# Exploratory Data Analysis of Haberman's Dataset

### Dataset Information:

The 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.

### Attribute Information:

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 (1 - The patient survived 5 years or longer, 2 - The patient died within 5 years)

### Objective:

The objective here is to classify whether or not a patient will survive for 5 years following a surgery for breast cancer based on the age of the patient, the year of operation and the number of positive axillary nodes detected.

### Importing and Cleaning of Data:

In this section, the data and the required libraries are imported and made ready for analysis.

In [1]:

```
# Importing the required library stack with their usual aliases

import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import seaborn as sns

import warnings                         # In order to supress any warnings
warnings.filterwarnings('ignore')
```

In [2]:

```
# Saved the csv file locally.

hb = pd.read_csv('haberman.csv')

hb.head()
```

Out[2]:

| | Age | Operation_Year | Axillary_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 |

In [3]:

```
# Usually, it is good practice to check for any null values in the data before proceeding with the
analysis.
Empty_Check = hb[hb.isnull().any(axis = 1)]
Empty_Check.empty
```

Out[3]:

```
True
```

In [4]:

```
# As we can see in the dataset, the survival statuses of the patients are represented numerically.
# Let us assign a better notation.
# A 'Yes' instead of a 1 signifying that the patient survived for over 5 years after the surgery.
# A 'No' instead of a 2 signifying that the patient survived for lesser than 5 years after the sur
gery.

hb['Survival_Status'] = hb['Survival_Status'].map({1:'Yes',2:'No'})
hb.head(10)
```

Out[4]:

| | Age | Operation_Year | Axillary_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 |

## High Level Statistics:

We answer some really basic questions about the data here like number of features, number of classes, number of datapoints etc.

In [5]:

```
# Shape of the data
print(hb.shape)

print('\n')

# Number of classes
print(hb['Survival_Status'].unique())

print('\n')

# Number of data points per class
print(hb['Survival_Status'].value_counts())

print('\n')

# General description of the data
print(hb.describe().round(2))
```

```
(306, 4)


['Yes' 'No']


Yes    225
No      81
Name: Survival_Status, dtype: int64


         Age  Operation_Year  Axillary_Nodes
```

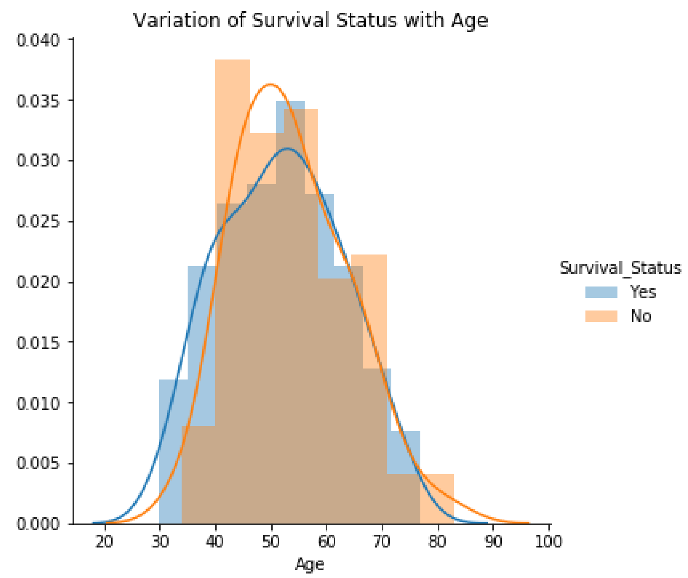
```
          Age   Operation_Year   Axillary_Nodes
count   306.00          306.00           306.00
mean     52.46           62.85             4.03
std      10.80            3.25             7.19
min      30.00           58.00             0.00
25%      44.00           60.00             0.00
50%      52.00           63.00             1.00
75%      60.75           65.75             4.00
max      83.00           69.00            52.00
```

## Univariate Analysis:

Here, we plot PDFs, CDFs, Box Plots on each feature and try to come to conclusions about the data and see which feature is useful in classification.

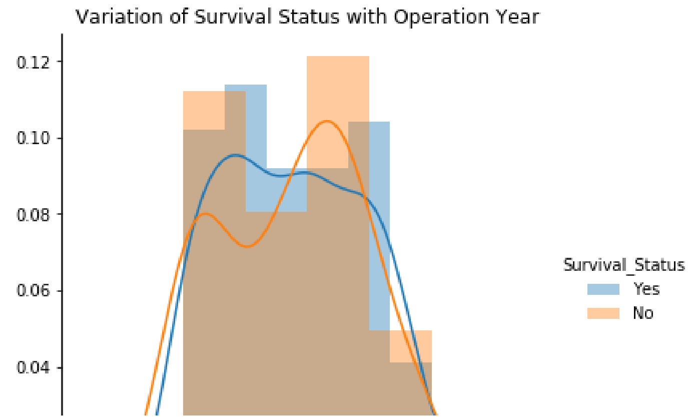
In [6]:

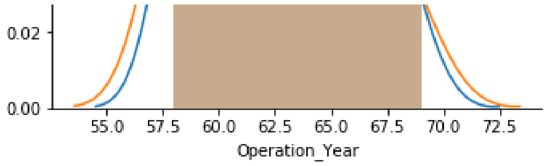
```
# 1.
# Plotting PDFs
# PDFs are basically a smoothened version of a histogram.
# They represent the probability that the variable takes a particular value.

sns.FacetGrid(hb, hue='Survival_Status',size = 5) \
    .map(sns.distplot,'Age') \
    .add_legend()
plt.title('Variation of Survival Status with Age')
plt.show()
```




In [7]:

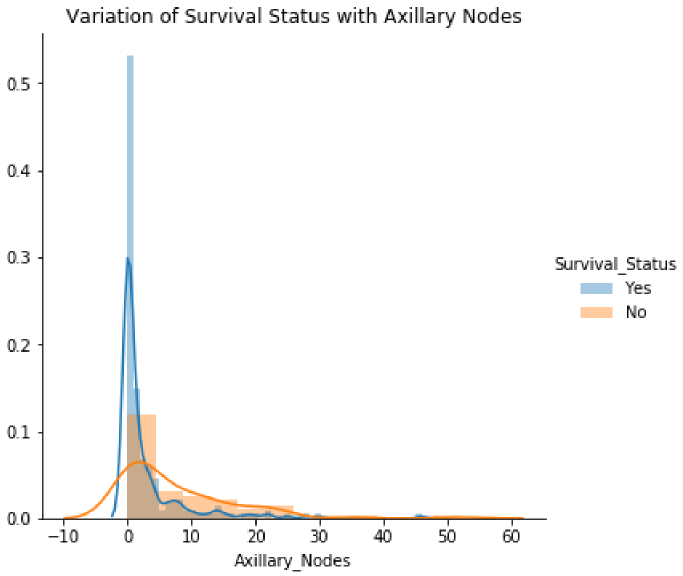
```
sns.FacetGrid(hb, hue='Survival_Status',size = 5) \
    .map(sns.distplot,'Operation_Year') \
    .add_legend()
plt.title('Variation of Survival Status with Operation Year')
plt.show()
```






In [8]:

```
sns.FacetGrid(hb, hue='Survival_Status',size = 5) \
    .map(sns.distplot,'Axillary_Nodes') \
    .add_legend()
plt.title('Variation of Survival Status with Axillary Nodes')
plt.show()
```



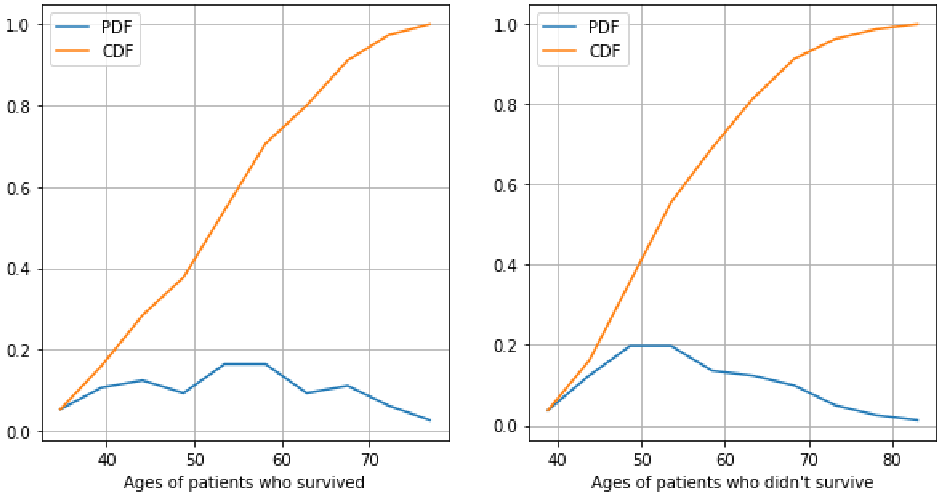

In [9]:

```
# In order to understand the data in more detail and how each feature
# is impacting the classification, we create a subset of the main dataframe.
# One subset has all the datapoints that lead to a 'Yes' and the other subset
# has all the datapoints that lead to a 'No'.

SS_Yes = hb[hb['Survival_Status'] == 'Yes']
SS_No = hb[hb['Survival_Status'] == 'No']
```

In [10]:

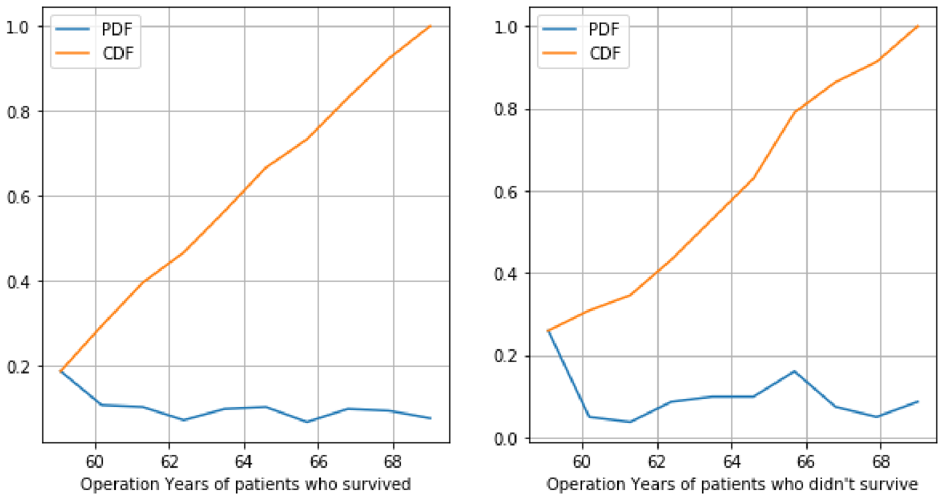
```
# 2.
# Plotting CDFs
# CDFs allow us to determine what percent of the datapoints in a dataset are below a particular va
lue.
plt.figure(figsize = (10,5))

plt.subplot(1,2,1)
counts , bin_edges = np.histogram(SS_Yes['Age'], density = True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,label='PDF')
plt.plot(bin_edges[1:], cdf,label='CDF')
plt.grid()
plt.legend()
plt.xlabel('Ages of patients who survived')

plt.subplot(1,2,2)
counts , bin_edges = np.histogram(SS_No['Age'], density = True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,label='PDF')
plt.plot(bin_edges[1:], cdf, label='CDF')
plt.grid()
plt.legend()
plt.xlabel('Ages of patients who didn\'t survive')
```

```
plt.show()
```




In [11]:

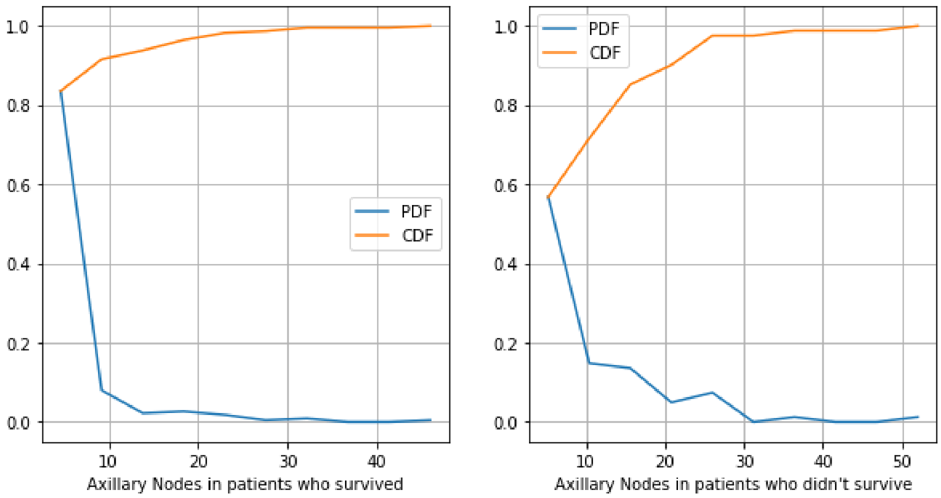
```
plt.figure(figsize = (10,5))

plt.subplot(1,2,1)
counts , bin_edges = np.histogram(SS_Yes['Operation_Year'], density = True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,label='PDF')
plt.plot(bin_edges[1:], cdf,label='CDF')
plt.grid()
plt.legend()
plt.xlabel('Operation Years of patients who survived')

plt.subplot(1,2,2)
counts , bin_edges = np.histogram(SS_No['Operation_Year'], density = True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,label='PDF')
plt.plot(bin_edges[1:], cdf,label='CDF')
plt.grid()
plt.legend()
plt.xlabel('Operation Years of patients who didn\'t survive')

plt.show()
```




In [12]:

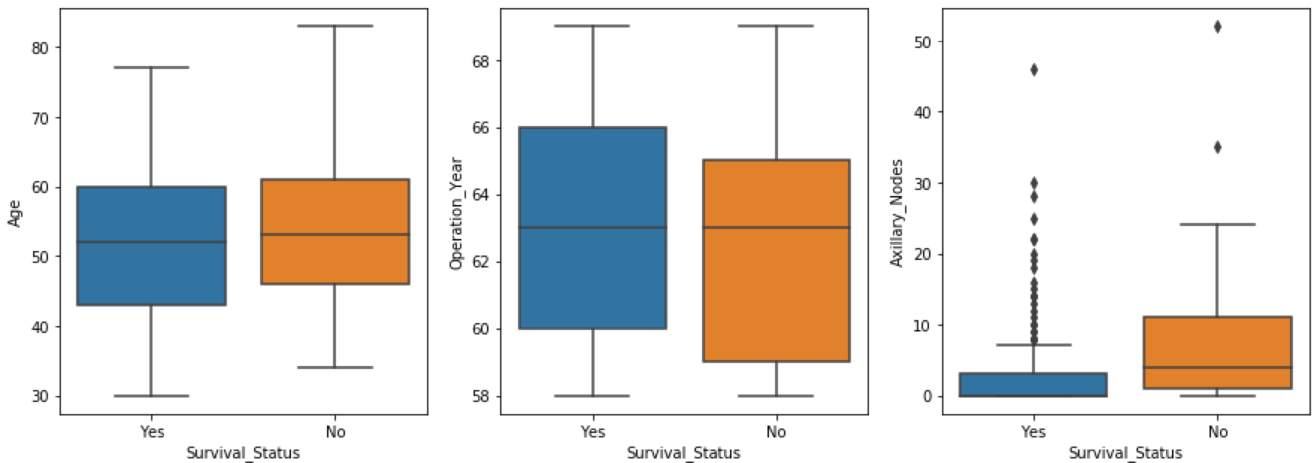
```
plt.figure(figsize = (10,5))

plt.subplot(1,2,1)
counts , bin_edges = np.histogram(SS_Yes['Axillary_Nodes'], density = True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
```

```
plt.plot(bin_edges[1:],pdf,label='PDF')
plt.plot(bin_edges[1:], cdf,label='CDF')
plt.grid()
plt.legend()
plt.xlabel('Axillary Nodes in patients who survived')

plt.subplot(1,2,2)
counts , bin_edges = np.histogram(SS_No['Axillary_Nodes'], density = True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,label='PDF')
plt.plot(bin_edges[1:], cdf,label='CDF')
plt.grid()
plt.legend()
plt.xlabel('Axillary Nodes in patients who didn\'t survive')

plt.show()
```




In [13]:

```
# 3.
# BOXPLOTS are a more visual and intuitive way of visualizing the dataset.
# There are 5 main lines in a box plot.
# The 3 lines in the middle represent the Inter-Quartile_Range, i.e. the 25th, 50th and 75th perce
ntile respectively.
# The lines at the bottom and the top are the whiskers which are the [Q1 - 1.5(IQR)] and the [Q3
+ 1.5(IQR)] respectively.
plt.figure(figsize = (15,5))

plt.subplot(131)
sns.boxplot(x='Survival_Status', y = 'Age', data = hb)
plt.subplot(132)
sns.boxplot(x='Survival_Status', y = 'Operation_Year', data = hb)
plt.subplot(133)
sns.boxplot(x='Survival_Status', y = 'Axillary_Nodes', data = hb)

plt.show()
```

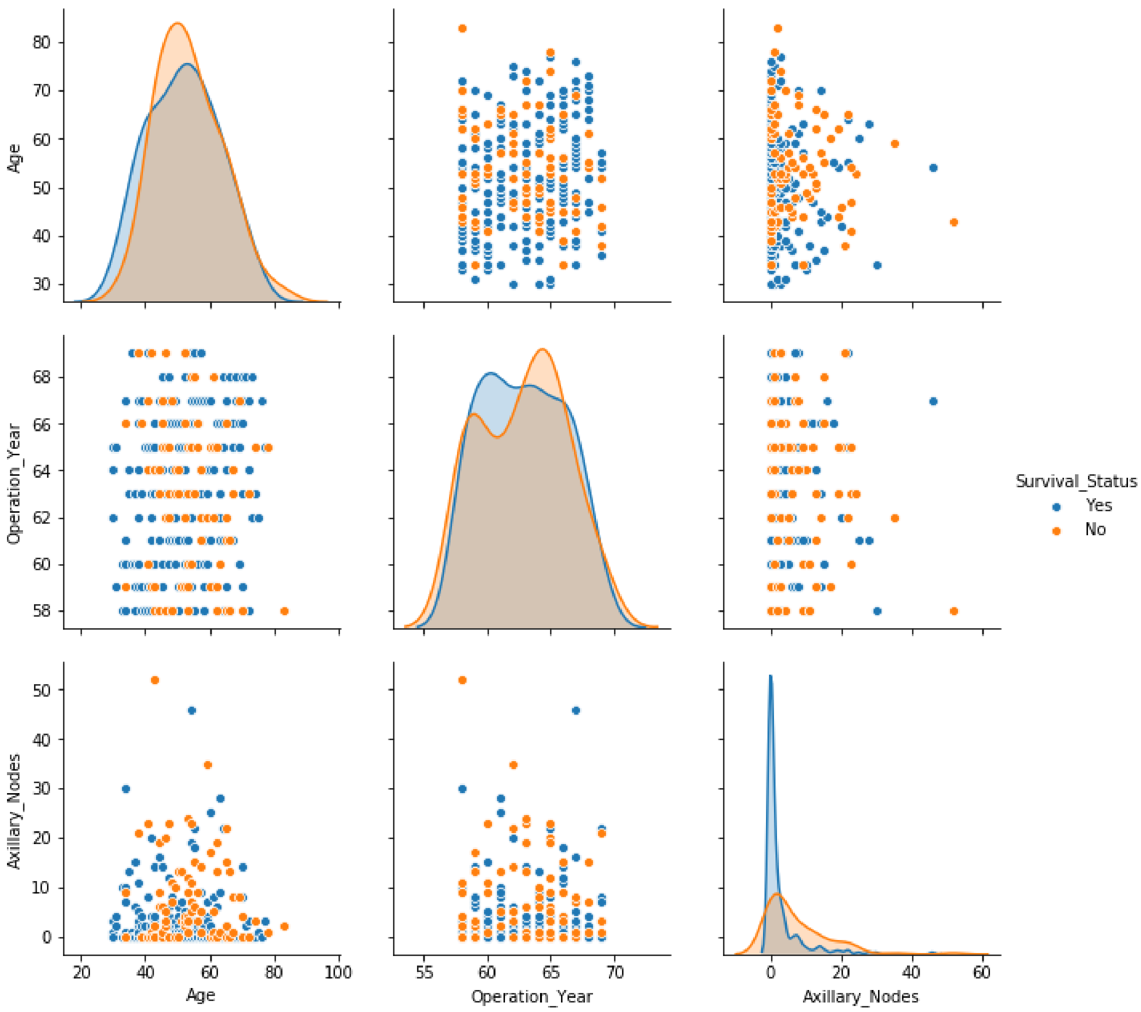


### Bivariate Analysis

Here we plot a pairplot to see which combination of features does a better job at classification

In [14]:

```
# Pairplot
sns.pairplot(hb,hue='Survival_Status',size = 3)
plt.show()
```




## Final Conclusions

*1. The number of rows (records of patients) are 306.*
*2. The number of classes are two, namely 'Yes' and 'No'.*
*3. There are 225 datapoints that result in a 'Yes'and 81 datapoints that result in a 'No'.*
*4. This is an imbalanced dataset.*
*5. The majority of patients that survived the treatment are in the ages between 50-60.*
*6. The majority of patients that didn't survive the treatment are around 50 years.*
*7. The number of Axillary Nodes found in patients are usually around (0-5) irrespective of their Survival Status.*
*8. About 90% of the patients that survived the surgery had less than 10 Axillary Nodes.*
*9. Roughly 70% of the patients that didn't survive the surgery had less than 10 Axillary Nodes.*
*10. In the case of Axillary Nodes, there seem to be quite a few number of outliers.*
*11. The ages of 50% of the patients who survived the treatment lie in between 43-60 roughly.*
*12. The ages of 50% of the patients who didn't survive the treatment are in between 46- 61 roughly.*
*13. Although there isn't much difference, the patients that couldn't survive the surgery are slightly older, on average, than those who did.*
*14. Similarly, the Operation Year of those patients who survived the surgery is sligjtly greater, on average, than those who didn't't.*
*15. The pairplot uses the three features to plot the graphs with combinations of features*
*16. Simply by looking, we can see that the plot between 'Operation_Year' and 'Axillary_Nodes' does the best job at classification*
*17. Although the classification is not perfect, it is better than the rest of the plots.*