In [45]:
```
pwd
```
Out[45]:
```
'C:\\Users\\Abhishek\\Desktop\\AppliedAI'
```

In [46]:
```
cd C:\Users\Abhishek\Desktop\AppliedAI
```
```
C:\Users\Abhishek\Desktop\AppliedAI
```

In [76]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

About the dataset

in this dataset 1st column denote the age of the patient and 2nd column represent the year when operation is done

3rd column represent the no of nodes and 4th one represent the survival status of patient. 1 represent he can survive and

2 represent he cant survive

In [59]:
```
#col_name=['Age','Operation_year','Nodes','Status']
df=pd.read_csv('haberman.csv')
df.head()
```
Out[59]:

	age	year	nodes	status

	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

Task

As a ml engineer our task is to predict the status of the patient if we know age,operation year,no of node

In [60]:
```
df.columns
```
Out[60]:
```
Index(['age', 'year', 'nodes', 'status'], dtype='object')
```

In [61]:
```
df.shape
```
Out[61]:
```
(306, 4)
```

Observation

This dataset have 4 column and 306 rows

In [62]:
```
df.describe()
```
Out[62]:

	age	year	nodes	status
count	306.000000	306.000000	306.000000	306.000000
mean	52.457516	62.852941	4.026144	1.264706

	age	year	nodes	status
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

In [64]:
```
df['status'].value_counts()
```

Out[64]:
```
1    225
2     81
Name: status, dtype: int64
```

Obervation

we can say that 225 patient survive and unfortunatily 81 patient not survive

and this dataset is balanced dataset

In [65]:
```
df.dtypes
```

Out[65]:
```
age       int64
year      int64
nodes     int64
status    int64
dtype: object
```

so here the datatype of each column is a string type of we have to convert all these value into int or float type

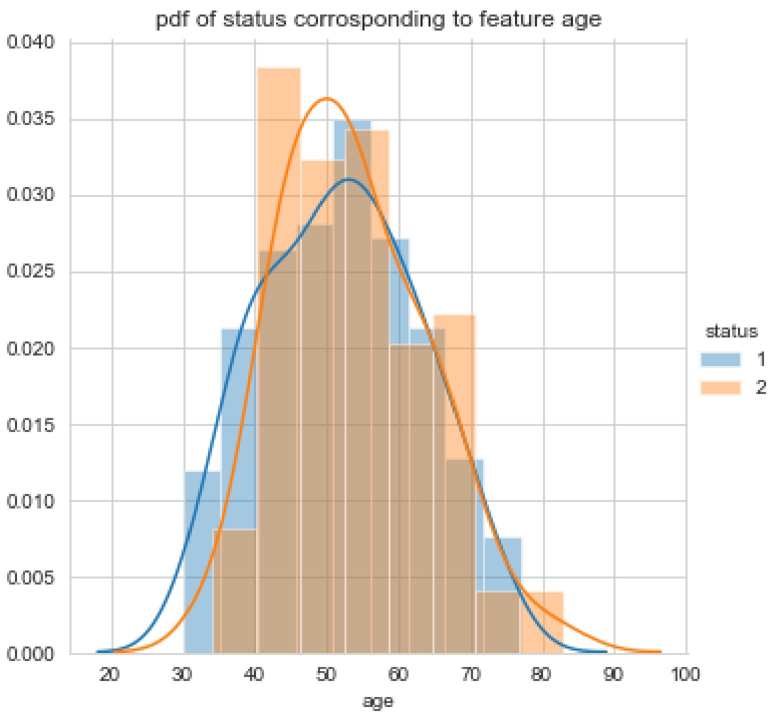
In [70]:
```
df[['age','year','nodes']]=df[['age','year','nodes']].astype(float)
df['status']=df['status'].astype('category')
df.dtypes
```

Out[70]:
```
age        float64
year       float64
nodes      float64
status    category
dtype: object
```

Univariate analysis

Histogram and pdf

In [79]:
```
sns.set_style('whitegrid')
sns.FacetGrid(df,hue='status',size=5).map(sns.distplot,'age',).add_lege
nd()
plt.title('pdf of status corrosponding to feature age')
plt.show()
```



Conclusion

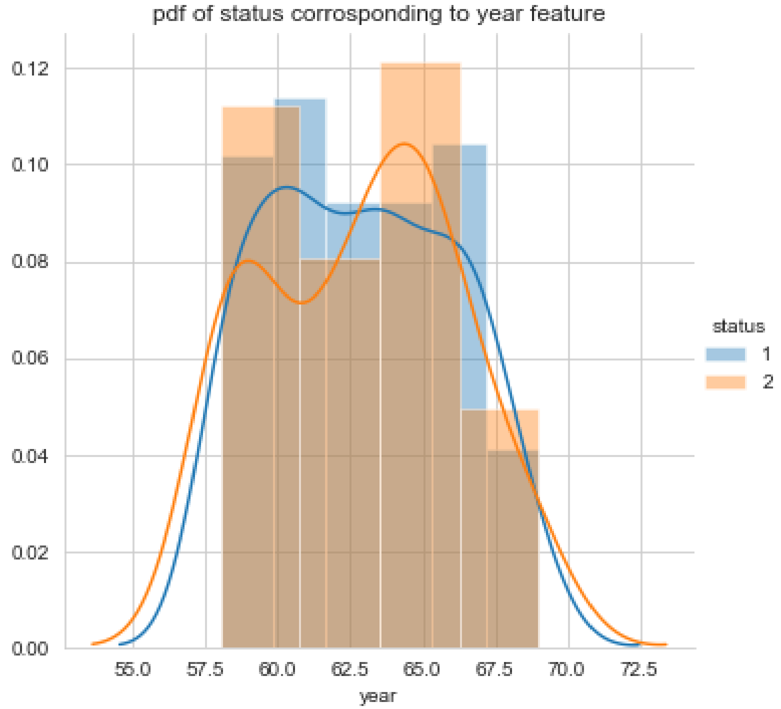
1.This histogram is overlapping each other

2.peolpe of age range between 40 to 60 are more likely to die

3.people of age less than 40 more probable to survive

In [80]:
```
sns.set_style('whitegrid')
sns.FacetGrid(df,hue='status',size=5).map(sns.distplot,'year').add_lege
nd()
```

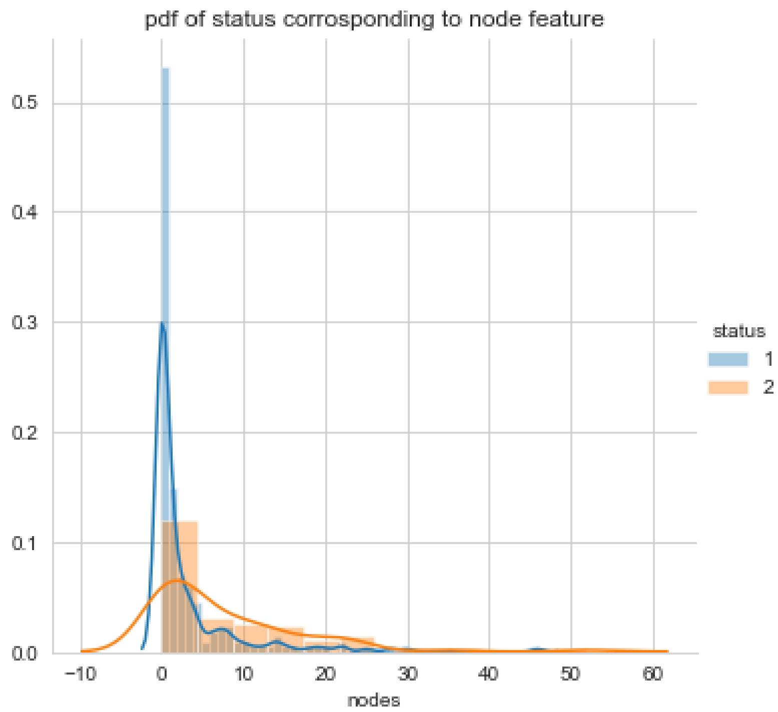
```
plt.title('pdf of status corrosponding to year feature')
plt.show()
```



conclusion

1.From the plot we can say that there is immense overlapping betwwen these two class

In [83]:
```
sns.set_style('whitegrid')
sns.FacetGrid(df,hue='status',size=5).map(sns.distplot,'nodes').add_leg
end()
plt.title('pdf of status corrosponding to node feature')
plt.show()
```



Conclusion

1.partially overlapping between these two class

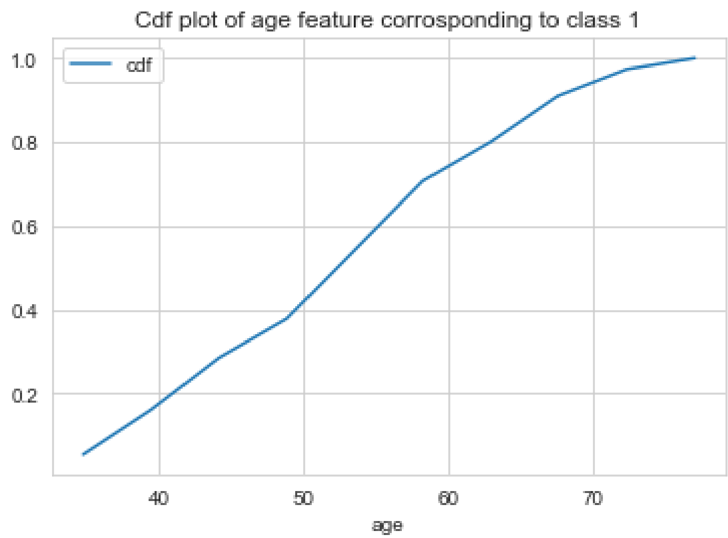
2.we can say that patient with 0 axil node survive

Univariate analysis using cdf

In [103]:
```
class_1=df.loc[df['status']==1]
class_2=df.loc[df['status']==2]
```

In [146]:
```
#plotting age feature corrosponding to class 1
counts,bin_edges=np.histogram(class_1['age'],bins=10,density=True)
pdf=counts/(sum(counts))
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],cdf,label='cdf')
plt.xlabel('age')
plt.title('Cdf plot of age feature corrosponding to class 1')
plt.legend()
plt.show()
```

```
[0.05333333 0.10666667 0.12444444 0.09333333 0.16444444 0.16444444
 0.09333333 0.11111111 0.06222222 0.02666667]
[30.  34.7 39.4 44.1 48.8 53.5 58.2 62.9 67.6 72.3 77. ]
```



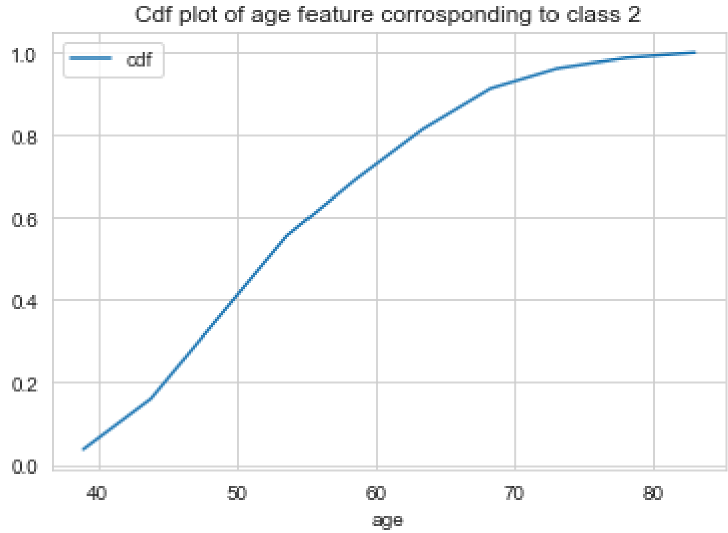
conclusion

it is clear that patient having age between 50 to 60 have greater rate of survival

Almost 90% who survived have the age less than or equal to 70

In [147]:
```
#plotting age feature corrosponding to class 2
counts,bin_edges=np.histogram(class_2['age'],bins=10,density=True)
pdf=counts/(sum(counts))
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],cdf,label='cdf')
plt.xlabel('age')
plt.title('Cdf plot of age feature corrosponding to class 2')
plt.legend()
plt.show()
```

```
[0.03703704 0.12345679 0.19753086 0.19753086 0.13580247 0.12345679
 0.09876543 0.04938272 0.02469136 0.01234568]
[34.  38.9 43.8 48.7 53.6 58.5 63.4 68.3 73.2 78.1 83. ]
```



conclusion

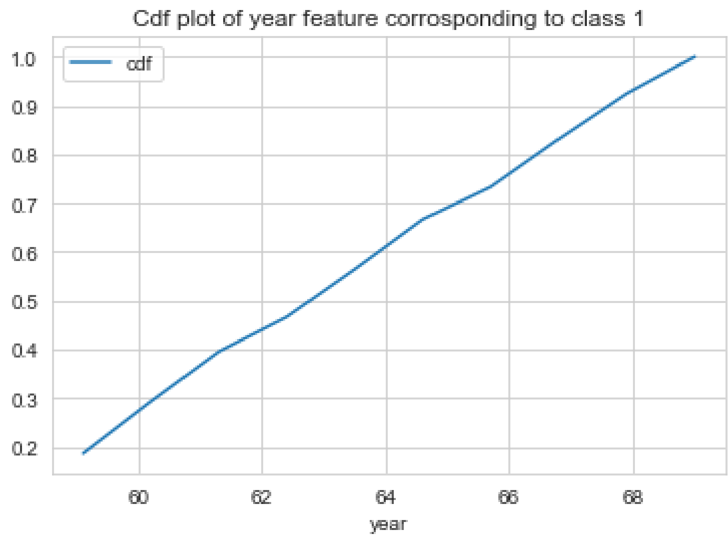
about 70% patient who died within 5 years have age equal to 60 yrs or less than 60 yrs

In [151]:

```
##plotting operation year feature corrosponding to class 1
counts,bin_edges=np.histogram(class_1['year'],bins=10,density=True)
pdf=counts/(sum(counts))
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],cdf,label='cdf')
plt.xlabel('year')
plt.title('Cdf plot of year feature corrosponding to class 1')
plt.legend()
plt.show()
```

```
[0.18666667 0.10666667 0.10222222 0.07111111 0.09777778 0.10222222
 0.06666667 0.09777778 0.09333333 0.07555556]
```

```
[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
```



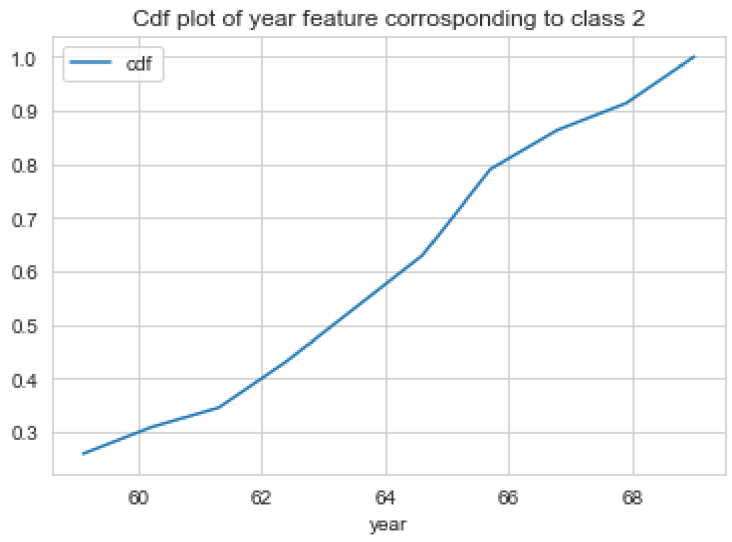
conclusion

about 60% patient those who survive their operation is done in before 1964

In [152]:
```
counts,bin_edges=np.histogram(class_2['year'],bins=10,density=True)
pdf=counts/(sum(counts))
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],cdf,label='cdf')
plt.xlabel('year')
plt.title('Cdf plot of year feature corrosponding to class 2')
plt.legend()
plt.show()
```

```
[0.25925926 0.04938272 0.03703704 0.08641975 0.09876543 0.09876543
 0.16049383 0.07407407 0.04938272 0.08641975]
```

```
[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
```

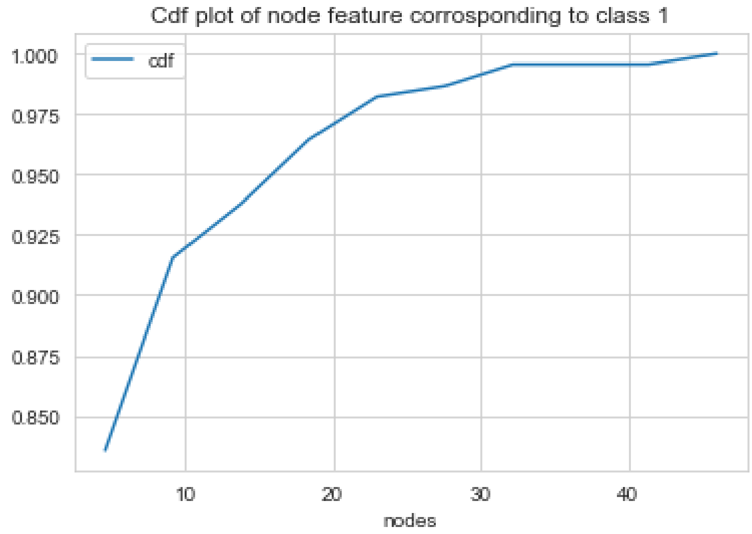


conclusion

about 90% patient who die there operation is done before 1968

In [154]:
```
counts,bin_edges=np.histogram(class_1['nodes'],bins=10,density=True)
pdf=counts/(sum(counts))
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],cdf,label='cdf')
plt.xlabel('nodes')
plt.title('Cdf plot of node feature corrosponding to class 1')
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. ]
```



conclusion

about 90% patient survive those have axil node 8.hence we can say that as much as the number of axil node in low the survival \

chance increase

counts,bin_edges=np.histogram(class_2['nodes'],bins=10,density=True) pdf=counts/(sum(counts)) print(pdf) print(bin_edges) cdf=np.cumsum(pdf) plt.plot(bin_edges[1:],cdf,label='cdf') plt.xlabel('nodes') plt.title('Cdf plot of node feature corrosponding to class 2') plt.legend() plt.show()

In [ ]:

```
#conclusion
#
```

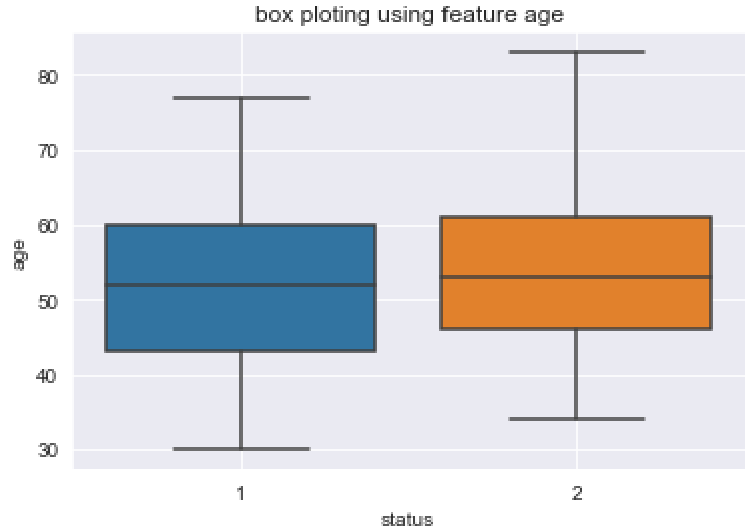
Mean median and standard deviation

In [99]:
```
#Mean, Variance, Std-deviation of age attribute
print('Mean of age attribute: ',np.mean(df["age"]))
print('median of age :',np.median(df['age']))
print('std_dev of age: ',np.std(df.age))
print('******************')
#Mean, Variance, Std-deviation of year attribute
print("Mean of  year: ",np.mean(df['year']))
print('median of year :',np.median(df['year']))
print('std of  year: ',np.std(df['year']))
```

```
Mean of age attribute:  52.45751633986928
median of age : 52.0
std_dev of age:  10.78578520363183
******************
Mean of  year:  62.85294117647059
median of year : 63.0
std of  year:  3.244090833563246
```

Box plot

In [124]:
```
sns.set_style('dark')
sns.boxplot(x='status',y='age',data=df)
plt.grid()
plt.title('box ploting using feature age')
plt.show()
```



conclusion

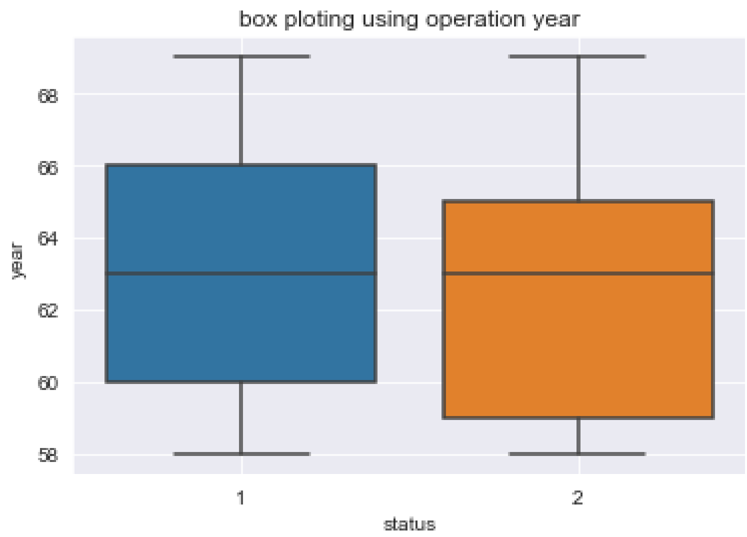
50% data point who survive their age belong between 43 to 60

50% data point who die their age belong between 46 to 62

from the box plot we can say that about 90 data overlap between these these box plot with same

median(~).Hence we can say that age feature is not sufficent to predict survival status

In [125]:
```
sns.set_style('dark')
sns.boxplot(x='status',y='year',data=df)
plt.grid()
plt.title('box ploting using operation year')
plt.show()
```

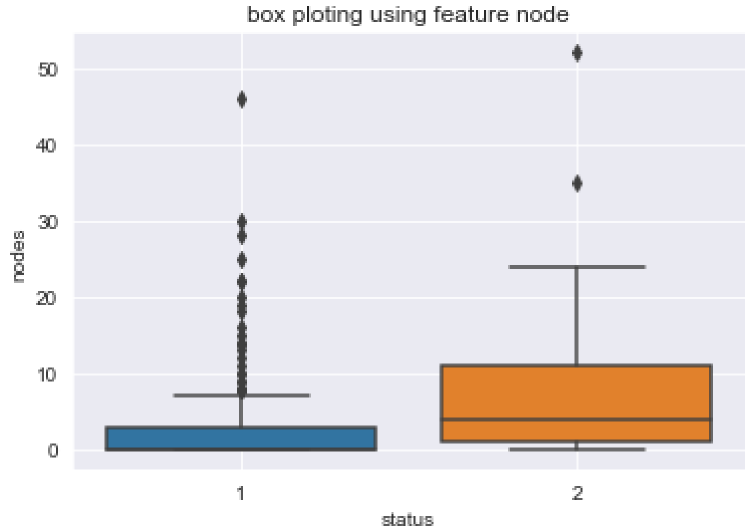


Conclusion

from the box plot we can say that about 80 data overlap between these these box plot with same

median(~).Hence we can say that operation year feature is not sufficent to predict survival status

In [127]:
```
sns.set_style('dark')
sns.boxplot(x='status',y='nodes',data=df)
plt.grid()
plt.title('box ploting using feature node')
plt.show()
```

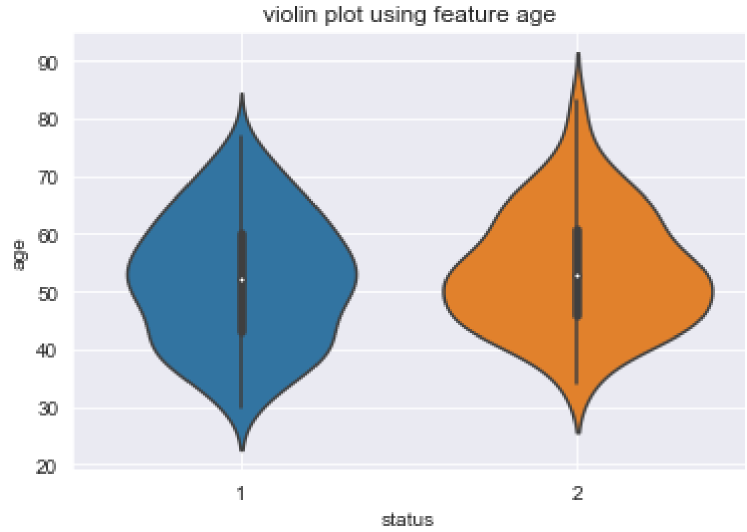


Conclusion

class_1(those who survive) have outlier but 50% survive those whose axil node no is less than 3

Violin plot

In [129]:
```
sns.violinplot(x='status',y='age',data=df)
plt.grid()
plt.title('violin plot using feature age')
plt.show()
```

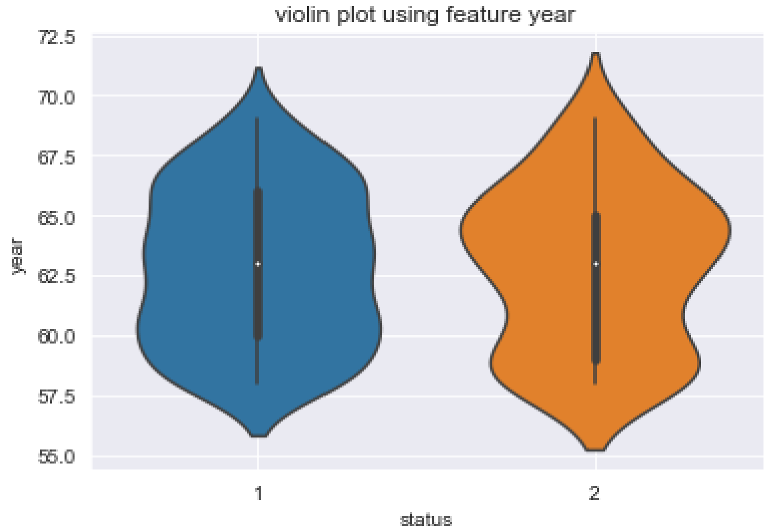


Conclusion

overlapping is seen upto 90% between both the class .so age feature is not sufficient to predict

the survival status

In [131]:
```
sns.violinplot(x='status',y='year',data=df)
plt.grid()
plt.title('violin plot using feature year')
plt.show()
```

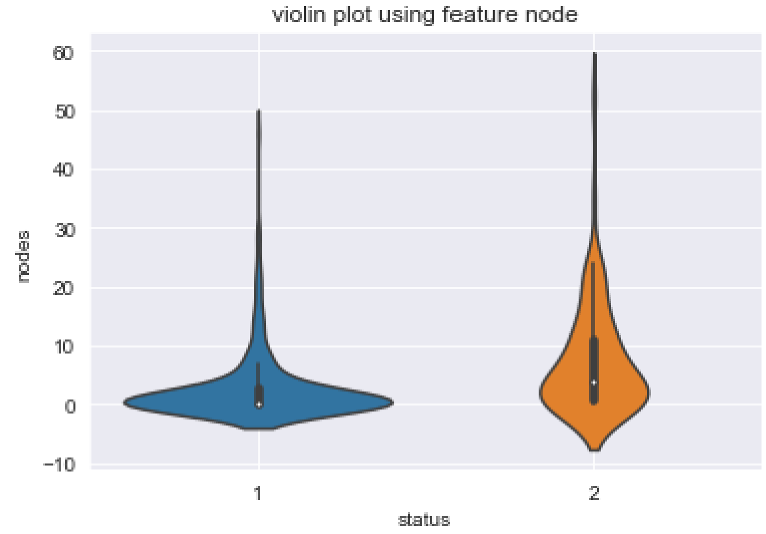


conclusion

here we also see about 90% datapoint overlap so we cant say operation year is sufficient to predict

survival status

In [134]:
```
sns.violinplot(x='status',y='nodes',data=df)
plt.grid()
plt.title('violin plot using feature node')
plt.show()
```



Conclusion

The survived patient having axil node equal to zero

patient who died had axil node greater than or equal to 1,and as the concentration of

axil node increased the patient is more likely to die

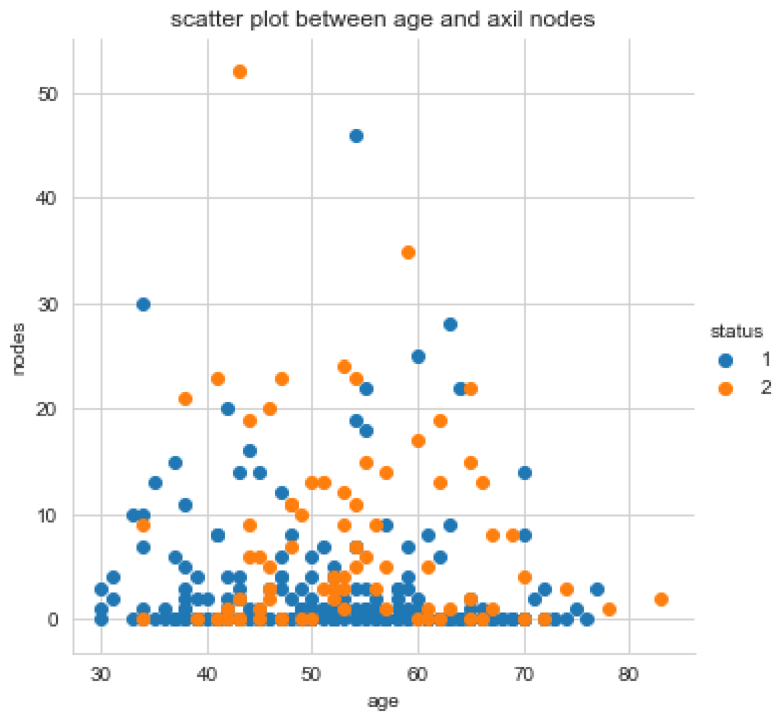
Bivariate analysis

In [136]:
```
sns.set_style('whitegrid')
sns.FacetGrid(df,hue='status',size=5).map(plt.scatter,'age','year').add
_legend()
plt.title('scatter plot between age and year')
plt.show()
```

Conclusion

their is about 90% overlap.so we cant separate the survival of patient on the basis of age and operation year

In [138]:
```
sns.set_style('whitegrid')
sns.FacetGrid(df,hue='status',size=5).map(plt.scatter,'age','nodes').ad
d_legend()
plt.title('scatter plot between age and axil nodes')
plt.show()
```

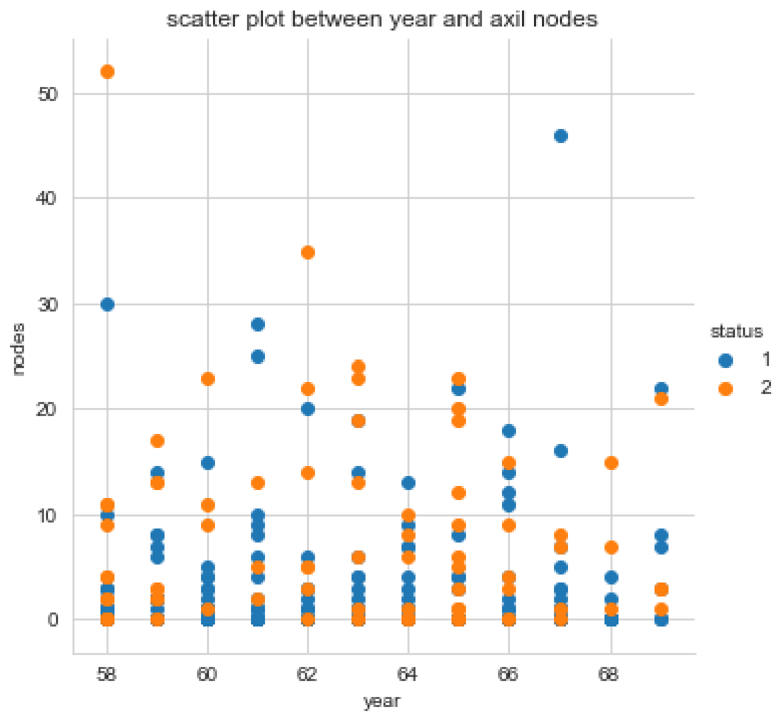


Conclusion

there is also a hue overlap about 90%.so we cant seperate survival of patient on the basis of age and axil node

In [140]:

```
sns.set_style('whitegrid')
sns.FacetGrid(df,hue='status',size=5).map(plt.scatter,'year','nodes').a
dd_legend()
plt.title('scatter plot between year and axil nodes')
plt.show()
```



Conclusion

there is also a hue overlap about (80 to 90)%.so we cant seperate survival of patient on the basis of age and axil node

Pair plot

In [143]:
```
plt.close();
sns.set_style("whitegrid");
sns.pairplot(df, hue="status", size=3,x_vars=['age','nodes','year'],y_v
ars=['age','nodes','year']);
plt.show()
```


age
nodes
year
status
1
2
80
70
60
50
40
30
20
10
0
68
66
64
62
60
58
20
40
60
80
100
age
0
20
40
60
nodes
55
60
65
70
year

Conclusion

it is very difficult to predict the survival of the patient who had undergone for cancer on thebasis

of these three feature because both the class about 80 to 90% overlapping each other

These two classes are linearly inseperable due to immense overlapping

we should collect more useful feature which are helpful to predict the survival of the patient

we need non_linear model then only we can predict the survival of the patient

order of usefullness of the feature is axil_node>operation_year>age

In [ ]: