# Exploratory_Data_Analysis_Assign

January 26, 2021

## 1 objective : Classify whether new patient can survive or not given x

Data-Set Link : https://www.kaggle.com/gilsousa/habermans-survival-data-set

Data-Set Description : 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.

Number of Instances: 306

Number of Attributes: 4 (including the class attribute)

Attribute Information: f1 : Age of patient at time of operation (numerical) f2 : Patient's year of operation (year - 1900, numerical) f3 : Number of positive axillary nodes detected (numerical) f4 : Survival status (class attribute) 1 = the patient survived 5 years or longer 2 = the patient died within 5 year Missing Attribute Values: None

[1]:
```
from google.colab import drive
drive.mount('/content/drive')
```

```
Mounted at /content/drive
```

[2]:
```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
import warnings
warnings.filterwarnings("ignore")

df = pd.read_csv('/content/drive/MyDrive/AAIC/Assignments/4.Exploratory Data␣
 ↪Analysis on Haberman Dataset/haberman.csv')

col = ['Age of patient at time of operation',
       'Patients year of operation',
       'Number of positive axillary nodes detected',
       'survival_status_after_5_years']

df.columns = col
```

## 2 High level statistics of the dataset

[3]:
```
# Number of Points , number of features, number of classes, data-points per␣
 ↪class.
print('Number of Points:',df.shape[0])
print('Number of features:',df.shape[1])
print('Number of classes:',set(df.iloc[:,-1]))
print('Number of data-points per class:\n',df['survival_status_after_5_years'].
 ↪value_counts())
```

```
Number of Points: 305
Number of features: 4
Number of classes: {1, 2}
Number of data-points per class:
 1    224
2     81
Name: survival_status_after_5_years, dtype: int64
```

OBS: It seems like data is imbalanced

[4]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 305 entries, 0 to 304
Data columns (total 4 columns):
 #   Column                                     Non-Null Count  Dtype
---  ------                                     --------------  -----
 0   Age of patient at time of operation        305 non-null    int64
 1   Patients year of operation                 305 non-null    int64
 2   Number of positive axillary nodes detected 305 non-null    int64
 3   survival_status_after_5_years              305 non-null    int64
dtypes: int64(4)
memory usage: 9.7 KB
```

[5]:
```
df.describe()
```

[5]:
```
       Age of patient at time of operation  ...  survival_status_after_5_years
count                           305.000000  ...                     305.000000
mean                             52.531148  ...                       1.265574
std                              10.744024  ...                       0.442364
min                              30.000000  ...                       1.000000
25%                              44.000000  ...                       1.000000
50%                              52.000000  ...                       1.000000
75%                              61.000000  ...                       2.000000
max                              83.000000  ...                       2.000000

[8 rows x 4 columns]
```

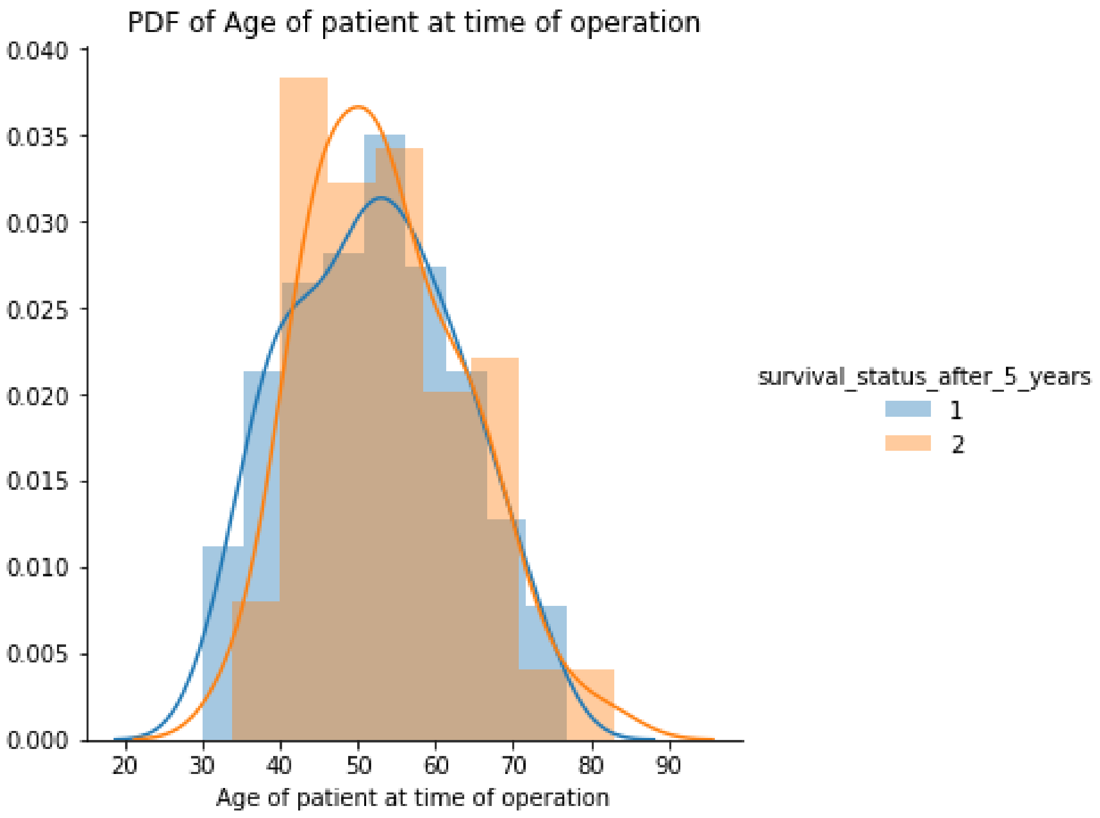
## 3 Perform Univaraite analysis(PDF, CDF, Boxplot, Voilin plots) to understand which features are useful towards classification.

[6]:
```
df.columns
```

[6]:
```
Index(['Age of patient at time of operation', 'Patients year of operation',
       'Number of positive axillary nodes detected',
       'survival_status_after_5_years'],
      dtype='object')
```

[7]:
```
x = ['Age of patient at time of operation',
     'Patients year of operation',
     'Number of positive axillary nodes detected']

for col in x:
    sns.FacetGrid(df, hue="survival_status_after_5_years", height=5) \
       .map(sns.distplot, col) \
       .add_legend();
    plt.title('PDF of {0}'.format(col))
    plt.show();
    print('*'*50)
```



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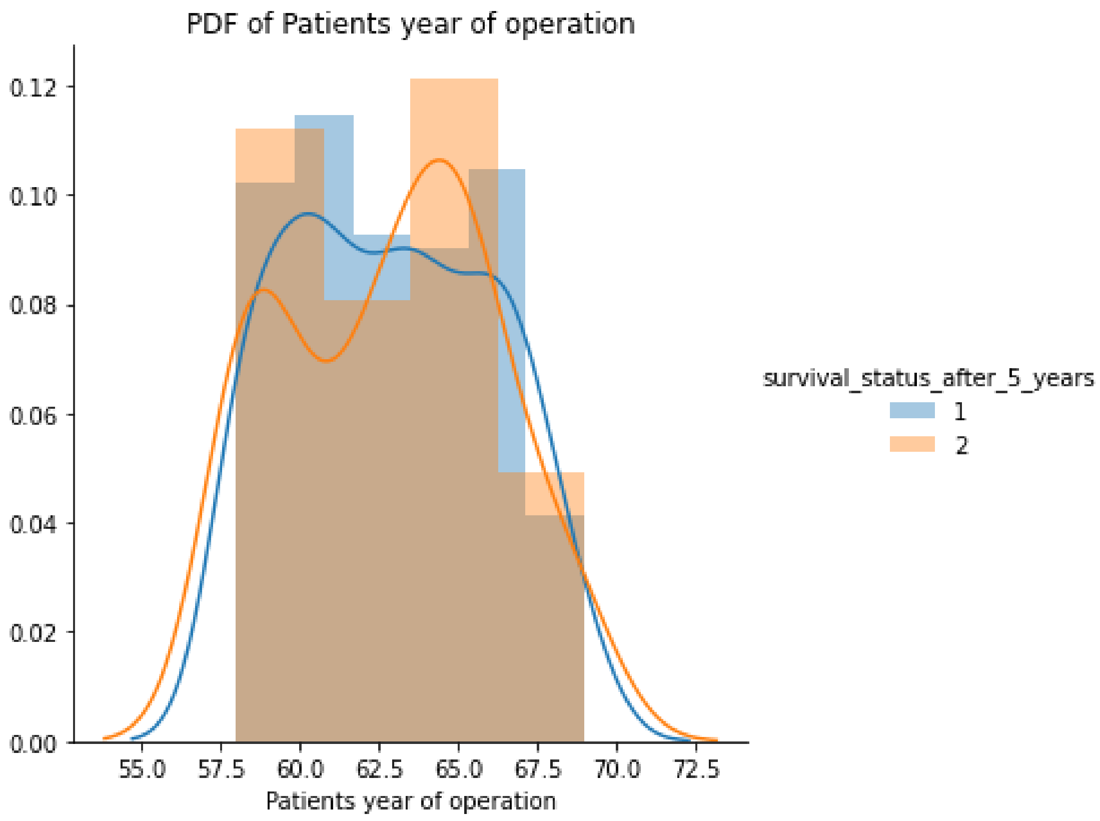
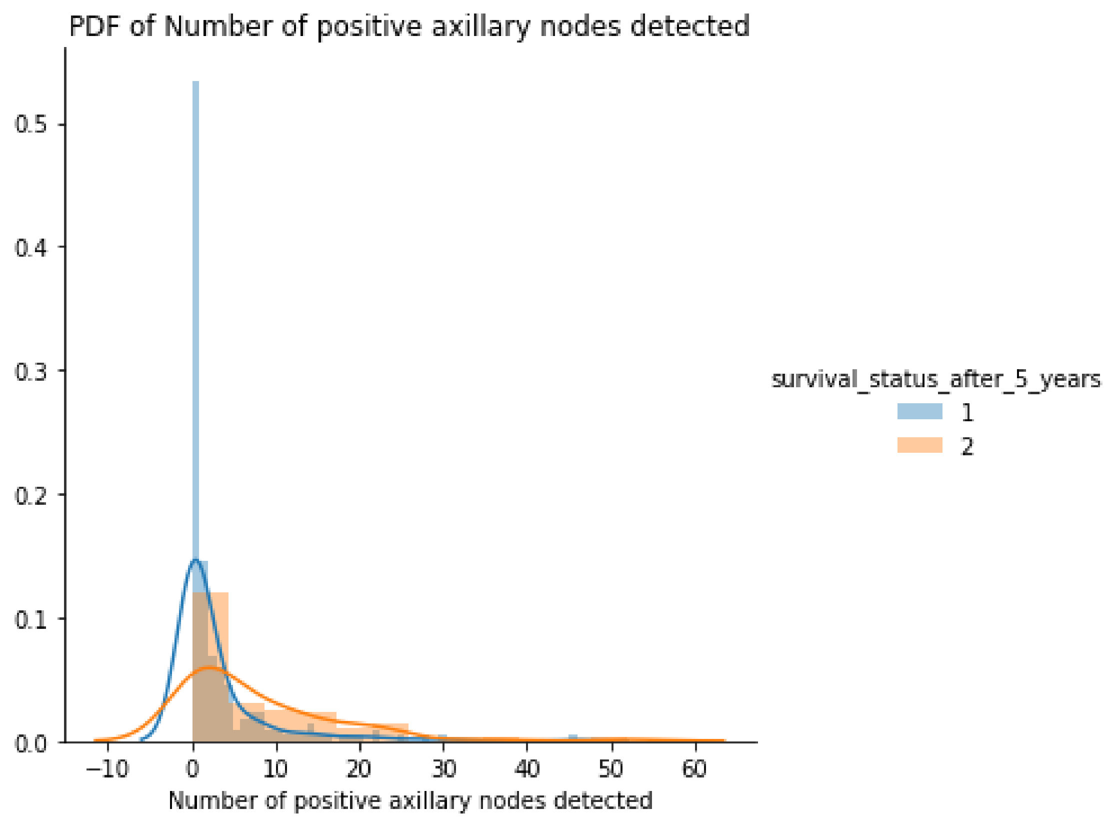

PDF of Patients year of operation
0.12
0.10
0.08
0.06
0.04
0.02
0.00
55.0
57.5
60.0
62.5
65.0
67.5
70.0
72.5
Patients year of operation
survival_status_after_5_years
1
2

**************************************************



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OBS: Here all the features are overlapping with the class labels, i.e the pdf plots of each feature w.r.t class labels are found to overlap their distribution, But for the feature " Number of positive axillary nodes detected " , after the count 5 there is a small gap b/w the distributions.

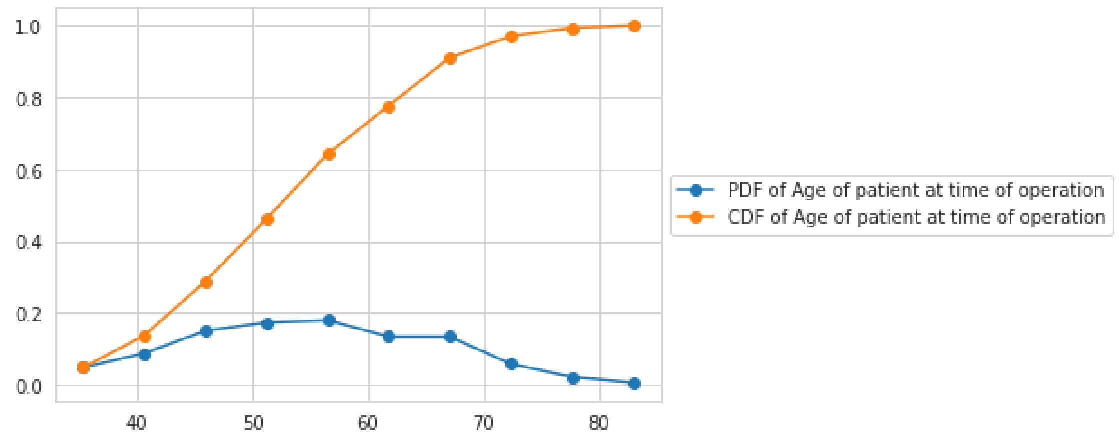
[15]:
```
df.columns
```

[15]:
```
Index(['Age of patient at time of operation', 'Patients year of operation',
       'Number of positive axillary nodes detected',
       'survival_status_after_5_years'],
      dtype='object')
```

[55]:
```
counts, bin_edges = np.histogram(df['Age of patient at time of operation'],␣
 ↪bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,'-o',label='PDF of Age of patient at time of␣
 ↪operation')
```

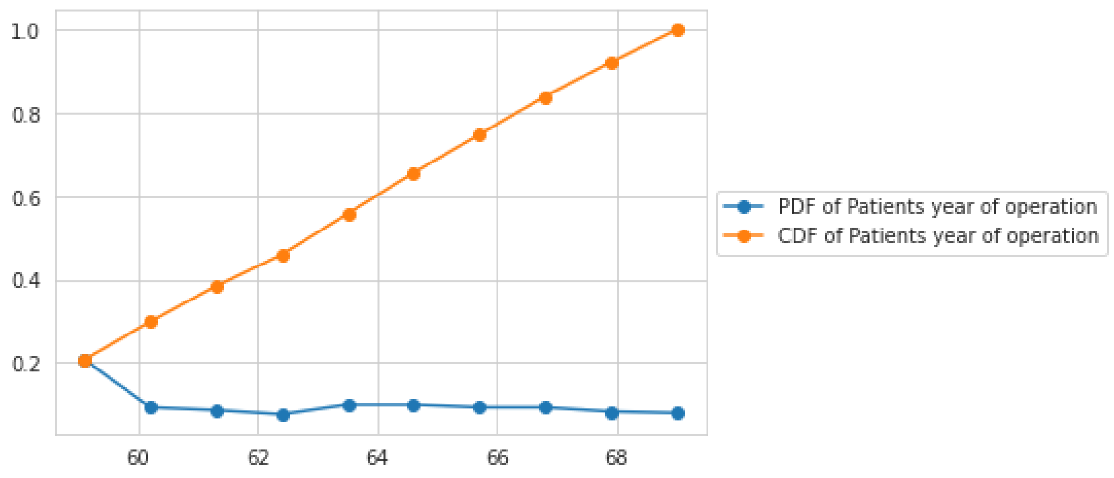
```
plt.plot(bin_edges[1:], cdf,'-o',label='CDF of Age of patient at time of␣
 ↪operation')
plt.legend(loc='center left',bbox_to_anchor=(1, 0.5))
plt.show()
```

```
[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. ]
```



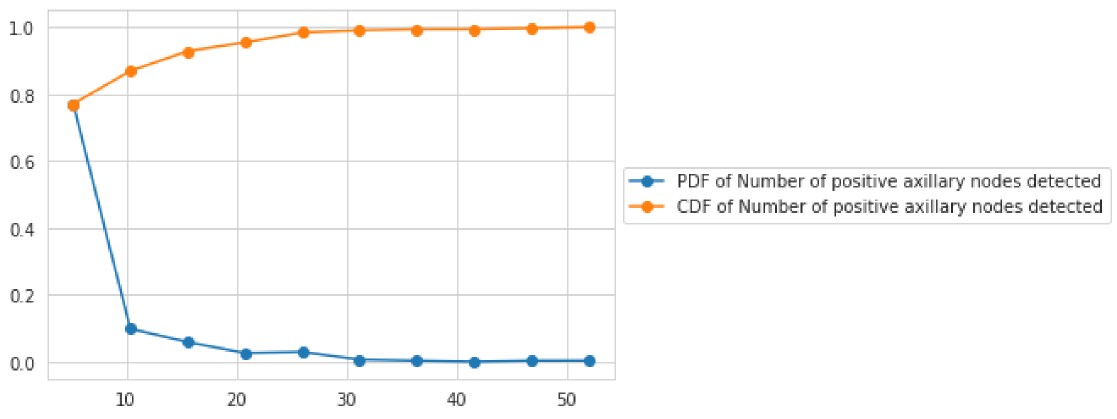
[56]:
```
counts, bin_edges = np.histogram(df['Patients year of operation'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,'-o',label='PDF of Patients year of operation')
plt.plot(bin_edges[1:], cdf,'-o',label='CDF of Patients year of operation')
plt.legend(loc='center left',bbox_to_anchor=(1, 0.5))
plt.show()
```

```
[0.20655738 0.09180328 0.0852459  0.07540984 0.09836066 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. ]
```

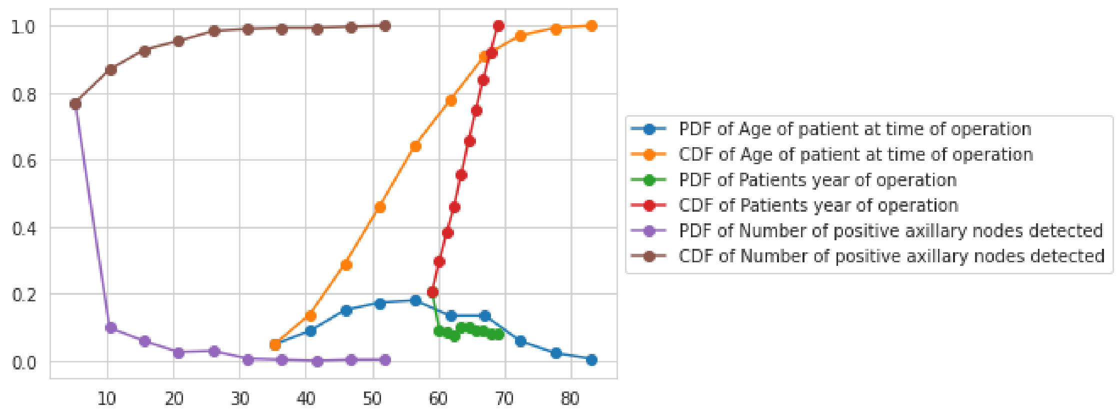


[57]:
```
counts, bin_edges = np.histogram(df['Number of positive axillary nodes␣
 ↪detected'], bins=10,
                                   density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,'-o',label='PDF of Number of positive axillary nodes␣
 ↪detected')
plt.plot(bin_edges[1:], cdf,'-o',label='CDF of Number of positive axillary␣
 ↪nodes detected')
plt.legend(loc='center left',bbox_to_anchor=(1, 0.5))
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. ]
```



[58]:
```
counts, bin_edges = np.histogram(df['Age of patient at time of operation'],␣
↪bins=10,
                                 density = True)
pdf = counts/(sum(counts))
#print(pdf);
#print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,'-o',label='PDF of Age of patient at time of␣
↪operation')
plt.plot(bin_edges[1:], cdf,'-o',label='CDF of Age of patient at time of␣
↪operation')

counts, bin_edges = np.histogram(df['Patients year of operation'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
#print(pdf);
#print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,'-o',label='PDF of Patients year of operation')
plt.plot(bin_edges[1:], cdf,'-o',label='CDF of Patients year of operation')

counts, bin_edges = np.histogram(df['Number of positive axillary nodes␣
↪detected'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
#print(pdf);
#print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf,'-o',label='PDF of Number of positive axillary nodes␣
↪detected')
plt.plot(bin_edges[1:], cdf,'-o',label='CDF of Number of positive axillary␣
↪nodes detected')
plt.legend(loc='center left',bbox_to_anchor=(1, 0.5))
plt.show();
```



[23]:
```
df.columns
```

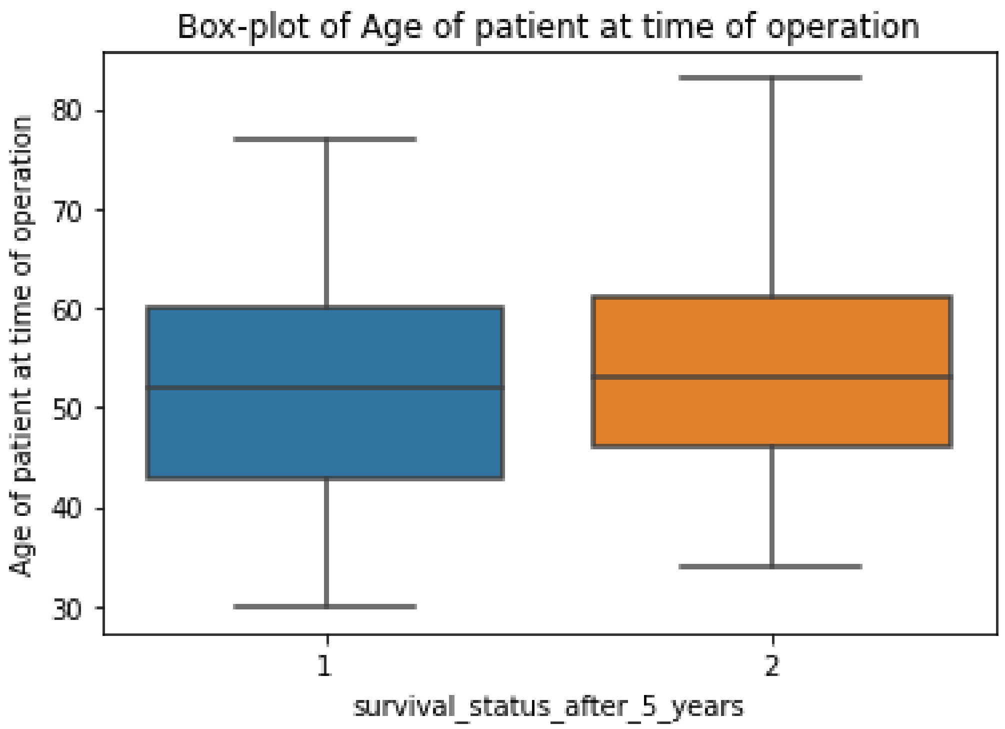
[23]:
```
Index(['Age of patient at time of operation', 'Patients year of operation',
       'Number of positive axillary nodes detected',
       'survival_status_after_5_years'],
      dtype='object')
```

[41]:
```
from prettytable import PrettyTable
t = PrettyTable(['Features','Medians', 'Quantiles' , '90th Percentiles' ,␣
 ↪'Median Absolute Deviation'])
#print(clf.best_estimator_,'\n',auc_test)
t.add_row(['Age of patient at time of operation',\
          (np.median(df['Age of patient at time of operation'])),\
           (np.percentile(df['Age of patient at time of operation'],np.
 ↪arange(0, 100, 25))),\
           (np.percentile(df['Age of patient at time of operation'],90)),
           (robust.mad(df['Age of patient at time of operation']))]
          )
t.add_row(['Patients year of operation',\
           (np.median(df['Patients year of operation'])),\
           (np.percentile(df['Patients year of operation'],np.arange(0, 100,␣
 ↪25))),\
           (np.percentile(df['Patients year of operation'],90)),\
           (robust.mad(df['Patients year of operation']))
           ])
t.add_row(['Number of positive axillary nodes detected',\
           (np.median(df['Number of positive axillary nodes detected'])),\
           (np.percentile(df['Number of positive axillary nodes detected'], np.
 ↪arange(0, 100, 25))),\
           (np.percentile(df['Number of positive axillary nodes detected'],␣
 ↪90)),\
           (robust.mad(df['Number of positive axillary nodes detected']))])
print(t)
```

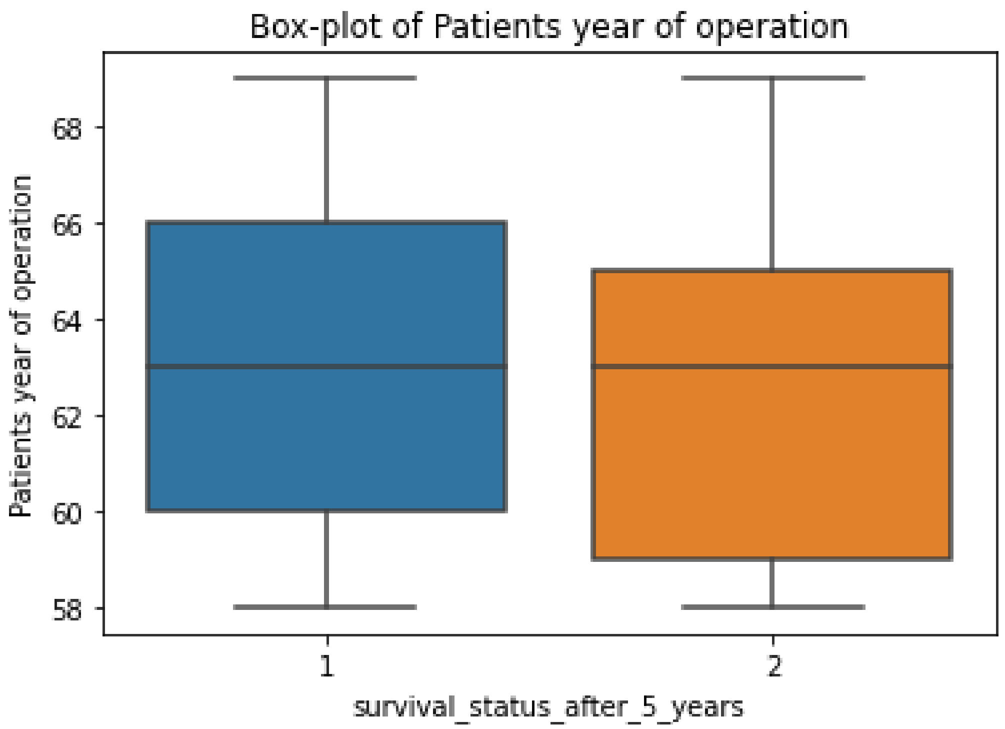
```
+-------------------------------------------+---------+------------------+----
--------------+--------------------------+
|                  Features                 | Medians |     Quantiles    |
90th Percentiles | Median Absolute Deviation |
+-------------------------------------------+---------+------------------+----
--------------+--------------------------+
|    Age of patient at time of operation    |   52.0  | [30. 44. 52. 61.] |
67.0        |      11.860817748044816    |
|         Patients year of operation        |   63.0  | [58. 60. 63. 66.] |
67.0        |      4.447806655516806     |
| Number of positive axillary nodes detected |   1.0   |   [0. 0. 1. 4.]   |
13.0        |      1.482602218505602     |
+-------------------------------------------+---------+------------------+----
--------------+--------------------------+
```

[ ]:

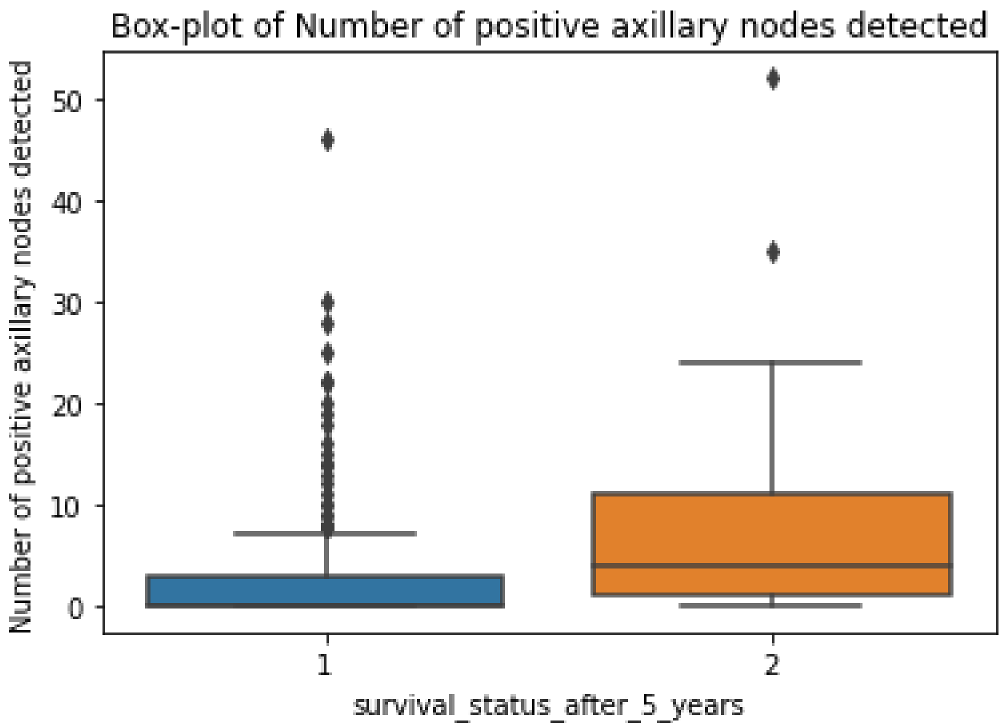
[8]:
```
for col in x:
    sns.boxplot(x='survival_status_after_5_years',y = col, data=df)
    plt.title('Box-plot of {0}'.format(col))
    plt.show()
    print('*'*50)
```



```
**************************************************
```


Box-plot of Patients year of operation
Patients year of operation
58
60
62
64
66
68
1
2
survival_status_after_5_years

**************************************************


Box-plot of Number of positive axillary nodes detected
Number of positive axillary nodes detected
0
10
20
30
40
50
1
2
survival_status_after_5_years

```
**************************************************
```

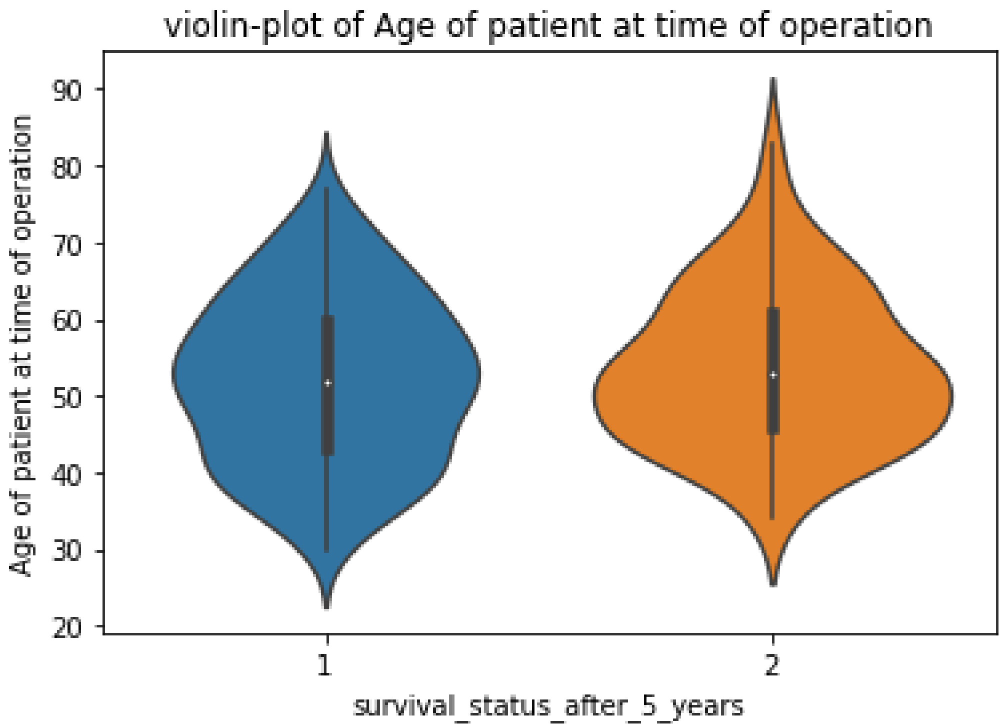
OBS: we can observe some difference in the box-plot curve for the feature " Number of positive axillary nodes detected ". I think this feature can be used in classification models

[ ]:

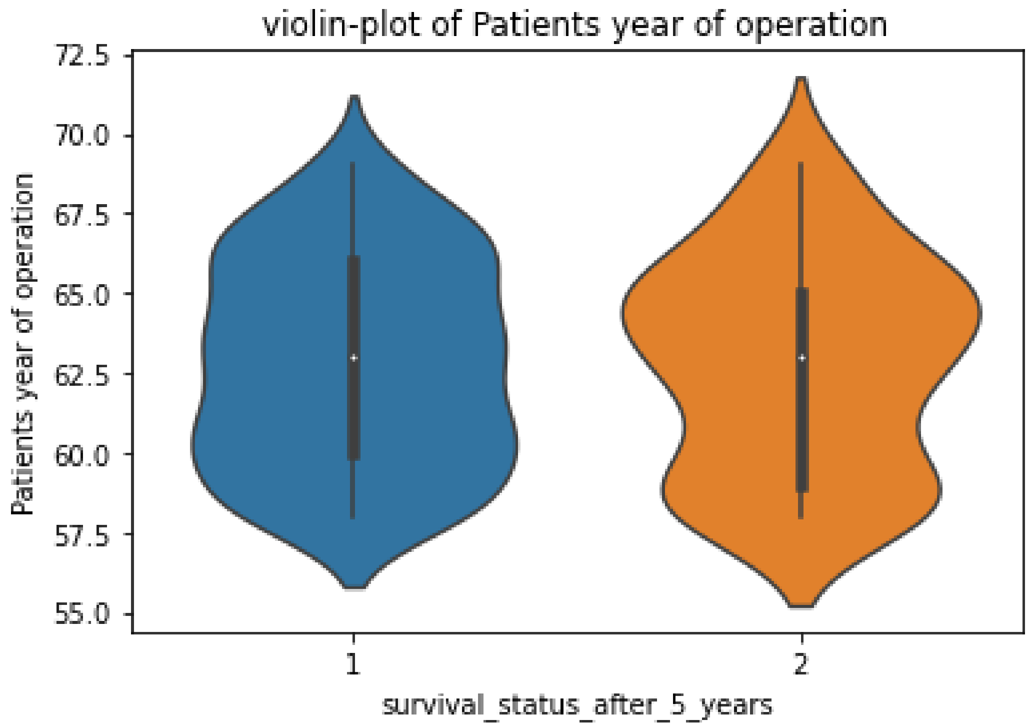
```

```

[9]:

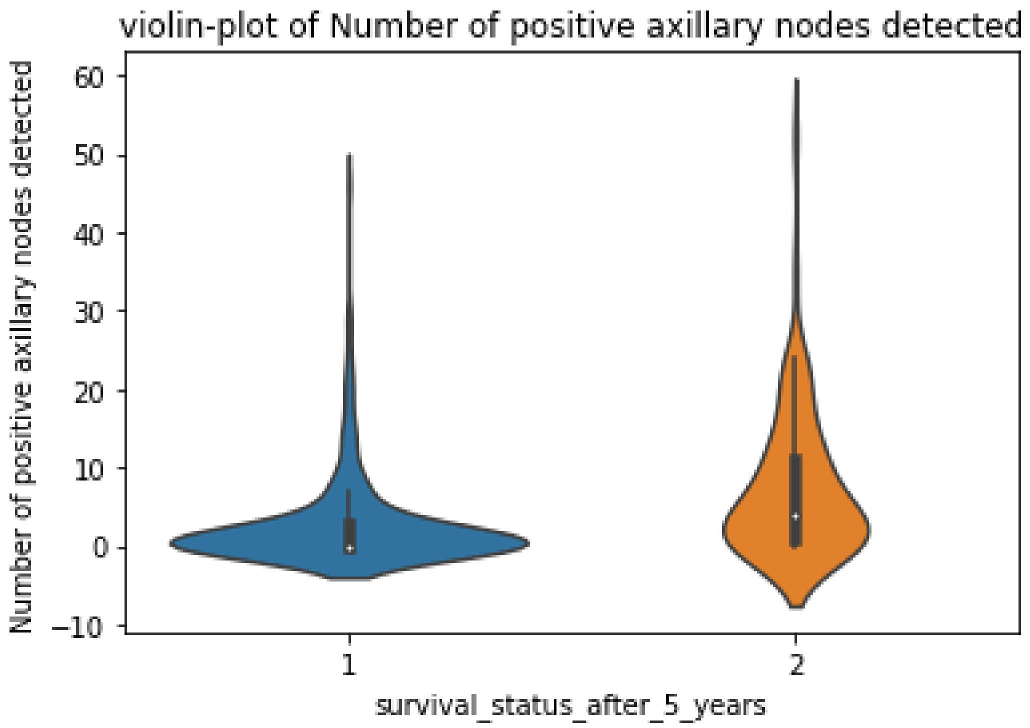
```
for col in x:
    sns.violinplot(x='survival_status_after_5_years',y = col, data=df)
    plt.title('violin-plot of {0}'.format(col))
    plt.show()
    print('*'*50)
```



```
**************************************************
```


violin-plot of Patients year of operation
Patients year of operation
72.5
70.0
67.5
65.0
62.5
60.0
57.5
55.0
1
2
survival_status_after_5_years

**************************************************


violin-plot of Number of positive axillary nodes detected
Number of positive axillary nodes detected
60
50
40
30
20
10
0
−10
1
2
survival_status_after_5_years

**************************************************

[ ]:

```
```

## 4 Perform Bi-variate analysis (scatter plots, pair-plots) to see if combinations of features are useful in classfication.

[10]:

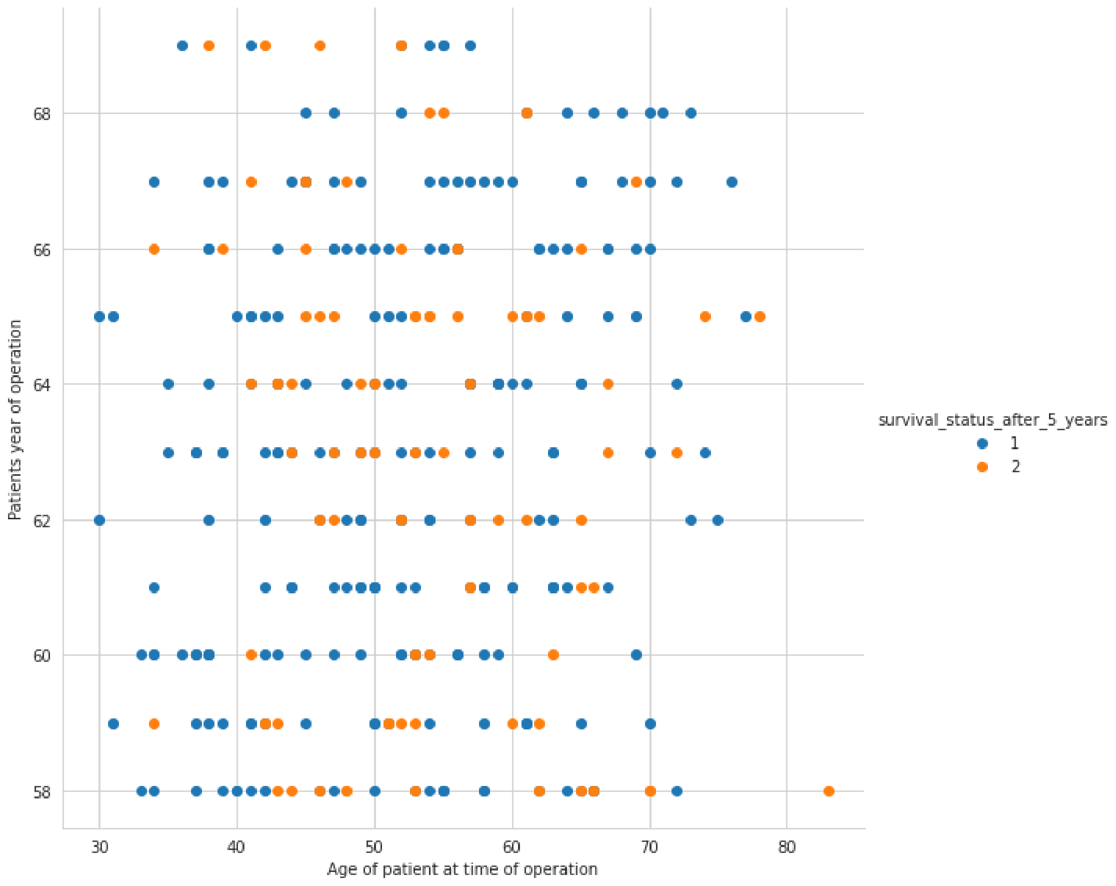
```
df.columns
```

[10]:

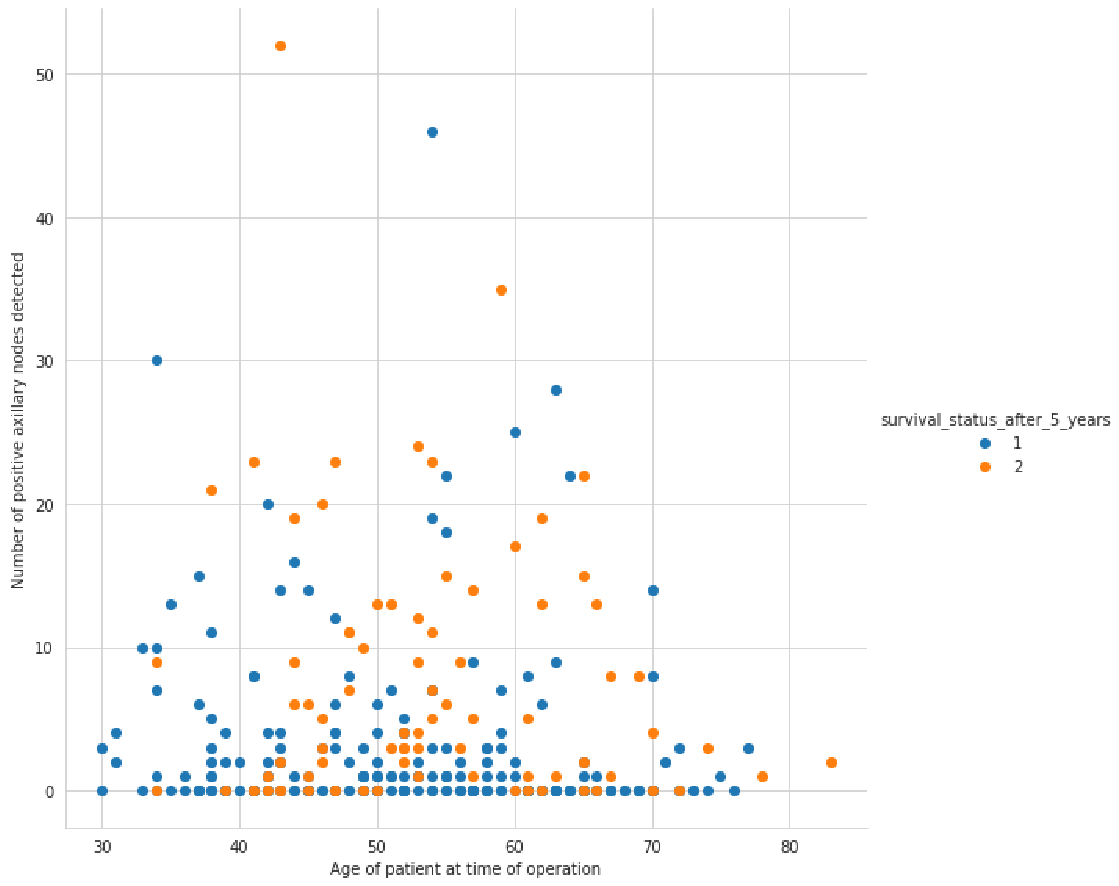
```
Index(['Age of patient at time of operation', 'Patients year of operation',
       'Number of positive axillary nodes detected',
       'survival_status_after_5_years'],
      dtype='object')
```

[11]:

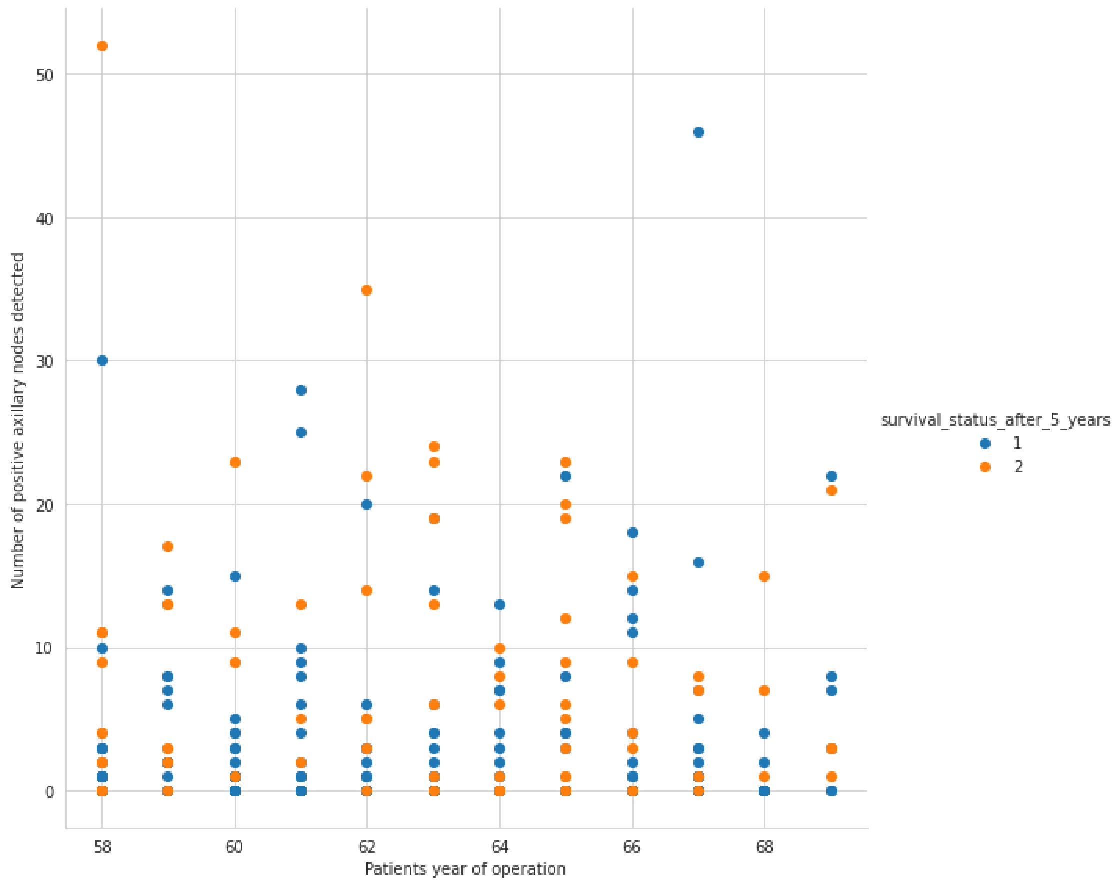
```
sns.set_style("whitegrid");
sns.FacetGrid(df, hue="survival_status_after_5_years", height=8) \
   .map(plt.scatter, 'Age of patient at time of operation', 'Patients year of␣
 ↪operation') \
   .add_legend();

plt.show();
```



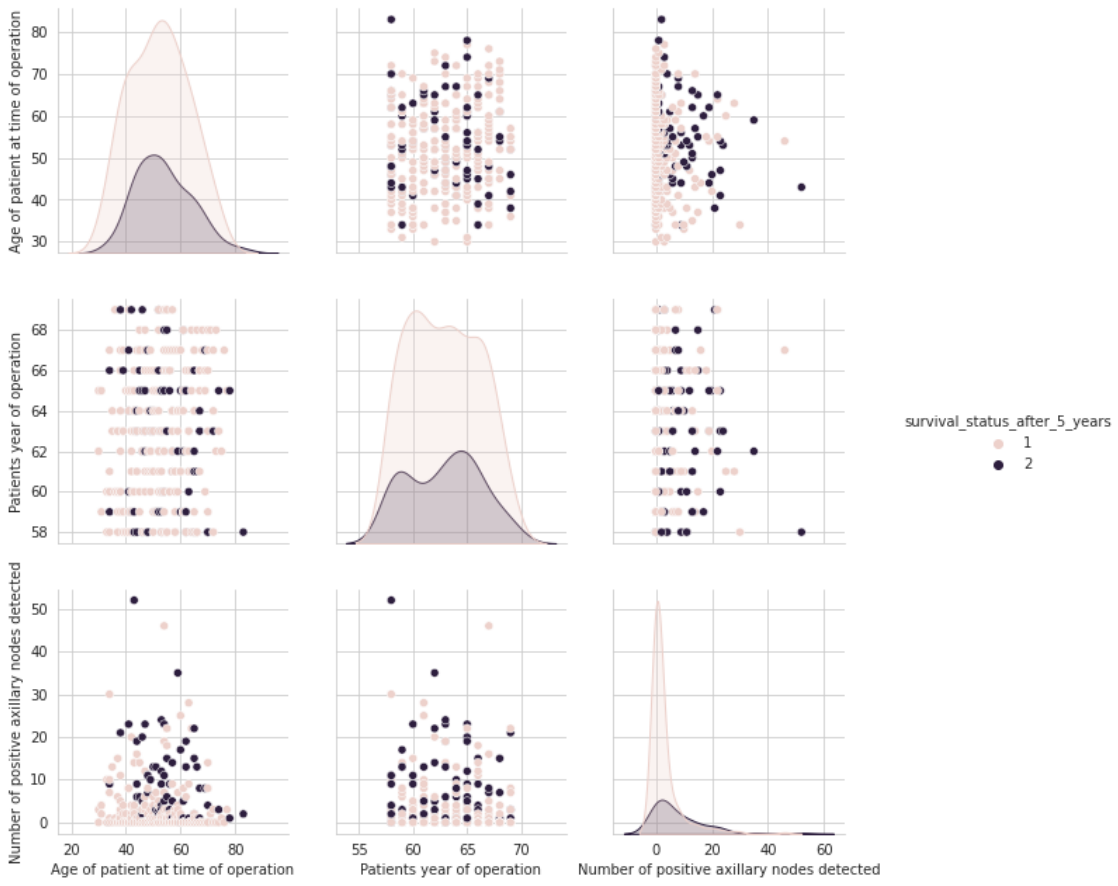
[12]:
```
sns.set_style("whitegrid");
sns.FacetGrid(df, hue="survival_status_after_5_years", height=8) \
   .map(plt.scatter, 'Age of patient at time of operation', 'Number of positive␣
 ↪axillary nodes detected') \
   .add_legend();
plt.show();
```



```
[13]: sns.set_style("whitegrid");
      sns.FacetGrid(df, hue="survival_status_after_5_years", height=8) \
         .map(plt.scatter, 'Patients year of operation','Number of positive axillary␣
       ↪nodes detected') \
         .add_legend();
      plt.show();
```



[14]:
```
sns.set_style("whitegrid");
sns.pairplot(df, hue="survival_status_after_5_years", height=3);
plt.show()
```



OBS: There is an overlap of data points in this scatter-plots. We cannot find a line/curve which divides this overlap until unless projected into 3-d or n-d.

```
[ ]:
```

```
[ ]:
```

```
[ ]:
```

```
[ ]:
```