Haberman’s Survival Data Set

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Overview: 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.

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

```
In [1]: import pandas as pd
```

```
In [2]: hmn = pd.read_csv('haberman.csv')
```

```
In [3]: #(Q) how many observations and features are there in the total dataset?
        print (hmn.shape)
```

```
(305, 4)
```

but, the kaggle website says there are 306 instances of data.
Read point 5 at https://www.kaggle.com/gilsousa/habermans-survival-data-set/data
also opening the original haberman.csv file in a text-editor like notepad++ shows 306 rows.
so where is the missing row? lets find out

```
In [4]: #view some data from the hmn dataframe
        hmn.head()
```

```
Out[4]:    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
```

seems like pandas is using up the first data row as the column header. Lets fix that;

```
In [5]: #read haberman.csv data-set again and add column headers
        hmn = pd.read_csv('haberman.csv' , names = ["age", "op-yr", "node", "class"])

        print (hmn.shape)
```

```
(306, 4)
```

```
In [6]: # view some random data to confirm everything is as expected
        hmn.sample(5)
```

```
Out[6]:      age  op-yr  node  class
        139   51     59     1      1
        64    43     64     0      2
        170   54     68     7      2
        237   61     59     0      1
        48    41     59     0      1
```

```
In [7]: #(Q) what are the columns in our dataset?
        print (hmn.columns)
```

```
Index(['age', 'op-yr', 'node', 'class'], dtype='object')
```

Column Information:

1. age: Age of patient at time of operation (numerical)
2. op-yr: Patient's calender year of operation (19xx, numerical)
3. node: Number of positive axillary nodes detected (numerical)
   - A positive axillary node is a lymph node in the area of the armpit (axilla) to which cancer has spread. See- https://en.wikipedia.org/wiki/Positive_axillary_lymph_node
4. class: Survival status (numerical)
   - 1 = the patient survived 5 years or longer after the operation
   - 2 = the patient died within 5 year of operation

OBJECTIVE:
Given a new patient's (age, year-of-operation, count-of-positive-nodes-detected) we want to build a model which predicts if the patient will survive for more than 5 years after the operation or not.

The following is the Exploratory Data Analysis for the same.

```
In [8]: #(Q) how many data points for each class are present?
        hmn["class"].value_counts()
```

```
Out[8]: 1    225
        2     81
        Name: class, dtype: int64
```

Conclusions:

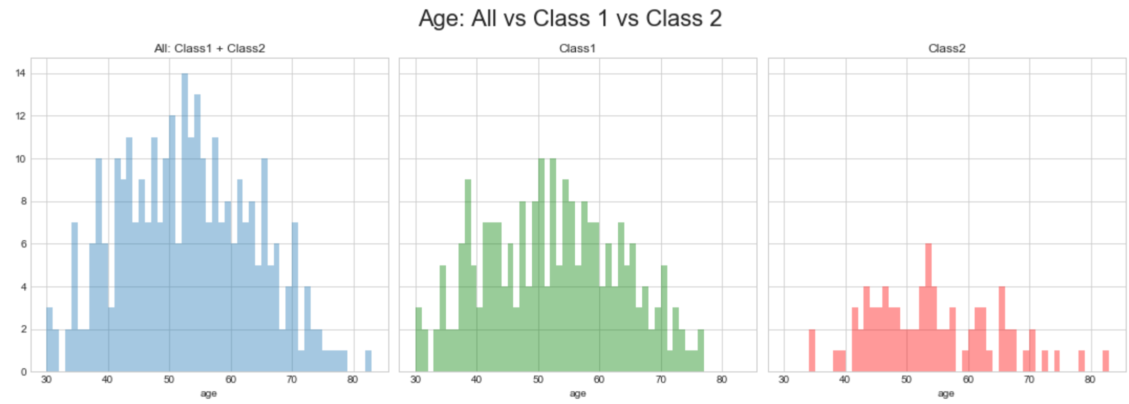
1. This is an imbalanced dataset.
   - ~**73.5%** survied for more than 5 yr after the operation
   - ~**26.5%** did not

```
In [9]: import seaborn as sns
        import matplotlib.pyplot as plt

        sns.set_style('whitegrid')
```

```
In [10]: #separating class1 and class2 dataset for better understanding and ease of working

         hmn_1 = hmn.loc[hmn['class']==1]
         hmn_2 = hmn.loc[hmn['class']==2]
```

First I'll try performing univariate analysis and see if the features individually reflect anything

```
In [11]: # 1. Studying 'age' feature

         fig, axs = plt.subplots(1, 3, sharex=True, sharey=True)

         plt.suptitle("Age: All vs Class 1 vs Class 2", y=1.06, fontsize=22)
         fig.set_figheight(5)
         fig.set_figwidth(15)

         axs[0].set_title('All: Class1 + Class2')
         sns.distplot(hmn['age'],
                      bins=range(min(hmn['age']), max(hmn['age']) + 1),
                      kde=False, ax=axs[0])

         axs[1].set_title('Class1')
         sns.distplot(hmn_1['age'],
                      bins=range(min(hmn_1['age']), max(hmn_1['age']) + 1),
                      color='g', kde=False, ax=axs[1])

         axs[2].set_title('Class2')
         sns.distplot(hmn_2['age'],
                      bins=range(min(hmn_2['age']), max(hmn_2['age']) + 1),
                      color='r', kde=False, ax=axs[2])

         plt.tight_layout()
         plt.show()
```



```
In [12]: hmn['age'].describe()
```

```
Out[12]: count    306.000000
         mean      52.457516
         std       10.803452
         min       30.000000
         25%       44.000000
         50%       52.000000
         75%       60.750000
         max       83.000000
         Name: age, dtype: float64
```

```
In [13]: hmn_1['age'].describe()
```

```
Out[13]: count    225.000000
         mean      52.017778
         std       11.012154
         min       30.000000
         25%       43.000000
         50%       52.000000
         75%       60.000000
         max       77.000000
         Name: age, dtype: float64
```

```
In [14]: hmn_2['age'].describe()
```

```
Out[14]: count    81.000000
         mean     53.679012
         std      10.167137
         min      34.000000
         25%      46.000000
         50%      53.000000
         75%      61.000000
         max      83.000000
         Name: age, dtype: float64
```

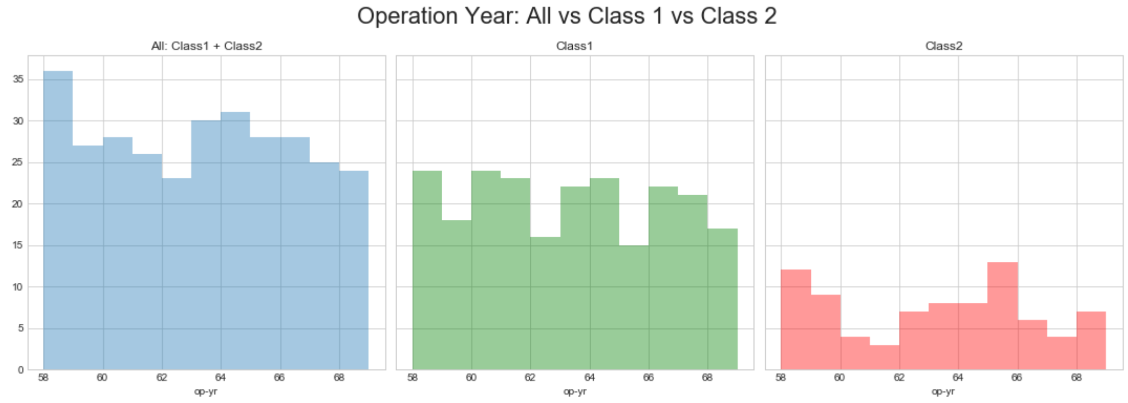
```
In [15]: print("Total: Number of Patient whose age <40 = {}"
               .format(len(hmn[hmn['age']<=40])))
         print("Class 1: Number of Patient whose age <40 = {}"
               .format(len(hmn_1[hmn_1['age']<=40])))
```

```
Total: Number of Patient whose age <40 = 43
Class 1: Number of Patient whose age <40 = 39
```

Conclusions:

1. **All** patients **< 34** years of age at the time of operation survived for more than 5 years
2. **No** patient **> 77** years of age at the time of operation survived for more than 5 years
3. If patient's age is **<= 40** at the time of operation, chances of survival for more than 5 years is significantly higher at **90%**(39/43)

```
In [16]: # 2. Studying 'op-yr' feature

         fig, axs = plt.subplots(1, 3, sharex=True, sharey=True)

         plt.suptitle("Operation Year: All vs Class 1 vs Class 2", y=1.06, fontsize=22)
         fig.set_figheight(5)
         fig.set_figwidth(15)

         axs[0].set_title('All: Class1 + Class2')
         sns.distplot(hmn['op-yr'],
                      bins=range(min(hmn['op-yr']), max(hmn['op-yr']) + 1),
                      kde=False, ax=axs[0])

         axs[1].set_title('Class1')
         sns.distplot(hmn_1['op-yr'],
                      bins=range(min(hmn_1['op-yr']), max(hmn_1['op-yr']) + 1),
                      color='g', kde=False, ax=axs[1])

         axs[2].set_title('Class2')
         sns.distplot(hmn_2['op-yr'],
                      bins=range(min(hmn_2['op-yr']), max(hmn_2['op-yr']) + 1),
                      color='r', kde=False, ax=axs[2])

         plt.tight_layout()
         plt.show()
```



```
In [17]: hmn['op-yr'].describe()

Out[17]: count    306.000000
         mean      62.852941
         std        3.249405
         min       58.000000
         25%       60.000000
         50%       63.000000
         75%       65.750000
         max       69.000000
         Name: op-yr, dtype: float64
```

```
In [18]: hmn_1['op-yr'].describe()
```

```
Out[18]: count    225.000000
         mean      62.862222
         std        3.222915
         min       58.000000
         25%       60.000000
         50%       63.000000
         75%       66.000000
         max       69.000000
         Name: op-yr, dtype: float64
```

```
In [19]: hmn_2['op-yr'].describe()
```

```
Out[19]: count    81.000000
         mean     62.827160
         std       3.342118
         min      58.000000
         25%      59.000000
         50%      63.000000
         75%      65.000000
         max      69.000000
         Name: op-yr, dtype: float64
```

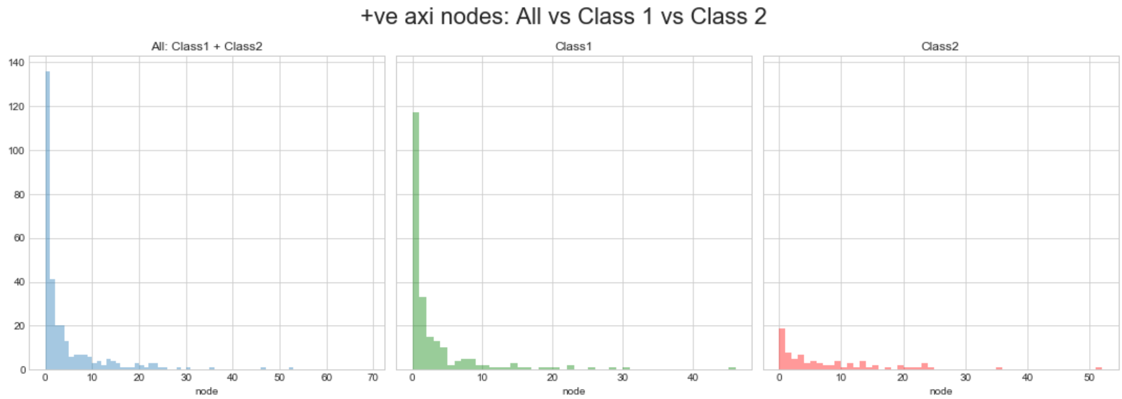
```
In [20]: # % patient distribution of class1 vs class2 for each year

         for i in range(min(hmn['op-yr']), max(hmn['op-yr']) + 1):
             total = len(hmn[hmn['op-yr']==i])
             class1 = len(hmn_1[hmn_1['op-yr']==i])
             print("year: 19{}, total-patient: {}, class1: {}%, class2: {}%"
                   .format(i,total,round(class1/total*100,2),round(100-(class1/total*100),2)))
```

```
year: 1958, total-patient: 36, class1: 66.67%, class2: 33.33%
year: 1959, total-patient: 27, class1: 66.67%, class2: 33.33%
year: 1960, total-patient: 28, class1: 85.71%, class2: 14.29%
year: 1961, total-patient: 26, class1: 88.46%, class2: 11.54%
year: 1962, total-patient: 23, class1: 69.57%, class2: 30.43%
year: 1963, total-patient: 30, class1: 73.33%, class2: 26.67%
year: 1964, total-patient: 31, class1: 74.19%, class2: 25.81%
year: 1965, total-patient: 28, class1: 53.57%, class2: 46.43%
year: 1966, total-patient: 28, class1: 78.57%, class2: 21.43%
year: 1967, total-patient: 25, class1: 84.0%, class2: 16.0%
year: 1968, total-patient: 13, class1: 76.92%, class2: 23.08%
year: 1969, total-patient: 11, class1: 63.64%, class2: 36.36%
```

Conclusions:

1. Year of Operation doesn't seem to have any prominent effect on patient's survival status.

```
In [21]: # 3. Studying 'node' feature

         fig, axs = plt.subplots(1, 3, sharey=True)

         plt.suptitle("+ve axi nodes: All vs Class 1 vs Class 2", y=1.06, fontsize=22)
         fig.set_figheight(5)
         fig.set_figwidth(15)

         axs[0].set_title('All: Class1 + Class2')
         sns.distplot(hmn['node'],
                      bins=range(min(hmn['node']), max(hmn['op-yr']) + 1),
                      kde=False, ax=axs[0])

         axs[1].set_title('Class1')
         sns.distplot(hmn_1['node'],
                      bins=range(min(hmn_1['node']), max(hmn_1['node']) + 1),
                      color='g', kde=False, ax=axs[1])

         axs[2].set_title('Class2')
         sns.distplot(hmn_2['node'],
                      bins=range(min(hmn_2['node']), max(hmn_2['node']) + 1),
                      color='r', kde=False, ax=axs[2])

         plt.tight_layout()
         plt.show()
```



```
In [22]: hmn['node'].describe()

Out[22]: count    306.000000
         mean       4.026144
         std        7.189654
         min        0.000000
         25%        0.000000
         50%        1.000000
         75%        4.000000
         max       52.000000
         Name: node, dtype: float64
```

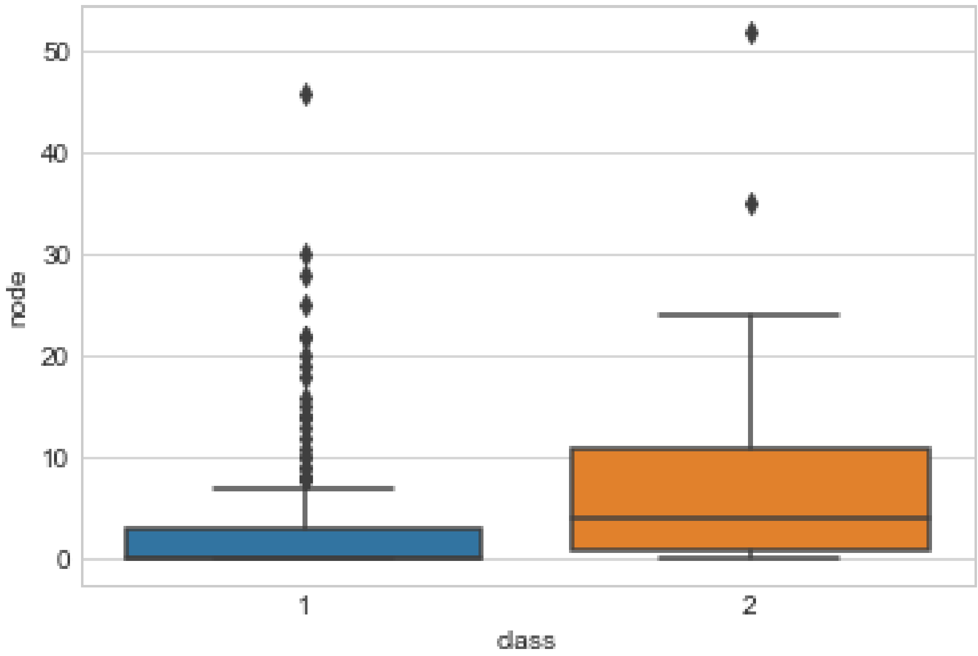
```
In [23]: hmn_1['node'].describe()
```

```
Out[23]: count    225.000000
         mean       2.791111
         std        5.870318
         min        0.000000
         25%        0.000000
         50%        0.000000
         75%        3.000000
         max       46.000000
         Name: node, dtype: float64
```

```
In [24]: hmn_2['node'].describe()
```

```
Out[24]: count    81.000000
         mean      7.456790
         std       9.185654
         min       0.000000
         25%       1.000000
         50%       4.000000
         75%      11.000000
         max      52.000000
         Name: node, dtype: float64
```

```
In [25]: sns.boxplot(x='class',y='node', data=hmn)
         plt.show()
```



```
In [26]: print("Total: Number of Patient with detected +ve node =0: {}"
                .format(len(hmn[hmn['node']==0])))
         print("Total: Number of Patient with detected +ve node <10: {}"
                .format(len(hmn[hmn['node']<10])))
```

```
Total: Number of Patient with detected +ve node =0: 136
Total: Number of Patient with detected +ve node <10: 263
```

Conclusions:

1. **44%** of patients are detected with 0 +ve axillary nodes
2. Though the maximum number of nodes detected for any patient is 52, **86%** of patients are detected with < 10 +ve axillary nodes
3. **75%** of patients who survived for more than 5 years after the operation had +ve axillary node <=3
4. **50%** of patients who did not survive for more than 5 years after the operation had +ve axillary node >4

Next I'll try bivariate analysis(age vs node-count) and check if they together reflect something more.

We already know that 75% patient who survive have +ve axillary node <=3

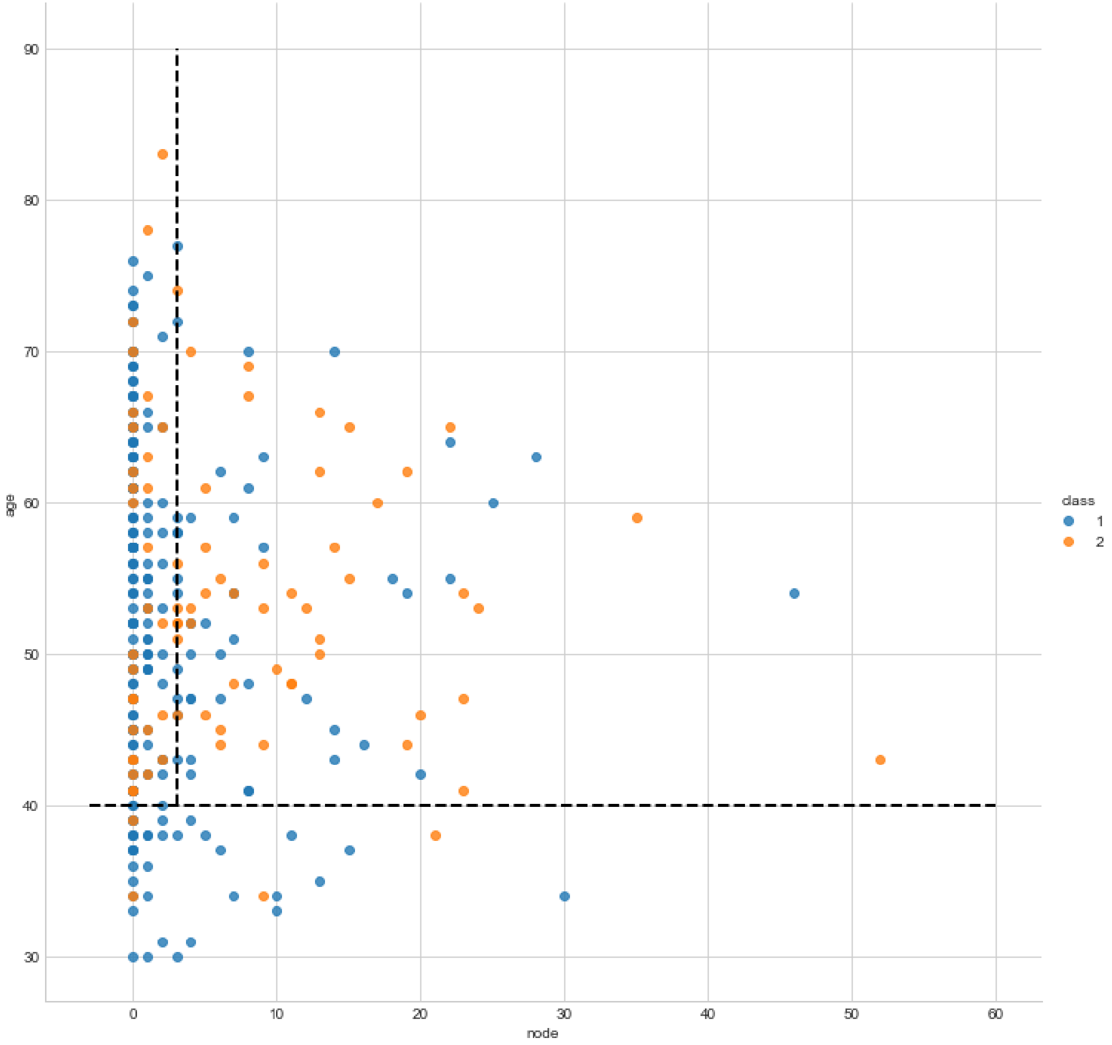
But what about those who do not survive in spite of <=3 +ve nodes detected. Do age play a factor there?

```
In [27]: #(Q) For class-2 patients with <=3 nodes, what were their age?

         hmn_2[hmn_2['node']<=3]['age'].describe()

Out[27]: count    39.000000
         mean     54.256410
         std      11.818179
         min      34.000000
         25%      45.000000
         50%      52.000000
         75%      62.500000
         max      83.000000
         Name: age, dtype: float64
```

Conclusions:

1. **75%** of patients who could not survive more than 5 yr had age **>45** at the time of operation

```
In [28]: sns.lmplot("node", "age", data=hmn, hue='class', fit_reg=False, size=10)

         plt.plot([-3, 60], [40, 40], 'k--', linewidth=2)
         plt.plot([3, 3], [40, 90], 'k--', linewidth=2)

         plt.show()
```



```
In [29]: print("Total: Number of Patient whose age >40 and node <=3 = {}"
               .format(len(hmn[(hmn['age']>40)&(hmn['node']<=3)])))
         print("Class1: Number of Patient whose age >40 and node <=3 = {}"
               .format(len(hmn_1[(hmn_1['age']>40)&(hmn_1['node']<=3)])))
         print()
         print("Total: Number of Patient whose age >40 and node >3 = {}"
               .format(len(hmn[(hmn['age']>40)&(hmn['node']>3)])))
         print("Class1: Number of Patient whose age >40 and node >3 = {}"
               .format(len(hmn_1[(hmn_1['age']>40)&(hmn_1['node']>3)])))
```

```
Total: Number of Patient whose age >40 and node <=3 = 187
Class1: Number of Patient whose age >40 and node <=3 = 150

Total: Number of Patient whose age >40 and node >3 = 76
Class1: Number of Patient whose age >40 and node >3 = 36
```

Conclusions:

- I divided the above scatterplot into 3 regions
- Calaulated % patient distribution of class-1 vs class-2 for each region.

Region	Condition	class-1 %	class-2 %
1	age <= 40	90	10
2	age > 40 & node <=3	80	20
3	age > 40 & node >3	47	53

- Build a pseudo model,

which Given a new patient's (age, year-of-operation, count-of-positive-nodes-detected), predicts if the patient will survive for more than 5 years after the operation or not.

```
In [30]: # Pseudo Model :

         def predict(age, opyr, node):

              '''This function returns
                 True: if a patient will survive for more than 5 years
                 False: otherwise
             '''

             if age<=40:
                 return True   # 90% success rate
             else:
                 if node<=3:
                     return True   # 80% success rate
                 else:
                     return
                     # I need some help here
                     # and would love to know how you would have analyzed this
```