Exploratory Data Analytics on Haberman's Survival Dataset

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1. Importing the necessary packages

In [2]:

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels.api as sm
```

2. About the dataset

The dataset contains cases from a study that was conducted between 1958 and 1970 at the University of Chicago's Billings Hospital on the survival of patients who had undergone surgery for breast cancer.

2.1 Loading the data

In [3]:

```
#Loading the data
haberman = pd.read_csv('Data/haberman.csv')
# Printing first ten records
print(haberman.head(10))
```

	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
5	33	58	10	1
6	33	60	0	1
7	34	59	0	2
8	34	66	9	2
9	34	58	30	1

2.2 Objective

To identify trends and pattrens in the survivability of the haberman's dataset.

3. Understanding Various High Level Information About The Dataset

- 1. How many data-points and features?
- 2. What are the column names/attributes/features/variables in our dataset?
- 3. How many data points for each class/feature/class label are present?
- 4. Other information about types of values in each column?

^{*}Assuming 'status' as our class label

In [4]:

```
print("Shape of the dataset :",haberman.shape)
print("\nColumns in dataset
                              :",list(haberman.columns))
print("\nData per each class :\n")
print(haberman['status'].value counts())
print("\n\n0ther information
print(haberman.describe().T)
Shape of the dataset: (306, 4)
Columns in dataset : ['age', 'year', 'nodes', 'status']
Data per each class
1
     225
2
      81
Name: status, dtype: int64
Other information
        count
                                      min
                                            25%
                                                  50%
                                                          75%
                                std
                                                                max
                    mean
        306.0
               52.457516
                          10.803452
                                     30.0
                                           44.0
                                                 52.0
                                                       60.75
                                                               83.0
age
                          3.249405 58.0
year
        306.0
              62.852941
                                           60.0
                                                 63.0
                                                       65.75
                                                              69.0
                4.026144
                           7.189654
                                                         4.00
                                                              52.0
nodes
        306.0
                                      0.0
                                            0.0
                                                  1.0
        306.0
                1.264706
                           0.441899
                                      1.0
                                            1.0
                                                   1.0
                                                         2.00
                                                               2.0
status
```

And from the above information we can understand that the haberman's dataset is **somewhat imbalanced** because there are 225 samples which indicate people who survived longer than 5 years. And only 81 samples which indicate people who died within 5 years. *But thinking intuitively this data is sufficent to make good inferences*.

4. Making some changes in dataset

4.1 Replacing the status values for better understanding

```
1 == Survived 5 years or longer
2 == Died within 5 years
```

In [5]:

```
for index,row in haberman.iterrows():
    if haberman.iloc[index,3]==1:
        haberman.iloc[index,3]='Survived 5 years or longer'
    if haberman.iloc[index,3]==2:
        haberman.iloc[index,3]='Died within 5 years'
print(haberman.head(5))
```

	age	year	nodes	S	tatus
0	<i>30</i>	64	1	Survived 5 years or lo	onger
1	<i>30</i>	62	3	Survived 5 years or lo	onger
2	<i>30</i>	65	0	Survived 5 years or lo	onger
3	31	59	2	Survived 5 years or lo	onger
4	31	65	4	Survived 5 years or lo	onger

4.2 Replacing the year values by appending '19' to every value

In [6]:

```
for index,row in haberman.iterrows():
    haberman.iloc[index,1]=int('19'+str(haberman.iloc[index,1]))
print(haberman.head(5))
```

```
age year nodes status
0 30 1964 1 Survived 5 years or longer
1 30 1962 3 Survived 5 years or longer
2 30 1965 0 Survived 5 years or longer
3 31 1959 2 Survived 5 years or longer
4 31 1965 4 Survived 5 years or longer
```

5. Bivariate Analysis on various features

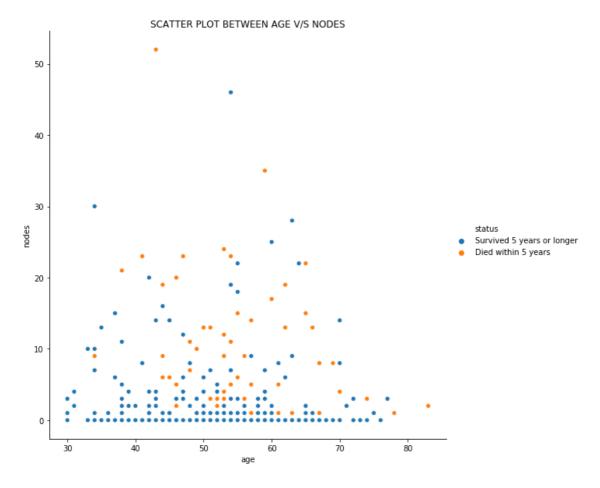
5.1. Age v/s Nodes (Scatter plot between age and nodes)

In [14]:

sns.relplot(x="age", y="nodes",hue="status",height=8,data=haberman)
plt.title("SCATTER PLOT BETWEEN AGE V/S NODES")

Out[14]:

Text(0.5, 1, 'SCATTER PLOT BETWEEN AGE V/S NODES')



Observations from the above scatter plot between age and nodes :

- People who had more than 50 auzillary lymph nodes did not survive and died within 5 years of operating.
- People who had age more than 80 did not survive and died within 5 years of operating.
- Clearly the above two observations can be considered as outliers for this dataset.

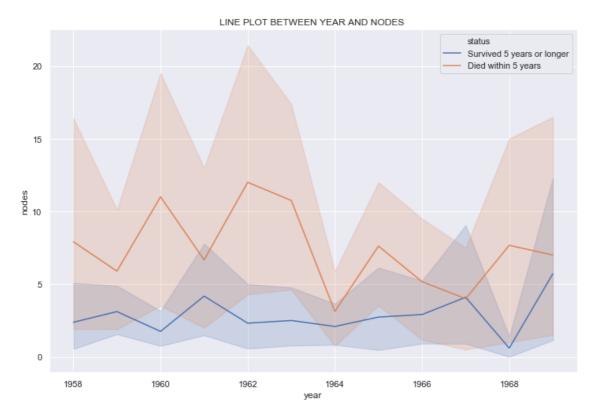
5.2. Years v/s Nodes (Line plot between year and nodes)

In [15]:

```
sns.set_style("whitegrid")
sns.set(rc={'figure.figsize':(12,8)})
sns.lineplot(x="year", y="nodes",hue="status",data=haberman)
plt.title("LINE PLOT BETWEEN YEAR AND NODES ")
```

Out[15]:

Text(0.5, 1.0, 'LINE PLOT BETWEEN YEAR AND NODES ')



If we want to find about the patients and their survival rate in different years, then the above plot can help us understand a little.

6. Univariate Analysis

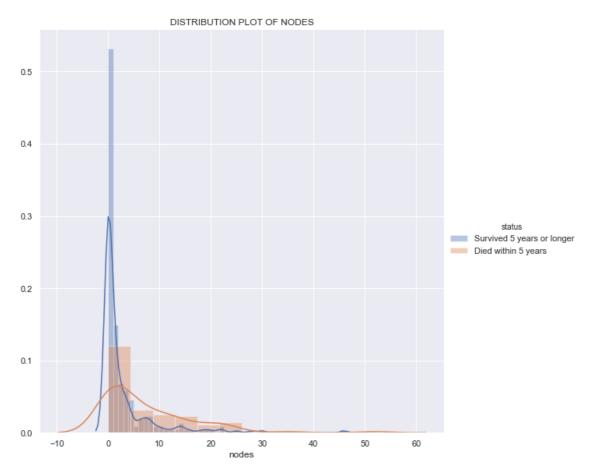
6.1. Distribution plot of lymph nodes

In [16]:

sns.FacetGrid(haberman, hue="status", height=8).map(sns.distplot, "nodes").add_l
egend()
plt.title("DISTRIBUTION PLOT OF NODES")

Out[16]:

Text(0.5, 1, 'DISTRIBUTION PLOT OF NODES')



From the above plot we can understand that :

- People who had lymph nodes between 0 to 5 have the highest survival rate which is more than 50%.
- Only 12-13% of the people who had 0-5 lymph nodes died within 5 years.
- For people who had more than 30 lymph nodes, it is harder to distinguish their survivability from the above plot.

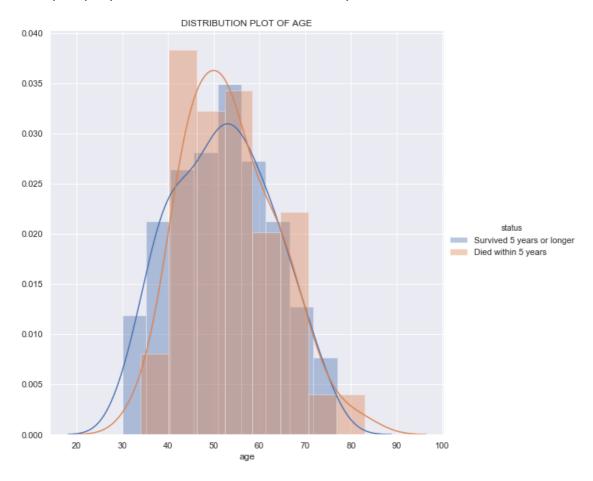
6.2. Distribution plot of age

In [17]:

 $sns.FacetGrid(haberman, hue="status", height=8).map(sns.distplot, "age").add_legend() plt.title("DISTRIBUTION PLOT OF AGE")$

Out[17]:

Text(0.5, 1, 'DISTRIBUTION PLOT OF AGE')



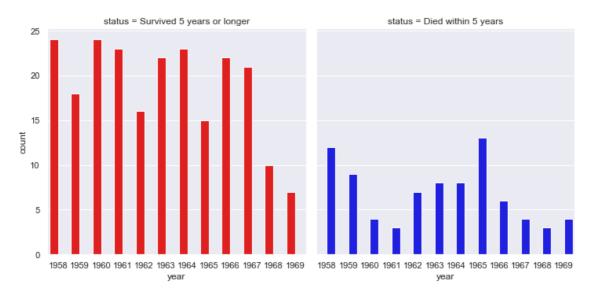
From the above plot we can understand that:

- People who were having an age between 51-56 relatively survived the most.(at 0.035 in distplot of age).
- Most of the people who were having an age between 40-45 died within 5 years of operating.
- People who were operated at ages 30-33, all of them survived.

6.3. Factor plot of years

In [25]:

FACTOR PLOT OF YEARS



From the above plot we can understand that :

- After 1958 the number of people died gradually decreased till 1961.
- And the trend of 1958-1961 can be seen again between 1965-1968.

6.4. Plotting PDF v/s CDF for age

As we are only concerned about the survival, we only consider the cases of people who survived 5 years or longer while plotting PDF and CDF.

In [28]:

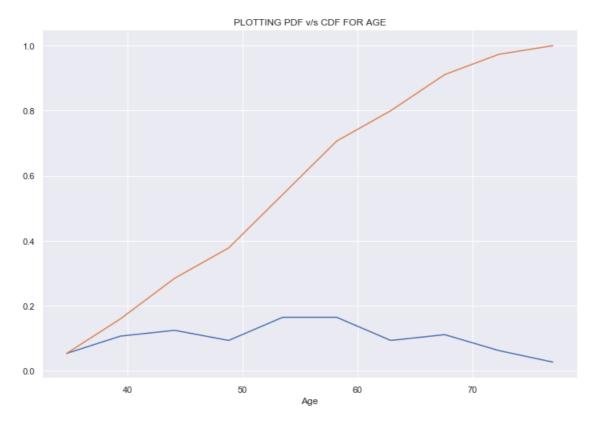
survived=haberman.loc[haberman['status']=='Survived 5 years or longer']
died=haberman.loc[haberman['status']=='Died within 5 years']

In [38]:

```
count1,binedges1 = np.histogram(survived['age'], bins=10, density = True)
pdf1=count1/sum(count1)
cdf1=np.cumsum(pdf1)
plt.plot(binedges1[1:],pdf1)
plt.plot(binedges1[1:], cdf1)
plt.xlabel("Age")
plt.xtitle("PLOTTING PDF v/s CDF FOR AGE")
```

Out[38]:

Text(0.5, 1.0, 'PLOTTING PDF v/s CDF FOR AGE')



From the above plot we can understand that :

• Interestingly 50% of the people ages are less than or equal to 52.(from CDF of age)

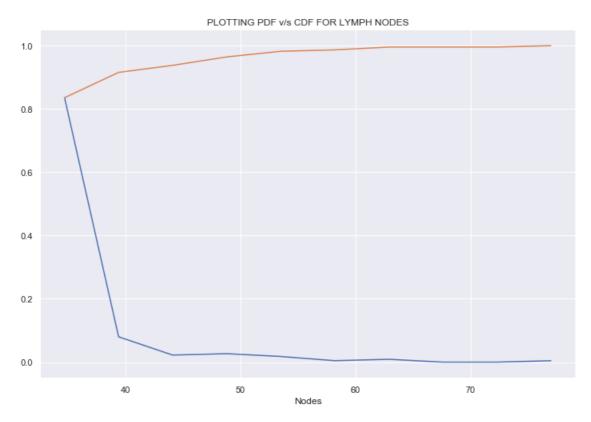
6.5. Plotting PDF v/s CDF for lymph nodes

In [39]:

```
count2,binedges2 = np.histogram(survived['nodes'], bins=10, density = True)
pdf2=count2/sum(count2)
cdf2=np.cumsum(pdf2)
plt.plot(binedges1[1:],pdf2)
plt.plot(binedges1[1:], cdf2)
plt.xlabel("Nodes")
plt.title("PLOTTING PDF v/s CDF FOR LYMPH NODES")
```

Out[39]:

Text(0.5, 1.0, 'PLOTTING PDF v/s CDF FOR LYMPH NODES')



From the above plot we can understand that:

• From the CDF of lymph nodes, 90% of people had less than 40 lymph nodes.

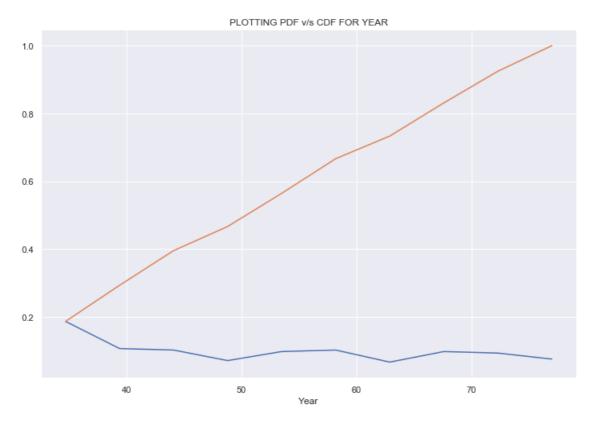
6.6 Plotting PDF v/s CDF for year

In [40]:

```
count3,binedges3 = np.histogram(survived['year'], bins=10, density = True)
pdf3=count3/sum(count3)
cdf3=np.cumsum(pdf3)
plt.plot(binedges1[1:],pdf3)
plt.plot(binedges1[1:], cdf3)
plt.xlabel("Year")
plt.title("PLOTTING PDF v/s CDF FOR YEAR")
```

Out[40]:

Text(0.5, 1.0, 'PLOTTING PDF v/s CDF FOR YEAR')



7. Multivariate Analysis

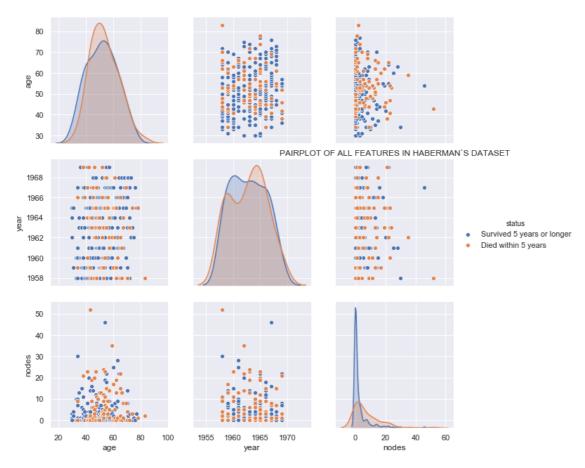
7.1. Pair plot of all the features

In [41]:

```
sns.pairplot(haberman, hue="status", height=3)
plt.title("PAIRPLOT OF ALL FEATURES IN HABERMAN'S DATASET")
```

Out[41]:

Text(0.5, 1, 'PAIRPLOT OF ALL FEATURES IN HABERMAN'S DATASET')



From pairplot of all the features we cannot make any inferences easily.

7.2. Heatmap of all features

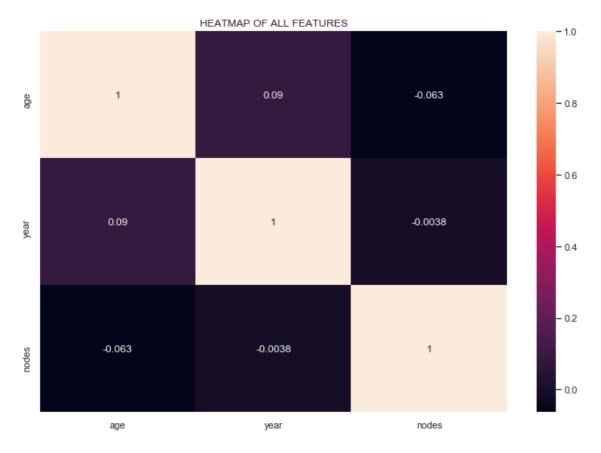
Probably the most heavily used summarization visualization is the correlation plot, in which measures the correlation between every pair of values in a dataset and plots a result in color.

In [42]:

```
h=haberman.corr()
sns.heatmap(h, annot=True)
plt.title("HEATMAP OF ALL FEATURES")
```

Out[42]:

Text(0.5, 1, 'HEATMAP OF ALL FEATURES')



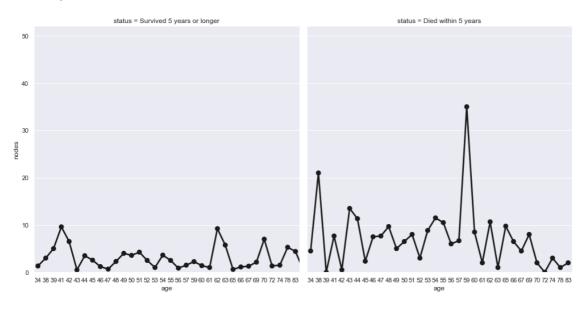
- The features **age** and **year** are **negatively correlated** with the feature **nodes**.
- The features age and year are positively correlated.

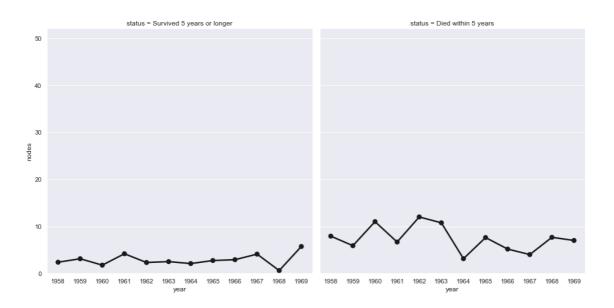
7.3. Multivariate Point Plot of age v/s nodes and year v/s nodes

In [48]:

MULTIVARIATE POINT PLOT OF AGE V/S NODES AND

YEAR V/S NODES





 Most of the people who had more than 10 lymph nodes did not survive and died within 5 years.

8. Understanding Central tendancy of various features in the data

In [20]:

```
print("People who lived 5 years or longer\n")
print(survived.describe().T)
print("\n_____\n")
print("People who dies within 5 years\n")
print(died.describe().T)
```

People who lived 5 years or longer

	count	mean	std	min	<i>25</i> %	<i>50</i> %	7
<i>5</i> %	max						
age	<i>225.0</i>	52.017778	11.012154	30.0	43.0	<i>52.0</i>	60.
•	77.0						
year	<i>225.0</i>	1962.862222	3.222915	1958.0	1960.0	1963.0	1966.
0 19	069.0						
nodes	225.0	2.791111	5.870318	0.0	0.0	0.0	3.
0	46.0						

People who dies within 5 years

count	mean	std	min	<i>25</i> %	<i>50</i> %	7
5% max age 81.0	53.679012	10.167137	34.0	46.0	53.0	61.
0 83.0 year 81.0	1962.827160	3.342118	1958.0	1959.0	1963.0	1965.
0 1969.0 nodes 81.0 0 52.0	7.456790	9.185654	0.0	1.0	4.0	11.

- 50% of people who survived had 0 lymph nodes.
- 50% of the people who died had atleast 4 lymph nodes.
- And 75% the people who had survived 5 years or longer had less than 4 lymph nodes.

9. Conclusions

- 1. The haberman's dataset can be used to understand the survivabilty of a person who has been operated for the breast cancer removal.
- 2. Age and Nodes together seems to be most important variables/features for predicting the survival.
- 3. The data is sufficient to build a basic classifier to predict the survival. But according to my opinion there need to be more features or more data for existing variables in order to make a robust model out of this dataset.
- 4. And from the above information we can understand that the haberman's dataset is **somewhat imbalanced** because there are 225 samples which indicate people who survived longer than 5 years. And only 81 samples which indicate people who died within 5 years. But thinking intuitively this data is sufficent to make good inferences.
- 5. People who had more than 50 auzillary lymph nodes did not survive and died within 5 years of operating.
- 6. People who had age more than 80 did not survive and died within 5 years of operating.
- 7. Clearly the above two observations can be considered as outliers for this dataset.
- 8. People who had lymph nodes between 0 to 5 have the highest survival rate which is more than 50%.
- 9. Only 12-13% of the people who had 0-5 lymph nodes died within 5 years.
- 10. For people who had more than 30 lymph nodes, it is harder to distinguish their survivability from the distribution plot of lymph nodes.
- 11. People who were having an age between 51-56 relatively survived the most.(at 0.035 in distplot of age).
- 12. Most of the people who were having an age between 40-45 died within 5 years of operating.
- 13. People who were operated at ages 30-33, all of them survived.
- 14. After 1958 the number of people died gradually decreased till 1961.
- 15. And the trend of 1958-1961 can be seen again between 1965-1968.
- 16. Interestingly 50% of the people ages are less than or equal to 52.(from CDF of age)
- 17. From the CDF of lymph nodes, 90% of people had less than 40 lymph nodes.
- 18. From pairplot of all the features we cannot make any inferences easily.
- 19. The features **age** and **year** are **negatively correlated** with the feature **nodes**.
- 20. The features age and year are positively correlated.
- 21. Most of the people who had more than 10 lymph nodes did not survive and died within 5 years.
- 22. 50% of people who survived had 0 lymph nodes.
- 23. 50% of the people who died had atleast 4 lymph nodes.
- 24. And 75% the people who had survived 5 years or longer had less than 4 lymph nodes.