# 3. Plotting for Exploratory data analysis (EDA)

# (3.1) Basic Terminology

- What is EDA?
- Data-point/vector/Observation
- Data-set.
- Feature/Variable/Input-variable/Dependent-varibale
- Label/Indepdendent-variable/Output-varible/Class/Classlabel/Response label
- Vector: 2-D, 3-D, 4-D,.... n-D

Q. What is a 1-D vector: Scalar

## (3.12) Exercise:

- Download Haberman Cancer Survival dataset from Kaggle. You may have to create a Kaggle account to download data. (<a href="https://www.kaggle.com/gilsousa/habermans-survival-data-set">https://www.kaggle.com/gilsousa/habermans-survival-data-set</a>)
- 2. Perform a similar alanlaysis as above on this dataset with the following sections:
- High level statistics of the dataset: number of points, numer of features, number of classes, data-points per class.
- Explain our objective.
- Perform Univaraite analysis(PDF, CDF, Boxplot, Voilin 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 classfication.
- Write your observations in english as crisply and unambigously as possible. Always quantify your results.

In [71]:

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

#Load haberman.csv into a pandas dataFrame.
haberman = pd.read_csv("haberman.csv")
haberman.head(10)
```

Out[71]:

	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
5	33	58	10	1
6	33	60	0	1
7	34	59	0	2
8	34	66	9	2
9	34	58	30	1

#### Here, the main objective of the analysis is to predict the survival status of patients

Features: age, year, lymph nodes

**Class Label: status** 

1 ==> means that a patient survied 5 years or longer

2 ==> means that a patient died within 5 years

In [72]:

haberman['status'].value\_counts()

Out[72]:

1 225

2 81

Name: status, dtype: int64

- It is evident that the number of patients who survived 5 years or longer are more than the number of patients who died within 5 years
- It is an imbalanced dataset

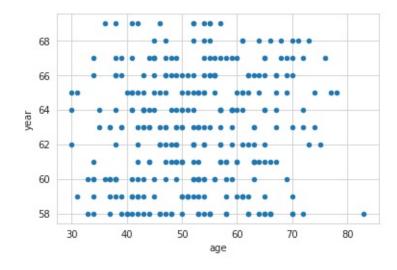
```
In [73]:
haberman.columns

Out[73]:
Index(['age', 'year', 'nodes', 'status'], dtyp
e='object')
```

# Checking if features age and year are useful for preditctive analysis

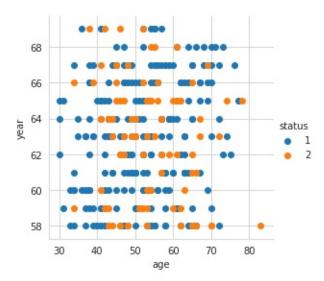
```
In [117]:
```

```
#2-D Scatter-Plot
haberman.plot(kind='scatter', x='age', y='year');
plt.show()
```



In [75]:

```
#2-D Scatter plot with color coding for each class
sns.set_style("whitegrid");
sns.FacetGrid(haberman, hue="status", size=4) \
    .map(plt.scatter, "age", "year") \
    .add_legend();
plt.show();
```

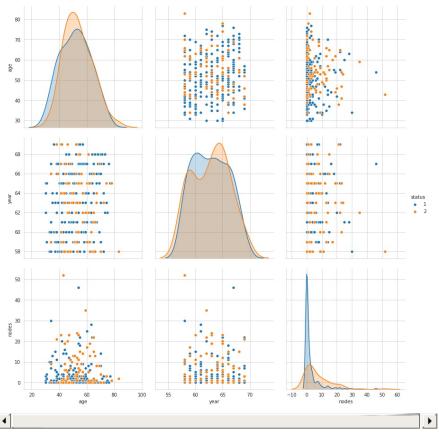


- There seems to be some separability between the two features based on class labels
- However,no solid conclusion can be made due to a lot of overlapping
- From the above 2D scatter-plot it is difficult to distinguish between the two classes as there is a lot of overlapping between the two and there is no clear separability

### **Seaborn Pairplot**

In [83]:

```
import warnings
warnings.filterwarnings("ignore")
plt.close();
sns.set_style("whitegrid");
sns.pairplot(haberman, hue= "status", vars=["age", "year", "n
odes"], size=4);
plt.show()
```

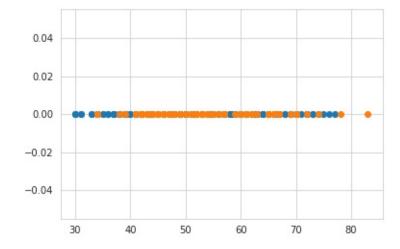


- The distributions are overlapping
  There is minimal separability between the datapoints based on target variable 'status'
  Difficult to make solid conclusions

# **Univariate Analysis**

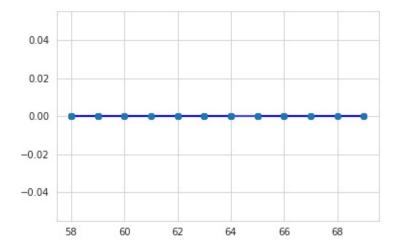
In [84]:

```
import numpy as np
survived=haberman.loc[haberman["status"] == 1]
died=haberman.loc[haberman["status"] == 2]
plt.plot(survived['age'],np.zeros_like(survived['age']),'o')
plt.plot(died['age'],np.zeros_like(died['age']),'o')
plt.show()
```



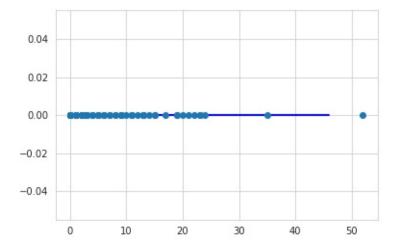
In [85]:

```
import numpy as np
survived=haberman.loc[haberman["status"] == 1]
died=haberman.loc[haberman["status"] == 2]
plt.plot(survived['year'], np.zeros_like(survived['age']), 'b')
plt.plot(died['year'], np.zeros_like(died['age']), 'o')
plt.show()
```



- There seems to be only one class that is visible on the graph.
- So this feature cannot be used to a patient's survival status based on year of operation

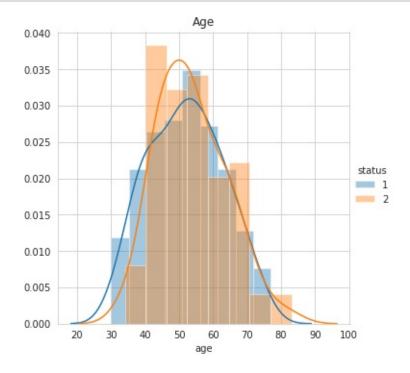
```
import numpy as np
survived=haberman.loc[haberman["status"] == 1]
died=haberman.loc[haberman["status"] == 2]
plt.plot(survived['nodes'], np.zeros_like(survived['age']), 'b')
plt.plot(died['nodes'], np.zeros_like(died['age']), 'o')
plt.show()
```



- If Number of positive auxillary nodes > 35: then the patient died
- But it is not a solid conclusion

```
In [97]:
```

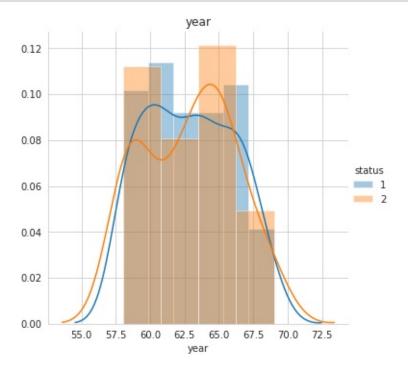
```
sns.FacetGrid(haberman, hue='status', size=5)\
   .map(sns.distplot, 'age')\
   .add_legend()
plt.title("Age")
plt.show();
```



- The distributions of datapoints belonging to class 1 and class 2 are overlapping
- There is no separability between the two distributions

```
In [98]:
```

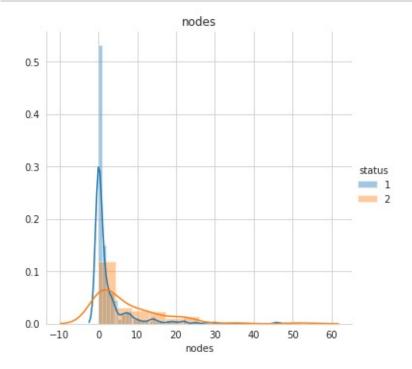
```
sns.FacetGrid(haberman, hue='status', size=5)\
   .map(sns.distplot, 'year')\
   .add_legend()
plt.title('year')
plt.show();
```



- Year of operation has no correlation with survival status
  The distributions of datapoints belonging to class 1 and class 2 are overlapping

```
In [99]:
```

```
sns.FacetGrid(haberman, hue='status', size=5)\
   .map(sns.distplot, 'nodes')\
   .add_legend()
plt.title('nodes')
plt.show();
```



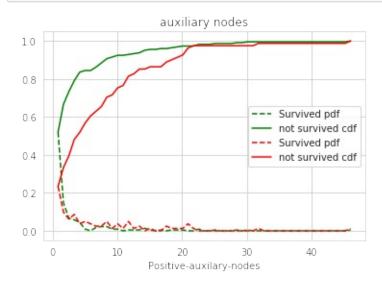
 Higer positive -auxilary-nodes does not gives guarantee for more survival

In [108]:

```
# now calculate the pdf & cdf for positive-auxilary nodes.

%matplotlib inline
# PDF & CDF
# compute pdf & cdf for survived

counts, bin_edges = np.histogram(survived['nodes'], bins = 55, density = True)
pdf = counts/sum(counts)
# print(pdf)
# print(bin_edges)
cdf=np.cumsum(pdf)
```



#### In [107]:

```
survived_status = survived['nodes'].describe()
not_survived_status =died['nodes'].describe()
# create dataframe to store the survived_status and not_survi
```

```
ved_status statistics.
df_nodes = pd.DataFrame(data={'Survived':survived_status,'Die
d':not_survived_status})
df_nodes
```

Out[107]:

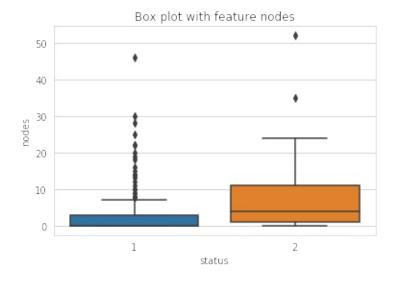
	Survived	Died
count	225.000000	81.000000
mean	2.791111	7.456790
std	5.870318	9.185654
min	0.000000	0.000000
25%	0.000000	1.000000
50%	0.000000	4.000000
75%	3.000000	11.000000
max	46.000000	52.000000

#### **Observations:**

- Most of patients have zero positive auxiliary nodesPatients having zero nodes died early and patients having almost 1 survived more

In [109]:

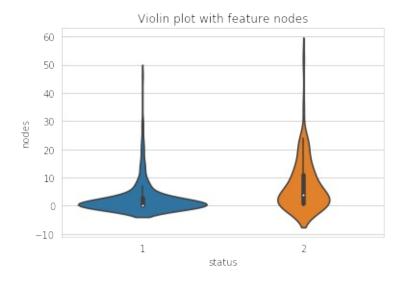
```
#Box-Plot
sns.boxplot(x='status',y='nodes', data=haberman)
plt.title('Box plot with feature nodes')
plt.show()
```



#### In [110]:

#### #Violin-plot

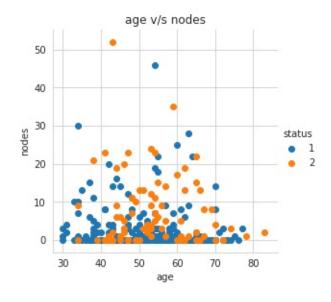
sns.violinplot(x="status", y="nodes", data=haberman, size=8)
plt.title('Violin plot with feature nodes')
plt.show()



# **Bi-Variate Analysis**

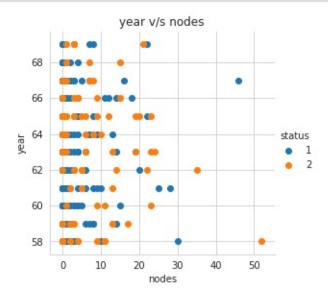
#### In [111]:

```
sns.set_style("whitegrid")
sns.FacetGrid(haberman, hue='status', size=4).map(plt.scatter, '
age', 'nodes').add_legend()
plt.title('age v/s nodes')
plt.show()
```



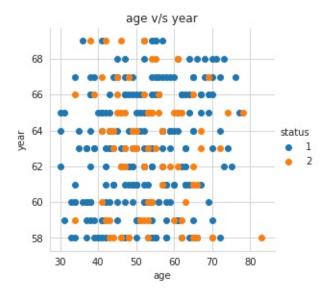
#### In [112]:

```
sns.set_style("whitegrid")
sns.FacetGrid(haberman, hue='status', size=4).map(plt.scatter,'
nodes', 'year').add_legend()
plt.title('year v/s nodes')
plt.show()
```



#### In [113]:

```
sns.set_style("whitegrid")
sns.FacetGrid(haberman, hue='status', size=4).map(plt.scatter,'
age', 'year').add_legend()
plt.title('age v/s year')
plt.show()
```



#### **Conclusions:**

- Age does not affect survival status.
- Year of operation does not have any affect on survival status
- Positve auxilary nodes has some affect on survival status
- If more number of Positve auxiliary nodes are detected then patients died within 5 years
- If less number of Positive auxiliary nodes are detected then patients survived for 5 years or more