In [1]:

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

Haberman's Survival Data Set

Objective

To predict whether the patient will survive after 5 years based on the patient's age, year of surgery and number of positive lymph nodes.

In [2]:

```
haberman = pd.read_csv("haberman.csv")
haberman.shape
```

Out[2]:

```
(306, 4)
```

In [3]:

```
haberman.head()
```

Out[3]:

	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

```
In [4]: haberman.columns
```

```
Out[4]: Index(['age', 'year', 'nodes', 'status'], dtype='object')
```

```
In [133]: haberman.status.unique()
```

```
Out[133]: array([1, 2], dtype=int64)
```

```
In [51]: haberman.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 306 entries, 0 to 305
Data columns (total 4 columns):
age       306 non-null int64
year      306 non-null int64
nodes     306 non-null int64
status    306 non-null int64
dtypes: int64(4)
memory usage: 9.6 KB
```

Observations

1. There are totally 306 observations
2. There are totally 3 features: Age of the patient, Year of Treatment and Number of positive lymph nodes
3. There are no missing values.
4. The class label is an integer with values 1 and 2, 1 indicating Patients Survived more than 5 years after the year of treatment and 2 indicating patients survived less than 5 years after the year of treatment.
5. The class label must be changed to a categorical variable.

Making the status as Categorical Variable

In [4]:
```
haberman["status"] = haberman["status"].map({1: "Survived after 5yrs", 2: "Not Survived after 5yrs"})
haberman.tail()
```

Out[4]:

	age	year	nodes	status
301	75	62	1	Survived after 5yrs
302	76	67	0	Survived after 5yrs
303	77	65	3	Survived after 5yrs
304	78	65	1	Not Survived after 5yrs
305	83	58	2	Not Survived after 5yrs

In [54]:
```
haberman["status"] = haberman["status"].astype("category")
haberman.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 306 entries, 0 to 305
Data columns (total 4 columns):
age       306 non-null int64
year      306 non-null int64
nodes     306 non-null int64
status    306 non-null category
dtypes: category(1), int64(3)
memory usage: 7.6 KB
```

Balanced or Imbalanced Data-set ?

In [55]:
```
haberman["status"].value_counts()
```

Out[55]:
```
Survived after 5 years        225
Not Survived after 5 years     81
Name: status, dtype: int64
```

```
In [60]: haberman["status"].value_counts(normalize = True)
```

```
Out[60]: Survived after 5 years        0.735294
         Not Survived after 5 years    0.264706
         Name: status, dtype: float64
```

Observation

The Class label is imbalanced with 73% of patient's status as Survived more than 5 years

Min, Max, Mean, Median and Quantiles

```
In [56]: haberman.describe()
```

```
Out[56]:
```

	age	year	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

Observations:

1. The age of the patients vary from 30 to 83 and the median is 52
2. The Surgery Year is between 1958 and 1969
3. The mean of all the patient's positive lymph nodes is 4 which is significanty greater than the median which is 1
4. Although, the positive lymph nodes of the patients vary between 0 and 52, 75 % of the patients have positive lymph nodes between 0 and 4, half of the patients have positive lymph nodes less than 2 and 25% of the patients have no positive lymph nodes at all.
5. Observation 3 and 4 indicate there are extreme values ie. outliers in our data set. Hence median and Median Absolute Deviation will be the most useful statistic to analyse our data than mean and standard deviation.

Max and Min Status-wise

In [31]:

```
g = haberman.groupby("status")
g.agg(['max','min'])
```

Out[31]:

	age		year		nodes	
	max	**min**	**max**	**min**	**max**	**min**
status						
Not Survived after 5yrs	83	34	69	58	52	0
Survived after 5yrs	77	30	69	58	46	0

Observations

1. Patients with age less than 34 have survived.
2. Patients with age greater than 77 have not survived.
3. Patients with nodes greater than 46 have not survived.

Median Absolute Deviation

In [39]:

```
nodes_of_survived = g.get_group("Survived after 5yrs")["nodes"]
nodes_of_not_survived = g.get_group("Not Survived after 5yrs")["nodes"]

survived_median = np.median(nodes_of_survived)
not_survived_median = np.median(nodes_of_not_survived)
survived_mad = robust.mad(nodes_of_survived, c = 1)
not_survived_mad = robust.mad(nodes_of_not_survived, c = 1)

print("Median of survived patients = {}".format(survived_median))
print("Median of not survived patients = {}".format(not_survived_median
))
print("\nMedian Absolute Deviation of survived patients = {}".format(su
rvived_mad))
print("Median Absolute Deviation of not survived patients = {}".format(
not_survived_mad))
```

```
Median of survived patients = 0.0
Median of not survived patients = 4.0

Median Absolute Deviation of survived patients = 0.0
Median Absolute Deviation of not survived patients = 4.0
```

Observation

1. From Median Absolute Deviation (MAD), we can infer, most of the survived patients have no nodes.
2. Nodes of most of the not survived patients vary between 0 and 8.

Percentiles

In [37]:

```
survived_90 = np.percentile(nodes_of_survived,90)
not_survived_90 = np.percentile(nodes_of_not_survived,90)
```

```
print("90th percentile nodes of survived = {}".format(survived_90))
print("90th percentile nodes of not survived = {}".format(not_survived_
90))
```

```
90th percentile nodes of survived = 8.0
90th percentile nodes of not survived = 20.0
```

Observations

1. 90% of the survived patients have nodes less than or equal to 8
2. 90% of the not survived patients have nodes less than or equal to 20

In [186]:

```
g.nodes.value_counts(normalize = True, bins = 5)
```

Out[186]:

```
status
Not Survived after 5yrs  (-0.053, 10.4]    0.716049
                         (10.4, 20.8]      0.185185
                         (20.8, 31.2]      0.074074
                         (41.6, 52.0]      0.012346
                         (31.2, 41.6]      0.012346
Survived after 5yrs      (-0.047, 9.2]     0.915556
                         (9.2, 18.4]       0.048889
                         (18.4, 27.6]      0.022222
                         (27.6, 36.8]      0.008889
                         (36.8, 46.0]      0.004444
Name: nodes, dtype: float64
```

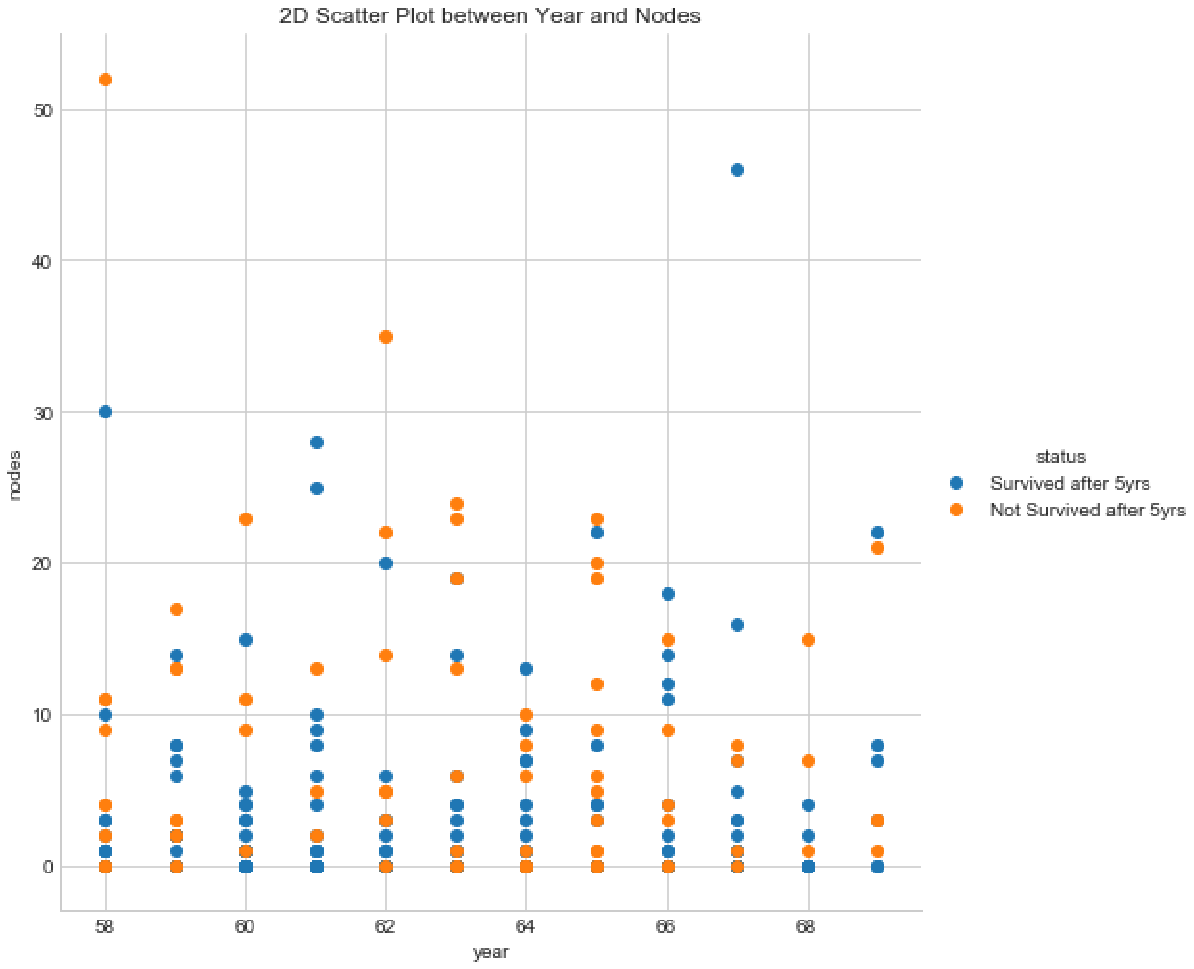
Observations

1. 71% of the not survived patients have nodes less than 11.
2. 91% of the survived patients have nodes less than 10
3. The Survival probability of patients decrease as the nodes increase.

Bivariate Analysis: 2 D Scatter Plot

In [142]:

```
sns.set_style("whitegrid")
sns.FacetGrid(haberman, hue = "status", size = 7).map(plt.scatter, "year", "nodes").add_legend()
plt.title("2D Scatter Plot between Year and Nodes")
plt.show()
```



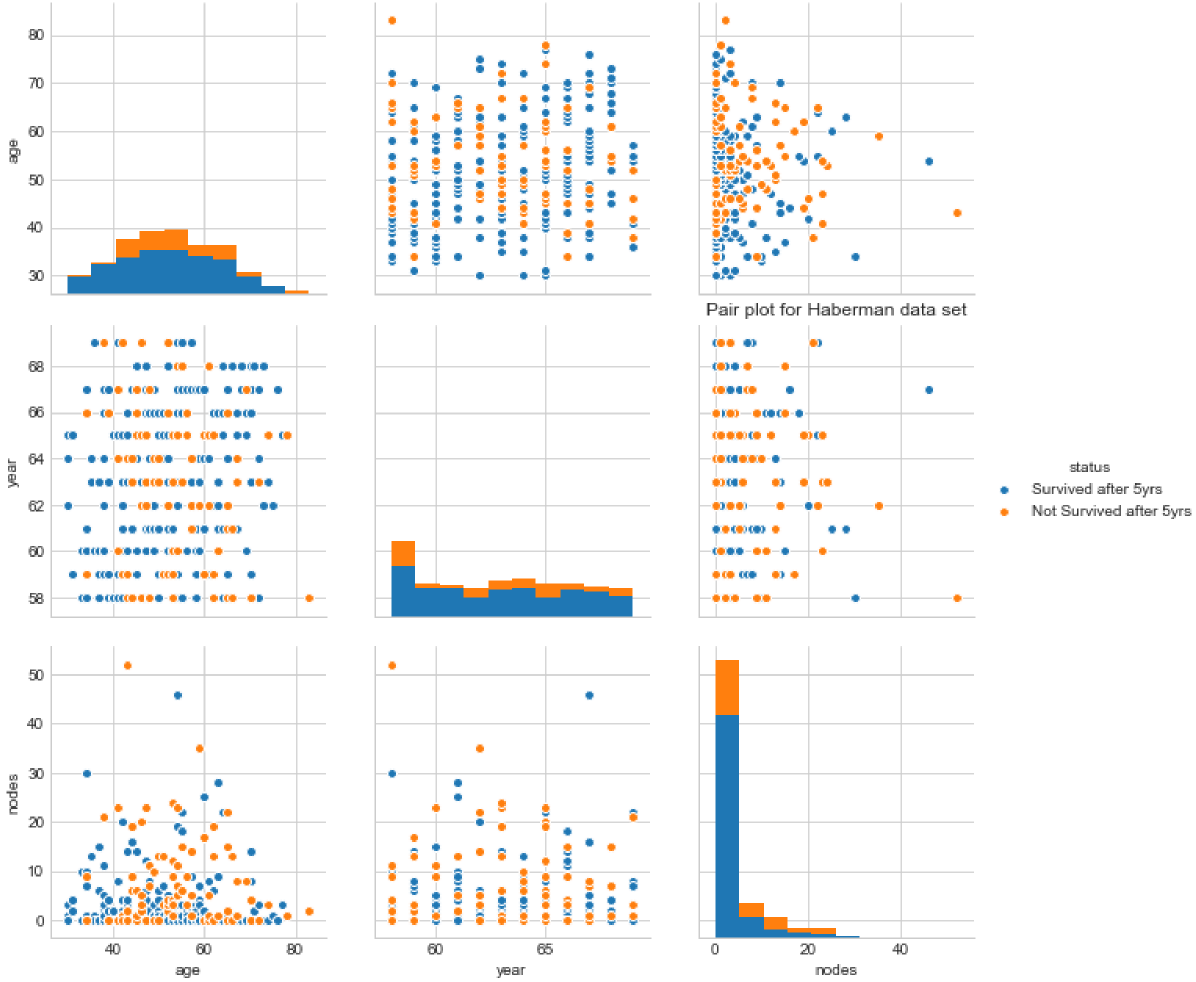
Observations

1. There are more number of patients with nodes less than 10, out of which patients survived after 5 years are higher.

Bivariate analysis - Pairplot

In [103]:

```
plt.close()
sns.set_style("whitegrid")
sns.pairplot(haberman, hue = "status", size = 3)
plt.show()
```



Observations

1. As the data points overlap each other massively, we couldn't derive any specific seperation threshold for distinguishing the class labels.
2. But with the nodes diagonal bar graph, we can infer, more than half of the survived patients have number of nodes less than 5.

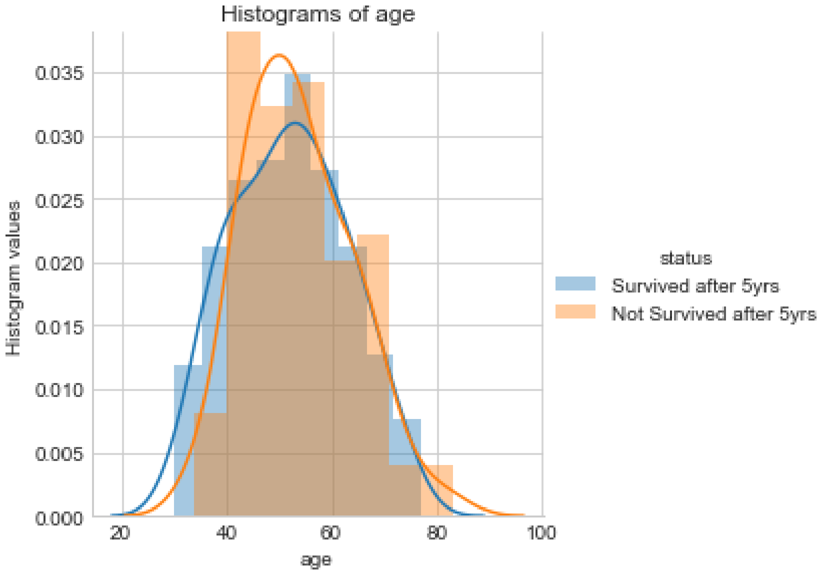
3. Hence we could infer nodes as the most useful feaure for predicting the survival of the patients.

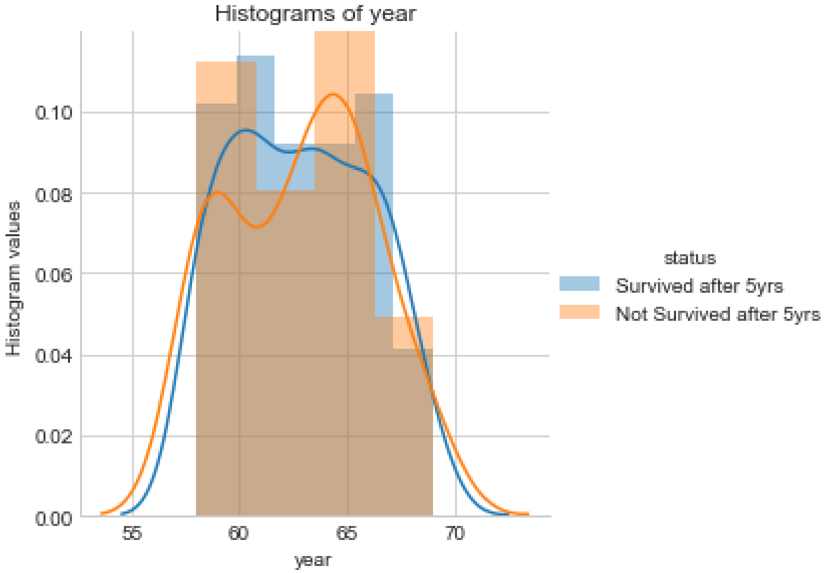
Univariate Analysis: Histograms

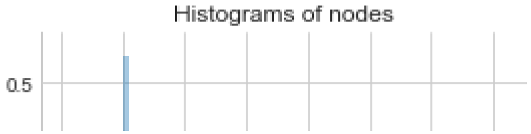
In [104]:

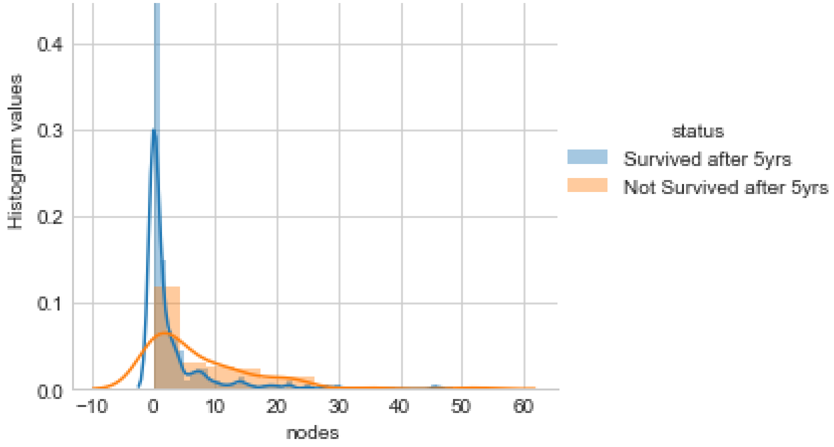
```
for feature in list(haberman.columns[:-1]):
    sns.FacetGrid(haberman, hue = "status", size = 4).map(sns.distplot, feature).add_legend()
    plt.title("Histograms of {}".format(feature))
    plt.ylabel("Histogram values")
plt.show()
```

```
C:\Users\sozhancompi\Anaconda3\lib\site-packages\matplotlib\axes\_axes.
py:6462: UserWarning: The 'normed' kwarg is deprecated, and has been re
placed by the 'density' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\sozhancompi\Anaconda3\lib\site-packages\matplotlib\axes\_axes.
py:6462: UserWarning: The 'normed' kwarg is deprecated, and has been re
placed by the 'density' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\sozhancompi\Anaconda3\lib\site-packages\matplotlib\axes\_axes.
py:6462: UserWarning: The 'normed' kwarg is deprecated, and has been re
placed by the 'density' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\sozhancompi\Anaconda3\lib\site-packages\matplotlib\axes\_axes.
py:6462: UserWarning: The 'normed' kwarg is deprecated, and has been re
placed by the 'density' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\sozhancompi\Anaconda3\lib\site-packages\matplotlib\axes\_axes.
py:6462: UserWarning: The 'normed' kwarg is deprecated, and has been re
placed by the 'density' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
C:\Users\sozhancompi\Anaconda3\lib\site-packages\matplotlib\axes\_axes.
py:6462: UserWarning: The 'normed' kwarg is deprecated, and has been re
placed by the 'density' kwarg.
  warnings.warn("The 'normed' kwarg is deprecated, and has been "
```


Histograms of age
Histogram values
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
20
40
60
80
100
age
status
🟦 Survived after 5yrs
🟧 Not Survived after 5yrs


Histograms of year
Histogram values
0.10
0.08
0.06
0.04
0.02
0.00
55
60
65
70
year
status
🟦 Survived after 5yrs
🟧 Not Survived after 5yrs


Histograms of nodes
0.5



Observation

To predict the survival, using nodes would be highly better than using age and using age is slightly better than using year.

We can infer few other minor points as below:

1. The probability of non survival is slightly higher for the age group 40 - 60.
2. The probability of survival is slightly higher for treatments done from the year 1958 to 1962.
3. The probability of not survival is slightly higher for treatments done from the year 1963 to 1966.
4. The probability of survival of patients having nodes less than 5 is drastically higher.

Univariate Analysis: PDFs and CDFs

In [75]:

```
plt.figure(figsize=(20,5))
nodes_of_survived = haberman.nodes[haberman.status == "Survived after 5yrs"]
nodes_of_not_survived = haberman.nodes[haberman.status == "Not Survived
```

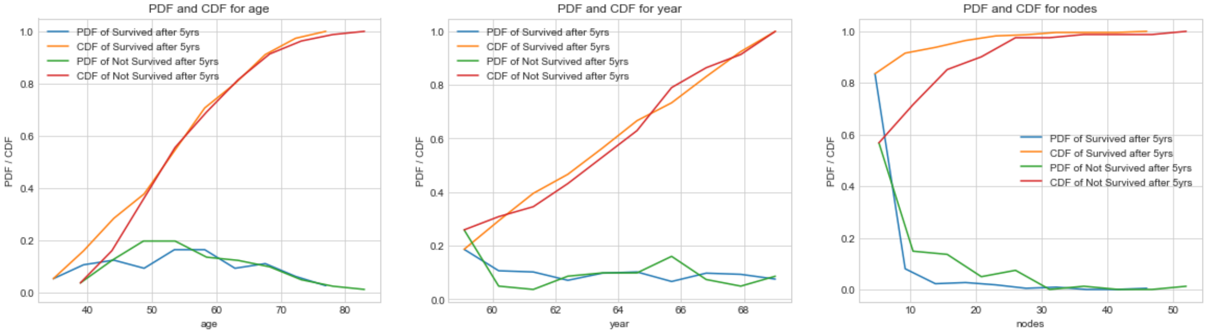
```
 after 5yrs"]
for idx,feature in enumerate(list(haberman.columns)[:-1]):
    plt.subplot(1, 3, idx + 1)

    for survival_status in list(haberman.status.unique()):
        print('-' * 30 + 'PDF and CDF of '+ survival_status + ' with re
spect to ' + feature + '-' * 30)
        hist, bin_edges = np.histogram(haberman[feature][haberman.statu
s == survival_status], bins = 10, density = True )

        print("\nHistogram values: {}".format(hist))
        print("\nBin Edges: {}".format(bin_edges))

        pdf = hist / sum(hist)
        print("\nPDF: {}".format(pdf))

        cdf = np.cumsum(pdf)
        print("\nCDF: {}\n".format(cdf))

        lines = plt.plot(bin_edges[1:], pdf, bin_edges[1:], cdf)

        plt.setp(lines[0],label = "PDF of {}".format(survival_status))
        plt.setp(lines[1],label = "CDF of {}".format(survival_status))

    plt.title("PDF and CDF for {}".format(feature))
    plt.xlabel(feature)
    plt.ylabel("PDF / CDF")
    plt.legend()

plt.show()
```

```
------------------------------PDF and CDF of Survived after 5yrs with r
espect to age------------------------------

Histogram values: [0.01134752 0.02269504 0.02647754 0.01985816 0.034988
18 0.03498818
 0.01985816 0.02364066 0.01323877 0.00567376]

Bin Edges: [30.  34.7 39.4 44.1 48.8 53.5 58.2 62.9 67.6 72.3 77. ]
```

```
PDF: [0.05333333 0.10666667 0.12444444 0.09333333 0.16444444 0.16444444
 0.09333333 0.11111111 0.06222222 0.02666667]

CDF: [0.05333333 0.16       0.28444444 0.37777778 0.54222222 0.70666667
 0.8        0.91111111 0.97333333 1.        ]

------------------------------PDF and CDF of Not Survived after 5yrs wi
th respect to age------------------------------

Histogram values: [0.00755858 0.02519526 0.04031242 0.04031242 0.027714
79 0.02519526
 0.02015621 0.01007811 0.00503905 0.00251953]

Bin Edges: [34.  38.9 43.8 48.7 53.6 58.5 63.4 68.3 73.2 78.1 83. ]

PDF: [0.03703704 0.12345679 0.19753086 0.19753086 0.13580247 0.12345679
 0.09876543 0.04938272 0.02469136 0.01234568]

CDF: [0.03703704 0.16049383 0.35802469 0.55555556 0.69135802 0.81481481
 0.91358025 0.96296296 0.98765432 1.        ]

------------------------------PDF and CDF of Survived after 5yrs with r
espect to year------------------------------

Histogram values: [0.16969697 0.0969697  0.09292929 0.06464646 0.088888
89 0.09292929
 0.06060606 0.08888889 0.08484848 0.06868687]

Bin Edges: [58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]

PDF: [0.18666667 0.10666667 0.10222222 0.07111111 0.09777778 0.10222222
 0.06666667 0.09777778 0.09333333 0.07555556]

CDF: [0.18666667 0.29333333 0.39555556 0.46666667 0.56444444 0.66666667
 0.73333333 0.83111111 0.92444444 1.        ]

------------------------------PDF and CDF of Not Survived after 5yrs wi
th respect to year------------------------------
```

```
Histogram values: [0.23569024 0.04489338 0.03367003 0.07856341 0.089786
76 0.08978676
 0.14590348 0.06734007 0.04489338 0.07856341]

Bin Edges: [58.  59.1 60.2 61.3 62.4 63.5 64.6 65.7 66.8 67.9 69. ]

PDF: [0.25925926 0.04938272 0.03703704 0.08641975 0.09876543 0.09876543
 0.16049383 0.07407407 0.04938272 0.08641975]

CDF: [0.25925926 0.30864198 0.34567901 0.43209877 0.5308642  0.62962963
 0.79012346 0.86419753 0.91358025 1.        ]

------------------------------PDF and CDF of Survived after 5yrs with r
espect to nodes------------------------------

Histogram values: [0.18164251 0.0173913  0.00483092 0.0057971  0.003864
73 0.00096618
 0.00193237 0.         0.         0.00096618]

Bin Edges: [ 0.   4.6  9.2 13.8 18.4 23.  27.6 32.2 36.8 41.4 46. ]

PDF: [0.83555556 0.08       0.02222222 0.02666667 0.01777778 0.00444444
 0.00888889 0.         0.         0.00444444]

CDF: [0.83555556 0.91555556 0.93777778 0.96444444 0.98222222 0.98666667
 0.99555556 0.99555556 0.99555556 1.        ]

------------------------------PDF and CDF of Not Survived after 5yrs wi
th respect to nodes------------------------------

Histogram values: [0.10921178 0.02849003 0.02611586 0.00949668 0.014245
01 0.
 0.00237417 0.         0.         0.00237417]

Bin Edges: [ 0.   5.2 10.4 15.6 20.8 26.  31.2 36.4 41.6 46.8 52. ]

PDF: [0.56790123 0.14814815 0.13580247 0.04938272 0.07407407 0.
 0.01234568 0.         0.         0.01234568]
```

```
CDF: [0.56790123 0.71604938 0.85185185 0.90123457 0.97530864 0.97530864
 0.98765432 0.98765432 0.98765432 1.        ]
```



Observations

Age Related observations:

1. For patients with age less than 50, the surivival probability is quite higher by around 10%.
2. Around 20% of the non-survival patient's age is 50.

Year related observations:

1. There is not much significant improvement in the patient survival probability year by year.

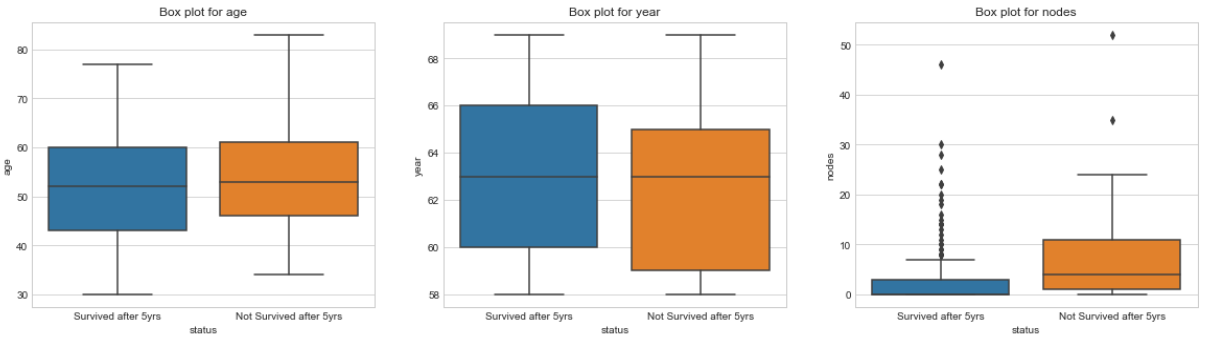
Nodes related observations:

1. Around 81% of the patients survived more than 5 years, have number of positive lymph nodes less than 5.
2. For patients with nodes less than 26, the survival probability is higher by around 5 to 20 %, with the probability difference decreasing as the nodes increasing.
3. For patients with nodes between 10 to 30, the non-survival probability is higher by around 5 to 10 %.

Univariate Analysis: Box Plot

In [190]:

```
plt.figure(1, figsize = (20,5))
for idx, feature in enumerate(list(haberman.columns)[:-1]):
    plt.subplot(1, 3, idx + 1)
    sns.boxplot(x = "status", y = feature, data = haberman)
    plt.title("Box plot for {}".format(feature))
plt.show()
```



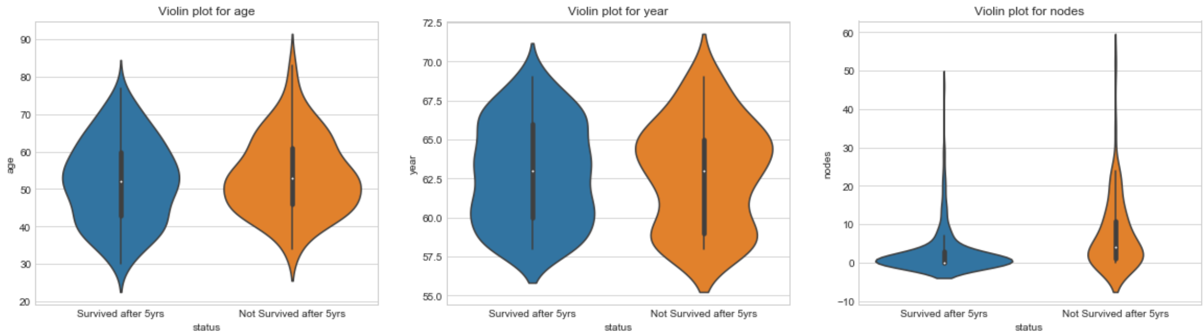
Observations

1. If I categorize patients with nodes lesser than 5 have survived more than 5 years, errorneously I'm likely to classify around 48% of patients not survived as patients survived and miss out 25% of the survived patients.
2. If I categorize patients with age lesser than 52 have survived more than 5 years, errorneously I'm likely to classify around 49% of patients not survived as survived and miss out 50% of the survived patients.
3. If I categorize patients undergone operations after the year 1963 as survived more than 5 years, errorneously I'm likely to classify around 50% of not survived as survived and miss out 50% of the survived patients.

Univariate Analysis: Violin Plot

In [191]:

```
plt.figure(1, figsize = (20,5))
for idx, feature in enumerate(list(haberman.columns)[:-1]):
    plt.subplot(1, 3, idx + 1)
    sns.violinplot(x = "status", y = feature, data = haberman)
    plt.title("Violin plot for {}".format(feature))
plt.show()
```



Observations

1. Most of the survivors after 5 years have number of positive lymph nodes between 0 and 5.
2. The probability of survival is most high for patients with age 53
3. The probability of non survival is most high for patients with age 50.
4. The probability of survival is most high for patients undergone operation in the year 1960.
5. The probability of non survival is most high patients undergone operation in the year 1964.
6. The probability of survival is most high for patients with no nodes.
7. The probability of non survival is most high for patients with nodes 3.

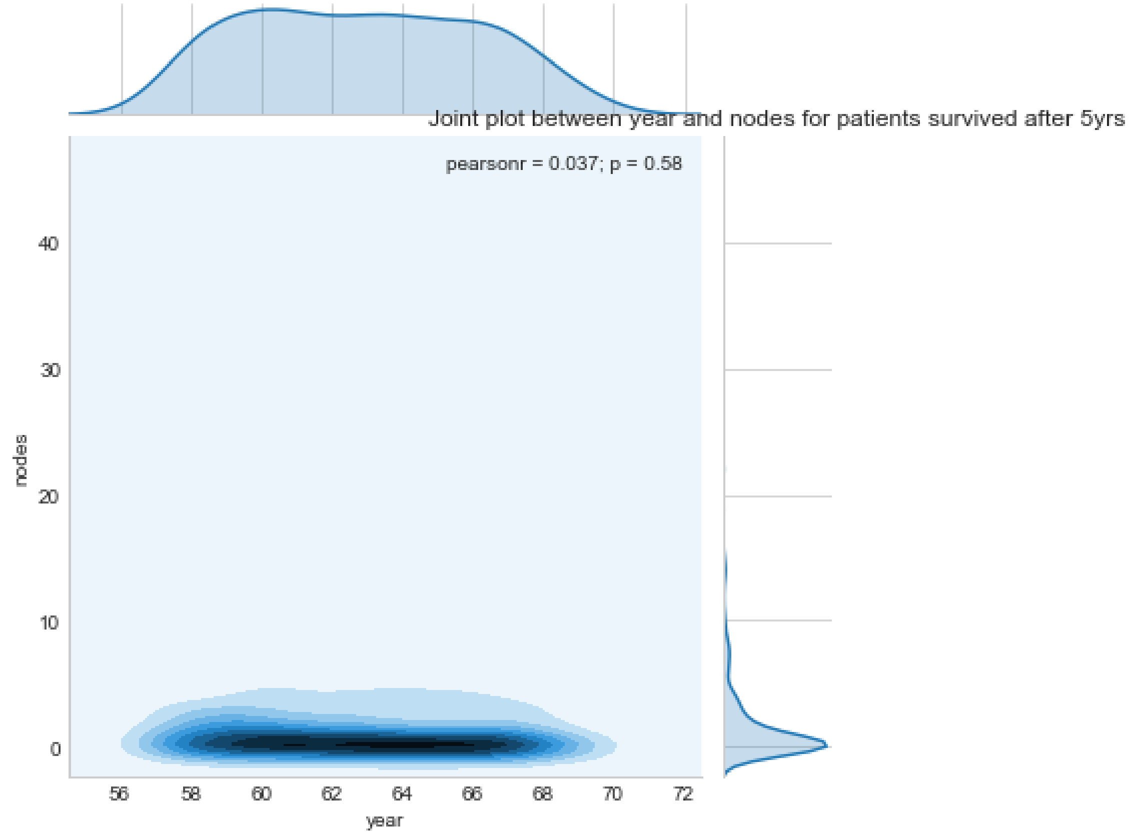
Bivariate Analysis - Joint plots

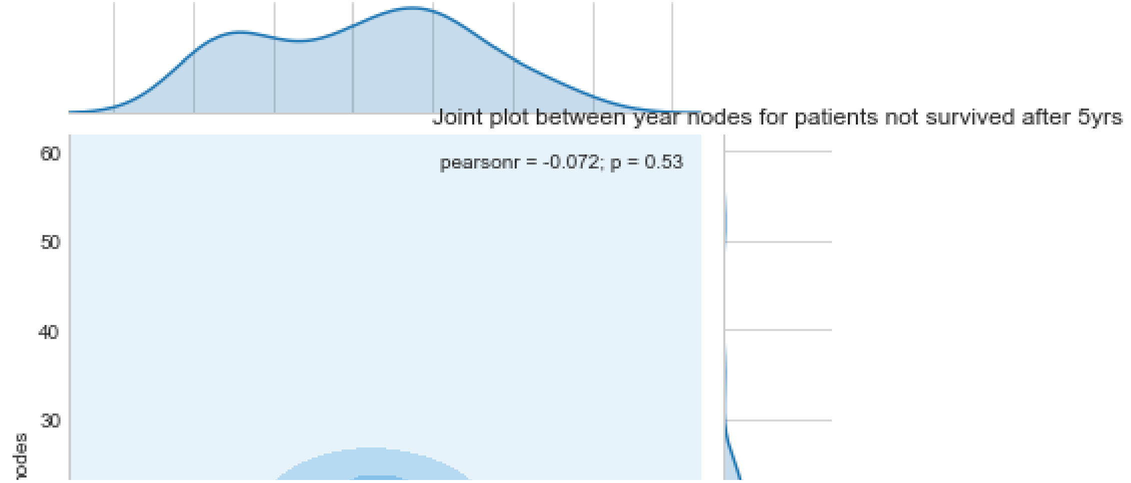
Joint Plot between year and nodes

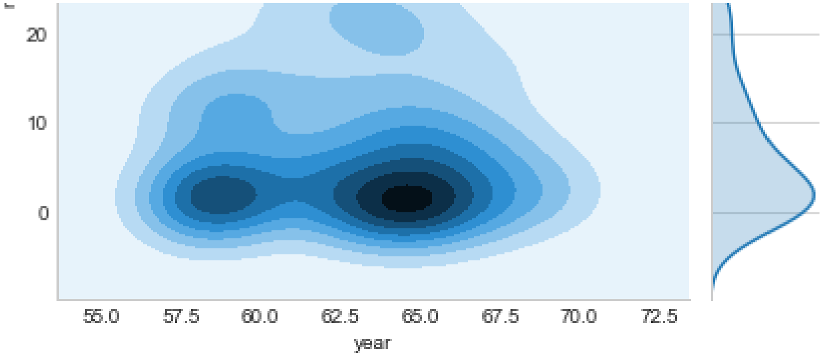
In [97]:

```
plt.figure(1)
sns.jointplot(x = "year", y = "nodes", data = haberman[haberman.status == "Survived after 5yrs"], kind = 'kde')
plt.title("Joint plot between year and nodes for patients survived after 5yrs")
plt.figure(2)
sns.jointplot(x = "year", y = "nodes", data = haberman[haberman.status == "Not Survived after 5yrs"], kind = 'kde')
plt.title("Joint plot between year nodes for patients not survived after 5yrs")
plt.show()
```

```
<Figure size 432x288 with 0 Axes>
```


Joint plot between year and nodes for patients survived after 5yrs
pearsonr = 0.037; p = 0.58
nodes
40
30
20
10
0
56
58
60
62
64
66
68
70
72
year


Joint plot between year nodes for patients not survived after 5yrs
pearsonr = -0.072; p = 0.53
60
50
40
30
nodes



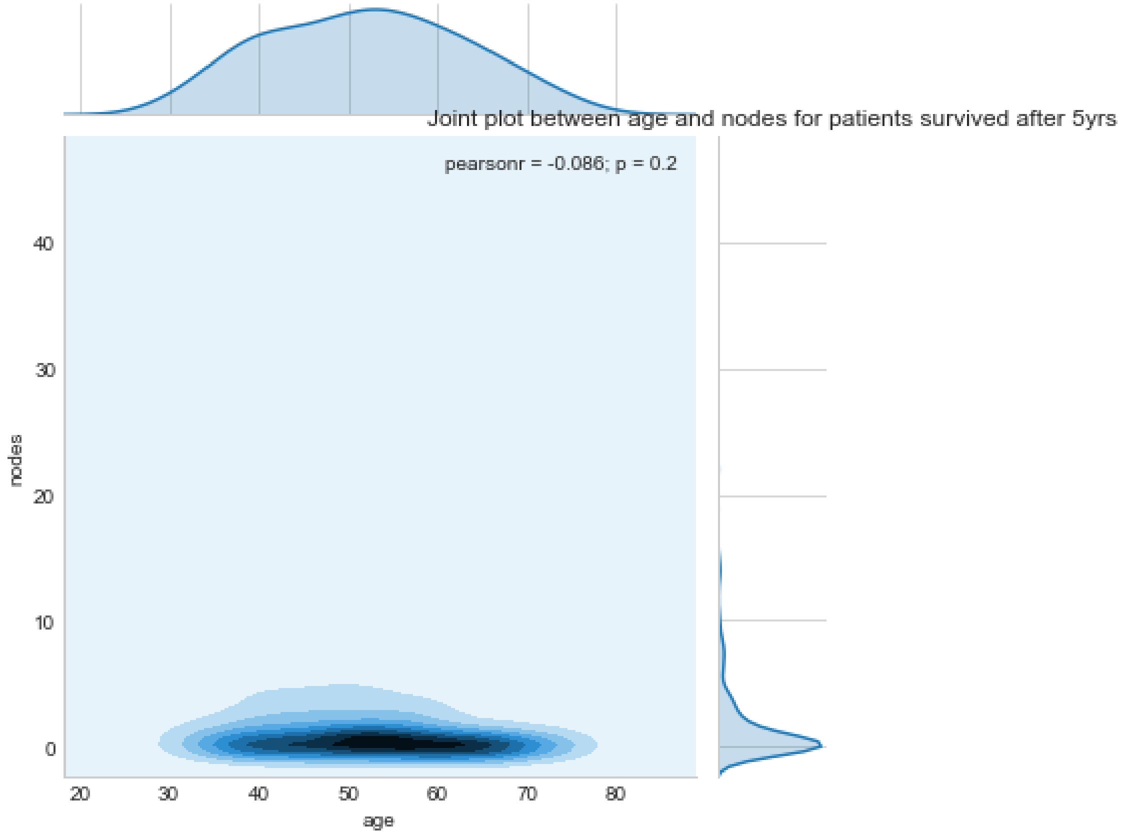
Observations

1. Most of the survived patients have undergone operation in the years between 1962 to 1966 and have no nodes
2. Most of the non survived patients have undergone operation in the years 1964 and 1965 and have nodes from 1 to 3.

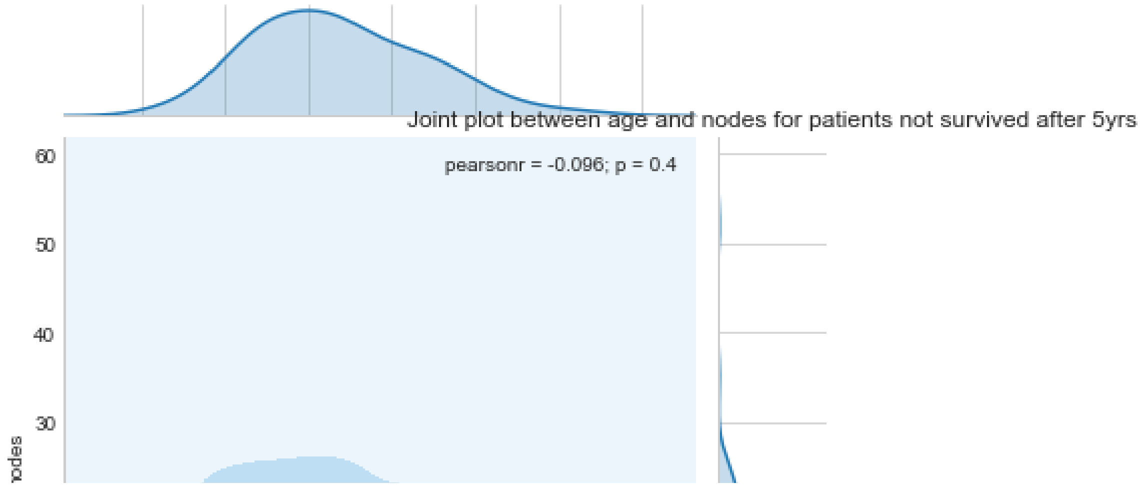
Joint plot between age and nodes

In [96]:
```
plt.figure(1)
sns.jointplot(x = "age", y = "nodes", data = haberman[haberman.status =
= "Survived after 5yrs"], kind = 'kde')
plt.title("Joint plot between age and nodes for patients survived after
 5yrs")
plt.figure(2)
sns.jointplot(x = "age", y = "nodes", data = haberman[haberman.status =
= "Not Survived after 5yrs"], kind = 'kde')
plt.title("Joint plot between age and nodes for patients not survived a
fter 5yrs")
plt.show()
```

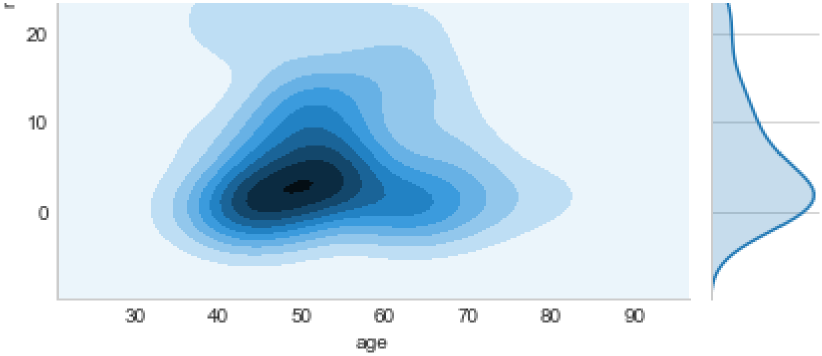
```
<Figure size 432x288 with 0 Axes>
```



Joint plot between age and nodes for patients survived after 5yrs



Joint plot between age and nodes for patients not survived after 5yrs



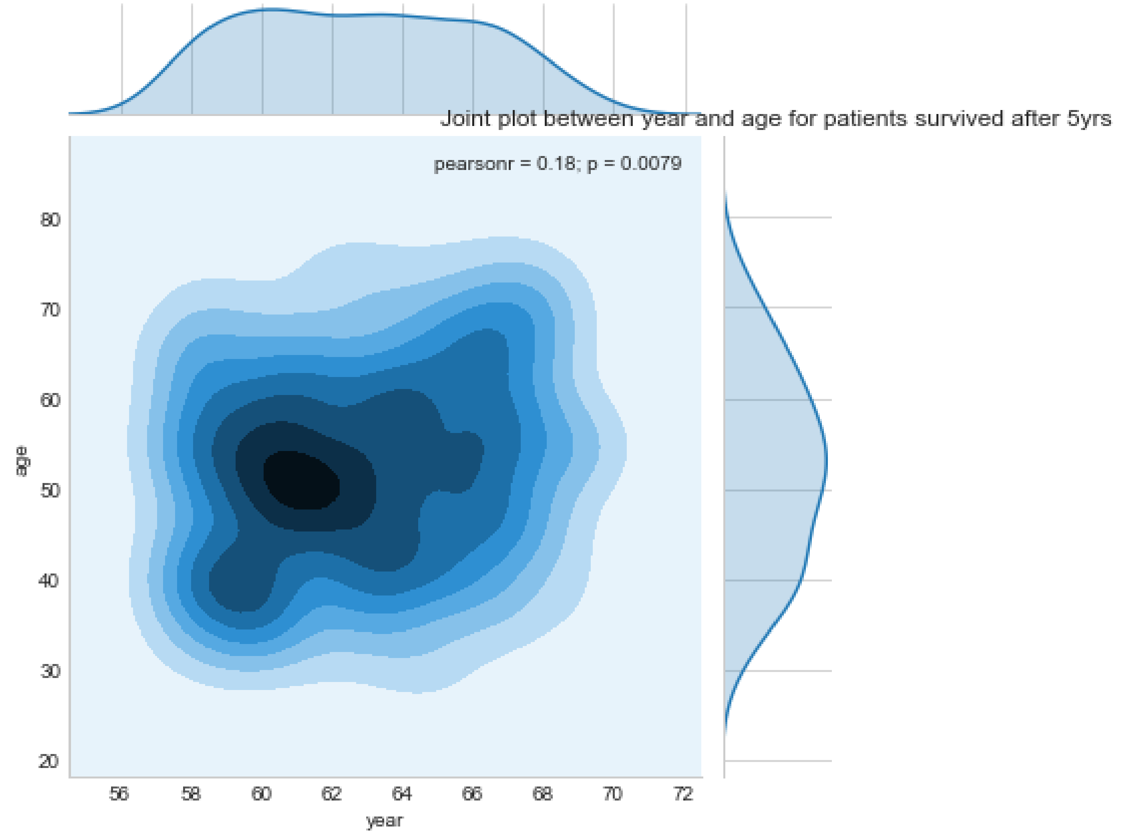
Observations

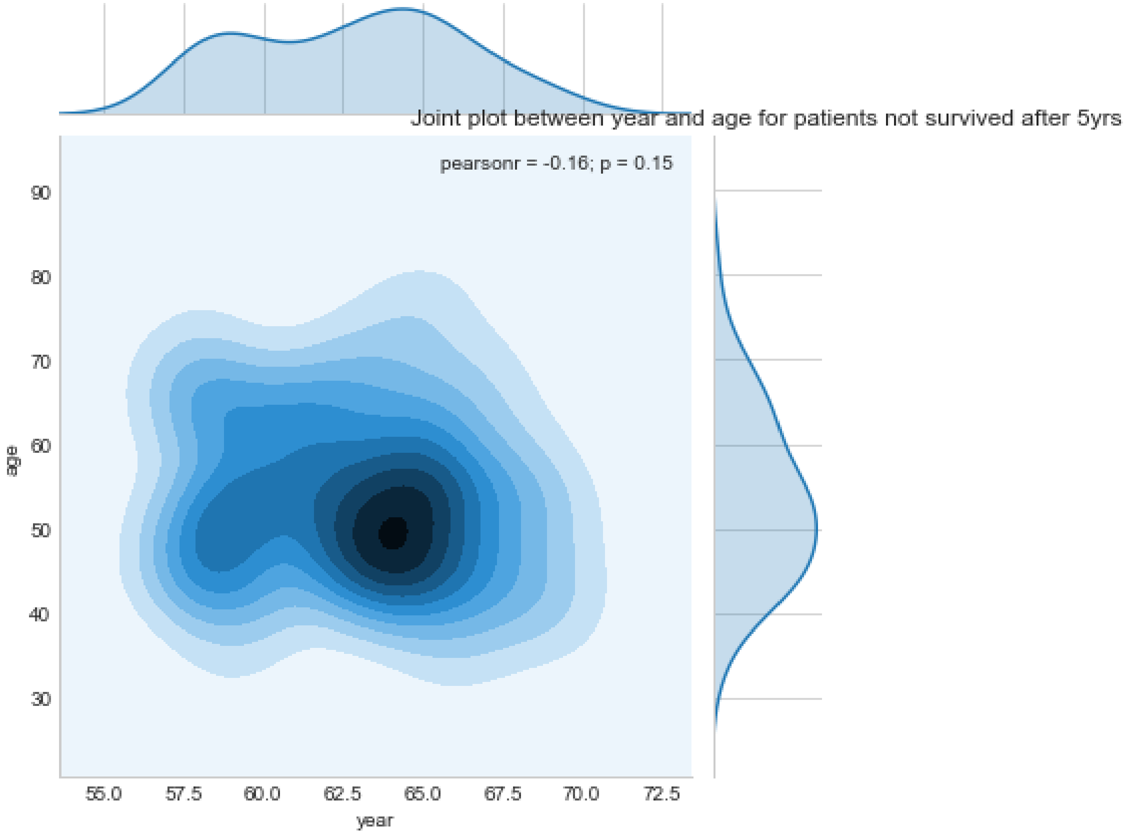
1. Most of the survived patient's age is between 50 to 63 and they have 0 to 2 nodes.
2. Most of the non-survived patient's age is 50 and 51 and they have nodes 3 to 4, but since the circle is smaller, this will sum up to a very small set of observations.

In [99]:

```
plt.figure(1)
sns.jointplot(x = "year", y = "age", data = haberman[haberman.status == "Survived after 5yrs"], kind = 'kde')
plt.title("Joint plot between year and age for patients survived after 5yrs")
plt.figure(2)
sns.jointplot(x = "year", y = "age", data = haberman[haberman.status == "Not Survived after 5yrs"], kind = 'kde')
plt.title("Joint plot between year and age for patients not survived after 5yrs")
plt.show()
```

```
<Figure size 432x288 with 0 Axes>
```


Joint plot between year and age for patients survived after 5yrs
pearsonr = 0.18; p = 0.0079
age
80
70
60
50
40
30
20
56
58
60
62
64
66
68
70
72
year



Observations

1. With operation year 1960 to 1962 and age 48 to 53, there are more number of survived patients.

2. With operation year 1963 and 1964 and age 48 to 51, there are more number of non-survived patients, but since the circle is smaller, this will sum up to a very small set of observations.

Conclusion

1. It is not possible to classify all the observations with simple if else constructs or by drawing a line, because the data points of both the classes overlap each other massively.

1. Yet, we can classify few of the data points (9 observations out of 306 observations) using simple if else construct. With respect to the given data set, we can predict the following:

   2.1 Patients with age less than 34 will survive more 5 years

   2.2 Patients with age more than 77 will not survive more than 5 years

   2.3 Patients with number of positive lymph nodes greater than 46 will not survive more than 5 years

1. For patients with age less than 50, we can predict the surivival probability will be quite higher by around 10%.

1. Although the number of positive lymph nodes of the patients will be widely spread between 0 to around 50, we can predict 75% of the patients will have number of positive lymph nodes less than 5, out of which around 81% of the patients will survive more than 5 years.

1. So we can predict around 60% of the patients, will have number of positive lymph nodes less than 5 and will survive more than 5 years. Hence the prediction is patients with positive lymph nodes less than 5, have around 60% of chance to survive more than 5 years.