# **Exploratory data Analysis for the Haberman dataset**

### **Basic Information About the Data**

- data is result of study conduted between the yeer 1958 abd 1970 at the university of chicago's Billings Hospital on the survival of patients who undergone for the breast cancer.
- · contains 4 attributes
- where feature values are ages , Op\_year , axil\_nodes.
- · target value is survival status of the patient.

## objective

import pandas as pd

Number of columns: 4

In [42]:

- · perform the analysis over the data
- · get as many findings as possible.

```
import seaborn as sns
         import matplotlib.pyplot as plt
         import numpy as np
         haberman = pd.read_csv('e:/data/haberman.csv')
In [43]:
In [44]:
         print(haberman.describe())
                          age
                                     year
                                                 nodes
                                                            status
                   306.000000
                               306.000000
                                           306.000000 306.000000
            count
            mean
                    52.457516
                                62.852941
                                              4.026144
                                                          1.264706
            std
                    10.803452
                                 3.249405
                                              7.189654
                                                          0.441899
            min
                    30.000000
                                58.000000
                                              0.000000
                                                          1.000000
            25%
                    44.000000
                                60.000000
                                                          1.000000
                                              0.000000
            50%
                    52.000000
                                63.000000
                                              1.000000
                                                          1.000000
            75%
                    60.750000
                                65.750000
                                              4.000000
                                                          2.000000
            max
                    83.000000
                                69.000000
                                             52.000000
                                                          2.000000
         print("Number of rows:",haberman.shape[0])
In [45]:
         print("Number of columns:", haberman.shape[1])
            Number of rows: 306
```

```
In [46]: print("Number of values\n" , haberman.status.value_counts())
    print("Percentages\n" , haberman.status.value_counts()/len(haberman)*100)
```

```
Number of values

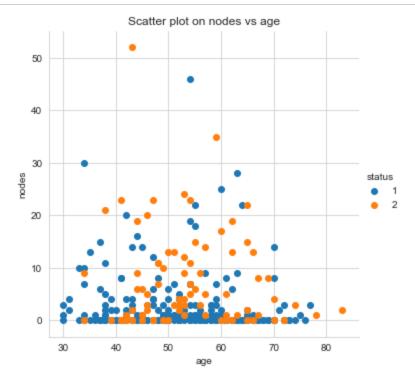
1 225
2 81
Name: status, dtype: int64
Percentages
1 73.529412
2 26.470588
Name: status, dtype: float64
```

#### **Observations**

• the data is imbalanced as number of 1's are greater than number of 2's

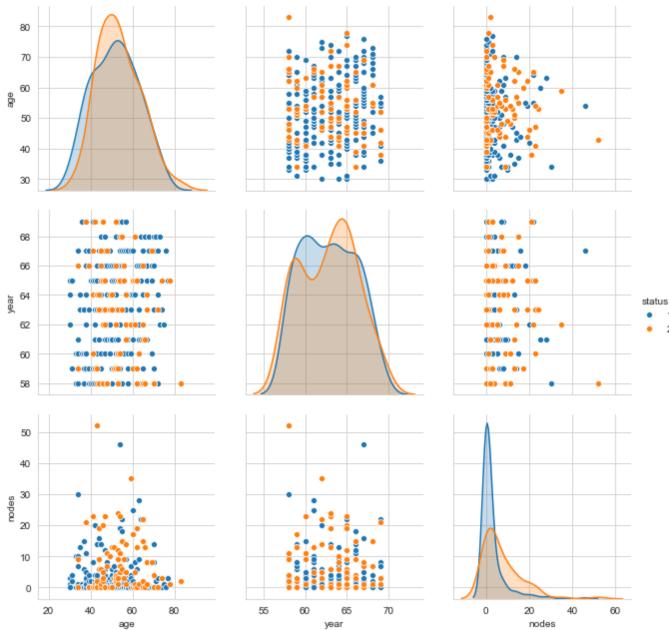
## Scatter Plot on the data

```
In [47]: sns.FacetGrid(haberman, hue="status",height=5).map(plt.scatter, "age" , "nodes").add_legend(
    plt.title('Scatter plot on nodes vs age')
    plt.show()
```

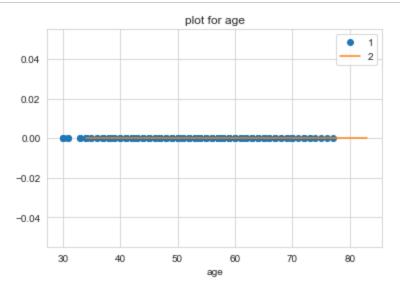


## **Pair Plot**

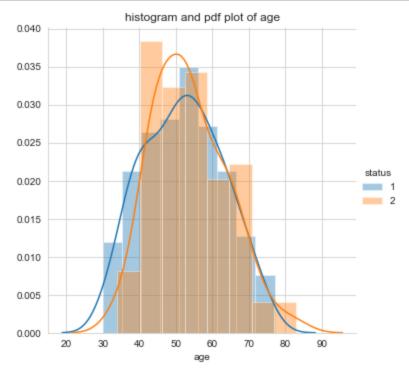
```
In [48]: plt.close();
    sns.set_style("whitegrid");
    sns.pairplot(haberman, hue="status", height=3 , vars = ['age','year','nodes'])
    plt.show()
```



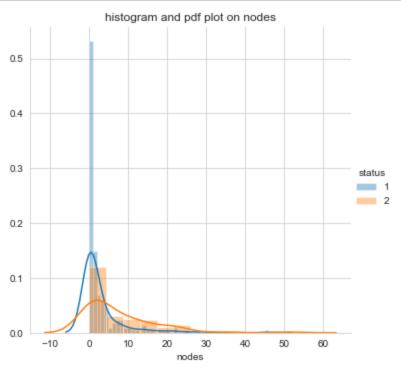
```
In [49]: haberman_survived = haberman.age.loc[haberman.status == 1]
    haberman_not_survived = haberman.age.loc[haberman.status == 2]
    one = plt.plot( haberman_survived ,np.zeros_like(haberman_survived) , 'o' ,label = '1')
    two = plt.plot(haberman_not_survived ,np.zeros_like(haberman_not_survived) , '-' , label = '
    plt.xlabel('age')
    plt.title('plot for age')
    plt.legend()
    plt.show()
```



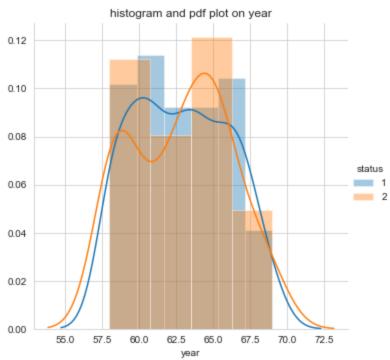
```
In [50]: sns.FacetGrid(haberman, hue="status", height=5) \
    .map(sns.distplot, "age") \
    .add_legend();
plt.title('histogram and pdf plot of age')
plt.show();
```



```
In [51]: sns.FacetGrid(haberman, hue="status", height=5) \
    .map(sns.distplot, "nodes") \
    .add_legend();
    plt.title('histogram and pdf plot on nodes')
    plt.show();
```

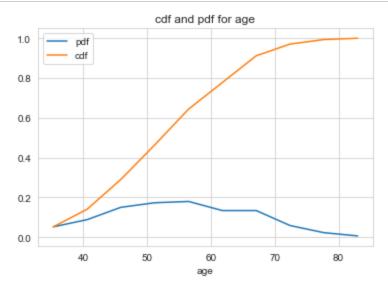


```
In [52]: sns.FacetGrid(haberman, hue="status", height=5) \
    .map(sns.distplot, "year") \
    .add_legend();
plt.title('histogram and pdf plot on year')
plt.show();
```

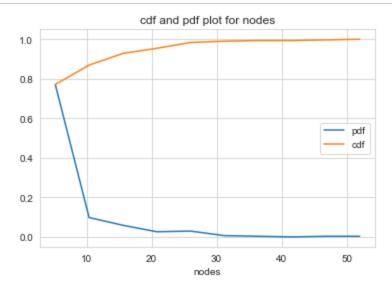


- from the above plot as the age increases the chances of survival goes down.
- as the number of nodes increases chances of survival goes down.
- from operation year 58 61 there are sligtly higher chance of survival.
- from operation year 63 66 there are slighly low chance of survival.

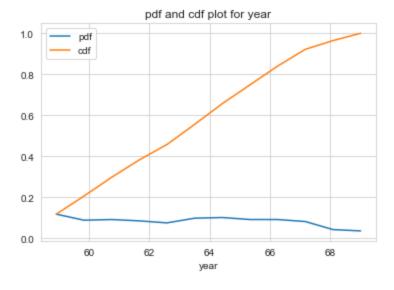
```
In [53]: counts, parts = np.histogram(haberman.age, bins = 10)
    pdf = counts/(sum(counts))
    cdf = np.cumsum(pdf)
    plt.xlabel('age')
    plt.plot(parts[1:],pdf , label = 'pdf')
    plt.plot(parts[1:], cdf ,label = 'cdf')
    plt.title('cdf and pdf for age')
    plt.legend()
    plt.show()
```



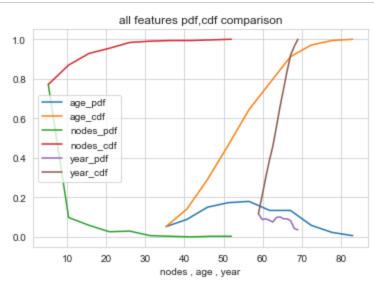
```
In [54]: counts, parts = np.histogram(haberman.nodes, bins = 10)
    pdf = counts/(sum(counts))
    cdf = np.cumsum(pdf)
    plt.xlabel('nodes')
    plt.plot(parts[1:],pdf , label = 'pdf')
    plt.plot(parts[1:], cdf , label = 'cdf')
    plt.title('cdf and pdf plot for nodes')
    plt.legend()
    plt.show();
```



```
In [55]: counts, parts = np.histogram(haberman.year, bins = 12)
    pdf = counts/(sum(counts))
    cdf = np.cumsum(pdf)
    plt.xlabel('year')
    plt.plot(parts[1:],pdf , label = 'pdf')
    plt.plot(parts[1:], cdf , label = 'cdf')
    plt.legend()
    plt.title('pdf and cdf plot for year')
    plt.show()
```



```
In [56]:
         counts, parts = np.histogram(haberman.age, bins = 10)
         pdf = counts/(sum(counts))
         cdf = np.cumsum(pdf)
         plt.plot(parts[1:],pdf , label = 'age_pdf')
         plt.plot(parts[1:], cdf , label = 'age_cdf')
         counts, parts = np.histogram(haberman.nodes, bins = 10)
         pdf = counts/(sum(counts))
         cdf = np.cumsum(pdf)
         plt.plot(parts[1:],pdf , label = 'nodes_pdf')
         plt.plot(parts[1:], cdf , label = 'nodes_cdf')
         counts, parts = np.histogram(haberman.year, bins = 12)
         pdf = counts/(sum(counts))
         cdf = np.cumsum(pdf)
         plt.xlabel('nodes , age , year')
         plt.plot(parts[1:],pdf , label = 'year_pdf' )
         plt.plot(parts[1:], cdf , label = 'year_cdf')
         plt.title('all features pdf,cdf comparison')
         plt.legend()
         plt.show();
```



Median, Percentile, Quantile, IQR, MAD

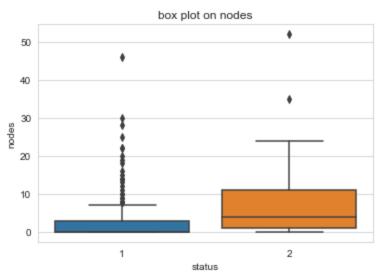
```
In [57]: | print("\nMedians:")
         print("age", np.median(haberman.age))
         print("nodes:" , np.median(haberman.nodes))
         print("Year:",np.median(haberman.year))
         print("\nQuantiles:")
         print("age:",np.percentile(haberman.age , [0,25,50,75]))
         print("nodes:", np.percentile(haberman.nodes , [0,25,50,75]))
         print("year:",np.percentile(haberman.year, [0,25,50,75]))
         print("\n90th Percentiles:")
         print("age:",np.percentile(haberman.age , 90))
         print("nodes:",np.percentile(haberman.nodes , 90))
         print("year:",np.percentile(haberman.year , 90))
         from statsmodels import robust
         print ("\nMedian Absolute Deviation")
         print("age:",robust.mad(haberman.age))
         print("nodes:",robust.mad(haberman.nodes))
         print("year:",robust.mad(haberman.year))
```

```
Medians:
age 52.0
nodes: 1.0
Year: 63.0
Quantiles:
          44. 52.
age: [30.
                       60.75]
nodes: [0. 0. 1. 4.]
                  63. 65.75]
year: [58. 60.
90th Percentiles:
age: 67.0
nodes: 13.0
year: 67.0
Median Absolute Deviation
age: 11.860817748044816
nodes: 1.482602218505602
```

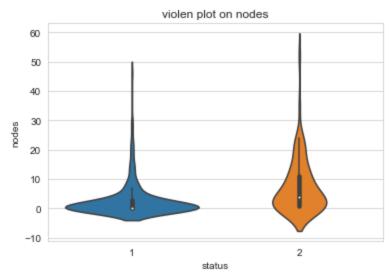
## **Box plot and Whiskers**

year: 4.447806655516806

```
In [58]: sns.boxplot(x='status',y='nodes', data=haberman)
  plt.title('box plot on nodes')
  plt.show()
```



```
In [59]: sns.violinplot(x="status", y="nodes", data=haberman)
   plt.title('violen plot on nodes')
   plt.show()
```



#### **Observations**

- as number of nodes increases chances of survival decreases.
- if a patient is having nodes close to 0 then it is having more chances of survival.

In [ ]:	
In [ ]:	