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.

Objective:

To predict whether the patient will survive after five years or not based on the attributes age,operation year and axil nodes

1. Environment Configuration

In [151]:
```python
# import all necessary packages
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
```

2. Loading The Data

Attribute Information:

Age ---- Age of patient at time of operation (numerical)

Op_year ----Patient's year of operation (numerical)

axil_nodes ----Number of positive axillary nodes detected (numerical)

Survival_status ----Survival status (class label)

1 = the patient survived 5 years or longer

2 = the patient died within 5 year

Here, Age, Op_year and axil_nodes are "variables" AND Survival_status is "class label"

In [152]:
```python
#Load the dataset
haber =pd.read_csv("D:\\haberman.csv")
print(haber)
```

```
     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
5    33  60   0    1
6    34  59   0    2
7    34  66   9    2
8    34  58  30    1
9    34  60   1    1
10   34  61  10    1
11   34  67   7    1
12   34  60   0    1
13   35  64  13    1
14   35  63   0    1
15   36  60   1    1
16   36  69   0    1
17   37  60   0    1
18   37  63   0    1
19   37  58   0    1
20   37  59   6    1
21   37  60  15    1
22   37  63   0    1
23   38  69  21    2
24   38  59   2    1
25   38  60   0    1
26   38  60   0    1
27   38  62   3    1
28   38  64   1    1
29   38  66   0    1
..   ..  ..  ..  ...
275  67  66   0    1
276  67  61   0    1
277  67  65   0    1
278  68  67   0    1
279  68  68   0    1
280  69  67   8    2
281  69  60   0    1
282  69  65   0    1
283  69  66   0    1
284  70  58   0    2
285  70  58   4    2
286  70  66  14    1
287  70  67   0    1
288  70  68   0    1
289  70  59   8    1
290  70  63   0    1
291  71  68   2    1
292  72  63   0    2
293  72  58   0    1
294  72  64   0    1
295  72  67   3    1
296  73  62   0    1
297  73  68   0    1
298  74  65   3    2
299  74  63   0    1
300  75  62   1    1
301  76  67   0    1
302  77  65   3    1
303  78  65   1    2
304  83  58   2    2

[305 rows x 4 columns]
```

In [153]:
```python
print(haber.columns)
```

```
Index(['30', '64', '1', '1.1'], dtype='object')
```

As,we have observed that our variable names/column names are in integer format we need to rename it so that we can access our column datapoints(data) easily.

Here we can can change column name with two approaches:

1. By directly assigning the names in list of columns,but A problem with this approach to change column names is that one has to change names of all the columns in the data frame. This approach would not work, if we want to change just change the name of one column.
2. By using the rename function We need to specify a mapper, a dictionary with old name as keys and new name as values.

In [154]:
```python
#Approach ii
haber.rename(columns={'30':'Age','64':'Op_year','1':'axil_nodes','float(1.1)':'Survival_status'},inp
lace=True)
print(haber.columns)
```

```
Index(['Age', 'Op_year', 'axil_nodes', '1.1'], dtype='object')
```

In [155]:
```python
#Approach i
haber.columns=['Age','Op_year','axil_nodes','Survival_status']
print(haber.columns)
```

```
Index(['Age', 'Op_year', 'axil_nodes', 'Survival_status'], dtype='object')
```

3. Data Preparation

In this phase you enhance the quality of the data and prepare it for use in subsequent steps.It ensures that the data is in a suitable format for use in your models.

In [156]:
```python
print(haber.shape)          #To check the no. of rows and columns in our dataset
```

```
(305, 4)
```

In [157]:
```python
haber.describe()
```

Out[157]:

	Age	Op_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 [158]:
```python
haber.isnull()              #To check if there are any null values in our dataset
```

Out[158]:

	Age	Op_year	axil_nodes	Survival_status
0	False	False	False	False
1	False	False	False	False
2	False	False	False	False
3	False	False	False	False
4	False	False	False	False
5	False	False	False	False
6	False	False	False	False
7	False	False	False	False
8	False	False	False	False
9	False	False	False	False
10	False	False	False	False
11	False	False	False	False
12	False	False	False	False
13	False	False	False	False
14	False	False	False	False
15	False	False	False	False
16	False	False	False	False
17	False	False	False	False
18	False	False	False	False
19	False	False	False	False
20	False	False	False	False
21	False	False	False	False
22	False	False	False	False
23	False	False	False	False
24	False	False	False	False
25	False	False	False	False
26	False	False	False	False
27	False	False	False	False
28	False	False	False	False
29	False	False	False	False
...	...	...	...	...
275	False	False	False	False
276	False	False	False	False
277	False	False	False	False
278	False	False	False	False
279	False	False	False	False
280	False	False	False	False
281	False	False	False	False
282	False	False	False	False
283	False	False	False	False
284	False	False	False	False
285	False	False	False	False
286	False	False	False	False
287	False	False	False	False
288	False	False	False	False
289	False	False	False	False
290	False	False	False	False
291	False	False	False	False
292	False	False	False	False
293	False	False	False	False
294	False	False	False	False
295	False	False	False	False
296	False	False	False	False
297	False	False	False	False
298	False	False	False	False
299	False	False	False	False
300	False	False	False	False
301	False	False	False	False
302	False	False	False	False
303	False	False	False	False
304	False	False	False	False

305 rows × 4 columns

In [179]:
```python
haber['Survival_status'].value_counts() #To check the count of the no. of people living for 5 year o
r above and 5 years and below"""
```

Out[179]:
```
1    224
2     81
Name: Survival_status, dtype: int64
```

Imbalanced dataset

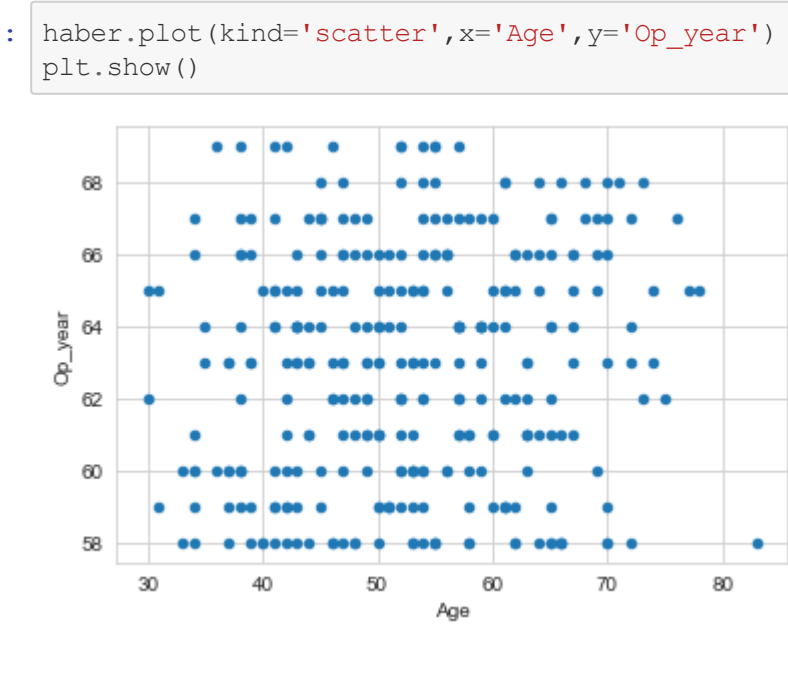
As, we can observe in the output above that the counts of number of people living more than 5 years and number of people living less than 5 years differ to a greater extent.Hence, our dataset is imbalanced.

4. Data Exploration

Data exploration is concerned with building a deeper understanding of your data. You try to understand how variables interact with each other, the distribution of the data, and whether there are outliers.

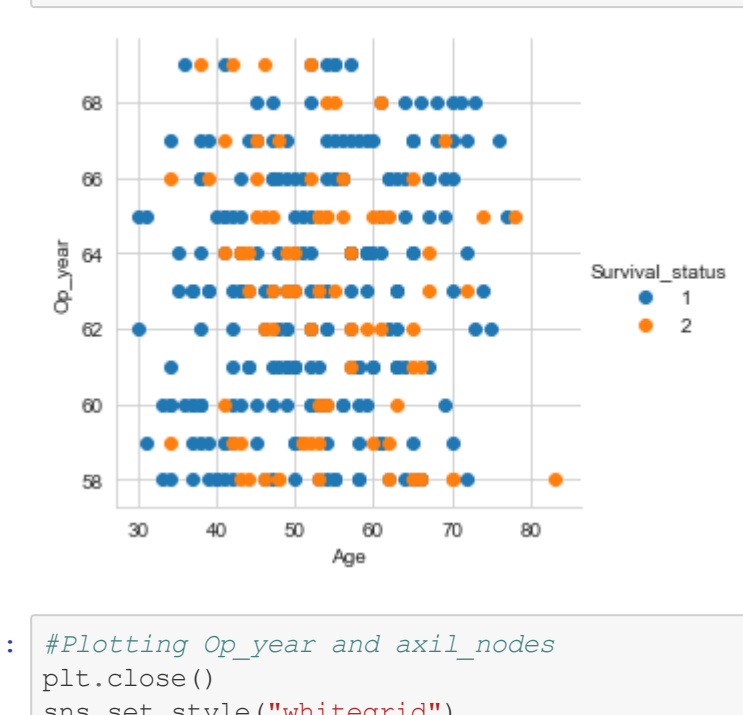
2-D Scatter Plot

In [160]:
```python
haber.plot(kind='scatter',x='Age',y='Op_year')
plt.show()
```

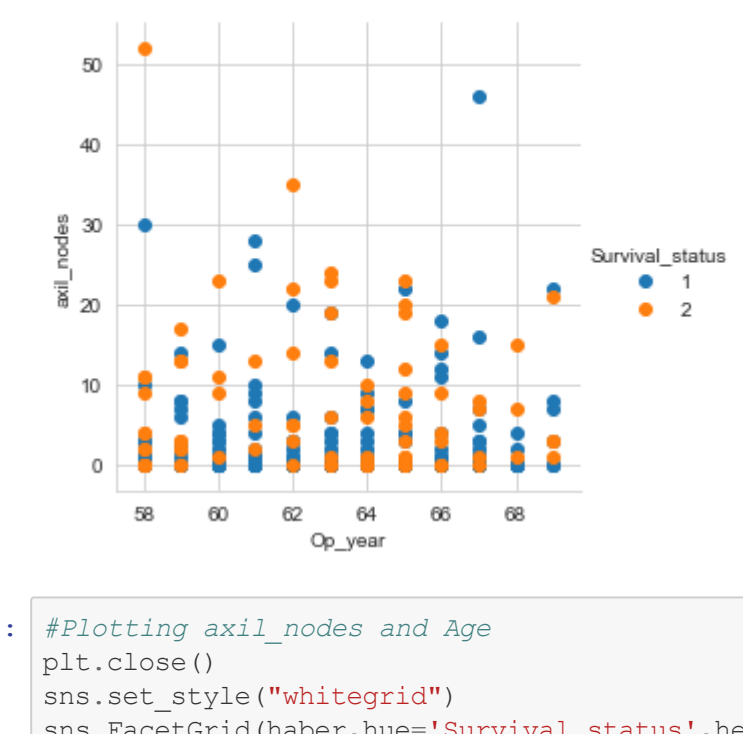


Here, we are scattering all the points on the graph.We can also scatter points using other combinations also like Op_year and axil_nodes,axil_nodes and Age.

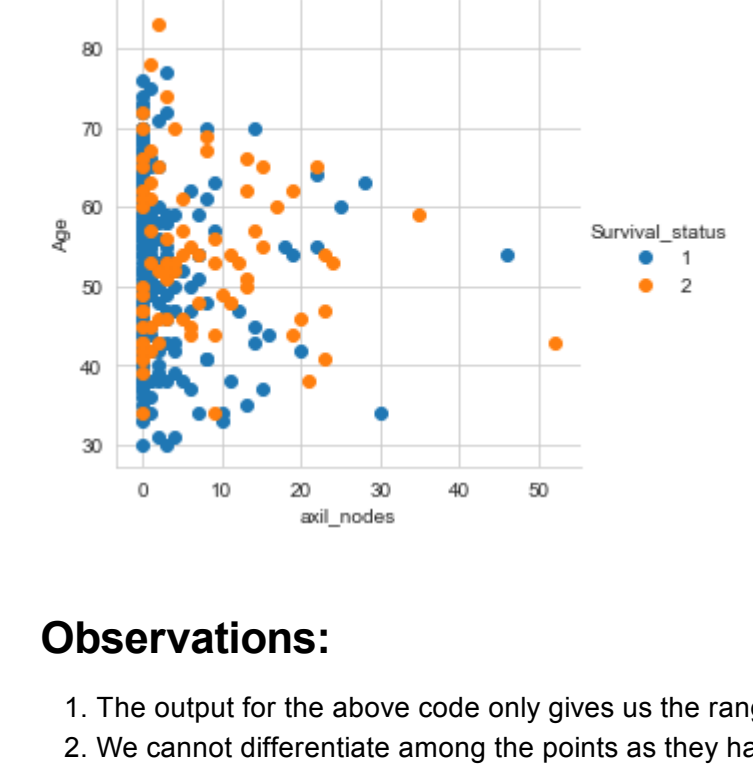
In [161]:
```python
#Here,we are coloring our points
#Plotting Age and Op_year
#The size attribute is updated as height
plt.close()
sns.set_style("whitegrid")
sns.FacetGrid(haber,hue='Survival_status',height=4)\
   .map(plt.scatter,"Age","Op_year").add_legend()
plt.show()
```



In [162]:
```python
#Plotting Op_year and axil_nodes
plt.close()
sns.set_style("whitegrid")
sns.FacetGrid(haber,hue='Survival_status',height=4)\
   .map(plt.scatter,"Op_year","axil_nodes").add_legend()
plt.show()
```



In [163]:
```python
#Plotting axil_nodes and Age
plt.close()
sns.set_style("whitegrid")
sns.FacetGrid(haber,hue='Survival_status',height=4)\
   .map(plt.scatter,"axil_nodes","Age").add_legend()
plt.show()
```



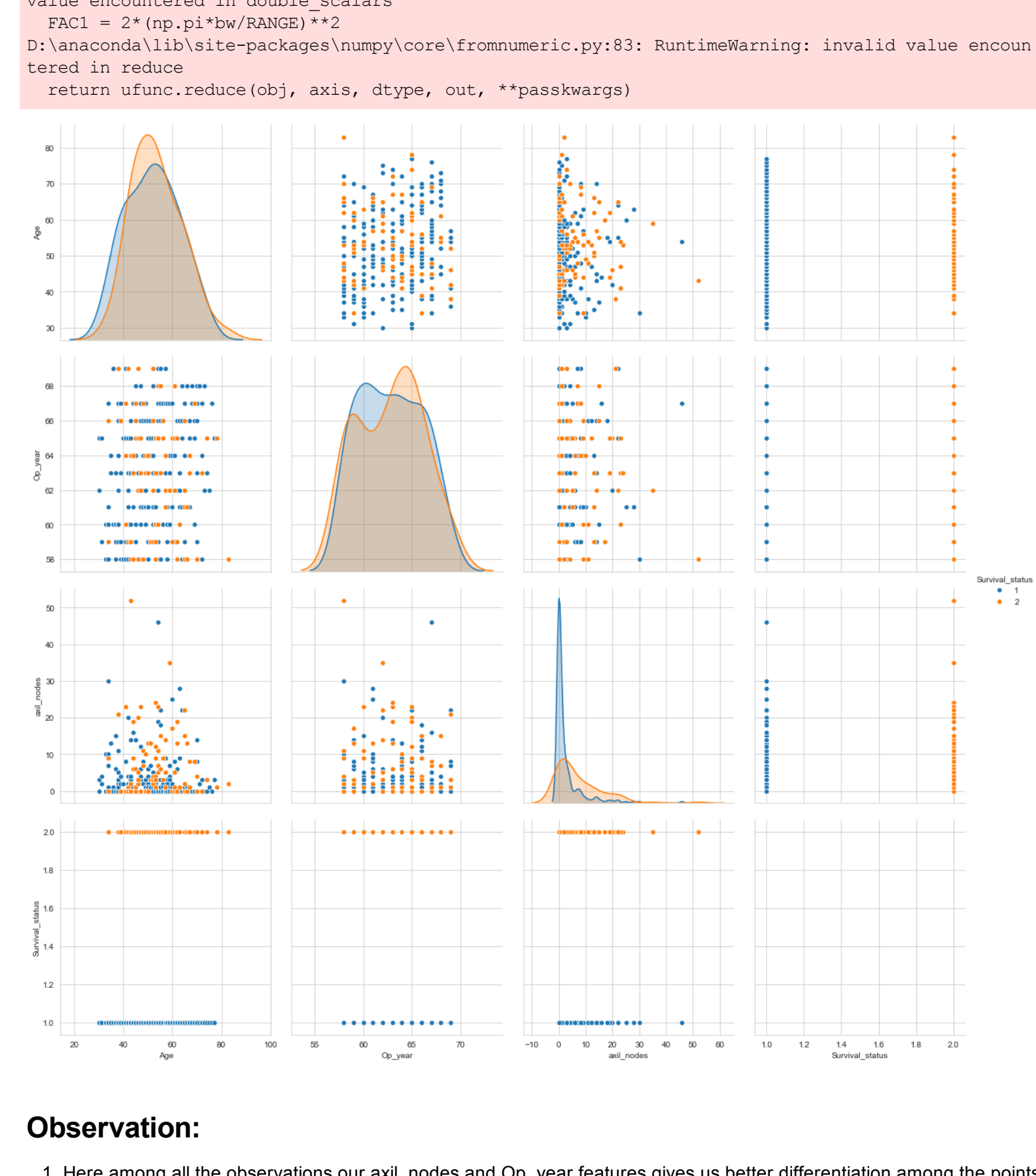
Observations:

1. The output for the above code only gives us the range of variables.
2. We cannot differentiate among the points as they have considerable overlapping.

Pair-plot

In [164]:
```python
# 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.
sns.pairplot(haber,hue="Survival_status",height=4)
plt.show()
```

```
D:\anaconda\lib\site-packages\scipy\stats\stats.py:1713: FutureWarning: Using a non-tuple sequen
ce for multidimensional indexing is deprecated; use `arr[tuple(seq)]` instead of `arr[seq]`. In
the future this will be interpreted as an array index, `arr[np.array(seq)]`, which will result e
ither in an error or a different result.
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
D:\anaconda\lib\site-packages\statsmodels\nonparametric\kde.py:488: RuntimeWarning: invalid valu
e encountered in true_divide
  binned = fast_linbin(X, a, b, gridsize) / (delta * nobs)
D:\anaconda\lib\site-packages\statsmodels\nonparametric\kdetools.py:34: RuntimeWarning: invalid
value encountered in double_scalars
  FAC1 = 2*(np.pi*bw/RANGE)**2
D:\anaconda\lib\site-packages\numpy\core\fromnumeric.py:83: RuntimeWarning: invalid value encoun
tered in reduce
  return ufunc.reduce(obj, axis, dtype, out, **passkwargs)
```



Observation:

1. Here,among all the observations our axil_nodes and Op_year features gives us better differentiation among the points.
2. But,we cannot seperate the points with simple linear seperation and by applying if-else condition to it.

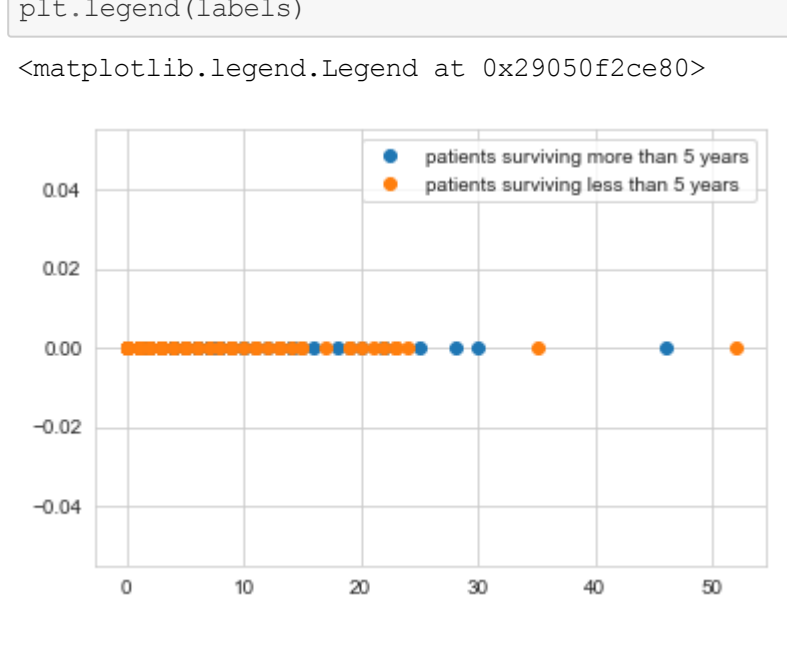
In [165]:
```python
haber.dtypes                #To find the datatype of each column
```

Out[165]:
```
Age                int64
Op_year            int64
axil_nodes         int64
Survival_status    int64
dtype: object
```

1-D Scatter Plot

In [170]:
```python
#Here, we seperate the no.of patients living more thaan 5 years and less than 5 years into two seper
ate variables
import numpy as np
labels = ["patients surviving more than 5 years","patients surviving less than 5 years"]
haber_more_than_5_years = haber.loc[haber["Survival_status"].astype(str) == "1"];
haber_less_than_5_years = haber.loc[haber["Survival_status"].astype(str) == "2"];
#We,plot the axil_nodes of the above two variables on x-axis and assign value 0 to y-axis
plt.plot(haber_more_than_5_years ["axil_nodes"], np.zeros_like(haber_more_than_5_years ['axil_nodes'
]), 'o')
plt.plot(haber_less_than_5_years ["axil_nodes"], np.zeros_like(haber_less_than_5_years ['axil_nodes'
]), 'o')
plt.legend(labels)
```

Out[170]: <matplotlib.legend.Legend at 0x29050f2ce80>

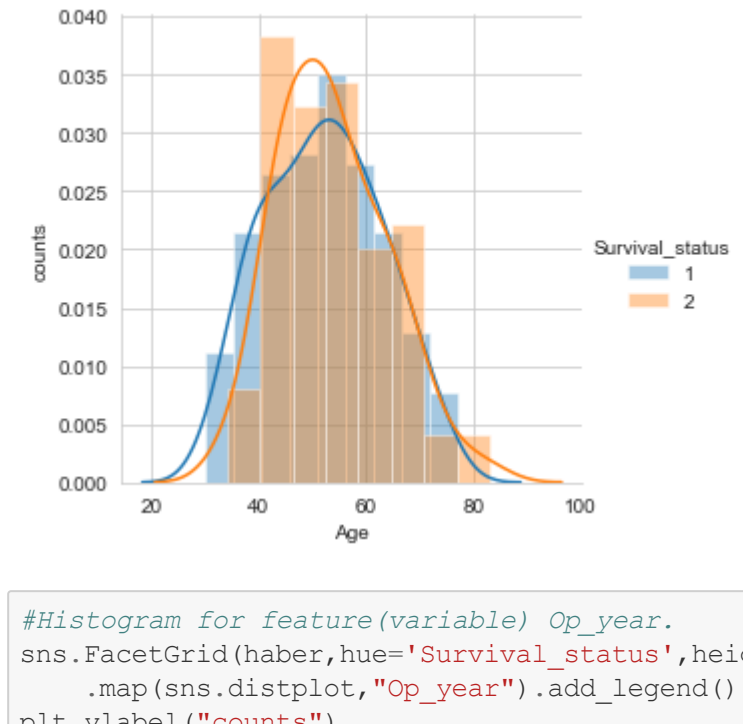


Observation:

1. They are very hard to make sense as points are overlapping alot.
2. They only help to visualize points in a particular window size.
3. To view these points we make use of Histograms.

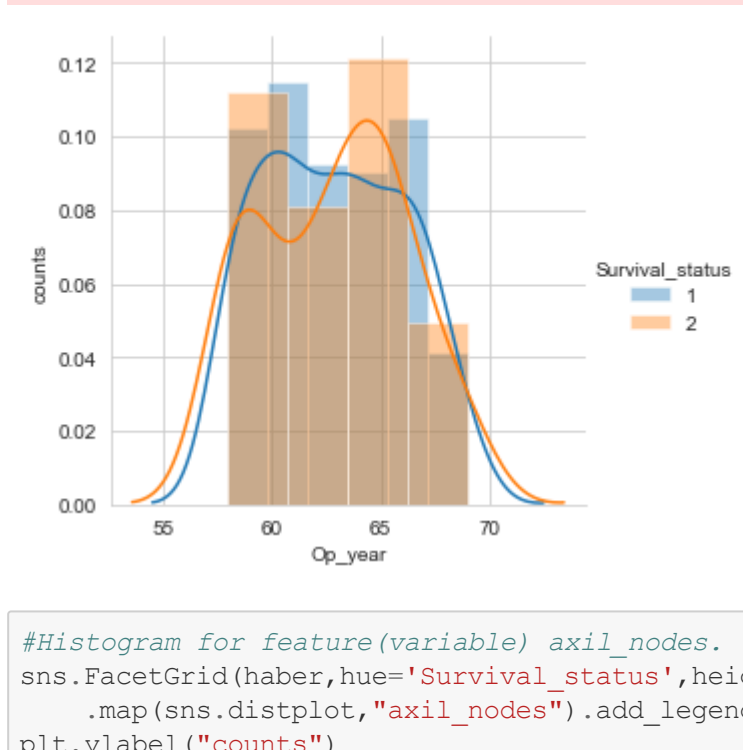
In [174]:
```python
#Histogram for feature(variable) Age.
sns.FacetGrid(haber,hue='Survival_status',height=4)\
    .map(sns.distplot,"Age").add_legend()
plt.ylabel("counts")
plt.show()
```

```
D:\anaconda\lib\site-packages\scipy\stats\stats.py:1713: FutureWarning: Using a non-tuple sequen
ce for multidimensional indexing is deprecated; use `arr[tuple(seq)]` instead of `arr[seq]`. In
the future this will be interpreted as an array index, `arr[np.array(seq)]`, which will result e
ither in an error or a different result.
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```



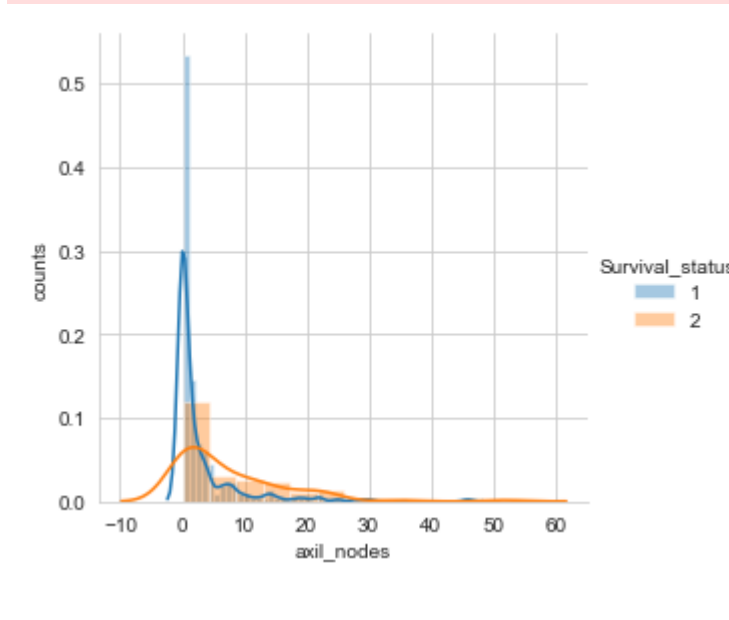
In [175]:
```python
#Histogram for feature(variable) Op_year.
sns.FacetGrid(haber,hue='Survival_status',height=4)\
    .map(sns.distplot,"Op_year").add_legend()
plt.ylabel("counts")
plt.show()
```

```
D:\anaconda\lib\site-packages\scipy\stats\stats.py:1713: FutureWarning: Using a non-tuple sequen
ce for multidimensional indexing is deprecated; use `arr[tuple(seq)]` instead of `arr[seq]`. In
the future this will be interpreted as an array index, `arr[np.array(seq)]`, which will result e
ither in an error or a different result.
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```



In [173]:
```python
#Histogram for feature(variable) axil_nodes.
sns.FacetGrid(haber,hue='Survival_status',height=4)\
    .map(sns.distplot,"axil_nodes").add_legend()
plt.ylabel("counts")
plt.show()
```

```
D:\anaconda\lib\site-packages\scipy\stats\stats.py:1713: FutureWarning: Using a non-tuple sequen
ce for multidimensional indexing is deprecated; use `arr[tuple(seq)]` instead of `arr[seq]`. In
the future this will be interpreted as an array index, `arr[np.array(seq)]`, which will result e
ither in an error or a different result.
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```



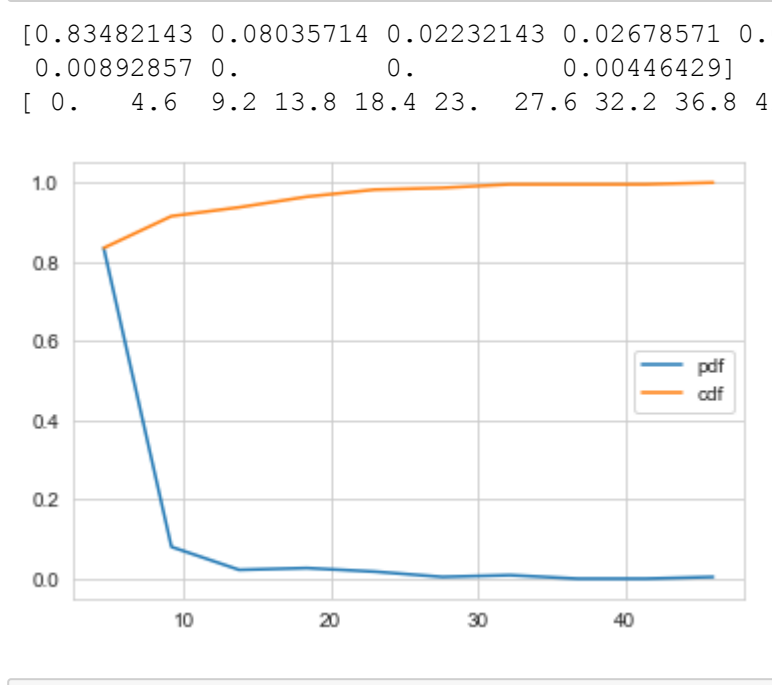
Observation:

1. Here,above the first two histograms are overlapping alot,the histogram for feature(variable) axil_node is a bit better among the three.
2. We can observe by seeing our histogram for feature(variable) axil_nodes that we have many points for patients surviving more than 5 years whose axil value is between 0 to 2.
3. We can also observe by seeing our histogram for feature(variable) axil_nodes that we have many points or patients surviving less than 5 years whose axil value is between 0 to 4.

PDF and CDF

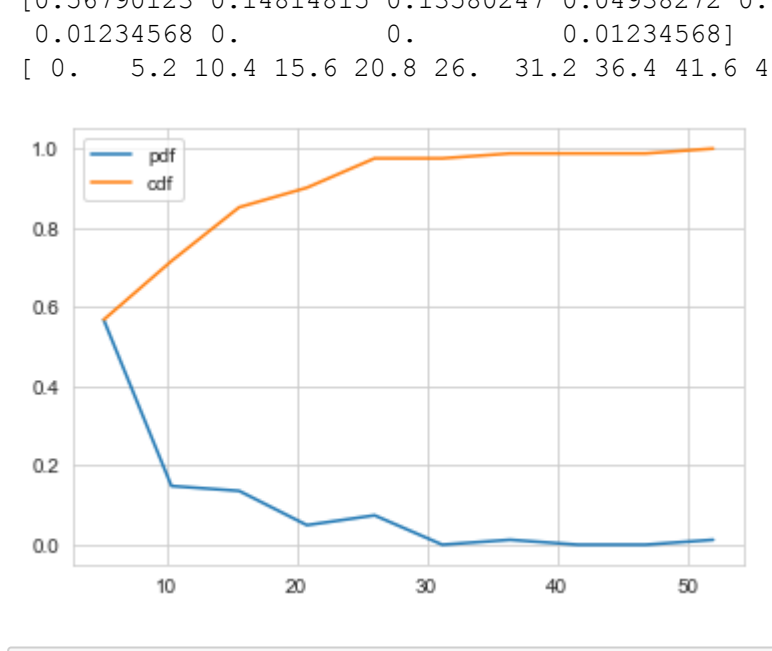
In [121]:
```python
#PDF's gives us the value and CDF's gives us the percentage of those values
counts, bin_edges = np.histogram(haber_more_than_5_years['axil_nodes'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)

labels = ["pdf","cdf"]
#compute CDF
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


#plt.show()
plt.legend(labels);
```

```
[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 [125]:
```python
counts, bin_edges = np.histogram(haber_less_than_5_years['axil_nodes'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)

labels = ["pdf","cdf"]
#compute CDF
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


#plt.show()
plt.legend(labels);
```

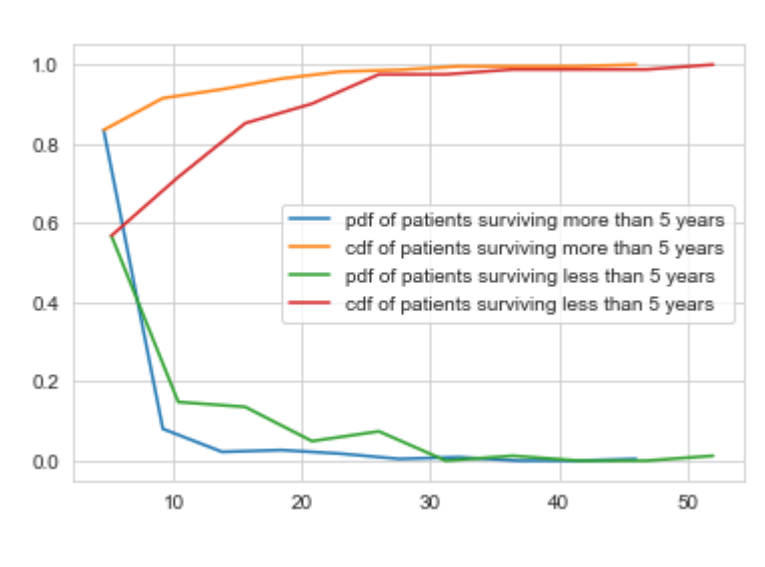
```
[0.56790123 0.14814815 0.13580247 0.04938272 0.07407407 0.
 0.01234568 0.         0.         0.01234568]
[ 0.   5.2 10.4 15.6 20.8 26.  31.2 36.4 41.6 46.8 52. ]
```



In [176]:
```python
labels = ["pdf of patients surviving more than 5 years","cdf of patients surviving more than 5 year
s","pdf of patients surviving less than 5 years","cdf of patients surviving less than 5 years"]
counts, bin_edges = np.histogram(haber_more_than_5_years['axil_nodes'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)

#compute CDF
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


counts, bin_edges = np.histogram(haber_less_than_5_years['axil_nodes'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)

#compute CDF
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)

#plt.show()
plt.legend(labels)
```

```
[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. ]
[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. ]
```

Out[176]: <matplotlib.legend.Legend at 0x29050dbf518>

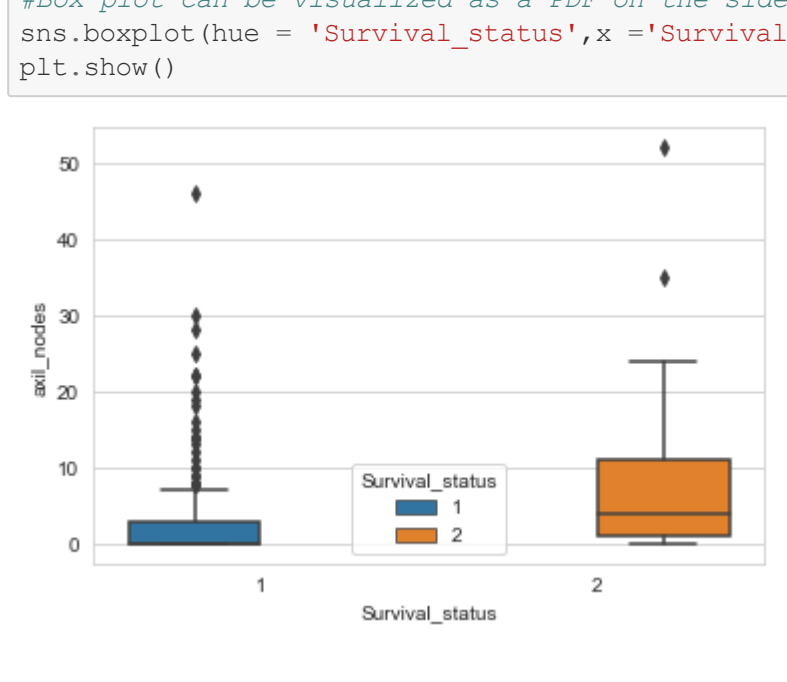


Observations:

1. We,can observe from the above graph that the percentage of patient surving for more than 5 years is 100% with axile value 30.
2. We can also observe that the percentage patient surviving less than 5 years is 100% with axile value 50.
3. So,we can partially conclude that a person should have a mid range of axile value i.e., between 30- 40 to survive for more than 5 years with accuracy 100%.

Box-plot and Whiskers

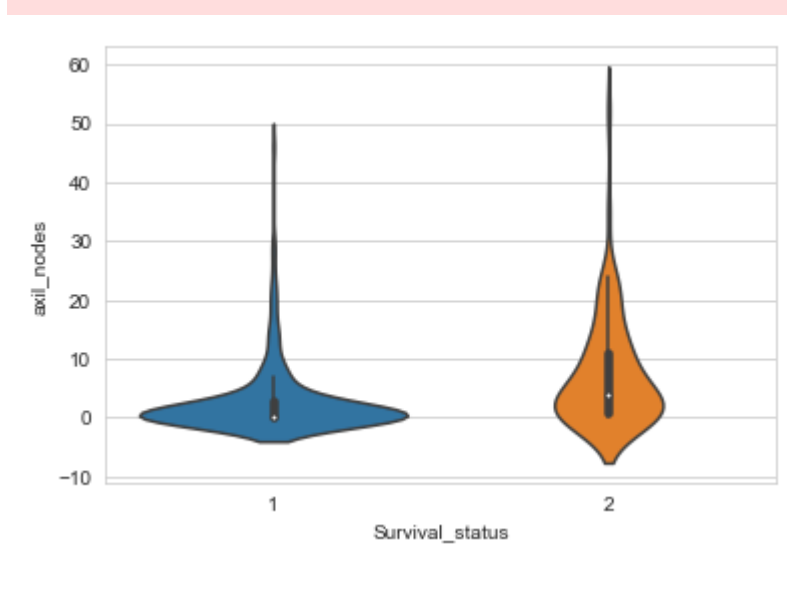
In [177]:
```python
#Box-plot with whiskers: another method of visualizing the  1-D scatter plot more intuitivey.
# The Concept of median, percentile, quantile.
#NOTE: IN the plot below, a technique call inter-quartile range is used in plotting the whiskers.
#Whiskers in the plot below donot correposnd to the min and max values.

#Box-plot can be visualized as a PDF on the side-ways.
sns.boxplot(hue = 'Survival_status',x ='Survival_status', y ='axil_nodes',data =haber)
plt.show()
```



Violin-plot

In [107]:
```python
# 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(hue='Survival_status',x ='Survival_status',y ='axil_nodes',data =haber)
plt.show()
```

```
D:\anaconda\lib\site-packages\scipy\stats\stats.py:1713: FutureWarning: Using a non-tuple sequen
ce for multidimensional indexing is deprecated; use `arr[tuple(seq)]` instead of `arr[seq]`. In
the future this will be interpreted as an array index, `arr[np.array(seq)]`, which will result e
ither in an error or a different result.
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```



Conclusion:

1. We can conclude that the feature(variable) axil_nodes is of great use to model the data and to give higher accuracy percent if plotted well.
2. We can see that the above plottings used Multivariate and Univariate are not efficient to predict this dataset.
3. PDF's and CDF's gives us more information to analyse our dataset.