# EDA on HABERMAN data-set

## Data-set contains 4 columns: age , year , nodes , status

- **age**: Age of patient at time of operation
- **year**: Operation Year
- **nodes**: Number of positive axillary nodes detected.
- **status**: 1 = the patient survived 5 years or longer, 2 = the patient died within 5 years

**OBJECTIVE: To perform Exploratory Data Analysis(EDA) on data-set**

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings("ignore")
```

```
from google.colab import files
files = files.upload()
```

Choose Files haberman (1).csv

- **haberman (1).csv**(application/vnd.ms-excel) - 3124 bytes, last modified: 10/7/2020 - 100% done

```
Saving haberman (1).csv to haberman (1).csv
```

```
df = pd.read_csv('haberman (1).csv')
df.head()
```

| | 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 |

# High level analysis:

```
print(df.shape)
df.info()
```

```
(306, 4)
<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
 1   year    306 non-null    int64
 2   nodes   306 non-null    int64
 3   status  306 non-null    int64
dtypes: int64(4)
memory usage: 9.7 KB
```

### observation: no presence of missing/null values

```
df.describe()
```

| | 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 |

### Observation: 75% (3rd quantile) of nodes are less than 4 , 75% of patients age is less than 60

```
df['nodes'].value_counts().head()
```

```
0    136
1     41
2     20
3     20
4     13
Name: nodes, dtype: int64
```

- Top 5 node values
- 0 nodes being the highest value(count = 136) followed by 1(count = 146)

```
df['age'].value_counts().head(10)
```

```
52    14
54    13
50    12
47    11
53    11
43    11
57    11
55    10
65    10
49    10
Name: age, dtype: int64
```

- top 10 ages of patients ranges from 49-52 years

```
df.groupby('status').count()
```

|  | age | year | nodes |
|---|---|---|---|
| **status** |  |  |  |
| **1** | 225 | 225 | 225 |
| **2** | 81 | 81 | 81 |

- Observation: there are more survivors compared to non-survivors

## Converting numerical feature - status(0 or 1) to categorical feature - survived (yes or no)

```
d = {1:'yes',2:'no'}
df['survived'] = df['status'].map(d)
df.head()
```

|  | age | year | nodes | status | survived |
|---|---|---|---|---|---|
| **0** | 30 | 64 | 1 | 1 | yes |
| **1** | 30 | 62 | 3 | 1 | yes |
| **2** | 30 | 65 | 0 | 1 | yes |
| **3** | 31 | 59 | 2 | 1 | yes |
| **4** | 31 | 65 | 4 | 1 | yes |

## Splitting data into survived and not survived data-frames

```
df_survived = df[df['survived']=='yes']
df_survived.head()
```

| | age | year | nodes | status | survived |
|---|---|---|---|---|---|
| **0** | 30 | 64 | 1 | 1 | yes |
| **1** | 30 | 62 | 3 | 1 | yes |
| **2** | 30 | 65 | 0 | 1 | yes |
| **3** | 31 | 59 | 2 | 1 | yes |
| **4** | 31 | 65 | 4 | 1 | yes |

```
df_notsurvived = df[df['survived']=='no']
df_notsurvived.head()
```

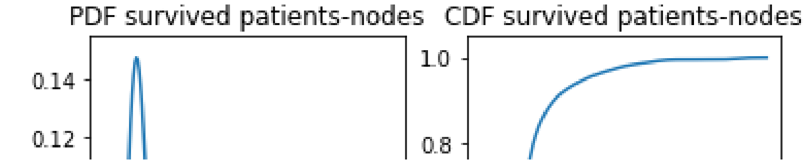
| | age | year | nodes | status | survived |
|---|---|---|---|---|---|
| **7** | 34 | 59 | 0 | 2 | no |
| **8** | 34 | 66 | 9 | 2 | no |
| **24** | 38 | 69 | 21 | 2 | no |
| **34** | 39 | 66 | 0 | 2 | no |
| **43** | 41 | 60 | 23 | 2 | no |

# Univariate Analysis

Survived Dataset:

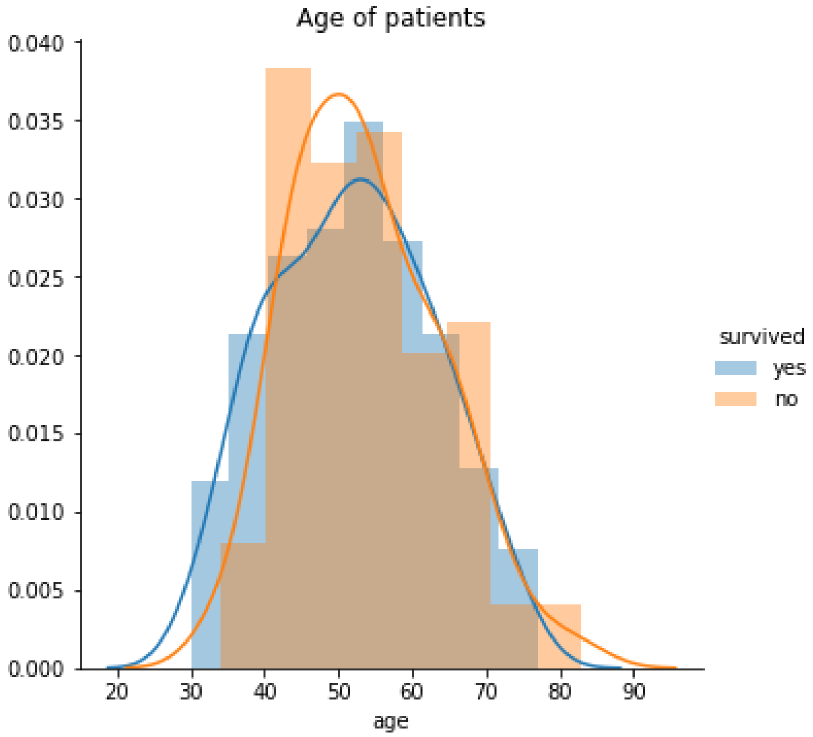
```
plt.subplot(1,2,1)
sns.kdeplot(data = df_survived , x = 'nodes',cumulative=False)
plt.title('PDF survived patients-nodes')

plt.subplot(1,2,2)
sns.kdeplot(data = df_survived , x = 'nodes',cumulative=True)
plt.title('CDF survived patients-nodes')
```

```
Text(0.5, 1.0, 'CDF survived patients-nodes')
```



Observation: Bulk of patients have nodes less than 15

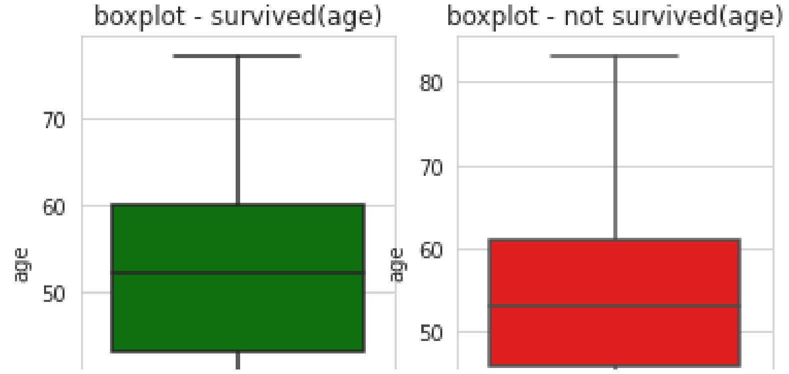
```
sns.FacetGrid(df, hue="survived", size=5) \
   .map(sns.distplot, "age") \
   .add_legend();
plt.title('Age of patients')
plt.show()
```



**Observations: No considerable difference in age of survived vs not survived patients**

```
sns.set_style('whitegrid')
plt.subplot(1,2,1)
sns.boxplot(data = df_survived , x = 'survived' , y = 'age',color = 'green')
plt.title('boxplot - survived(age)')

plt.subplot(1,2,2)
sns.boxplot(data = df_notsurvived , x = 'survived' , y = 'age' , color = 'red')
plt.title('boxplot - not survived(age)')
```

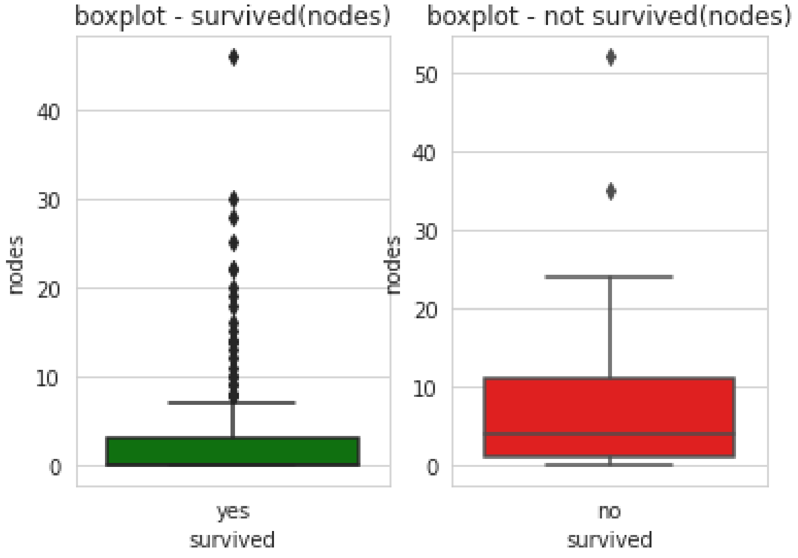
```
Text(0.5, 1.0, 'boxplot - not survived(age)')
```



### Observations: No considerable difference in age of survived vs not survived patients

```
sns.set_style('whitegrid')
plt.subplot(1,2,1)
sns.boxplot(data = df_survived , x = 'survived' , y = 'nodes',color = 'green')
plt.title('boxplot - survived(nodes)')

plt.subplot(1,2,2)
sns.boxplot(data = df_notsurvived , x = 'survived' , y = 'nodes' , color = 'red')
plt.title('boxplot - not survived(nodes)')
print('survived nodes mean:  '+str(df_survived['nodes'].mean()))
print('not-survived nodes mean:  '+str(df_notsurvived['nodes'].mean()))
```

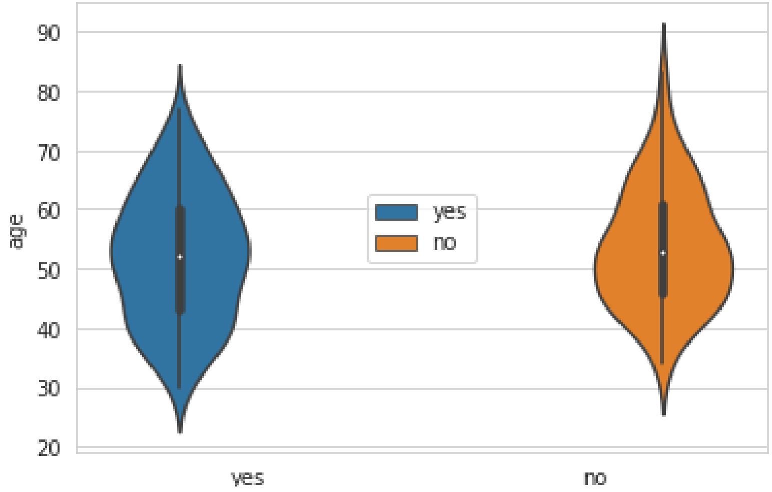
```
survived nodes mean:  2.7911111111111113
not-survived nodes mean:  7.45679012345679
```



### Observations: survived patients have very few nodes with mean 2.7 compared to not-survived patients with mean 7.4

```
sns.set_style('whitegrid')
sns.violinplot(x="survived", y="age", data = df,hue = 'survived')
plt.legend(loc='center')
```

```
<matplotlib.legend.Legend at 0x7f04b44214a8>
```



**Observations:**

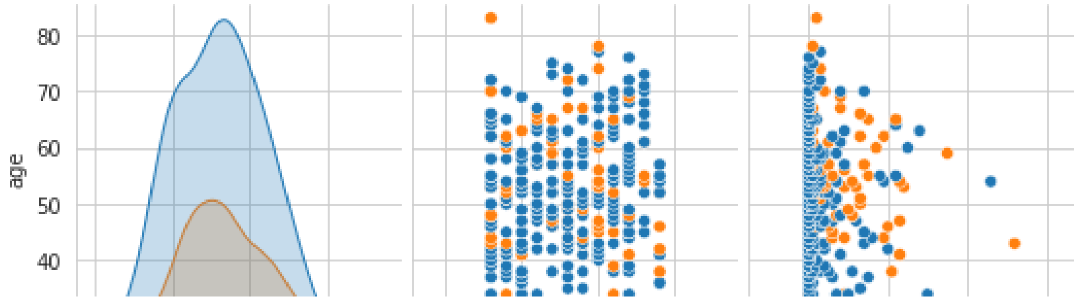
**1. Very few patients are aged above 75 years in survived data , hence it can be noted that most patients above 75 years have not survived**

**2. Most patients below 30 years have survived**

# Bivariate Analysis

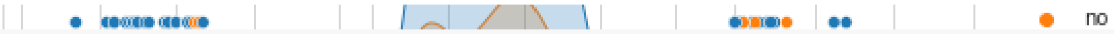
```
#pair plot 3x3

sns.set_style('whitegrid')
sns.pairplot(data = df , hue = 'survived',vars=['age','year','nodes'])
```

```
<seaborn.axisgrid.PairGrid at 0x7f04b39ec1d0>
```



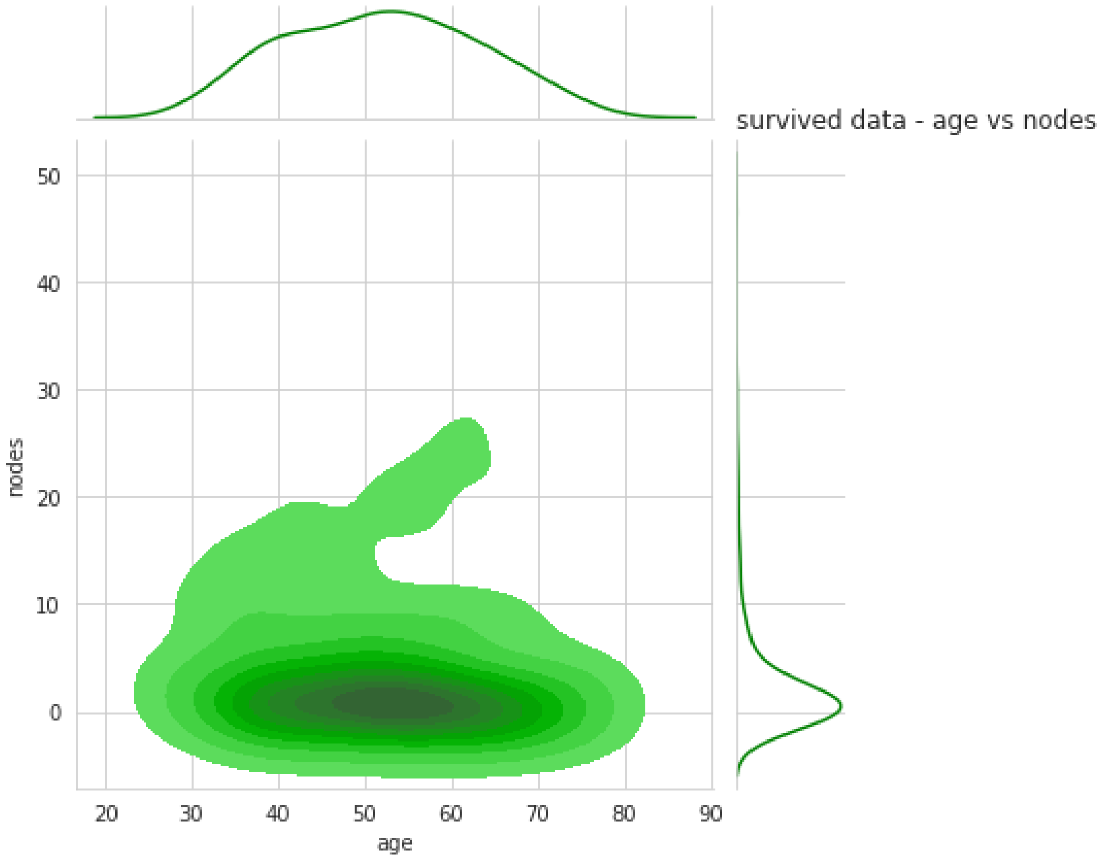
Observations:

- There is considerable overlap between features
- No single feature can be used to classify
- nodes vs age seems to provide better classification



```
#joint plot

sns.jointplot(data = df_survived , x = 'age' , y='nodes' , kind = 'kde',shade = True,co
plt.title('survived data - age vs nodes',loc='left',)
```

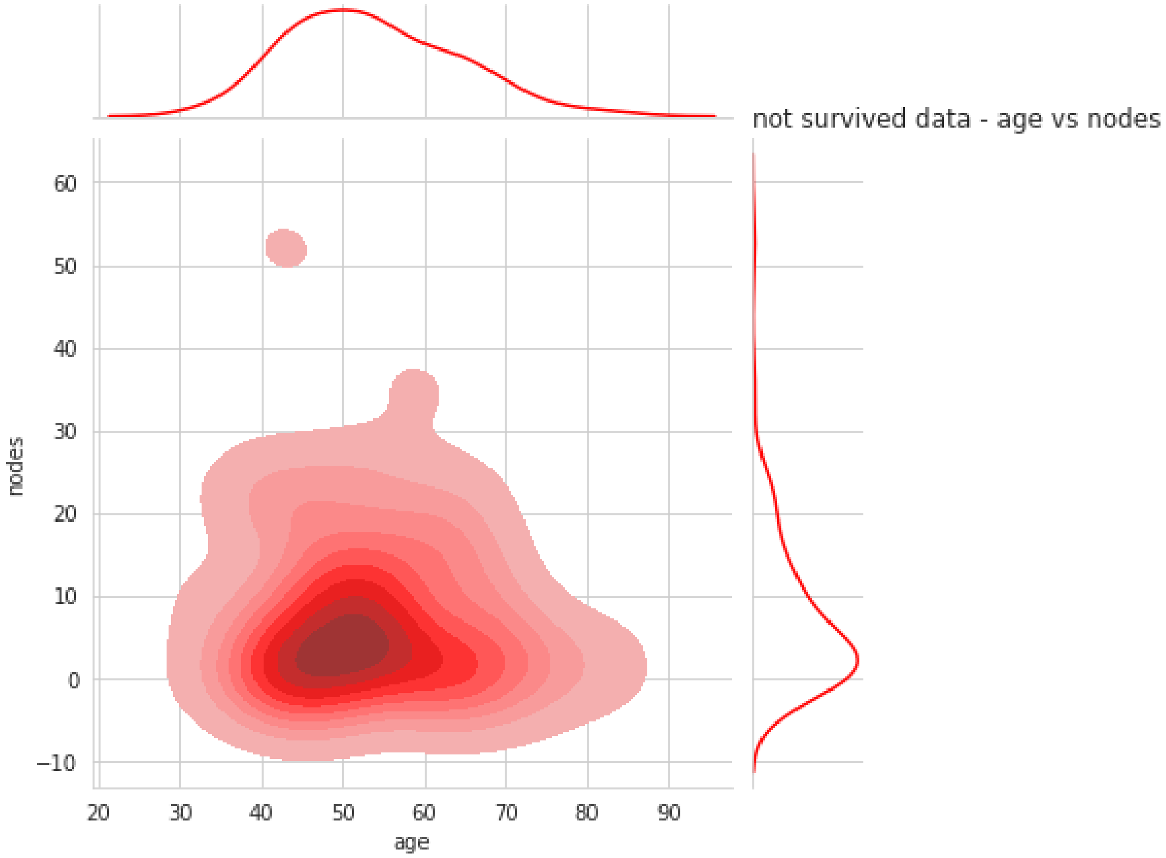
```
Text(0.0, 1.0, 'survived data - age vs nodes')
```



**Observations: Patients aged between 35-75 with less than 4 nodes have greatest chance of survival**

```
#joint plot

sns.jointplot(data = df_notsurvived , x = 'age' , y='nodes' , kind = 'kde',shade = True
sns.jointplot(data = df_notsurvived , x = 'age' , y= 'nodes' , kind = 'kde' ,shade = True
plt.title('not survived data - age vs nodes',loc='left',)
```

```
Text(0.0, 1.0, 'not survived data - age vs nodes')
```



### Observations: Patients with higher number of nodes(5-30) have least chance of survival

```
#survived patients:
print('--- SURVIVED PATIENTS ---')
print("Mean age:  "+str(np.mean(df_survived['age'])))
print("Mean number of nodes:  "+str(np.mean(df_survived['nodes'])))
print('90th percentile - number of nodes: '+str(np.percentile(df_survived['nodes'],90))
print("")
print("")
print('--- DEAD PATIENTS ---')
print("Mean age:  "+str(np.mean(df_notsurvived['age'])))
print("Mean number of nodes:  "+str(np.mean(df_notsurvived['nodes'])))
print('90th percentile - number of nodes: '+str(np.percentile(df_notsurvived['nodes'],9
```

```
--- SURVIVED PATIENTS ---
Mean age:  52.017777777777778
Mean number of nodes:  2.7911111111111113
90th percentile - number of nodes: 8.0


--- DEAD PATIENTS ---
Mean age:  53.67901234567901
Mean number of nodes:  7.45679012345679
90th percentile - number of nodes: 20.0
```

# SUMMARY

- Due to significant overlap in data, perfectly classifing features can't be obtained
- Of the three features , nodes is the most important feature followed by age
- Patients having nodes less than 4 have greatest chance of survival
- Patients below age of 35 and age above 75 have highest chance of survival