1. Exploratory Data Analysis of Hebarman Survival Data Set

Description:-

The dataset contains cases from a study that was conducted between 1958 and 1970 at the university of chicago's billings hospital on survival of patients who had undergone surgery for breast cancer

Attributes/Features Information :- (from kaggle)

1. There are 4 features including class label/dependent variable.
2. 30 - It represents age of patient at the time of operation(numerical)
3. 64 - It represents year of operation(numerical)
4. 1 - It tells no of +ve auxillry node detected(numerical)
5. 1.1 - Survival status 1 = the patient survived 5 years or longer 2 = the patient died within 5 year

In [4]:

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

In [5]:

```
# Data source :- https://www.kaggle.com/gilsousa/habermans-survival-data-set
# Read the dataset using pandas library
haber = pd.read_csv("haberman.csv")
```

(1.1) High Level Statistics of Dataset

In [8]:

```
#how many rows and columns?
haber.shape
```

Out[8]:

```
(305, 4)
```

In [9]:

```
#Top 5 rows and all columns
haber.head()
```

Out[9]:

	30	64	1	1.1
0	30	62	3	1
1	30	65	0	1
2	31	59	2	1
3	31	65	4	1
4	33	58	10	1

observations :-

1. Haberman dataset contains 305 rows and 4 columns
2. From above we can see that, columns are not having names
3. From kaggle adding the names of columns

In [34]:

```
#naming the columns
print(haber.columns)
haber.columns = ["age","operation_year","axil_nodes","survival_status"]
print(haber.head())
```

```
Index(['age', 'opertion_year', 'axil_nodes', 'survival_status'], dtype='object')
   age  operation_year  axil_nodes  survival_status
0   30              62           3                1
1   30              65           0                1
2   31              59           2                1
3   31              65           4                1
4   33              58          10                1
```

observations:-

1. First column contains age of patients
2. Second column contains opeartion year of patients
3. Third column contains number of axil nodes, which are responsible for cancer
4. Fourth coulmn contains :-

   1 = person survived after 5 years,

   2 = person died befor 5 years

In [35]:

```
haber.describe()
```

Out[35]:

	age	operation_year	axil_nodes	survival_status
count	305.000000	305.000000	305.000000	305.000000
mean	52.531148	62.849180	4.036066	1.265574
std	10.744024	3.254078	7.199370	0.442364
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%	61.000000	66.000000	4.000000	2.000000
max	83.000000	69.000000	52.000000	2.000000

In [36]:

```
haber.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 305 entries, 0 to 304
Data columns (total 4 columns):
age                305 non-null int64
operation_year     305 non-null int64
axil_nodes         305 non-null int64
survival_status    305 non-null int64
dtypes: int64(4)
memory usage: 9.6 KB
```

In [37]:

```
haber["survival_status"].value_counts()
```

```
haber['survival_status'].value_counts()
```

Out[37]:

```
1    224
2     81
Name: survival_status, dtype: int64
```

observations:-

```
1. clearly knowing that, haberman dataset is unbalanced dataset
   224:- people lived after 5 years
    81:- people dead before 5 years
```

(1.2) Objective :-

Our objective is to predict whether the patient will survive after 5 years or not based on this 4 features (age , operation_year, axil_nodes, survival_status)

BI-VARIATE ANALYSIS

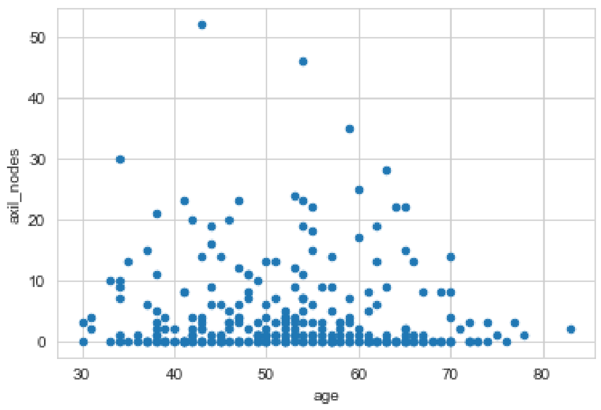
(1.3) 2-D Scatter Plot

In [38]:

```
#scatterplot
haber.plot(kind ="scatter", x ="age",y ="axil_nodes")
```

Out[38]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x203ee127a58>
```

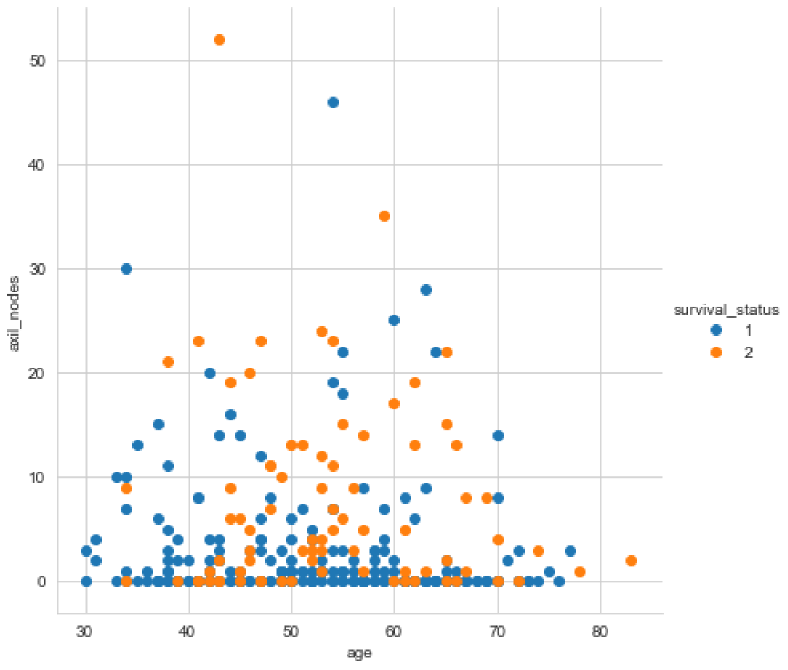


observation:-

```
Maximum number of people are having zero axil_nodes
```

In [39]:

```
# 2-D Scatter plot with color-coding for each flower type/class.
# Here 'sns' corresponds to seaborn.
sns.set_style("whitegrid")
sns.FacetGrid(haber,hue="survival_status",height=6)\
   .map(plt.scatter,"age","axil_nodes")\
   .add_legend()
plt.show()
```



observations:-

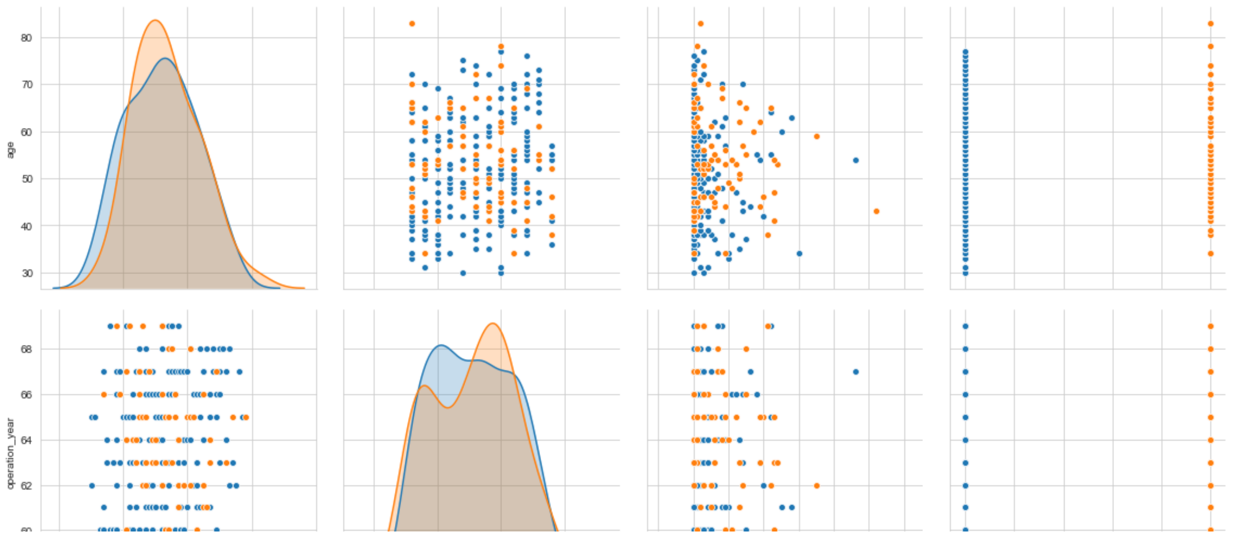
```
1.it is difficult to classify orange and blue points
2.But mostly people lies on zero axil_nodes
3.From this 2-d sactterplot we cannot make take decision , because it is not clearly
classified
4.For good analysis of data , pair plots are used
```

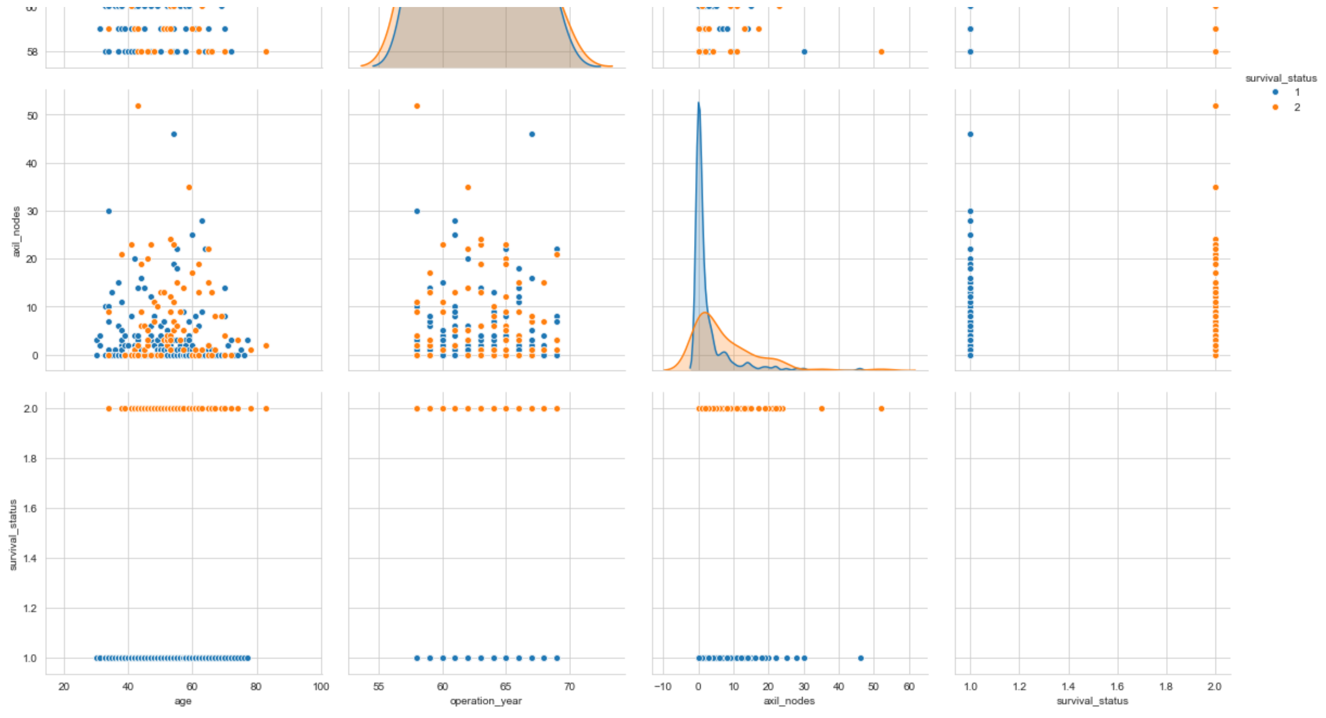
3-D Satter plot

(1.4) Pair Plot

In [40]:

```
# pairwise scatter plot: Pair-Plot
# Dis-advantages:
##Can be used when number of features are high.
##Cannot visualize higher dimensional patterns in 3-D and 4-D.
#Only possible to view 2D patterns
plt.close()
sns.set_style("whitegrid")
sns.pairplot(haber,hue ="survival_status",height=4)
plt.show()
```





observation:-

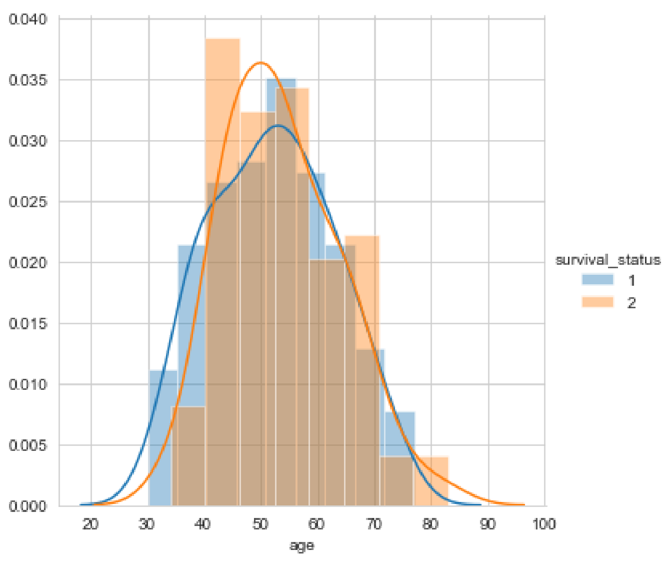
```
1. By scattering the data points between axil_nodes and age,we can see the better
seperation between the two
clases than other scatter plots
2. Remaining plots are extremely overlapped
```

UNIVARIATE ANALYSIS

(1.5) Histogram,PDF,CDF

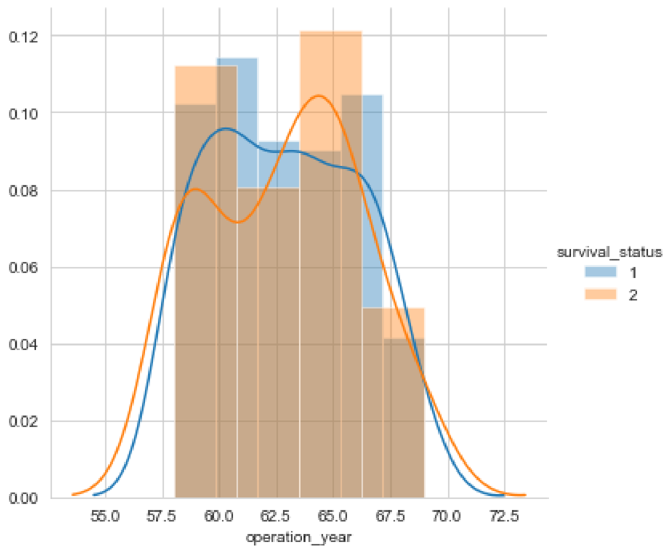
In [44]:

```
sns.FacetGrid(haber,hue="survival_status",height=5)\
   .map(sns.distplot,"age")\
   .add_legend()
plt.show()
```



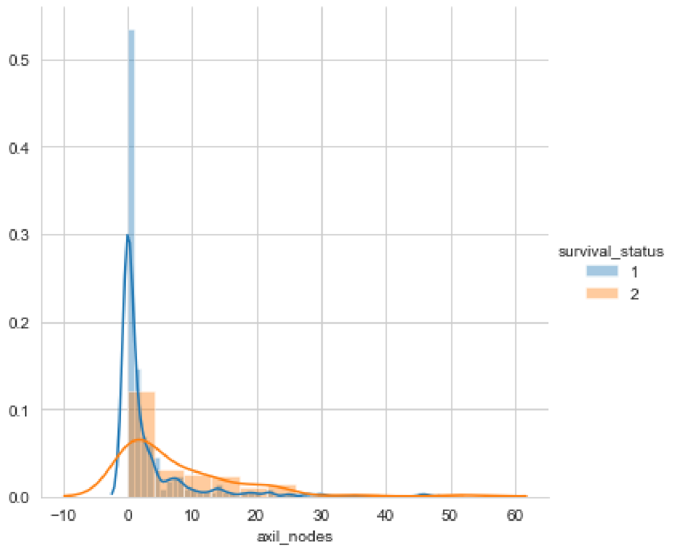
In [45]:

```
sns.FacetGrid(haber,hue="survival_status",height=5)\
    .map(sns.distplot,"operation_year")\
    .add_legend()
plt.show()
```



In [46]:

```
sns.FacetGrid(haber,hue="survival_status",height=5)\
    .map(sns.distplot,"axil_nodes")\
    .add_legend()
plt.show()
```



observations:-

```
1.From pdfs of this "age vs survival_status" and  "operation_year vs survival_status" plots
we cannot classify , because
 it is overlapped more
2.From pdf of "axil_nodes vs survival_status"  as there is difference between the
distributions for both classes.
 From that distribution we can infer that most survival patients have fallen in to zero axi
l_nodes.
```

CDF

In [54]:

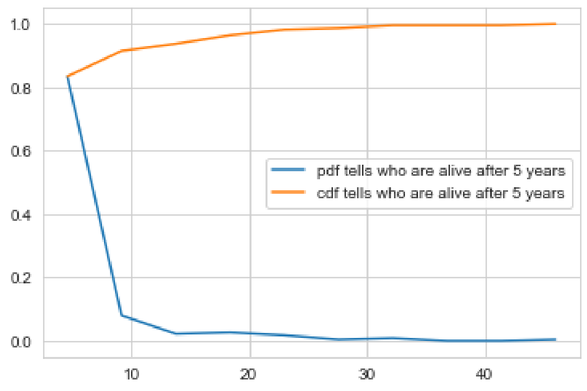
```
#dividing the dataset according to survial_status
#in survival status dataset have two classes 1,2
```

```
#consider survival_status aliveafter5= 1, deadbefore5 =2
alive_after5= haber.loc[haber["survival_status"]==1]
dead_before5 = haber.loc[haber["survival_status"]==2]
```

In [58]:

```
counts,bin_edges = np.histogram(alive_after5["axil_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)
plt.legend(["pdf tells who are alive after 5 years","cdf tells who are alive after 5 years"])
plt.show()
```

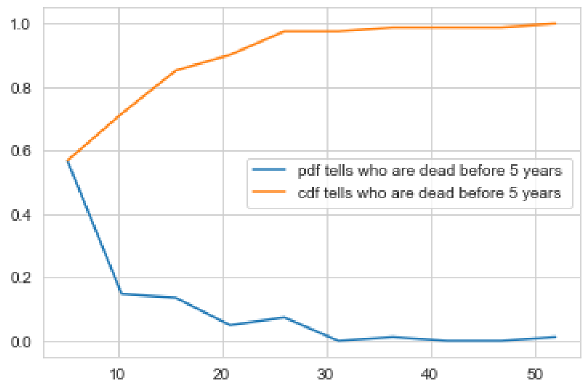
```
[0.83482143 0.08035714 0.02232143 0.02678571 0.01785714 0.00446429
 0.00892857 0.         0.         0.00446429]
[ 0.   4.6  9.2 13.8 18.4 23.  27.6 32.2 36.8 41.4 46. ]
```



In [59]:

```
counts,bin_edges = np.histogram(dead_before5["axil_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)
plt.legend(["pdf tells who are dead before 5 years","cdf tells who are dead before 5 years "])
plt.show()
```

```
[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. ]
```



(1.6) Mean, Variance and Std-dev

In [88]:

```
#Mean, Variance, Std-deviation
print("Mean for alive_after5:")
print(np.mean(alive_after5["age"]))
print(np.mean(alive_after5["axil_nodes"]))
print(np.mean(alive_after5["operation_year"]))

print("\n Mean for dead_before5:")
print(np.mean(dead_before5["age"]))
print(np.mean(dead_before5["axil_nodes"]))
print(np.mean(dead_before5["operation_year"]))

#std_deviation
print("\nstd_deviation for alive_after5:")
print(np.std(alive_after5["age"]))
print(np.std(alive_after5["axil_nodes"]))
print(np.std(alive_after5["operation_year"]))

print("\n std_dead_before5:")
print("std_deviation for alive_after5")
print(np.std(dead_before5["age"]))
print(np.std(dead_before5["axil_nodes"]))
print(np.std(dead_before5["operation_year"]))

#variance
print("\nvariance for alive_after5:")
print(np.var(alive_after5["age"]))
print(np.var(alive_after5["axil_nodes"]))
print(np.var(alive_after5["operation_year"]))

print("\n variance for dead_before5:")
print(np.var(dead_before5["age"]))
print(np.var(dead_before5["axil_nodes"]))
print(np.var(dead_before5["operation_year"]))
```

```
Mean for alive_after5:
52.11607142857143
2.799107142857143
62.857142857142854

 Mean for dead_before5:
53.67901234567901
7.45679012345679
62.82716049382716

std_deviation for alive_after5:
10.913004640364269
5.869092706952767
3.2220145175061514

 std_dead_before5:
std_deviation for alive_after5
10.10418219303131
9.128776076761632
3.3214236255207883

variance for alive_after5:
119.09367028061209
34.44624920280616
10.381377551020398

 variance for dead_before5:
102.09449778997102
83.3345526596555
11.031854900167659
```

In [71]:

```
print("overall summary statistics of patients alive after 5 years")
alive_after5.describe()
```

```
overall summary statistics of patients alive after 5 years
```

Out[71]:

	age	operation_year	axil_nodes	survival_status
count	224.000000	224.000000	224.000000	224.0
mean	52.116071	62.857143	2.799107	1.0
std	10.937446	3.229231	5.882237	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

In [72]:

```
print("overall summary statistics of patients dead before 5 years")
dead_before5.describe()
```

```
overall summary statistics of patients dead before 5 years
```

Out[72]:

	age	operation_year	axil_nodes	survival_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:-

```
1.From both the tables we can observe that almost for all the features the statistics are s
imilar except for axil_nodes.
2.The mean of axil_nodes is more for people who died within 5 years than people who have su
rvived for more than 5 years
```

(1.7) Median, Percentile, Quantile, IQR, MAD

In [87]:

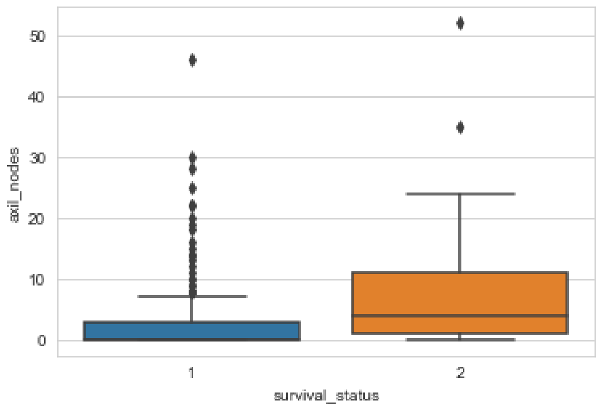
```
#Median, Quantiles, Percentiles, IQR.
print("\nMedians:")
print(np.median(alive_after5["axil_nodes"]))
#Median with outlier
print(np.median(np.append(alive_after5["axil_nodes"],60)))
print(np.median(dead_before5["axil_nodes"]))

print("\nQuantiles:")
print(np.percentile(alive_after5["axil_nodes"],np.arange(0,100,25)))
print(np.percentile(dead_before5["axil_nodes"],np.arange(0,100,25)))

print("\n90th Percentiles:")
print(np.percentile(alive_after5["axil_nodes"],90))
print(np.percentile(dead_before5["axil_nodes"],90))

from statsmodels import robust
print("\n Median Absolute Deviation:")
print(robust.mad(alive_after5["axil_nodes"]))
print(robust.mad(dead_before5["axil_nodes"]))
```

```
Medians:
0.0
0.0
4.0

Quantiles:
[0. 0. 0. 3.]
[ 0.  1.  4. 11.]

90th Percentiles:
8.0
20.0

 Median Absolute Deviation:
0.0
5.930408874022408
```

1.8 Box plot and Whiskers

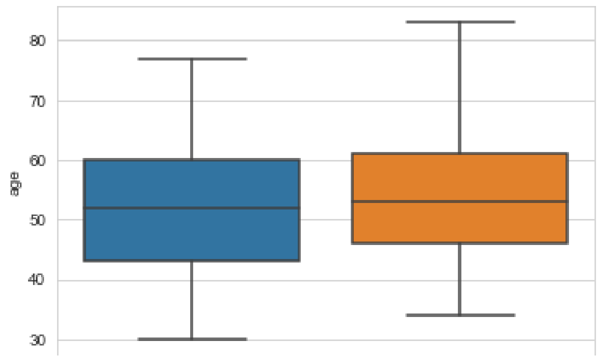
In [79]:

```
#Box-plot with whiskers: another method of visualizing the  1-D scatter plot more intuitivey.
# The Concept of median, percentile, quantile.
# How to draw the box in the box-plot?
# How to draw whiskers: [no standard way] Could use min and max or use other complex statistical t
echniques.
# IQR like idea.

#NOTE: IN the plot below, a technique call inter-quartile range is used in plotting the whiskers.
#Whiskers in the plot below donot correposnd to the min and max values.

#Box-plot can be visualized as a PDF on the side-ways.

sns.boxplot(x = "survival_status", y = "axil_nodes", data =haber)
plt.show()
```



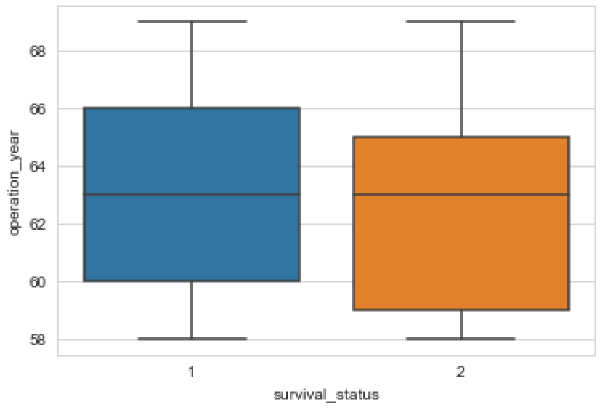
In [80]:

```
sns.boxplot(x="survival_status",y = "age",data=haber)
plt.show()
```



In [82]:

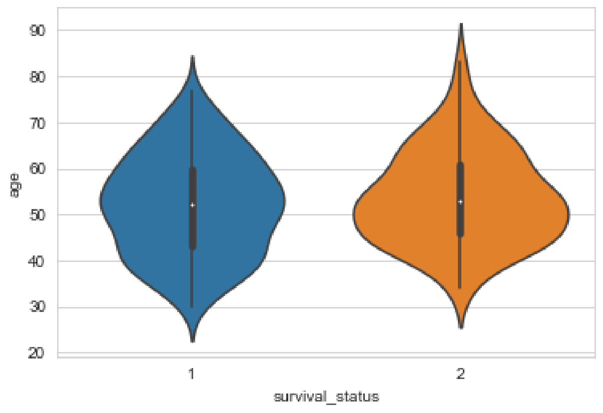
```
sns.boxplot(x="survival_status",y="operation_year",data=haber)
plt.show()
```



1.9 Violin plots

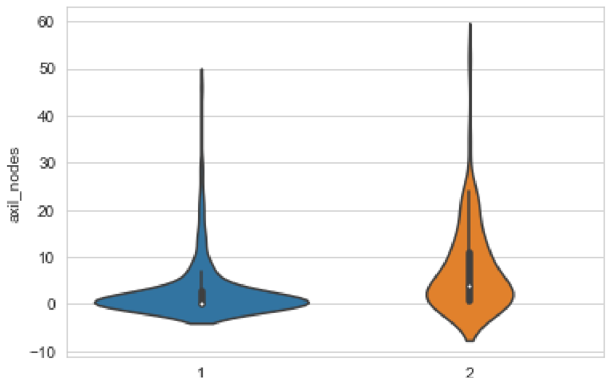
In [84]:

```
# A violin plot combines the benefits of the previous two plots
#and simplifies them

# Denser regions of the data are fatter, and sparser ones thinner
#in a violin plot

sns.violinplot(x="survival_status",y="age", data =haber, size=8)
plt.show()
```



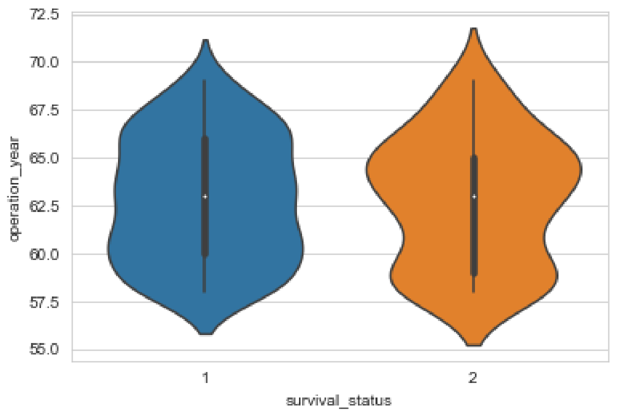
In [85]:

```
sns.violinplot(x="survival_status",y="axil_nodes",data=haber,size =8)
plt.show()
```



In [86]:

```
sns.violinplot(x="survival_status", y="operation_year",data=haber,size=8)
plt.show()
```



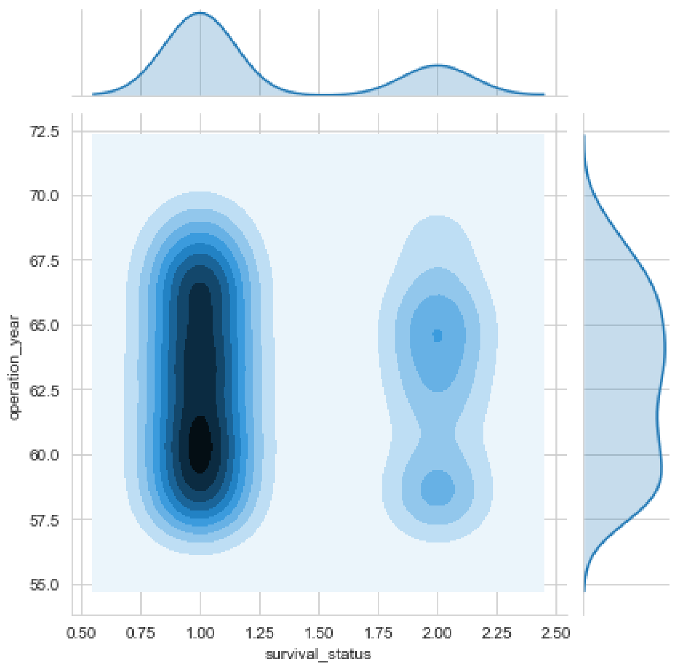
observations:-

```
1.Axil_nodes of survival_status is dense from 0 to 5
2.More than 5 years 80% of people have less than or equal to 5 axil_nodes
3. (46-62) age group patients were dead year between 1959 to 1965
4. (42-60) age group patients are alive year between 1960 to 1966
```

Countour Plot

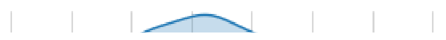
In [89]:

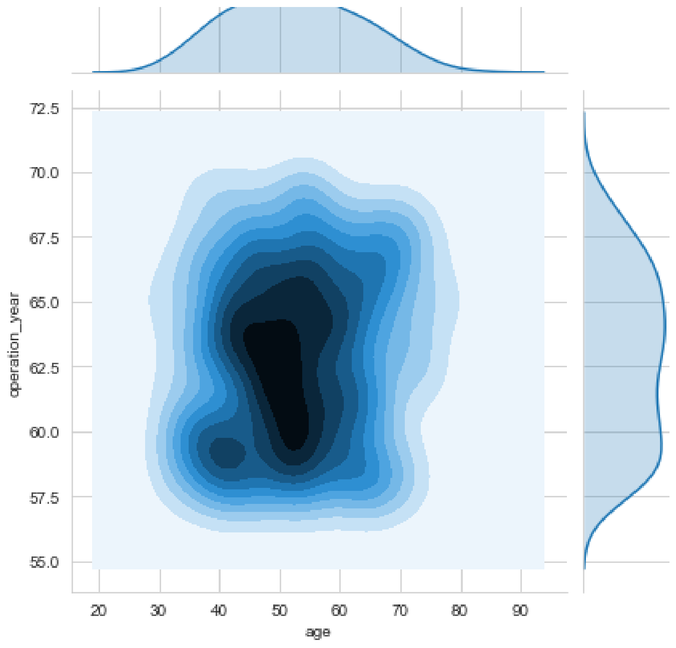
```
sns.jointplot(x="survival_status",y="operation_year",data=haber,kind="kde")
plt.show()
```



In [90]:

```
sns.jointplot(x="age",y="operation_year",data=haber,kind="kde")
plt.show()
```





conclusions:-

1. The given dataset is imbalanced as it does not contain equal number data points means class labels
2. The given dataset is not linearly seperable from each, there is huge overlapping between classlabels so it is difficult to classify.
3. Somehow, axil_nodes vs age gives some geometrical idea of classification of survival_status
4. we cannot make model using simple if_else conditions, we should use some advance techniques to solve

ASSIGNMENT -1

B MUKUNDA REDDY

```
In [ ]:
```