Haberman_Dataset_Analysis

July 9, 2018

```
In [2]: **Overview**
        The dataset given contains the data collected during a study conducted between 1958 an
        Hospital on the survivality of patients who underwent breast cancer treatment.

        column |  content
          1st  :  age of patients
          2nd  :  year of operation
          3rd  :  positive axillary nodes detected
          4th  :  survival status
                  1 = patient survived 5 or more years after the treatement.
                  2 = patient died within 5 years of the treatement.

        **Objective**
        1. To analyse the dataset and build a model that can predict the survivality of a patie
           nodes as input.
```

```
In [2]: import pandas as pd
        import matplotlib.pyplot as plt
        import seaborn as sns
        import numpy as np
```

```
In [3]: # Reading data from haberman.csv dataset
        df = pd.read_csv('haberman.csv')
```

```
In [4]: # Getting number of datapoints and attributes
        df.shape
```

```
Out[4]: (306, 4)
```

```
In [5]: df.head()
```

```
Out[5]:    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
```

```
In [6]: # Since the dataset lacks column labels . We will read the data by adding column label
        # Here age = age of patient.
        #      year = year of operation.
        #      nodes = number of positive axillary nodes detected.(Lymph nodes).
        #      status = this shows that a patient was able to survive for more than 5 years or
        df = pd.read_csv('haberman.csv',names=['age','year','nodes','status'])
```

```
In [7]: # Getting first few datapoints
        df.head()
```

```
Out[7]:    age  year  nodes  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 [8]: # Here we need labels in the status column instead of integral value .
        df['status'].unique()
```

```
Out[8]: array([1, 2], dtype=int64)
```

```
In [9]: # Hence we will replace 1 with 'survived' and 2 with 'died'
        df['status'] = df['status'].apply(lambda x:'survived' if x==1 else 'died')
```

```
In [10]: df.head()
```

```
Out[10]:    age  year  nodes    status
         0   30    64      1  survived
         1   30    62      3  survived
         2   30    65      0  survived
         3   31    59      2  survived
         4   31    65      4  survived
```

```
In [12]: # Getting the stastical overwiew of the dataset
         df.describe()
```

```
Out[12]:               age        year       nodes
         count  307.000000  307.000000  307.000000
         mean    52.384365   62.856678    4.016287
         std     10.861674    3.244751    7.179974
         min     30.000000   58.000000    0.000000
         25%     44.000000   60.000000    0.000000
         50%     52.000000   63.000000    1.000000
         75%     60.500000   65.500000    4.000000
         max     83.000000   69.000000   52.000000
```

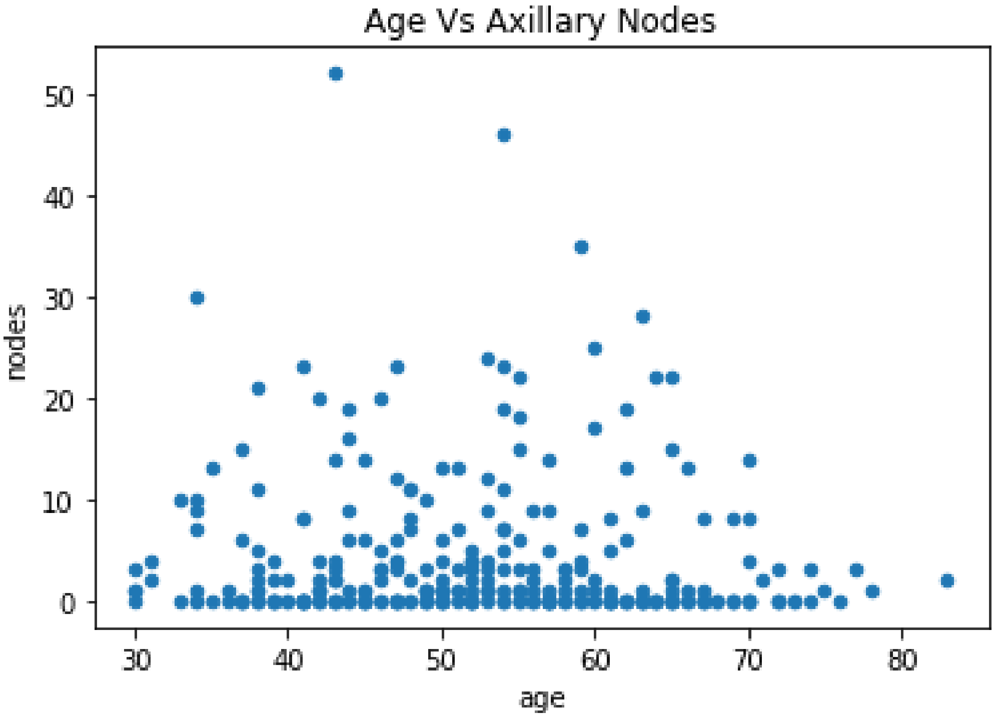
```
In [ ]: **Observations**
        1. Min age of patients is 30 and max age is 83 but 75% of the patients are below the ag
        2. Mean age of the patients is below 53 year.
        3. 75% of the patients were treated before 1965.
        4. 75% of the patients have axillary nodes less than or equal to 4 although tha maximu
        5. Moreover 50% of the patients had axillary nodes less than or equal to 1.
```

```
In [13]: # Count the number of patients who survived or died after the treatement.
         df['status'].value_counts()
```

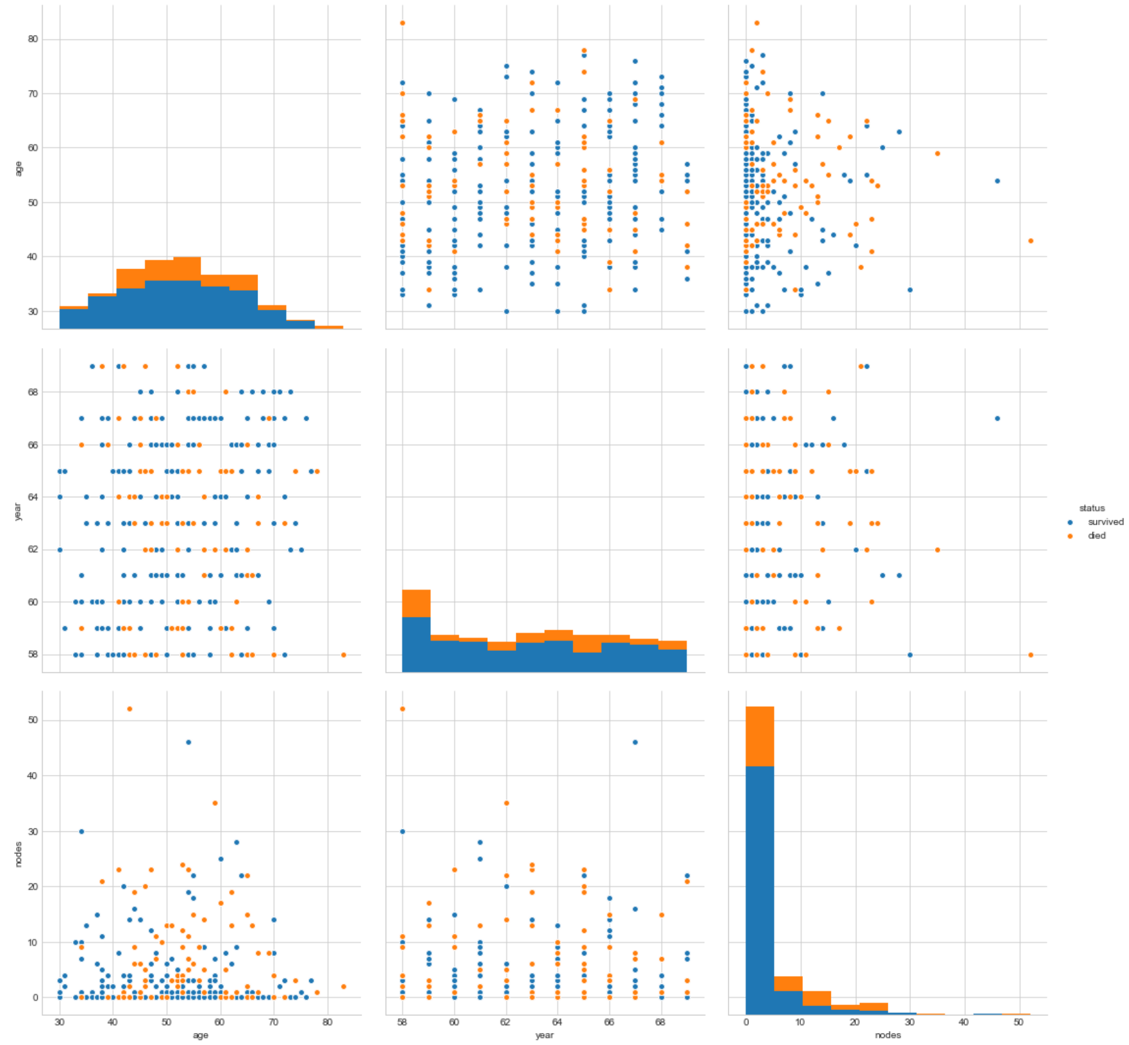
```
Out[13]: survived    226
         died         81
         Name: status, dtype: int64
```

```
In [ ]: **Observations**
        1. 73.61% of the patients survived and 26.28% of the patients died after 5 years of th
        2. The given data is imbalanced.
```

```
In [14]: # Multivariate Analysis
         df.plot(kind='scatter',x='age',y='nodes')
         plt.title('Age Vs Axillary Nodes')
         plt.show()
```



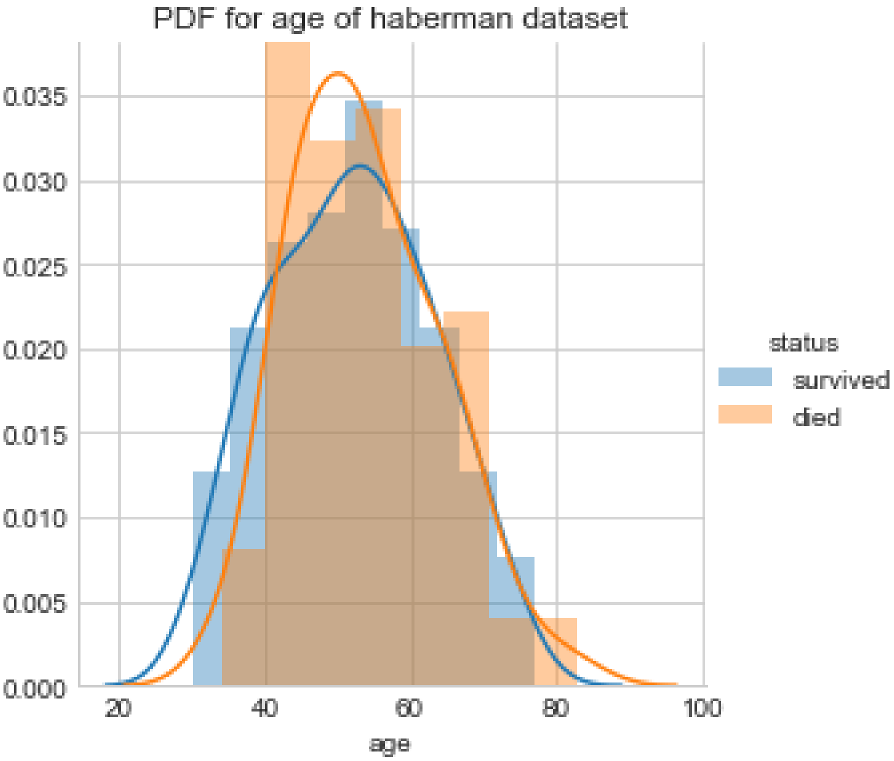
```
In [15]: # let us plot some more plots
         sns.set_style('whitegrid');
         sns.pairplot(df,hue='status',size=5)
         plt.show()
```



```
In [ ]: **Observations**
        1. From graph number 2 (age vs nodes ): We can observe that patients of age 40 and belo
                                                survival.
        2. From graph number 2 (age vs nodes) : We can observe that patients having age betwee
                                                or equal to 4 have a very high probability of s
```

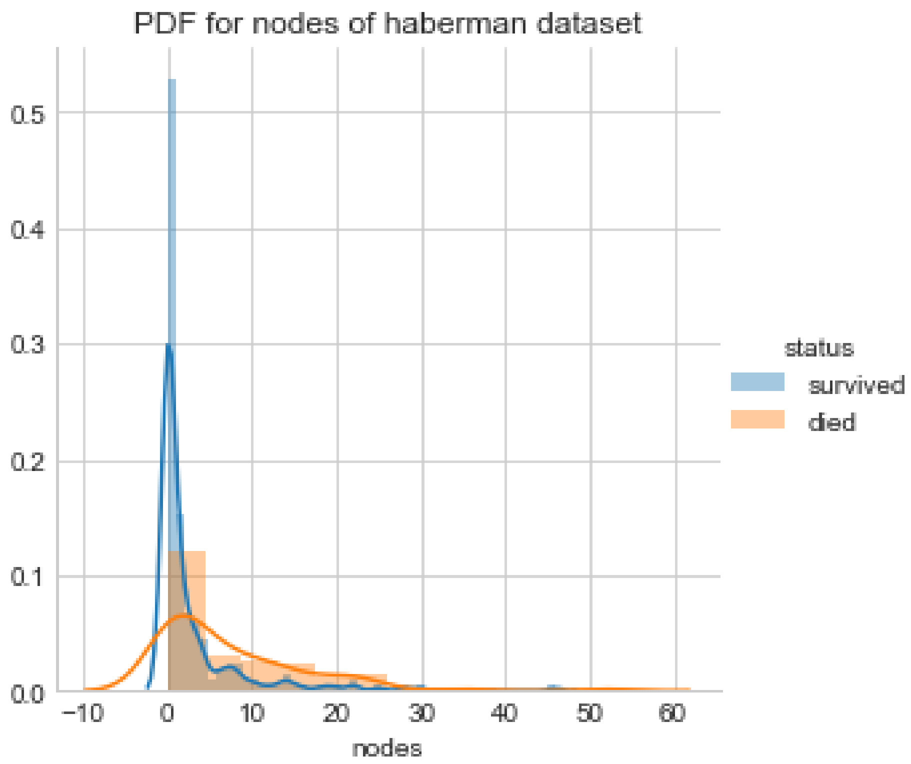
```
In [16]: haberman_survived = df.loc[df['status']=='survived'] # Patients who survived 5 years
         haberman_died = df.loc[df['status']=='died'] # Patients who counld't survive 5 years.
```

```
In [125]: plt.close();
          sns.set_style('whitegrid');
          sns.FacetGrid(df,hue='status',size=4) \
             .map(sns.distplot,'age') \
             .add_legend();
          plt.title('PDF for age of haberman dataset')
          plt.show()
```



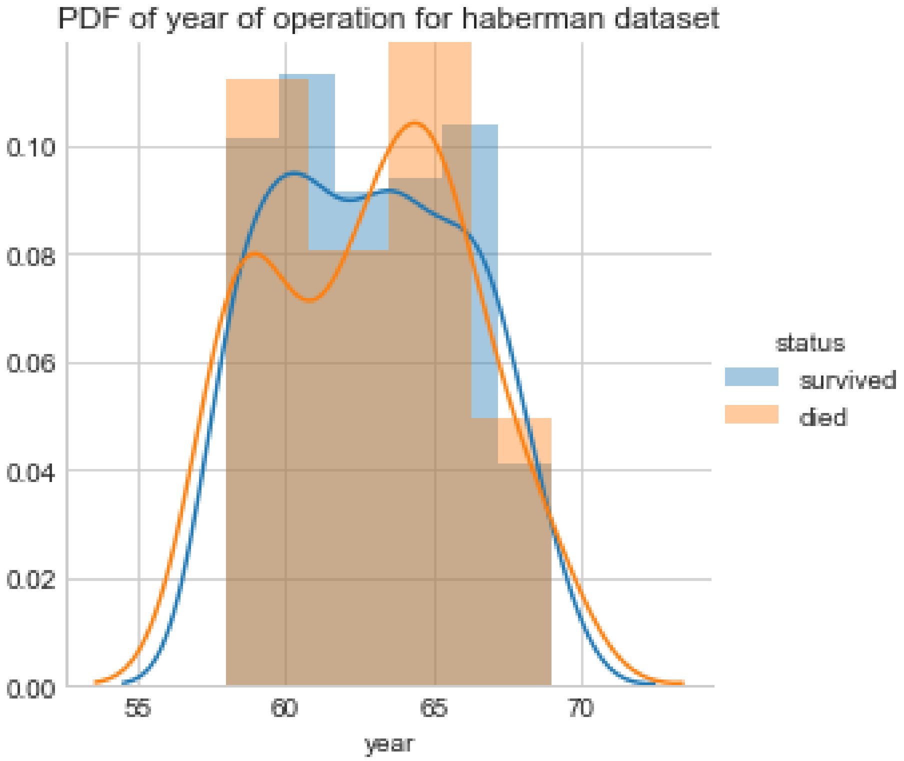
```
In [ ]: **Observation**
        1. The pdf of class haberman_survived and haberman_died are highly overlapped.
```

```
In [124]: sns.set_style('whitegrid')
          sns.FacetGrid(df,hue='status',size=4) \
             .map(sns.distplot,'nodes') \
             .add_legend();
          plt.title('PDF for nodes of haberman dataset')
          plt.show()
```



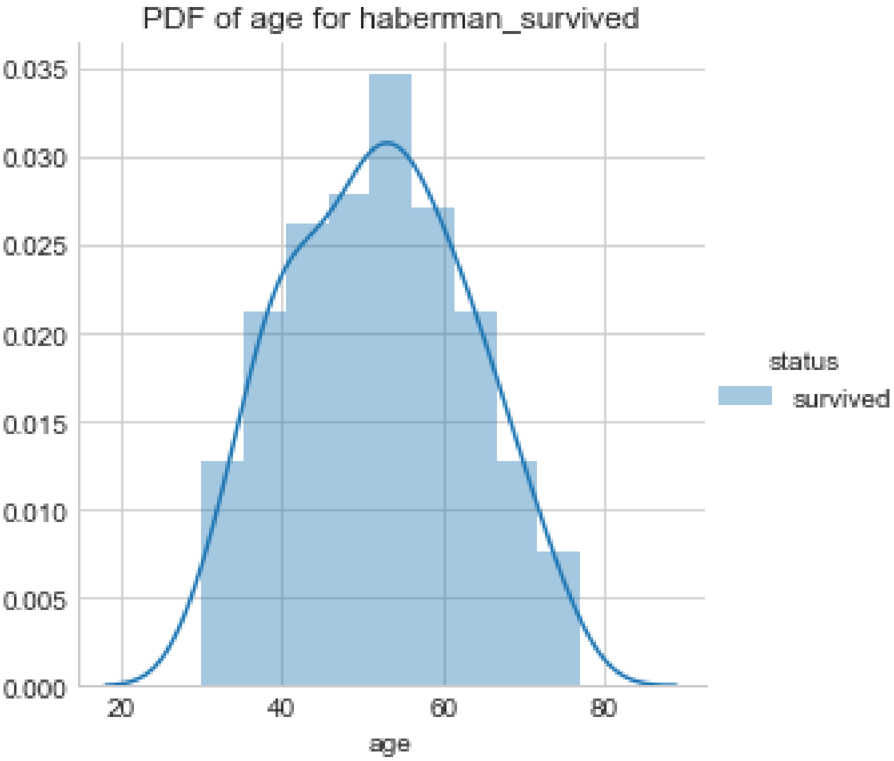
```
In [ ]: **Observation**
        1. The pdf of class haberman_survived and haberman_died are highly overlapped and we ca
```

```
In [17]: sns.set_style('whitegrid')
         sns.FacetGrid(df,hue='status',size=4) \
            .map(sns.distplot,'year') \
            .add_legend();
         plt.title('PDF of year of operation for haberman dataset')
         plt.show()
```



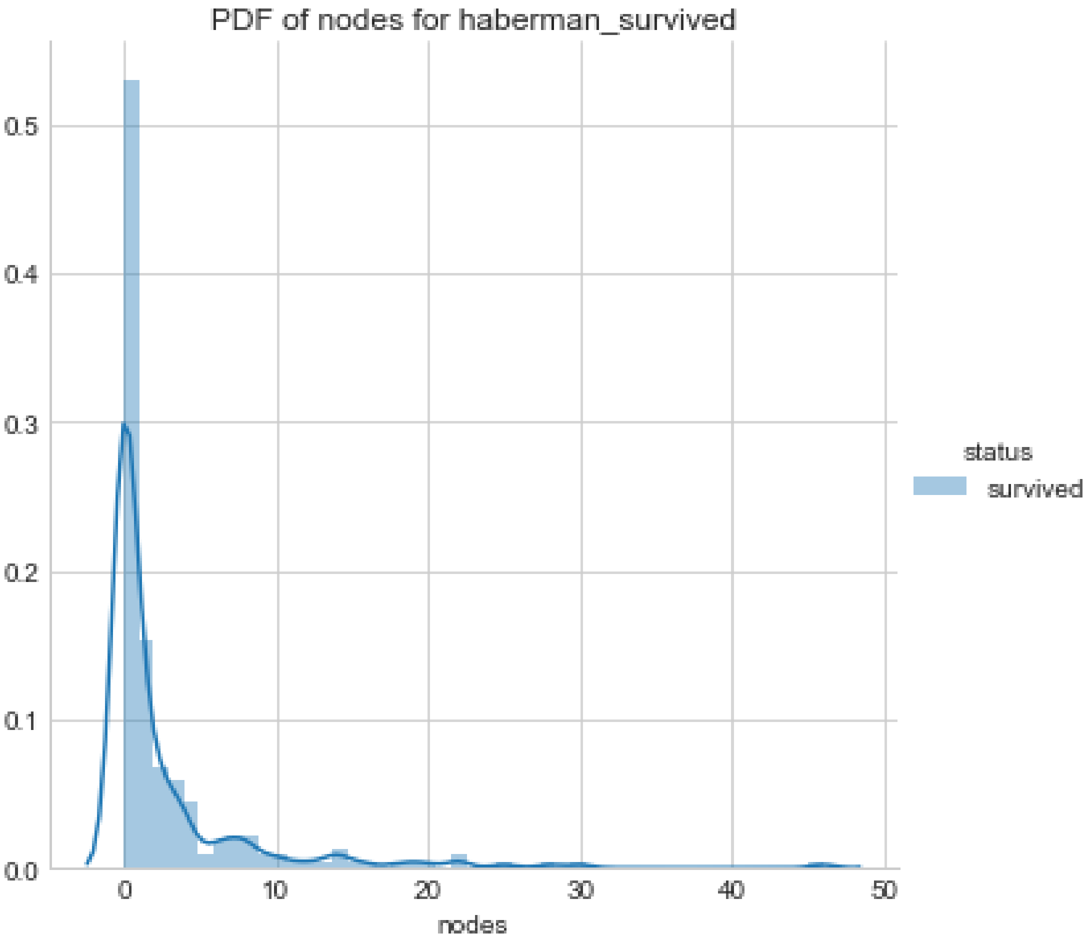
```
In [ ]: **Observation**
        1. The pdf of class haberman_survived and haberman_died are highly overlapped.
```

```
In [61]: # Univariate analysis for class haberman_survived
         # HISTOGRAM , PDFs
         sns.set_style('whitegrid')
         sns.FacetGrid(haberman_survived,hue='status',size=4) \
            .map(sns.distplot,'age') \
            .add_legend();
         plt.title('PDF of age for haberman_survived')
         plt.show()
```



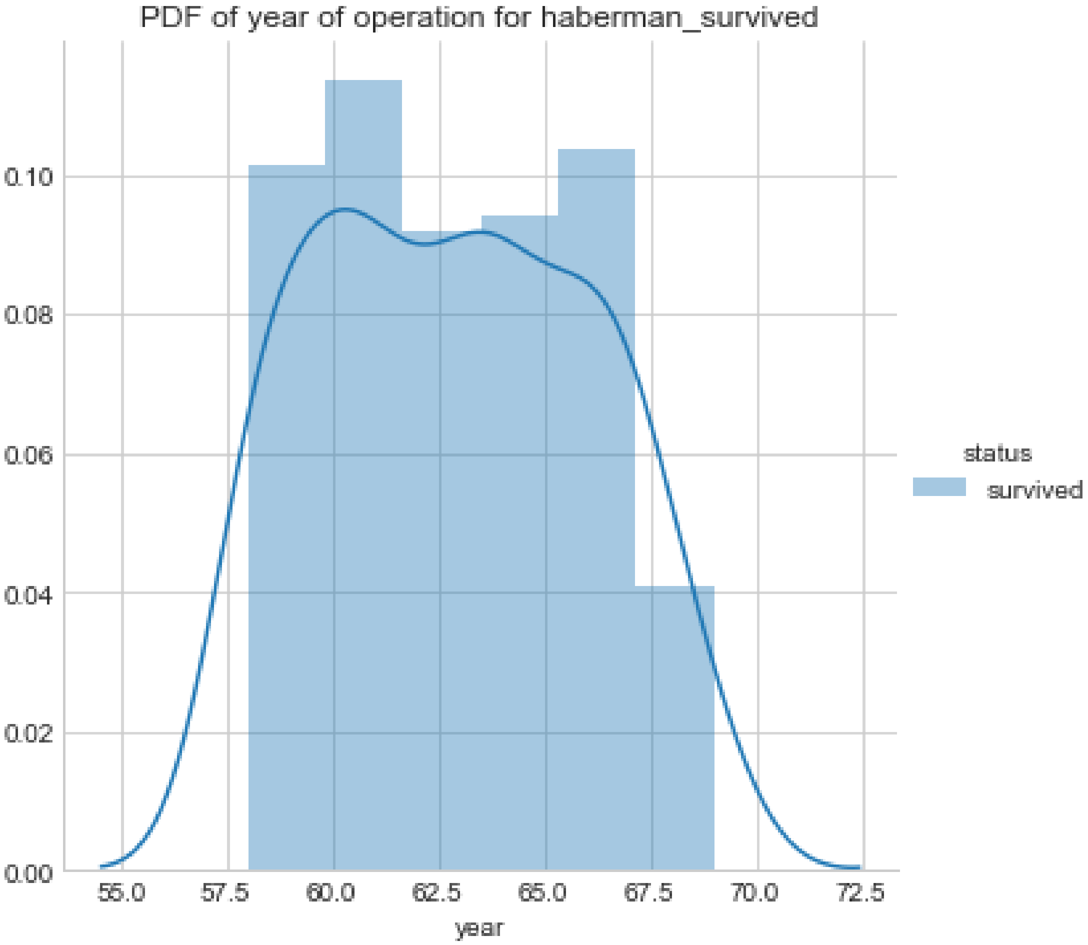
```
In [ ]: **observations**
        1. Maximum number of patients who survived the operation were of age between 40 and 60
        2. No patient survived for more than 5 years whose age is more than 77 years.
```

```
In [168]: sns.set_style('whitegrid')
          sns.FacetGrid(haberman_survived,hue='status',size=5) \
             .map(sns.distplot,'nodes') \
             .add_legend();
          plt.title('PDF of nodes for haberman_survived')
          plt.show()
```



```
In [ ]: **observations**
        1. Maximum number of patients who survived the operation had nodes less than 5.
```

```
In [169]: sns.set_style('whitegrid')
          sns.FacetGrid(haberman_survived,hue='status',size=5) \
             .map(sns.distplot,'year') \
             .add_legend();
          plt.title('PDF of year of operation for haberman_survived')
          plt.show()
```

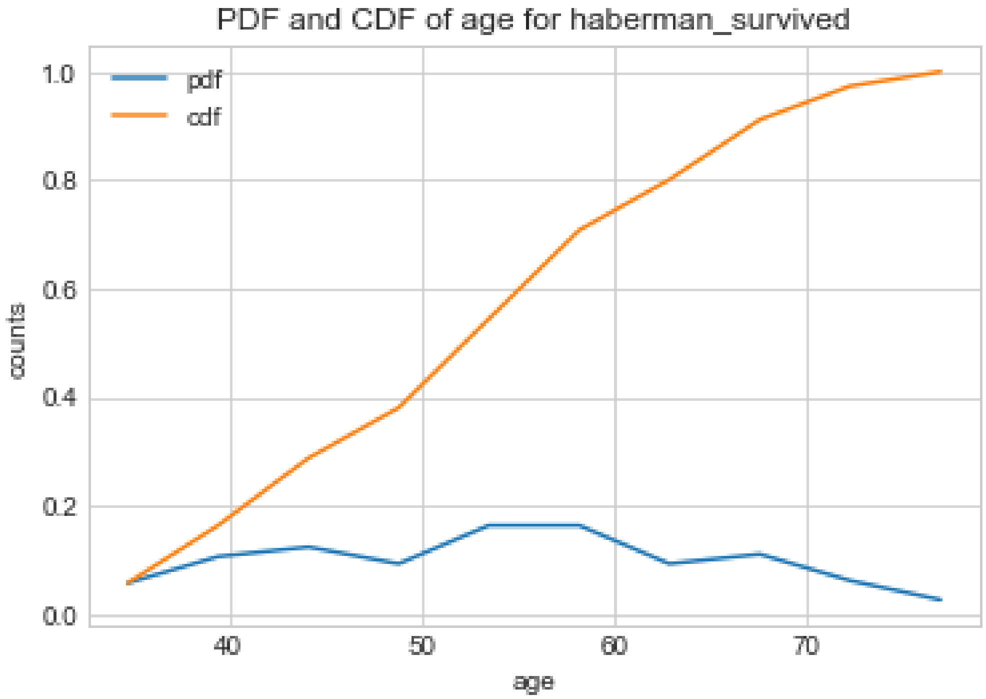


```
In [ ]: **Observation**
        1. The year of operation does not play any significant role in the survival of the pat
```

```
In [149]: # PDFs , CDFs For class haberman_survived
          haberman_survived=haberman_survived.sort_values(['age']) # sorted the dataset on age

          counts,bin_edges = np.histogram(haberman_survived['age'],bins=10,density=True)

          pdf = counts/(sum(counts))
          print(pdf);
          print(bin_edges);

          cdf = np.cumsum(pdf)
          plt.plot(bin_edges[1:],pdf)
          plt.plot(bin_edges[1:],cdf)
          plt.xlabel('age')
          plt.ylabel('counts')
```

```
         plt.title('PDF and CDF of age for haberman_survived')
         plt.legend(['pdf','cdf'])  # This takes a list as argument (each for pdf and cdf)
         plt.show()
```

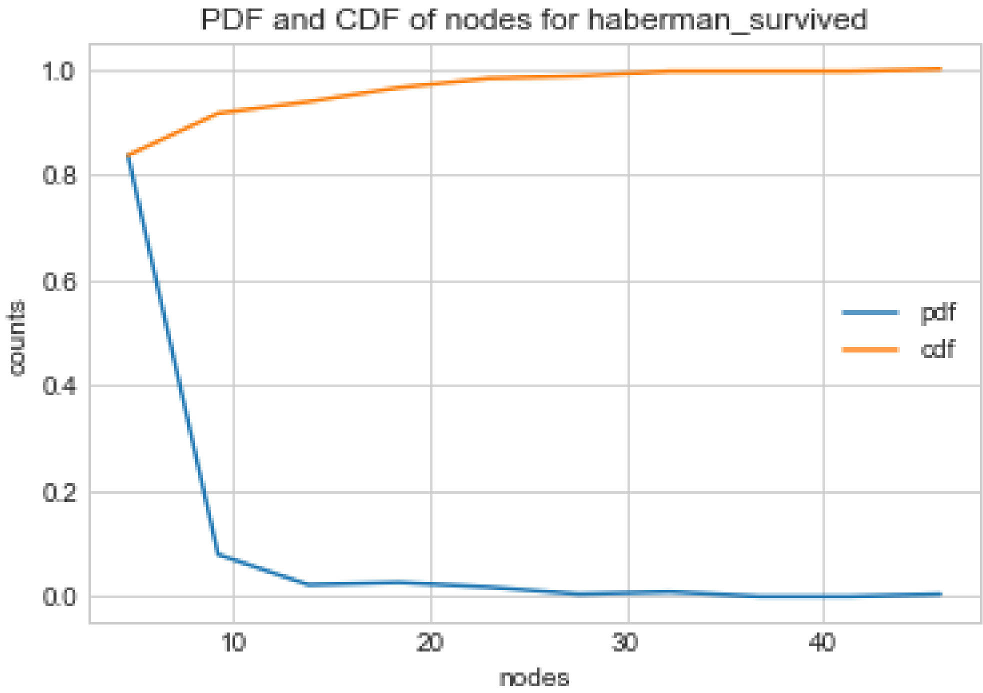
```
[0.05752212 0.10619469 0.12389381 0.09292035 0.16371681 0.16371681
 0.09292035 0.11061947 0.0619469  0.02654867]
[30.  34.7 39.4 44.1 48.8 53.5 58.2 62.9 67.6 72.3 77. ]
```



```
In [ ]: **Observation**
        1. 50% of the patients who survived for 5 or more years are less than 54 years of age a
```

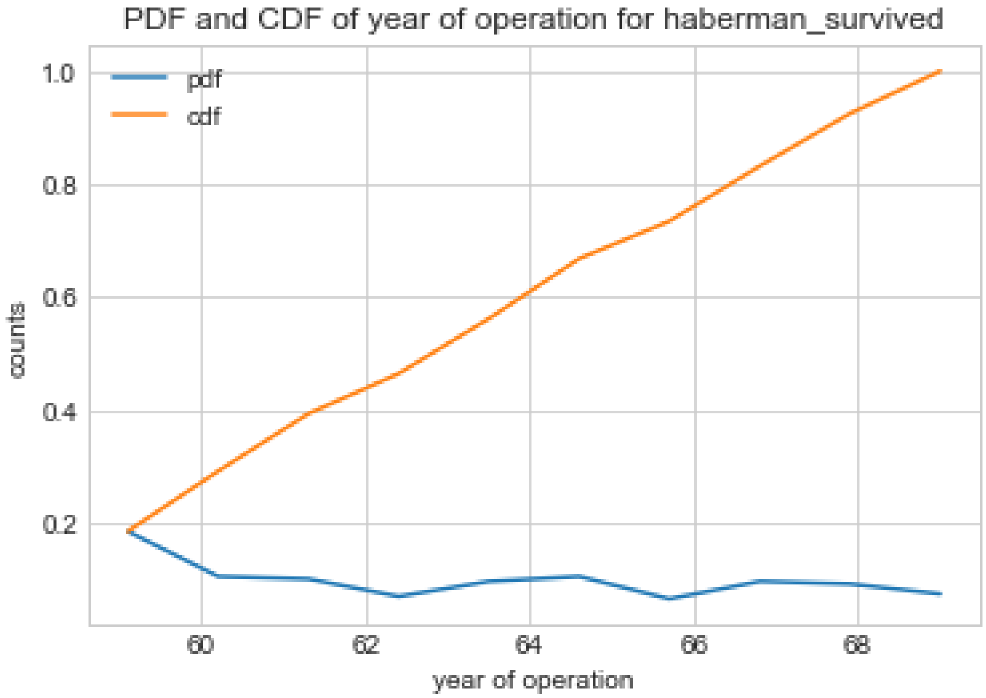
```
In [46]: # CDF and PDF of axillary nodes
         haberman_survived=haberman_survived.sort_values(['nodes']); # sorted the dataset on a

         counts,bin_edges = np.histogram(haberman_survived['nodes'],bins=10,density=True)

         pdf = counts/(sum(counts))
         print(pdf);
         print(bin_edges);

         cdf = np.cumsum(pdf)
         plt.plot(bin_edges[1:],pdf)
         plt.plot(bin_edges[1:],cdf)
         plt.xlabel('nodes')
         plt.ylabel('counts')
         plt.title('PDF and CDF of nodes for haberman_survived')
         plt.legend(['pdf','cdf'])
         plt.show()
```

```
[0.83628319 0.07964602 0.02212389 0.02654867 0.01769912 0.00442478
 0.00884956 0.         0.         0.00442478]
[ 0.   4.6  9.2 13.8 18.4 23.  27.6 32.2 36.8 41.4 46. ]
```



```
In [ ]: **Observations**
        1. 82% of the patients who survived for 5 or more years had nodes less than 4.
        2. More than 95% of the patients who survived for 5 or more years had number of nodes

In [157]: # PDF , CDF of age of operation.
          haberman_survived=haberman_survived.sort_values(['year']); # sorted the dataset on a

          counts,bin_edges = np.histogram(haberman_survived['year'],bins=10,density=True)

          pdf = counts/(sum(counts))
          print(pdf);
          print(bin_edges);

          cdf = np.cumsum(pdf)
          plt.plot(bin_edges[1:],pdf)
          plt.plot(bin_edges[1:],cdf)
          plt.xlabel('year of operation')
          plt.ylabel('counts')
          plt.title('PDF and CDF of year of operation for haberman_survived')
          plt.legend(['pdf','cdf'])
          plt.show()
```

```
[0.18584071 0.10619469 0.10176991 0.07079646 0.09734513 0.10619469
 0.06637168 0.09734513 0.09292035 0.07522124]
[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
```



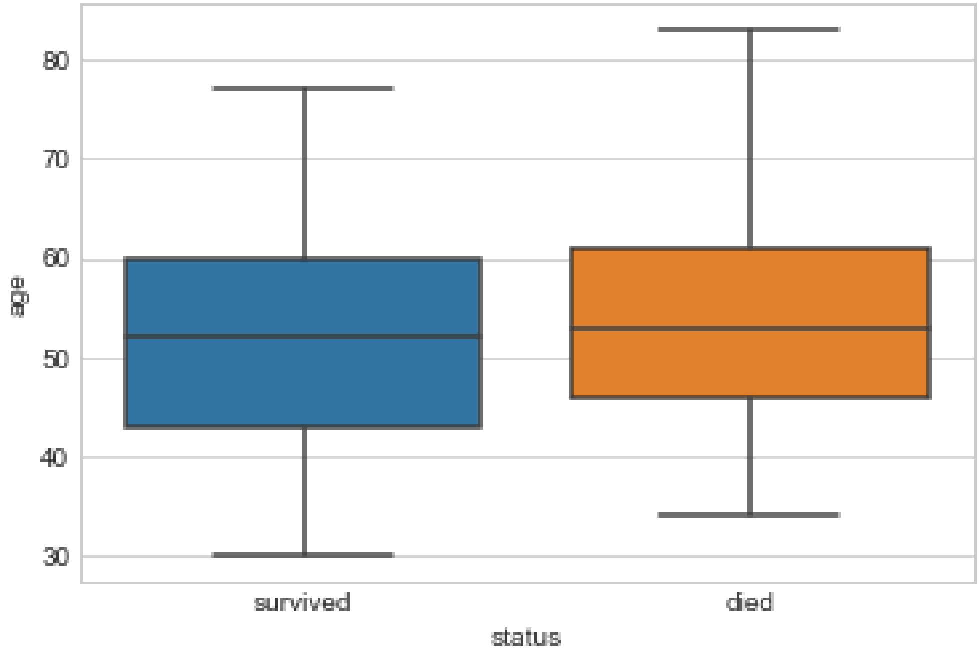
```
In [69]: ###### Medians,Quantiles,Percentiles,MAD

         print("Medians:")
         print('***************')
         print("Median age of all the patients",np.median(df['age']))
         print("Median nodes of all the patients",np.median(df['nodes']))
         print("Median age of all the patients who survived for 5 or more years",np.median(habe
         print("Median nodes of all the patients who survived for 5 or more years",np.median(ha
         print("Median age of all the patients who died within 5 years",np.median(haberman_diec
         print("Median node of all the patients who died within 5 years",np.median(haberman_die

         print("***************")
         print("Quantiles")
         print("***************")
         print("Quantile age of all the patients",np.percentile(df['age'],np.arange(0,100,25)))
         print("Quantile node of all the patients",np.percentile(df['nodes'],np.arange(0,100,25
         print("Quantile age of patients who survived for 5 or more years",np.percentile(haberm
         print("Quantile node of patients who survived 5 or more years",np.percentile(haberman_
         print("Quantile age of patients who died within 5 years",np.percentile(haberman_died[
         print("Quantile node of patients who died within 5 years ",np.percentile(df['nodes'],n

         print("***************")
         print("Percentiles")
         print("***************")
         print("90 percentile age of all patients",np.percentile(df['age'],90))
         print("90 percentile node of all patients",np.percentile(df['nodes'],90))
         print("90 percentile age of patients who survived 5 or more years",np.percentile(haber
         print("90 percentile node of patients who survived 5 or more years",np.percentile(habe
         print("90 percentile age of patients who died within 5 years",np.percentile(haberman_d
         print("90 percentile age of patients who died within 5 years",np.percentile(haberman_d

         print("***************")
         print("Median Absolute Deviation") # MAD = (median of (summation(x-median)))^2
         print("***************")
         from statsmodels import robust
         print("MAD of age of all the patients",robust.mad(df['age']))
         print("MAD of nodes of all the patients",robust.mad(df['nodes']))
         print("MAD of age of all the patients who survived for 5 or more years",robust.mad(hab
         print("MAD of nodes of all the patients who survived for 5 or more years",robust.mad(h
         print("MAD of age of all the patients who died within5 years",robust.mad(haberman_died
         print("MAD of age of all the patients who died within 5 years",robust.mad(haberman_die
```

```
Medians:
***************
Median age of all the patients 52.0
Median nodes of all the patients 1.0
Median age of all the patients who survived for 5 or more years 52.0
Median nodes of all the patients who survived for 5 or more years 0.0
Median age of all the patients who died within 5 years 53.0
Median node of all the patients who died within 5 years 4.0
***************
Quantiles
***************
Quantile age of all the patients [30.  44.  52.  60.5]
Quantile node of all the patients [0. 0. 1. 4.]
Quantile age of patients who survived for 5 or more years [30. 43. 52. 60.]
Quantile node of patients who survived 5 or more years [0. 0. 0. 3.]
Quantile age of patients who died within 5 years [34. 46. 53. 61.]
Quantile node of patients who died within 5 years  [0. 0. 1. 4.]
***************
```

```
Percentiles
***************
90 percentile age of all patients 67.0
90 percentile node of all patients 13.0
90 percentile age of patients who survived 5 or more years 67.0
90 percentile node of patients who survived 5 or more years 8.0
90 percentile age of patients who died within 5 years 67.0
90 percentile age of patients who died within 5 years 20.0
***************
Median Absolute Deviation
***************
MAD of age of all the patients 11.860817748044816
MAD of nodes of all the patients 1.482602218505602
MAD of age of all the patients who survived for 5 or more years 13.343419966550417
MAD of nodes of all the patients who survived for 5 or more years 0.0
MAD of age of all the patients who died within5 years 11.860817748044816
MAD of age of all the patients who died within 5 years 5.930408874022408
```

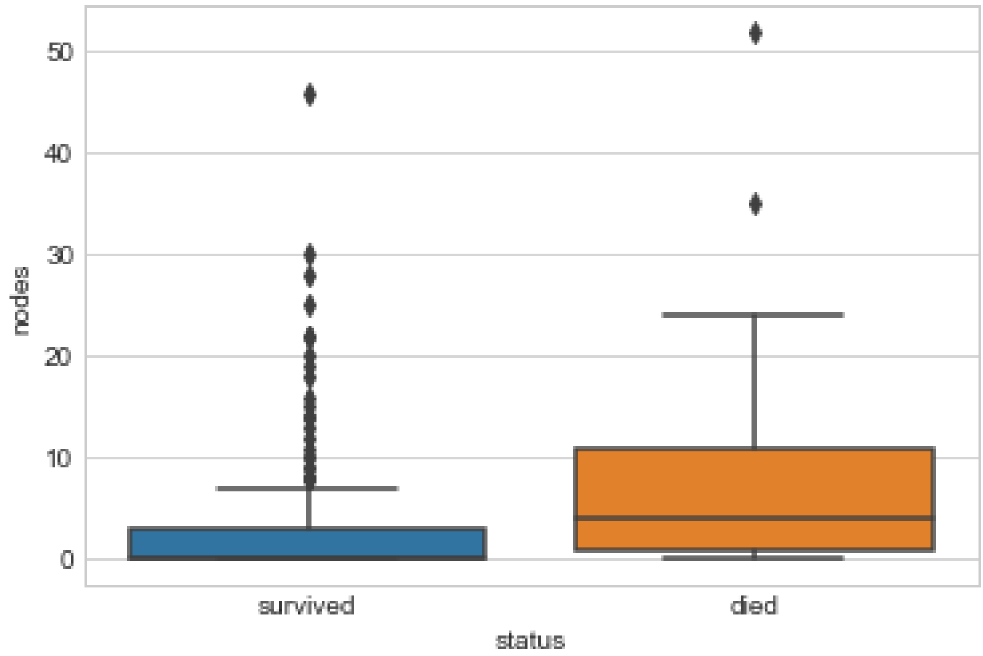
```
In [ ]: **Observations**
        1.50% of all the patients are below the age of 52.
        2.50% of all the patients have nodes below or equal to 1.
        3.All the patient of age below 34 survived.
        4.90% of the patients who survived had node less than or equal to 8.
```

```
In [173]: # BOX PLOT WITH WHISKERS FOR haberman dataset

          sns.boxplot(x='status',y='age',data=df)
          plt.show()
```



```
In [ ]: **Observations**
        1. 50% of the patients who survived were having between 42 and 60.
        2. 50% of the patients who died were having age between 46 and 62.
        3. None of the patients died who had age less than 34.
```

```
In [54]: sns.boxplot(x='status',y='nodes',data=df)
         plt.show()
```

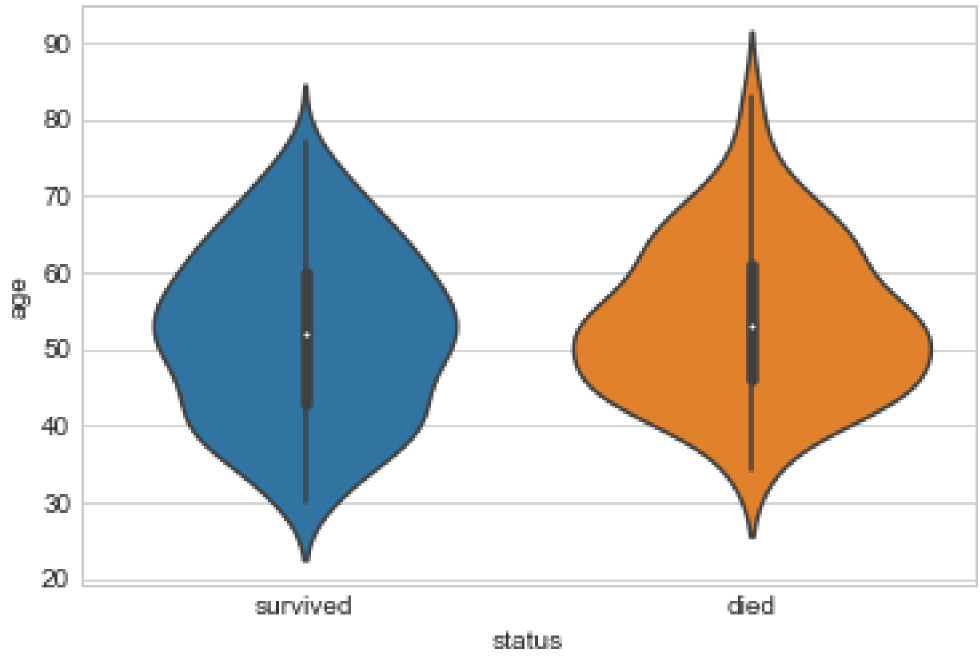


```
In [57]: print("Number of patients having zero nodes : {}".format(len(df[df['nodes']==0])))
         print("Number of patients having nodes less than 10 : {}".format(len(df[df['nodes']<1
```

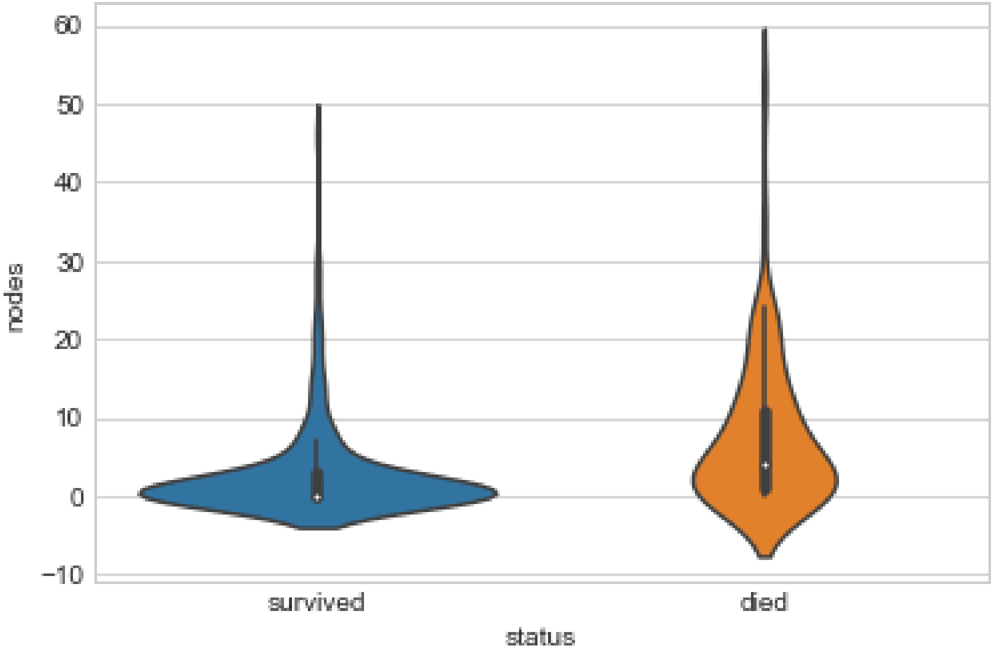
```
Number of patients having zero nodes : 136
Number of patients having nodes less than 10 : 264
```

```
In [ ]: **Observations**
        1.44% of the patients have zero positive axillary nodes.
        2.86.2% of the patients have positive axillary nodes less than 10.
```

```
In [62]: # Violin Plots
         sns.violinplot(x='status',y='age',data=df,size=8)
         plt.show()
```

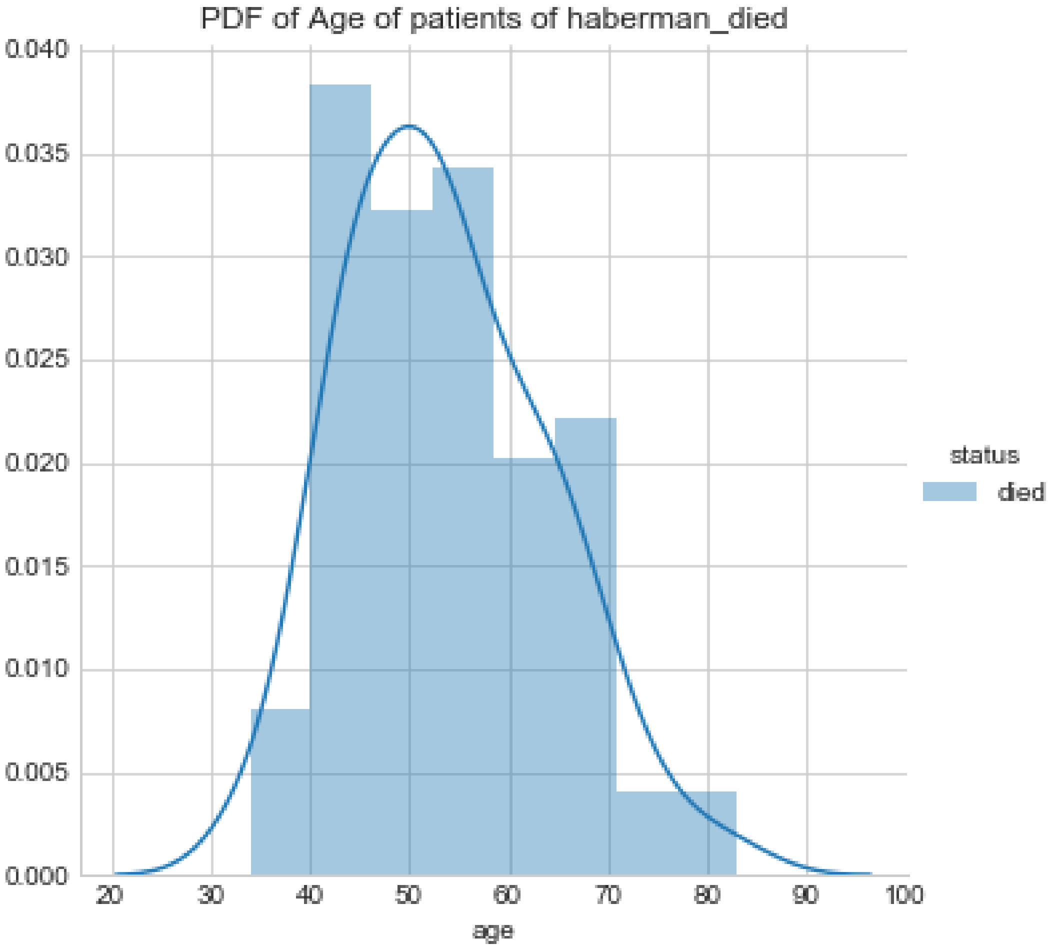


```
In [63]: sns.violinplot(x='status',y='nodes',data=df,size=8)
         plt.show()
```



```
In [ ]: **Observation**
        1. Not much useful for classification.
```

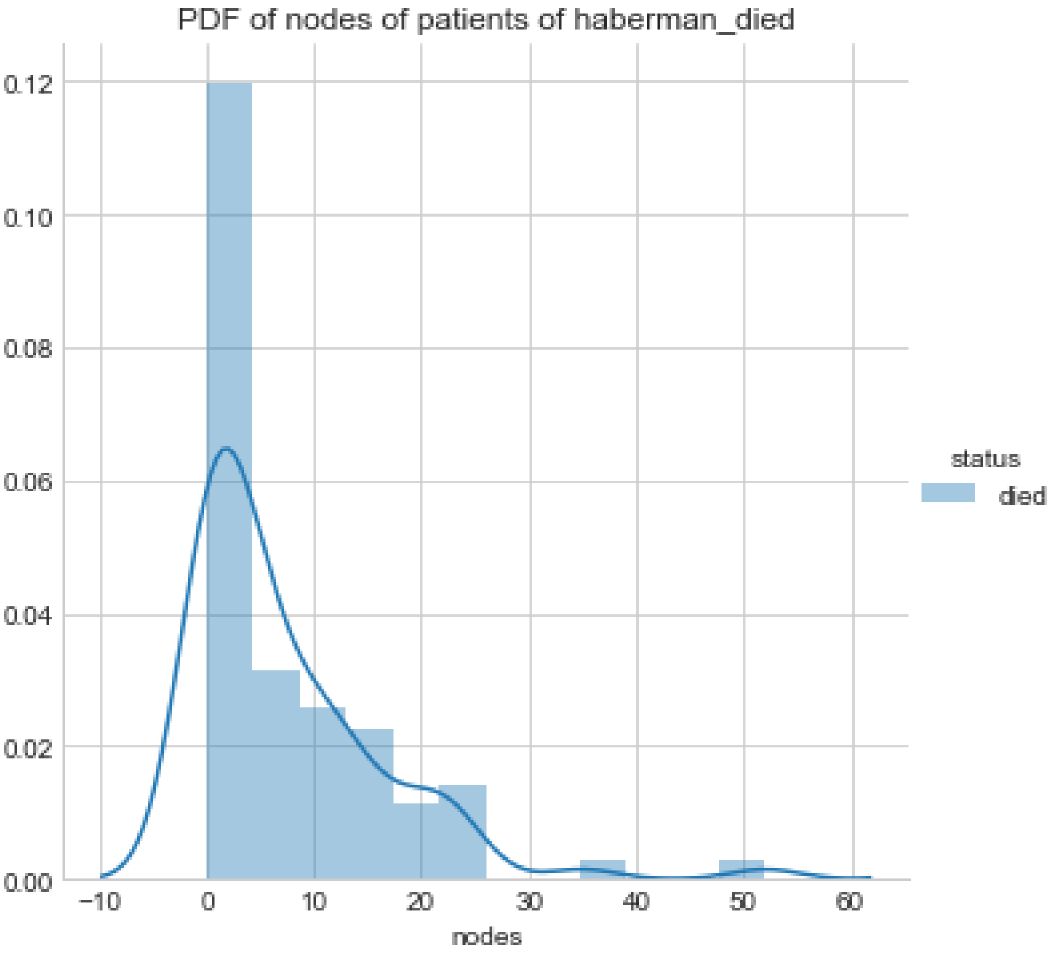
```
In [51]: # Haberman_died class analysis
         sns.set_style('whitegrid')
         sns.FacetGrid(haberman_died,hue='status',size=5) \
            .map(sns.distplot,'age') \
            .add_legend();
         plt.title("PDF of Age of patients of haberman_died")
         plt.show()
```



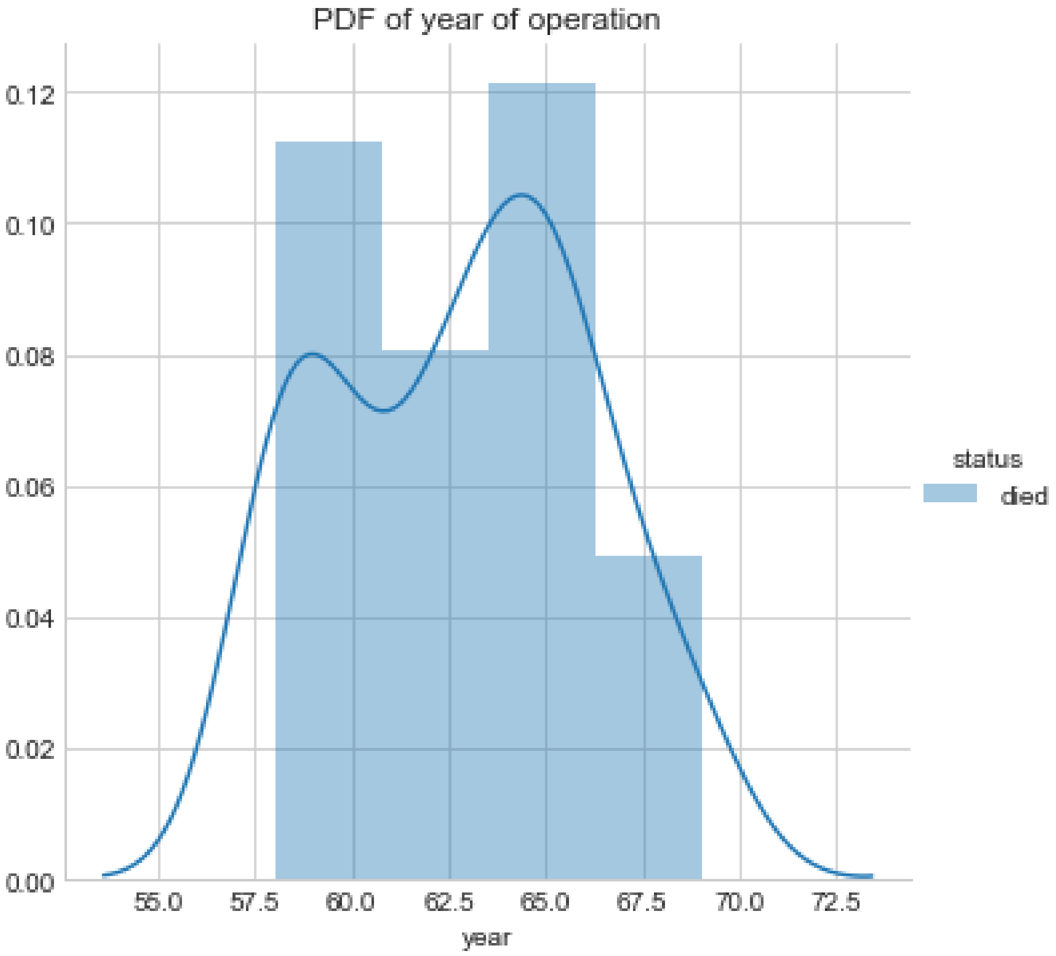
```
In [ ]: **Observation**
        1. None of the patients having age less than 34 died within 5 years of the treatement.
```

```
In [52]: sns.set_style('whitegrid')
         sns.FacetGrid(haberman_died,hue='status',size=5) \
            .map(sns.distplot,'nodes') \
            .add_legend();
```

```
plt.title("PDF of nodes of patients of haberman_died")
plt.show()
```

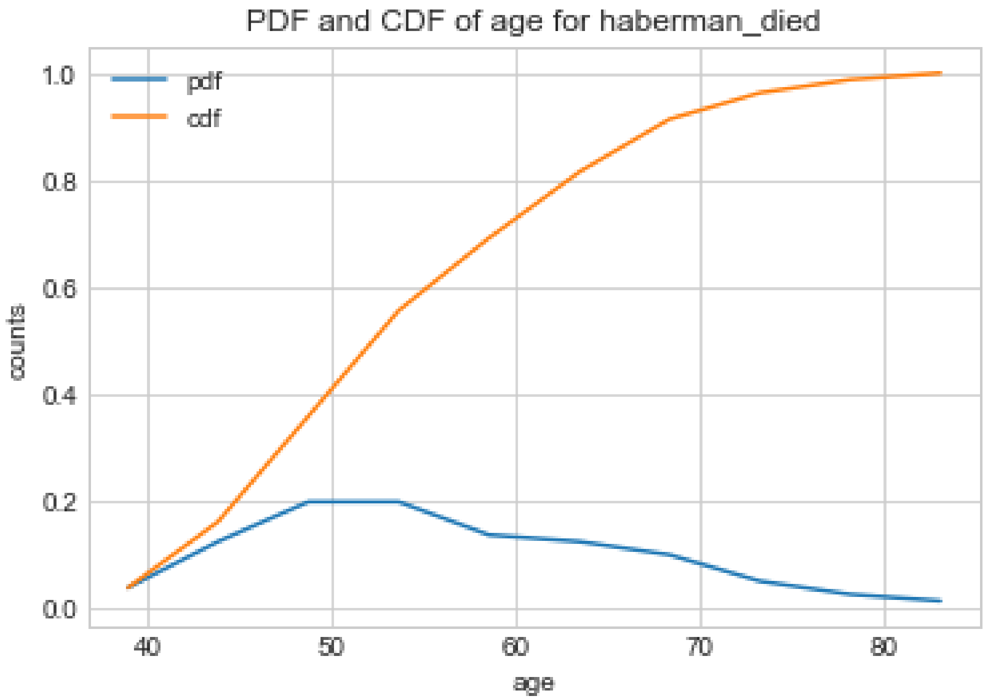


```
In [53]: sns.set_style('whitegrid')
         sns.FacetGrid(haberman_died,hue='status',size=5) \
            .map(sns.distplot,'year') \
            .add_legend();
         plt.title("PDF of year of operation")
         plt.show()
```



```
In [58]: # PDFs , CDFs For class haberman_died
         haberman_died=haberman_died.sort_values(['age']) # sorted the dataset on age

         counts,bin_edges = np.histogram(haberman_died['age'],bins=10,density=True)

         pdf = counts/(sum(counts))
         print(pdf);
         print(bin_edges);

         cdf = np.cumsum(pdf)
         plt.plot(bin_edges[1:],pdf)
         plt.plot(bin_edges[1:],cdf)
         plt.xlabel('age')
         plt.ylabel('counts')
         plt.title('PDF and CDF of age for haberman_died')
         plt.legend(['pdf','cdf'])  # This takes a list as argument (each for pdf and cdf)
         plt.show()
```

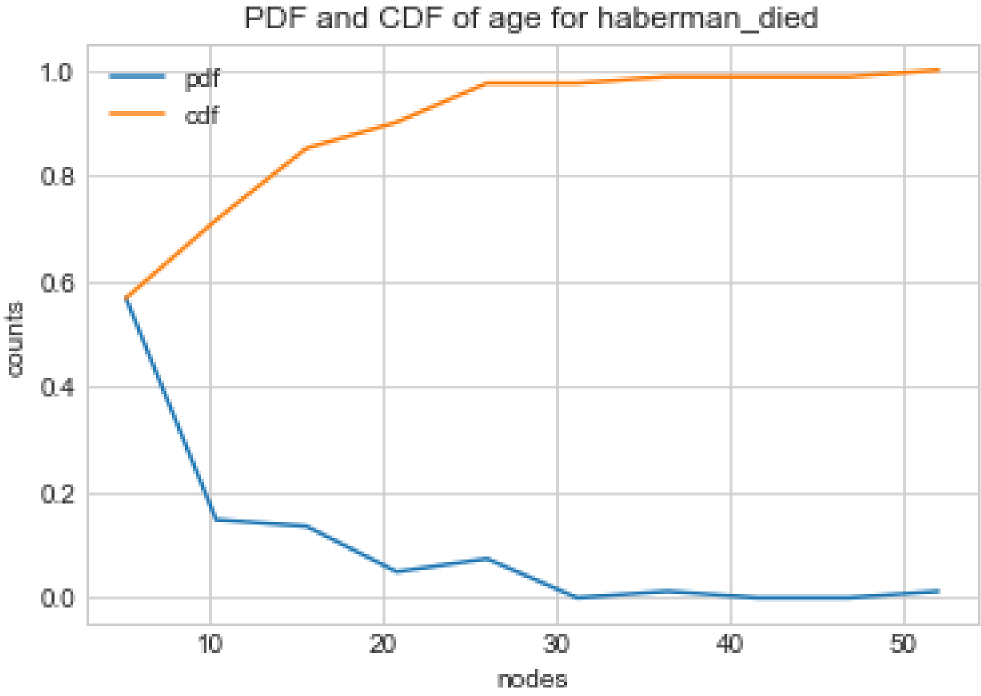
```
[0.03703704 0.12345679 0.19753086 0.19753086 0.13580247 0.12345679
 0.09876543 0.04938272 0.02469136 0.01234568]
[34.   38.9 43.8 48.7 53.6 58.5 63.4 68.3 73.2 78.1 83. ]
```



```
In [59]: # PDFs , CDFs For class haberman_died
         haberman_died=haberman_died.sort_values(['nodes']) # sorted the dataset on nodes

         counts,bin_edges = np.histogram(haberman_died['nodes'],bins=10,density=True)

         pdf = counts/(sum(counts))
         print(pdf);
         print(bin_edges);

         cdf = np.cumsum(pdf)
         plt.plot(bin_edges[1:],pdf)
         plt.plot(bin_edges[1:],cdf)
         plt.xlabel('nodes')
         plt.ylabel('counts')
         plt.title('PDF and CDF of age for haberman_died')
         plt.legend(['pdf','cdf'])  # This takes a list as argument (each for pdf and cdf)
         plt.show()
```

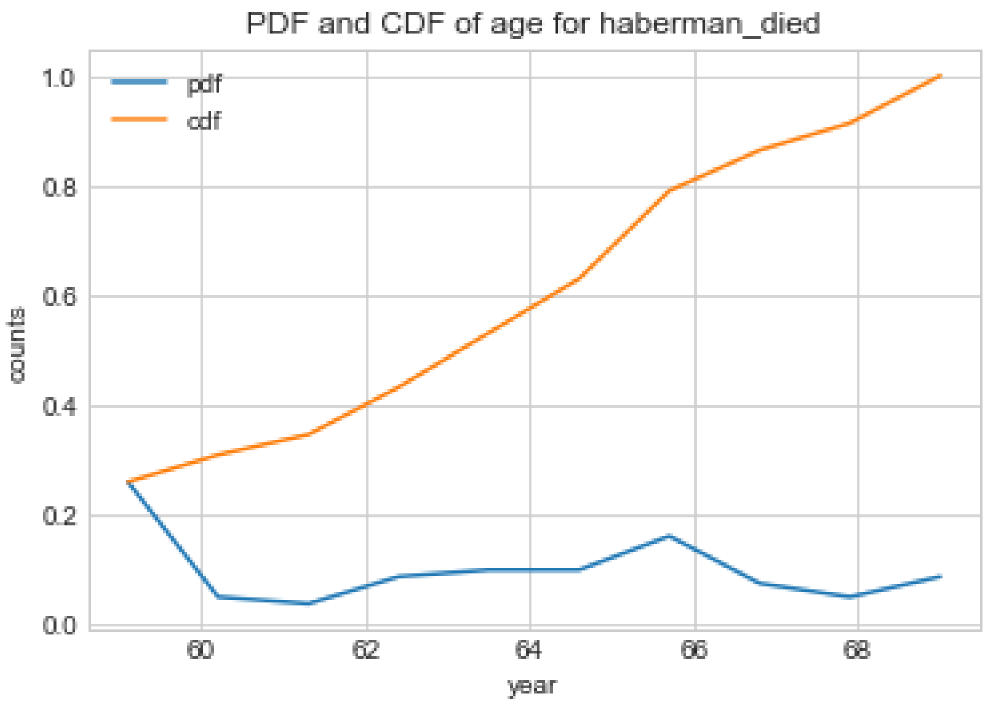
```
[0.56790123 0.14814815 0.13580247 0.04938272 0.07407407 0.
 0.01234568 0.         0.         0.01234568]
```

```
[ 0.   5.2 10.4 15.6 20.8 26.  31.2 36.4 41.6 46.8 52. ]
```



```
In [60]: # PDFs , CDFs For class haberman_died
         haberman_died=haberman_died.sort_values(['year']) # sorted the dataset on year

         counts,bin_edges = np.histogram(haberman_died['year'],bins=10,density=True)

         pdf = counts/(sum(counts))
         print(pdf);
         print(bin_edges);

         cdf = np.cumsum(pdf)
         plt.plot(bin_edges[1:],pdf)
         plt.plot(bin_edges[1:],cdf)
         plt.xlabel('year')
         plt.ylabel('counts')
         plt.title('PDF and CDF of age for haberman_died')
         plt.legend(['pdf','cdf'])  # This takes a list as argument (each for pdf and cdf)
         plt.show()
```

```
[0.25925926 0.04938272 0.03703704 0.08641975 0.09876543 0.09876543
 0.16049383 0.07407407 0.04938272 0.08641975]
[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
```



```
In [33]: # We will move proceed our analysis based on the results abtained from scatter plots.
         # Now we will focus on age group of less than 40 and between 50 and 60.
         # We will also focus on analysing the number of nodes of these age group patients.
         haberman_below_40 = df.loc[df['age']<=40]
```

```
In [35]: haberman_below_40['status'].value_counts()
```

```
Out[35]: survived    40
         died         4
         Name: status, dtype: int64
```

```
In [ ]: **Observations**
        1. 90.90% of the patient having age <=40  survived for more than 5 years.
        2. 9.10% of the patients having age <=40 died within 5 years of the  treatement.
```

```
In [77]: # Collecting datapoints having age less than or equal to 40 and node less than 3
         haberman_below_40_nodes_below_3 = haberman_below_40.loc[df['nodes']<3]
```

```
In [78]: haberman_below_40_nodes_below_3['status'].value_counts()
```

```
Out[78]: survived    27
         died         2
         Name: status, dtype: int64
```

```
In [ ]: **Observation**
        1. 93.10% of the patients having age <= 40 and nodes < 3  survived for more than 5 yea
        2. 6.90% of patients having age <=40 and nodes <3 died within 5 years of the treatemen
```

```
In [53]: # Patients between 50 and 60 years of age
         haberman_betw_50_60 = df.loc[60 - df['age']<=10]
```

```
In [55]: haberman_betw_50_60['nodes'].value_counts()
```

```
Out[55]: 0     83
         1     26
         3     13
         2     10
         4      7
         7      5
         9      4
         5      4
         8      4
         13     4
         6      3
         22     3
         15     2
         14     2
         19     2
         35     1
         12     1
         11     1
         17     1
         18     1
         23     1
         24     1
         25     1
         28     1
         46     1
         Name: nodes, dtype: int64
```

```
In [ ]: **Observations**
        1. 67.03% of patients having age between 50 an 60 have nodes lesss than or equal to 3.
```

```
In [97]: haberman_betw_50_60['status'].value_counts()
```

```
Out[97]: survived    132
         died         50
         Name: status, dtype: int64
```

```
In [ ]: **Observations**
        1. 75.52% of the patients between the age of 50 and 60 survived for 5 or more years af
        2. 24.48% of the patients bbetween the age of 50 and 60 died within 5 years of the trea
```

```
In [79]: #Patients of age between 50 and 60 and having nodes lasss than 3
         haberman_betw_50_60_nodes_below_3 = haberman_betw_50_60.loc[haberman_betw_50_60['nodes
```

```
In [80]: haberman_betw_50_60_nodes_below_3['status'].value_counts()
```

```
Out[80]: survived    102
         died         17
         Name: status, dtype: int64
```

```
In [ ]: **Observations**
        1. 85.71% of the patients between the age 50 and 60 survived if the patients have less
        2. 14.29% of the patients between the age 50 and 60 died if they have 3 or more nodes
```

```
In [38]: df['nodes'].value_counts()
```

```
Out[38]: 0     136
         1      42
         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: nodes, dtype: int64
```

```
In [71]: # Since max patients had nodes less than or equal to 3
         # We will find how many patients out of this survived
         haberman_nodes_below_4 = df[df['nodes']<4]
```

```
In [72]: haberman_nodes_below_4['status'].value_counts()
```

```
Out[72]: survived    179
         died         39
         Name: status, dtype: int64
```

```
In [ ]: **Observations**
        1. 82.11% of the patients having nodes less than 4 survived and rest 17.89% died.
```

```
In [ ]: ###### Conclusion =======>
        1. The given data is imbalanced as 73.5% of datapoints belong to class1(survived) and
        2. 75% of the patients have age less than 60 although max age is 83.
        3. 75% of the patients have axillary nodes less than 4.
        4. 44% of the patients have 0 axillary nodes and 86.2% have less than 10
           axillary nodes although max nodes detected was 52.
        5. 90.90% of the patients having age <=40 survived for more than 5 years.
        6. 93.10% of the patients having age <=40 and nodes <=3 survived for more than 5 years
        7. All the patients survived for 5or more years who had age less than 34.
        8. 85.71% of the patients having age >=50 and age <=60 and axillary nodes <3
           survived for more than 5 years.
```

```
In [102]: # Now we will make a simple model to predict the survivability of the patients under

          def predict_survivality(age,year,nodes):
              '''This function predicts that whether a patient
                 will survive for 5 or more years after the treatement is
                 done or not.'''
              if age<34: # 100% accuracy
                  return 'Patient will survive'
              if age<=40:   # 90.90% accuracy
                  if nodes < 3:  #93.10% accuracy
                      return 'Patient will survive for 5 or more years'
                  else:
                      return 'Patient may or may not survive for 5 or more year'
              elif age>=50 and age<=60: # 75.52% accuracy
                  if nodes <3:            # 85.71% accuracy
                      return 'Patient will survive for 5 or more years'
                  else:
                      return 'Patient may or may not survive for 5 years'
              else:
                  return 'Patient may or may not survive for 5 or more years'

          predict_survivality(55,71,3)
```

```
Out[102]: 'patient may or may not survive for 5 years'
```