Haberman's survival dataset

- Title: Haberman's Survival Data
- Sources: (a) Donor: Tjen-Sien Lim (limt@stat.wisc.edu) (b) Date: March 4, 1999
- Number of Instances: 306
- Number of Attributes: 4 (including the class attribute)
- Attribute Information:
    - 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 2 = the patient died within 5 year

Importing dataset and going through summary statistics

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import os
import seaborn as sns
import warnings

warnings.filterwarnings("ignore")
```

```
path = "/content/sample_data/haberman.csv"
```

```
df = pd.read_csv(path)
```

```
df.head()
```

```
        age  year  nodes  status
```

```
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
 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
```

Observations

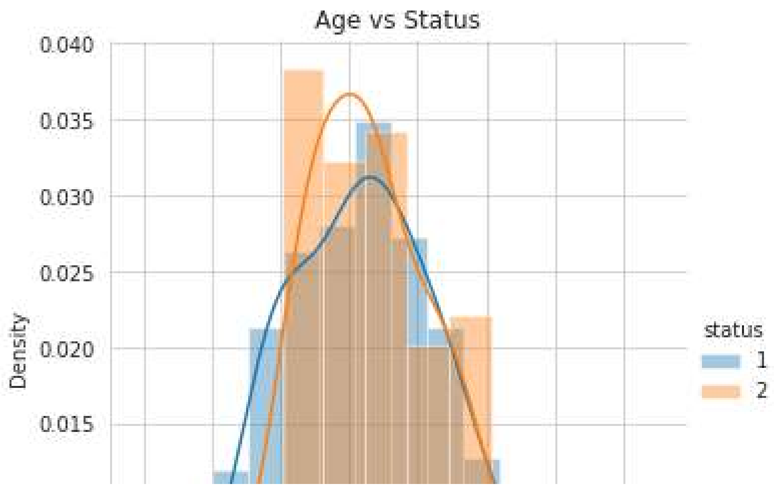
- There are 306 entries
- No missing values
- 4 attributes including class attribute

Objective

Attributes - Age of patient,year of operation,Number of positive axillary nodes to be used to predict if a patient will survive after 5 years

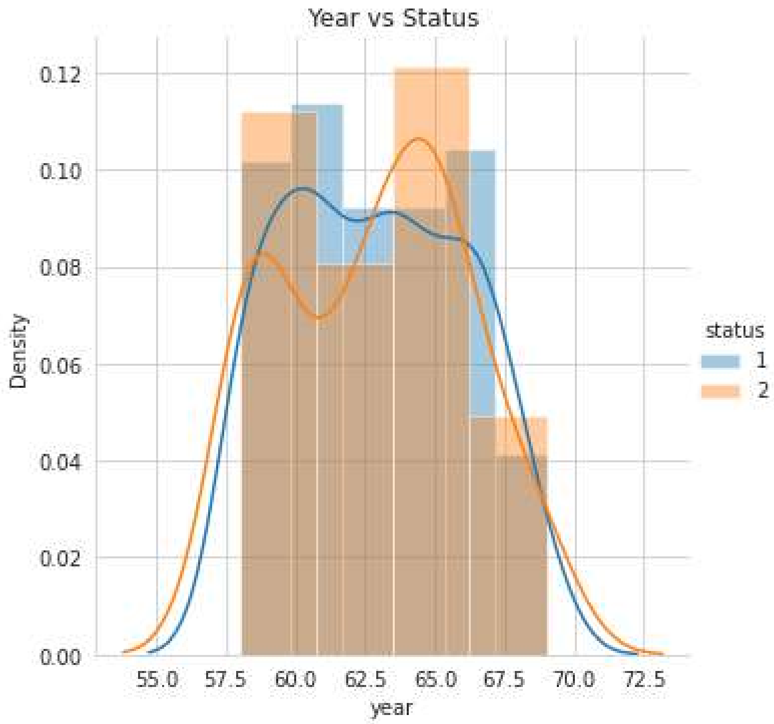
Plotting 1-D histograms

```
#Plotting 1-D histograms on attributes

sns.FacetGrid(df, hue="status", size=5) \
   .map(sns.distplot, "age") \
   .add_legend();

plt.title("Age vs Status")
plt.show();
```



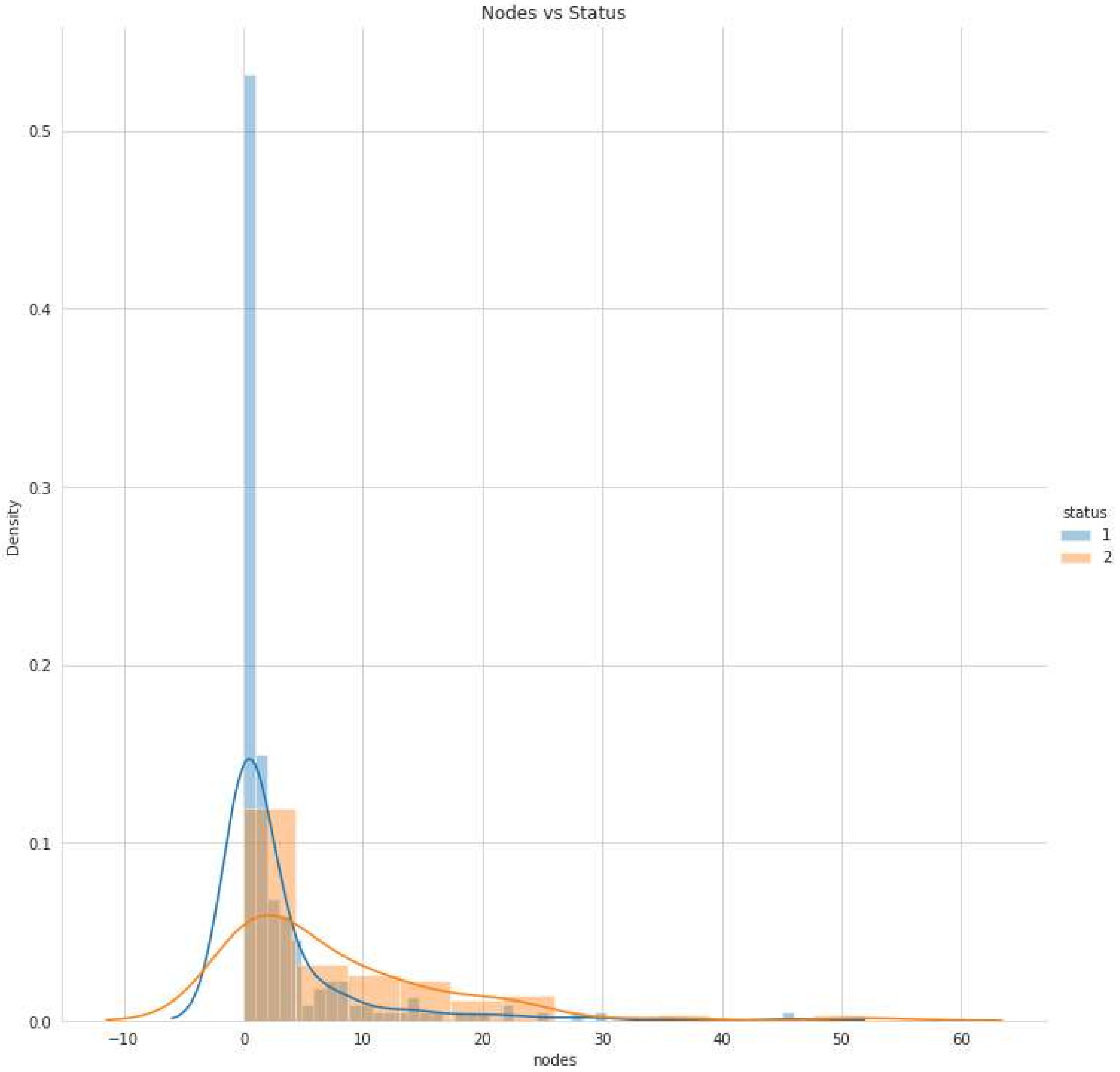
- Age alone can't determine whether the patient will live after 5 years as there is no clear separation between attributes
- Lesser the age, more the chances that patient will live after 5 years
- above age of 90 the chances of surving after surgery is nil

```
sns.FacetGrid(df, hue="status", size=5) \
   .map(sns.distplot, "year") \
   .add_legend();

plt.title("Year vs Status")
plt.show();
```



- There is no clear relation b/w year and status

```
sns.FacetGrid(df, hue="status", size=10) \
   .map(sns.distplot, "nodes") \
   .add_legend();

plt.title("Nodes vs Status")
plt.show();
```



- Patients with 1 & 2 axilary nodes have the highest survival rate
- For patients above 55 axilary nodes the survival rate is nil

- Axilary nodes are the only attribute which provides some significant information about the survival rate of patients

Descriptive statistics

```
#Splitting the dataframe into survived and died

haberman_survived = df.loc[df["status"]==1]
haberman_dead = df.loc[df["status"]==2]
```

```
#Descriptive statistics of both dataframes

haberman_survived.describe()
```

	age	year	nodes	status
count	225.000000	225.000000	225.000000	225.0
mean	52.017778	62.862222	2.791111	1.0
std	11.012154	3.222915	5.870318	0.0
min	30.000000	58.000000	0.000000	1.0
25%	43.000000	60.000000	0.000000	1.0
50%	52.000000	63.000000	0.000000	1.0
75%	60.000000	66.000000	3.000000	1.0
max	77.000000	69.000000	46.000000	1.0

- mean of 2.79 and 75% quartile value of 3 indicates that most of the survived patients (75%) were having 3 or less nodes
- Chances of a person surviving with higher number of nodes is very low

```
haberman_dead.describe()
```

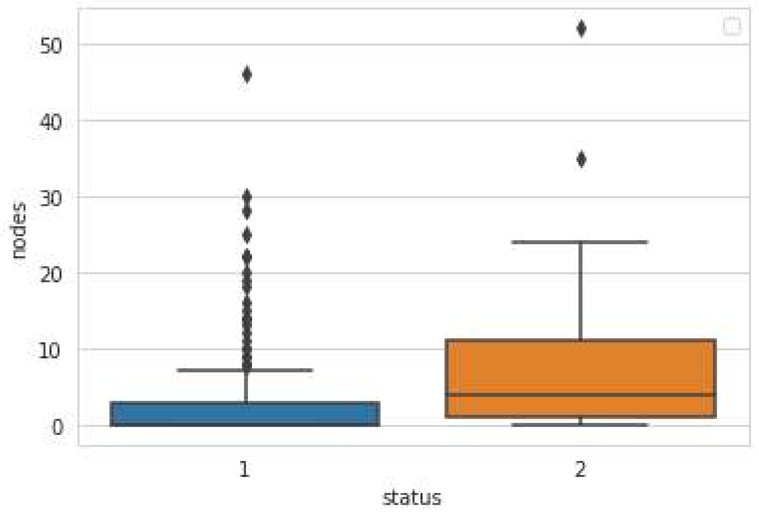
	age	year	nodes	status
count	81.000000	81.000000	81.000000	81.0
mean	53.679012	62.827160	7.456790	2.0
std	10.167137	3.342118	9.185654	0.0
50%	53.000000	63.000000	4.000000	2.0

- 50 percentile value of axilary nodes for died patients is 4. Which indicates that lesser number of nodes does not guarantee that patient will survive

Box Plot

```
#Plotting box plots
sns.boxplot(x='status',y='nodes', data=df)
plt.legend()
plt.show()
```

```
No handles with labels found to put in legend.
```

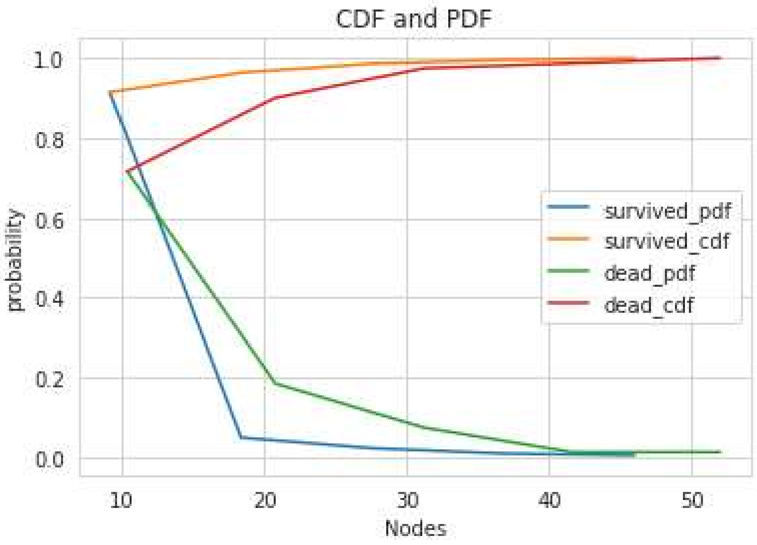


- There are many outlier points for survived class
- Though 75th percentile of survived class is at node = 5, there are many exceptions on that

CDF and PDF

```
#Plotting PDF and CDF of nodes on both dataframes

counts,bin_edges = np.histogram(haberman_survived["nodes"],bins =5,density = True)

pdf = counts/(sum(counts))
```

```
cdf = np.cumsum(pdf)

plt.plot(bin_edges[1:],pdf,label = "survived_pdf")
plt.plot(bin_edges[1:],cdf,label = "survived_cdf")

counts,bin_edges = np.histogram(haberman_dead["nodes"],bins =5,density = True)

pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)

plt.plot(bin_edges[1:],pdf,label = "dead_pdf")
plt.plot(bin_edges[1:],cdf,label = "dead_cdf")
plt.xlabel("Nodes")
plt.ylabel("probability")
plt.title("CDF and PDF")
plt.legend()
plt.show()
```

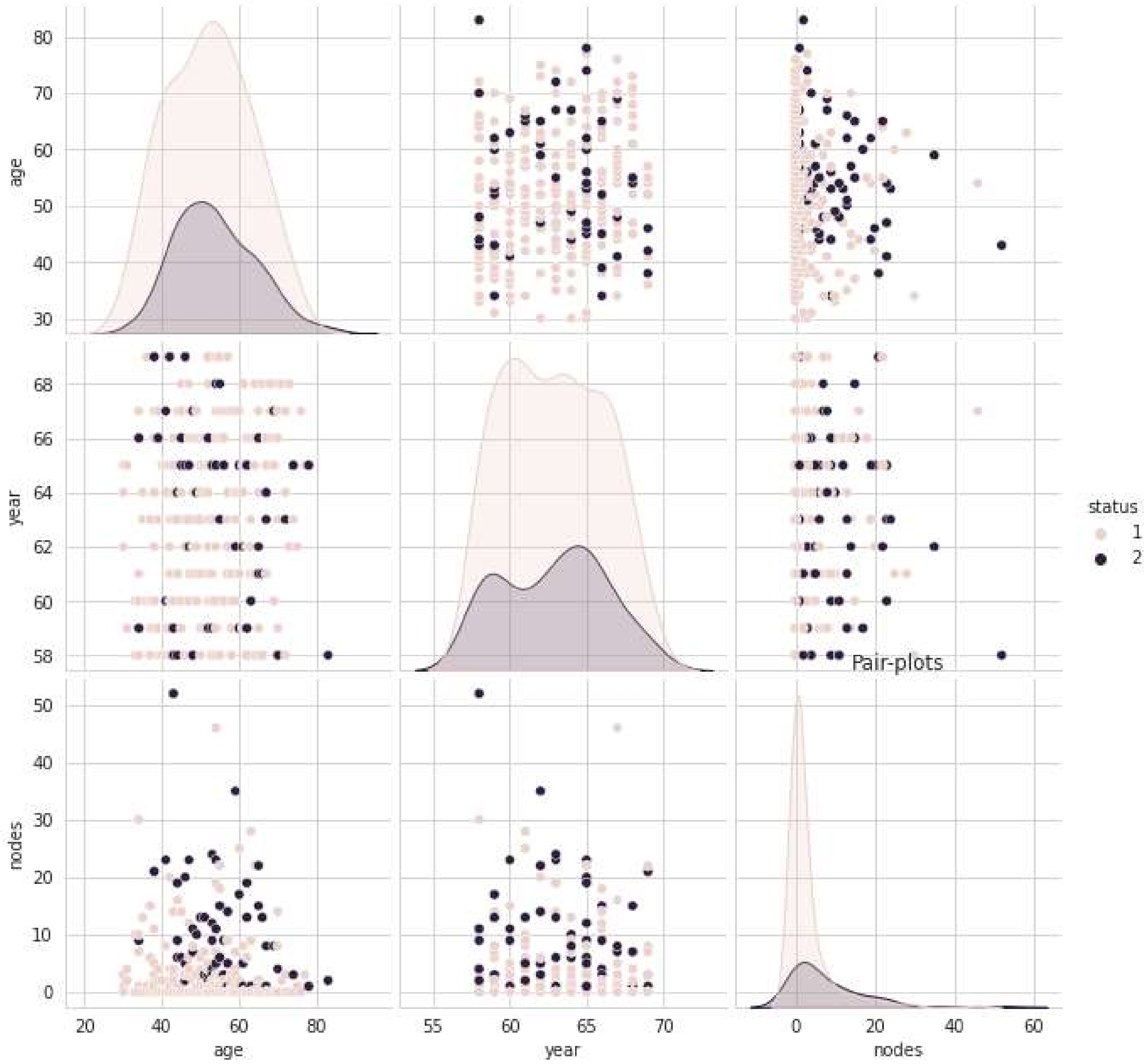


- The above plot re-validtaes the descriptive statistics that lesser number of nodes does not guarantee that patient will survive
- Higher number of occurances of patients dying and surviving are at lowe nodes
- CDF shows that patients with lower nodes have better chances of surviving but its not guranteed

Pair Plots

```
#Plotting pair-plots

sns.set_style("whitegrid");
sns.pairplot(df, hue="status", size=3);
```

```
    plt.show()
```



Conclusions

- There is no clear separation of classes on any of the sctter plots
- patients having age less than 40 and axilary nodes less than 10 have very high chance of surviving
- The survival rate of patients having nodes less than 5 have improved after year 1965

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