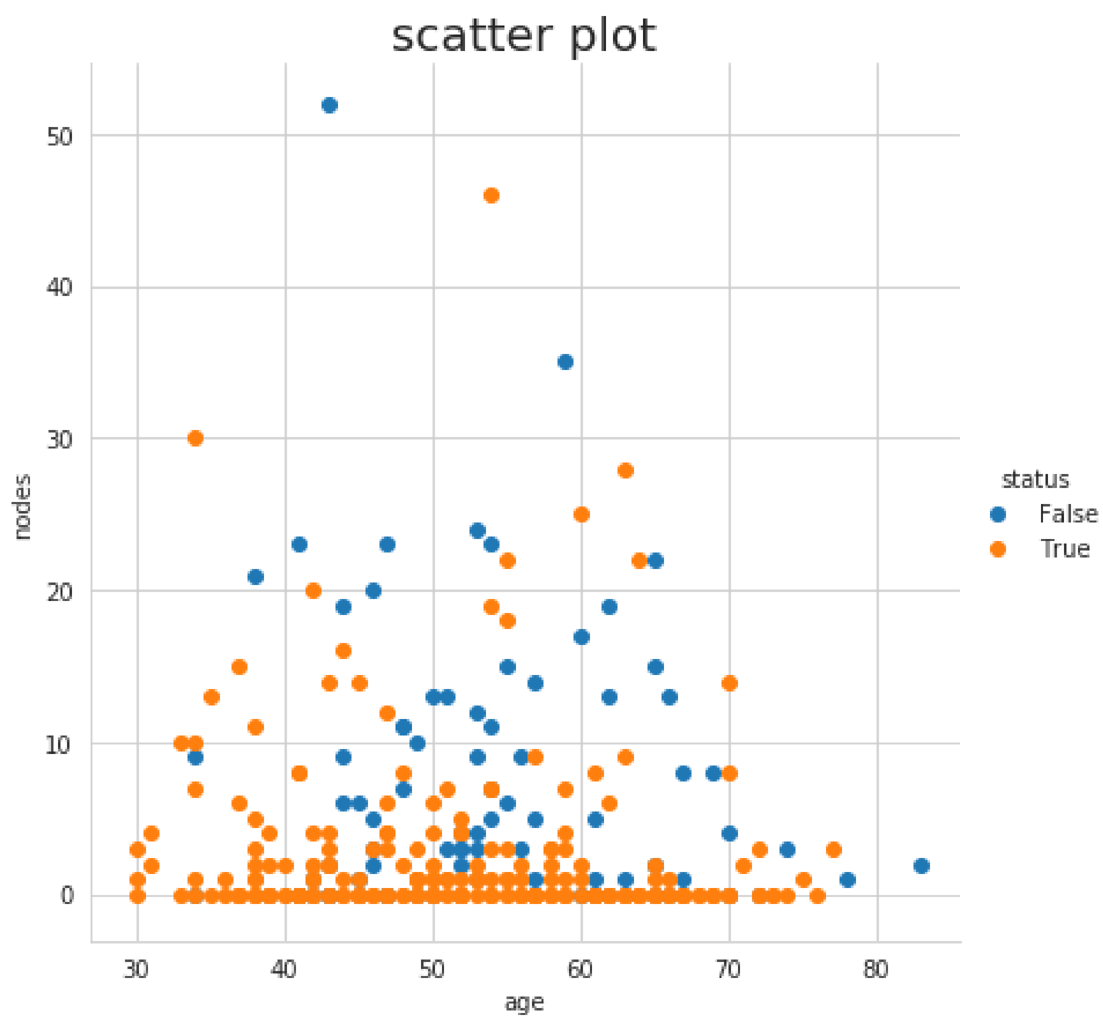


Observation: From 1960 to 1964, more operations done on the patients in the age group 45 to 55.

scatter plot

[49]:
```
sns.set_style("whitegrid")
sns.FacetGrid(haberman_dataset, hue = "status" , height = 6)\
 .map(plt.scatter,"age","nodes")\
 .add_legend()

plt.title('scatter plot',fontsize=20)
plt.show()
```



Cumulative Distribution Function(CDF)

[17]:
```
status_yes = haberman_dataset[haberman_dataset['status']==1]
status_yes.describe()
```

[17]:

	age	year	nodes
count	225.000000	225.000000	225.000000
mean	52.017778	62.862222	2.791111
std	11.012154	3.222915	5.870318
min	30.000000	58.000000	0.000000
25%	43.000000	60.000000	0.000000
50%	52.000000	63.000000	0.000000
75%	60.000000	66.000000	3.000000
max	77.000000	69.000000	46.000000

[18]:
```
status_no=haberman_dataset[haberman_dataset['status']==0]
status_no.describe()
```

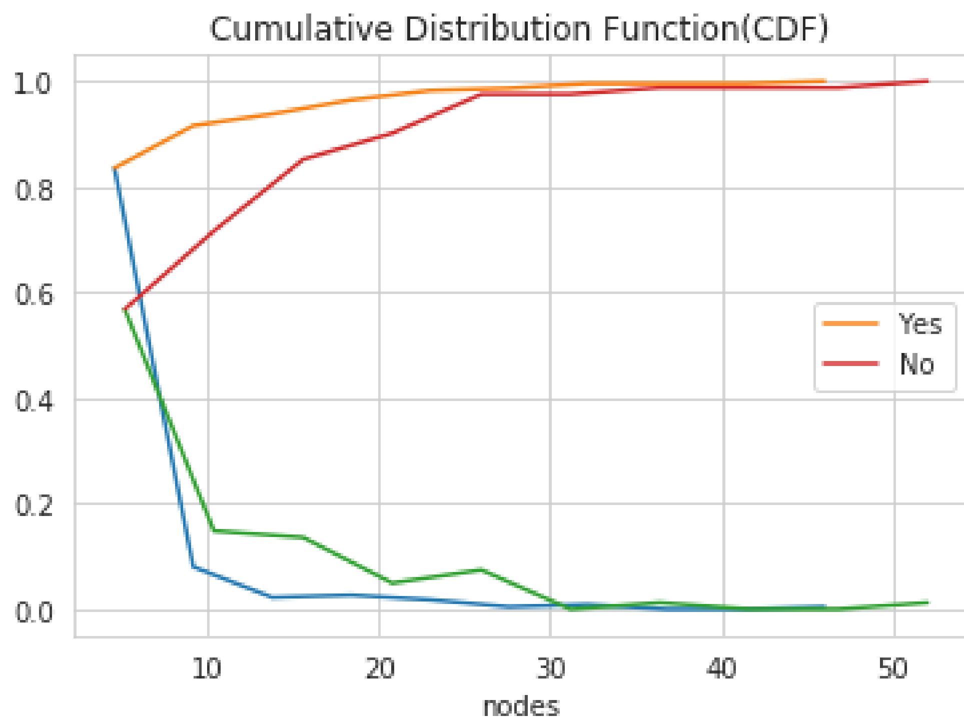
[18]:

```
             age       year      nodes
count  81.000000  81.000000  81.000000
mean   53.679012  62.827160   7.456790
std    10.167137   3.342118   9.185654
min    34.000000  58.000000   0.000000
25%    46.000000  59.000000   1.000000
50%    53.000000  63.000000   4.000000
75%    61.000000  65.000000  11.000000
max    83.000000  69.000000  52.000000
```

[32]:

```
counts1, bin_edges1 = np.histogram(status_yes['nodes'], bins=10, density = True)
pdf1 = counts1/(sum(counts1))
print(pdf1);
print(bin_edges1)
cdf1 = np.cumsum(pdf1)
plt.plot(bin_edges1[1:], pdf1)
plt.plot(bin_edges1[1:], cdf1, label = 'Yes')
plt.xlabel('nodes')
print("***********************************************************")
counts2, bin_edges2 = np.histogram(status_no['nodes'], bins=10, density = True)
pdf2 = counts2/(sum(counts2))
print(pdf2);
print(bin_edges2)
cdf2 = np.cumsum(pdf2)
plt.plot(bin_edges2[1:], pdf2)
plt.plot(bin_edges2[1:], cdf2, label = 'No')
plt.xlabel('nodes')
plt.title('Cumulative Distribution Function(CDF)')
plt.legend()
plt.show()
```

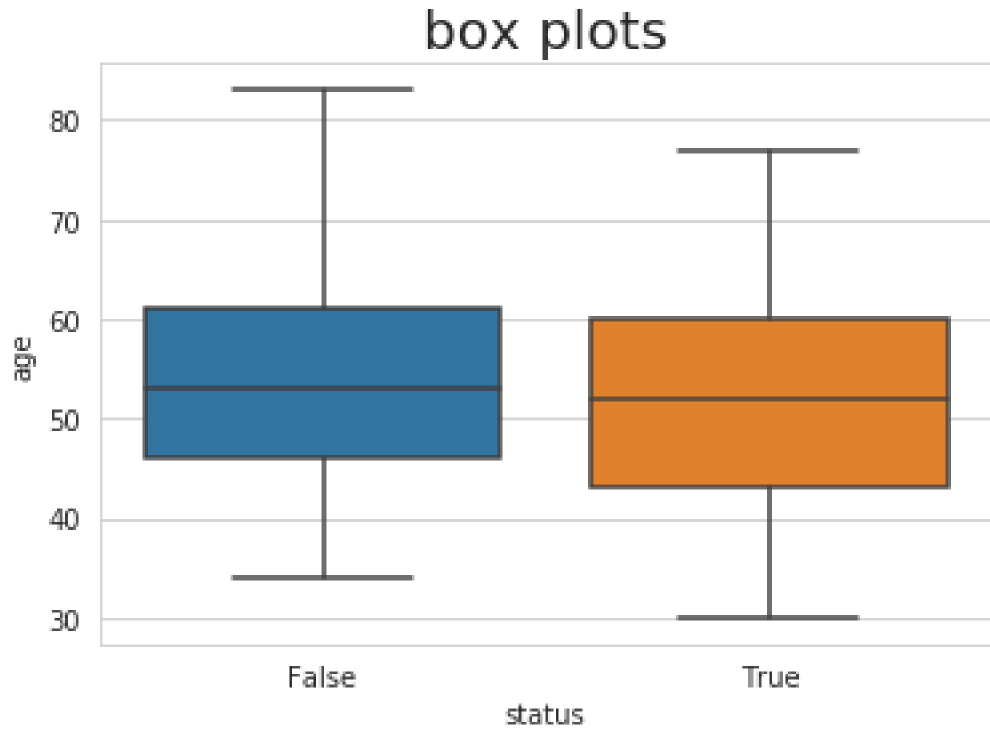
```
[0.83555556 0.08       0.02222222 0.02666667 0.01777778 0.00444444
 0.00888889 0.         0.         0.00444444]
[ 0.   4.6  9.2 13.8 18.4 23.  27.6 32.2 36.8 41.4 46. ]
***********************************************************
[0.56790123 0.14814815 0.13580247 0.04938272 0.07407407 0.
 0.01234568 0.         0.         0.01234568]
[ 0.   5.2 10.4 15.6 20.8 26.  31.2 36.4 41.6 46.8 52. ]
```

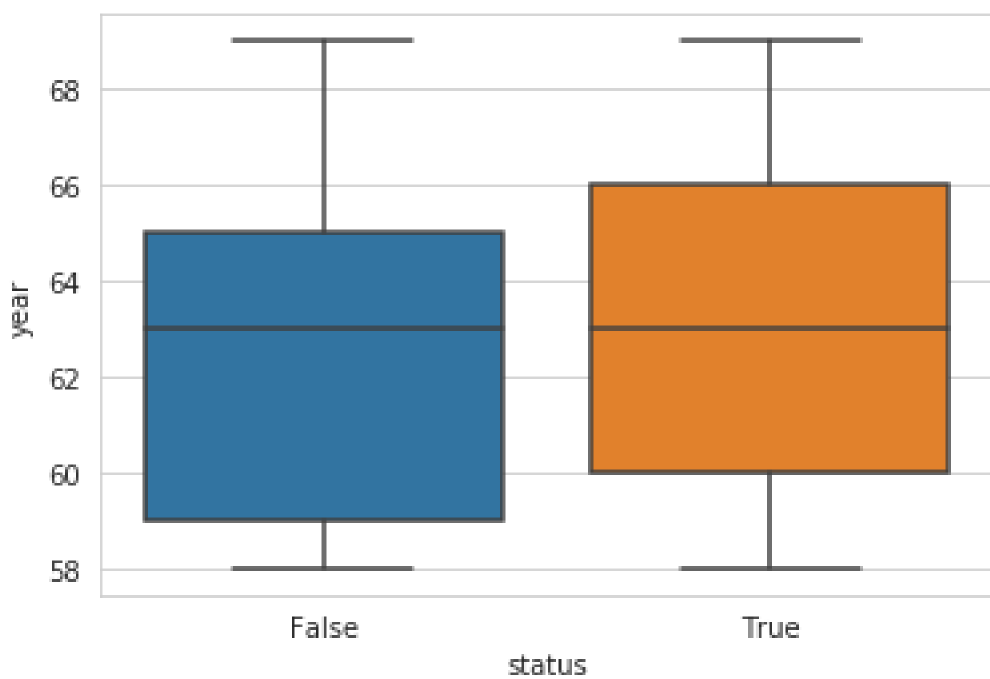


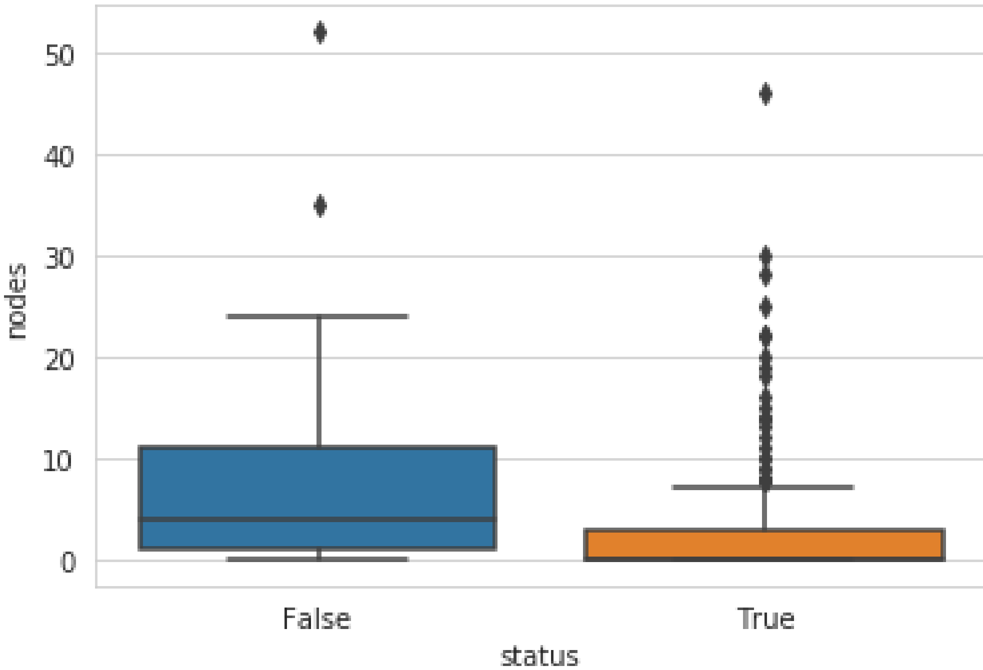
observation 83.55% of the patients who have survived had nodes in the range of 0–4.6

box plots and violin plot

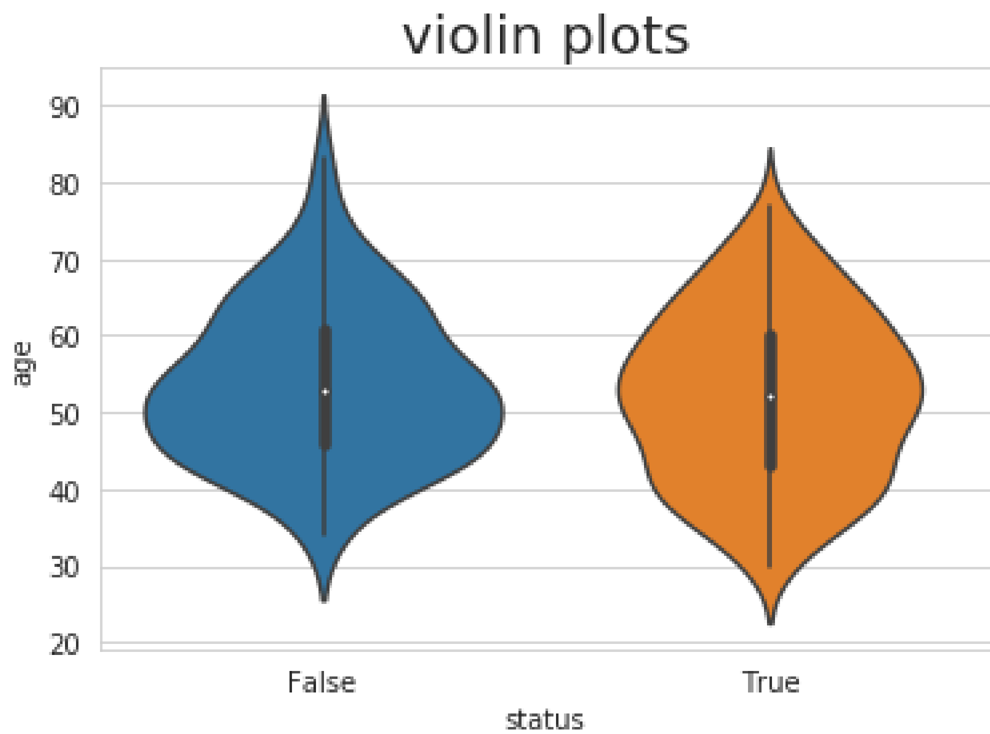
[44]:
```
sns.boxplot(x='status',y='age',data=haberman_dataset)
plt.title('box plots',fontsize=20)
plt.show()
sns.boxplot(x='status',y='year',data=haberman_dataset)
plt.show()
sns.boxplot(x='status',y='nodes',data=haberman_dataset)
plt.show()
```

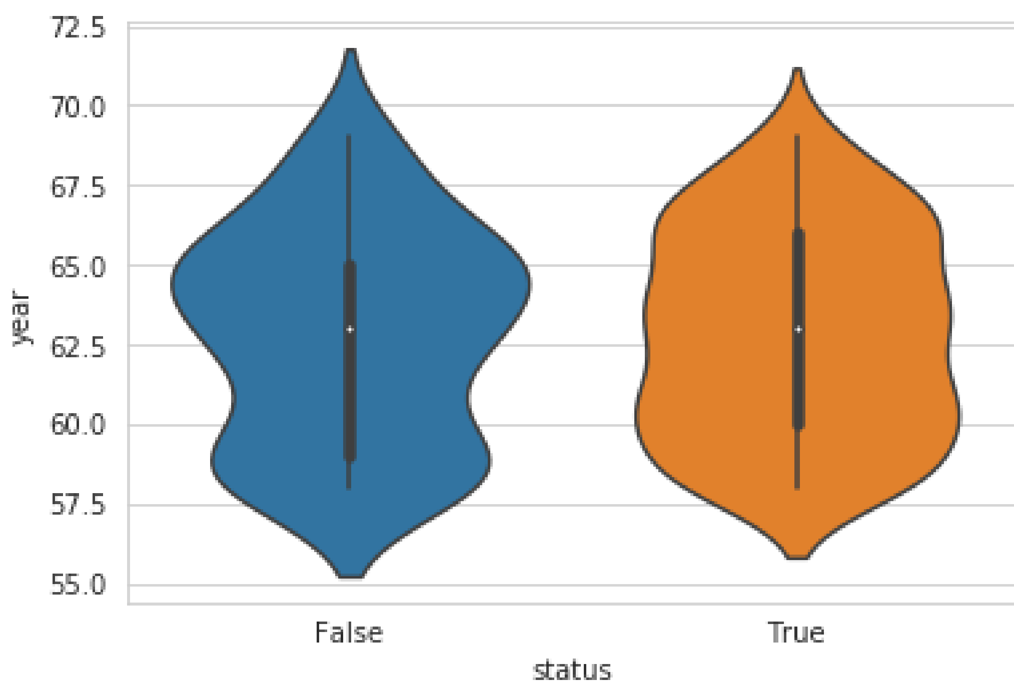

box plots
80
70
60
50
40
30
age
False
True
status


68
66
64
62
60
58
year
False
True
status



[46]:
```
sns.violinplot(x="status",y="age",data = haberman_dataset,height = 10)
plt.title("violin plots",fontsize=20)
plt.show()
sns.violinplot(x="status",y="year",data = haberman_dataset,height = 10)
plt.show()
sns.violinplot(x="status",y="nodes",data = haberman_dataset,height = 10)
plt.show()
```


violin plots
90
80
70
60
50
40
30
20
age
False
True
status


72.5
70.0
67.5
65.0
62.5
60.0
57.5
55.0
year
False
True
status