3.1 EDA on Haberman Dataset

In [18]:
```
import warnings

warnings.filterwarnings("ignore")
```

In [3]:
```
#importing all the libraries

import pandas as pd
import seaborn as sns
import numpy as np
import matplotlib.pyplot as plt
import matplotlib.patches as mpatches
haberman = pd.read_csv("habermans.csv")
haberman.head()
```

Out[3]:

	age	op_year	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

In [4]:
```
# data-points and features?
print (haberman.shape)
```

```
(306, 4)
```

In [5]:
```
#name column names in our dataset?
print (haberman.columns)
```

```
Index(['age', 'op_year', 'axil_nodes', 'survival_status'], dtype='objec
t')
```

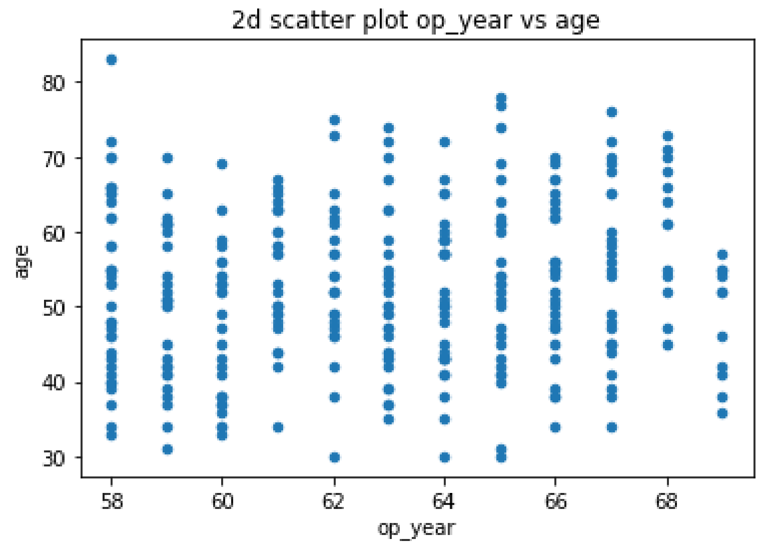
In [7]:
```
#how many datapoints for each  status is present
haberman["survival_status"].value_counts()
```

Out[7]:
```
1    225
2     81
Name: survival_status, dtype: int64
```

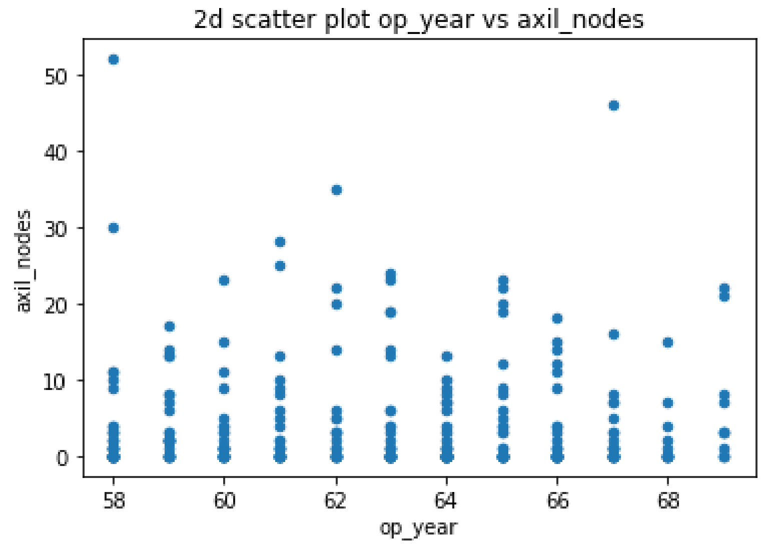
observation:It concludes that 225 (status -1) patients are survived more than 5 years, and 81 (status-2) patients are survived less than 5 years

(3.2) 2-D Scatter Plot

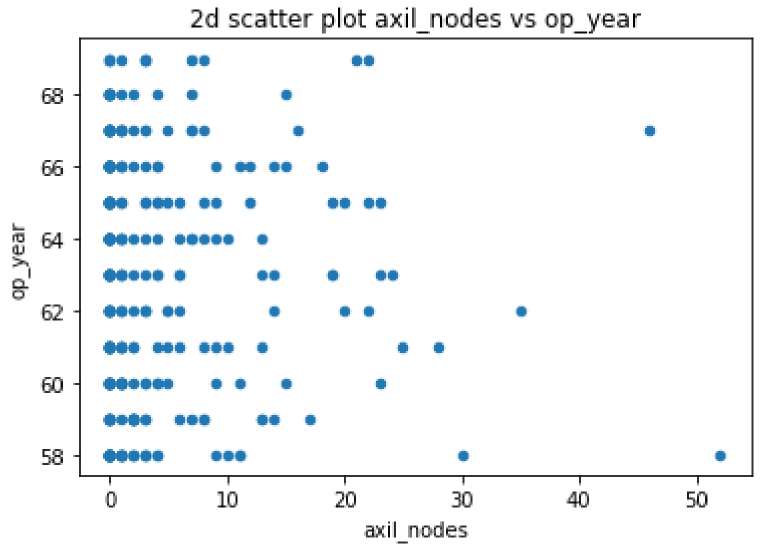
In [8]:
```
haberman.plot(kind='scatter', x='op_year', y='age') ;
plt.title('2d scatter plot op_year vs age')
#plt.grid()
plt.show()
```



In [9]:
```
haberman.plot(kind='scatter', x='op_year', y='axil_nodes') ;
plt.title('2d scatter plot op_year vs axil_nodes')
plt.show()
```

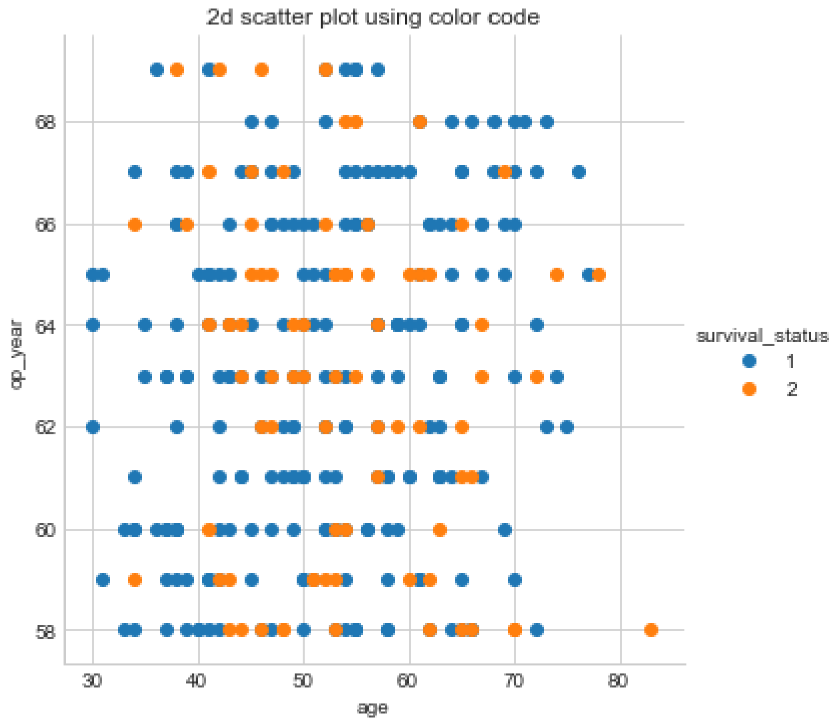


In [10]:
```
haberman.plot(kind='scatter', x='axil_nodes', y='op_year') ;
plt.title('2d scatter plot axil_nodes vs op_year')
plt.show()
```

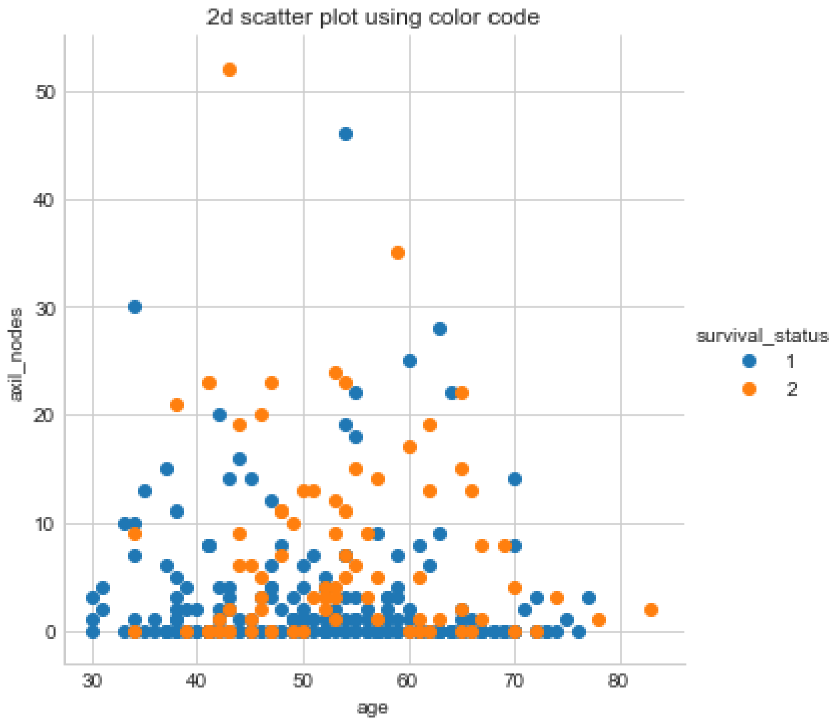


observation: in 2d scatter plot i had drawn 3 plots in between age,year,nodes it shows all the data in overlap fashoin and also in same color unable to distinguish between the data

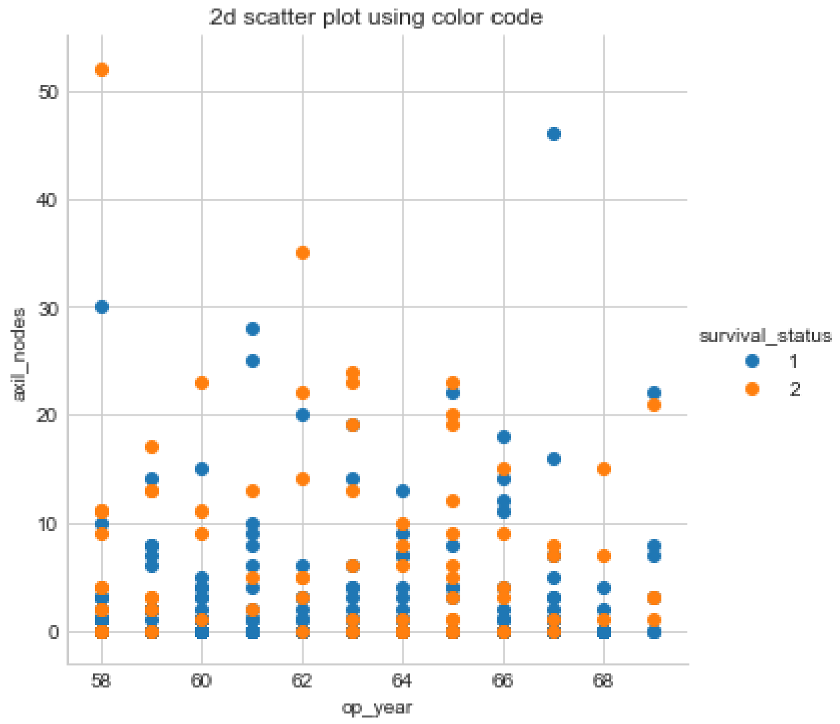
In [11]:
```
#2d scatter plot using color code for the survival status in haberman
import seaborn as sns
import matplotlib.pyplot as plt
sns.set_style("whitegrid");
sns.FacetGrid(haberman, hue="survival_status", size=5)\
   .map(plt.scatter, "age", "op_year")\
   .add_legend();
plt.title('2d scatter plot using color code')
plt.show();
```



In [12]:
```
import seaborn as sns
import matplotlib.pyplot as plt
sns.set_style("whitegrid");
sns.FacetGrid(haberman, hue="survival_status", size=5)\
   .map(plt.scatter, "age", "axil_nodes")\
   .add_legend();
plt.title('2d scatter plot using color code')
plt.show();
```



In [14]:
```python
import seaborn as sns
import matplotlib.pyplot as plt
sns.set_style("whitegrid");
sns.FacetGrid(haberman, hue="survival_status", size=5)\
   .map(plt.scatter, "op_year", "axil_nodes")\
   .add_legend();
plt.title('2d scatter plot using color code')
plt.show();
```

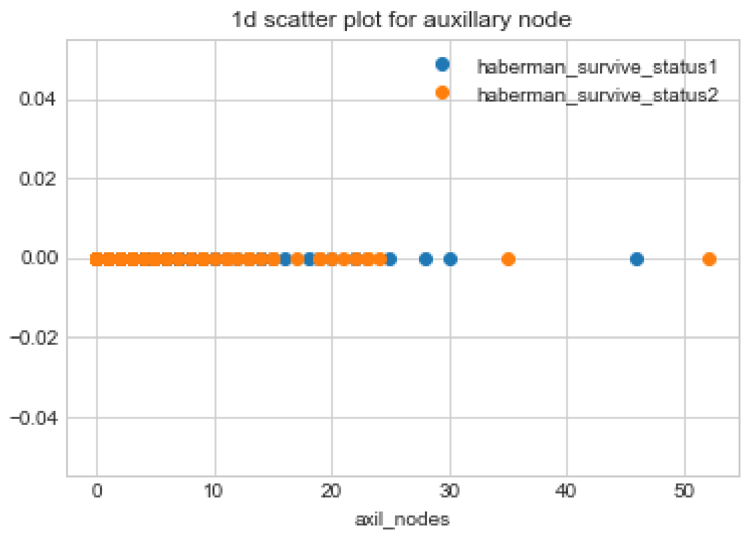


observation: i have imported function like facetgrid from seaborn library due to which we are able to distinguish between the colors since both colors are still overlapping cannot differnetiate for survival status

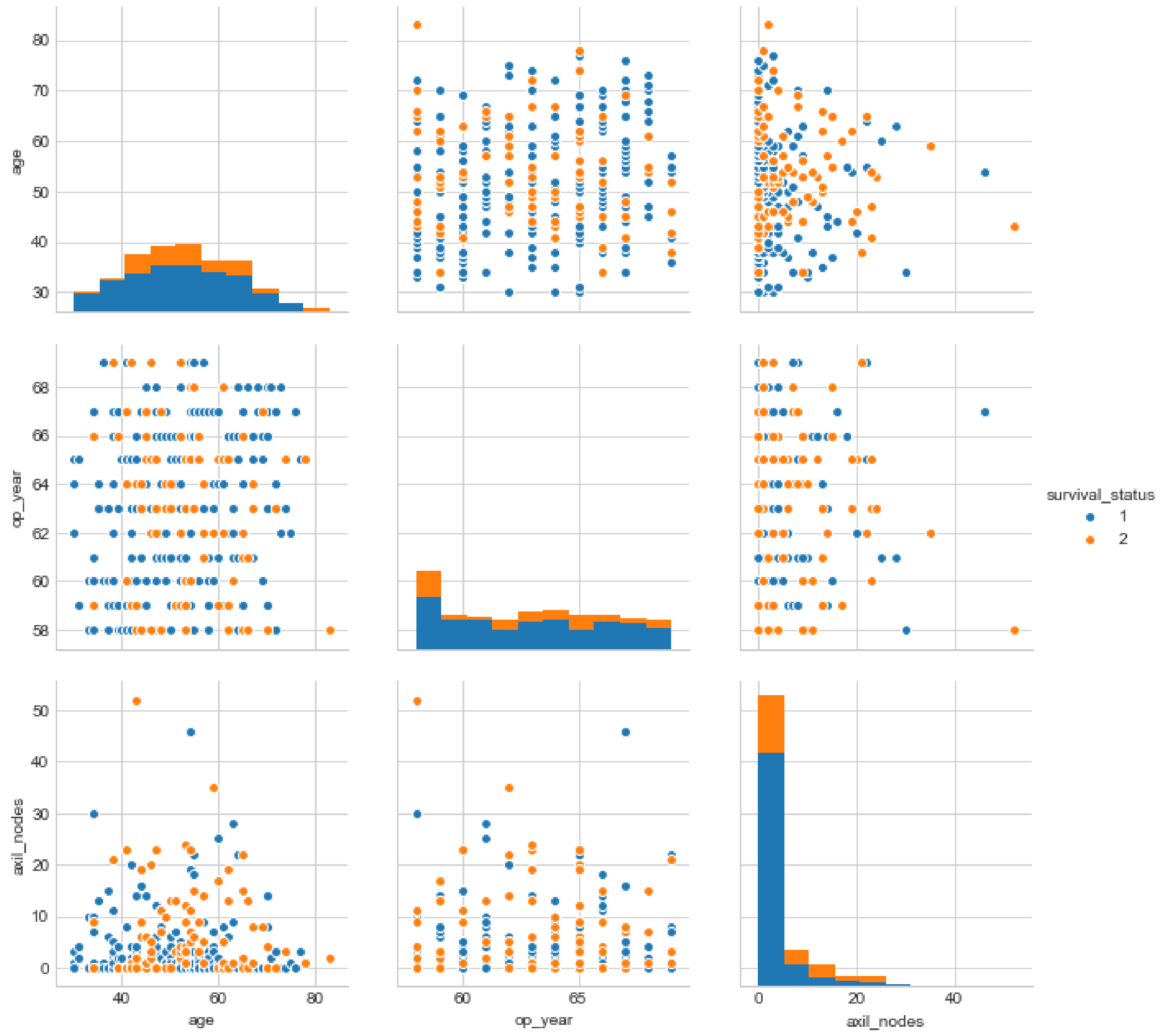
(3.3) Pair-plot

In [50]:
```
#1-D scatter plot of auxillary nodes
import numpy as np
haberman_survive_status1 = haberman.loc[haberman["survival_status"] ==
1];
haberman_survive_status2 = haberman.loc[ haberman["survival_status"] ==
 2];
plt.plot(haberman_survive_status1["axil_nodes"], np.zeros_like(haberman
_survive_status1['axil_nodes']), 'o')
```

```
plt.plot(haberman_survive_status2["axil_nodes"], np.zeros_like(haberman
_survive_status2['axil_nodes']), 'o')
plt.xlabel('axil_nodes')
plt.title('1d scatter plot for auxillary node')
plt.gca().legend(('haberman_survive_status1','haberman_survive_status2'
))




plt.show()
```



In [16]:
```
sns.set_style("whitegrid");
sns.pairplot(haberman, hue="survival_status", size=3, vars = ['age', 'o
p_year', 'axil_nodes'])


plt.show()
```

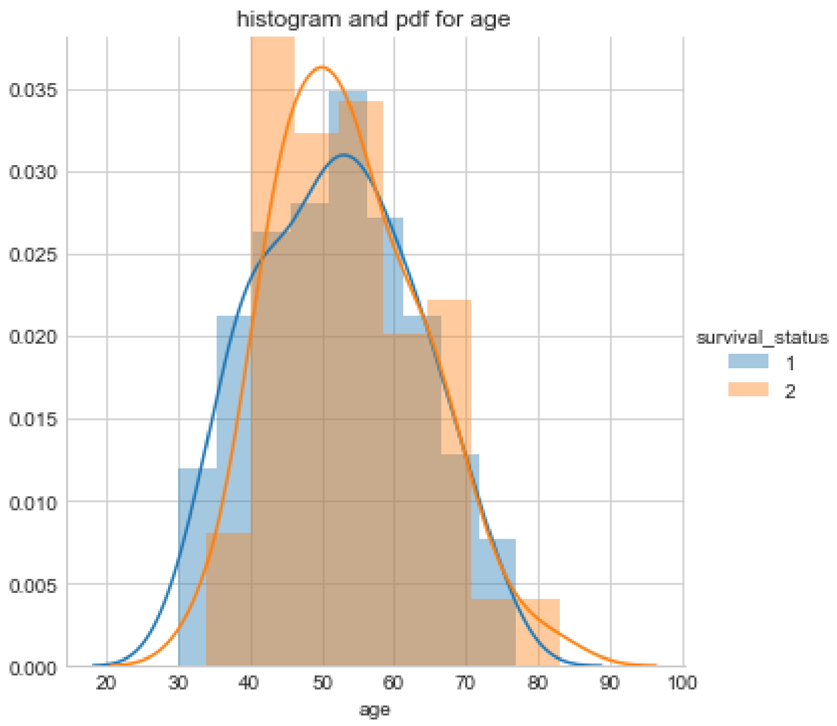


observation:

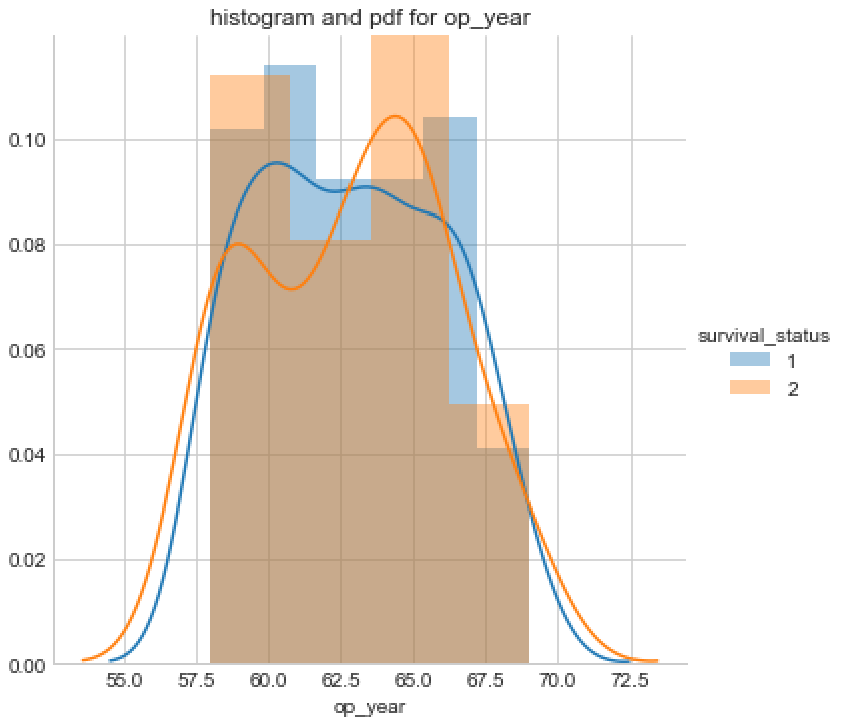
Above upper diagnoal and lower diagnoal graphs are same, only the axis between them are interchanged .and also all the datapoints are in overlapped state cannot distinguish between them.

(3.4) Histogram, PDF, CDF

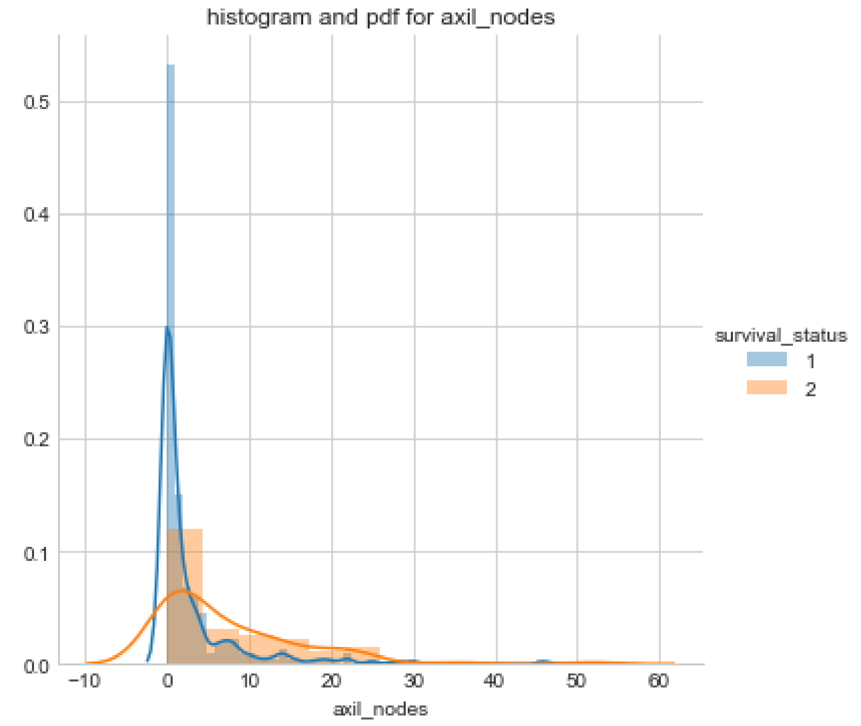
In [19]:
```
sns.FacetGrid(haberman, hue="survival_status", size=5)\
   .map(sns.distplot, "age")\
   .add_legend();
plt.title('histogram and pdf for age')
plt.show();
```



In [20]:
```
sns.FacetGrid(haberman, hue="survival_status", size=5) \
   .map(sns.distplot, "op_year") \
   .add_legend();
plt.title('histogram and pdf for op_year')
plt.show();
```



In [21]:
```
sns.FacetGrid(haberman, hue="survival_status", size=5) \
   .map(sns.distplot, "axil_nodes") \
   .add_legend();
plt.title('histogram and pdf for axil_nodes')
plt.show();
```

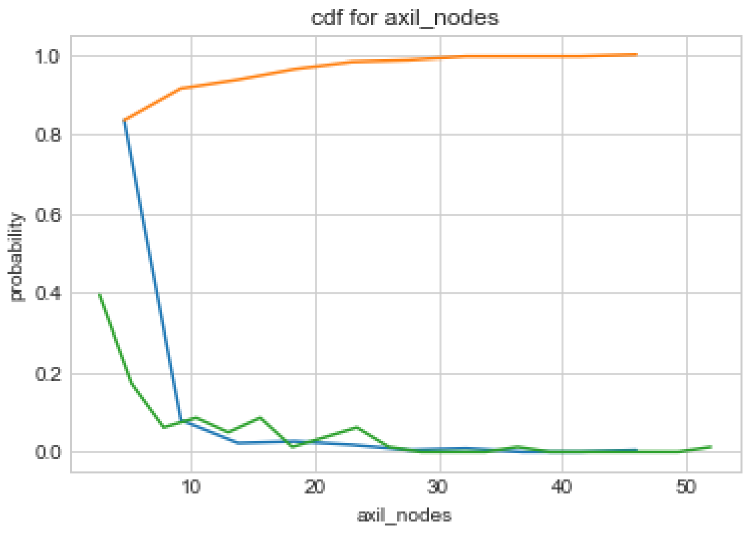


observation:

- plot-1 : Major overlapping is observed, which tells us that survival chances are irrespective of a person’s age.
- plot-2 : There is major overlapping observed.
- plot-3 : Patients with no nodes or 1 node are more likely to survive. There are very few chances of surviving if there are 25 or more nodes.

In [55]:
```
#plotting cdf for nodes
counts, bin_edges = np.histogram(haberman_survive_status1['axil_nodes'
], bins=10,
                                              density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges);
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)
plt.xlabel('axil_nodes')
plt.ylabel('probability')



counts, bin_edges = np.histogram(haberman_survive_status2['axil_nodes'
], bins=20,
                                 density = True)
pdf = counts/(sum(counts))
plt.plot(bin_edges[1:],pdf);
plt.title('cdf for axil_nodes')

plt.show();
```

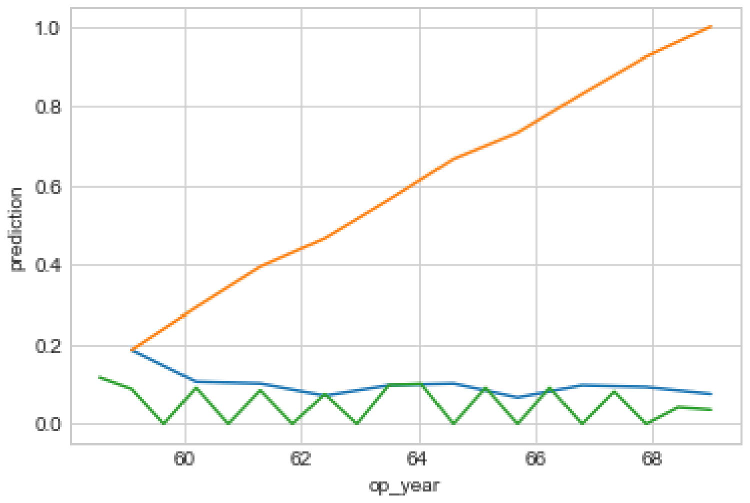
```
[0.83555556 0.08       0.02222222 0.02666667 0.01777778 0.00444444
 0.00888889 0.         0.         0.00444444]
[ 0.   4.6  9.2 13.8 18.4 23.  27.6 32.2 36.8 41.4 46. ]
```



```
In [56]: #plotting cdf for year
```

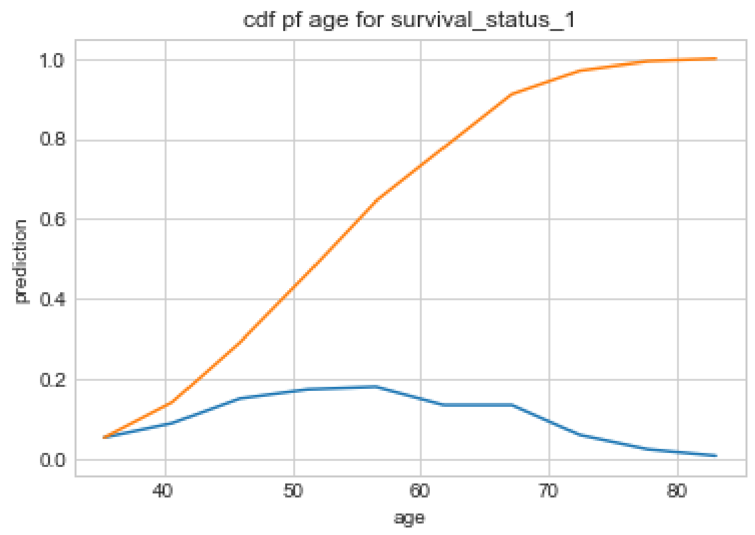
```
counts, bin_edges = np.histogram(haberman_survive_status1['op_year'], b
ins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges);
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)
plt.xlabel('op_year')
plt.ylabel('prediction')


counts, bin_edges = np.histogram(haberman['op_year'], bins=20,
                              density = True)
pdf = counts/(sum(counts))
plt.plot(bin_edges[1:],pdf);


plt.show();
```

```
[0.18666667 0.10666667 0.10222222 0.07111111 0.09777778 0.10222222
 0.06666667 0.09777778 0.09333333 0.07555556]
[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
```



In [47]:
```
#plotting cdf for ages
counts, bin_edges = np.histogram(haberman['age'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges);
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)
plt.xlabel('age')
plt.ylabel('prediction')
plt.title('cdf pdf age for survival_status_1')


counts, bin_edges = np.histogram(haberman['age'], bins=20,
                                density = True)
pdf = counts/(sum(counts))
plt.plot(bin_edges[1:],pdf);

plt.show();
```

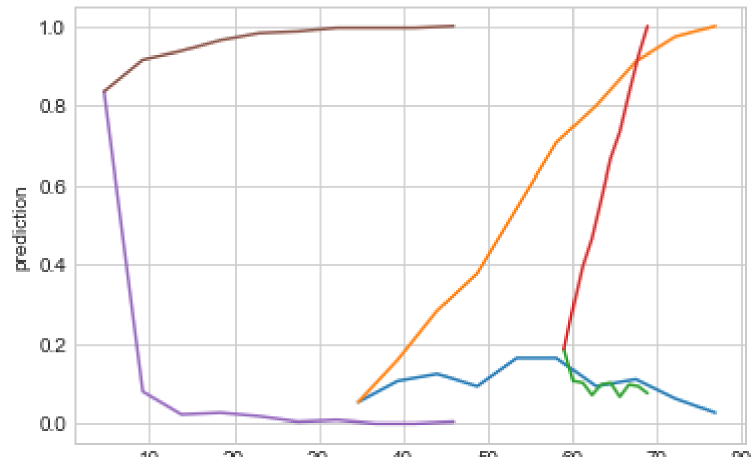
```
[0.05228758 0.08823529 0.1503268  0.17320261 0.17973856 0.13398693
 0.13398693 0.05882353 0.02287582 0.00653595]
[30.  35.3 40.6 45.9 51.2 56.5 61.8 67.1 72.4 77.7 83. ]
```



In [57]:
```
#plotting cdf at a time for all the features
counts, bin_edges = np.histogram(haberman_survive_status1['age'], bins=
10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


# op_year
counts, bin_edges = np.histogram(haberman_survive_status1['op_year'], b
ins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)
```

```
# axil_nodes
counts, bin_edges = np.histogram(haberman_survive_status1['axil_nodes'
], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)
plt.ylabel('prediction')


plt.show();
```

```
[0.05333333 0.10666667 0.12444444 0.09333333 0.16444444 0.16444444
 0.09333333 0.11111111 0.06222222 0.02666667]
[30.  34.7 39.4 44.1 48.8 53.5 58.2 62.9 67.6 72.3 77. ]
[0.18666667 0.10666667 0.10222222 0.07111111 0.09777778 0.10222222
 0.06666667 0.09777778 0.09333333 0.07555556]
[58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]
[0.83555556 0.08       0.02222222 0.02666667 0.01777778 0.00444444
 0.00888889 0.         0.         0.00444444]
[ 0.   4.6  9.2 13.8 18.4 23.  27.6 32.2 36.8 41.4 46. ]
```



(3.5) Mean, Variance and Std-dev

In [26]:

```
import numpy as np
print("Means for axil node feature")
print('mean for survival status-1 people',np.mean(haberman_survive_stat
us1['axil_nodes']))
print('mean for survival status-2 people',np.mean(haberman_survive_stat
us1['axil_nodes']))
print('Mean with an outlier')
print('meanfor survival status-1 people',np.mean(np.append(haberman_sur
vive_status1['axil_nodes'],50))); #added outier point to find out the m
ean
print('mean for survival status-2 people',np.mean(haberman_survive_stat
us2['axil_nodes']))


print("\nStd-dev:");
print('standard deviation of status_1 people :',np.std(haberman_survive
_status1['axil_nodes']))
print('standard deviation of status_1 people:',np.std(haberman_survive_
status2['axil_nodes']))
```

```
Means for axil node feature
mean for survival status-1 people 2.7911111111111113
mean for survival status-2 people 2.7911111111111113
Mean with an outlier
meanfor survival status-1 people 3.0
mean for survival status-2 people 7.45679012345679

Std-dev:
standard deviation of status_1 people : 5.857258449412131
standard deviation of status_1 people: 9.128776076761632
```

3.6 Median, Percentile, Quantile, IQR, MAD

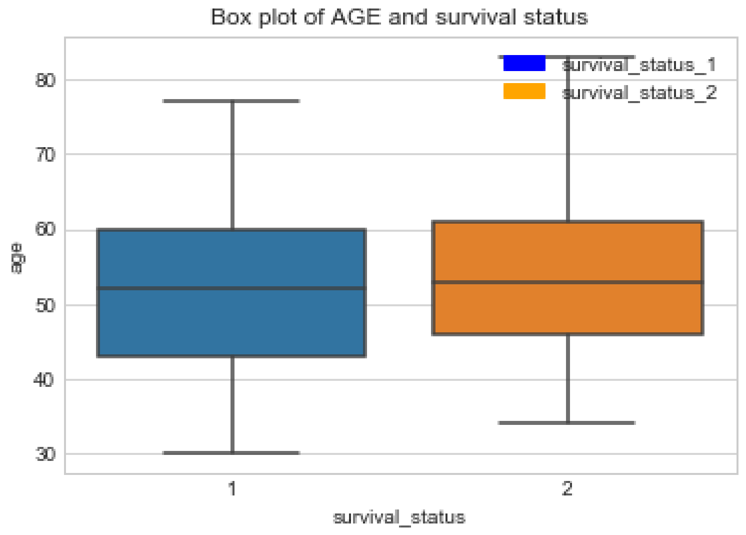
In [27]:
```python
import numpy as np
print("\nMedians:")
print(np.median(haberman_survive_status1["axil_nodes"]))
#Median with an outlier
print(np.median(np.append(haberman_survive_status1["axil_nodes"],50)))
print(np.median(haberman_survive_status2["axil_nodes"]))



print("\nQuantiles:")
print(np.percentile(haberman_survive_status1["axil_nodes"],np.arange(0,
 100, 25)))
print(np.percentile(haberman_survive_status2["op_year"],np.arange(0, 10
0, 25)))


print("\n90th Percentiles:")
print(np.percentile(haberman_survive_status1["axil_nodes"],90))
print(np.percentile(haberman_survive_status2["axil_nodes"],90))


from statsmodels import robust
print ("\nMedian Absolute Deviation")
print(robust.mad(haberman_survive_status1["axil_nodes"]))
print(robust.mad(haberman_survive_status2["axil_nodes"]))
```

```
Medians:
0.0
0.0
4.0

Quantiles:
[0. 0. 0. 3.]
[58. 59. 63. 65.]

90th Percentiles:
8.0
20.0
```

```
Median Absolute Deviation

0.0
5.930408874022408
```

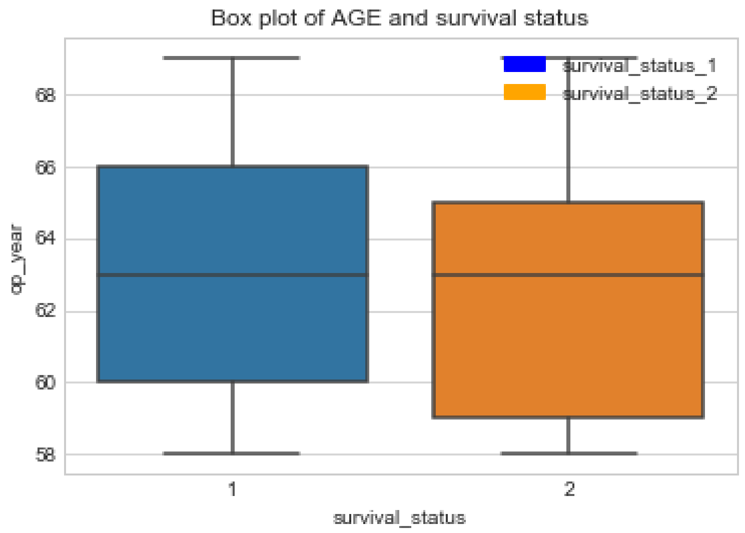
(3.7) Box plot and Whiskers

In [41]:
```
sns.boxplot(x='survival_status',y='age', data=haberman).set_title('Box
 plot of AGE and survival status')
blue_patch = mpatches.Patch(color='blue', label='survival_status_1')
orange_patch = mpatches.Patch(color='orange', label='survival_status_2'
)
plt.legend(handles=[blue_patch,orange_patch],loc=1)
plt.show()
```

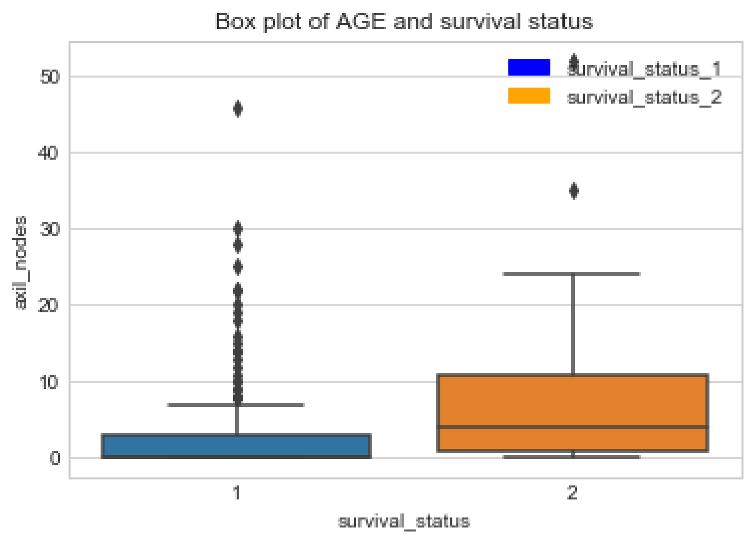


In [32]:
```
sns.boxplot(x='survival_status',y='op_year', data=haberman).set_title(
'Box plot of AGE and survival status')
blue_patch = mpatches.Patch(color='blue', label='survival_status_1')
orange_patch = mpatches.Patch(color='orange', label='survival_status_2'
)
```

```
plt.legend(handles=[blue_patch,orange_patch],loc=1)
plt.show()
```

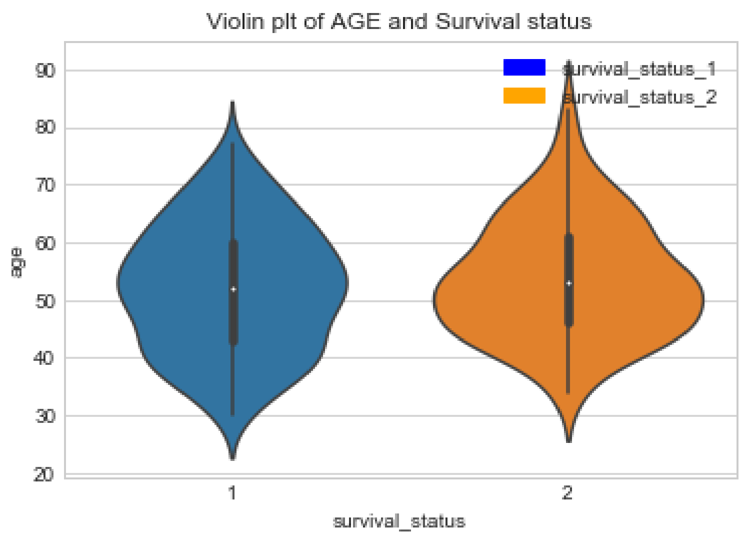


In [34]:
```
sns.boxplot(x='survival_status',y='axil_nodes', data=haberman).set_titl
e('Box plot of AGE and survival status')
blue_patch = mpatches.Patch(color='blue', label='survival_status_1')
orange_patch = mpatches.Patch(color='orange', label='survival_status_2'
)
plt.legend(handles=[blue_patch,orange_patch],loc=1)
plt.show()
```

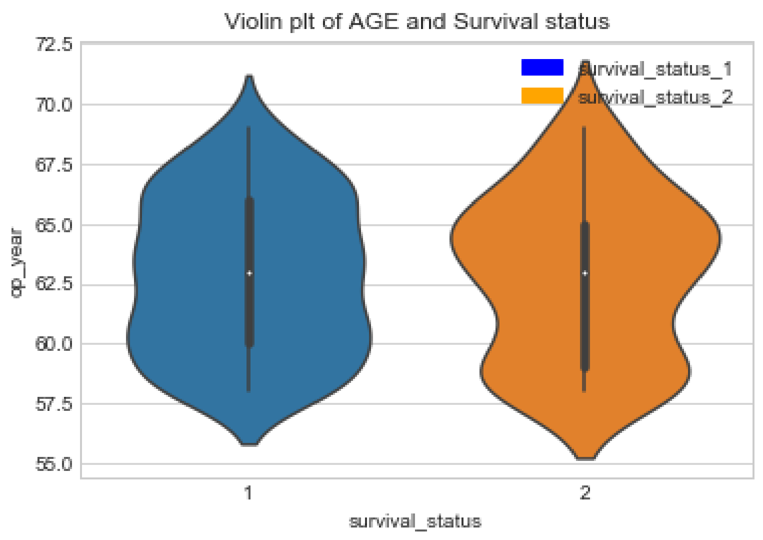


(3.8) Violin plots

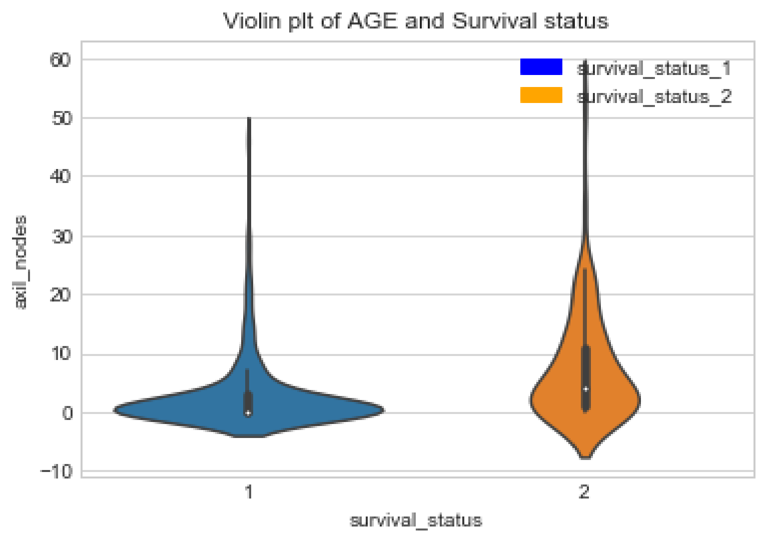
In [35]:
```
sns.violinplot(x="survival_status", y="age", data=haberman, size=8)
plt.title('Violin plt of AGE and Survival status')
blue_patch = mpatches.Patch(color='blue', label='survival_status_1')
orange_patch = mpatches.Patch(color='orange', label='survival_status_2'
)
plt.legend(handles=[blue_patch,orange_patch],loc=1)
plt.show()
```



In [37]:
```
sns.violinplot(x="survival_status", y="op_year", data=haberman, size=8)
plt.title('Violin plt of AGE and Survival status')
blue_patch = mpatches.Patch(color='blue', label='survival_status_1')
orange_patch = mpatches.Patch(color='orange', label='survival_status_2'
)
plt.legend(handles=[blue_patch,orange_patch],loc=1)
plt.show()
```

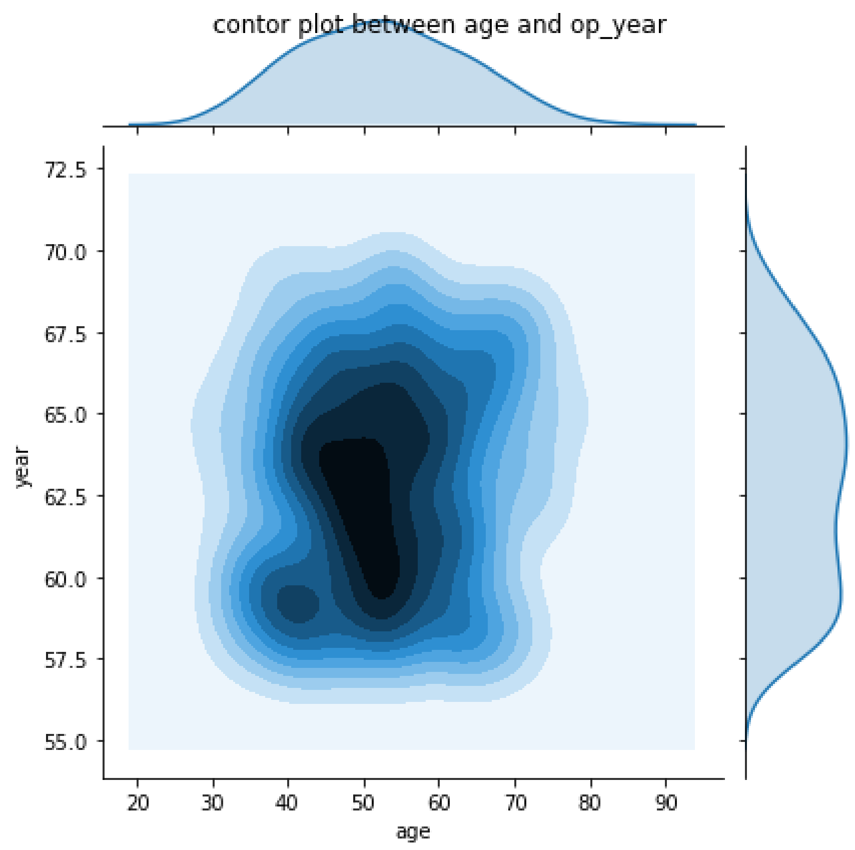


In [42]:
```
sns.violinplot(x="survival_status", y="axil_nodes", data=haberman, size
=8)
plt.title('Violin plt of AGE and Survival status')
blue_patch = mpatches.Patch(color='blue', label='survival_status_1')
orange_patch = mpatches.Patch(color='orange', label='survival_status_2'
)
plt.legend(handles=[blue_patch,orange_patch],loc=1)
plt.show()
```

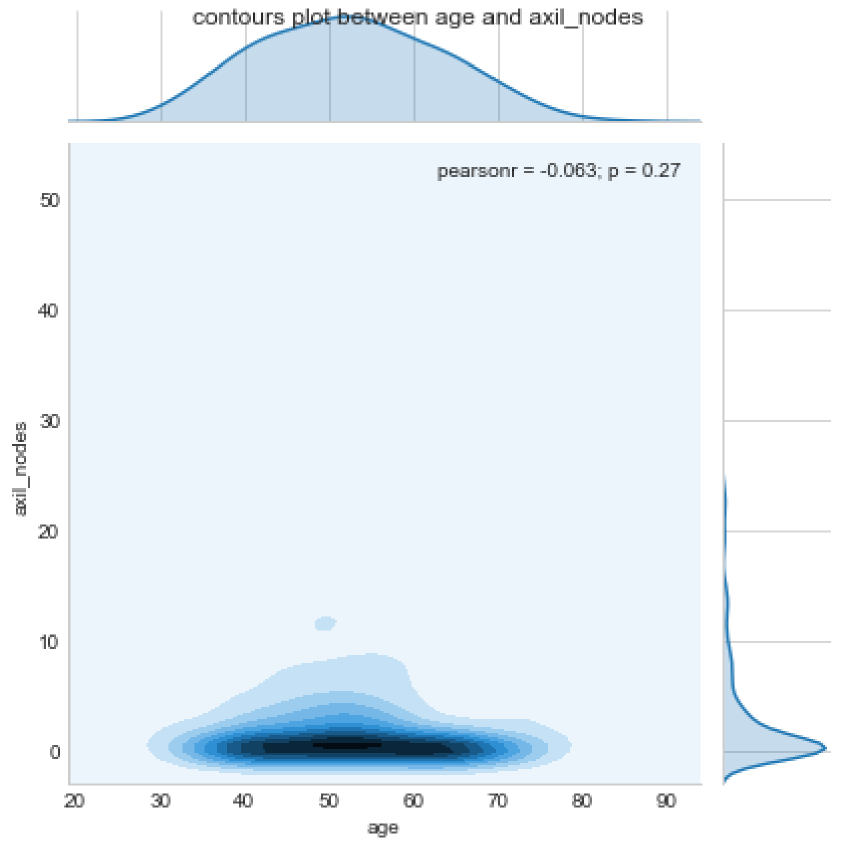


(3.9) Multivariate probability density, contour plot.

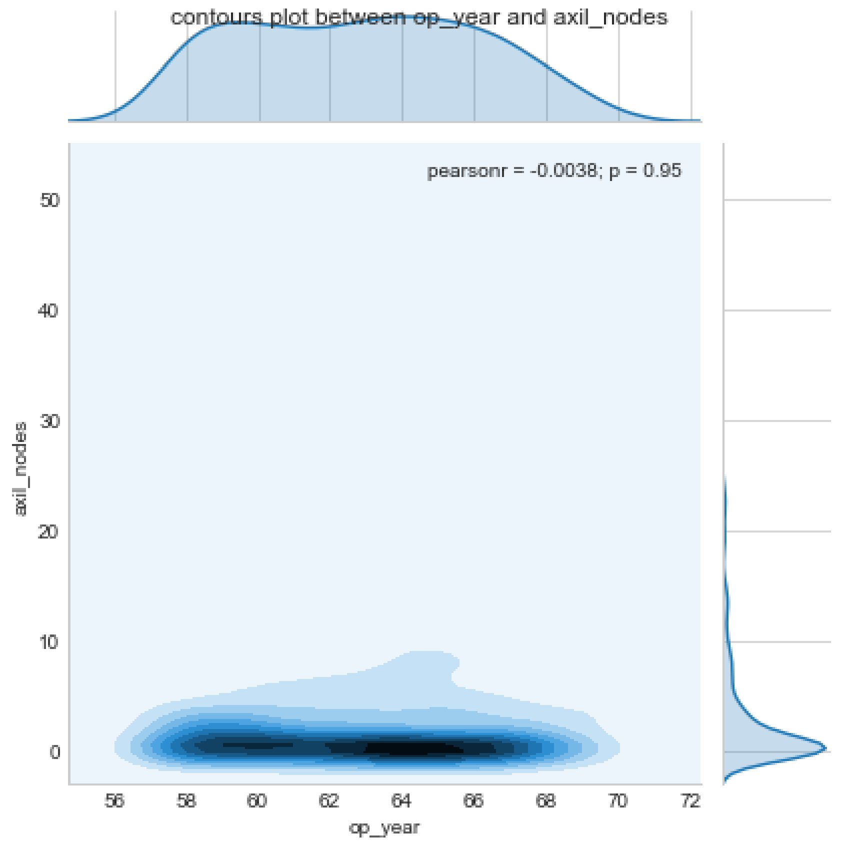
In [34]:
```
#2D Density plot, contors-plot
import seaborn as sns
sns.jointplot(x="age", y="year", data=haberman, kind="kde");
plt.suptitle('contor plot between age and op_year')
plt.show();
```



In [39]:
```
#2D Density plot, contors-plot
import seaborn as sns
sns.jointplot(x="age", y="axil_nodes", data=haberman, kind="kde");
plt.suptitle('contours plot between age and axil_nodes')
plt.show();
```



In [40]:
```
#2D Density plot, contors-plot
import seaborn as sns
sns.jointplot(x="op_year", y="axil_nodes", data=haberman, kind="kde");
plt.suptitle('contours plot between op_year and axil_nodes')
plt.show();
```



conclusion:

- Patient’s age and operation year alone are not deciding factors for his/her survival.
- if number of auxillary nodes are less chances of surviving is more i can say Survival chance is inversely proportional to the number of positive axillary nodes.But, We also saw that the absence of positive axillary nodes cannot always guarantee survival.
- The objective of classifying the survival status of a patient based on the given features is a difficult task as the data is imbalanced.