```
# Importing Required Libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

```
# Loding the dataset
haberman = pd.read_csv("haberman.csv")
haberman.head()
```

	age	year	nodes	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

1.1 Analyze high level statistics of the dataset:

```
print(haberman.shape)
```

```
(306, 4)
```

```
print(haberman.columns)
```

```
Index(['age', 'year', 'nodes', 'status'], dtype='object')
```

Number of data points: 306

Number of features: 4 (including class attribute[Status])

```
print(haberman.info())
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 306 entries, 0 to 305
Data columns (total 4 columns):
 #   Column  Non-Null Count  Dtype
---  ------  --------------  -----
 0   age     306 non-null    int64
 1   year    306 non-null    int64
```

```
     2   nodes   306 non-null    int64
     3   status  306 non-null    int64
    dtypes: int64(4)
    memory usage: 9.7 KB
    None
```

Feature Info:

Age: Age of patient at the time of operation (Numerical)

Year: Patient's year of operation (Numerical)

Nodes: Number of positive axillary nodes detected (Numerical)

Status: Survival status (Numerical)

1: patient survived 5 years or longer

2: patient died within 5 years

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

```
    1    225
    2     81
    Name: status, dtype: int64
```

Observation:

The Haberman is imbalanced dataset as the number of datapoints for each class is different

1.2 Objective:

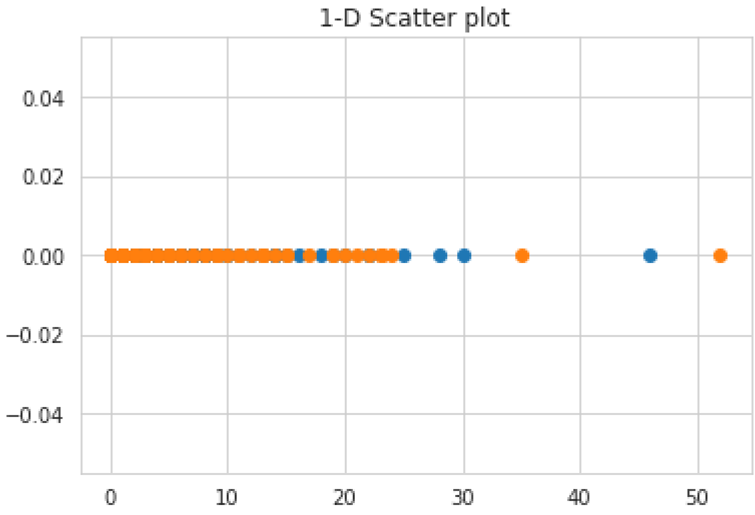
- Classify the patient survival status whether
  he/she will survive 5 years or longer Or
  he/she will survive 5 year or less, based on given attributes

1-D Scatter Plot

From the given dataset we are ploting datapoints for axillary nodes with the survival Status

```
survive = haberman.loc[haberman['status'] == 1] # status 1 is survived
dead = haberman.loc[haberman['status']==2]  # status 2 is not nor survived
```

```
plt.plot(survive["nodes"],np.zeros_like(survive['nodes']),'o')
plt.plot(dead["nodes"],np.zeros_like(dead['nodes']),'o')
plt.title('1-D Scatter plot')
plt.show()
```



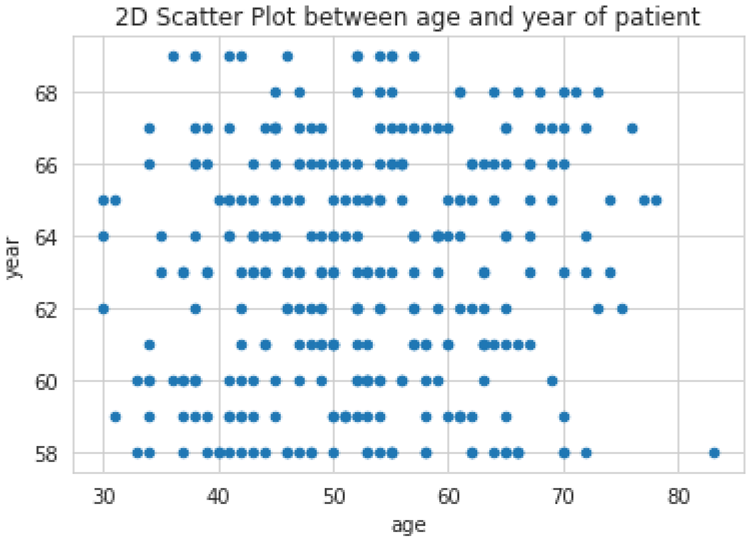
Observations:

1. A lot of overlapping datapoints at every instance
2. We must try to plot 2-d scatter plot

2-D Scatter Plot

We are now ploting each pair of features from given attributes

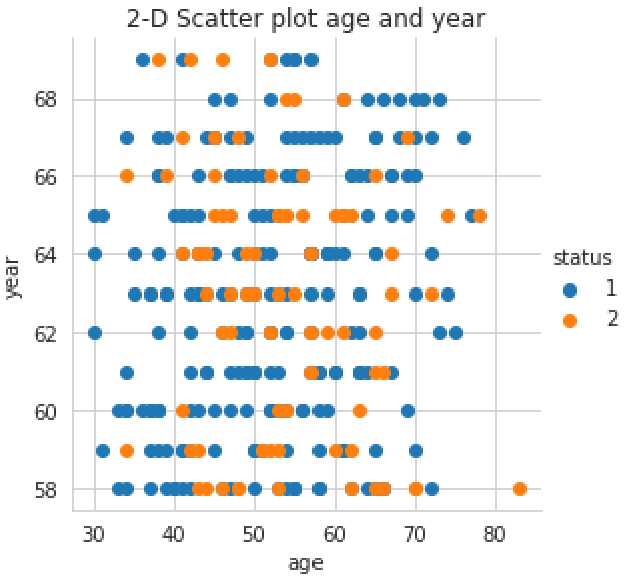
```
haberman.plot(kind='scatter', x='age', y='year')
plt.title('2D Scatter Plot between age and year of patient')
plt.show()
```



Observation:

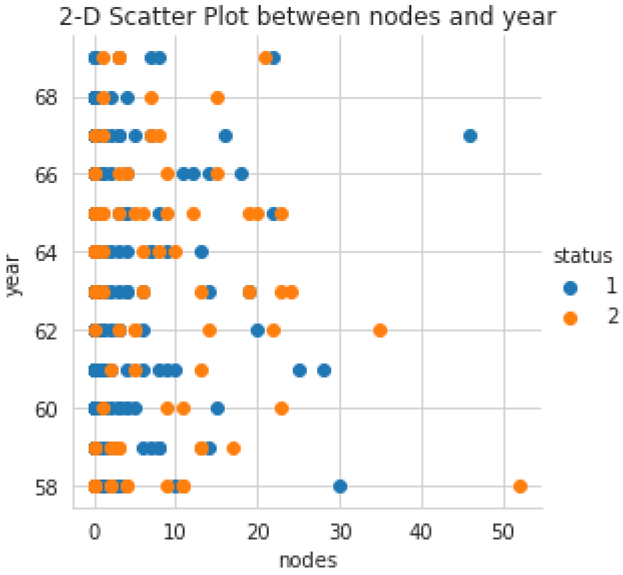
1. We are not able to make sense out of it
2. Lets try it out with giving some color to each features data points

```
# 2-D Scatter plot with color-coding for each status
# seaborn is refferred as sns
# age & year
sns.set_style('whitegrid')
sns.FacetGrid(haberman, hue='status', size=4)\
              .map(plt.scatter, "age", "year")\
              .add_legend()
plt.title('2-D Scatter plot age and year')
plt.show()
```



```
# age & nodes
sns.set_style('whitegrid')
sns.FacetGrid(haberman, hue='status', size=4)\
              .map(plt.scatter, "age", "nodes")\
              .add_legend()
plt.title('2-D Scatter plot between age and nodes')
plt.show()
```

```
# nodes & year
sns.set_style('whitegrid')
sns.FacetGrid(haberman, hue='status', size=4)\
              .map(plt.scatter, "nodes", "year")\
              .add_legend()
plt.title('2-D Scatter Plot between nodes and year')
plt.show()
```



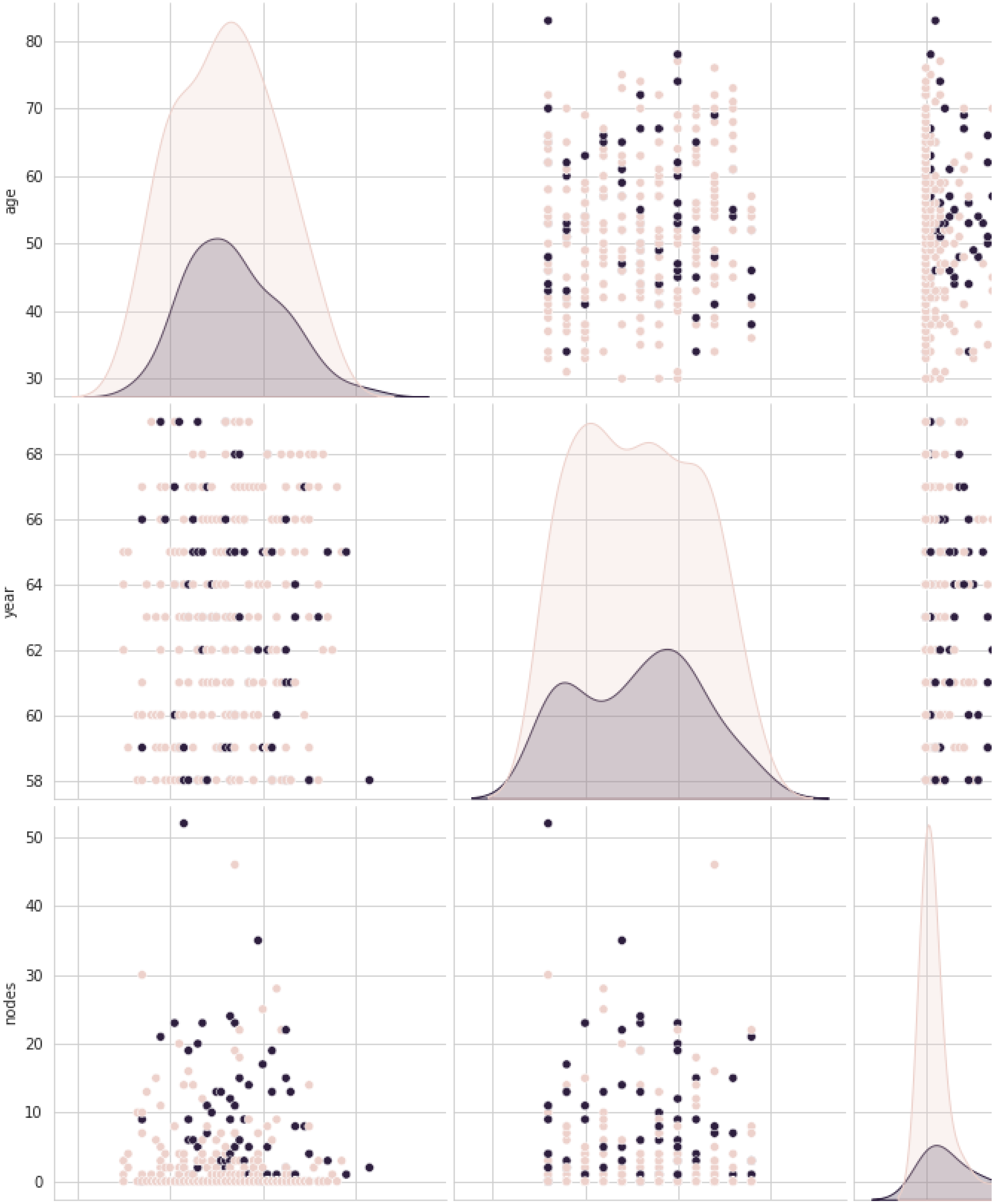
Observations:

1. Neither of the parameter were able to clearly distinguish between status 1 and 2.
2. We should come up with other plot for diff features for better understanding

Pair Plot

Most of the time there can be multiple features in dataset we need to gain insights as n-dimension. But we human can not see dimensions more 3-d, so to gain more insights from n-d dataset we use pair plots to get all combinations of features plotted against each other.

```
plt.close()
sns.set_style("whitegrid")
sns.pairplot(haberman, hue="status", height=4);
plt.title('Pair plot')
plt.show()
# Note: The Diagonal element if PDF of each combination
```



Observations:

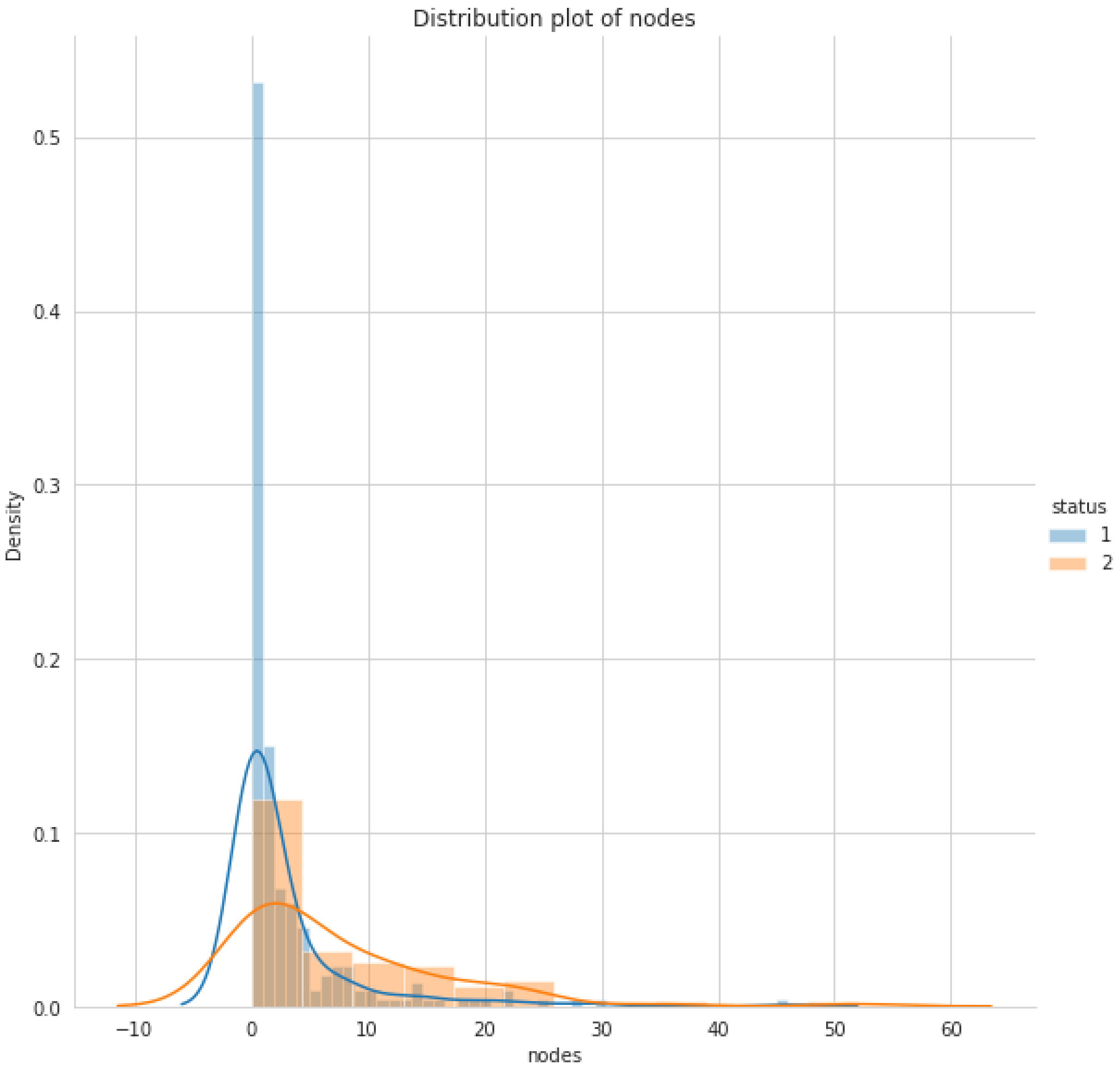
1. scatter plot between "age and nodes" is comparatively better than other scatter plot which we can classify the status.

2. younger people have higher chances of survival

3. Adding if..else condition we can build a simple model

Histogram, PDF's, CDF's

```
# distribution plot of nodes
sns.FacetGrid(haberman, hue="status", height=8)\
              .map(sns.distplot, "nodes")\
              .add_legend();
plt.title('Distribution plot of nodes')
plt.show()
```

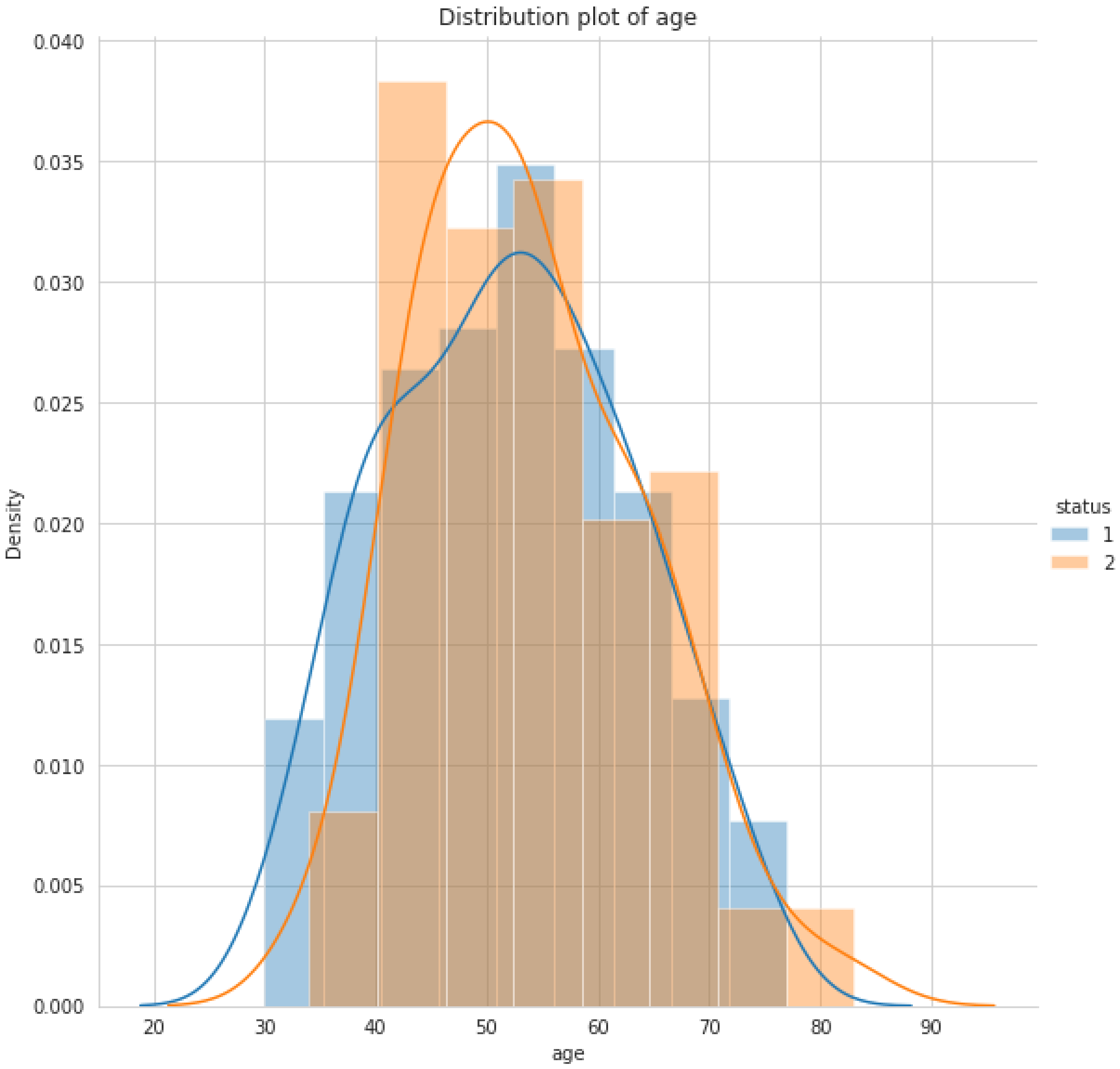


Observations:

1. There is denser region near 0-5 for the PDF(Its the probability of (status) over the max value from x-axis) of node column.

2. Which means patients with lower node have better probability of surviving

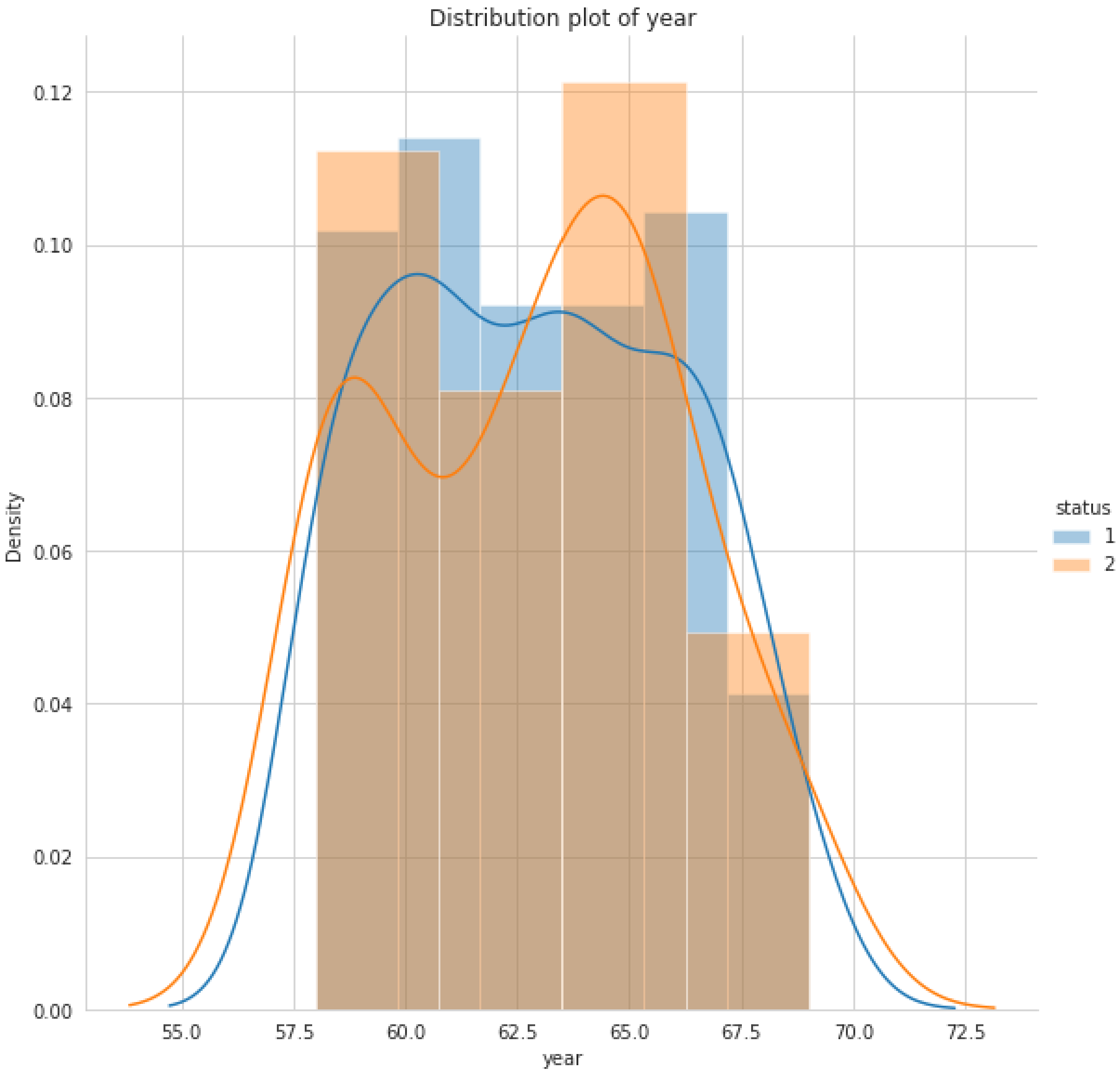
```
# distribution plot of age
sns.FacetGrid(haberman, hue="status", height=8)\
              .map(sns.distplot, "age")\
              .add_legend();
plt.title('Distribution plot of age')
plt.show()
```



Observations:

1. We can not classify because its overlapping
2. we can try with other feature as well

```
# distribution plot of year
sns.FacetGrid(haberman, hue="status", height=8)\
              .map(sns.distplot, "year")\
              .add_legend();
plt.title('Distribution plot of year')
plt.show()
```



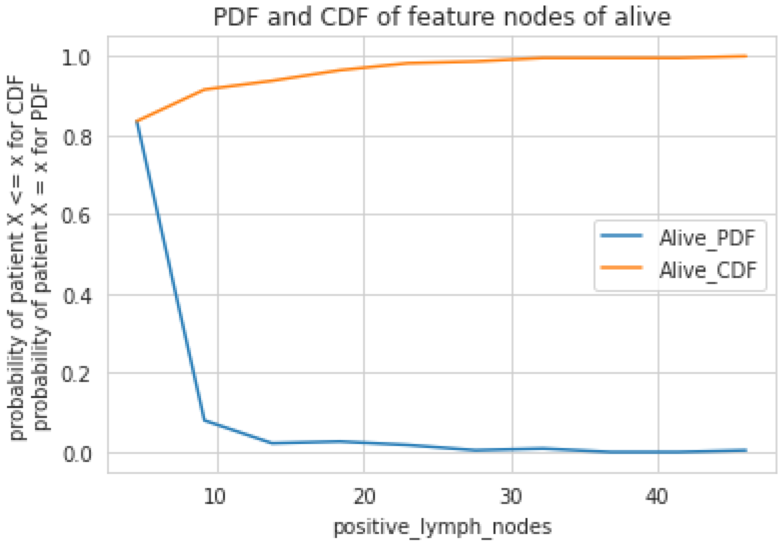
Observations:

1. we can not classify both the classed , both are massively overlapped
2. We can try with other plots to classify

Cumulative Density Function(CDF)

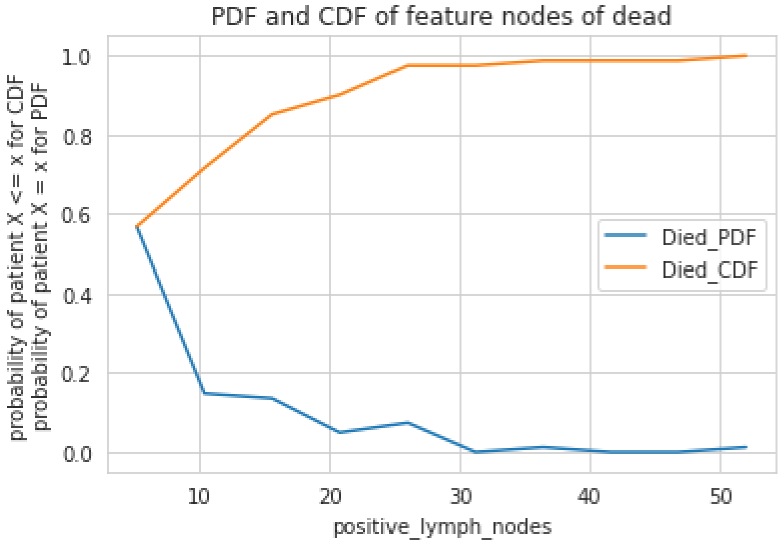
```
# Need for Cumulative Distribution Function (CDF)
# We can visually see what percentage of survival have
#Plot CDF of positive lymph nodes
counts, bin_edges = np.histogram(survive['nodes'],bins=10,density=True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.legend('status')
plt.legend(['Alive_PDF','Alive_CDF'])
plt.xlabel('positive_lymph_nodes')
plt.ylabel('probability of patient X <= x for CDF\nprobability of patient X = x for PDF')
plt.title('PDF and CDF of feature nodes of alive')
```

```
Text(0.5, 1.0, 'PDF and CDF of feature nodes of alive')
```



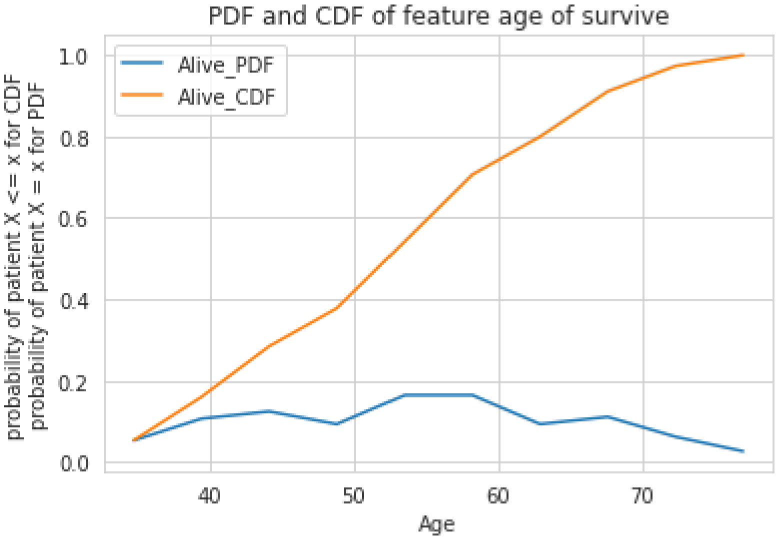
```
# We can visually see what percentage of died have
#Plot CDF of positive lymph nodes
counts, bin_edges = np.histogram(dead['nodes'],bins=10,density=True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.legend('status')
plt.legend(['Died_PDF','Died_CDF'])
plt.title('PDF and CDF of feature nodes of dead')
plt.xlabel('positive_lymph_nodes')
plt.ylabel('probability of patient X <= x for CDF\nprobability of patient X = x for PDF')
```

```
Text(0, 0.5, 'probability of patient X <= x for CDF\nprobability of patient X = x for PI
```



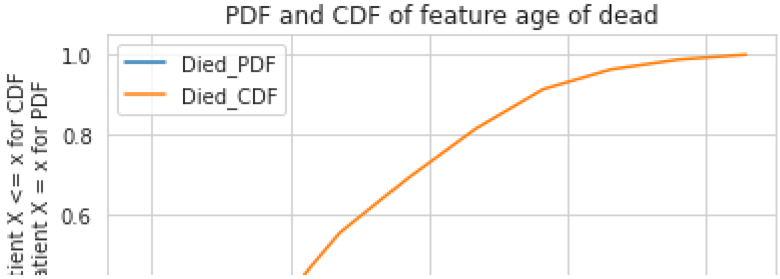
```
# Need for Cumulative Distribution Function (CDF) and PDF
# We can visually see what percentage of survival have
counts, bin_edges = np.histogram(survive['age'],bins=10,density=True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.legend('status')
plt.legend(['Alive_PDF','Alive_CDF'])
plt.xlabel('Age')
plt.ylabel('probability of patient X <= x for CDF\nprobability of patient X = x for PDF')
plt.title('PDF and CDF of feature age of survive')
```

```
Text(0.5, 1.0, 'PDF and CDF of feature age of survive')
```



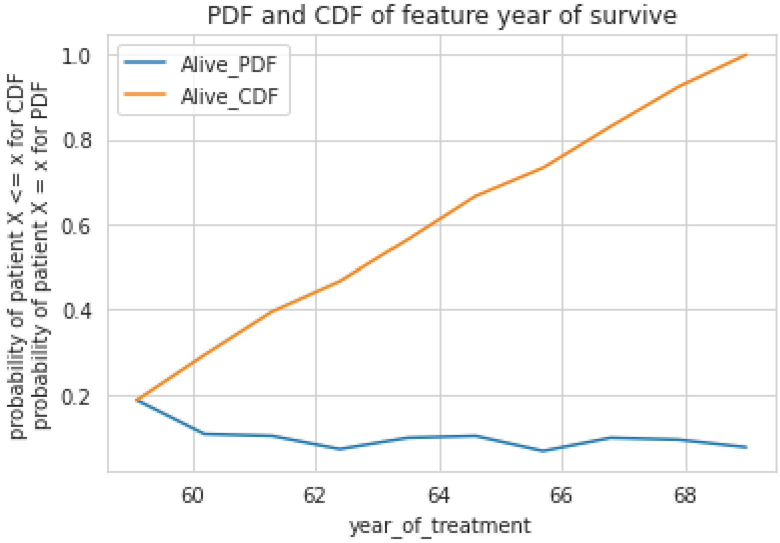
```
# We can visually see what percentage of died have
counts, bin_edges = np.histogram(dead['age'],bins=10,density=True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.legend('status')
plt.legend(['Died_PDF','Died_CDF'])
plt.xlabel('Age')
plt.ylabel('probability of patient X <= x for CDF\nprobability of patient X = x for PDF')
plt.title('PDF and CDF of feature age of dead')
```

```
Text(0.5, 1.0, 'PDF and CDF of feature age of dead')
```



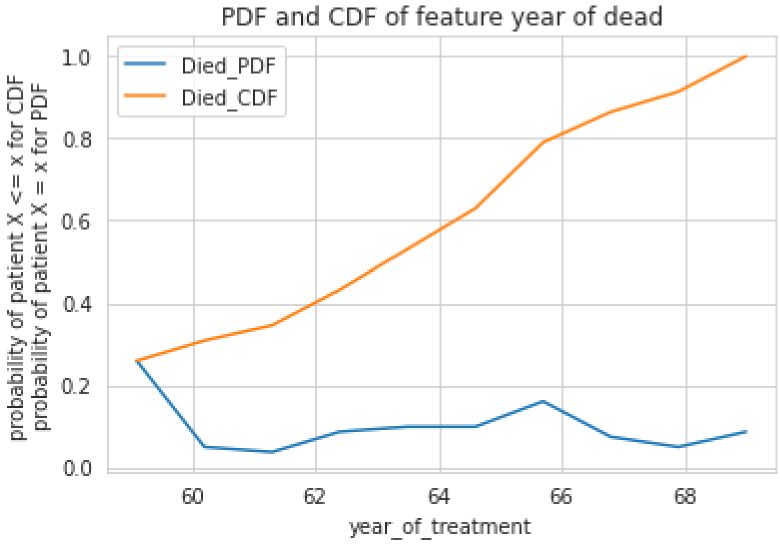
```
# Need for Cumulative Distribution Function (CDF) and PDF
# We can visually see what percentage of survival have
counts, bin_edges = np.histogram(survive['year'],bins=10,density=True)
pdf = counts/(sum(counts))
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:],cdf)
plt.legend('status')
plt.legend(['Alive_PDF','Alive_CDF'])
plt.xlabel('year_of_treatment')
plt.ylabel('probability of patient X <= x for CDF\nprobability of patient X = x for PDF')
plt.title('PDF and CDF of feature year of survive')
```

```
Text(0.5, 1.0, 'PDF and CDF of feature year of survive')
```



```
# We can visually see what percentage of died have
counts, bin_edges = np.histogram(dead['year'],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.legend('status')
plt.legend(['Died_PDF','Died_CDF'])
plt.xlabel('year_of_treatment')
plt.ylabel('probability of patient X <= x for CDF\nprobability of patient X = x for PDF')
plt.title('PDF and CDF of feature year of dead')
```

```
Text(0.5, 1.0, 'PDF and CDF of feature year of dead')
```



Observations from PDF's and CDF's:

1. We can see from the 1st plot of CDF and PDF, the probability of survival is around 82% when lymph nodes are less.
2. In the 2nd plot, the probability of patient who survived is 58% and had lymph node less than 10
3. In the 5th plot, the probability of patient who survived is 18% when they had treatment before the age 60
4. So eventually the probability of patients survival is high when he/she has node range in(0-9).

Mean,Variance and Standard Deviation

```
# Mean of nodes
print('Means of nodes')
print(np.mean(survive['nodes']))
# added outlier value to see mean of survival
print(np.mean(np.append(survive['nodes'],80)))
print(np.mean(dead['nodes']))
# added outlier value to see mean of dead
print(np.mean(np.append(dead['nodes'],80)))
print('\nStd Deviation of nodes')
print(np.std(survive['nodes']))
print(np.std(dead['nodes']))
```

```
Means of nodes
2.7911111111111113
3.1327433628318584
7.45679012345679
8.341463414634147

Std Deviation of nodes
```

```
5.857258449412131
```

Median, Pencentile, Quantile, IQR, MAD(Median Absolute Deviation)

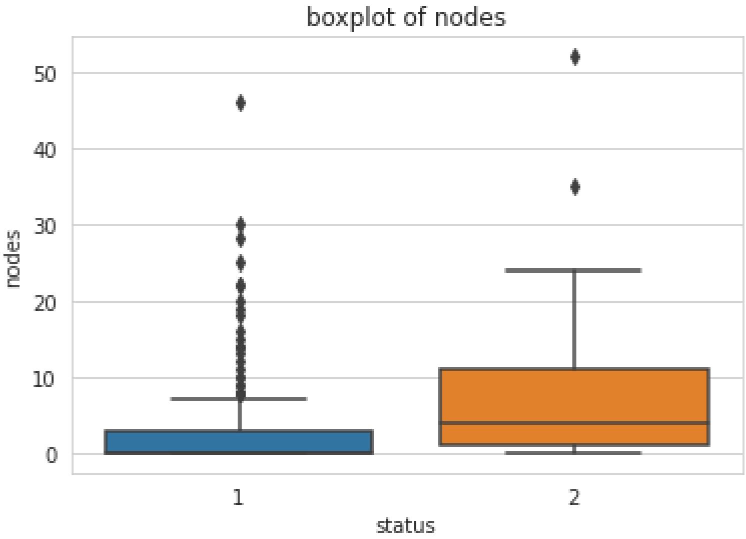
```
# Median of node
print('Median of nodes')
print(np.median(survive['nodes']))
# Median with outlier
print(np.median(np.append(survive['nodes'],80)))
print(np.median(dead['nodes']))
# Median with outlier
print(np.median(np.append(dead['nodes'],80)))

# quantiles of node
print("\nQuantiles")
print(np.percentile(survive['nodes'],np.arange(0,100,25)))
print(np.percentile(dead['nodes'],np.arange(0,100,25)))

# 90th percentile of node
print("\n90th Percentile")
print(np.percentile(survive['nodes'],90))
print(np.percentile(dead['nodes'],90))

# Median Absolute Deviation
from statsmodels import robust
print("\nMAD(Median Absolute Deviation)")
print(robust.mad(survive['nodes']))
print(robust.mad(dead['nodes']))
```

```
Median of nodes
0.0
0.0
4.0
4.0

Quantiles
[0. 0. 0. 3.]
[ 0.  1.  4. 11.]

90th Percentile
8.0
20.0

MAD(Median Absolute Deviation)
0.0
5.930408874022408
```

Boxplot and Whiskers

```
# boxplot of nodes with respect to status
```

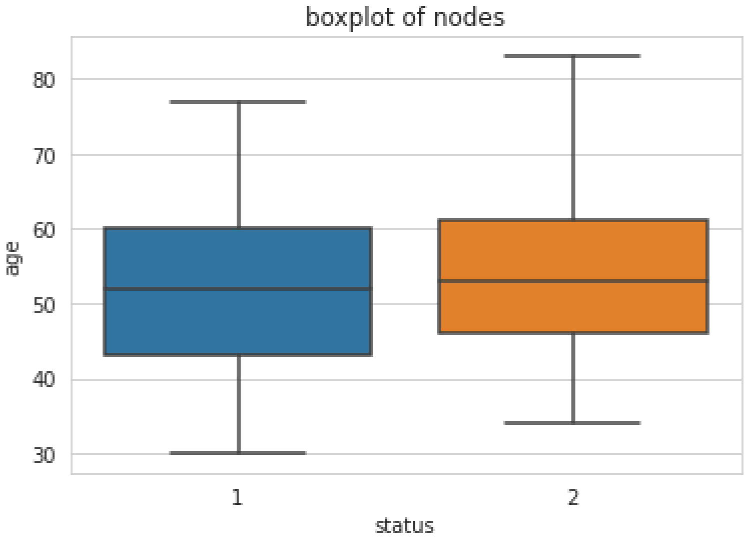
```
sns.boxplot(x="status", y="nodes", data=haberman)
plt.title('boxplot of nodes')
plt.show()
```



Observation:

1. If you see status 2 is having 75th percentile is higher
2. Means 75% of patient will die if they have more nodes
3. The lesser nodes you have the more chances you have to survive

```
# boxplot of age with respect to status
sns.boxplot(x="status", y="age", data=haberman)
plt.title('boxplot of nodes')
plt.show()
```



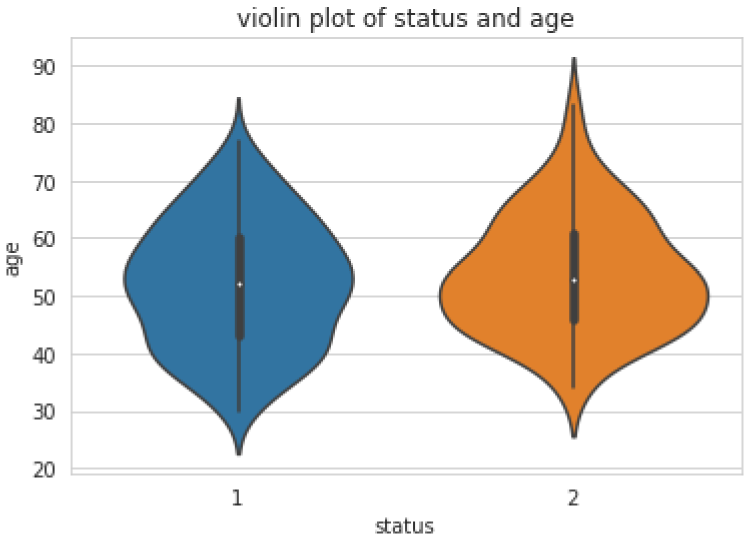
Observation:

1. Probability of older patient to die is bit more than young patient

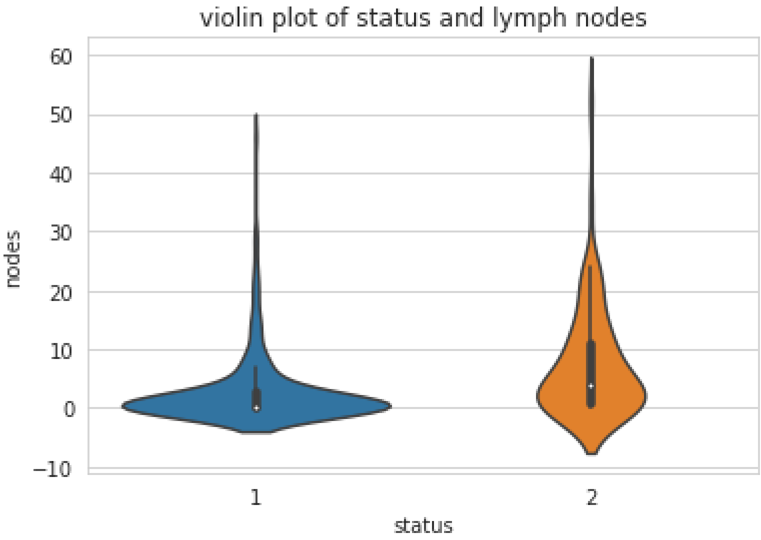
Violin plots

- A violin plot combines the benefits of the previous two plots and simplifies them
- Denser regions of the data are fatter, and sparser ones thinner in a violin plot

```
# violin plot of age
sns.violinplot(x="status", y="age", data=haberman, size=8)
plt.title('violin plot of status and age')
plt.show()
```



```
# violon plot of nodes
sns.violinplot(x="status", y="nodes", data=haberman, size=8)
plt.title('violin plot of status and lymph nodes')
plt.show()
```



Observation:

1. The survival plot where node is less than 5 is denser
2. Where Non survival plot is denser when nodes are more.
3. Clearly less nodes have more chances of survival

Final Observations/Conclusions

From Pair plots and Scatter plots

- scatter plot between "age and nodes" is comparatively better than other scatter plot which we can classify the status.
- younger people have higher chances of survival

From Distribution plots CDF's and PDF's

- postive_lymph_nodes feature is better one to classify the status
- Patients having less node will have more chances of survival
- Probability of survival is around 82% when lymph nodes are less.
- Probability of patient who survived is 58% and had lymph node less than 10

From Box plots and Whiskers

- status of die is having 75th percentile higher which Means 75% of patient will die if they have more nodes
- Status of alive's 75th percentile is lesser which means 75% of patient will survive if lymph nodes are less than 10

From Violin plots

- The survival plot where node is less than 5 is denser
- Where Non survival plot is denser when nodes are more

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