# **Big Data Analysis Lab-01**

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## **Question 1**

- 1. Download Haberman Cancer Survival dataset from Kaggle. You may have to create a Kaggle account to download data. (<a href="https://www.kaggle.com/gilsousa/habermans-survival-data-set">https://www.kaggle.com/gilsousa/habermans-survival-data-set</a> (<a href="https://www.kaggle.com/gilsous
- Mention High level statistics of the dataset: number of points, number of features, number of classes, data-points per class.
- 3. Explain our objective.
- 4. Perform Univariate analysis (PDF, CDF, Boxplot, Violin plots) to understand which features are useful towards classification
- 5. Perform Bi-variate analysis (scatter plots, pair-plots) to see if combinations of features are useful in classification.
- 6. Most important Write your observations in English words to summarize patient condition.

```
In [1]: import pandas as pd
   import matplotlib.pyplot as plt
   import numpy as np
   from scipy.stats import norm
   import seaborn as sns
   import warnings
   warnings.filterwarnings("ignore")
   %matplotlib inline
   sns.set_style("whitegrid")

In [2]: df = pd.read_csv('haberman.csv', header=None)
   column_name = ["age", "year", "nodes", "status"]
   df.columns = column_name
   df.head()
```

### Out[2]:

	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 [3]: df.info()

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 306 entries, 0 to 305
Data columns (total 4 columns):
# Column Non-Null Count Dtype
           -----
0
   age
           306 non-null
                          int64
           306 non-null
                        int64
1 year
2 nodes
           306 non-null
                         int64
   status 306 non-null
                          int64
dtypes: int64(4)
memory usage: 9.7 KB
```

```
In [4]: df.describe()
```

### Out[4]:

	age	year	nodes	status
count	306.000000	306.000000	306.000000	306.000000
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	0.000000	1.000000
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

```
In [5]: df.shape
Out[5]: (306, 4)
In [6]: df['status'].value_counts()
Out[6]: 1
             225
        2
              81
        Name: status, dtype: int64
In [7]: df.isnull().sum()
Out[7]: age
                  0
        year
                  0
        nodes
        status
        dtype: int64
```

The Haberman's survival dataset consists of 4 attributes: Age of patient at time of operation (numerical)

Patient's year of operation (year - 1900, numerical)

Number of positive axillary nodes detected (numerical)

Survival status (class attribute)

1 = the patient survived 5 years or longer (225 records)

2 = the patient died within 5 year (81 records)

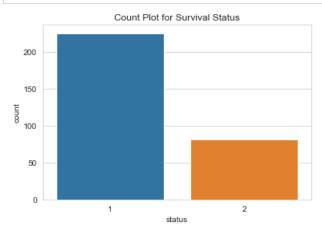
The dataset contains 306 instances and there are no missing values.

## Objective:

Our objective is to predict whether a patient can be saved from cancer or not by performing exploratory data analysis. We try to find out which features are useful for the classification with the help of univariate and bivariate analysis.

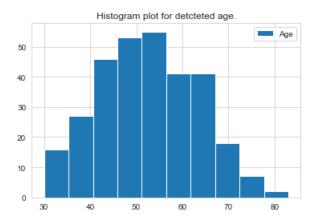
## **Univariate Analysis**

```
In [8]: sns.countplot(x = df['status']).set_title('Count Plot for Survival Status')
plt.show()
```



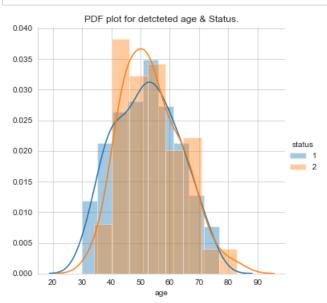
```
In [9]: plt.hist(df["age"],label="Age")
    plt.legend()
    plt.title("Histogram plot for detcteted age.")
```

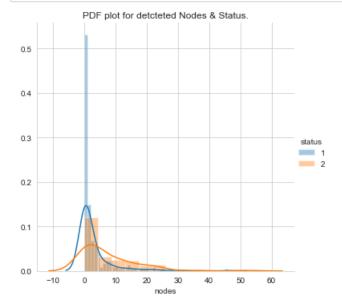
Out[9]: Text(0.5, 1.0, 'Histogram plot for detcteted age.')

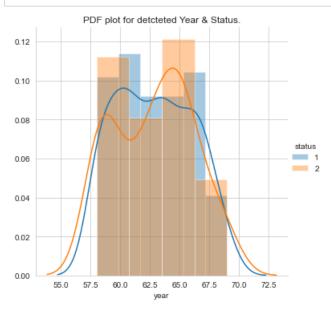


PDF - (Probability Density Function) PDF shows the density of that data or number of data present on that point. PDF will be a peak like structure represents high peak if more number of data present or else it will be flat/ small peak if number of data present is less. It is smooth graph plot using the edges of histogram.

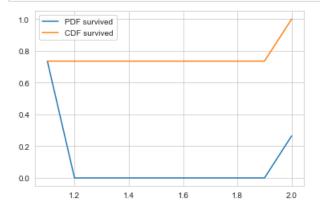
CDF - (Cumulative Distribution Function) CDF is representation of cumulative data of PDF ie. it will plot a graph by considering PDF for every data point cumulatively.



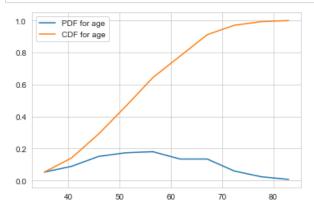




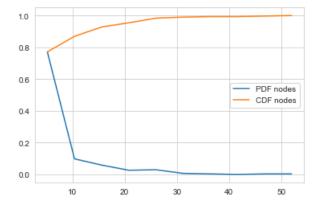
```
In [13]: # PDF and CDF
    count, bin_edges = np.histogram(df['status'], bins=10, density=True)
    pdf = count/(sum(count))
    cdf = np.cumsum(pdf)
    plt.plot(bin_edges[1:], pdf, label='PDF survived')
    plt.plot(bin_edges[1:], cdf, label='CDF survived')
    plt.legend()
    plt.show()
```



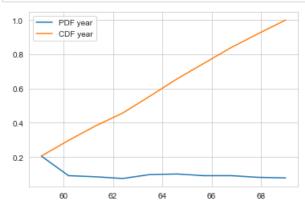
```
In [14]:
    count, bin_edges = np.histogram(df['age'], bins=10, density=True)
    pdf = count/(sum(count))
    cdf = np.cumsum(pdf)
    plt.plot(bin_edges[1:], pdf, label='PDF for age')
    plt.plot(bin_edges[1:], cdf, label='CDF for age')
    plt.legend()
    plt.show()
```



```
In [15]: count, bin_edges = np.histogram(df['nodes'], bins=10, density=True)
    pdf = count/(sum(count))
    cdf = np.cumsum(pdf)
    plt.plot(bin_edges[1:], pdf, label='PDF nodes')
    plt.plot(bin_edges[1:], cdf, label='CDF nodes')
    plt.legend()
    plt.show()
```

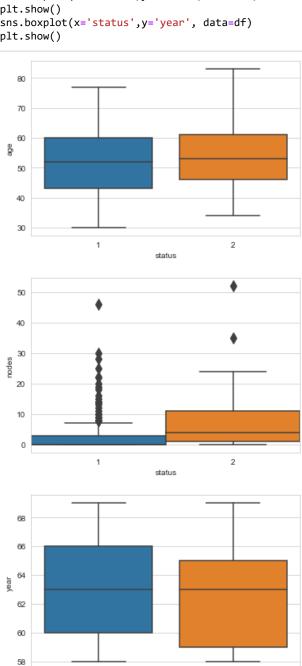


```
In [16]:
    count, bin_edges = np.histogram(df['year'], bins=10, density=True)
    pdf = count/(sum(count))
    cdf = np.cumsum(pdf)
    plt.plot(bin_edges[1:], pdf, label='PDF year')
    plt.plot(bin_edges[1:], cdf, label='CDF year')
    plt.legend()
    plt.show()
```



## **Boxplots and Violin Plots**

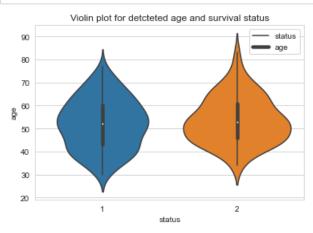
```
In [17]:
    sns.boxplot(x='status',y='age',data=df)
    plt.show()
    sns.boxplot(x='status',y='nodes', data=df, width=1.0, fliersize=10)
    plt.show()
    sns.boxplot(x='status',y='year', data=df)
    plt.show()
```



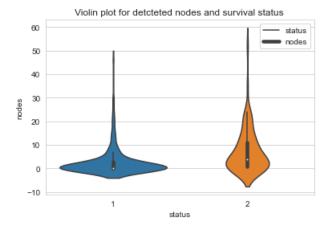
2

status

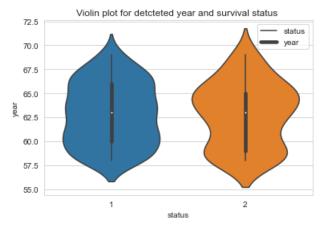
# In [18]: # A violin plot combines the benefits of the previous two plots and simplifies #Denser regions of the data are fatter, and sparser ones thinner. sns.violinplot(x="status", y="age", data=df, size=8) plt.title("Violin plot for detcteted age and survival status") plt.legend(labels=["status", "age"]) plt.show()



```
In [19]: sns.violinplot(x="status", y="nodes", data=df, size=8)
    plt.title("Violin plot for detcteted nodes and survival status ")
    plt.legend(labels=["status", "nodes"])
    plt.show()
```



```
In [20]: sns.violinplot(x="status", y="year", data=df, size=8)
    plt.title("Violin plot for detcteted year and survival status ")
    plt.legend(labels=["status","year"])
    plt.show()
```



From the above box plots and violin plots, we can say that people in age group of 30-34 have 100% survival rate and patients of age around 78 could not survive for 5 years after the surgery. Also 50 percentile of people that survived have node 0.

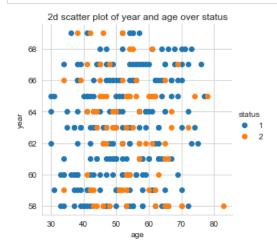
```
In [21]: df.corr()
```

## Out[21]:

	age	year	nodes	status
age	1.000000	0.089529	-0.063176	0.067950
year	0.089529	1.000000	-0.003764	-0.004768
nodes	-0.063176	-0.003764	1.000000	0.286768
status	0.067950	-0.004768	0.286768	1.000000

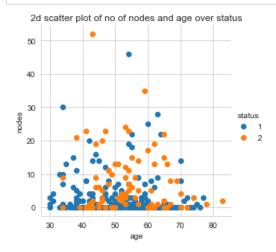
## **Bivariate analysis - Scatter and Pair Plots**

```
In [22]: sns.FacetGrid(df, hue="status", height=4) \
     .map(plt.scatter, "age", "year") \
     .add_legend()
    plt.title("2d scatter plot of year and age over status")
    plt.show()
```

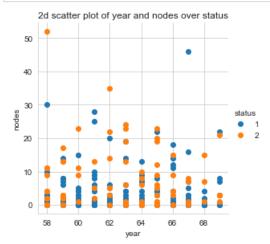


From this plot we can say that, people with age between 30 and 40 operated in 1958,1960,1961,1962,1963,1964,1965,1967,1969 have survived.

```
In [23]:
    sns.set_style("whitegrid");
    sns.FacetGrid(df, hue="status", height=4) \
        .map(plt.scatter, "age", "nodes") \
        .add_legend();
    plt.title("2d scatter plot of no of nodes and age over status")
    plt.show();
```

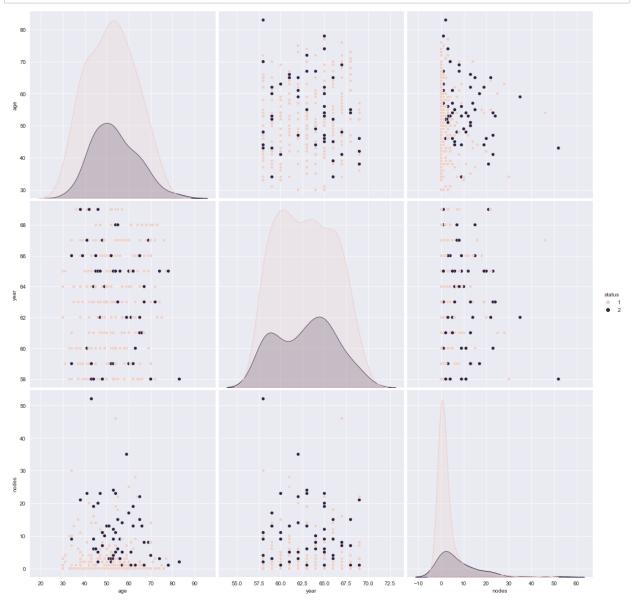


The points in the above scatter plot are randomly scattered and no line can seperate the classes.



The points in the above scatter plot are randomly scattered and no line can seperate the classes.

```
In [25]: plt.close();
    sns.set_style("darkgrid");
    sns.pairplot(df, hue="status", height=5);
    plt.show()
```



From the pair plot, we can say that the features 'age' and 'nodes' can be helpful. And in most of the plots we can observe an overlap of points.

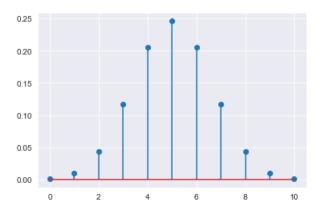
# **Question 2**

What is the probability of observing different numbers of heads in 10 tosses with a fair coin? Find which distribution will get apply and plot it. Write a python script to draw the distribution. Hints: Binomial Distribution.

```
In [26]: from scipy.stats import binom
    num_trials = 10
    heads_probability = .5

probs = [binom.pmf(i, num_trials, heads_probability) for i in range(11)]
plt.stem(list(range(11)), probs)
```

#### Out[26]: <StemContainer object of 3 artists>



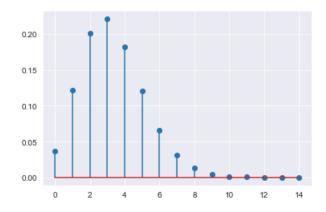
From the graph above, we can see that it's most likely to observe 5 heads in 10 tosses. Binomial Distribution can be used model binary data like yes or no.

## **Question 3**

Imagine you have a machine learning model deployed in the cloud and receiving requests from your customers in real-time. How much cloud resources do you need to pay for in order to be 99% sure you can serve all the traffic that arrives at the model in any one-minute period? (Note: 3.3 requests on average based on your traffic data). Draw the distribution using python. Hints: Poisson distribution

```
In [27]: from scipy.stats import poisson
    rate = 3.3
    probs = [poisson.pmf(i, rate) for i in range(15)]
    plt.stem(list(range(15)), probs)
```

Out[27]: <StemContainer object of 3 artists>



```
In [28]: simulated_request_per_minute = poisson.rvs(3.3, size=1_000_000)
np.percentile(simulated_request_per_minute, 99)
```

Out[28]: 8.0

The cloud resources do you need to pay for in order to be 99% sure you can serve all the traffic that arrives at the model in

any one-minute period would be 8.

Poisson distribution describes events that occur at some rate over time od space. It can be used to conduct queueing simulations that help allocate resources.

# **CONCLUSION:**

Univariate (PDF, CDF, box plots, violin plots) and bivariate analysis (scatter plots, pair plots) was performed on the Haberman's Cancer Survival data. Also, the probability distribution (Binomial and Poisson Distribution) graphs were drawn.