HABERMAN'S SURVIVAL

Data Description

The Haberman's survival 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.

Attribute Information

- 1. Age of patient at time of operation (numerical)
- 2. Patient's year of operation (year 1900, numerical)
- 3. Number of positive axillary nodes detected (numerical)
- 4. Survival status (class attribute) 1 = the patient survived 5 years or longer 2 = the patient died within 5 years

In [46]:

```
same#Import Necessary Libraries/Packages
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

In [47]:

```
#Reading the file
df = pd.read_csv('/home/sampath/Documents/Haberman-Cancer-Survival-Dataset-maste
r/haberman.csv')
```

In [48]:

```
#check the top 5 rows
df.head()
```

Out[48]:

	30	64	1	1.1
0	30	62	3	1
1	30	65	0	1
2	31	59	2	1
3	31	65	4	1
4	33	58	10	1

Findings:

1. Column names are missing in the dataset and hence adding the column names

In [49]:

```
#Renaming the column names as its too big
df.columns = ['Age','Year','Nodes','Survival_status']
df.head()
```

Out[49]:

	Age	Year	Nodes	Survival_status
0	30	62	3	1
1	30	65	0	1
2	31	59	2	1
3	31	65	4	1
4	33	58	10	1

In [50]:

```
#Finding total number of datapoints(rows) and columns in our dataset df.shape
```

Out[50]:

(305, 4)

In [51]:

```
#Checking if there are any null values
df.isnull().sum()
```

Out[51]:

Age 0
Year 0
Nodes 0
Survival_status 0
dtype: int64

In [52]:

df.info()

dtypes: int64(4) memory usage: 9.6 KB

In [53]:

```
#Checking if the data is Balanced or Imbalanced
df['Survival_status'].value_counts()
```

Out[53]:

224
 81

Name: Survival_status, dtype: int64

Findings:

- 1. There are 305 rows(data-points) and 4 columns(Features).
- 2. There are no null values in the dataset.
- 3. All the columns are of type int.
- 4. There are 224 survival records and 81 not survived records in the give n dataset. Hence it is clear that the given dataset is imbalanced.

In [54]:

```
df.describe()
```

Out[54]:

	Age	Year	Nodes	Survival_status
count	305.000000	305.000000	305.000000	305.000000
mean	52.531148	62.849180	4.036066	1.265574
std	10.744024	3.254078	7.199370	0.442364
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%	61.000000	66.000000	4.000000	2.000000
max	83.000000	69.000000	52.000000	2.000000

Findings

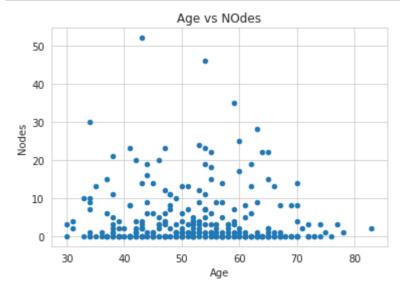
- 1. Age range of patients are between 30 to 83 with median of 52.
- 2. Nodes range from 0 to 52.
- 3. 75% of patients have nodes less than 5 and 25% of the patients have 0 nodes.

BI-VARIATE ANALYSIS

2-D SCATTER PLOT

In [55]:

```
df.plot(kind='scatter', x='Age', y='Nodes');
plt.title('Age vs NOdes')
plt.show()
```



Findings:

1. Most of the people have 0 nodes.

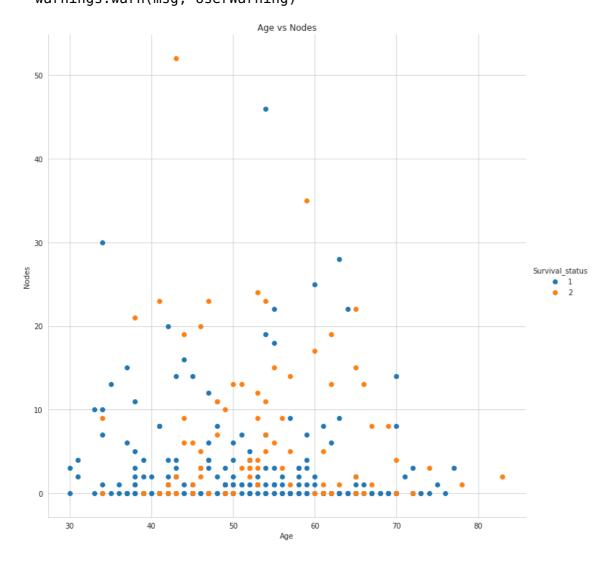
2-D SCATTER PLOT WITH COLOR-CODING

In [56]:

```
sns.set_style('whitegrid')
sns.FacetGrid(df, hue='Survival_status', size = 10) \
.map(plt.scatter,'Age','Nodes').add_legend()

plt.title('Age vs Nodes')
plt.show()
```

/home/sampath/anaconda3/lib/python3.7/site-packages/seaborn/axisgri
d.py:230: UserWarning: The `size` paramter has been renamed to `heig
ht`; please update your code.
 warnings.warn(msg, UserWarning)



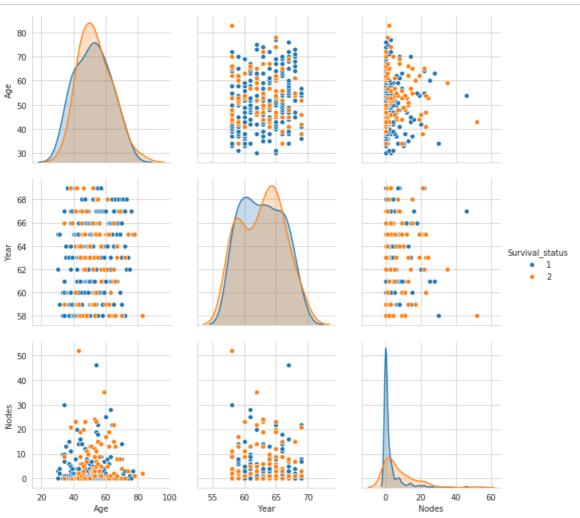
Findings:

- 1. Most of the patients have 0 Nodes.
- 2. Blue(Survived) and Orange(not survived) points are not well seperated, so we cannot make any decision by looking at this Age vs Nodes graph regarding the patient survival.
- 3. Hence we need to check the pair/combination of features to make good d esicion/combination.
- 4. Number of combination of features is 3C2 = 3, which will plot using Pa ir-plot.

Pair-Plot

In [57]:

```
#Analyzing data using pair plots
plt.close()
sns.set_style('whitegrid')
sns.pairplot(df, hue = 'Survival_status', height = 3, vars = ['Age', 'Year', 'Node
s'])
plt.show()
```



Finding_2:

- 1. Age between 30 to 40 and year of operation between 58(approx) to 65 has quite good survival status who survived
- 2. Nodes signififies the Survival_status
- 2.1 Lesser the number of nodes higher the chance of patient being survived.
- 2.2 Higher the number of nodes lesser the chance of patient being sur vived.

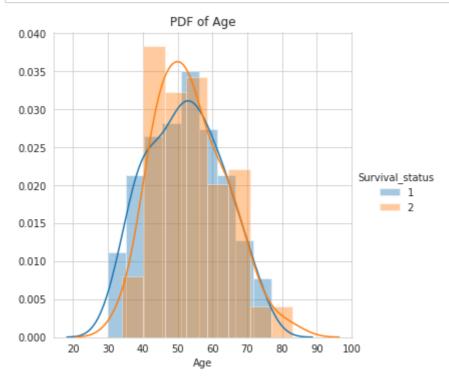
UNIVARIATE ANALYSIS

HISTOGRAM, PDF, CDF

1. 'AGE'

In [58]:

```
#Drawing Histogram and understanding effect Age
sns.FacetGrid(df,hue='Survival_status',height=5).map(sns.distplot,'Age').add_leg
end()
plt.title('PDF of Age')
plt.show()
```



In [59]:

```
#plotting CDF
count, bin_edges = np.histogram(df['Age'], bins=10, density = True)
pdf = count/(sum(count))
print(pdf)
print(bin_edges)

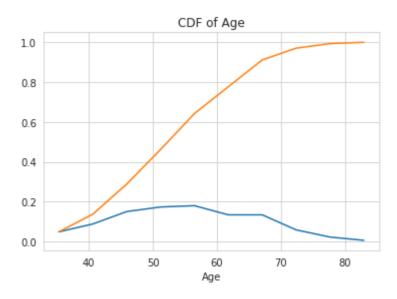
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.title('CDF of Age')
plt.xlabel('Age')

#Note: I have selected bins as 10 since it has quite less number of data points.
We can select any data points in the range of 5 to 20.
```

```
[0.04918033 0.08852459 0.15081967 0.17377049 0.18032787 0.13442623 0.13442623 0.05901639 0.02295082 0.00655738] [30. 35.3 40.6 45.9 51.2 56.5 61.8 67.1 72.4 77.7 83. ]
```

Out[59]:

Text(0.5, 0, 'Age')



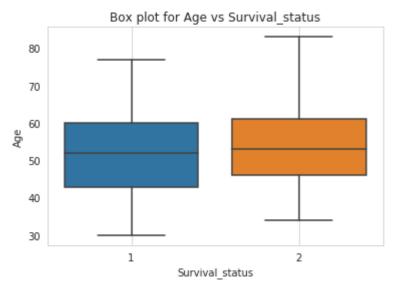
Finding_3:

1. There are approx 95% of the people below age group of 70.

Note: This is just finding from above graph, age is not an significant factor to distinguish between survival_status as seen clearly from the pairplot graph

In [60]:

```
#plotting boxplot
sns.boxplot(x='Survival_status', y='Age', data= df)
plt.grid()
plt.title('Box plot for Age vs Survival_status')
plt.show()
```



Finding_4:

- 1. People who are in the range between 30 to 35(Approx) irrespective of Year of operation and Positive nodes have survived.
- 2. People whose age is above 75 irrespective of Year_of_operation and Positive_nodes have not survived.

In [61]:

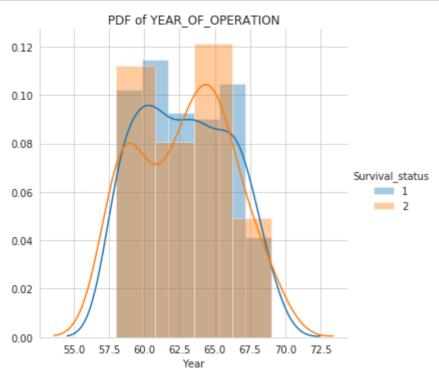
```
sns.violinplot(x='Survival_status',y='Age',data = df , size = 6)
plt.title('Violin plot for Age vs Survival_status')
plt.show()
```



2. Year

In [62]:

```
sns.FacetGrid(df,hue='Survival_status',height=5).map(sns.distplot,'Year').add_le
gend()
plt.title('PDF of YEAR_OF_OPERATION')
plt.show()
```

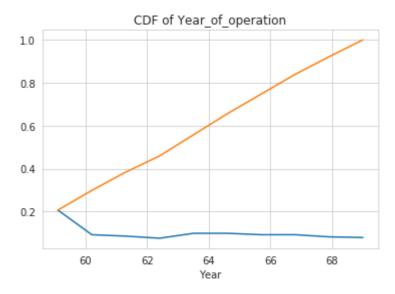


In [63]:

```
#plotting cdf
count,bin_edges = np.histogram(df['Year'], bins = 10, density = True)
pdf = count/(sum(count))
print(pdf)
print(bin_edges)

cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.title('CDF of Year_of_operation')
plt.xlabel('Year')
plt.show()
```

```
[0.20655738 0.09180328 0.0852459 0.07540984 0.09836066 0.09180328 0.09180328 0.08196721 0.07868852]
[58. 59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69.]
```



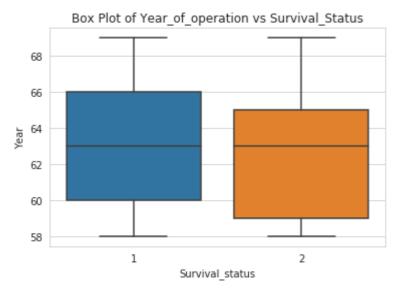
Finding_4:

1. Almost 79% of people had undergone operation in the year range 1958 to $1966\,$

Note: Again the above info is just for understanding as this data will not help us in understanding the survival status

In [64]:

```
#Box plot
sns.boxplot(x='Survival_status', y='Year', data= df)
plt.title('Box Plot of Year_of_operation vs Survival_Status')
plt.show()
```



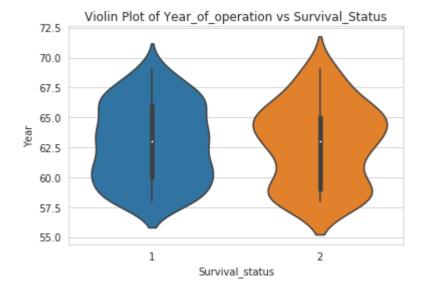
From the above boxplot it is hard to retrive any information

In [65]:

```
sns.violinplot(x='Survival_status',y='Year',data=df ,size= 6)
plt.title('Violin Plot of Year_of_operation vs Survival_Status')
```

Out[65]:

Text(0.5, 1.0, 'Violin Plot of Year_of_operation vs Survival_Status')



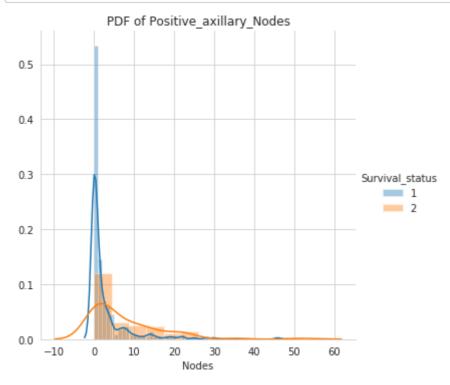
Finding_5:

1. From the above graphs we were not able to retrive any kind of informat ion regarding survival_status hence we can say Year_of_operation doesnot play any significant role in identifying the Survival status

3. Nodes

In [66]:

```
sns.FacetGrid(df,hue='Survival_status',height=5).map(sns.distplot,'Nodes').add_l
egend()
plt.title('PDF of Positive_axillary_Nodes')
plt.show()
```



Finding_5:

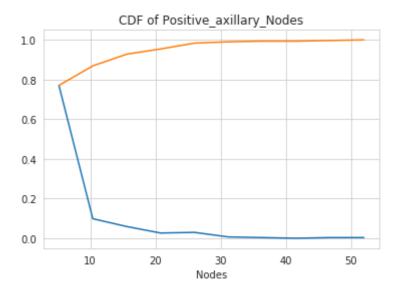
- 1. From the above graph we can say that there are approx 55% of people su rvived having Positive_Lymph_nodes between 0-2 and around 12% of people w ho died as well having nodes in this range
- 2. If positive nodes is higher then there is less chance of patient being survived.
- 3. Most of the people have zero positive_Lymph_nodes.

In [67]:

```
#cdf
count,bin_edges = np.histogram(df['Nodes'],bins=10,density= True)
pdf = count/(sum(count))
print(pdf)
print(bin_edges)

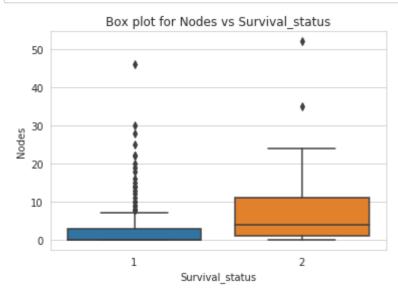
cdf =np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.xlabel('Nodes')
plt.title('CDF of Positive_axillary_Nodes')
plt.show()
```

```
[0.7704918 0.09836066 0.05901639 0.02622951 0.0295082 0.00655738 0.00327869 0. 0.00327869 0.00327869]
[0. 5.2 10.4 15.6 20.8 26. 31.2 36.4 41.6 46.8 52.]
```



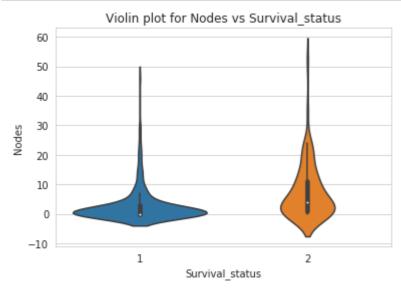
In [68]:

```
#boxplot
sns.boxplot(x='Survival_status',y='Nodes', data=df)
plt.title('Box plot for Nodes vs Survival_status')
plt.show()
```



In [69]:

```
sns.violinplot(x='Survival_status',y='Nodes',data=df ,size=6)
plt.title('Violin plot for Nodes vs Survival_status')
plt.show()
```



In [70]:

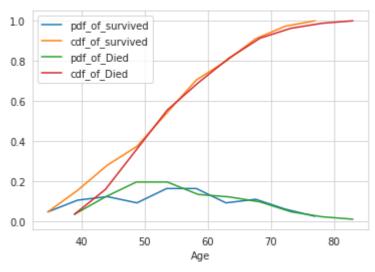
```
#Drawing PDF and CDF for survival status
Survived = df.loc[df['Survival_status'] == 1]
Died = df.loc[df['Survival_status'] == 2]
```

In [71]:

```
count,bin_edges = np.histogram(Survived['Age'],bins=10,density=True)
pdf = count/(sum(count))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
label = ['pdf_of_survived','cdf_of_survived','pdf_of_Died','cdf_of_Died']

count,bin_edges = np.histogram(Died['Age'],bins=10,density=True)
pdf = count/(sum(count))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.xlabel('Age')
plt.legend(label)

plt.show()
```



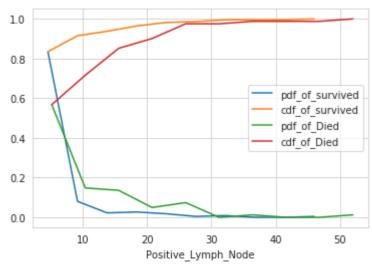
Finding_6:

- 1. Almost 15% of the people among survived have age less than 36(Approx)
- 2. After age above 75 we can see there is a high chance of death.
- 3. The number of nodes from 0 to 5 is highly densed.

In [72]:

```
count,bin_edges = np.histogram(Survived['Nodes'],bins=10,density=True)
pdf = count/(sum(count))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
label = ['pdf_of_survived','cdf_of_survived','pdf_of_Died','cdf_of_Died']

count,bin_edges = np.histogram(Died['Nodes'],bins=10,density=True)
pdf = count/(sum(count))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.xlabel('Positive_Lymph_Node')
plt.legend(label)
plt.show()
```



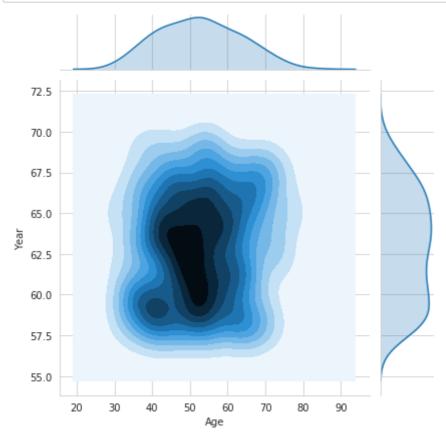
Finding_7:

1. People having positive_lymph_node more than 46 have died.

Contour plot

In [73]:

```
sns.jointplot(x="Age", y="Year", data=df, kind="kde");
plt.show()
```



Findings:

1. There are more number of people who have undergone operation during th e year 59-64 and between the ages 42-64

CONCLUSION:

- The given dataset is Imbalanced since there is no equal number of Observation for our Dependent Variable
- We cannot differentiate our Dependent Variable since all the Independent Variables have overlapping.

OBSERVATIONS:

1. People who are in the AGE range between 30 to 35(Approx) irrespective of Year of operation and Positive nodes have survived.

- 2. People whose age is above 75 irrespective of Year_of_operation and Po sitive nodes have not survived.
- 3. From the above graph we can say that there are approx 55% of people s urvived having Positive_Lymph_nodes between 0-2 and around 12% of people who died as well having nodes in this range.
- 4. If positive nodes is higher then there is less chance of patient bein g survived.
- 5. Most of the people have zero positive Lymph nodes.
- 6. Almost 15% of the people among survived have age less than 36(Appro x).
- 7. After age > 75 we can see there is a high chance of death.
- 8. People having positive_lymph_node more than 46 have died.
- 9. Age between 30 to 40 and year of operation between 58(approx) to 65 h as quite good survival_status who survived.
- 10. Lesser the number of nodes higher the chance of patient being survive d.
- 11. Higher the number of nodes lesser the chance of patient being survive d.
- 12. There are more number of people who have undergone operation during the Year_of_operation 59-64 and between the ages 42-64.

ın [1:			