

EDA_Haberman_Dataset

December 15, 2018

0.1 EDA - Haberman's Survival Data

0.2 Assignment description

- Download Haberman Cancer Survival dataset from Kaggle. You may have to create a Kaggle account to download data. (<https://www.kaggle.com/gilsousa/habermans-survival-dataset>)
- Perform a similar analysis as above on this dataset with the following sections:
- High level statistics of the dataset: number of points, number of features, number of classes, data-points per class.
- Explain our objective.
- Perform Univariate analysis(PDF, CDF, Boxplot, Violin plots) to understand which features are useful towards classification.
- Perform Bi-variate analysis (scatter plots, pair-plots) to see if combinations of features are useful in classification.
- Write your observations in english as crisply and unambiguously as possible. Always quantify your results.

0.3 Dataset qualitative description

Dataset source: (a) Donor: Tjen-Sien Lim (limt@stat.wisc.edu) (b) Date: March 4, 1999

Features 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)

Axillary nodes drain lymph vessels from the lateral quadrants of the breast, and are clinically significant in breast cancer.

Classes * 1 (survived) = the patient survived 5 years or longer * 2 (died) = the patient died within 5 year

```
In [5]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

```
In [6]: haberman = pd.read_csv('./haberman.csv',
                                names = ["age", "operation_year", "axillary_nodes", "survival_status"],

                                # preprocessing to facilitate the analysis
                                haberman.loc[haberman.survival_status == 1, 'survival_status'] = 'survived'
                                haberman.loc[haberman.survival_status == 2, 'survival_status'] = 'died'
```

```
In [7]: # first dataset visualization
print(haberman)
print(haberman.describe())
```

	age	operation_year	axillary_nodes	survival_status
0	30	64	1	survived
1	30	62	3	survived
2	30	65	0	survived
3	31	59	2	survived
4	31	65	4	survived
5	33	58	10	survived
6	33	60	0	survived
7	34	59	0	died
8	34	66	9	died
9	34	58	30	survived
10	34	60	1	survived
11	34	61	10	survived
12	34	67	7	survived
13	34	60	0	survived
14	35	64	13	survived
15	35	63	0	survived
16	36	60	1	survived
17	36	69	0	survived
18	37	60	0	survived
19	37	63	0	survived
20	37	58	0	survived
21	37	59	6	survived
22	37	60	15	survived
23	37	63	0	survived
24	38	69	21	died
25	38	59	2	survived
26	38	60	0	survived
27	38	60	0	survived
28	38	62	3	survived
29	38	64	1	survived
..
276	67	66	0	survived
277	67	61	0	survived
278	67	65	0	survived
279	68	67	0	survived
280	68	68	0	survived
281	69	67	8	died
282	69	60	0	survived
283	69	65	0	survived
284	69	66	0	survived
285	70	58	0	died
286	70	58	4	died
287	70	66	14	survived

288	70	67	0	survived
289	70	68	0	survived
290	70	59	8	survived
291	70	63	0	survived
292	71	68	2	survived
293	72	63	0	died
294	72	58	0	survived
295	72	64	0	survived
296	72	67	3	survived
297	73	62	0	survived
298	73	68	0	survived
299	74	65	3	died
300	74	63	0	survived
301	75	62	1	survived
302	76	67	0	survived
303	77	65	3	survived
304	78	65	1	died
305	83	58	2	died

[306 rows x 4 columns]

	age	operation_year	axillary_nodes
count	306.000000	306.000000	306.000000
mean	52.457516	62.852941	4.026144
std	10.803452	3.249405	7.189654
min	30.000000	58.000000	0.000000
25%	44.000000	60.000000	0.000000
50%	52.000000	63.000000	1.000000
75%	60.750000	65.750000	4.000000
max	83.000000	69.000000	52.000000

0.3.1 1 High level statistics of the dataset

```
In [8]: print(haberman.columns)
        print(haberman.shape)
        # number of points: 306
        # number of features: 3
        # number of classes: 2

        gb = haberman.groupby('survival_status')
        print(gb.count())

        # data-points per class:
        # 1 (the patient survived 5 years or longer): 225
        # 2 (the patient died within 5 year): 81
```

```
Index(['age', 'operation_year', 'axillary_nodes', 'survival_status'], dtype='object')
(306, 4)
```

	age	operation_year	axillary_nodes
survival_status			
died	81	81	81
survived	225	225	225

0.3.2 2 Objective

Classify a new patient that did a surgery for breast cancer as belonging to one of the 2 classes, given the 3 features described in the "Dataset qualitative description" section.

0.3.3 3 Univariate analysis

3.1 PDF

```
In [9]: sns.set_style('whitegrid')
```

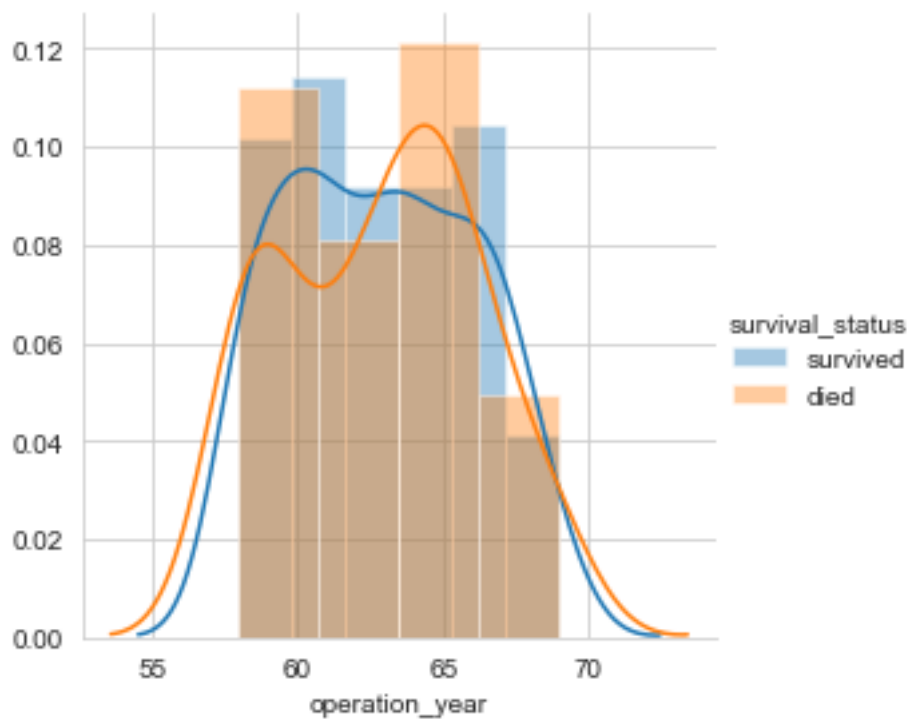
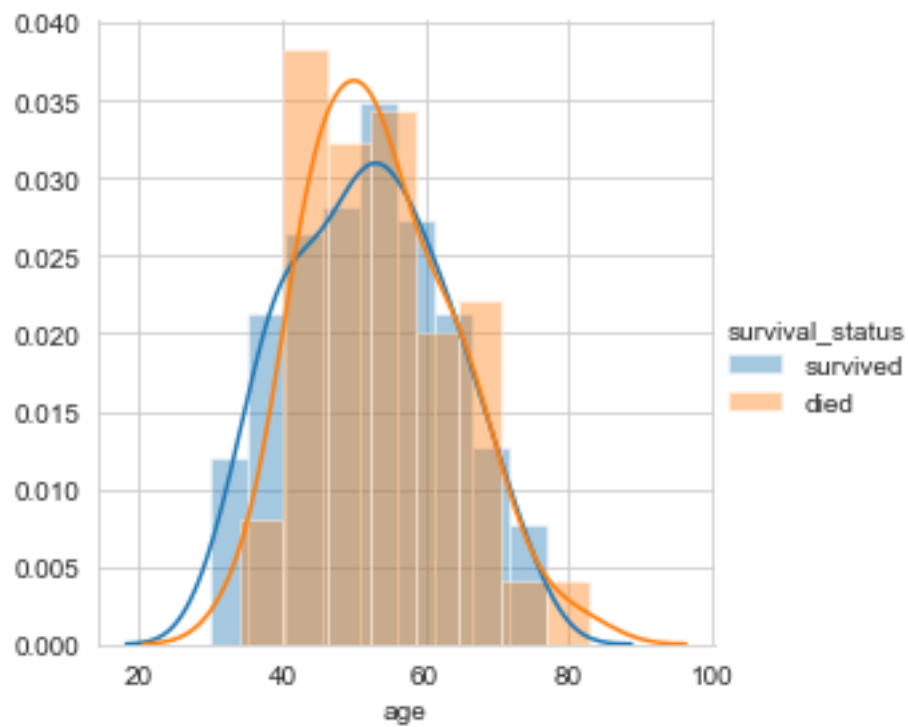
```
sns.FacetGrid(haberman, hue='survival_status', height=4) \
    .map(sns.distplot, 'age') \
    .add_legend()
```

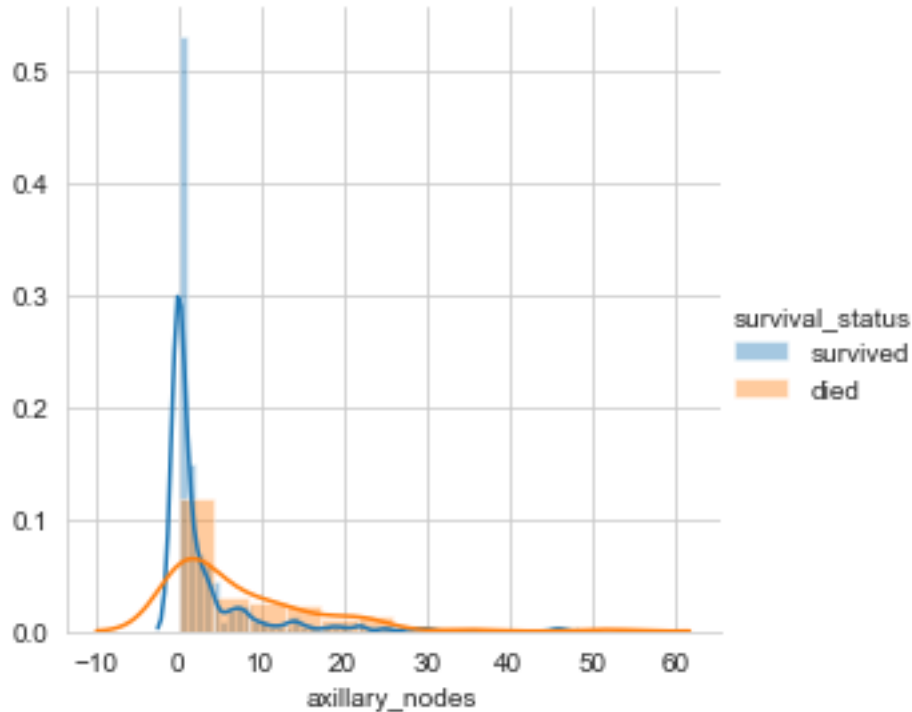
```
sns.FacetGrid(haberman, hue='survival_status', height=4) \
    .map(sns.distplot, 'operation_year') \
    .add_legend()
```

```
sns.FacetGrid(haberman, hue='survival_status', height=4) \
    .map(sns.distplot, 'axillary_nodes') \
    .add_legend()
```

```
plt.show()
```

```
/Users/gustavo.fonseca/anaconda3/lib/python3.7/site-packages/scipy/stats/stats.py:1713: FutureWarning
    return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```





3.1.1 Observation(s) Age and Operation_year graphs: * They both assume a normal distribution; * Both of their classes overlap tremendously, therefore, they do not appear to be separable.

Axillary_nodes graph: * It assumes a right skewed form; * Both classes overlap; * The PDF of the survived class is much higher in approx 0 axillary_nodes.

3.2 CDF Based on the PDF plot, age and operation_year do not appear as promising for univariate analysis as axillary_nodes. Hence, only the axillary nodes' CDF is plotted for further visualization and analysis.

```
In [10]: # divide the classes to perform separate analysis
haberman_survived = haberman.loc[haberman["survival_status"] == "survived"];
haberman_died = haberman.loc[haberman["survival_status"] == "died"];

In [11]: plt.figure(1)
plt.title('Axillary nodes PDF / CDF')

# survived
counts, bin_edges = np.histogram(haberman_survived.axillary_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)
```

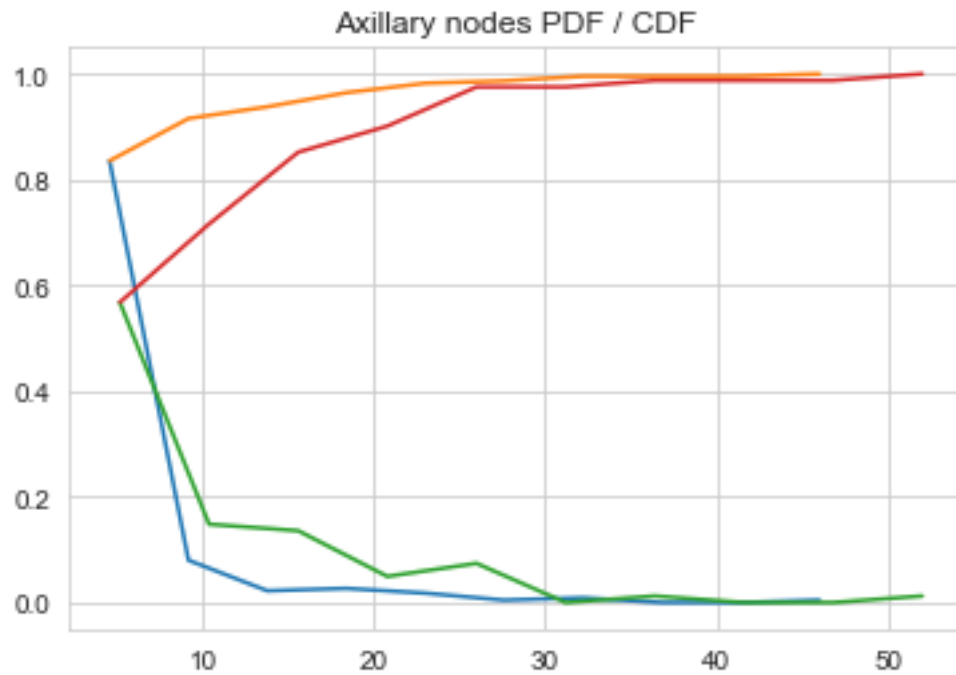
```

# died
counts, bin_edges = np.histogram(haberman_died.axillary_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()

```



3.2.2 Observations

- At the 10 axillary nodes removal lies: approx 90% of all survivals and 70% of all non-survivals;
- With only one feature, it doesn't seem to exist a basic model capable of separating both classes efficiently.

3.3 Box and Whiskers

In [12]: plt.close()

```

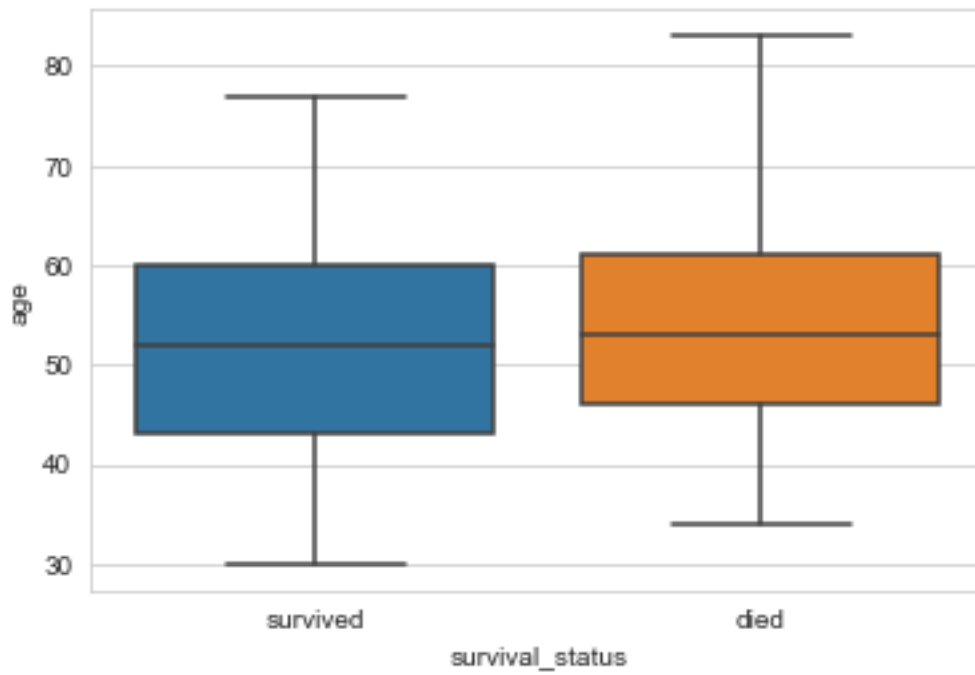
plt.figure(1)
sns.boxplot(x='survival_status', y='age', data=haberman)

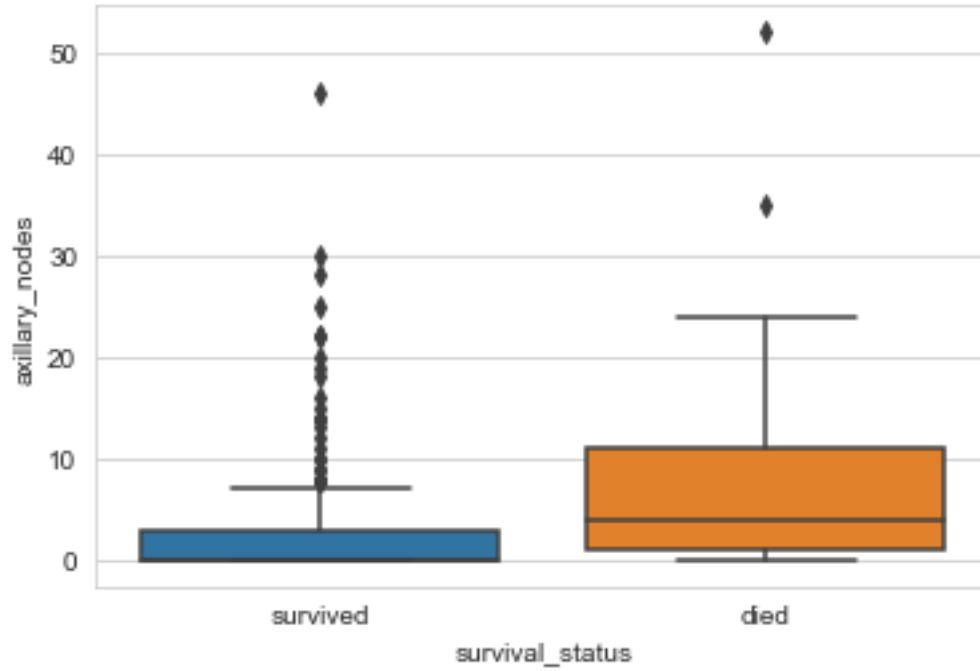
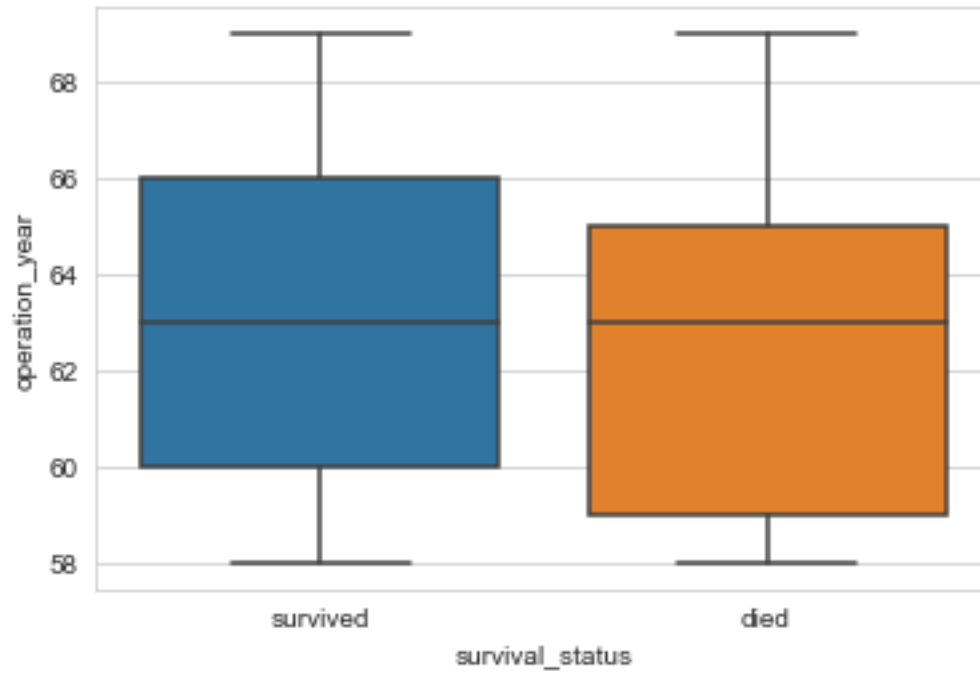
```

```
plt.figure(2)
sns.boxplot(x='survival_status', y='operation_year', data=haberman)

plt.figure(3)
sns.boxplot(x='survival_status', y='axillary_nodes', data=haberman)

plt.show()
```





3.3.1 Observations Age graph: * Both classes have a very similar median, ranging between 52 - 54; * Even though both classes' boxes are in a similar range, older patients seem to die more frequently.

Operation year: * Both classes seem to have an identical median, approx 63; * Both classes lies in a similar range, but patients who have an older operation year, seem to die more frequently.

Axillary nodes: * There are a significant number of outliers; * It appears to be the most promising feature to reach the objective of this model; * Patients that remove less axillary_nodes appears to have a higher survival chance;

3.4 Violin

```
In [13]: plt.close()
```

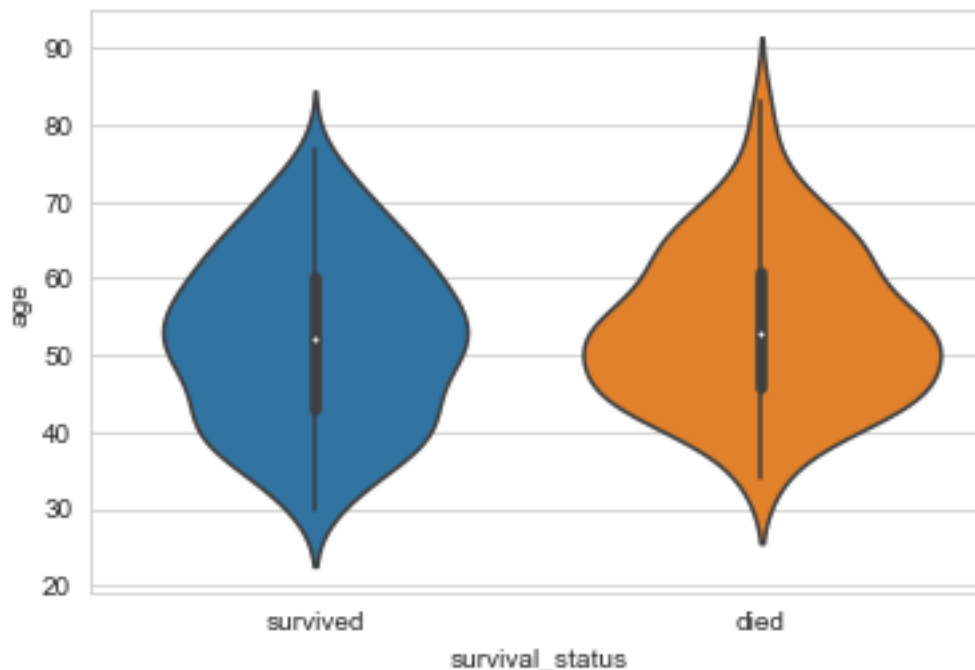
```
plt.figure(1)
sns.violinplot(x="survival_status", y="age", data=haberman, size=8)

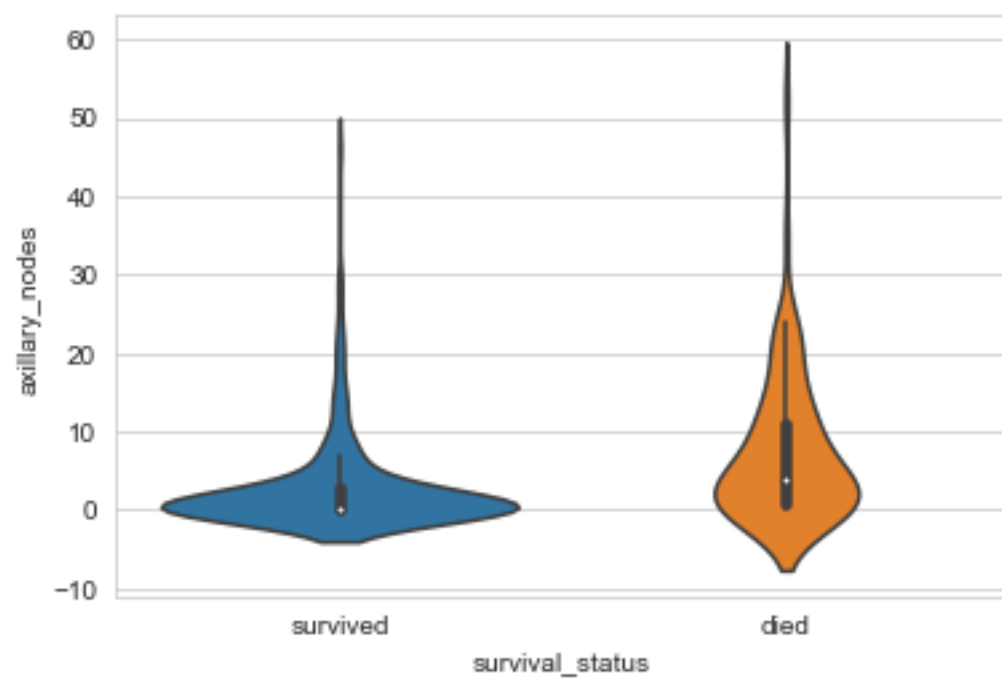
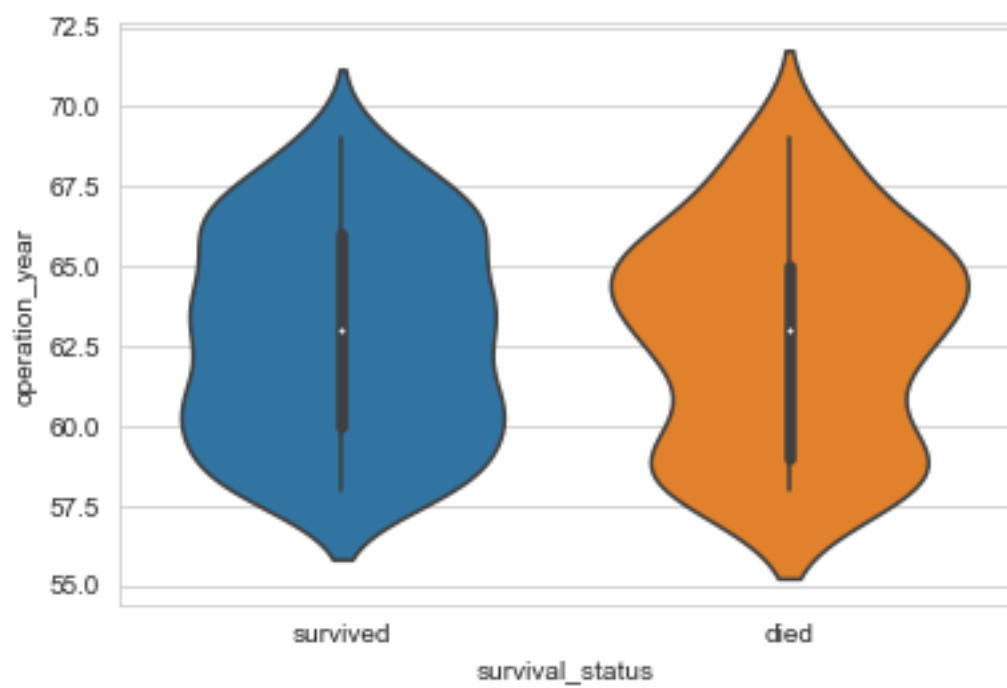
plt.figure(2)
sns.violinplot(x="survival_status", y="operation_year", data=haberman, size=8)

plt.figure(3)
sns.violinplot(x="survival_status", y="axillary_nodes", data=haberman, size=8)

plt.show()
```

```
/Users/gustavo.fonseca/anaconda3/lib/python3.7/site-packages/scipy/stats/stats.py:1713: FutureWarning
return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```





3.4.1 Observations

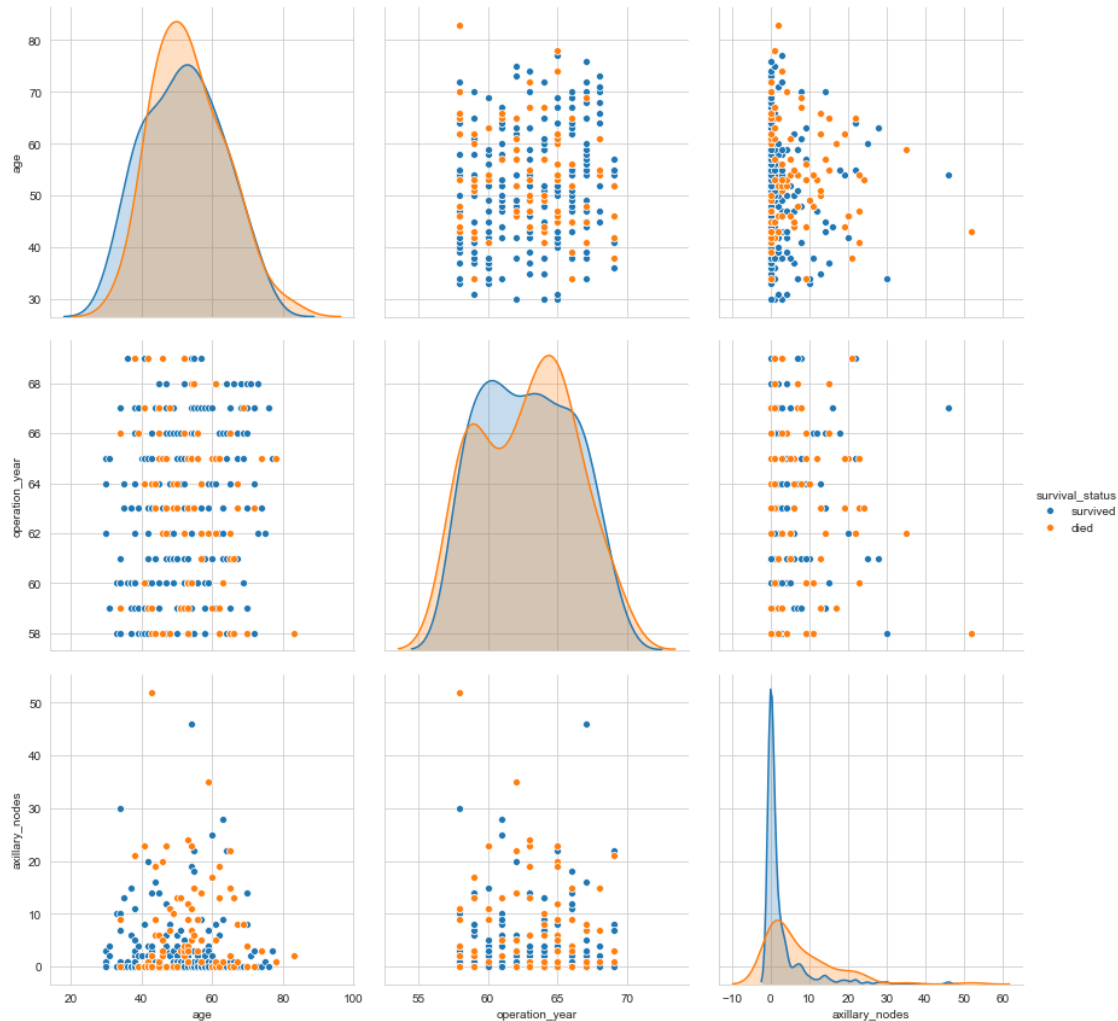
- The violin plot shows that patients that remove 0 axillary nodes have a high probability of survival.

0.3.4 4. Bivariate analysis

4.1 Pair plots

```
In [14]: plt.close();  
sns.set_style("whitegrid");  
sns.pairplot(haberman, hue="survival_status", height=4);  
plt.show()
```

```
/Users/gustavo.fonseca/anaconda3/lib/python3.7/site-packages/scipy/stats/stats.py:1713: FutureWarning  
return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```



4. 2 Observations

- Apparently there is no pair of features that could linearly separate both classes effectively;
- The most promising feature for classification seems to be axillary_nodes;
- We can't build a simple model with 'if' and 'else' to separate both classes efficiently.