Exploratory Data Analysis on Haberman Survival Data Set

Exercise :

1. Download Haberman Cancer Survival dataset from Kaggle. You may have to create a Kaggle account to donwload data. (https://www.kaggle.com/gilsousa/habermans-survival-data-set)
2. Perform a similar alanlaysis as above on this dataset with the following sections:
3. High level statistics of the dataset: number of points, numer of features, number of classes, data-points per class.
4. Explain our objective.
5. Perform Univaraite analysis(PDF, CDF, Boxplot, Voilin plots) to understand which features are useful towards classification.
6. Perform Bi-variate analysis (scatter plots, pair-plots) to see if combinations of features are useful in classfication.
7. Write your observations in english as crisply and unambigously as possible. Always quantify your results.

Information regarding data set :

1. **Title**: Haberman's Survival Data
2. **Sources**: (a) Donor: Tjen-Sien Lim (limt@stat.wisc.edu) (b) Date: March 4, 1999
3. **Relevant Information**: 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.
4. **Past Usage**:

   - Haberman, S. J. (1976). Generalized Residuals for Log-Linear Models, Proceedings of the 9th International Biometrics Conference, Boston, pp. 104-122.
   - Landwehr, J. M., Pregibon, D., and Shoemaker, A. C. (1984), Graphical Models for Assessing Logistic Regression Models (with discussion), Journal of the American Statistical Association 79: 61-83.
   - Lo, W.-D. (1993). Logistic Regression Trees, PhD thesis, Department of Statistics, University of Wisconsin, Madison, WI.

Objective :

> It is a classification problem, where we have to analyze and provide observation which evaluates whether a patient would survive a cancer treatment or not.

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:
```
# Load heberman.csv in panda's daraframe.
haberman = pd.read_csv("haberman.csv")
haberman
```

```
Out[2]:
```

	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
5	33	60	0	1
6	34	59	0	2
7	34	66	9	2
8	34	58	30	1
9	34	60	1	1
10	34	61	10	1
11	34	67	7	1
12	34	60	0	1
13	35	64	13	1
14	35	63	0	1
15	36	60	1	1
16	36	69	0	1
17	37	60	0	1
18	37	63	0	1
19	37	58	0	1
20	37	59	6	1
21	37	60	15	1
22	37	63	0	1
23	38	69	21	2
24	38	59	2	1
25	38	60	0	1
26	38	60	0	1
27	38	62	3	1
28	38	64	1	1
29	38	66	0	1
...	...	...	...	...
275	67	66	0	1
276	67	61	0	1
277	67	65	0	1
278	68	67	0	1
279	68	68	0	1
280	69	67	8	2
281	69	60	0	1
282	69	65	0	1
283	69	66	0	1
284	70	58	0	2
285	70	58	4	2
286	70	66	14	1
287	70	67	0	1
288	70	68	0	1
289	70	59	8	1
290	70	63	0	1
291	71	68	2	1
292	72	63	0	2

	30	64	1	1.1
293	72	58	0	1
294	72	64	0	1
295	72	67	3	1
296	73	62	0	1
297	73	68	0	1
298	74	65	3	2
299	74	63	0	1
300	75	62	1	1
301	76	67	0	1
302	77	65	3	1
303	78	65	1	2
304	83	58	2	2

305 rows × 4 columns

(Q) how many data-points and features?

In [3]:
```
print("Number of data-points present in dataset is {0}".format(haberman.shape[0]))
print("Number of features/classes present in dataset is {0}".format(haberman.shape[1]))
```

```
Number of data-points present in dataset is 305
Number of features/classes present in dataset is 4
```

(Q) What are the column/attribute names and their information in our dataset?

In [4]:
```
for column in haberman:
    if haberman.columns.get_loc(column) == 0:
        print("Column name is {0} : It represent age of patient at time of operation (numerical)\n".fo
rmat(column))
    elif haberman.columns.get_loc(column) == 1:
        print("Column name is {0} : Patient's year of operation (year - 1900, numerical)\n".format(col
umn))
    elif haberman.columns.get_loc(column) == 2:
        print("Column name is {0} : Number of positive axillary nodes detected (numerical)\n".format(c
olumn))
    elif haberman.columns.get_loc(column) == 3:
        print("Column name is {0} : Survival status (class attribute)".format(column))
        print("\t\t\t -- 1 = the patient survived 5 years or longer")
        print("\t\t\t -- 2 = the patient died within 5 year")
```

```
Column name is 30 : It represent age of patient at time of operation (numerical)

Column name is 64 : Patient's year of operation (year - 1900, numerical)

Column name is 1 : Number of positive axillary nodes detected (numerical)

Column name is 1.1 : Survival status (class attribute)
                         -- 1 = the patient survived 5 years or longer
                         -- 2 = the patient died within 5 year
```

In [5]:
```
haberman.columns
```

Out[5]:
```
Index(['30', '64', '1', '1.1'], dtype='object')
```

In [6]:
```
# Rename columns for better understanding also modify data for "survival_status" column.
# 1 --> Yes if the patient survived 5 years or longer
# 2 --> No the patient died within 5 year

haberman.columns = ['Patient_age', 'Year_of_operation','Axillary_nodes','Survival_status']
haberman['Survival_status'] = haberman['Survival_status'].apply(lambda x: "Yes" if x == 1 else "No")
haberman
```

Out[6]:

	Patient_age	Year_of_operation	Axillary_nodes	Survival_status
0	30	62	3	Yes
1	30	65	0	Yes
2	31	59	2	Yes
3	31	65	4	Yes
4	33	58	10	Yes
5	33	60	0	Yes
6	34	59	0	No
7	34	66	9	No
8	34	58	30	Yes
9	34	60	1	Yes
10	34	61	10	Yes
11	34	67	7	Yes
12	34	60	0	Yes
13	35	64	13	Yes
14	35	63	0	Yes
15	36	60	1	Yes
16	36	69	0	Yes
17	37	60	0	Yes
18	37	63	0	Yes
19	37	58	0	Yes
20	37	59	6	Yes
21	37	60	15	Yes
22	37	63	0	Yes
23	38	69	21	No
24	38	59	2	Yes
25	38	60	0	Yes
26	38	60	0	Yes
27	38	62	3	Yes
28	38	64	1	Yes
29	38	66	0	Yes
...	...	...	...	...
275	67	66	0	Yes
276	67	61	0	Yes
277	67	65	0	Yes
278	68	67	0	Yes
279	68	68	0	Yes
280	69	67	8	No
281	69	60	0	Yes
282	69	65	0	Yes
283	69	66	0	Yes
284	70	58	0	No
285	70	58	4	No
286	70	66	14	Yes
287	70	67	0	Yes
288	70	68	0	Yes
289	70	59	8	Yes
290	70	63	0	Yes
291	71	68	2	Yes
292	72	63	0	No

	Patient_age	Year_of_operation	Axillary_nodes	Survival_status
293	72	58	0	Yes
294	72	64	0	Yes
295	72	67	3	Yes
296	73	62	0	Yes
297	73	68	0	Yes
298	74	65	3	No
299	74	63	0	Yes
300	75	62	1	Yes
301	76	67	0	Yes
302	77	65	3	Yes
303	78	65	1	No
304	83	58	2	No

305 rows × 4 columns

(Q) How many data points for each class are present?

In [7]:
```
# From above table we can easily find that we have to classify data on the basis of "Survival_status"
# Yes = the patient survived 5 years or longer
# No = the patient died within 5 year.
# It is an imbalanced datasets as number of value counts are far away from each other.

haberman['Survival_status'].value_counts()
```

Out[7]:
```
Yes    224
No      81
Name: Survival_status, dtype: int64
```

In [8]:
```
# Similarly, another finding can be done on the basis of "Year_of_operation"
# It is a partially balanced datasets as number of value counts are not far away from each other.

haberman['Year_of_operation'].value_counts()
```

Out[8]:
```
58    36
64    30
63    30
66    28
65    28
60    28
59    27
61    26
67    25
62    23
68    13
69    11
Name: Year_of_operation, dtype: int64
```

Note :

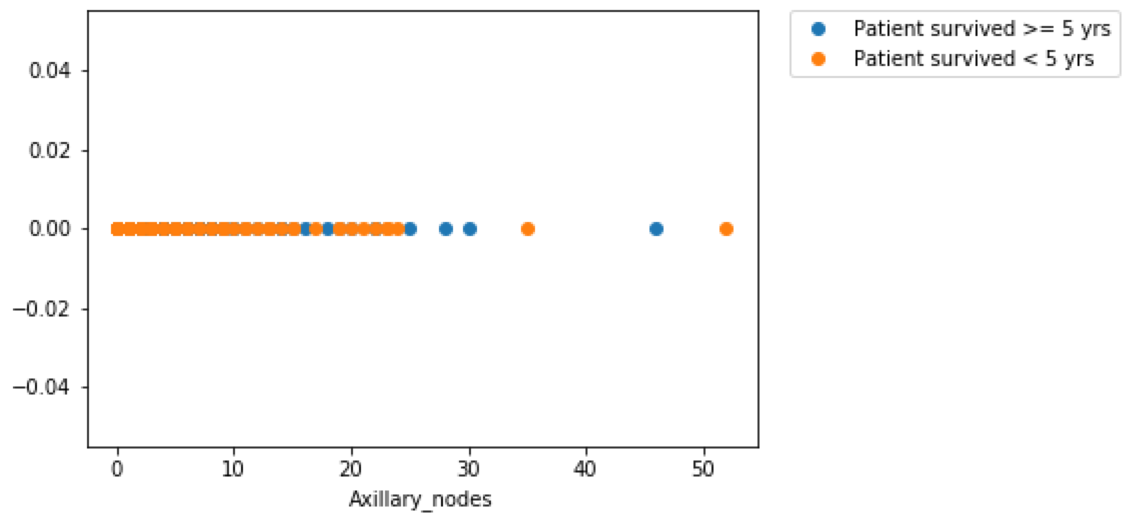
Even though the dataset is not balanced in the case of survival status, still we can perform univariate and bivariate analysis on the feature.

(1) Univariate Analysis :

(1.1) 1D Scatter Plot :

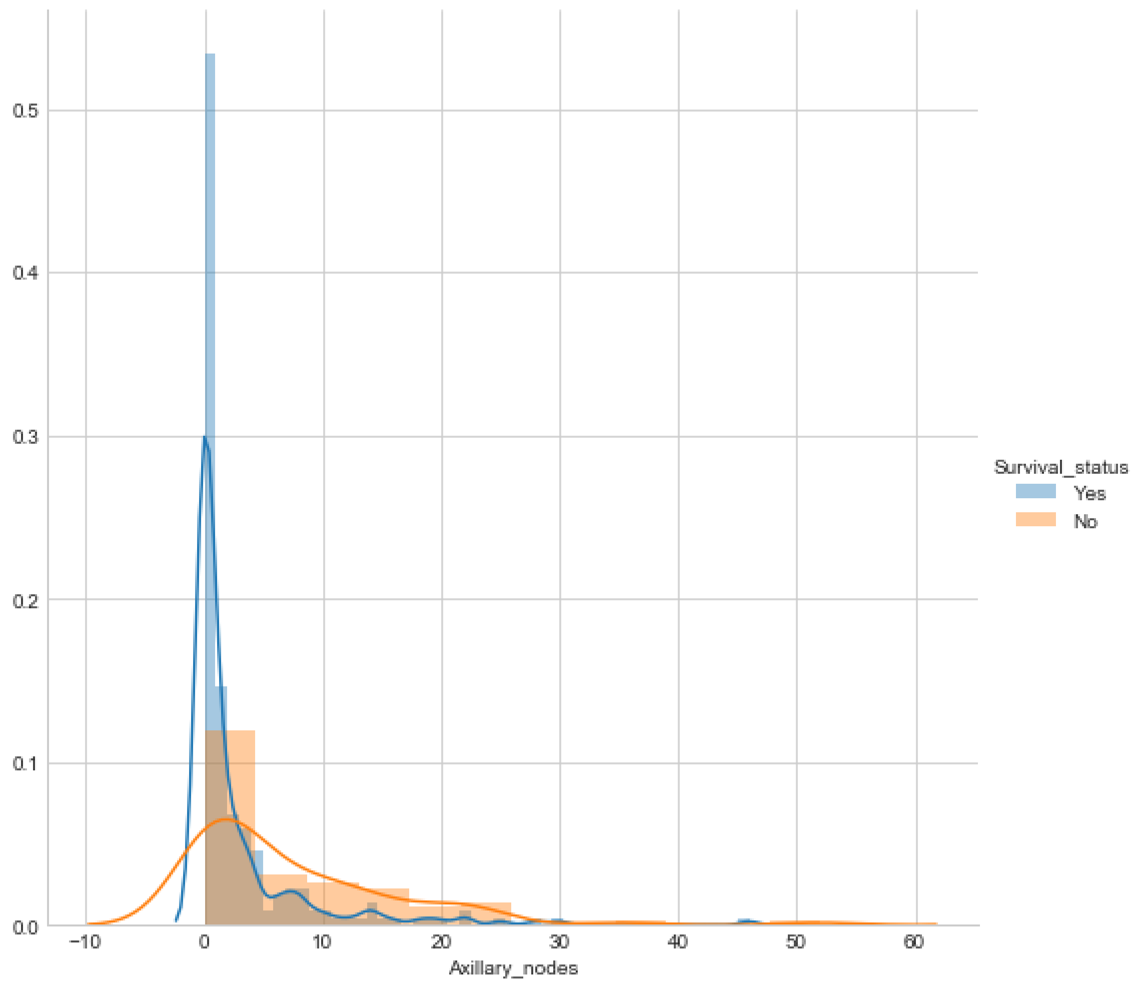
By our understanding we know that,
A more number of positive axillary lymph node are bad for the patient survival.

In [9]:
```
haberman_yes = haberman.loc[haberman["Survival_status"] == "Yes"]
haberman_no = haberman.loc[haberman["Survival_status"] == "No"]
plt.plot(haberman_yes["Axillary_nodes"], \
         np.zeros_like(haberman_yes['Axillary_nodes']), 'o', \
         label="Patient survived >= 5 yrs")

plt.plot(haberman_no["Axillary_nodes"], \
         np.zeros_like(haberman_no['Axillary_nodes']), \
         'o', label="Patient survived < 5 yrs")

plt.xlabel('Axillary_nodes')
plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0.)
plt.show()
```

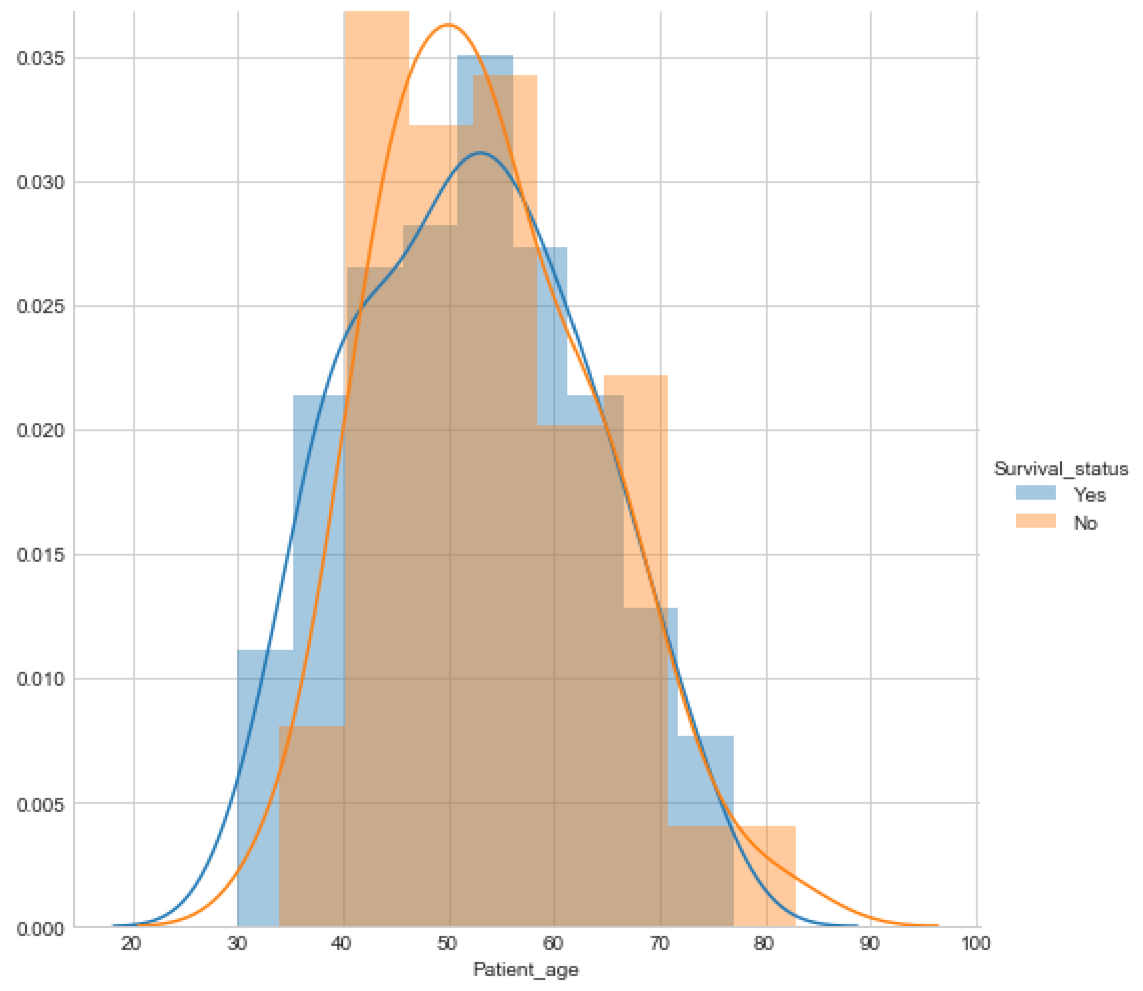


(1.2) Histograms and Probability Density Functions (PDF) :

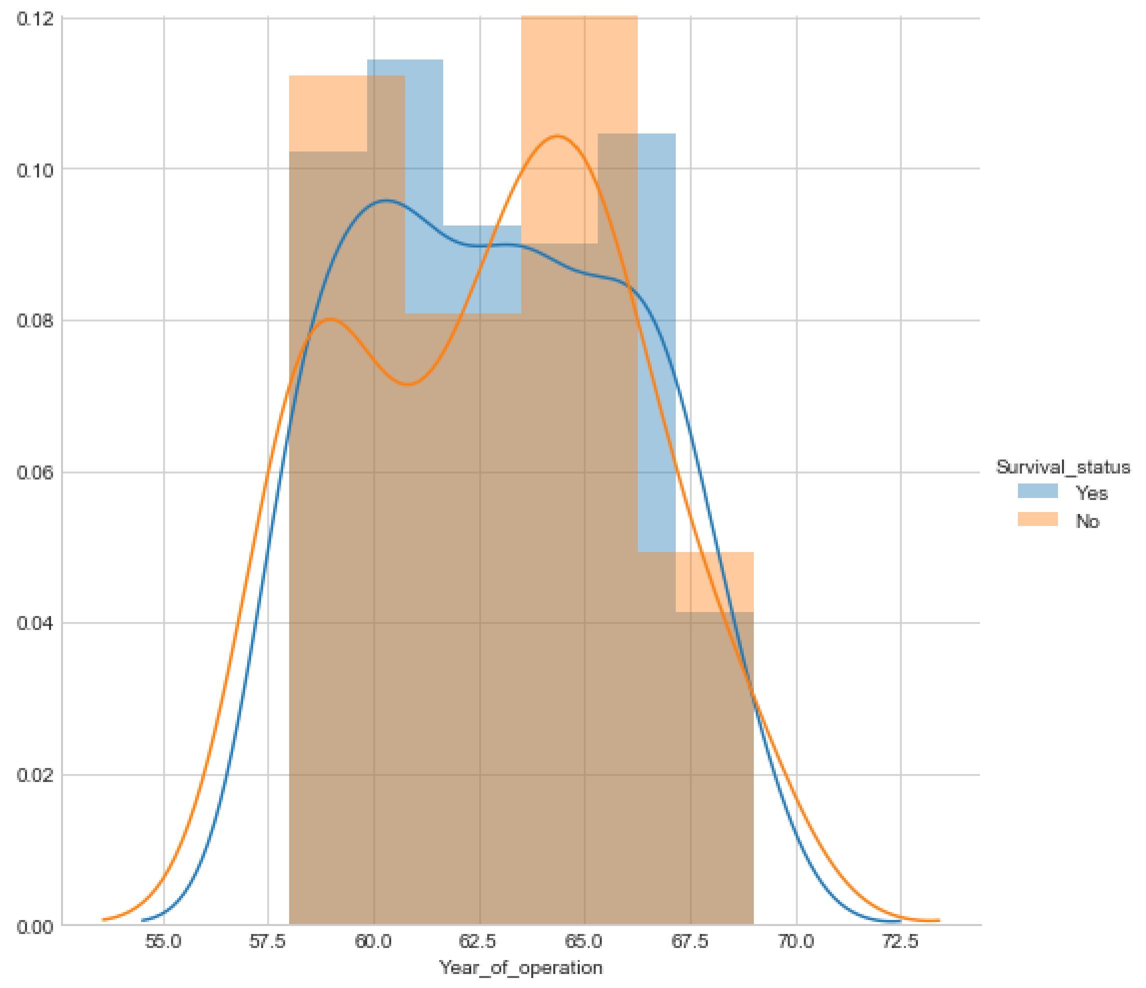
In [10]:
```
# Histograms and Probability Density Functions (PDF) of Axillary_nodes
sns.set_style("whitegrid");
sns.FacetGrid(haberman,hue="Survival_status",size=7) \
   .map(sns.distplot,"Axillary_nodes") \
   .add_legend()
plt.show();
```



In [11]:
```
# Histograms and Probability Density Functions (PDF) of Patient_age
sns.FacetGrid(haberman,hue="Survival_status",size= 7) \
   .map(sns.distplot,"Patient_age") \
   .add_legend()
plt.show()
```



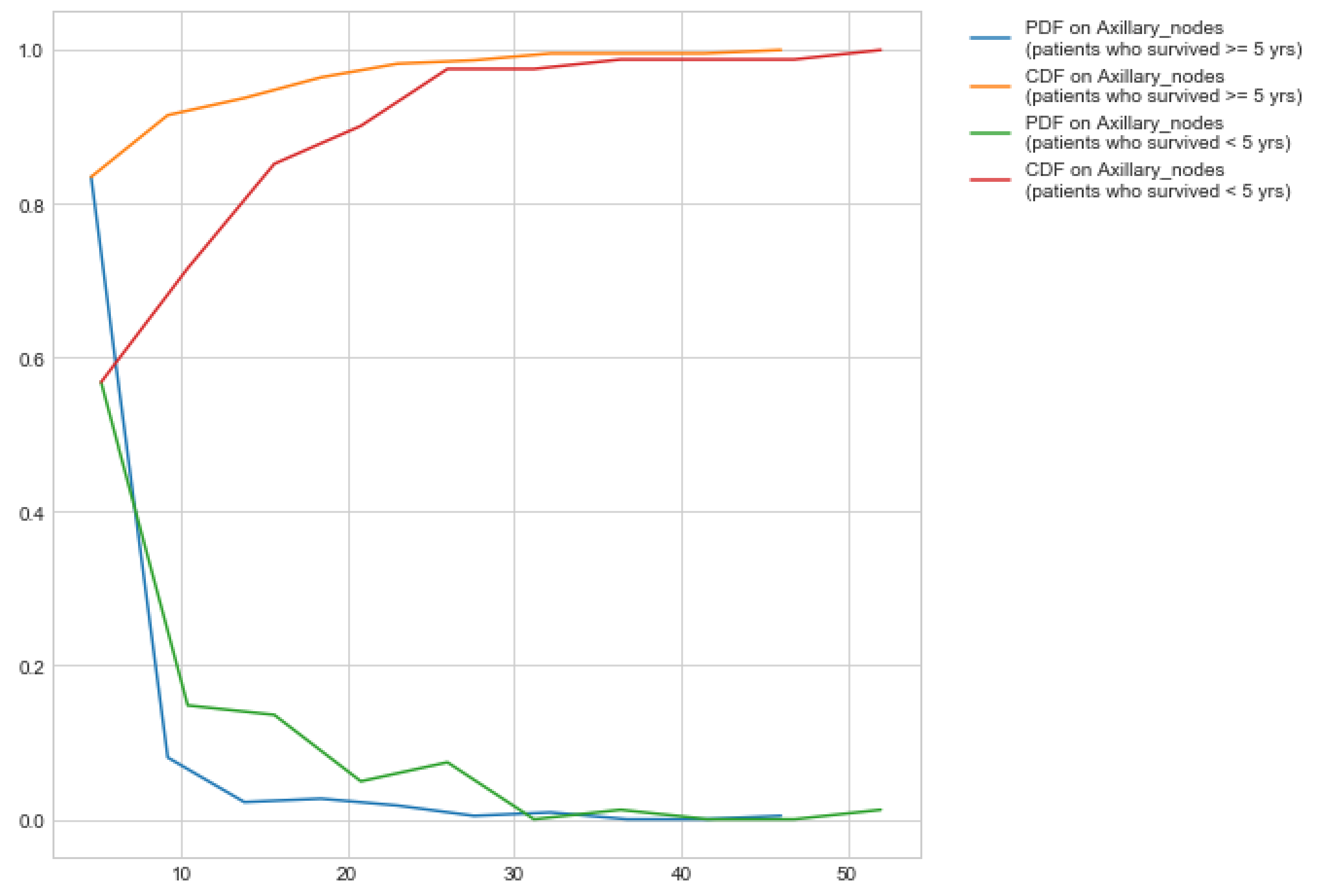
In [12]:
```
# Histograms and Probability Density Functions (PDF) of Year_of_operation
sns.FacetGrid(haberman,hue="Survival_status",size=7) \
   .map(sns.distplot,"Year_of_operation") \
   .add_legend()
plt.show()
```



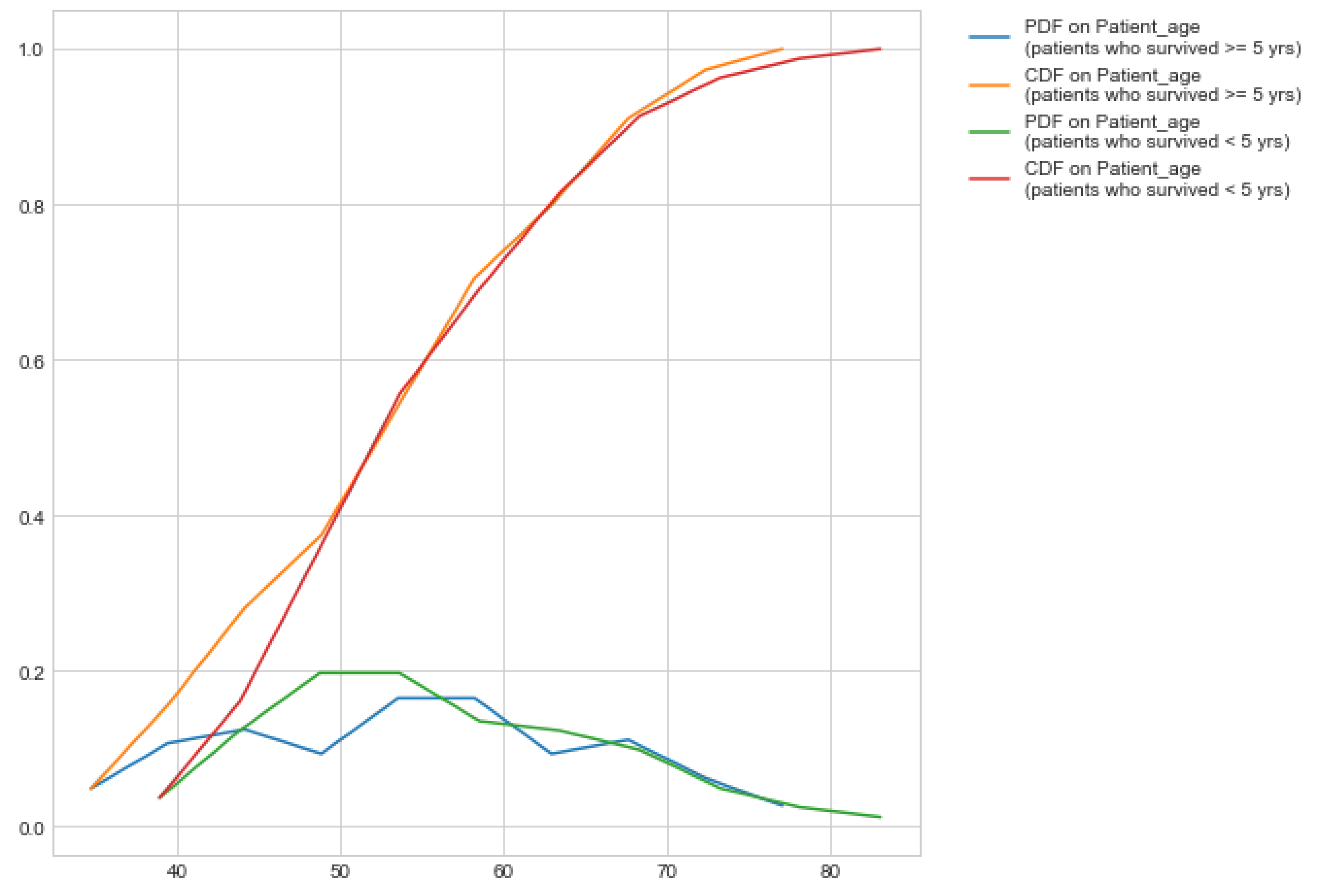
(1.3) Cumulative Distribution Functions (CDF) :

In [13]:
```python
# Cumulative Density Functions (CDF) for patients who survived >= 5 and < 5
def showCDF(feature):
    print("\nCumulative Density Functions (CDF) of "+feature+" (patients who survived >= 5 yrs) :-  \n
")
    count,bin_edges = np.histogram(haberman_yes[feature],bins=10,density=True)

    pdf = count/(sum(count))

    print("PDF : \n",pdf)
    print("\nBin Edges : \n",bin_edges)

    cdf = np.cumsum(pdf)
    plt.figure(figsize=(8, 8))
    plt.plot(bin_edges[1:],pdf,label="PDF on "+feature+" \n(patients who survived >= 5 yrs)")
    plt.plot(bin_edges[1:],cdf,label="CDF on "+feature+" \n(patients who survived >= 5 yrs)")
    plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0.)
    print("\n------------------------------------------------------------------------------------
\n")

    print("\nCumulative Density Functions (CDF) of "+feature+" (patients who survived < 5 yrs) :- \n")
    count,bin_edges = np.histogram(haberman_no[feature],bins=10,density=True)

    pdf = count/(sum(count))

    print("PDF : \n",pdf)
    print("\nBin Edges : \n",bin_edges)

    cdf = np.cumsum(pdf)
    plt.plot(bin_edges[1:],pdf,label="PDF on "+feature+"\n(patients who survived < 5 yrs)")
    plt.plot(bin_edges[1:],cdf,label="CDF on "+feature+"\n(patients who survived < 5 yrs)")
    plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0.)
    print("\n------------------------------------------------------------------------------------
\n")
    plt.show()


showCDF("Axillary_nodes")
showCDF("Patient_age")
showCDF("Year_of_operation")
```

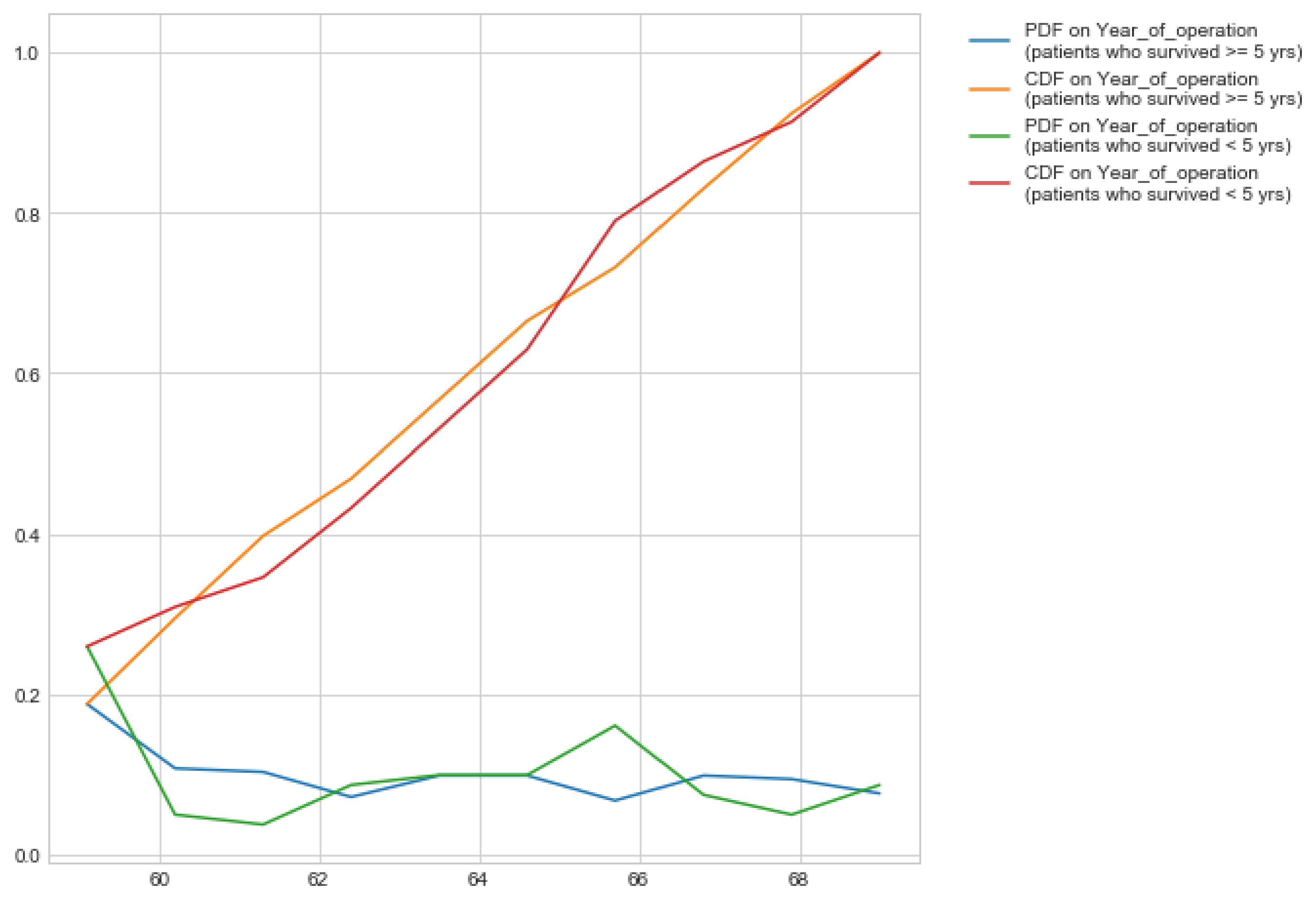
```
Cumulative Density Functions (CDF) of Axillary_nodes (patients who survived >= 5 yrs) :-

PDF :
 [ 0.83482143  0.08035714  0.02232143  0.02678571  0.01785714  0.00446429
  0.00892857  0.          0.          0.00446429]

Bin Edges :
 [  0.    4.6   9.2  13.8  18.4  23.   27.6  32.2  36.8  41.4  46. ]

------------------------------------------------------------------------------------------


Cumulative Density Functions (CDF) of Axillary_nodes (patients who survived < 5 yrs) :-

PDF :
 [ 0.56790123  0.14814815  0.13580247  0.04938272  0.07407407  0.
  0.01234568  0.          0.          0.01234568]

Bin Edges :
 [  0.    5.2  10.4  15.6  20.8  26.   31.2  36.4  41.6  46.8  52. ]

------------------------------------------------------------------------------------------
```



```
Cumulative Density Functions (CDF) of Patient_age (patients who survived >= 5 yrs) :-

PDF :
 [ 0.04910714  0.10714286  0.125       0.09375     0.16517857  0.16517857
  0.09375     0.11160714  0.0625      0.02678571]

Bin Edges :
 [ 30.   34.7  39.4  44.1  48.8  53.5  58.2  62.9  67.6  72.3  77. ]

------------------------------------------------------------------------------------------

Cumulative Density Functions (CDF) of Patient_age (patients who survived < 5 yrs) :-

PDF :
 [ 0.03703704  0.12345679  0.19753086  0.19753086  0.13580247  0.12345679
  0.09876543  0.04938272  0.02469136  0.01234568]

Bin Edges :
 [ 34.   38.9  43.8  48.7  53.6  58.5  63.4  68.3  73.2  78.1  83. ]

------------------------------------------------------------------------------------------
```

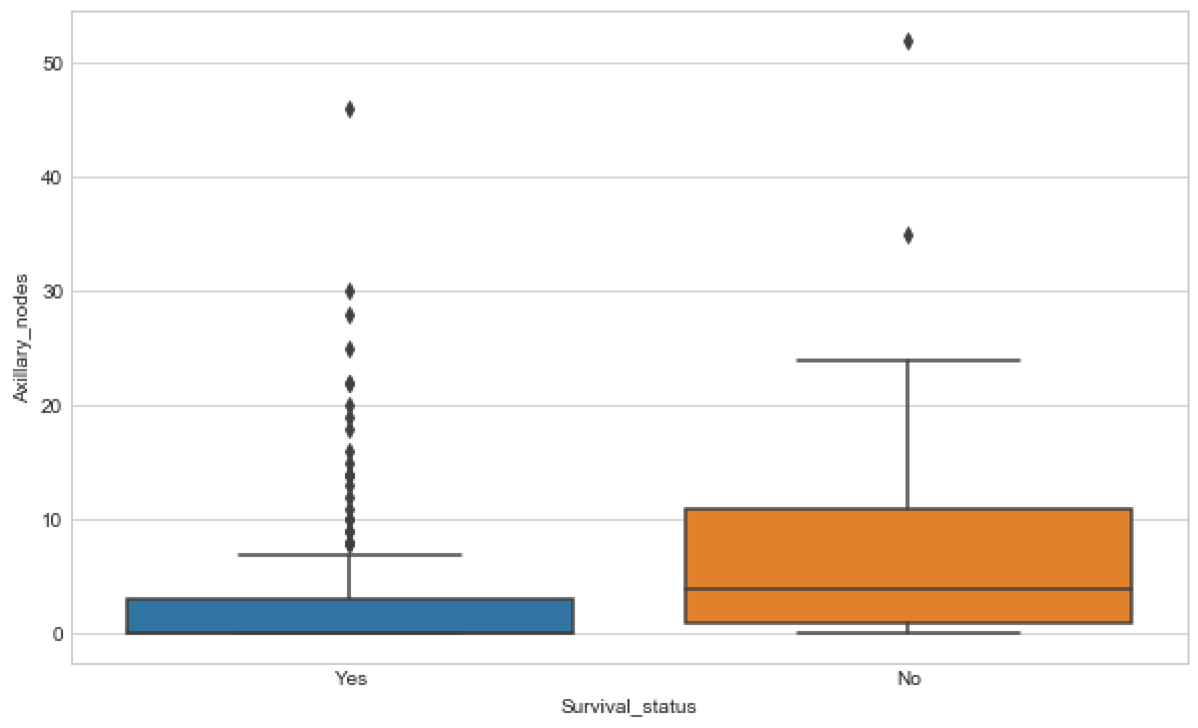


```
Cumulative Density Functions (CDF) of Year_of_operation (patients who survived >= 5 yrs) :-

PDF :
 [ 0.1875      0.10714286  0.10267857  0.07142857  0.09821429  0.09821429
  0.06696429  0.09821429  0.09375     0.07589286]

Bin Edges :
 [ 58.   59.1  60.2  61.3  62.4  63.5  64.6  65.7  66.8  67.9  69. ]

-------------------------------------------------------------------------------------------


Cumulative Density Functions (CDF) of Year_of_operation (patients who survived < 5 yrs) :-

PDF :
 [ 0.25925926  0.04938272  0.03703704  0.08641975  0.09876543  0.09876543
  0.16049383  0.07407407  0.04938272  0.08641975]

Bin Edges :
 [ 58.   59.1  60.2  61.3  62.4  63.5  64.6  65.7  66.8  67.9  69. ]

-------------------------------------------------------------------------------------------
```



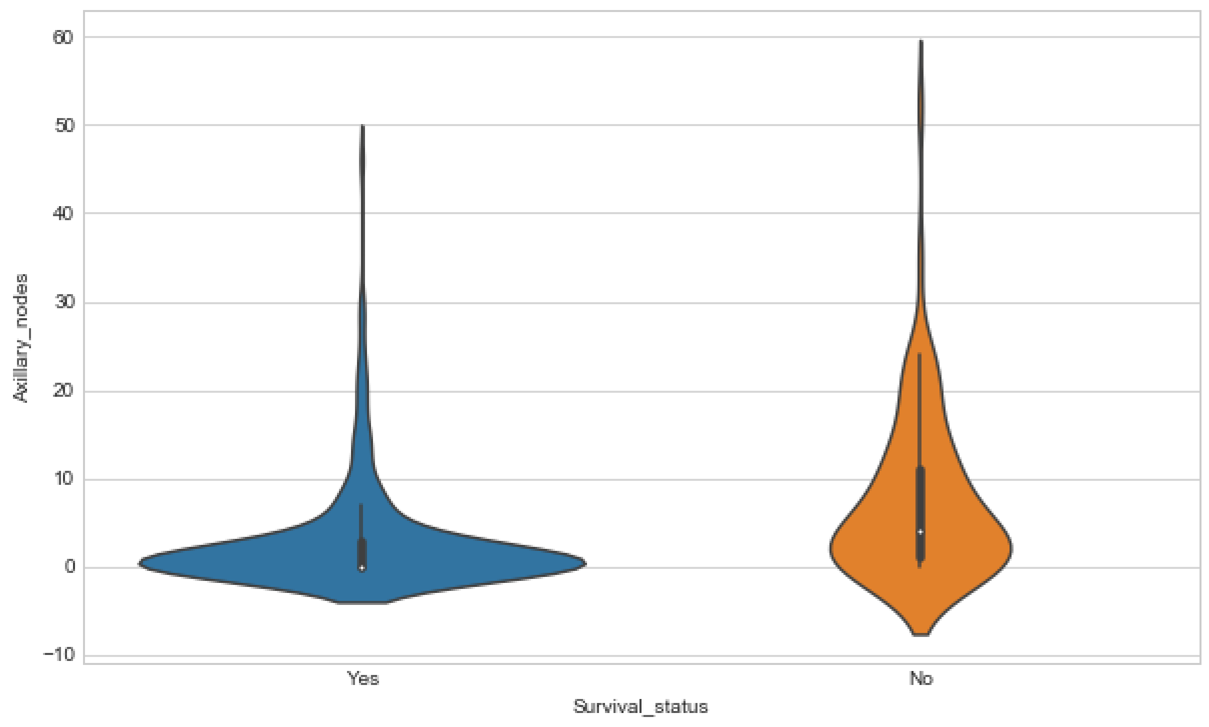
(1.4) Box-plot with whiskers

In [14]:
```
# Box-plot with whiskers is an another method of visualizing the 1-D scatter plot more intuitivey.
plt.figure(figsize=(10, 6))
sns.boxplot(x="Survival_status",y="Axillary_nodes",data=haberman)
plt.show()
```



(1.5) Violin plot

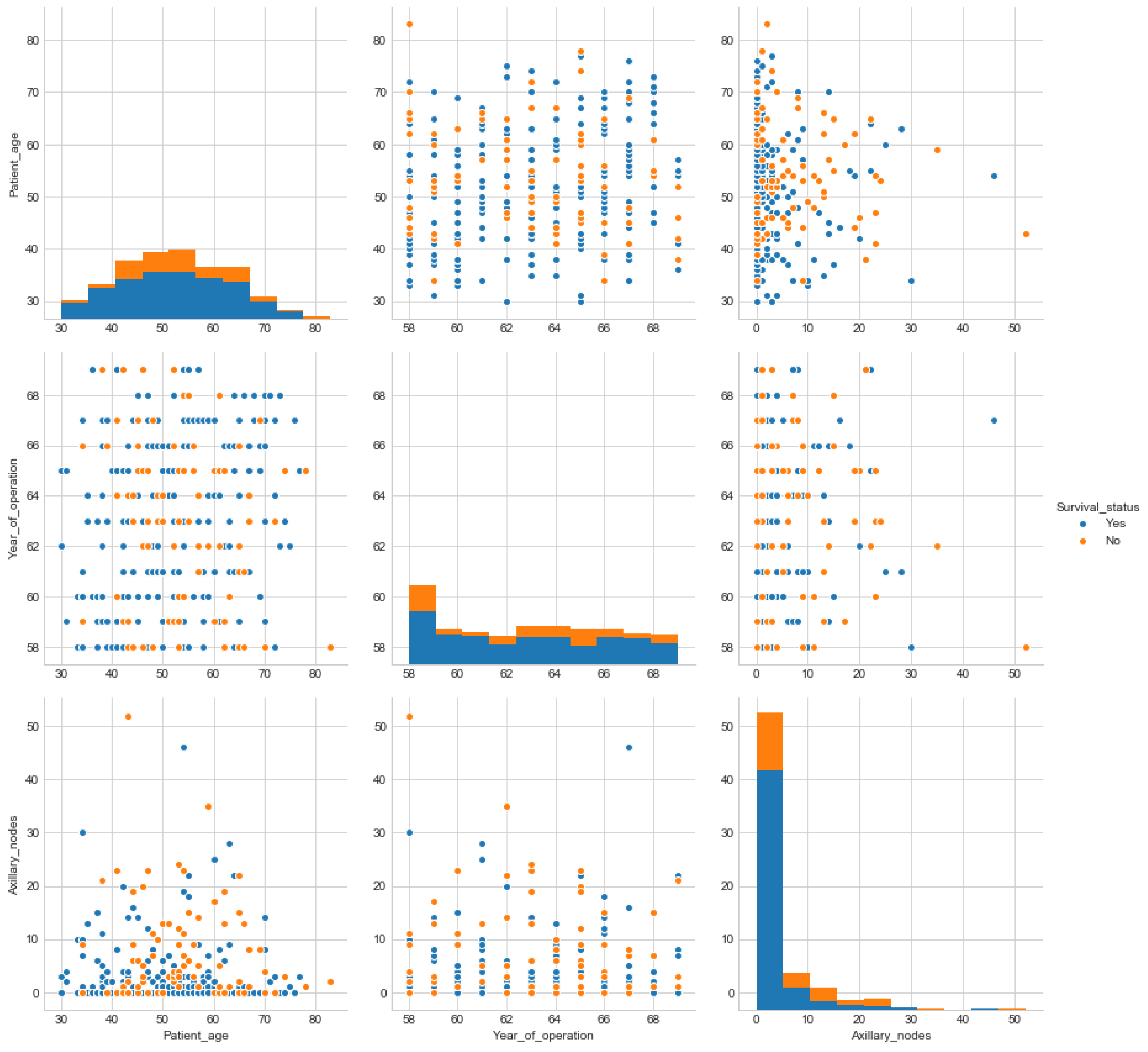
In [15]:
```
# A violin plot combines the benefits of the both, PDF and BoxPlot, and simplifies them.
plt.figure(figsize=(10, 6))
sns.violinplot(x="Survival_status",y="Axillary_nodes",data=haberman)
plt.show()
```



(2) Bivariate Analysis :

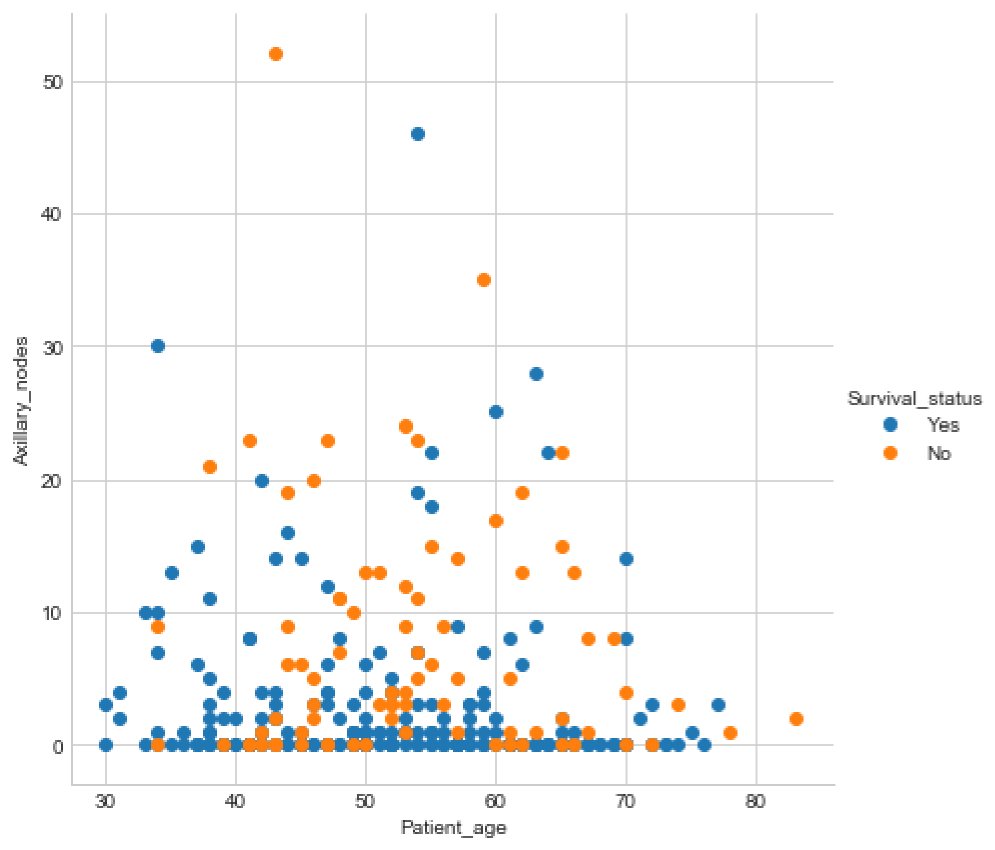
(2.1) Pair Plot

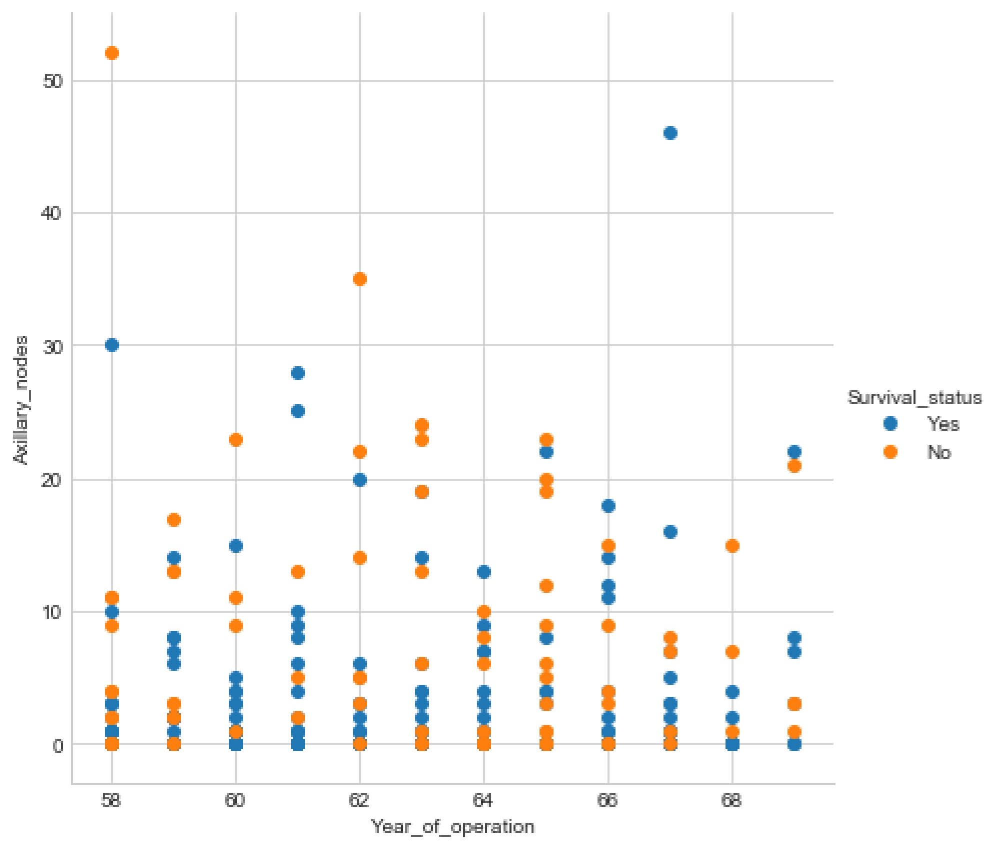
In [16]:
```
# Pair plots are used when number of features are more than 2, to see different
# combinations of features with each other.
# NOTE: the diagnol elements are PDFs for each feature. PDFs are expalined below.
# ,vars=["Patient_age","Year_of_operation","Axillary_nodes"]
plt.close();
sns.set_style("whitegrid")
sns.pairplot(haberman,hue="Survival_status",size=4)
plt.show()
```

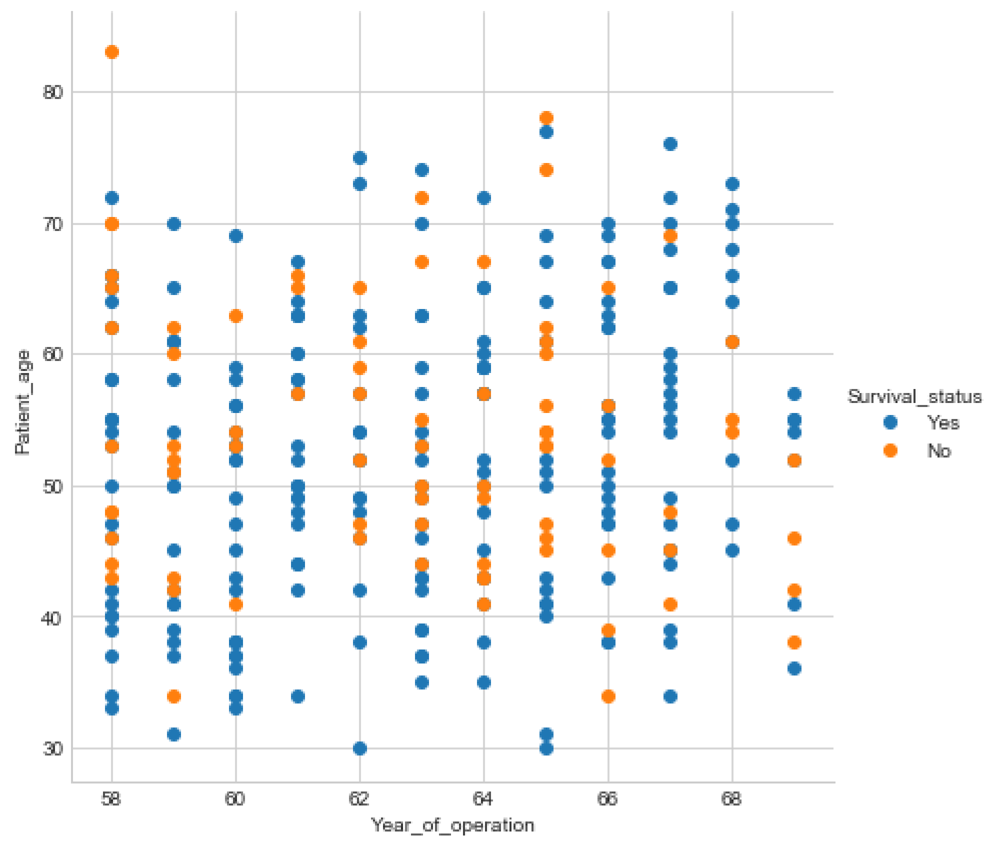


(2.2) 2D-Scatter plot

In [17]:
```
# 2D-Scatter plots is used when number of features is 2.
# Note: From above pair plot figure we can take,
# Axillary_nodes and Patient_age as two features for scatter plot.

sns.set_style("whitegrid")
sns.FacetGrid(haberman,hue="Survival_status",size=6) \
   .map(plt.scatter,'Patient_age','Axillary_nodes') \
   .add_legend()
plt.show()

sns.set_style("whitegrid")
sns.FacetGrid(haberman,hue="Survival_status",size=6) \
   .map(plt.scatter,'Year_of_operation','Axillary_nodes') \
   .add_legend()
plt.show()

sns.set_style("whitegrid")
sns.FacetGrid(haberman,hue="Survival_status",size=6) \
   .map(plt.scatter,'Year_of_operation','Patient_age') \
   .add_legend()
plt.show()
```







Observations :

1. From univariate analysis we found that Axillary_nodes is useful feature for furhter analysis.
2. From bivariate analysis we found that, in correspondence with Axillary_nodes, we can pair two more features like Patient_age and Year_of_operation.
3. All patients who has 0 Axillary_nodes, have greater chance of survival.
4. No patient has survived whose Axillary_nodes is greater than 50.
5. So whether a patient would survive a cancer treatment or not is dependent on Axillary_nodes.if 0 then he/she has high chance of survival and above 50 has low chance of survival.