Exploratory Data Analysis on Haberman's dataset

Dataset:

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

Columns of dataset:

- age = Age of patient at time of operation (numerical)
- Op Year = Operated year
- axil nodes = Number of axillary nodes.
- Surv_status = 1(the patient survived 5 years or longer,2(the patient died within 5 years)

Objective:

- To analyse whether the patient will survive or not depending on age of patient, operated year, auxillary nodes.
- Independent variable : age,Op_Year,axil_nodes,Surv_status
- Dependent variable(class) : Surv_status

Loading and visualizing data

```
In [12]:
```

```
# import dataset and store it as dataframe.
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
do = pd.read csv(r'C:\Users\Friend\AI\datasets\haberman.csv',header = None)
# Assigning feature labels to columns.
do.columns = ['age','Op Year','axil nodes','Surv status']
# Converting class label from numeric to string.
label = do['Surv_status']
def renaming(x):
   if x == 1:
       return 'positive'
   else:
       return 'negative'
label = label.map(renaming)
data['Surv_status'] = label
# print data to check data
print(data.head())
# print data to check data
print(data.tail())
  age Op_Year axil_nodes Surv_status
0
```

```
Name: Surv_status, dtype: int64
```

High level statistics of dataset

```
In [13]:
# Number of points and features
print('number of data points are {} \nnumber of features are {}'.format(data.shape[0],data.shape[1]))
number of data points are 306
number of features are 4
In [14]:
# Names of features (column names)
print(data.columns)
Index(['age', 'Op_Year', 'axil_nodes', 'Surv_status'], dtype='object')
In [15]:
# Data-Points per class
print (data['Surv_status'].value_counts())
positive
            225
negative
            81
Name: Surv_status, dtype: int64
In [17]:
# Is dataset balanced/imbalaced?
gl = data.groupby('Surv status')
gl['Surv status'].count()
Out[17]:
Surv status
negative
            81
          225
positive
Name: Surv_status, dtype: int64
Observations:
 • Since there is no uniformity in class, this dataset could be considered as imbalanced data set. Typically the
In [19]:
# Survival Status occured in each year
operated_years = data.groupby('Op_Year')
for operated_year,Status in operated_years:
   print(operated_year)
    print(Status['Surv status'].value counts())
58
positive
            24
            12
negative
Name: Surv_status, dtype: int64
positive
          18
           9
negative
Name: Surv status, dtype: int64
positive
            24
negative
Name: Surv_status, dtype: int64
```

```
positive 23
negative
Name: Surv_status, dtype: int64
positive 16
negative
Name: Surv status, dtype: int64
positive
negative 8
Name: Surv_status, dtype: int64
positive 23
negative 8
Name: Surv_status, dtype: int64
positive 15 negative 13
           13
negative
Name: Surv_status, dtype: int64
positive 22
negative
Name: Surv status, dtype: int64
positive 21 negative 4
Name: Surv_status, dtype: int64
positive
negative
Name: Surv_status, dtype: int64
positive
           4
negative
Name: Surv status, dtype: int64
```

Observations:

- In 1958, we could see the highest number (24) of survivals.
- In 1965, we could see the lowest number of deaths(13).

In [57]:

```
# compute statistical values
print (data.describe())
```

	age	Op Year	axil nodes	Surv status
count	306.000000	306.000000	306.000000	306.000000
mean	52.457516	62.852941	4.026144	1.264706
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

Observations:

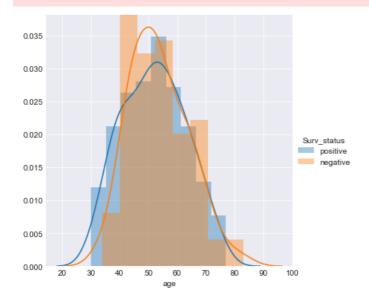
- Total number of patients that underwent treatment is 306.
- Age of patients vary from 30 to 83
- This dataset corresponds to patients treated from the year 1958 to 1969.
- There are patients who doesnt have axil nodes. Perhaps 75% of the patients had max of 4 lymph nodes.

Univariate Analysis

PDF

```
# PDF plot taking 'age' as variable.
sns.FacetGrid(data, hue = 'Surv_status', size = 5).map(sns.distplot, 'age').add_legend()
sns.set_style('darkgrid')
plt.show()

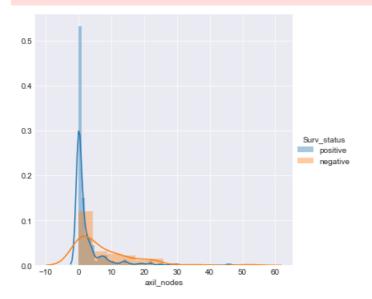
C:\Users\Friend\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: UserWarning: The 'normed' kw
arg is deprecated, and has been replaced by the 'density' kwarg.
   warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\Friend\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: UserWarning: The 'normed' kw
arg is deprecated, and has been replaced by the 'density' kwarg.
   warnings.warn("The 'normed' kwarg is deprecated, and has been "
```



In [23]:

```
# PDF plot taking 'axil_nodes' as variable.
sns.FacetGrid(data, hue = 'Surv_status', size = 5) .map(sns.distplot, 'axil_nodes') .add_legend()
sns.set_style('darkgrid')
plt.show()
```

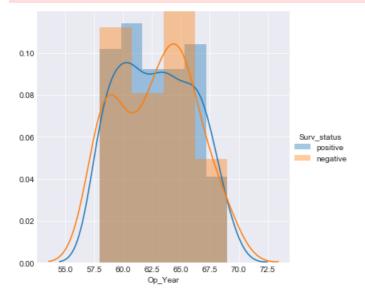
C:\Users\Friend\Anaconda3\lib\site-packages\matplotlib\axes_axes.py:6462: UserWarning: The 'normed' kw arg is deprecated, and has been replaced by the 'density' kwarg.
 warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\Friend\Anaconda3\lib\site-packages\matplotlib\axes_axes.py:6462: UserWarning: The 'normed' kw arg is deprecated, and has been replaced by the 'density' kwarg.
 warnings.warn("The 'normed' kwarg is deprecated, and has been "



In [25]:

```
sns.FacetGrid(data, hue = 'Surv_status', size = 5).map(sns.distplot, 'Op_Year').add_legend()
sns.set_style('darkgrid')
plt.show()

C:\Users\Friend\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: UserWarning: The 'normed' kw
arg is deprecated, and has been replaced by the 'density' kwarg.
    warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\Friend\Anaconda3\lib\site-packages\matplotlib\axes\_axes.py:6462: UserWarning: The 'normed' kw
arg is deprecated, and has been replaced by the 'density' kwarg.
    warnings.warn("The 'normed' kwarg is deprecated, and has been "
```



CDF

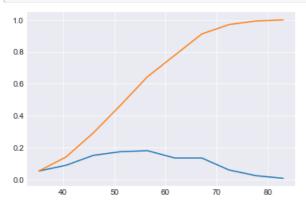
In [26]:

```
# calculate mass and bar width ranges.
count,bar_width = np.histogram(data['age'],bins = 10,density = True)

# plot pdf and cdf
pdf = count/(sum(count))
plt.plot(bar_width[1:],pdf)

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

plt.show()
```



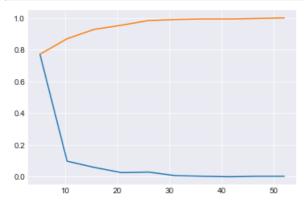
In [27]:

```
# calculate mass and bar width ranges.
count,bar_width = np.histogram(data['axil_nodes'],bins = 10,density = True)
# plot pdf
```

```
pdf = count/(sum(count))
plt.plot(bar_width[1:],pdf)

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

plt.show()
```

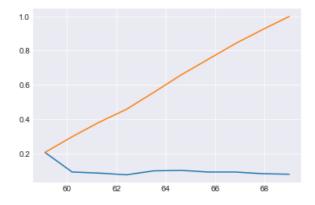


In [28]:

```
# calculate mass and bar width ranges.
count,bar_width = np.histogram(data['Op_Year'],bins = 10,density = True)

# plot pdf
pdf = count/(sum(count))
plt.plot(bar_width[1:],pdf)

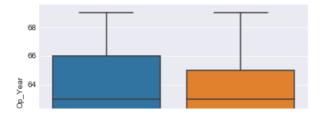
# plot CDF
cdf = np.cumsum(pdf)
plt.plot(bar_width[1:],cdf)
plt.show()
```

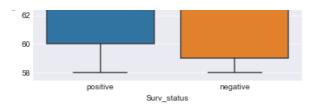


Box plot

In [29]:

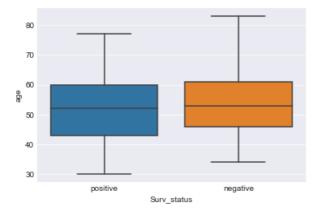
```
sns.boxplot(x = 'Surv_status',y = 'Op_Year',data = data)
sns.set_style('darkgrid')
plt.show()
```





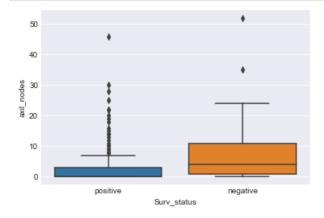
In [30]:

```
sns.boxplot(x = 'Surv_status',y = 'age',data = data)
sns.set_style('darkgrid')
plt.show()
```



In [31]:

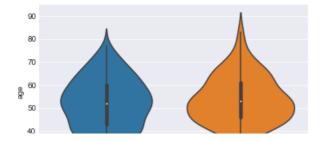
```
sns.boxplot(x = 'Surv_status',y = 'axil_nodes',data = data)
sns.set_style('darkgrid')
plt.show()
```



Violin plot

In [32]:

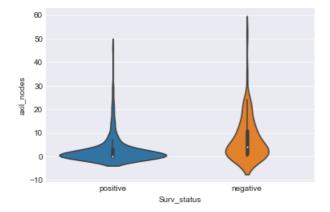
```
sns.violinplot(x ='Surv_status' ,y = 'age',data = data)
sns.set_style('darkgrid')
plt.show()
```



```
20 positive negative Surv_status
```

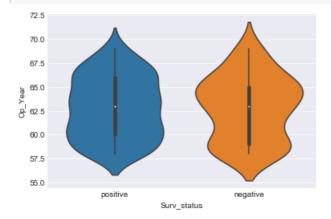
In [33]:

```
sns.violinplot(x ='Surv_status' ,y = 'axil_nodes',data = data)
sns.set_style('darkgrid')
plt.show()
```



In [40]:

```
sns.violinplot(x ='Surv_status',y = 'Op_Year',data = data)
sns.set_style('darkgrid')
plt.show()
```



Observations of Univariate Analysis:

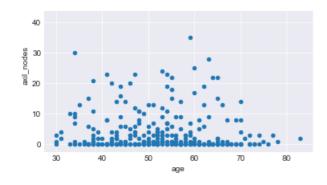
- Patients who have beentreated after 1966 has high chances of survival.
- 75% of patients who have survived more than 5 years have less than around 4 lymph nodes

Bivariate analysis

2D-Scatter Plot

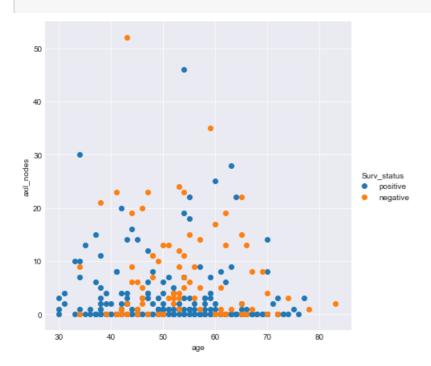
In [35]:

```
data.plot(kind = 'scatter', x = 'age', y = 'axil_nodes')
plt.show()
```



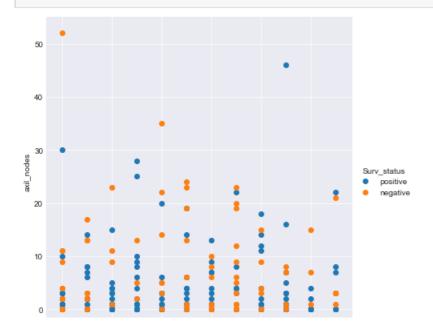
In [36]:

```
sns.FacetGrid(data, hue = 'Surv_status', size = 6) .map(plt.scatter, 'age', 'axil_nodes') .add_legend()
sns.set_style('darkgrid')
plt.show()
```



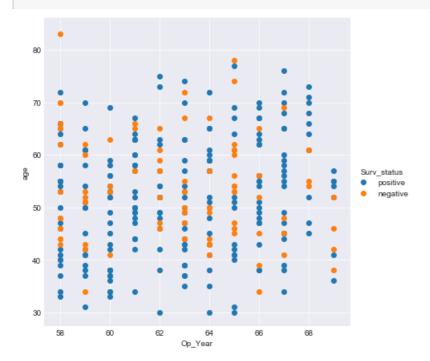
In [37]:

```
sns.FacetGrid(data,hue = 'Surv_status',size = 6).map(plt.scatter,'Op_Year','axil_nodes').add_legend()
sns.set_style('darkgrid')
plt.show()
```



In [38]:

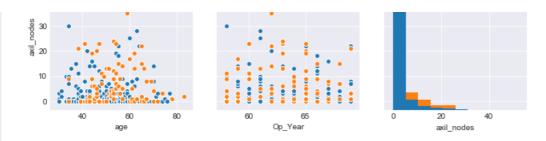
```
sns.FacetGrid(data,hue = 'Surv_status',size = 6).map(plt.scatter,'Op_Year','age').add_legend()
sns.set_style('darkgrid')
plt.show()
```



Pair plot

```
In [39]:
sns.pairplot(data, hue = 'Surv status', size = 3)
sns.set_style('darkgrid')
plt.show()
  80
                                  70
                                           9Ge
  50
```





Observations of Bivariate Analysis:

- By scatter plot drawn across all the features of dataset, we can see that the plot output does not provide us any result.
- None of the features distinguishes the class label.
- Data has thoroughly scattered across all the plot, and hence a distinct analysis could not be made using pair plot.