EDA on Haberman Dataset

The dataset is of shape (306, 4)

Out of 4 columns, first 3 columns are independent features

The attributes are as follows:

```
    Column 1 - Age of the patient diagnosed of Breast Cancer
    Column 2 - The year of operation
    Column 3 - Number of positive auxilary nodes detected
    Column 4 - Survival Status (Class based)
                -- 1 -> Patient survived for 5 or more than 5 years
                -- 2 -> Patient died within 5 years
```

Objective:

```
    - Explore the dataset and perform Univariate, Bi-variate analysis.
    - Derive usefull information about the data which can be used in classification.
    - Write down your observations.
```

1. Setup

In [1]:

```python
# import packages

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

In [2]:

```
# read the csv file using pandas

df = pd.read_csv(
    "haberman.csv", header = None,
    names = ['age', 'year_of_operation', 'positive_axil_nodes', 'survival_status']
)
df.head()
```

Out[2]:

	age	year_of_operation	positive_axil_nodes	survival_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

2. Data Preparation

In [3]:

```
# let's see if there are any missing values
df.isnull().values.any()
```

Out[3]:

```
False
```

In [4]:

```
df['age'].values
```

Out[4]:

```
array([30, 30, 30, 31, 31, 33, 33, 34, 34, 34, 34, 34, 34, 34, 35, 35, 36,
       36, 37, 37, 37, 37, 37, 37, 38, 38, 38, 38, 38, 38, 38, 38, 38, 38,
       39, 39, 39, 39, 39, 39, 40, 40, 40, 41, 41, 41, 41, 41, 41, 41, 41,
       41, 41, 42, 42, 42, 42, 42, 42, 42, 42, 42, 43, 43, 43, 43, 43, 43,
       43, 43, 43, 43, 43, 44, 44, 44, 44, 44, 44, 44, 45, 45, 45, 45, 45,
       45, 45, 45, 45, 46, 46, 46, 46, 46, 46, 46, 47, 47, 47, 47, 47, 47,
       47, 47, 47, 47, 47, 48, 48, 48, 48, 48, 48, 48, 49, 49, 49, 49, 49,
       49, 49, 49, 49, 49, 50, 50, 50, 50, 50, 50, 50, 50, 50, 50, 50, 50,
       51, 51, 51, 51, 51, 51, 52, 52, 52, 52, 52, 52, 52, 52, 52, 52, 52,
       52, 52, 52, 53, 53, 53, 53, 53, 53, 53, 53, 53, 53, 53, 54, 54, 54,
       54, 54, 54, 54, 54, 54, 54, 54, 54, 54, 55, 55, 55, 55, 55, 55, 55,
       55, 55, 55, 56, 56, 56, 56, 56, 56, 56, 57, 57, 57, 57, 57, 57, 57,
       57, 57, 57, 57, 58, 58, 58, 58, 58, 58, 58, 59, 59, 59, 59, 59, 59,
       59, 59, 60, 60, 60, 60, 60, 60, 61, 61, 61, 61, 61, 61, 61, 61, 61,
       62, 62, 62, 62, 62, 62, 62, 63, 63, 63, 63, 63, 63, 63, 63, 64, 64,
       64, 64, 64, 65, 65, 65, 65, 65, 65, 65, 65, 65, 65, 66, 66, 66, 66,
       66, 67, 67, 67, 67, 67, 67, 68, 68, 69, 69, 69, 69, 70, 70, 70, 70,
       70, 70, 70, 71, 72, 72, 72, 72, 73, 73, 74, 74, 75, 76, 77, 78, 8
3], dtype=int64)
```

In [5]:

```
# check if all the data in the rows are numerical
df_temp = df.applymap(lambda x: isinstance(x, int))
df_temp.all()
```

Out[5]:

```
age                    True
year_of_operation      True
positive_axil_nodes    True
survival_status        True
dtype: bool
```

In [6]:

```
# let's change the name of target column name and it's values for simplicity
df = df.rename(columns={'survival_status': 'survival_after_five_years'})
df['survival_after_five_years'] = df['survival_after_five_years'].apply(lambda x: "aliv
e" if x == 1 else "not_alive")
df.head(10)
```

Out[6]:

	age	year_of_operation	positive_axil_nodes	survival_after_five_years
0	30	64	1	alive
1	30	62	3	alive
2	30	65	0	alive
3	31	59	2	alive
4	31	65	4	alive
5	33	58	10	alive
6	33	60	0	alive
7	34	59	0	not_alive
8	34	66	9	not_alive
9	34	58	30	alive

In [7]:

```
# changing the last column datatype into category
df['survival_after_five_years'] = df['survival_after_five_years'].astype('category')
df['survival_after_five_years'].dtype
```

Out[7]:

```
category
```

Observations

```
- There are no missing values in the dataset
- All the data points are integers
- Converted last column datatype into category
```

3. High level statistics of the dataset

In [8]:

```
print("Total data points:", df.shape[0])
print("Total features in the data:", df.shape[-1]-1) #last column being a dependent var
iable (outcome)
df_counts = df['survival_after_five_years'].value_counts()
print("There are", len(df_counts), "classes in this dataset")
print('***********************')
print("The counts of each classes are:")
# for col, val in df_counts.items():
#         print(col, '-', val)
print(df_counts)
print('***********************')
```

```
Total data points: 306
Total features in the data: 3
There are 2 classes in this dataset
***********************
The counts of each classes are:
alive        225
not_alive     81
Name: survival_after_five_years, dtype: int64
***********************
```

In [9]:

```
df_survived = df[ df['survival_after_five_years'] == "alive" ]
df_not_survived = df[ df['survival_after_five_years'] == "not_alive" ]
```

In [10]:

```
# high level statistics of people who survived
df_survived.describe()
```

Out[10]:

	age	year_of_operation	positive_axil_nodes
count	225.000000	225.000000	225.000000
mean	52.017778	62.862222	2.791111
std	11.012154	3.222915	5.870318
min	30.000000	58.000000	0.000000
25%	43.000000	60.000000	0.000000
50%	52.000000	63.000000	0.000000
75%	60.000000	66.000000	3.000000
max	77.000000	69.000000	46.000000

In [11]:

```
# high level statistics of people who did not survive
df_not_survived.describe()
```

Out[11]:

	age	year_of_operation	positive_axil_nodes
count	81.000000	81.000000	81.000000
mean	53.679012	62.827160	7.456790
std	10.167137	3.342118	9.185654
min	34.000000	58.000000	0.000000
25%	46.000000	59.000000	1.000000
50%	53.000000	63.000000	4.000000
75%	61.000000	65.000000	11.000000
max	83.000000	69.000000	52.000000

Observations

```
        - There are a total of 306 data points in the dataset.
        - There are three independent variables and one dependent variable.
        - The dataset is imbalanced.
        - Seperated data into two dataframes based on their survival to find out the
    ir respective high level information
          seperately, which is as follows:
              1) The range of age of a person who survived in the given data is from
     30 to 77 whereas for a person who
                 did not survive had an age range of 34 to 83.
              2) 75% of people who survived had a maximum of 3 positive axillary nod
    es whereas 75% of people who did not
                 survive had a maximum of 11 positive auxillary nodes.
              3) The mean of positive nodes of people who survived is 2.79 and that
     for people who did not survive is
                 7.45 which is higher. But there are instances where people did not
     survive with 0 positive nodes (min 0).
```

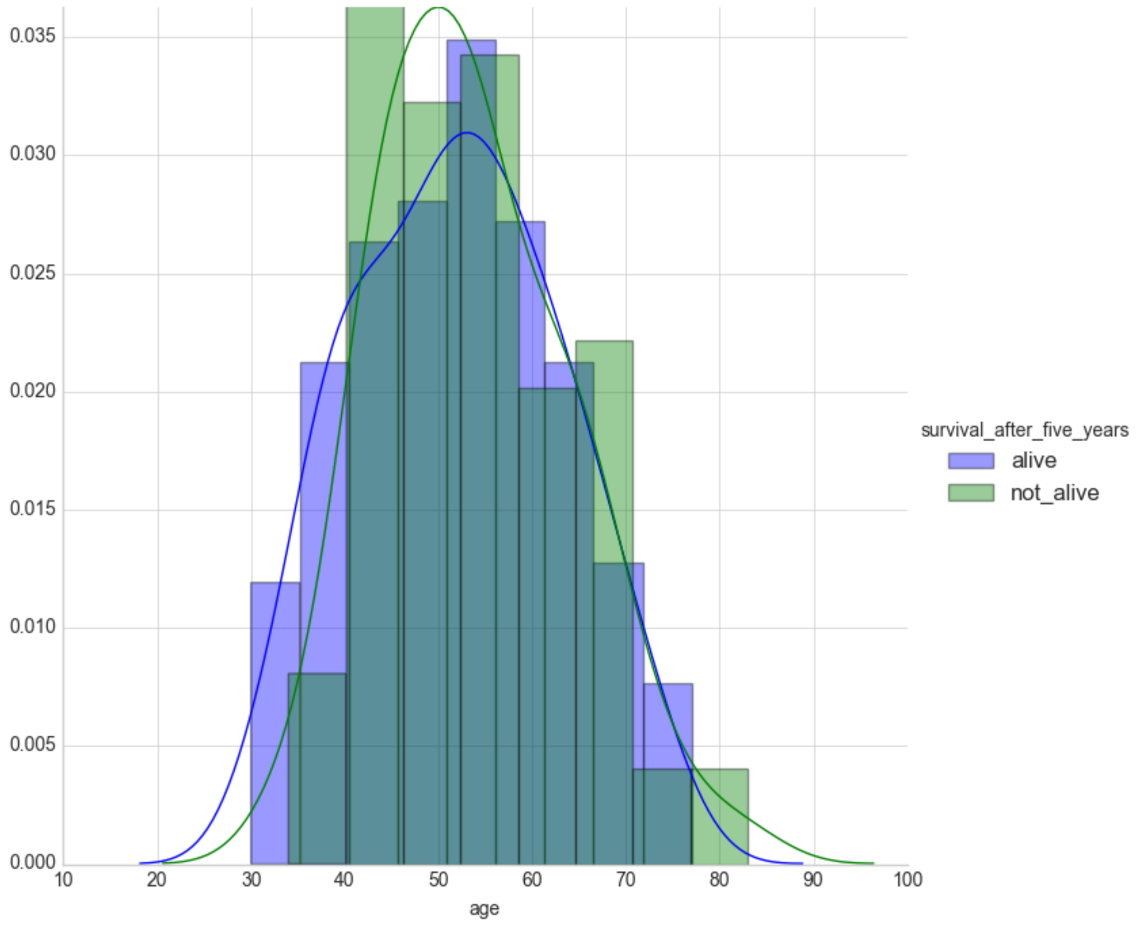
4. Univariate Analysis

Histograms with PDF

In [12]:

```
# Histogram with age

sns.set_style('whitegrid')
sns.FacetGrid(df, hue='survival_after_five_years', size=7).map(sns.distplot, 'age').add
_legend()
plt.show()
```

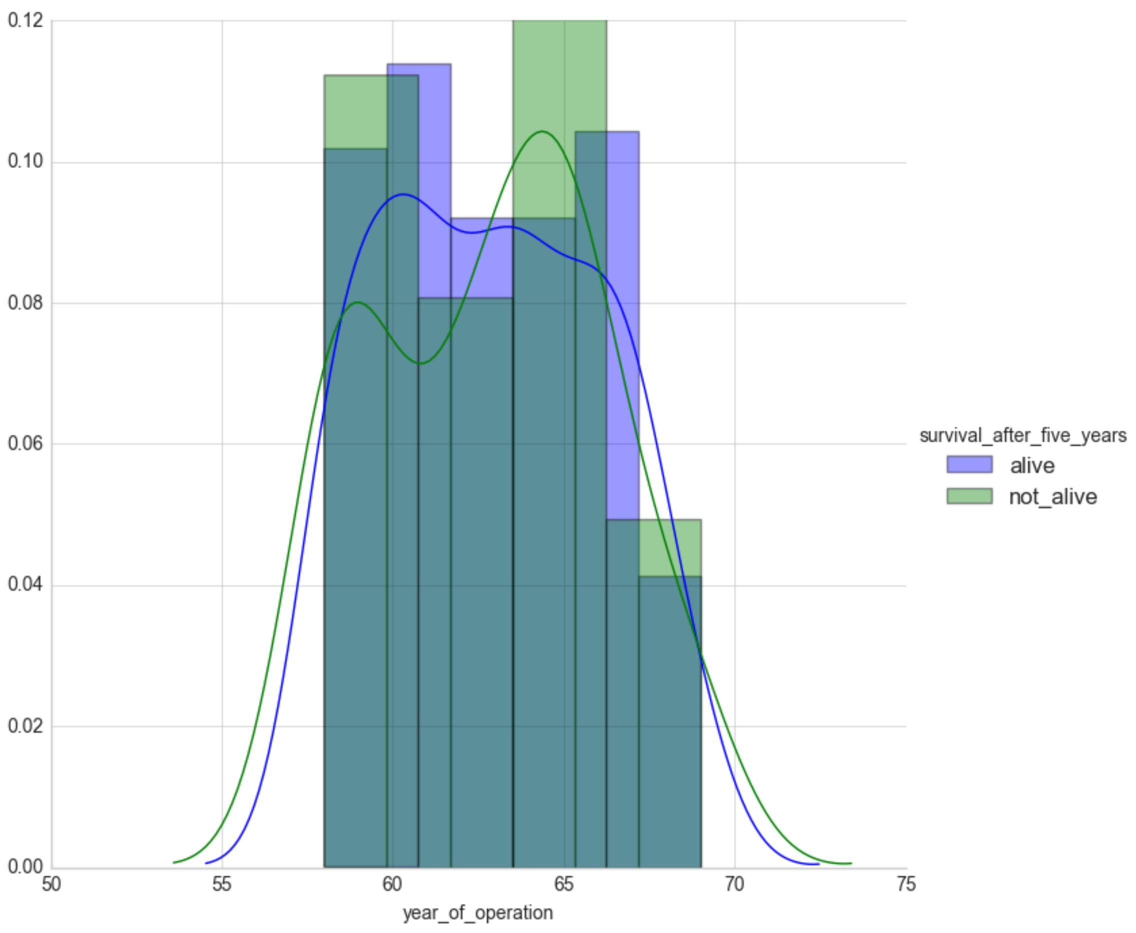
```
C:\Program Files\Anaconda3\lib\site-packages\statsmodels\nonparametric\kde
tools.py:20: VisibleDeprecationWarning: using a non-integer number instead
of an integer will result in an error in the future
  y = X[:m/2+1] + np.r_[0,X[m/2+1:],0]*1j
```



In [13]:

```
# histogram with year_of_operation

sns.set_style('whitegrid')
sns.FacetGrid(df, hue='survival_after_five_years', size=7).map(sns.distplot, 'year_of_o
peration').add_legend()
plt.show()
```

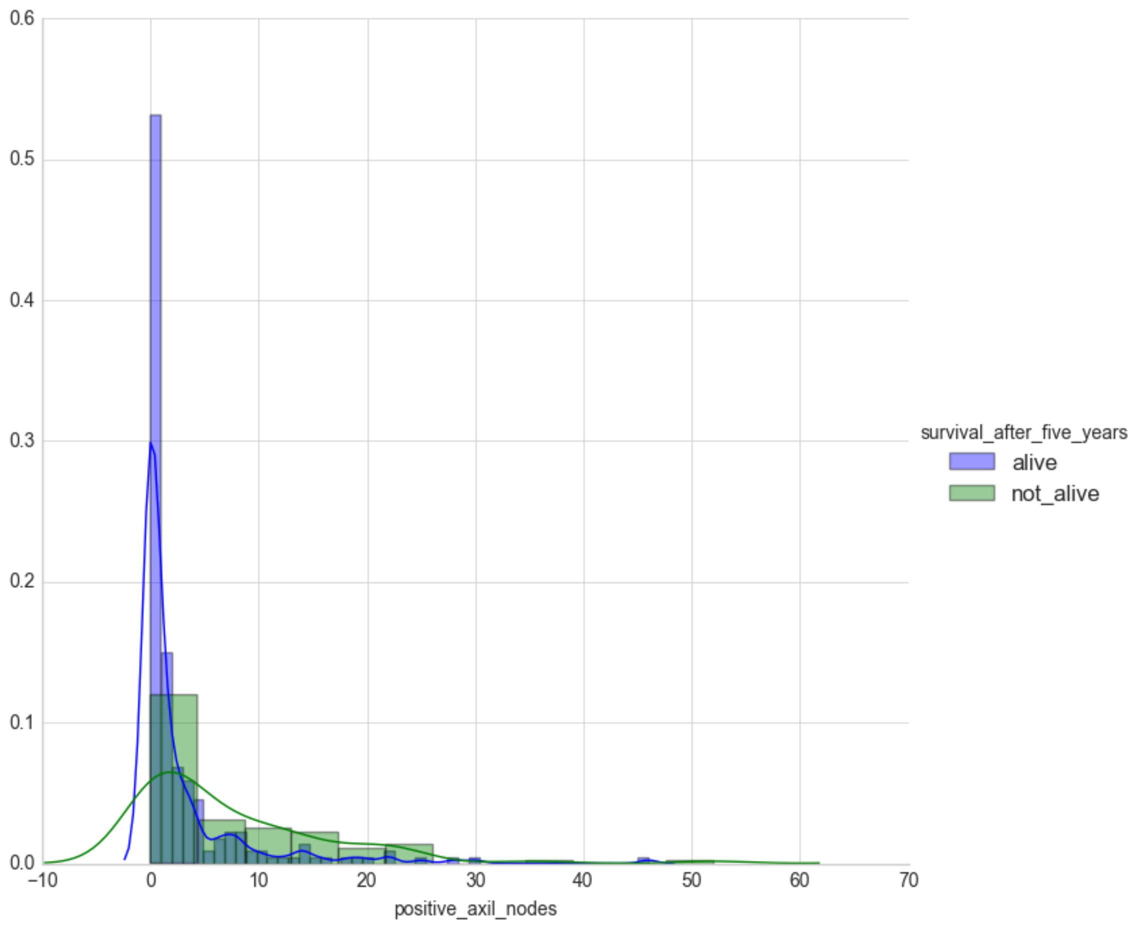
```
C:\Program Files\Anaconda3\lib\site-packages\statsmodels\nonparametric\kde
tools.py:20: VisibleDeprecationWarning: using a non-integer number instead
of an integer will result in an error in the future
  y = X[:m/2+1] + np.r_[0,X[m/2+1:],0]*1j
```



In [14]:

```
# histogram with number of positive auxillary nodes

sns.set_style("whitegrid")
sns.FacetGrid(df, hue="survival_after_five_years", size=7).map(sns.distplot, "positive_
axil_nodes").add_legend()
plt.show()
```

```
C:\Program Files\Anaconda3\lib\site-packages\statsmodels\nonparametric\kde
tools.py:20: VisibleDeprecationWarning: using a non-integer number instead
of an integer will result in an error in the future
  y = X[:m/2+1] + np.r_[0,X[m/2+1:],0]*1j
```



Observations

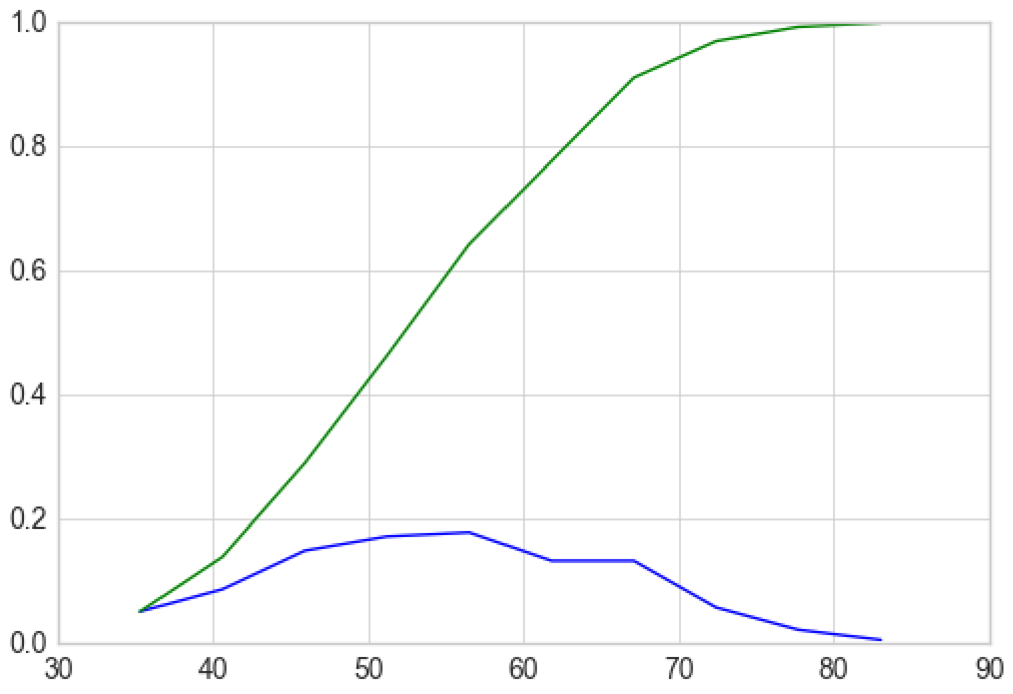
```
- Classification based on single variable is quite impossible as dependent varia
bles overlap a lot, maybe looking into
  two features (bivariate) at a time will help.
- Statistically speaking, the survival of people with 0-2 positive axillary node
s occupies highest percentage amongst the
  total people who survived.
- The number of people having positive axillary nodes decreases rapidly as we mo
ve right on the x-axis.
```

CDF and PDF

In [15]:

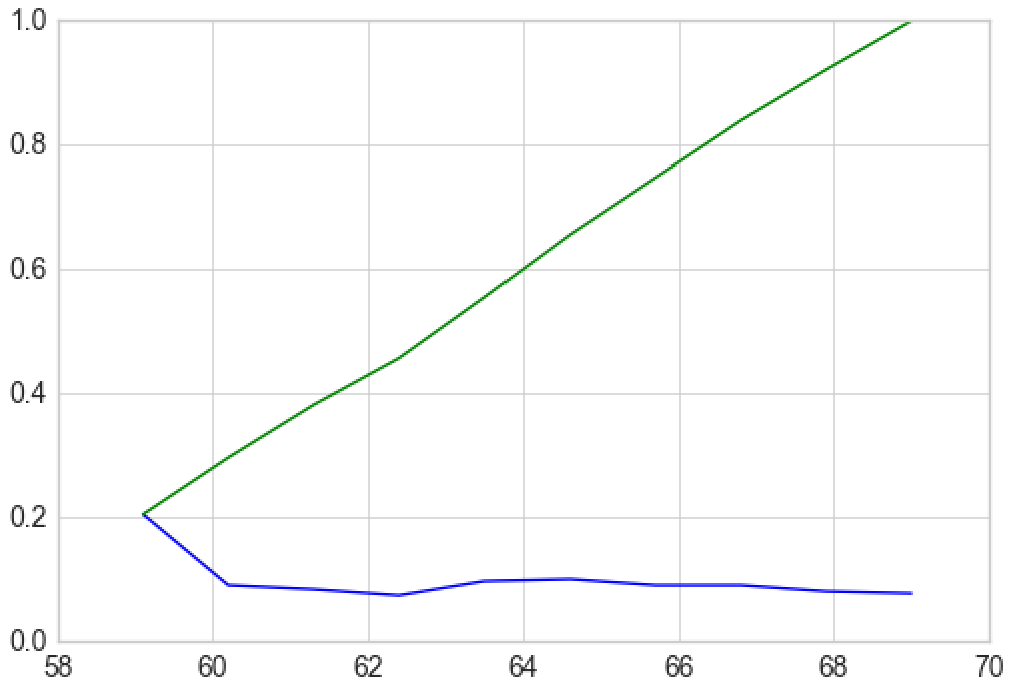
```
# cdf and pdf with age

counts, bin_edges = np.histogram(df['age'], bins=10, density=True)
pdf = counts/(sum(counts))

cdf = np.cumsum(pdf)

print(pdf)
print(cdf)
print(counts)
print(bin_edges)

plt.plot(bin_edges[1:], pdf)
plt.plot(bin_edges[1:], cdf)

plt.show()
```

```
[ 0.05228758  0.08823529  0.1503268   0.17320261  0.17973856  0.13398693
  0.13398693  0.05882353  0.02287582  0.00653595]
[ 0.05228758  0.14052288  0.29084967  0.46405229  0.64379085  0.77777778
  0.91176471  0.97058824  0.99346405  1.        ]
[ 0.00986558  0.01664817  0.02836355  0.03267974  0.03391294  0.02528055
  0.02528055  0.01109878  0.00431619  0.0012332 ]
[ 30.   35.3  40.6  45.9  51.2  56.5  61.8  67.1  72.4  77.7  83. ]
```



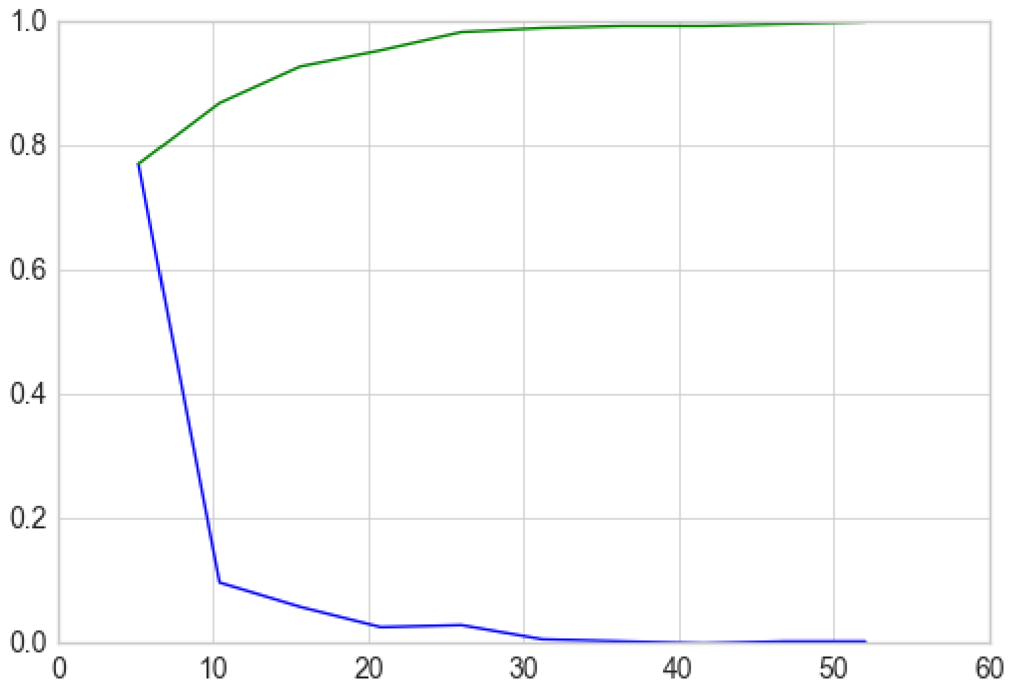
In [16]:

```
# cdf and pdf with year of operation

counts, bin_edges = np.histogram(df['year_of_operation'], bins=10, density=True)
pdf = counts/(sum(counts))

cdf = np.cumsum(pdf)

plt.plot(bin_edges[1:], pdf)
plt.plot(bin_edges[1:], cdf)

plt.show()
```



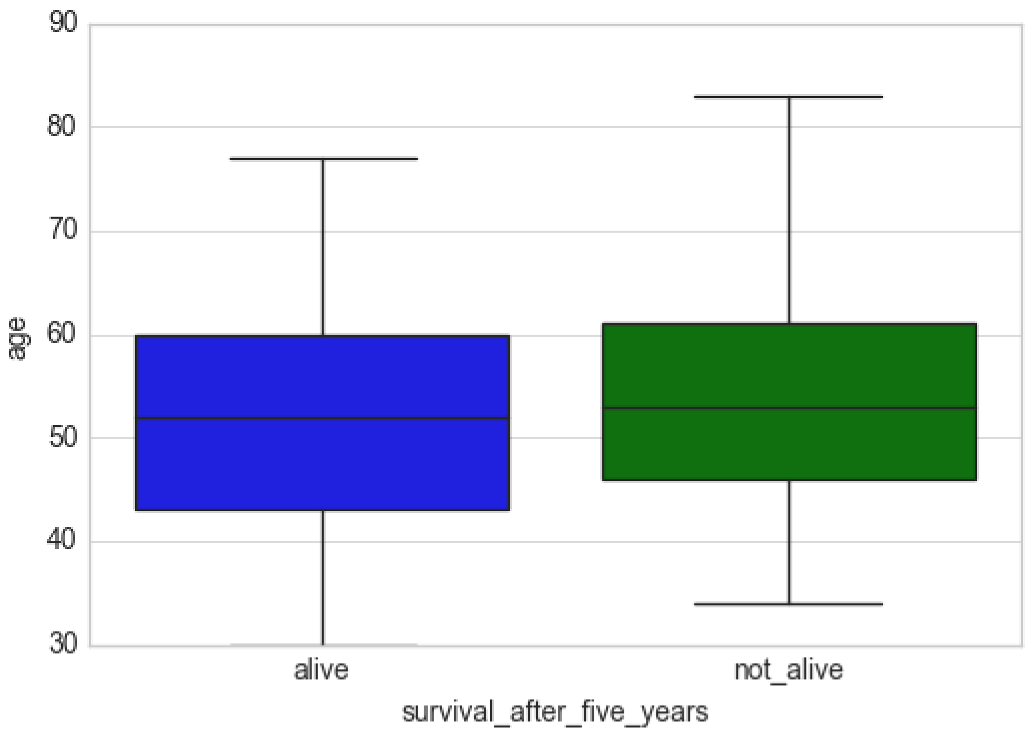
In [30]:

```
# cdf and pdf with positive auxillary nodes

counts, bin_edges = np.histogram(df['positive_axil_nodes'], bins=10, density=True)
pdf = counts/(sum(counts))

cdf = np.cumsum(pdf)

plt.plot(bin_edges[1:], pdf)
plt.plot(bin_edges[1:], cdf)

plt.show()
```



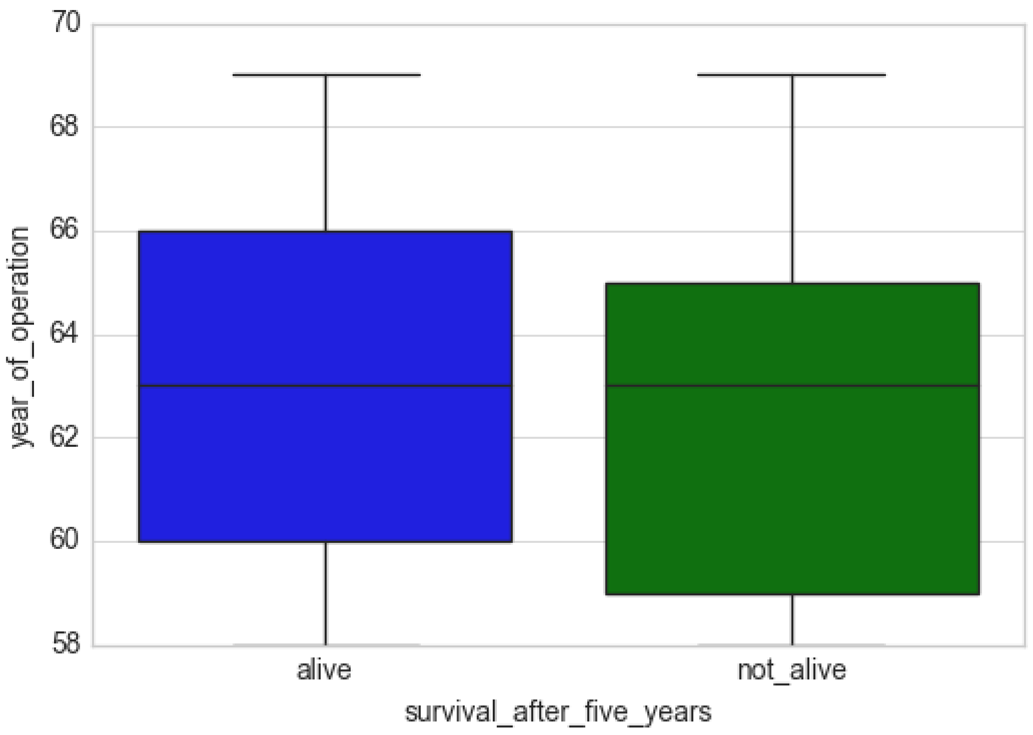
In [32]:

```
# box plot for age

sns.boxplot(data=df, x="survival_after_five_years", y="age")
plt.show()
```



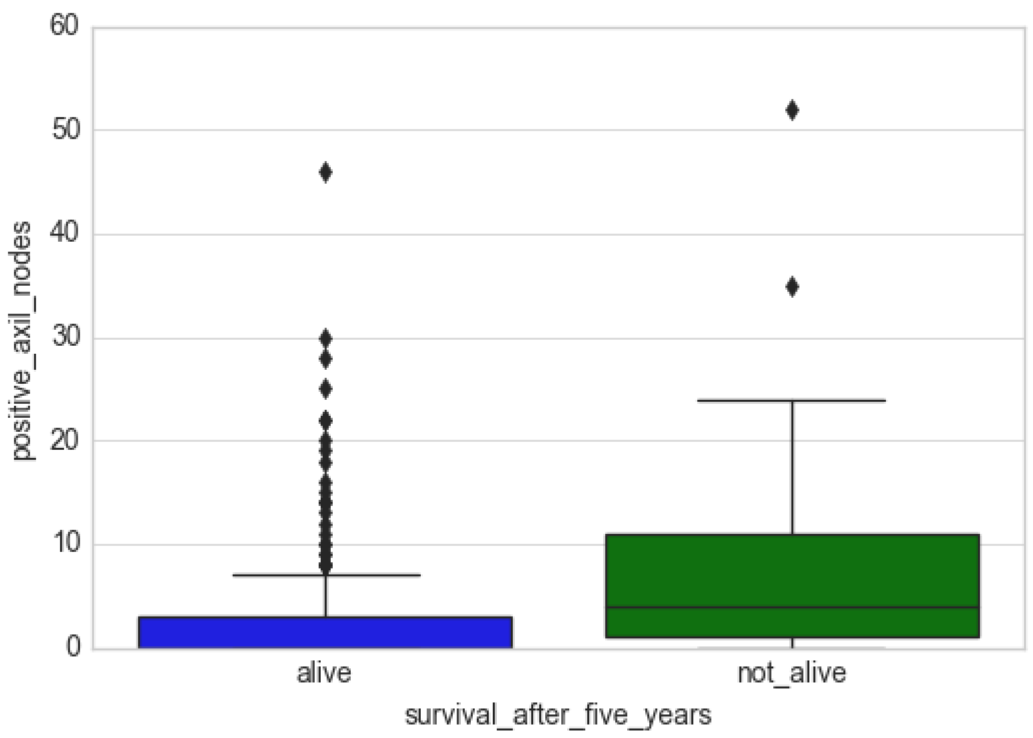
In [19]:

```
# box plot for year of operation

sns.boxplot(data=df, x="survival_after_five_years", y="year_of_operation")
plt.show()
```



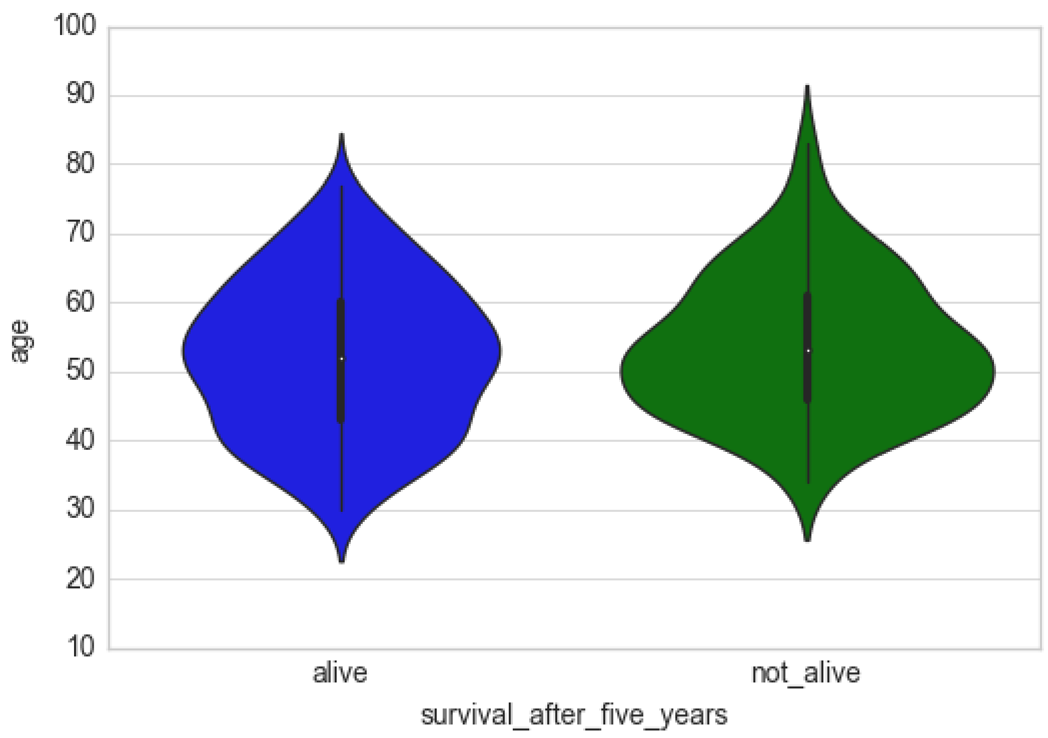
In [36]:

```
# box plot for positive axillary nodes

sns.boxplot(data=df, x="survival_after_five_years", y="positive_axil_nodes")
plt.show()
```



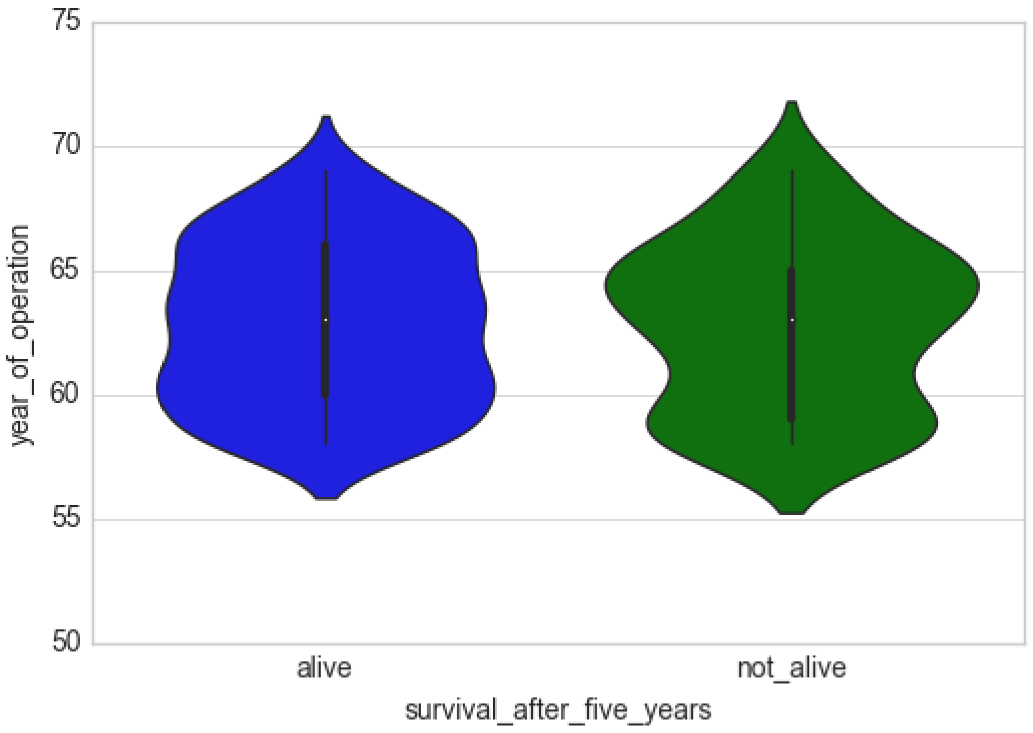
In [21]:

```
# violin plot for age

sns.violinplot(data=df, x="survival_after_five_years", y="age")
plt.show()
```



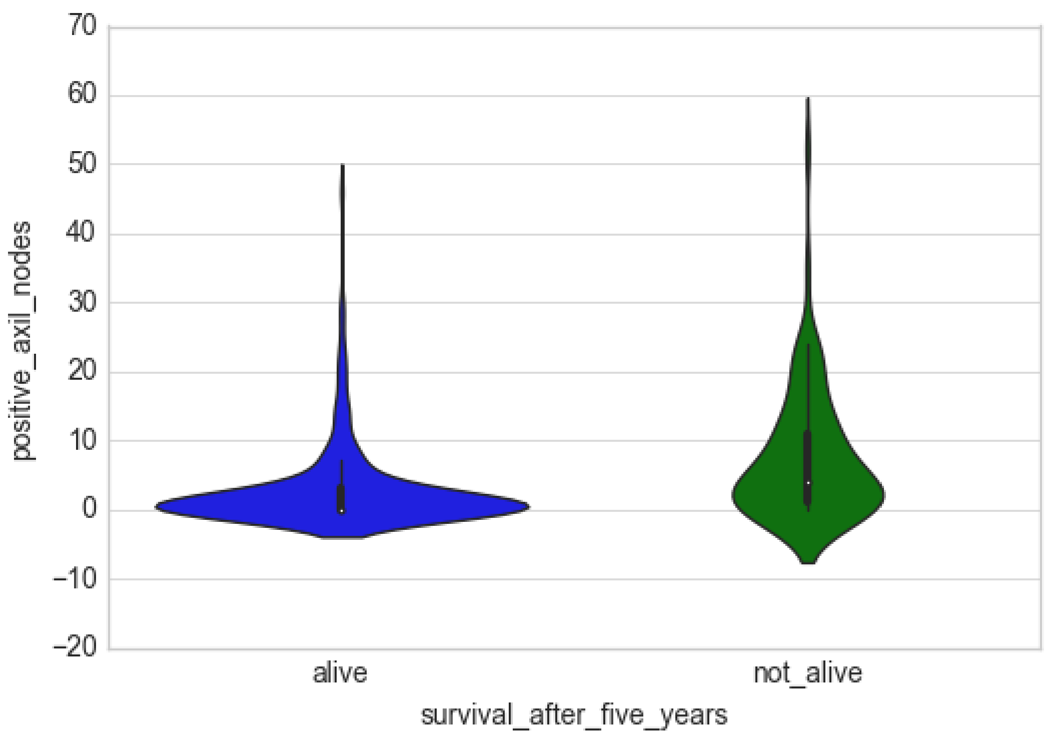
In [22]:

```
# violin plot for year of operation

sns.violinplot(data=df, x="survival_after_five_years", y="year_of_operation")
plt.show()
```



In [23]:

```
# violin plot for positive axillary nodes

sns.violinplot(data=df, x="survival_after_five_years", y="positive_axil_nodes")
plt.show()
```



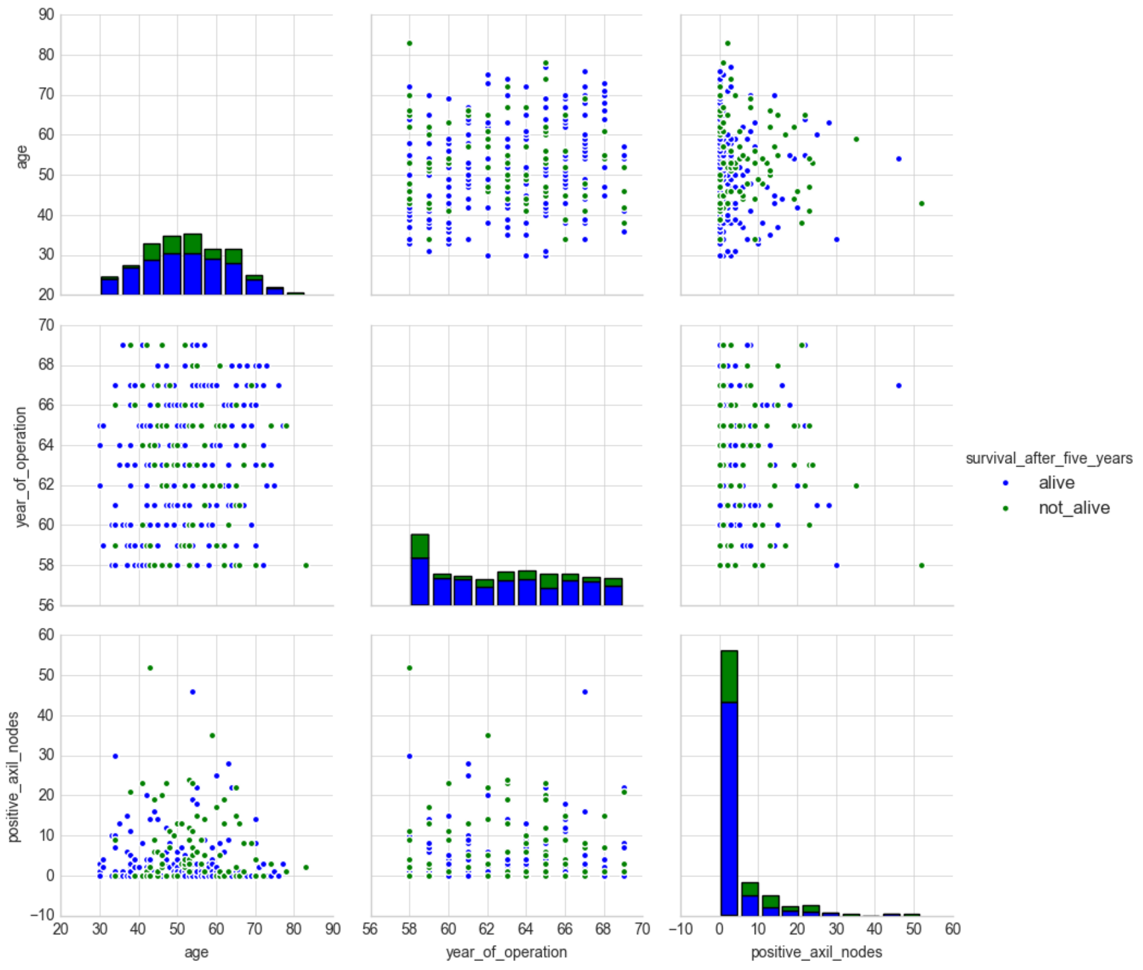
Observations

```
- Approximately 20% of patients fall into 50-60 age bracket.
- The number of positive lymph mostly occur in the range of 0-10.
- There are so many outliers in the box plot for positive axillary nodes (weir
d).
- There are patients who did not survive with 0 positive axillary nodes.
```

5. Bivariate Analysis

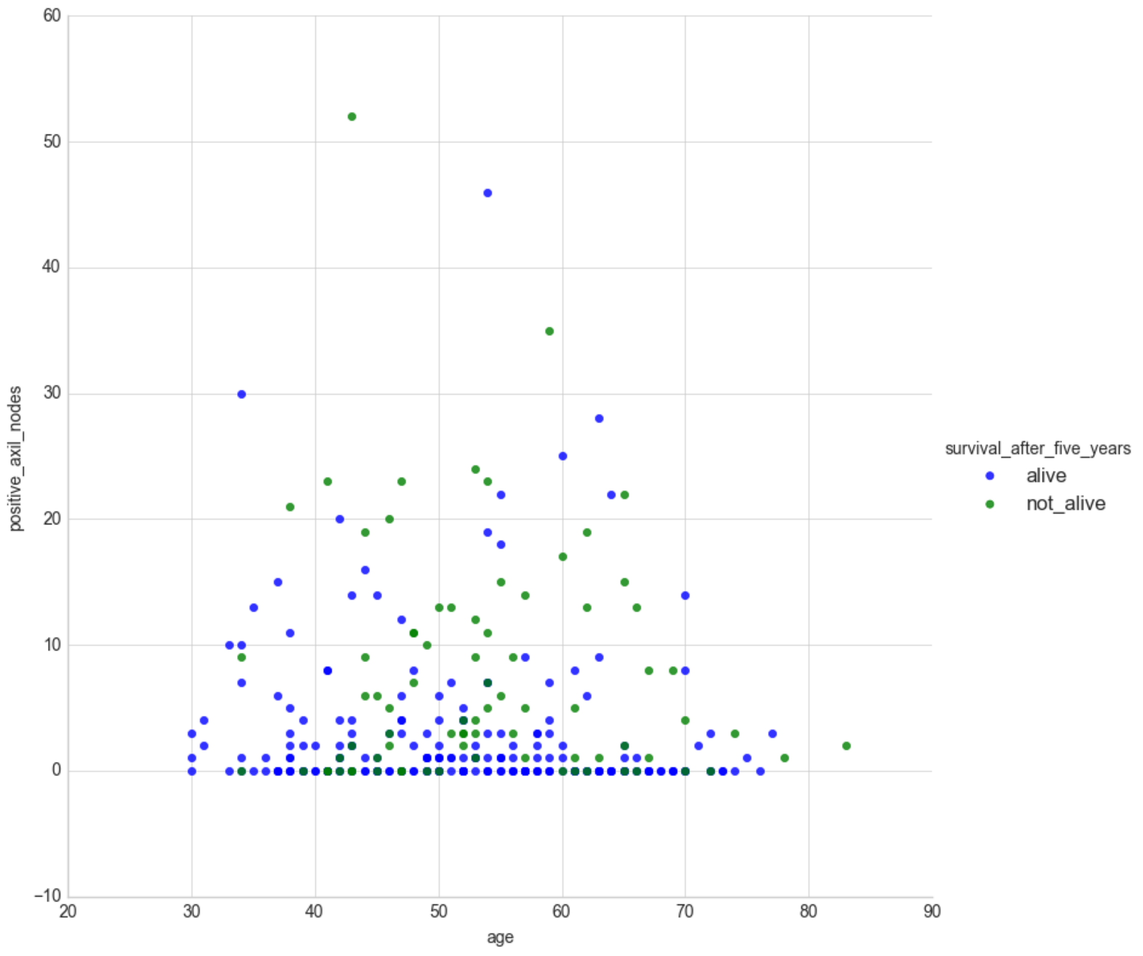
In [24]:

```
# pair plot

sns.set_style("whitegrid")
sns.pairplot(data=df, hue="survival_after_five_years", size=3)
plt.show()
```



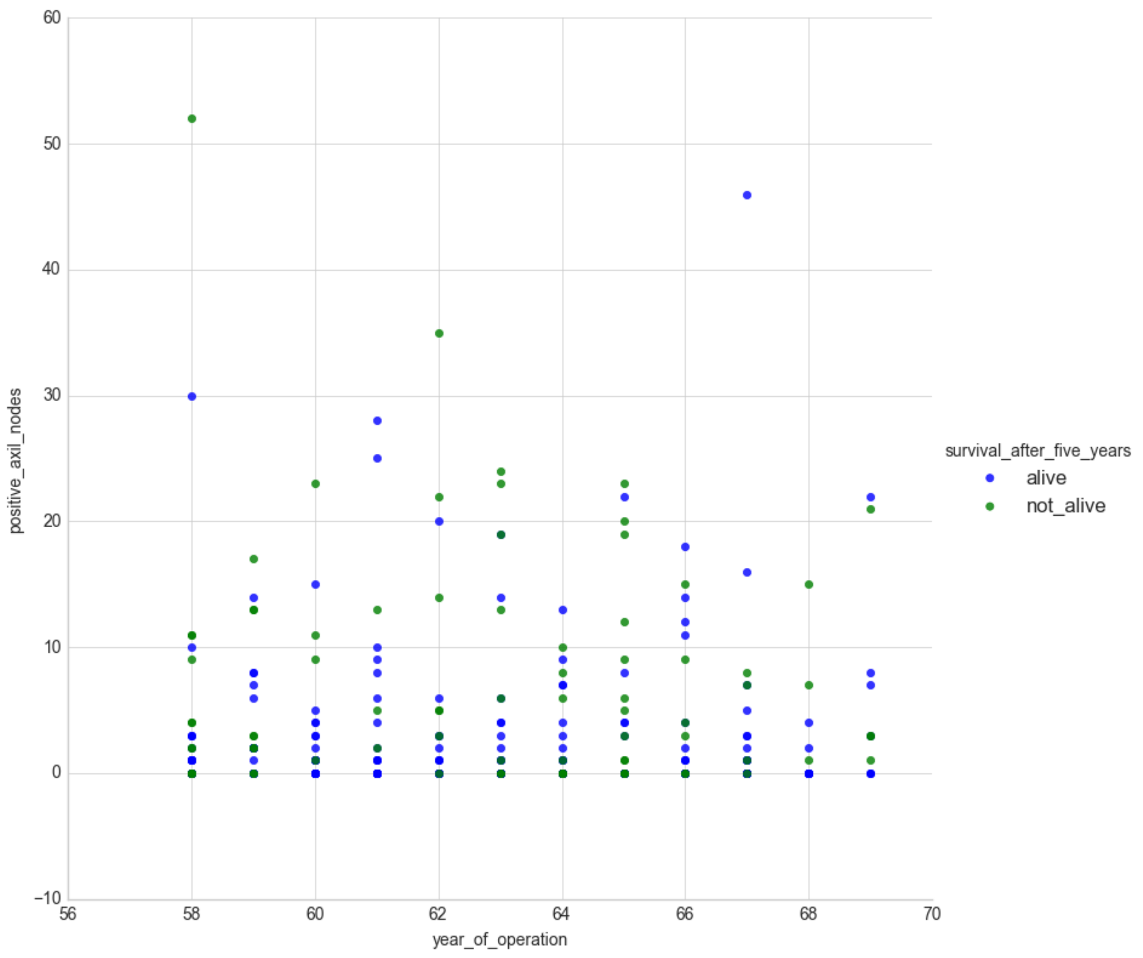
In [25]:

```
# let's use lmplot function in seaborn for a scatter plot

sns.lmplot("age", "positive_axil_nodes", data=df, hue="survival_after_five_years", fit_
reg=False, size=8)
plt.show()
```



In [26]:

```
sns.lmplot("year_of_operation", "positive_axil_nodes", data=df, hue="survival_after_fiv
e_years", fit_reg=False, size=8)
plt.show()
```



Observations

```
- There seems to be no dependency of year_of_operation and age on positive_axil_
nodes.
- The data is highly overlapping even in bivariate analysis.
```

Conclusions

```
- From univariate and bivariate analysis, no single/double features are solely r
esponsible for patient's survival.
- This is because the features are overlapping and there is no clear seperation.
 This will lead to high error rates.
- Positive axillary nodes alone also cannot be a deciding factor of patient's su
rvival because there are few people who
  did not survive with 0 nodes.
- Statistically speaking, the chances of survival is high if positive axillary n
odes is < 3.
```