Hberman_Assignment

June 27, 2019

1 Exploratory Data Analysis Of Haberman Cancer Survival Dataset

What is Haberman Dataset?

It is a dataset that contains datas from a study 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.

2 Importing libraries and the dataset

Coloumn names is not provided in the dataset.

```
[0]: import pandas as pd
   import matplotlib.pyplot as plt
   import numpy as np
   import seaborn as sns
   from google.colab import files
[0]: haberman = files.upload()
   <IPython.core.display.HTML object>
   Saving haberman.csv to haberman.csv
[0]: haberman = pd.read csv("haberman.csv")
[0]: #How many datapoints?
   haberman.shape
[0]: (305, 4)
      The dataset contains 305 Rows and 4 Coloumn.
[0]: #What are the column names in the dataset?
   haberman.columns
[0]: Index(['30', '64', '1', '1.1'], dtype='object')
```

```
[0]: haberman.columns = ["Age", "Operation_Year", "Axil_Nodes", "Survival_Status"] haberman.columns
```

Names of the column was referred from the dataset provided.

[0]: haberman.head()

[0]:		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

The first 5 datapoints are printed here.

- First column shows the age of patients
- Second column shows the year each patient had undergone the surgery during 1958 and 1970
- Third column shows the number of numbers of tumors they found
- Fourth column shows the survival status of the patients.

If the value is 1 - The patient survived 5 years or more If the value is 2 - The patient survived less than 5 years

[0]: haberman.describe()

[0]:		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

Age

- The age of the patients vary from 30 to 83 with a mean of 52.
- 75% of the patients were almost 61 years old.

Operation_Year

- Oldest patient to have the surgery was 69 years old and the youngest was 58 years old .With a mean of age 62.
- 75% of the patients had operation at the age 66.

Axil_Nodes

- More than 25% of the patients had no positive lymph nodes and 75% of the patient had less than 5 positive lymph nodes
- 52 positive lymph was found in a single patient.

Survival_Status

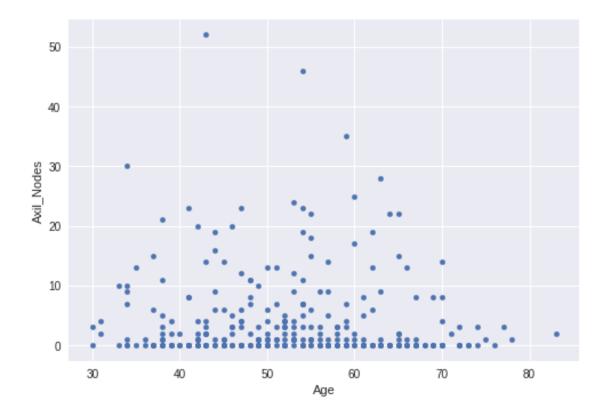
• More than 50% of the patients survived 5 years or more.

[0]: habe	erman["Axil_Nodes"].value_counts()
[0]: 0	136
1	40
2	20
3	20
4	13
6	7
7	7
8	7
5	6
9	6
13	5
14	4
11	4
10	3
15	3
19	3
22	3
23	3
12	2
20	2
46	1
16	1
17	1
18	1
21	1
24	1
25	1
28	1
30	1
35	1
52	1
Name	e: Axil_Nodes, dtype: int64

3 2-D Scatterplot

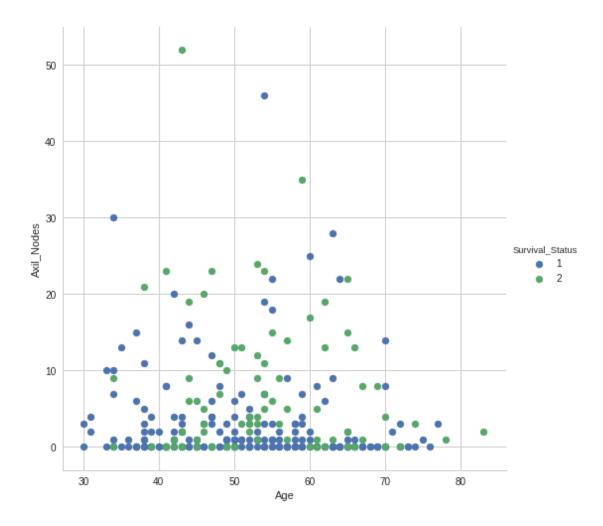
```
[0]: haberman.plot(kind='scatter', x='Age', y='Axil_Nodes')
plt.show()
```

'c' argument looks like a single numeric RGB or RGBA sequence, which should be avoided as value-mapping will have precedence in case its length matches with 'x' & 'y'. Please use a 2-D array with a single row if you really want to specify the same RGB or RGBA value for all points.



Majority of the patients had no sign of positive lymph nodes

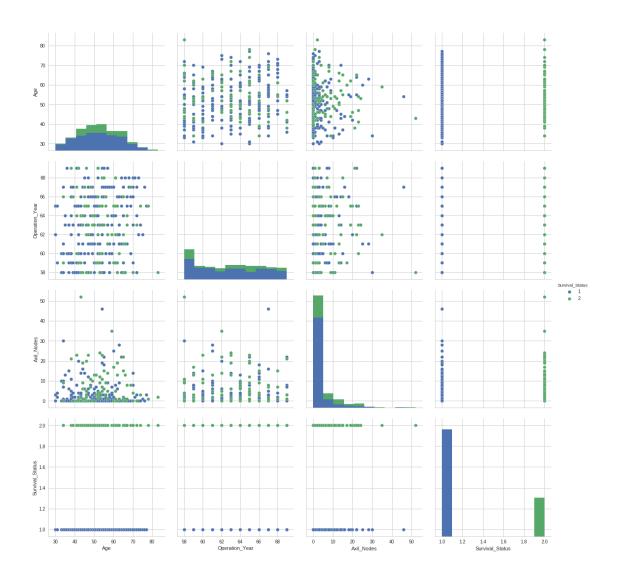
```
[0]: sns.set_style("whitegrid");
sns.FacetGrid(haberman, hue="Survival_Status", size = 7) \
.map(plt.scatter, "Age", "Axil_Nodes") \
.add_legend();
plt.show()
```



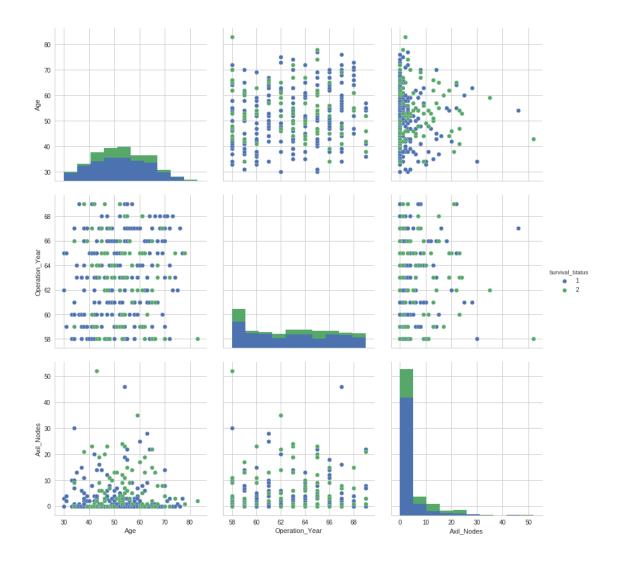
- Most of the patients had 0 positive lymph nodes.
- Most of the patients with no positive lymph nodes have survived 5 years or more.

#Pair-Plot

```
[0]: plt.close()
    sns.set_style("whitegrid");
    sns.pairplot(haberman, hue="Survival_Status", size = 4);
    plt.show()
```



The plots with x axis or y axis as Survival Status is not a helpful study.



• Plot between Axil Nodes and Age is very understanding. Most of the patient who survived have no positive lymph nodes.

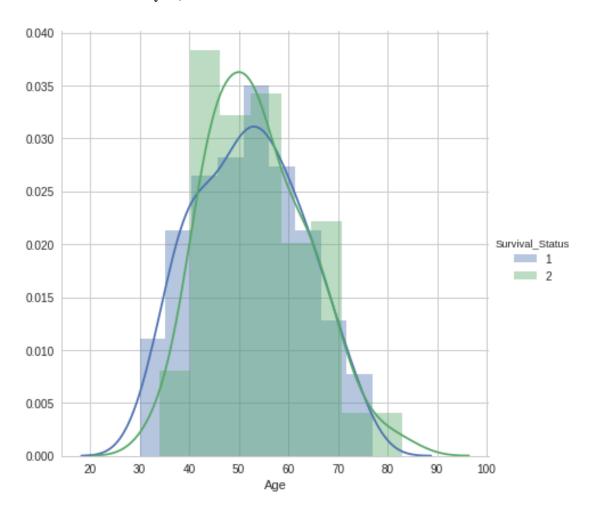
#Histogram

```
[0]: plt.close()
sns.FacetGrid(haberman, hue="Survival_Status", size = 6) \
.map(sns.distplot, "Age") \
.add_legend();
plt.show()
```

/usr/local/lib/python3.6/dist-packages/matplotlib/axes/_axes.py:6521: MatplotlibDeprecationWarning:

The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1.

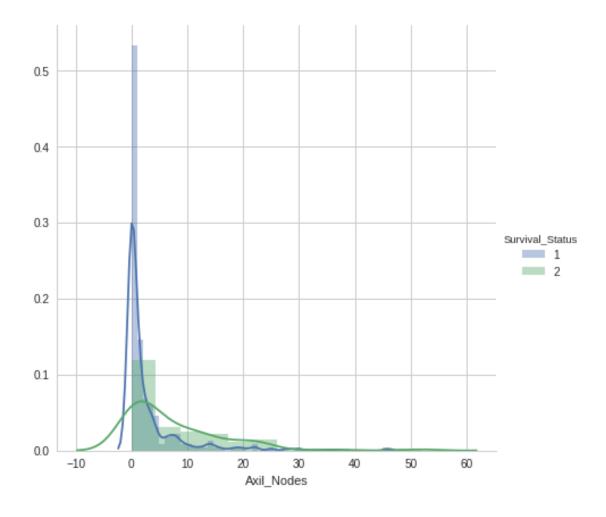
```
Use 'density' instead.
  alternative="'density'", removal="3.1")
```



```
[0]: plt.close()
sns.FacetGrid(haberman, hue="Survival_Status", size = 6) \
.map(sns.distplot,"Axil_Nodes") \
.add_legend();
plt.show()
```

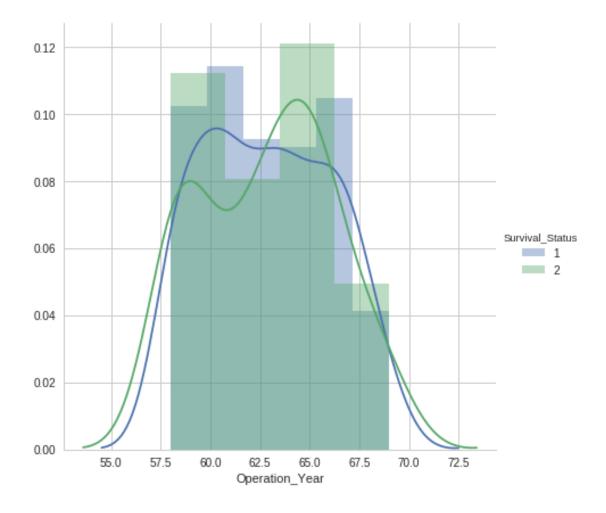
/usr/local/lib/python3.6/dist-packages/matplotlib/axes/_axes.py:6521:
MatplotlibDeprecationWarning:
The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1.
Use 'density' instead.

alternative="'density'", removal="3.1")



```
[0]: plt.close()
sns.FacetGrid(haberman, hue="Survival_Status", size = 6) \
.map(sns.distplot, "Operation_Year") \
.add_legend();
plt.show()
```

/usr/local/lib/python3.6/dist-packages/matplotlib/axes/_axes.py:6521:
MatplotlibDeprecationWarning:
The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1.
Use 'density' instead.
 alternative="'density'", removal="3.1")



Histogram of Axil nodes shows us that most of the patients who survived for 5 or more years had no positive lymph nodes.

#CDF

```
[0]: alive = haberman.loc[haberman["Survival_Status"] == 1] dead = haberman.loc[haberman["Survival_Status"] == 2]
```

The dataset is divided into two set based on the survival status

```
[0]: counts , bin_edges = np.histogram(alive['Axil_Nodes'], bins = 10, density = □

→True)

pdf = counts/(sum(counts))

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

plt.legend(['Pdf of the patients who survived more than 5 years'],['CDF of the □

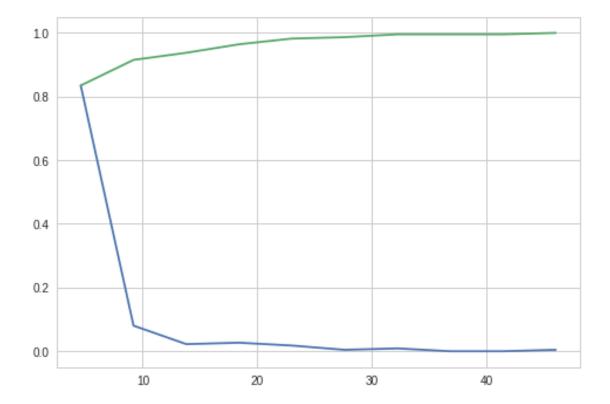
→patients who survived more than 5 years'])
```

```
plt.show()
```

/usr/local/lib/python3.6/dist-packages/matplotlib/legend.py:798: UserWarning: Legend does not support 'Pdf of the patients who survived more than 5 years' instances.

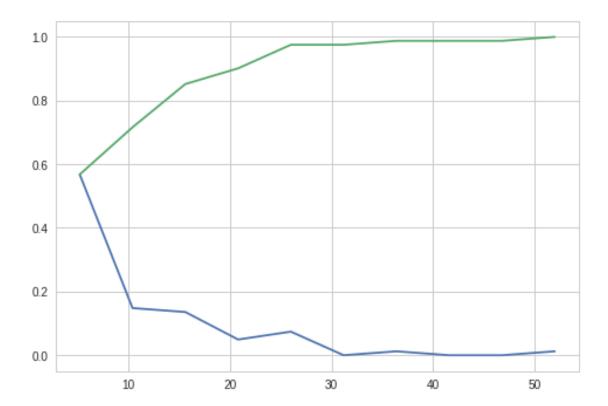
A proxy artist may be used instead.

See: http://matplotlib.org/users/legend_guide.html#creating-artistsspecifically-for-adding-to-the-legend-aka-proxy-artists "aka-proxy-artists".format(orig_handle)



/usr/local/lib/python3.6/dist-packages/matplotlib/legend.py:798: UserWarning: Legend does not support 'Pdf of the patients who died in 5 years' instances. A proxy artist may be used instead.

See: http://matplotlib.org/users/legend_guide.html#creating-artistsspecifically-for-adding-to-the-legend-aka-proxy-artists "aka-proxy-artists".format(orig_handle)



#Mean, Variance and Std-dev

Let us see the mean , variance and std deviation of patients who lived more than 5 years and less than 5 years.

```
[0]: print("Patients who survived for more than 5 years") alive.describe()
```

Patients who survived for more than 5 years

[0]:		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

```
77.000000
                            69.000000
                                         46.000000
                                                                 1.0
    max
[0]: print("Patients who survived less than 5 years")
    dead.describe()
   Patients who survived less than 5 years
[0]:
                 Age Operation_Year
                                       Axil_Nodes Survival_Status
                           81.000000
                                        81.000000
    count 81.000000
                                                               81.0
                                                                2.0
                           62.827160
                                         7.456790
   mean
           53.679012
   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
                                                                2.0
    75%
           61.000000
                           65.000000
                                        11.000000
           83.000000
                           69.000000
                                        52.000000
                                                                2.0
   max
      #Median, Percentiles, Quantiles, IQR and MAD
[0]: print("Medians:")
    print(np.median(alive['Axil_Nodes']))
    print(np.median(dead['Axil_Nodes']))
    print("")
    print("Quantiles:")
    print(np.percentile(alive['Axil_Nodes'],np.arange(0,100,25)))
    print(np.percentile(dead['Axil_Nodes'],np.arange(0,100,25)))
    print("")
    print("50th percentile")
    print(np.percentile(alive['Axil_Nodes'],50))
    print(np.percentile(dead['Axil_Nodes'],50))
   Medians:
   0.0
   4.0
   Quantiles:
   [0. 0. 0. 3.]
   [ 0. 1. 4. 11.]
   50th percentile
   0.0
   4.0
[0]: from statsmodels import robust as rb
[0]: print("MAD")
    print(rb.mad(alive['Axil_Nodes']))
```

```
print(rb.mad(dead['Axil_Nodes']))
```

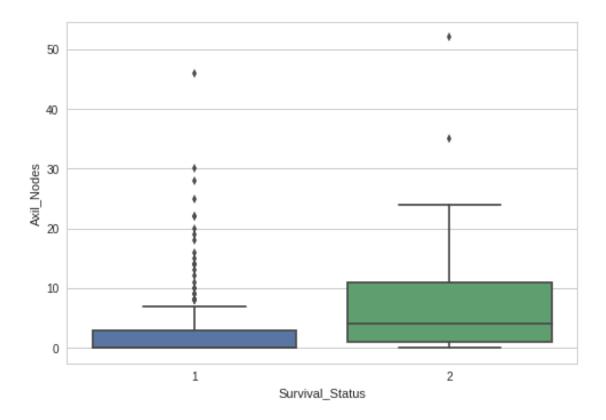
MAD 0.0

5.930408874022408

#Box plot and Whiskers

```
[0]: sns.boxplot(x="Survival_Status", y="Axil_Nodes", data = haberman,) plt.show()
```

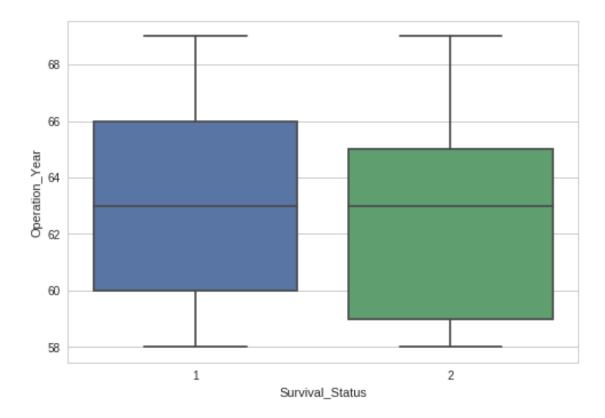
/usr/local/lib/python3.6/dist-packages/seaborn/categorical.py:454:
FutureWarning: remove_na is deprecated and is a private function. Do not use.
box_data = remove_na(group_data)



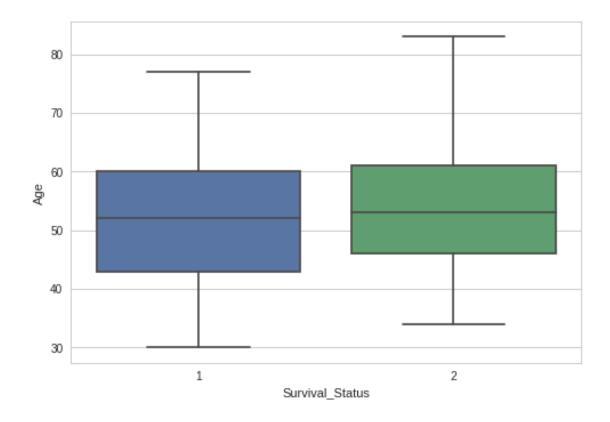
• Most of the patients with less number of positive lymph survived more than patients with more number of positive lymph

```
[0]: sns.boxplot(x="Survival_Status", y="Operation_Year", data = haberman) plt.show()
```

/usr/local/lib/python3.6/dist-packages/seaborn/categorical.py:454:
FutureWarning: remove_na is deprecated and is a private function. Do not use.
box_data = remove_na(group_data)



/usr/local/lib/python3.6/dist-packages/seaborn/categorical.py:454:
FutureWarning: remove_na is deprecated and is a private function. Do not use.
box_data = remove_na(group_data)



- Patients who survived more than 5 years aged more than 40 to 60 years old
- Patients who survived less than 5 years aged between 45 to 60+ years old

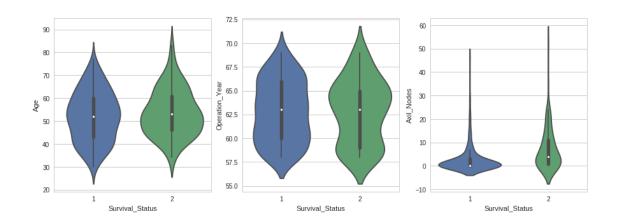
#Violin Plot

```
[0]: fig, axes = plt.subplots(1,3,figsize=(15,5))

for idx, feature in enumerate(list(haberman.columns)[:-1]):
    sns.violinplot(x="Survival_Status", y=feature,data=haberman, ax=axes[idx])

plt.show()
```

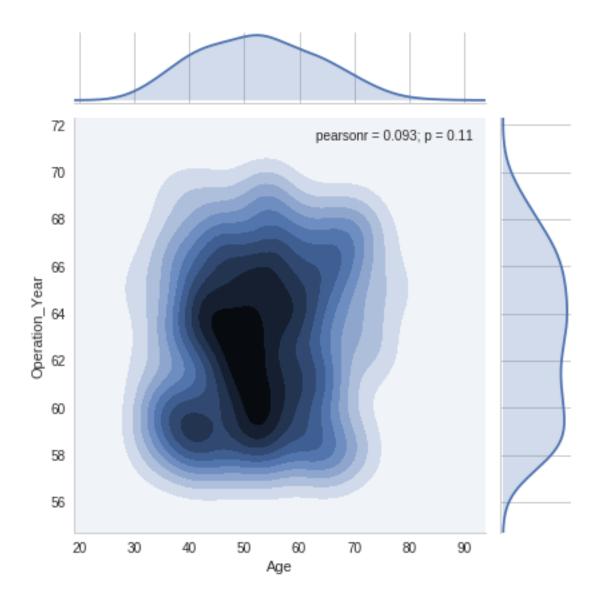
```
/usr/local/lib/python3.6/dist-packages/seaborn/categorical.py:588:
FutureWarning: remove_na is deprecated and is a private function. Do not use.
  kde_data = remove_na(group_data)
/usr/local/lib/python3.6/dist-packages/seaborn/categorical.py:816:
FutureWarning: remove_na is deprecated and is a private function. Do not use.
  violin_data = remove_na(group_data)
```



- 80% of the patients have less than or equal to 5 lymph survived more than 5 years.
- Number of positive lymph nodes of the survivors is more from 0 to 5

#Contour plot

```
[0]: sns.jointplot(x="Age", y="Operation_Year", data = haberman, kind = "kde") plt.show()
```



• Most of the patients have undergone operation between the age 40 to 60 years old.