Exploratory data analysis of Haberman Dataset.

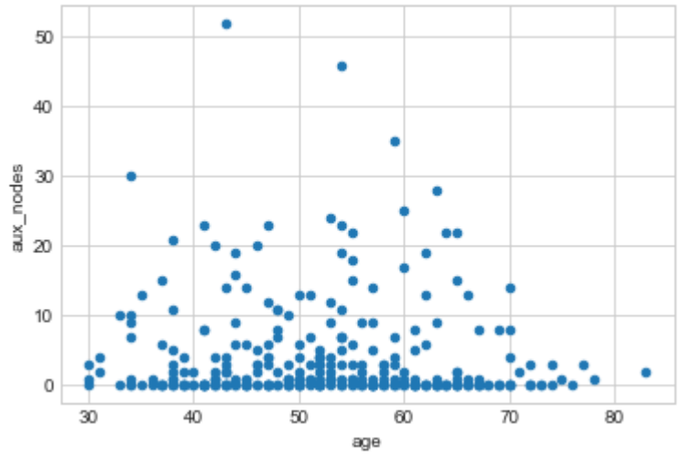
In [ ]:
```
## Description
# 1. Age of patient at time of diagnosis
# 2. Year of treatment
# 3. Auxiliary nodes detected
# 4. status of survival. 1=patient alive after 5 yrs, 2=patient died within 5
 yrs.
```

In [6]:
```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
hbm = pd.read_csv('haberman.csv', header=None)
hbm.columns = ['age', 'year', 'aux_nodes', 'status']
print(hbm.columns)

#modifying status of survival. 1=alive after 5 years of traetment, 2=dead afte
r 5 years of treatment.
hbm["status"] = hbm["status"].map({1:"alive", 2:"died"})
```

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

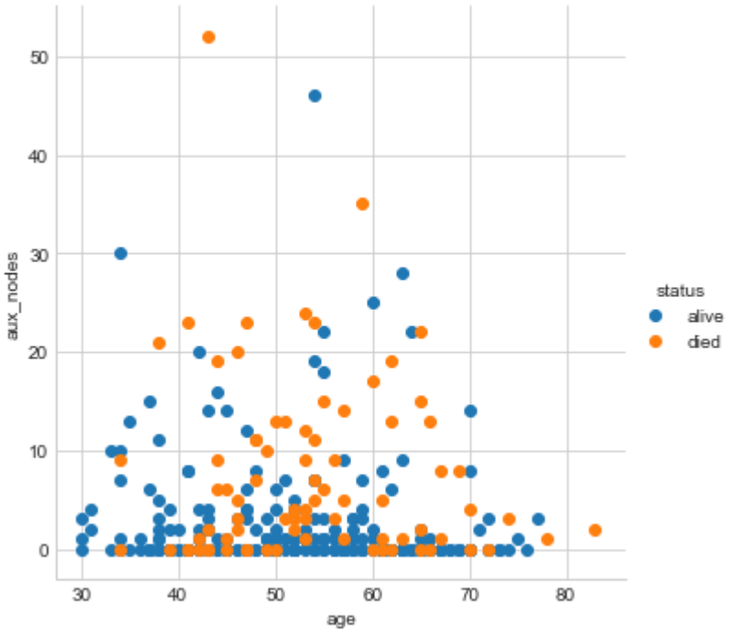
2-D Scatter Plot of age w.r.t auxilary lymph nodes

In [13]:
```
hbm.plot(kind='scatter', x='age', y='aux_nodes');
plt.show()
```



Observation: From the above observation, we can observe that majority of the patient's auxiliary nymph nodes effected ranges from (0-5).

In [3]:
```
#2-D Scatter plot for survival status of patient
#We compare age with no of aux node affected

sns.set_style("whitegrid");
sns.FacetGrid(hbm, hue="status", size=5) \
    .map(plt.scatter, 'age', 'aux_nodes') \
    .add_legend();
plt.show();
```



Observation: We cannot distinguish any result clearly from the above 2-D scatter plot.

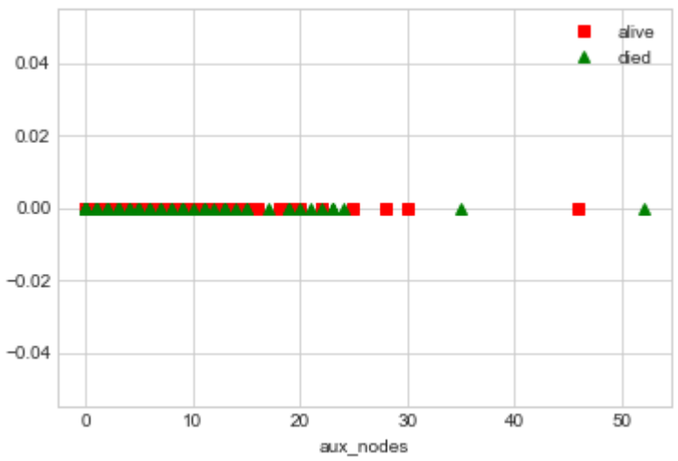
Pair Plot

In [4]:
```
plt.close();
sns.set_style("whitegrid");
sns.pairplot(hbm, hue="status", size=2);
plt.show()
```

Observation: The above pairplot doesnt give any clear idea. The above observations are still valid here.

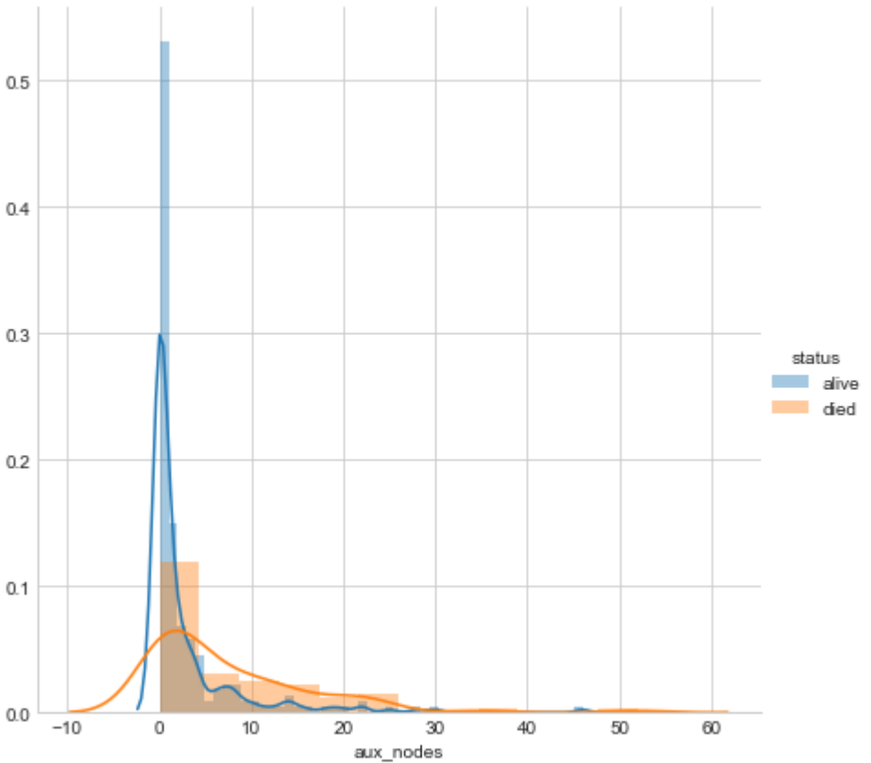
Histogram, PDF, CDF

In [22]:
```
#1-D Scatter plot using one feature
#1-D Scatter plot of aux_nodes

hbm_alive = hbm.loc[hbm["status"] == "alive" ];
hbm_died = hbm.loc[hbm["status"] == "died"];

plt.plot(hbm_alive["aux_nodes"], np.zeros_like(hbm_alive["aux_nodes"]), 'rs',
label='alive')
plt.plot(hbm_died["aux_nodes"], np.zeros_like(hbm_died["aux_nodes"]), 'g^', la
bel='died')
plt.xlabel("aux_nodes")
plt.legend()
plt.show()
```



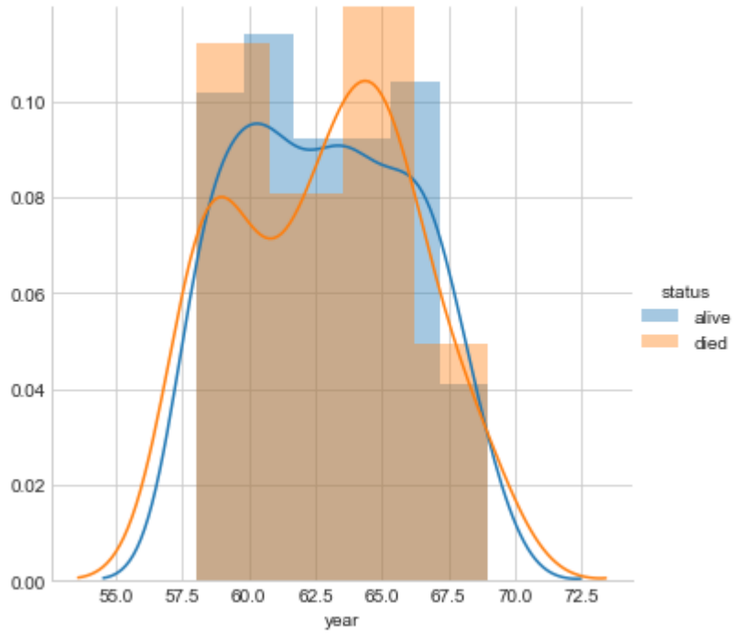
Observation: Most of the auxiliary lymph nodes are concentrated in the range (0-25).

In [23]:
```
#1-D Histogram plot of aux-nodes
sns.FacetGrid(hbm, hue="status", size=6) \
    .map(sns.distplot, "aux_nodes") \
    .add_legend();
plt.show();
```



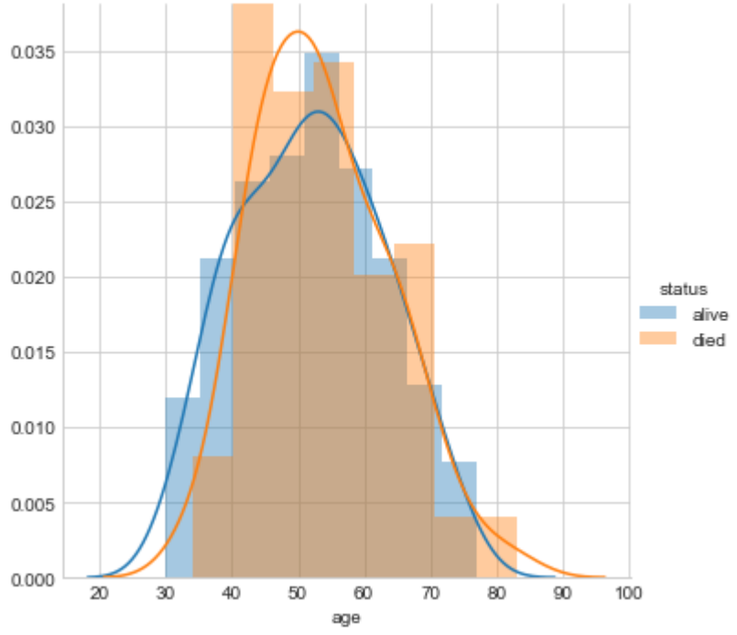
Observation: Most of the Patients having aux-nodes 0, are alive after 5 years of operation.

In [24]:
```
#1-D Histogram plot of year
sns.FacetGrid(hbm, hue="status", size=5) \
    .map(sns.distplot, "year") \
    .add_legend();
plt.show();
```



observation: No significant result can be observed.

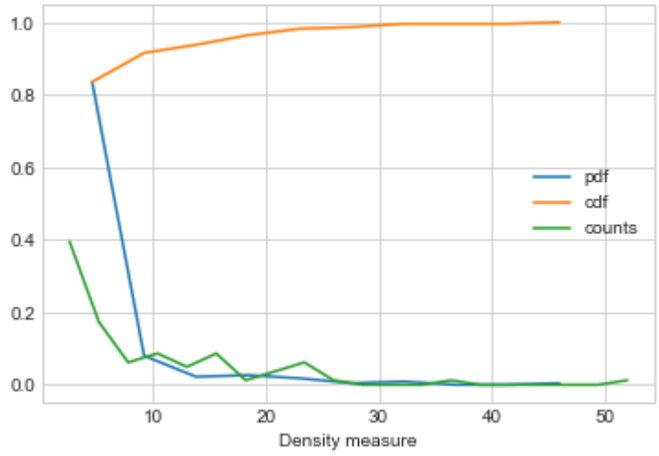
In [25]:
```
#1-D Histogram plot of age

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



In [ ]:
```
observation:
No significant result can be observed.
```

In [27]:
```
#CDF (Cumulative Distribution Function)
#Plotting CDF of aux nodes

counts, bin_edges = np.histogram(hbm_alive['aux_nodes'], bins=10, density =
True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges);
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:], pdf, label="pdf");
plt.plot(bin_edges[1:], cdf, label="cdf")

counts, bin_edges = np.histogram(hbm_died['aux_nodes'], bins=20,
                                 density = True)
pdf = counts/(sum(counts))
plt.plot(bin_edges[1:],pdf, label="counts");
plt.xlabel("Density measure")
plt.legend()
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. ]
```



Mean, Varience and Std-dev

In [32]:
```
print("Means of Aux-Nodes: ")
print(np.mean(hbm_alive["aux_nodes"]))
print(np.mean(hbm_died["aux_nodes"]))

print("\nMeans of Age: ")
print(np.mean(hbm_alive["age"]))
print(np.mean(hbm_died["age"]))

print("\nMeans of Year of Treatment: ")
print(np.mean(hbm_alive["year"]))
print(np.mean(hbm_died["year"]))
```

```
Means of Aux-Nodes:
2.7911111111111113
7.45679012345679

Means of Age:
52.01777777777778
53.67901234567901

Means of Year of Treatment:
62.86222222222222
62.82716049382716
```

In [35]:
```
print("Standard Deviation of aux nodes: ");
print(np.std(hbm_alive['aux_nodes']));
print(np.std(hbm_died['aux_nodes']));

print("\nStandard Deviation of age: ");
print(np.std(hbm_alive['age']));
print(np.std(hbm_died['age']));
```

```
Standard Deviation of aux nodes:
5.857258449412131
9.128776076761632

Standard Deviation of age:
10.98765547510051
10.10418219303131
```

Median, Percentile, Quantile, IQR, MAD

In [43]:
```
import numpy as np
print("\nMedians of aux nodes:")
print(np.median(hbm_alive["aux_nodes"]))
print(np.median(hbm_died["aux_nodes"]))

print("\nMedians of age of patient:")
print(np.median(hbm_alive["age"]))
print(np.median(hbm_died["age"]))

print("\nMedians of year of treatment:")
print(np.median(hbm_alive["year"]))
print(np.median(hbm_died["year"]))
```

```
Medians of aux nodes:
0.0
4.0

Medians of age of patient:
52.0
53.0

Medians of year of treatment:
63.0
63.0
```

In [44]:
```
#Quantiles
print("\nQuantiles for aux nodes:")
print(np.percentile(hbm_alive["aux_nodes"],np.arange(0, 100, 25)))
print(np.percentile(hbm_died["aux_nodes"],np.arange(0, 100, 25)))

print("\nQuantiles for year:")
print(np.percentile(hbm_alive["year"],np.arange(0, 100, 25)))
print(np.percentile(hbm_died["year"],np.arange(0, 100, 25)))

print("\nQuantiles for age:")
print(np.percentile(hbm_alive["age"],np.arange(0, 100, 25)))
print(np.percentile(hbm_died["age"],np.arange(0, 100, 25)))
```

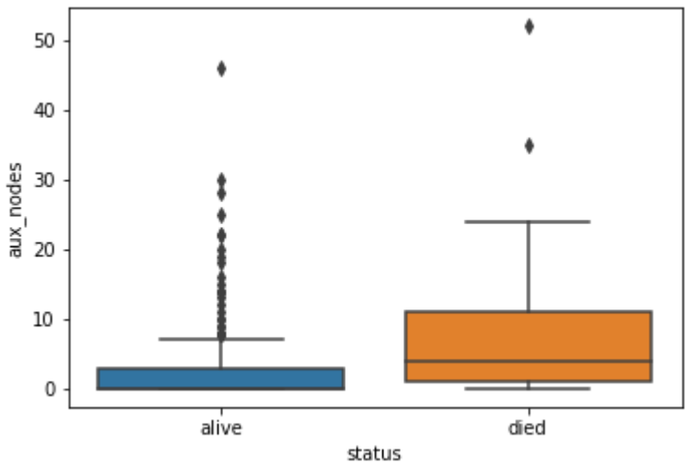
```
Quantiles for aux nodes:
[0. 0. 0. 3.]
[ 0.  1.  4. 11.]

Quantiles for year:
[58. 60. 63. 66.]
[58. 59. 63. 65.]

Quantiles for age:
[30. 43. 52. 60.]
[34. 46. 53. 61.]
```

In [49]:
```
#Median absolute Deviation
from statsmodels import robust
print ("\nMedian Absolute Deviation")
print(robust.mad(hbm_alive["aux_nodes"]))
print(robust.mad(hbm_died["aux_nodes"]))
```

```
Median Absolute Deviation
0.0
5.930408874022408
```

Box plot and Whiskers

In [4]:
```
sns.boxplot(x='status', y='aux_nodes', data=hbm)
plt.show()
```

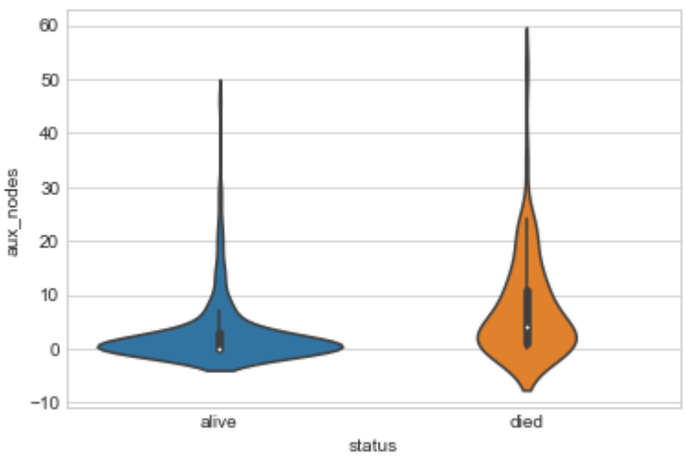


Observations:

1. since the quantiles (25% and 50%) in case of alive peoples are concentrated within zero. we can easily conclude that most of the patients having lymph nodes = 0 were alive after 5 years of treatment.
2. the patients having less lymph node affected were alive after 5 years of treatment.
3. the whiskers are much lower in case of alive peoples than the died ones.
4. most of the died patients had higher auxiliary lymph nodes.

Violin plots

In [37]:
```
sns.violinplot(x="status", y='aux_nodes', data=hbm, size=8)
plt.show()
```



observations:

1. since the alive violin plot has fatter area on the range (0-5). so we can conclude that most of the patients in that area were alive after 5 years of treatment.
2. since the died violin plot has diversed area. so we can say that patients who died had variable auxiliary lymph nodes.

Conclusions:

1. Maximum number of patients have auxiliary lymph nodes of 0.
2. Most of the patients are of age 52-53.
3. The year in which most of the patients are treated is 1963.
4. Most of the Patients having aux-nodes 0, are alive after 5 years of operation.
5. The patients who had higher auxiliary lymph nodes died after 5 years of treatment.