What is Haberman's Survival Data Set ?

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.

Ojective:

Perform the exploratory data analysis on breast cancer patients.

In [1]:

```
#import the library numpy matplotlib,seaborn,pandas

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

%matplotlib inline
```

In [2]:

```
# Download the Haberman's Survival Data Set from "https://www.kaggle.com/gilsousa/haber
mans-survival-data-set"

#load the Haberman's Survival Data Set
df = pd.read_csv("haberman.csv") # assume that i am loading the data in current dirceto
ry

# here columns are not more expressable so here i am setting the columns names

col = ['Age','Year-of-operation','Positive-auxilary-nodes','Status']
df = pd.read_csv("haberman.csv",names = col)
df.head()
```

Out[2]:

	Age	Year-of-operation	Positive-auxilary-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]:

```
# how many data points and features are there.
df.shape
```

Out[3]:

```
(306, 4)
```

In [4]:

```
# Now what are the columns name of our data set

print(df.columns)
```

```
Index(['Age', 'Year-of-operation', 'Positive-auxilary-nodes', 'Status'], d
type='object')
```

In [5]:

```
# print the number of class in data set.
df['Status'].value_counts()

# Here  is 2 class and this data set is imbalnced because class1 have 225 data points a
nd class2 have 81 data points
```

Out[5]:

```
1    225
2     81
Name: Status, dtype: int64
```

In [6]:

```
# count,mean ,standard deviation(std),minimum(min),First quartile(25%),Second quartile
(50%),Third quartile(75%), maximum(max) for each
# feature of dataset.

df.describe()
```

Out[6]:

	Age	Year-of-operation	Positive-auxilary-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

Observations about Haberman dataset:

1. Numbers of rows(training data) is: 306
2. Numbers of features(columns) is: 4
3. Year operation of patient show last 2 digits of years.
4. This dataset contain two class(it can be said binary classification):
5. Status 1 = the patient survived 5 years or longer
6. Status 2 = the patient died within 5 year
7. class 1's , 225 patient survived for 5 years or longer
8. class 2 's, 85 patient died within 5 years
9. It is Imbalance data set because class 1 has 225 data point and class 2 has 81 data point.

In [7]:

```
# calculate the percentage  of each class
df['Status'].value_counts()*100/df.shape[0]
```

Out[7]:

```
1    73.529412
2    26.470588
Name: Status, dtype: float64
```

Observation:

- 73% of class 1 pateints survived 5 years or more
- 26% of class 2 patients dies within 5 years

Univariate analysis:

In [8]:

```
survived = df.loc[df['Status']== 1]
not_survived = df.loc[df['Status'] == 2]
```

In [9]:

```
print("Patients survied 5 years or more")
survived.describe()
```

Patients survied 5 years or more

Out[9]:

	Age	Year-of-operation	Positive-auxilary-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

In [10]:

```
print("Patients died within 5 years")
not_survived.describe()
```

Patients died within 5 years

Out[10]:

	Age	Year-of-operation	Positive-auxilary-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
min	34.000000	58.000000	0.000000	2.0
25%	46.000000	59.000000	1.000000	2.0
50%	53.000000	63.000000	4.000000	2.0
75%	61.000000	65.000000	11.000000	2.0
max	83.000000	69.000000	52.000000	2.0

Observation:

- Patients survived 5 years or more
  - Mean = 2.791111
  - 75%(third quartile) = 3.00000
- Patients died within 5 years
  - Mean = 7.456790
  - 75%(thirs quartile) = 3.000000
- Here increaase in standard deviation,so we can say that patients who had more positive-auxilary-nodes died early.

1. Age Feature :

let us do more analysis on each features.

In [11]:

```
survived_status = survived['Age'].describe()
not_survived_status =not_survived['Age'].describe()

# create dataframe to store the survived_status and not_survived_status statistics.
df1_age = pd.DataFrame(data={'Survived':survived_status,'Died':not_survived_status})


df1_age
```

Out[11]:

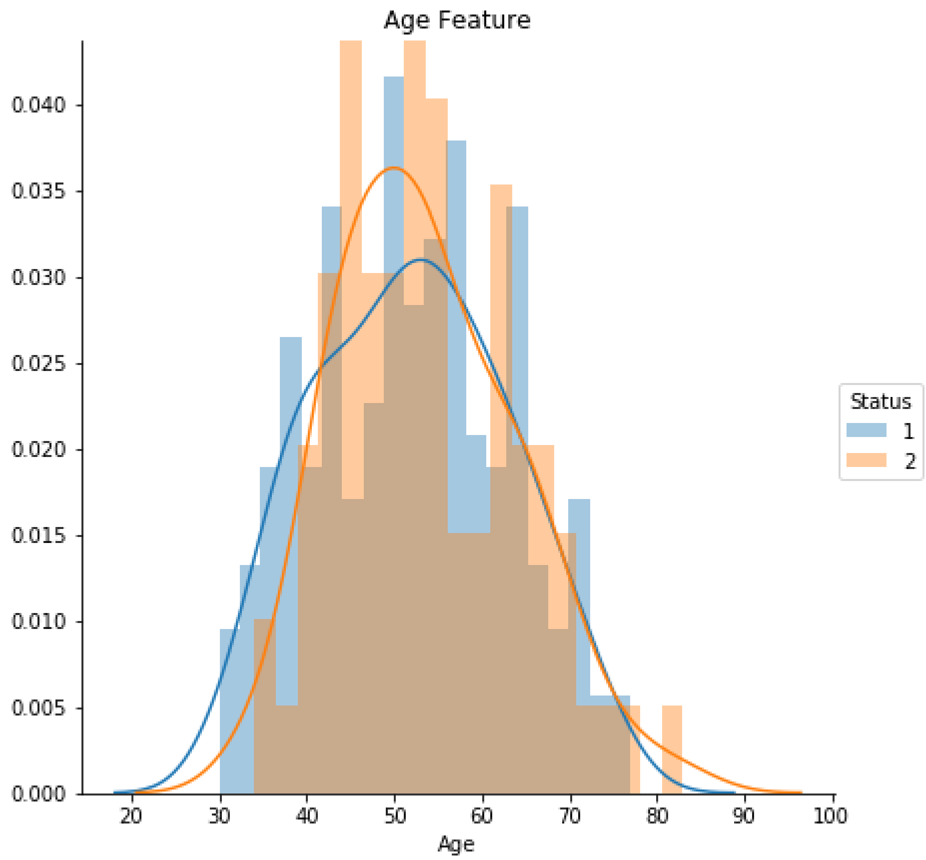
	Died	Survived
count	81.000000	225.000000
mean	53.679012	52.017778
std	10.167137	11.012154
min	34.000000	30.000000
25%	46.000000	43.000000
50%	53.000000	52.000000
75%	61.000000	60.000000
max	83.000000	77.000000

Observation:

- Mean of Died patients roughly equal Mean of Survived patients
- Std of Died patients roughly equal std of Survived patients
- It is not making so much clear. i.e age of patients does not effect on patient's status

In [12]:

```
sns.FacetGrid(df,hue = 'Status',size =6).map(sns.distplot,'Age',bins = 20).add_legend()
plt.title("Age Feature")
plt.show()
```

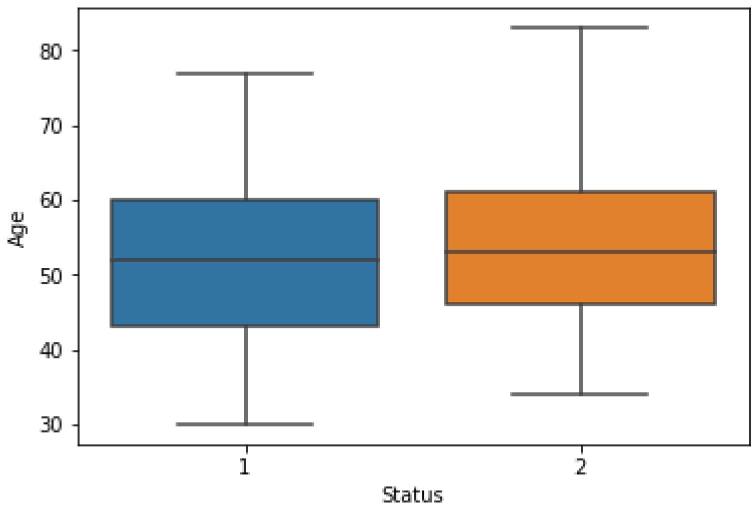


In [13]:

```
# draw the boxplot for age feature:
sns.boxplot(x = 'Status',y = 'Age',data = df)
```

Out[13]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x17b9160e668>
```

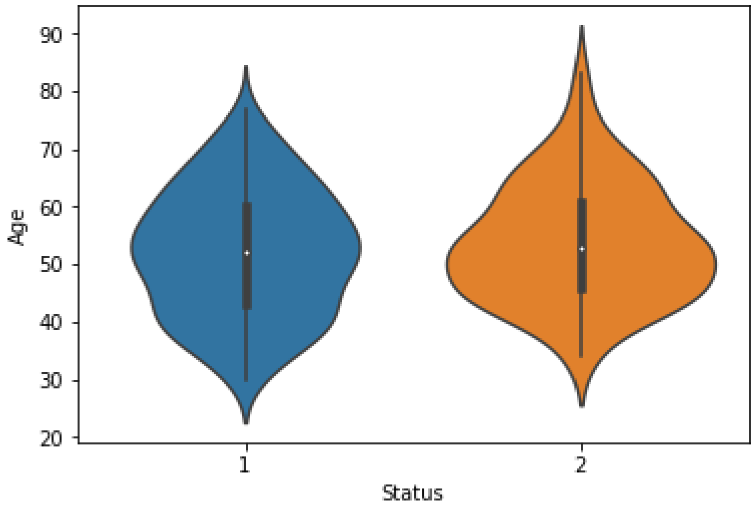


In [14]:

```
#  drwa the violoin plot for age feature:
sns.violinplot(x = 'Status',y = 'Age',data = df,size = 6)
```

Out[14]:

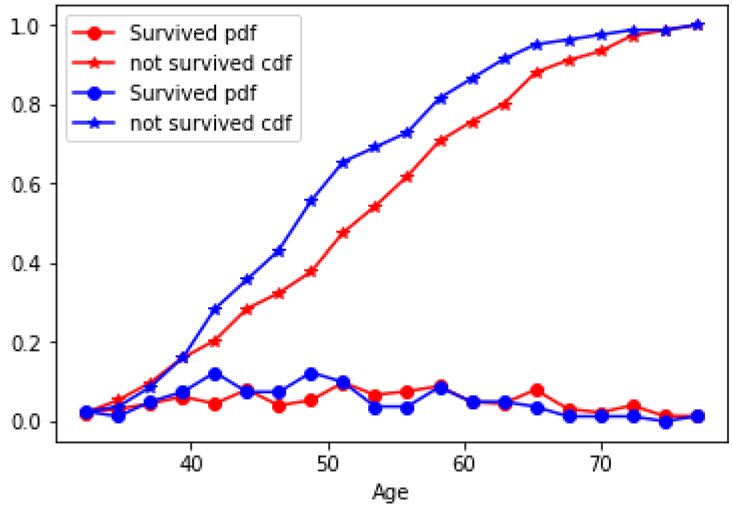
```
<matplotlib.axes._subplots.AxesSubplot at 0x17b917e7400>
```



In [15]:

```
# now plot the pdf and cdf for Age

%matplotlib inline
# PDF & CDF
# compute pdf & cdf for survived

counts, bin_edges = np.histogram(survived['Age'],bins = 20,density = True)
pdf = counts/sum(counts)
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,"ro-",label = "Survived pdf")
plt.plot(bin_edges[1:],cdf,"r*-",label = "not survived cdf")


# compute pdf & cdf for not_survived

counts,bin_edgs = np.histogram(not_survived['Age'],bins= 20,density = True)
pdf = counts/sum(counts)
print(pdf)
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,'bo-',label = "Survived pdf")
plt.plot(bin_edges[1:],cdf,'b*-',label = "not survived cdf")
plt.legend()
plt.xlabel("Age")

plt.show()
```

```
[ 0.02222222  0.03111111  0.04444444  0.06222222  0.04444444  0.08
  0.04
  0.05333333  0.09777778  0.06666667  0.07555556  0.08888889  0.04888889
  0.04444444  0.08        0.03111111  0.02222222  0.04        0.01333333
  0.01333333]
[ 30.    32.35  34.7   37.05  39.4   41.75  44.1   46.45  48.8   51.15
  53.5   55.85  58.2   60.55  62.9   65.25  67.6   69.95  72.3   74.65
 77.  ]
[ 0.02469136  0.01234568  0.04938272  0.07407407  0.12345679  0.07407407
  0.07407407  0.12345679  0.09876543  0.03703704  0.03703704  0.08641975
  0.04938272  0.04938272  0.03703704  0.01234568  0.01234568  0.01234568
  0.          0.01234568]
[ 30.    32.35  34.7   37.05  39.4   41.75  44.1   46.45  48.8   51.15
  53.5   55.85  58.2   60.55  62.9   65.25  67.6   69.95  72.3   74.65
 77.  ]
```



Observation:

- survived and not survuved patients have similar pdf and cdf.ie huge overlap
- Age feature is not relevent to determine status of patients.

2.Year-of-operation Feature:

In [16]:

```
survived_status = survived['Year-of-operation'].describe()
not_survived_status =not_survived['Year-of-operation'].describe()

# create dataframe to store the survived_status and not_survived_status statistics.
df1_year = pd.DataFrame(data={'Survived':survived_status,'Died':not_survived_status})


df1_year
```

Out[16]:

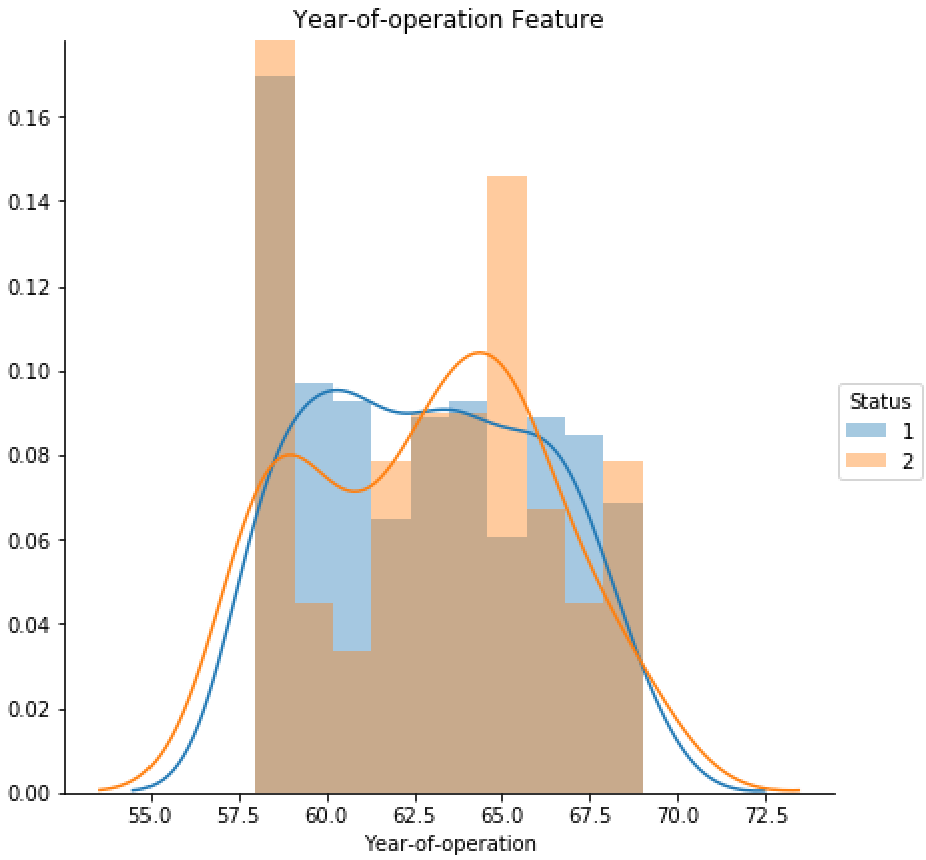
	Died	Survived
count	81.000000	225.000000
mean	62.827160	62.862222
std	3.342118	3.222915
min	58.000000	58.000000
25%	59.000000	60.000000
50%	63.000000	63.000000
75%	65.000000	66.000000
max	69.000000	69.000000

Observation:

- survived and not_survied patients have similar statistics
- It does not make any sense.

In [17]:

```
sns.FacetGrid(df,hue = 'Status',size =6).map(sns.distplot,'Year-of-operation',bins = 10
).add_legend()
plt.title("Year-of-operation Feature")
plt.show()
```



Observation:

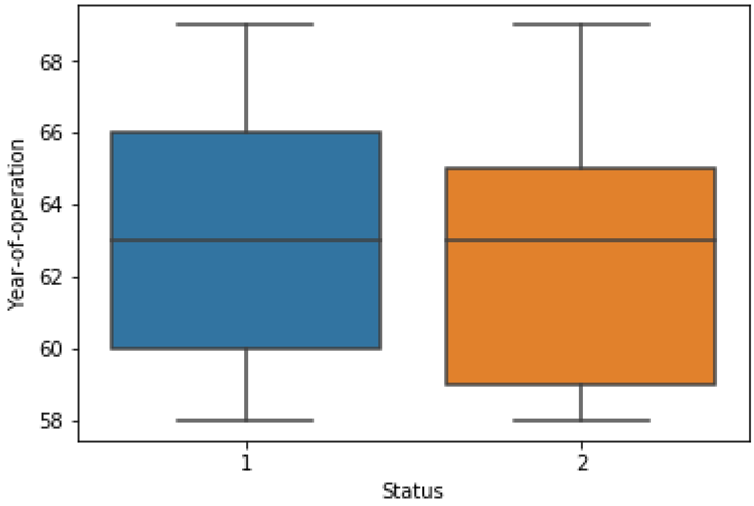
- Year of opeartion of patients does not classified .
- It is not useful feature to determine status of patients.

In [18]:

```
# draw the boxplot for year-of-operation feature:

sns.boxplot(x = 'Status',y = 'Year-of-operation',data = df)
```

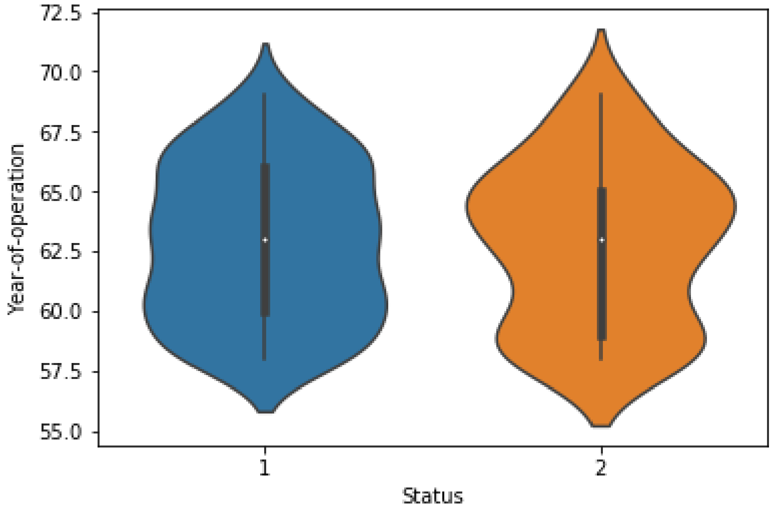
Out[18]:

<matplotlib.axes._subplots.AxesSubplot at 0x17b91891a20>



In [19]:

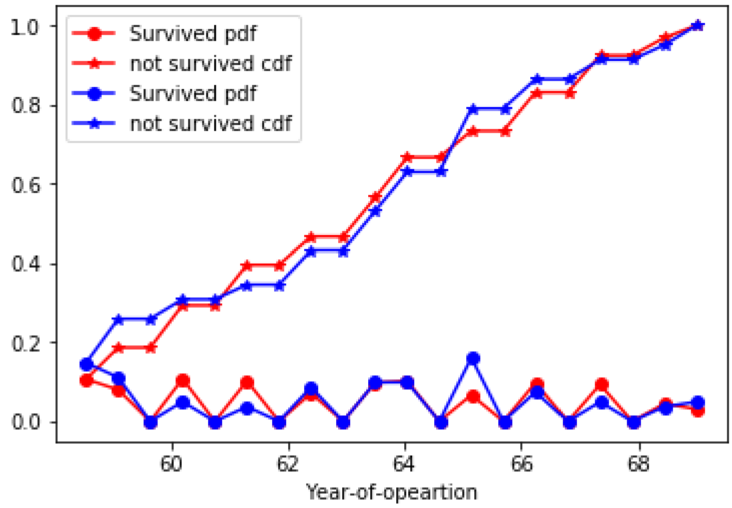
```
# draw th violinplot for year-of-operation feature:

sns.violinplot(x = 'Status',y = 'Year-of-operation',data = df)
plt.show()
```



In [20]:

```
# now calculate pdf & cdf for year-of-operation

%matplotlib inline
# PDF & CDF
# compute pdf & cdf for survived

counts, bin_edges = np.histogram(survived['Year-of-operation'],bins = 20,density = True
)
pdf = counts/sum(counts)
print(pdf)
print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,"ro-",label = "Survived pdf")
plt.plot(bin_edges[1:],cdf,"r*-",label = "not survived cdf")


# compute pdf & cdf for not_survived

counts,bin_edgs = np.histogram(not_survived['Year-of-operation'],bins= 20,density = Tru
e)
pdf = counts/sum(counts)
print(pdf)
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,'bo-',label = "Survived pdf")
plt.plot(bin_edges[1:],cdf,'b*-',label = "not survived cdf")
plt.legend()
plt.xlabel("Year-of-opeartion")

plt.show()
```

```
[ 0.10666667  0.08        0.          0.10666667  0.          0.10222222
  0.          0.07111111  0.          0.09777778  0.10222222  0.
  0.06666667  0.          0.09777778  0.          0.09333333  0.
  0.04444444  0.03111111]
[ 58.    58.55  59.1   59.65  60.2   60.75  61.3   61.85  62.4   62.95
  63.5   64.05  64.6   65.15  65.7   66.25  66.8   67.35  67.9   68.45  6
9.  ]
[ 0.14814815  0.11111111  0.          0.04938272  0.          0.03703704
  0.          0.08641975  0.          0.09876543  0.09876543  0.
  0.16049383  0.          0.07407407  0.          0.04938272  0.
  0.03703704  0.04938272]
[ 58.    58.55  59.1   59.65  60.2   60.75  61.3   61.85  62.4   62.95
  63.5   64.05  64.6   65.15  65.7   66.25  66.8   67.35  67.9   68.45  6
9.  ]
```



Observation:

- survived and not_survived patients have similar plots and vital overlap
- It is not useful feature to determine status of patients.

3. Positive-auxilary-nodes Feature:

In [21]:

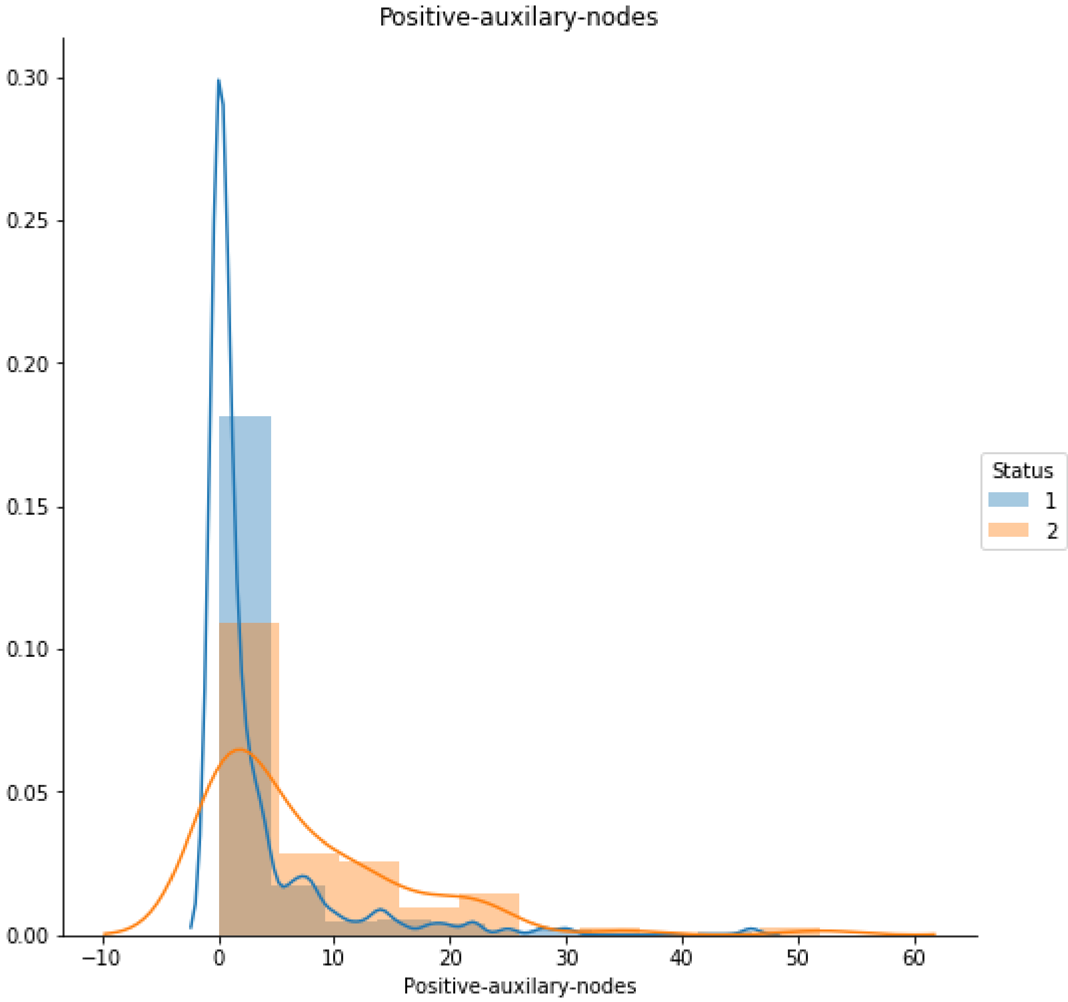
```
survived_status = survived['Positive-auxilary-nodes'].describe()
not_survived_status =not_survived['Positive-auxilary-nodes'].describe()

# create dataframe to store the survived_status and not_survived_status statistics.
df1_nodes = pd.DataFrame(data={'Survived':survived_status,'Died':not_survived_status})


df1_nodes
```

Out[21]:

	Died	Survived
count	81.000000	225.000000
mean	7.456790	2.791111
std	9.185654	5.870318
min	0.000000	0.000000
25%	1.000000	0.000000
50%	4.000000	0.000000
75%	11.000000	3.000000
max	52.000000	46.000000

In [22]:

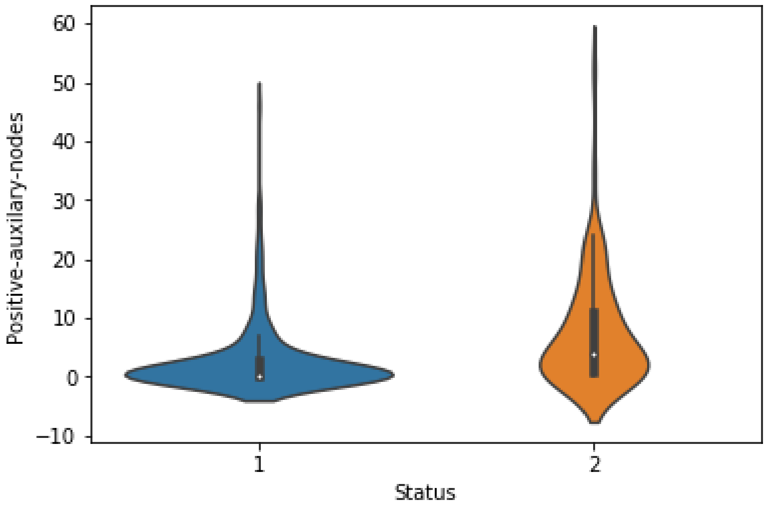
```
sns.FacetGrid(df,hue = 'Status',size =7).map(sns.distplot,'Positive-auxilary-nodes',bin
s = 10).add_legend()
plt.title("Positive-auxilary-nodes")
plt.show()
```



- Most of patients have zero positive auxilary nodes
- If positive nodes is higher then there is less chance for survival
- If there is low or zero nodes then ,it is not surety that patients survived more yeras
- Patients having zero nodes died early and patients having almost 1 survived more.
- Higer positive -auxilary-nodes does not gives guarantee for more survival

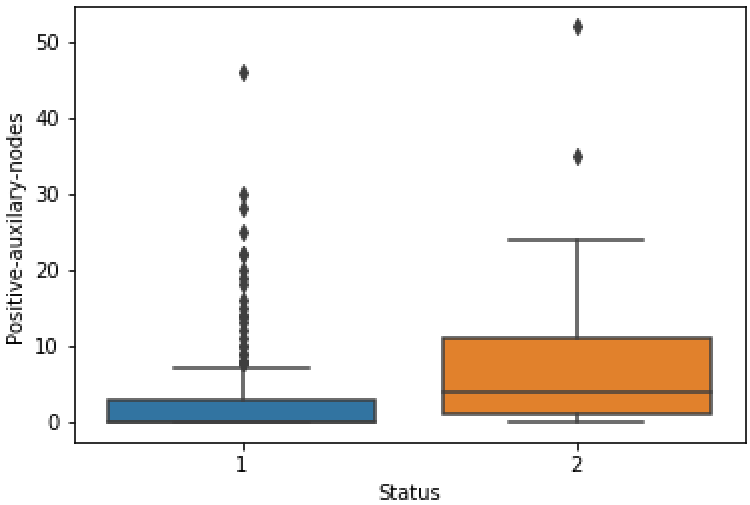
In [23]:

```
# draw the violinplot for Positive-auxilary-nodes

sns.violinplot(x= 'Status',y = 'Positive-auxilary-nodes',data = df)
plt.show()
```



In [24]:

```
# draw the boxplot for Positive-auxilary-nodes

sns.boxplot(x = 'Status',y = 'Positive-auxilary-nodes',data = df)
plt.show()
```

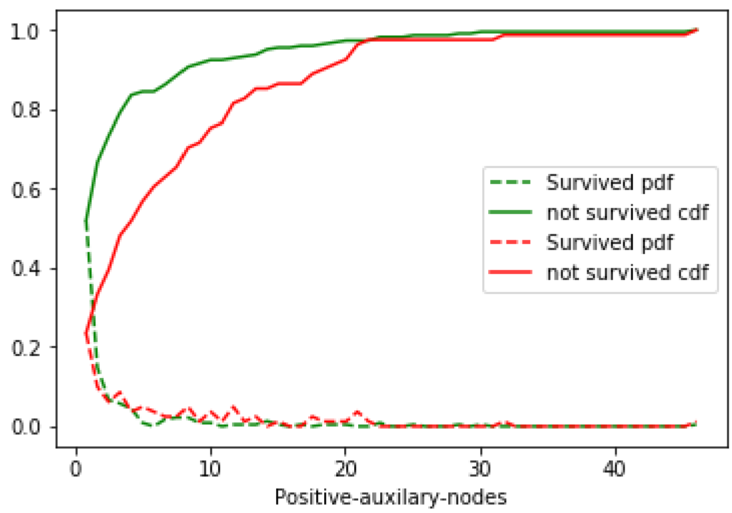


Observation:

- 75% of survived patients and 50% of not_survives patients have positive-auxilary-nodes < 4

In [25]:

```
# now calculate the pdf & cdf for positive-auxilary nodes.

%matplotlib inline
# PDF & CDF
# compute pdf & cdf for survived

counts, bin_edges = np.histogram(survived['Positive-auxilary-nodes'],bins = 55,density
= True)
pdf = counts/sum(counts)
# print(pdf)
# print(bin_edges)
cdf=np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,"--g",label = "Survived pdf")
plt.plot(bin_edges[1:],cdf,"g",label = "not survived cdf")


# compute pdf & cdf for not_survived

counts,bin_edgs = np.histogram(not_survived['Positive-auxilary-nodes'],bins= 55,density
 = True)
pdf = counts/sum(counts)
#print(pdf)
# print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,'--r',label = "Survived pdf")
plt.plot(bin_edges[1:],cdf,'r',label = "not survived cdf")
plt.legend()
plt.xlabel("Positive-auxilary-nodes")

plt.show()
```



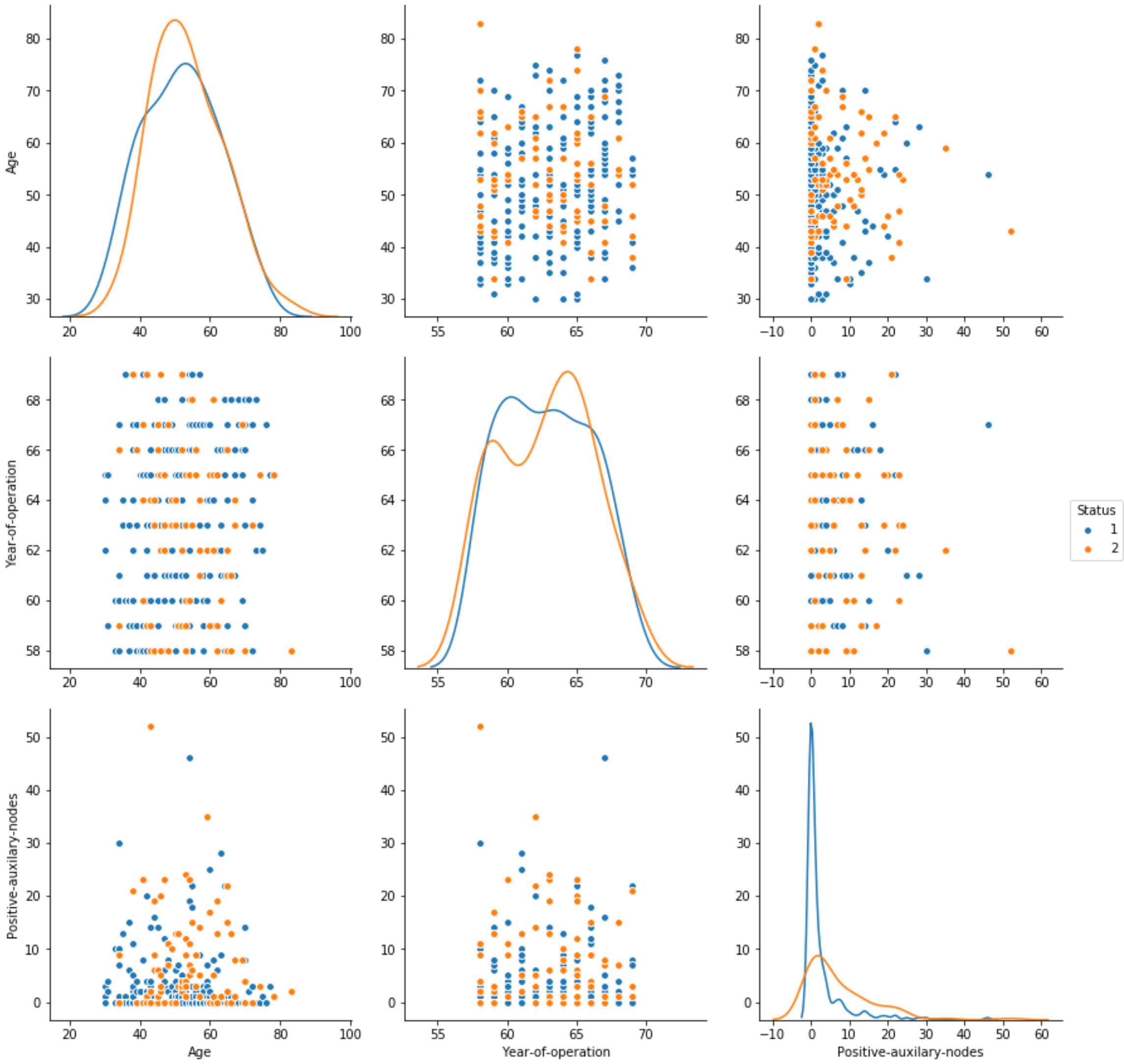
Observation:

- if postive-auxilary nodes is 1 then, then we will misclassify the data roughly 50% of survived and 20% of not_survived
- if positive-auxilary node is 4 the, we will misclassify the data roughly 15% of survived and roughly 50% of not_survived
- if positive-auxilary node is 10 the, we will misclassify the data roughly 10% of survived and roughly 70% of not_survived

Bivariate Analysis:

In [26]:

```
# plot the 3*3 grid for haberman dataset


# sns.set_style("whitegrid")
sns.pairplot(df,hue = 'Status',vars = ['Age','Year-of-operation','Positive-auxilary-nod
es'],diag_kind = 'kde',
           size =4);
plt.show()
```



Observation:

- Year-of-operation does not play any role with with others features.

Obsevation:

- Age does not effect on survival status.
- Year-of -opeartion does not effect on survival status
- Positve -auxilary-nodes afffect on survival status
    - if more numbers of Positve -auxilary-nodes deetcted then patients died within 5 years
    - if less numbers of Positve -auxilary-nodes detected then patients survived for 5 years or more