# My Analysis Of Haberman's Survival Data

January 20, 2019

# 1 The dataset contains 305 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.

Attributes of Data : 1. Age of patient at time of operation (numerical) 2. Patient's year of operation (year - 1900, numerical) 3. Number of positive axillary nodes detected (numerical) 4. Survival status (class attribute) 1 = the patient survived 5 years or longer (class attribute)2 = the patient died within 5 year

## 1.1 Importing the dataset

```
In [1]: # Importing all libraries needed for exploratory data analysis of this dataset
        import pandas as pd
        import numpy as np
        import seaborn as sns
        import matplotlib.pyplot as plt
```

```
In [2]: cancer_data = pd.read_csv('./InputFile/haberman.csv')
```

```
In [3]: cancer_data.head(4)
```

```
Out[3]:    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
```

## 1.2 Preparing the data

```
In [4]: cancer_data.columns = ["age_of_patient","year_of_operation","pos_axil_nodes","survival
```

```
In [5]: cancer_data.head(3)
```

```
Out[5]:    age_of_patient  year_of_operation  pos_axil_nodes  \
        0              30                 62               3
        1              30                 65               0
        2              31                 59               2

           survival_status_after_5_years
        0                              1
        1                              1
        2                              1
```

```
In [6]: cancer_data.tail(4)
```

```
Out[6]:      age_of_patient  year_of_operation  pos_axil_nodes  \
        301              76                 67               0
        302              77                 65               3
        303              78                 65               1
        304              83                 58               2

             survival_status_after_5_years
        301                              1
        302                              1
        303                              2
        304                              2
```

```
In [7]: # changeing status from 1,2 to yes and no
        cancer_data.survival_status_after_5_years = cancer_data.survival_status_after_5_years.r
```

```
In [8]: cancer_data.shape
```

```
Out[8]: (305, 4)
```

```
In [9]: cancer_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 305 entries, 0 to 304
Data columns (total 4 columns):
age_of_patient                   305 non-null int64
year_of_operation                305 non-null int64
pos_axil_nodes                   305 non-null int64
survival_status_after_5_years    305 non-null object
dtypes: int64(3), object(1)
memory usage: 9.6+ KB
```

We have no missing value in the dataset

### 1.2.1 Our Goal is to find the relationship of survival_status and other features, so that in future we can build machine learning model using these features.

### 1.2.2 Minimum number of records required to build a model = 2exp(number of features), which is 8 in our case and since we have 305 records, we can make a machine learning model using this data

### 1.2.3 Descriptive Statistics of data

```
In [10]: cancer_data.describe()
```

```
Out[10]:        age_of_patient  year_of_operation  pos_axil_nodes
         count      305.000000         305.000000      305.000000
         mean        52.531148          62.849180        4.036066
         std         10.744024           3.254078        7.199370
         min         30.000000          58.000000        0.000000
         25%         44.000000          60.000000        0.000000
         50%         52.000000          63.000000        1.000000
         75%         61.000000          66.000000        4.000000
         max         83.000000          69.000000       52.000000
```

```
In [11]: cancer_data['survival_status_after_5_years'].value_counts(normalize = True)
```

```
Out[11]: Yes    0.734426
         No     0.265574
         Name: survival_status_after_5_years, dtype: float64
```

**Key Observations:**

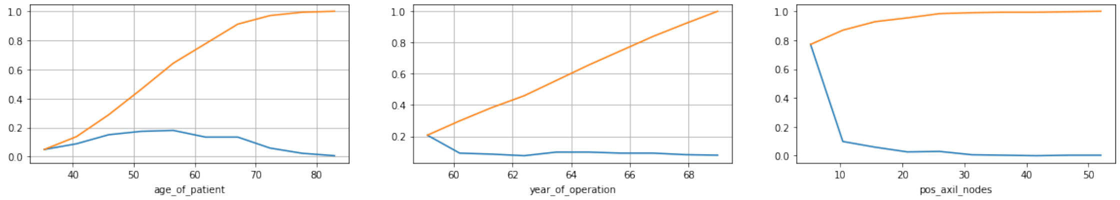
```
1. Data is imbalanced as we expected from domain knowledge
2. Only 25% of the patients are under the age of 44 years, meaning most of the pateints are ove
3. 75% of the patients has less than 4 axillary lymph nodes.
4. 73.44 % of the patients survived after 5 years.
```

## 1.3 Inferential statistics

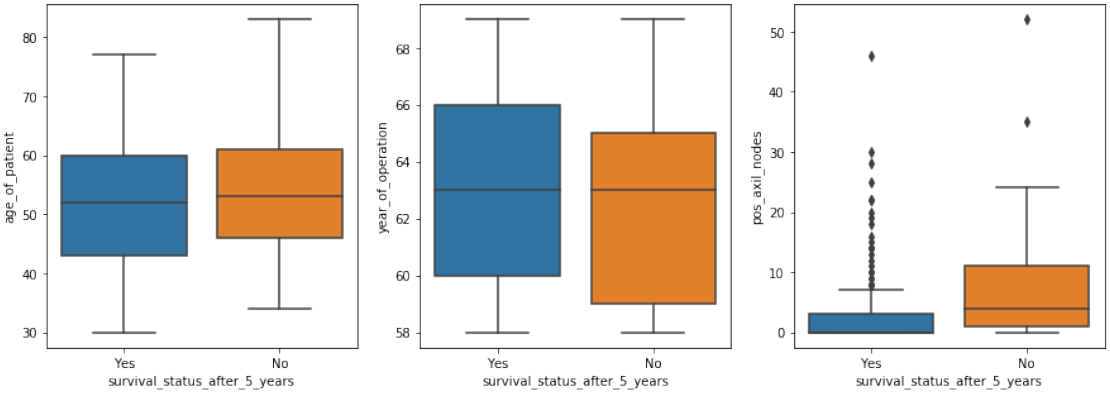
### Univariate Analysis

```
In [12]: """  https://www.kaggle.com/gokulkarthik/haberman-s-survival-exploratory-data-analysi
         * Distribution plots are used to visually assess how the data points are distributed 
         * Usually the data points are grouped into bins and the height of the bars representi
         number of data points lying within that group. (histogram)
         * Probality Density Function (PDF) is the probabilty that the variable takes a value 
         * Kernel Density Estimate (KDE) is the way to estimate the PDF. The area under the KD
         * Here the height of the bar denotes the percentage of data points under the correspo
         * The cumulative distribution function (cdf) is the probability that the variable tak
         """
         plt.figure(figsize = (20,3))
         for idx,feature in enumerate(list(cancer_data.columns)[:-1]):
             counts,binsize = np.histogram(cancer_data[feature],bins = 10,density = True)
             pdf = counts/sum(counts)
             cdf = np.cumsum(pdf)
             print("*******PDF OF {} IS ********".format(feature))
             print("BINSIZE --{}".format(binsize))
             print("PDF --{}".format(pdf))
             plt.grid()
             plt.subplot(1,3,idx+1)
             plt.plot(binsize[1:],pdf,binsize[1:],cdf)
             plt.xlabel(feature)
```

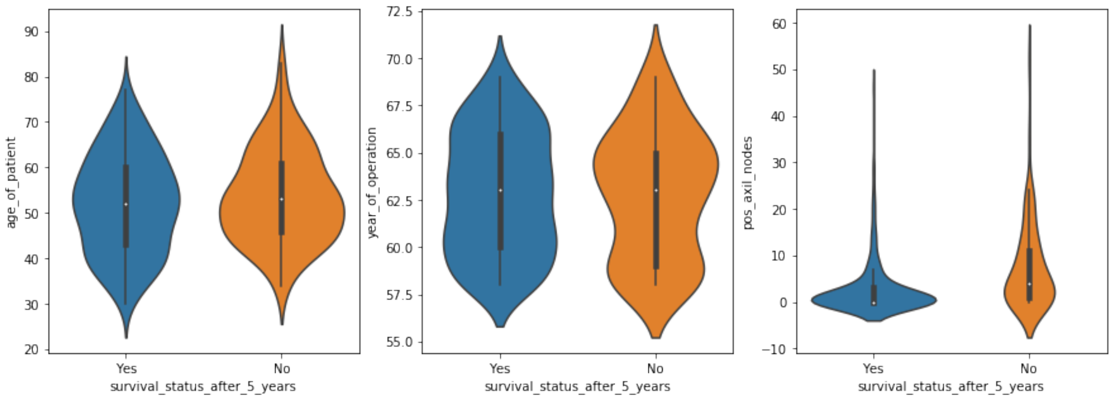
```
*******PDF OF age_of_patient IS ********
BINSIZE --[30.  35.3 40.6 45.9 51.2 56.5 61.8 67.1 72.4 77.7 83. ]
PDF --[0.04918033 0.08852459 0.15081967 0.17377049 0.18032787 0.13442623
 0.13442623 0.05901639 0.02295082 0.00655738]
*******PDF OF year_of_operation IS ********
BINSIZE --[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
PDF --[0.20655738 0.09180328 0.0852459  0.07540984 0.09836066 0.09836066
 0.09180328 0.09180328 0.08196721 0.07868852]
*******PDF OF pos_axil_nodes IS ********
BINSIZE --[ 0.   5.2 10.4 15.6 20.8 26.  31.2 36.4 41.6 46.8 52. ]
PDF --[0.7704918  0.09836066 0.05901639 0.02622951 0.0295082  0.00655738
 0.00327869 0.         0.00327869 0.00327869]
```



```
In [13]: """
         Box plot takes a less space and visually represents the five number summary of the da
         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
         """
         fig, axes = plt.subplots(1, 3, figsize=(15, 5))
         for idx, feature in enumerate(list(cancer_data.columns)[:-1]):
             sns.boxplot( x='survival_status_after_5_years', y=feature, data=cancer_data, ax=a
         plt.show()
```



```
In [14]: """
         Violin Plots are the combination of PDF and Box Plots.
         """
         fig,axes = plt.subplots(1,3,figsize = (15,5))
         for idx, feature in enumerate(list(cancer_data.columns[:-1])):
             sns.violinplot(x= 'survival_status_after_5_years',y=feature,data=cancer_data,ax =
```



### 1.3.1 Observations:

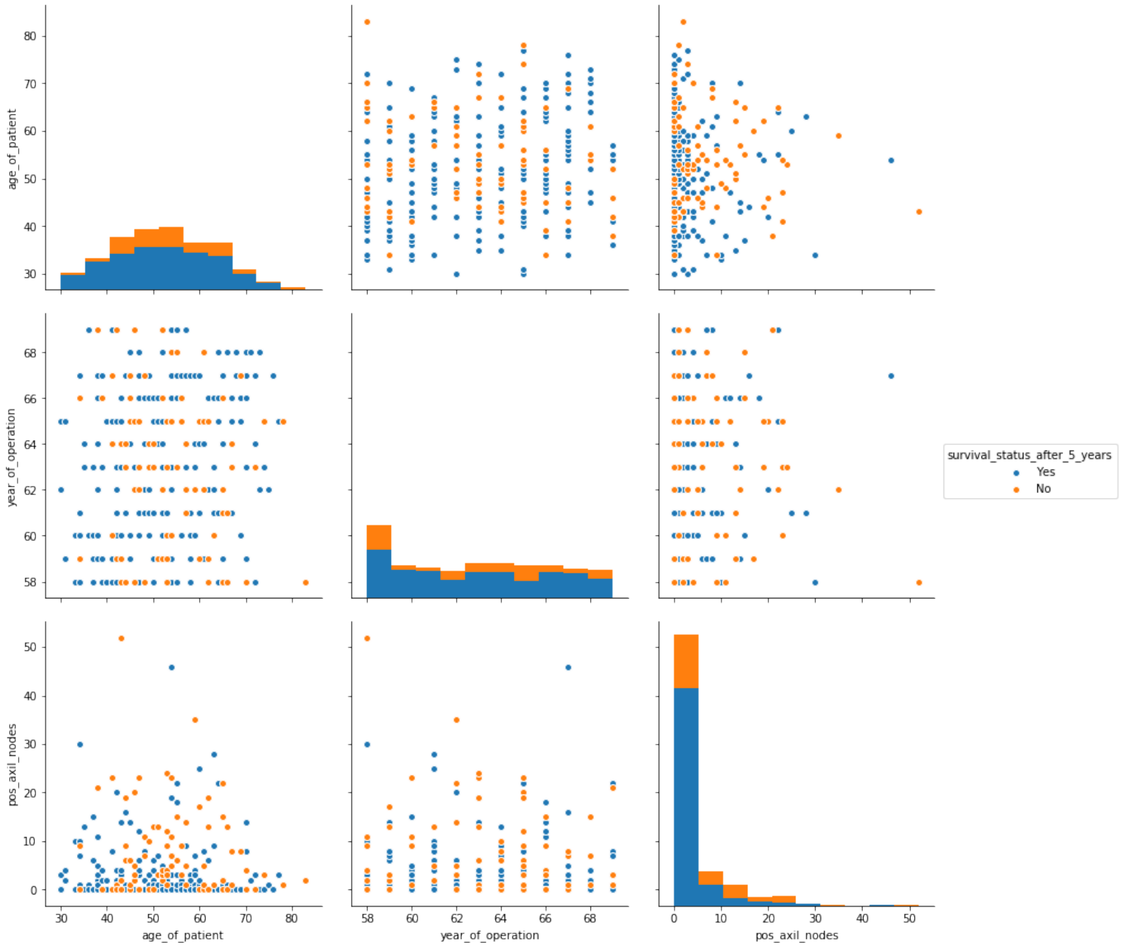
1. Patients above age 78 could not survive after 5 years.
2. 80% of the patients have less than or equal to 5 nodes.
3. Patients treated after 1965 have the slighly higher chance of surviving after 5 years

### 1.3.2 Multivariate Analysis

```
In [17]: plt.figure(figsize = (15,4))
         sns.pairplot(cancer_data,hue="survival_status_after_5_years",size = 4)

Out[17]: <seaborn.axisgrid.PairGrid at 0x22d3c649be0>

<Figure size 1080x288 with 0 Axes>
```

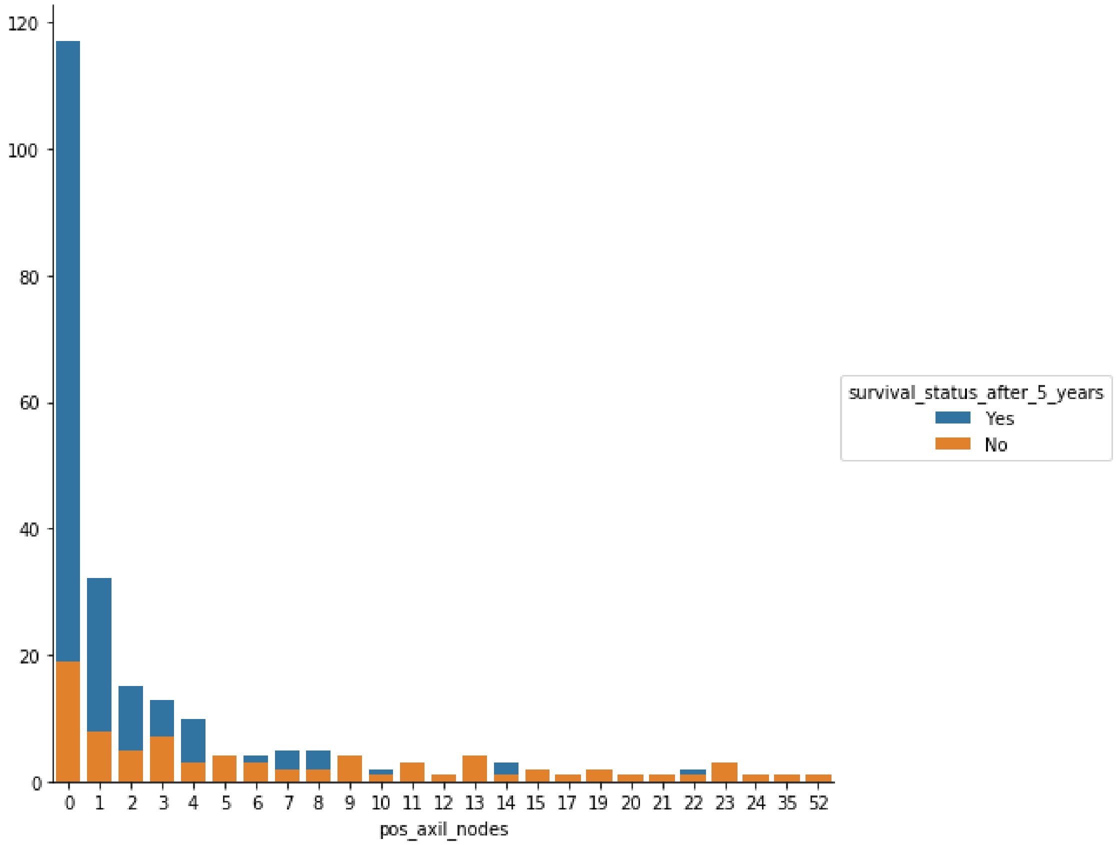


No way to classify the target variable using given features

```
In [19]: sns.FacetGrid(cancer_data,hue = "survival_status_after_5_years",size  =7).map(sns.cou

C:\ProgramData\Anaconda3\lib\site-packages\seaborn\axisgrid.py:703: UserWarning: Using the cou
  warnings.warn(warning)


Out[19]: <seaborn.axisgrid.FacetGrid at 0x22d3d7707b8>
```



Patients with few axil nodes has better chance of surviving after 5 years