EXPLORATORY DATA ANALYSIS: HABERMAN DATASET

A. DATASET INFORMATION

About the Dataset :- The Haberman's Survival Dataset contains cases from a study that was conducted between 1958 and 1970 at the University of Chicagos Billings Hospital on the survival of patients who had undergone surgery for breast cancer.

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

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

B. OBJECTIVE

To predict whether the patient will survive after 5 years or not based upon the patient's age, year of treatment and the number of positive lymph nodes

C. DATASET CONFIGURATION

1. ENVIRONMENT SETUP

In [1]:
```python
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
import warnings
warnings.filterwarnings('ignore') ## ignore all the warnings
from statsmodels import robust ## for Median Absolute Deviation
```

2. LOADING THE DATASET

In [2]:
```python
haberman=pd.read_csv("haberman.csv")
```

D. HIGH LEVEL STATISTICS OF THE DATASET

In [3]:
```python
# haberman.describe()
print(haberman.head(15))
```

```
    age  operation_year  axil_nodes  survival_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
10   34              60           1                1
11   34              61          10                1
12   34              67           7                1
13   34              60           0                1
14   35              64          13                1
```

1. NUMBER OF POINTS

In [4]:
```python
print (haberman.shape)
```

```
(306, 4)
```

In [5]:
```python
haberman["survival_status"].value_counts()
```

Out[5]:
```
1    225
2     81
Name: survival_status, dtype: int64
```

In [6]:
```python
haberman.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 306 entries, 0 to 305
Data columns (total 4 columns):
age                306 non-null int64
operation_year     306 non-null int64
axil_nodes         306 non-null int64
survival_status    306 non-null int64
dtypes: int64(4)
memory usage: 9.6 KB
```

In [7]:
```python
# Class Label "survival_status" are now to labelled as {1:"yes",2:"no"} stating "yes" as survived and "no" as Dead Not Survived
haberman['survival_status'] = haberman['survival_status'].map({1:"yes", 2:"no"})
print(haberman.head(15)) ## we are displaying 1st 15 lines
```

```
    age  operation_year  axil_nodes survival_status
0    30              64           1             yes
1    30              62           3             yes
2    30              65           0             yes
3    31              59           2             yes
4    31              65           4             yes
5    33              58          10             yes
6    33              60           0             yes
7    34              59           0              no
8    34              66           9              no
9    34              58          30             yes
10   34              60           1             yes
11   34              61          10             yes
12   34              67           7             yes
13   34              60           0             yes
14   35              64          13             yes
```

In [8]:
```python
## CHECKING THE UPDATED SURVIVAL STATUS
haberman["survival_status"].value_counts()
```

Out[8]:
```
yes    225
no      81
Name: survival_status, dtype: int64
```

In [9]:
```python
## CHECKING THE UPDATED INFO ABOUT THE CHANGED DATATYPE OF OUR CLASS LABEL
haberman.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 306 entries, 0 to 305
Data columns (total 4 columns):
age                306 non-null int64
operation_year     306 non-null int64
axil_nodes         306 non-null int64
survival_status    306 non-null object
dtypes: int64(3), object(1)
memory usage: 9.6+ KB
```

OBSERVATION

1. Dataset is UNBALANCED but complete as no values are missing
2. Our CLASS LABEL ie survival_status is INTERGER and needs to converted to valid CATEGORICAL datatype
3. Class Label "survival_status" are now to labelled as {1:"yes",2:"no"} stating "yes" as survived and "no" as Dead Not Survived

2. NUMBER OF FEATURES

In [10]:
```python
print (haberman.columns)
```

```
Index(['age', 'operation_year', 'axil_nodes', 'survival_status'], dtype='object')
```

In [11]:
```python
## Last column is our CATEGORY that is the DEPENDENT VARIABLE, therefore it is not considered as a feature
print (haberman.columns[:-1])
```

```
Index(['age', 'operation_year', 'axil_nodes'], dtype='object')
```

3. NUMBER OF CLASSES

In [12]:
```python
print(haberman["survival_status"].unique())
```

```
['yes' 'no']
```

4. DATAPOINTS PER NUMBER OF CLASS

In [13]:
```python
print(haberman.groupby("survival_status").count())
```

```
                 age  operation_year  axil_nodes
survival_status
no                81              81          81
yes              225             225         225
```

5. MEAN, MAD & STD. DEVIATION

In [14]:
```python
haberman_yes=haberman.loc[haberman["survival_status"]=="yes"]
haberman_no=haberman.loc[haberman["survival_status"]=="no"]

print("SURVIVAL_STATUS: YES , COUNT",haberman_yes["survival_status"].count())
print("hi")
print("VARIABLE       MEAN             MEDIAN    STD. DEVIATION        MAD")
print("age          ",np.mean(haberman_yes["age"]),"  ",np.median(haberman_yes["age"]),"  ",np.std(haberman_yes["age"]),"   ",robust.mad(haberman_yes["age"]))
print("opYear       ",np.mean(haberman_yes["operation_year"]),"  ",np.median(haberman_yes["operation_year"]),"  ",np.std(haberman_yes["operation_year"]),"   ",robust.mad(haberman_yes["operation_year"]))
print("axilnodes    ",np.mean(haberman_yes["axil_nodes"]),"  ",np.median(haberman_yes["axil_nodes"]),"  ",np.std(haberman_yes["axil_nodes"]),"   ",robust.mad(haberman_yes["axil_nodes"]))
print("\n")
# includeInDescribe=['ag','opYear','axilNodes']
perc=[.0,.25,.50,.75,.1]


print("SURVIVAL_STATUS: NO , COUNT",haberman_no["survival_status"].count())
print("VARIABLE       MEAN             MEDIAN    STD. DEVIATION        MAD")
print("age          ",np.mean(haberman_no["age"]),"  ",np.median(haberman_no["age"]),"  ",np.std(haberman_no["age"]),"   ",robust.mad(haberman_no["age"]))
print("opYear       ",np.mean(haberman_no["operation_year"]),"  ",np.median(haberman_no["operation_year"]),"  ",np.std(haberman_no["operation_year"]),"   ",robust.mad(haberman_no["operation_year"]))
print("axilnodes    ",np.mean(haberman_no["axil_nodes"]),"  ",np.median(haberman_no["axil_nodes"]),"  ",np.std(haberman_no["axil_nodes"]),"   ",robust.mad(haberman_no["axil_nodes"]))
print("\n\n")

print("SURVIVAL STATUS: YES -> DESCRIBE")
print(haberman_yes.describe(percentiles=perc))
print("\n\n")
print("SURVIVAL STATUS: NO -> DESCRIBE")
print(haberman_no.describe(percentiles=perc))
# print(haberman.describe(percentiles=perc))
```

```
SURVIVAL_STATUS: YES , COUNT 225
hi
VARIABLE       MEAN             MEDIAN    STD. DEVIATION        MAD
age          52.01777777777778    52.0    10.98765547510051     13.343419966550417
opYear       62.86222222222222    63.0    3.2157452144021956     4.447806655516806
axilnodes    2.7911111111111113    0.0    5.857258449412131     0.0


SURVIVAL_STATUS: NO , COUNT 81
VARIABLE       MEAN             MEDIAN    STD. DEVIATION        MAD
age          53.67901234567901    53.0    10.10418219303131     11.860817748044816
opYear       62.82716049382716    63.0    3.3214236255207883    4.447806655516806
axilnodes    7.45679012345679     4.0     9.128776076761632     5.930408874022408


SURVIVAL STATUS: YES -> DESCRIBE
              age  operation_year  axil_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
0%      30.000000       58.000000    0.000000
10%     38.000000       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


SURVIVAL STATUS: NO -> DESCRIBE
             age  operation_year  axil_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
0%     34.000000       58.000000    0.000000
10%    42.000000       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
```

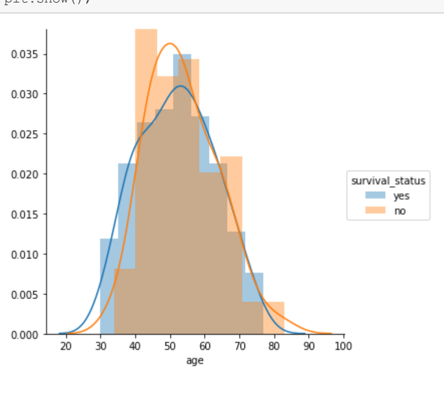
OBSERVATION

1. This is Binary Classification Problem, where we need to predict whether the patient will survive after 5 years or not based upon the patient's age, year of treatment and the number of positive lymph nodes
2. 50% of the Patients are below the age of 54.

E. UNIVARIATE ANALYSIS

1. HISTOGRAM

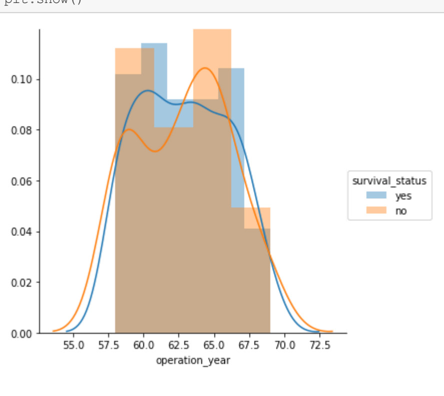
In [15]:
```python
## PATIENT AGE
sns.FacetGrid(haberman,hue="survival_status",size=5)\
    .map(sns.distplot,"age")\
    .add_legend();

plt.show();
```



OBSERVATION

1. Patients with age range 40-60 have survived the most.

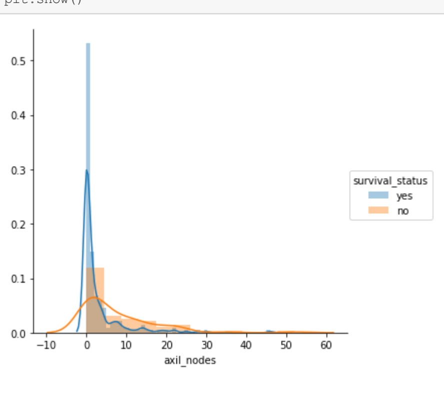
In [16]:
```python
sns.FacetGrid(haberman,hue="survival_status",size=5)\
    .map(sns.distplot,"operation_year")\
    .add_legend();
plt.show()
```



OBSERVATION

1. Operation year having range (63-66) had highest successfull survival rate
2. Operation year 60 had highest un-successfull rate

In [17]:
```python
sns.FacetGrid(haberman,hue="survival_status",size=5)\
    .map(sns.distplot,"axil_nodes")\
    .add_legend();

plt.show()
```

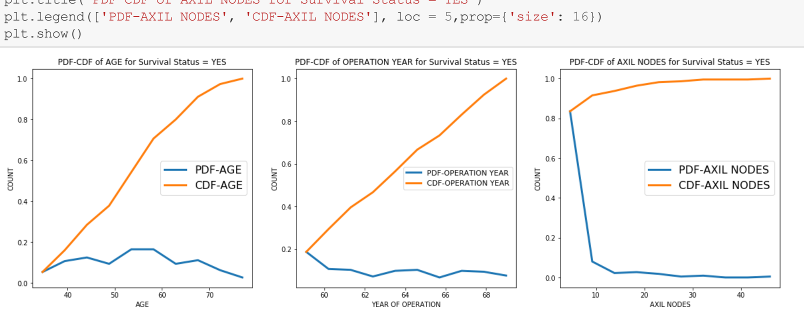


OBSERVATION

1. As we can clearly see, axil node=0 has the highest Survival rate.

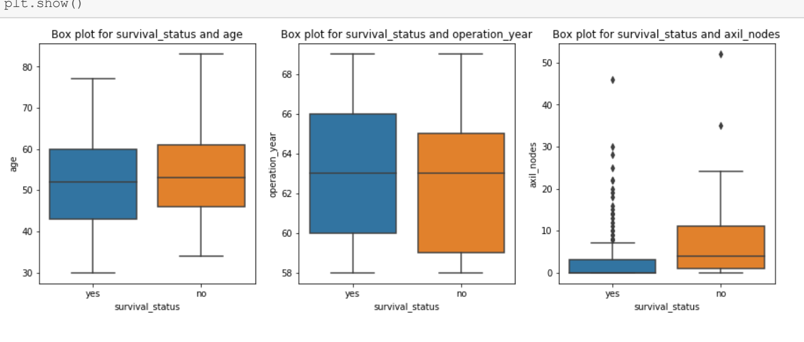
2. PDF & CDF

In [18]:
```python
##haberman
plt.figure(figsize=(20,6))
plt.subplot(131) ##(1=no. of rows, 3= no. of columns, 1=1st figure,2,3,4 boxes)
counts,bin_edges=np.histogram(haberman_yes["age"],bins=10,density=True)
pdf=counts/sum(counts)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,linewidth=3.0)
plt.plot(bin_edges[1:],cdf,linewidth=3.0)
plt.ylabel("COUNT")
plt.xlabel('AGE')
plt.title('PDF-CDF of AGE for Survival Status = YES')
plt.legend(['PDF-AGE', 'CDF-AGE'], loc = 5,prop={'size': 16})

plt.subplot(132)
counts,bin_edges=np.histogram(haberman_yes["operation_year"],bins=10,density=True)
pdf=counts/sum(counts)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,linewidth=3.0)
plt.plot(bin_edges[1:],cdf,linewidth=3.0)
plt.ylabel("COUNT")
plt.xlabel('YEAR OF OPERATION')
plt.title('PDF-CDF of OPERATION YEAR for Survival Status = YES')
plt.legend(['PDF-OPERATION YEAR', 'CDF-OPERATION YEAR'], loc = 5,prop={'size': 11})

plt.subplot(133)
counts,bin_edges=np.histogram(haberman_yes["axil_nodes"],bins=10,density=True)
pdf=counts/sum(counts)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,linewidth=3.0)
plt.plot(bin_edges[1:],cdf,linewidth=3.0)
plt.ylabel("COUNT")
plt.xlabel('AXIL NODES')
plt.title('PDF-CDF of AXIL NODES for Survival Status = YES')
plt.legend(['PDF-AXIL NODES', 'CDF-AXIL NODES'], loc = 5,prop={'size': 16})
plt.show()
```



3. BOX PLOT & WHISKERS

In [19]:
```python
# Box plot takes a less space and visually represents the five number summary of the data points in a box.
# The outliers are displayed as points outside the box.
# 1. Q1 - 1.5*IQR
# 2. Q1 (25th percentile)
# 3. Q2 (50th percentile or median)
# 4. Q3 (75th percentile)
# 5. Q3 + 1.5*IQR
# Inter Quartile Range = Q3 -Q1

figure, axes = plt.subplots(1, 3, figsize=(15, 5))
for idx, feature in enumerate(list(haberman.columns)[:-1]):
    mystr="Box plot for survival_status and "+feature
    sns.boxplot( x='survival_status', y=feature, data=haberman, ax=axes[idx]).set_title(mystr)
plt.show()
```

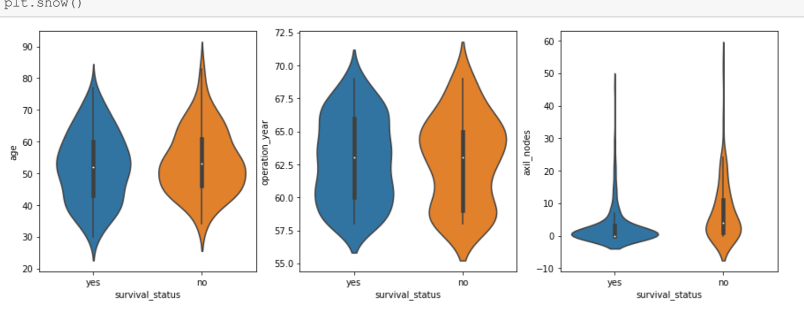


OBSERVATION

1. From AXIL_NODE and SURVIVAL_STATUS, we can conclude that higher the axil_nodes, higher the chances of their death.

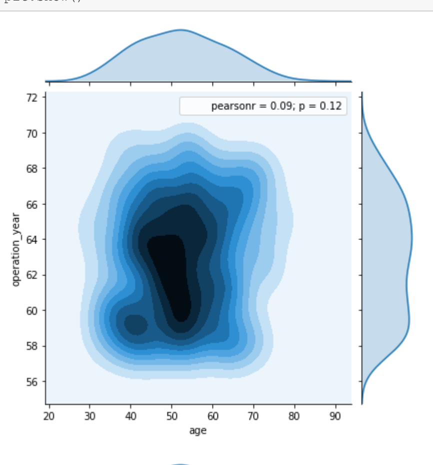
4. VIOLIN PLOT

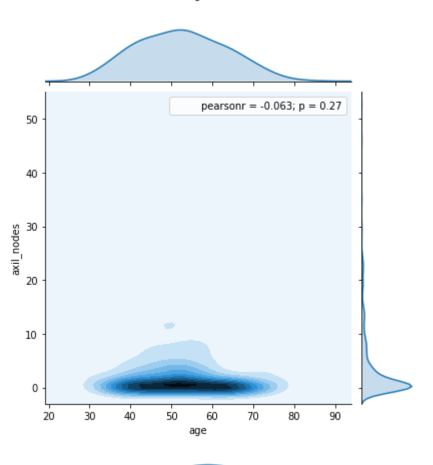
In [20]:
```python
# A violin plot combines the benefits of BoxPlot and Univariate Histogram PDF plots
#and simplifies them
# Denser regions of the data are fatter, and sparser ones thinner
#in a violin plot

fig, axes = plt.subplots(1, 3, figsize=(15, 5))
for idx, feature in enumerate(list(haberman.columns)[:-1]):
#     print(idx,feature)
    sns.violinplot( x='survival_status', y=feature, data=haberman, ax=axes[idx])
plt.show()
```

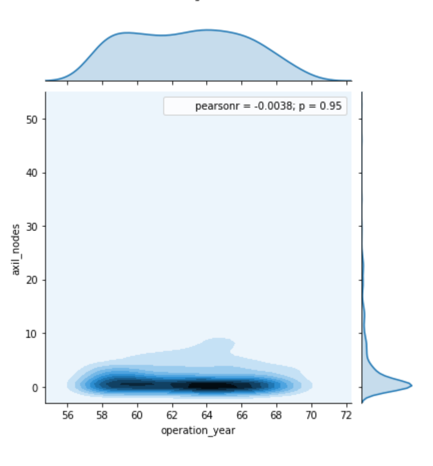


5. CONTOUR PLOT

In [21]:
```python
#2D Density plot, contors-plot
sns.jointplot(x="age",y="operation_year",data=haberman, kind="kde")
plt.show()

sns.jointplot(x="age",y="axil_nodes",data=haberman, kind="kde")
plt.show()

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







F. BI-VARIATE ANALYSIS

1. PAIR PLOTS

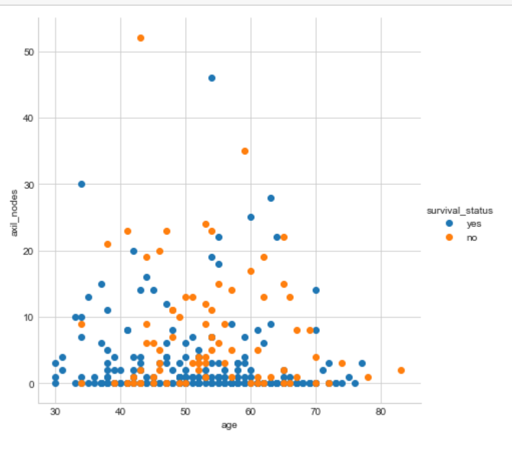
In [22]:
```python
plt.close() ## close previous show()
sns.set_style("whitegrid")
sns.pairplot(haberman,hue="survival_status",vars=["age","operation_year","axil_nodes"],size=3.5,plot_kws=dict(s=70),diag_kind = 'kde')
plt.show()
```

OBSERVATION

As we can see all the above Pair Plots, we can say that they are not Linearly Separable.

2. SCATTER PLOTS

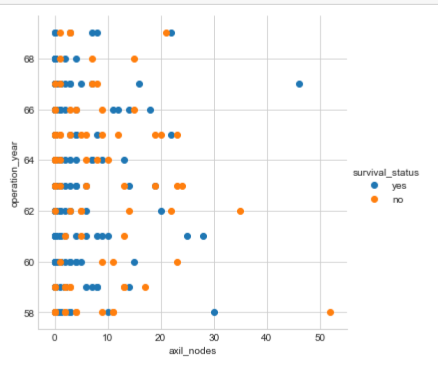
In [23]:
```python
## AGE <> AXIL NODES
# haberman.plot(kind='scatter', x='age', y='axil_nodes') ;
# plt.show()

sns.set_style("whitegrid");
sns.FacetGrid(haberman, hue="survival_status", size=6) \
   .map(plt.scatter, "age", "axil_nodes") \
   .add_legend();
plt.show();
```



OBSERVATION

1. Patients with Age < 40 and axil < 30 have higher chances of survival.
2. Patients with Age > 50 and Axil > 10 are more likely to die.

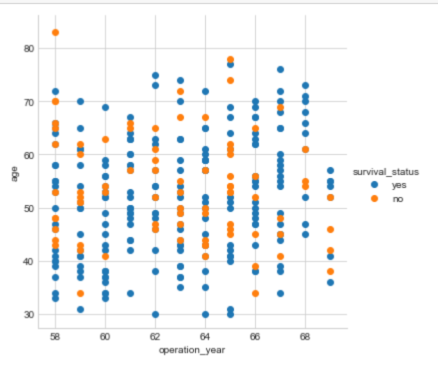
In [24]:
```python
## AXIL NODES <> OPERATION YEAR
sns.set_style("whitegrid");
sns.FacetGrid(haberman, hue="survival_status", size=5) \
   .map(plt.scatter, "axil_nodes", "operation_year") \
   .add_legend();

plt.show();
```



OBSERVATION

1. People with axil nodes more than 50 have higher rate of non survival.

In [25]:
```python
## AGE <> OPERATION YEAR
sns.set_style("whitegrid");
sns.FacetGrid(haberman, hue="survival_status", size=5) \
   .map(plt.scatter, "operation_year", "age") \
   .add_legend();
plt.show();
```



OBSERVATION

1. Operation year 60, 61 and 68 has more survival rate.

G. ALL OBSERVATIONS

1. Dataset is UNBALANCED but complete as no values are missing
2. Our CLASS LABEL ie survival_status is INTERGER and needs to converted to valid CATEGORICAL datatype
3. Class Label "survival_status" are now to labelled as {1:"yes",2:"no"} stating "yes" as survived and "no" as Dead Not Survived.
4. This is Binary Classification Problem, where we need to predict whether the patient will survive after 5 years or not based upon the patient's age, year of treatment and the number of positive lymph nodes
5. 50% of the Patients are below the age of 54.
6. Operation year having range (63-66) had highest successfull survival rate
7. Operation year 60 had highest un-successfull rate. Patients with age range 40-60 have survived the most.
8. As we can clearly see, axil node=0 has the highest Survival rate.
9. From AXIL_NODE and SURVIVAL_STATUS, we can conclude that higher the axil_nodes, higher the chances of their death.
10. As we can see all the above Pair Plots, we can say that they are not Linearly Separable.
11. Patients with Age < 40 and axil < 30 have higher chances of survival.
12. Patients with Age > 50 and Axil > 10 are more likely to die
13. People with axil nodes more than 50 have higher rate of non survival.
14. Operation year 60, 61 and 68 has more survival rate.