Haberman_Exploratory_Analysis

August 11, 2018

1 Perform EDA on Haberman Dataset

1.0.1 Data Description:

The dataset contains a study conducted between 1958 and 1970 at the University of Chicago on **survival of patients** who had undergone surgery for breast cancer.

1.0.2 Data Attributes:

1. Age of patient
2. Patient's year of operation
3. Number of positive lymph nodes detected
4. Survival Status (1 = survived 5 years; 2 = died within 5 year)

1.0.3 Objective:

To analyze the data to know, how to predict a patient will survive or not, based on his age, number of positive lymph nodes and year in which the operation was conducted.

1.1 1. Load Data

```
In [46]: import pandas as pd
         import seaborn as sns
         import matplotlib.pyplot as plt
         import numpy as np


         # Load haberman.csv into a pandas dataFrame.
         # Survival data of patients who had undergone surgery for breast cancer
         haberman = pd.read_csv("haberman.csv")

         # (Q) how many data-points and features?
         print (haberman.shape)

         # See the input data.
         haberman.head(5)
         # Identified the columns doesnt have header information.
```

```
(305, 4)
```

```
Out[46]:    30  64   1  1.1
         0  30  62   3    1
         1  30  65   0    1
         2  31  59   2    1
         3  31  65   4    1
         4  33  58  10    1
```

```
In [47]: # Give column names based on attribute information
         haberman.columns = ['Age', 'Year', 'Nodes', 'Survived']

         # See the input data.
         haberman.head(5)
```

```
Out[47]:    Age  Year  Nodes  Survived
         0   30    62      3         1
         1   30    65      0         1
         2   31    59      2         1
         3   31    65      4         1
         4   33    58     10         1
```

2 2. Input Data Analysis & Preparation

```
In [48]: # Check characteristics of data.
         haberman.info()
         haberman.describe()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 305 entries, 0 to 304
Data columns (total 4 columns):
Age         305 non-null int64
Year        305 non-null int64
Nodes       305 non-null int64
Survived    305 non-null int64
dtypes: int64(4)
memory usage: 9.6 KB
```

```
Out[48]:               Age        Year       Nodes    Survived
         count  305.000000  305.000000  305.000000  305.000000
         mean    52.531148   62.849180    4.036066    1.265574
         std     10.744024    3.254078    7.199370    0.442364
         min     30.000000   58.000000    0.000000    1.000000
         25%     44.000000   60.000000    0.000000    1.000000
         50%     52.000000   63.000000    1.000000    1.000000
         75%     61.000000   66.000000    4.000000    2.000000
         max     83.000000   69.000000   52.000000    2.000000
```

```
In [49]: # To make 4th column (class label), more meaningful, replace with Survival Status
         haberman.loc[haberman['Survived'] == 1, 'Survived'] = "yes"
         haberman.loc[haberman['Survived'] == 2, 'Survived'] = "no"

         #(Q) How many data points for each class are present?
         haberman["Survived"].value_counts()

Out[49]: yes    224
         no      81
         Name: Survived, dtype: int64
```

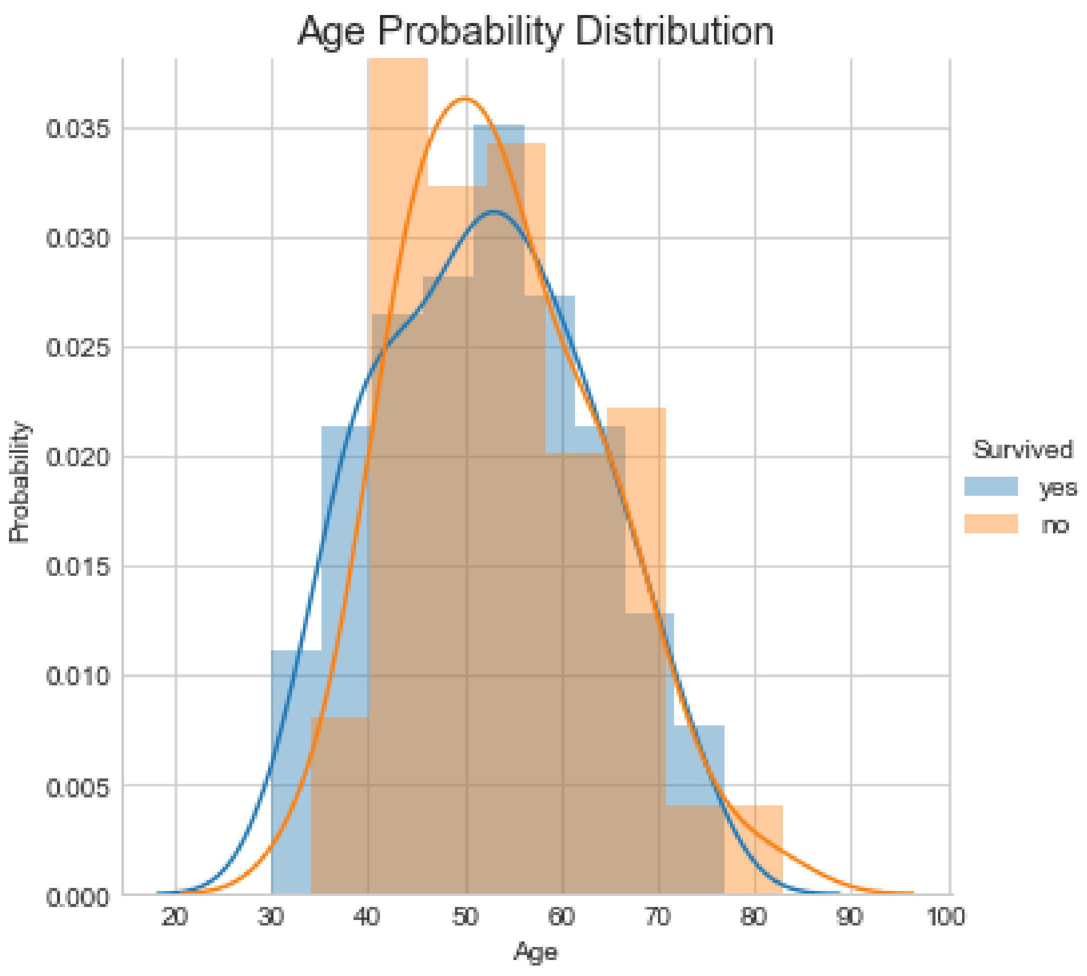
3 3. Univariate Analysis

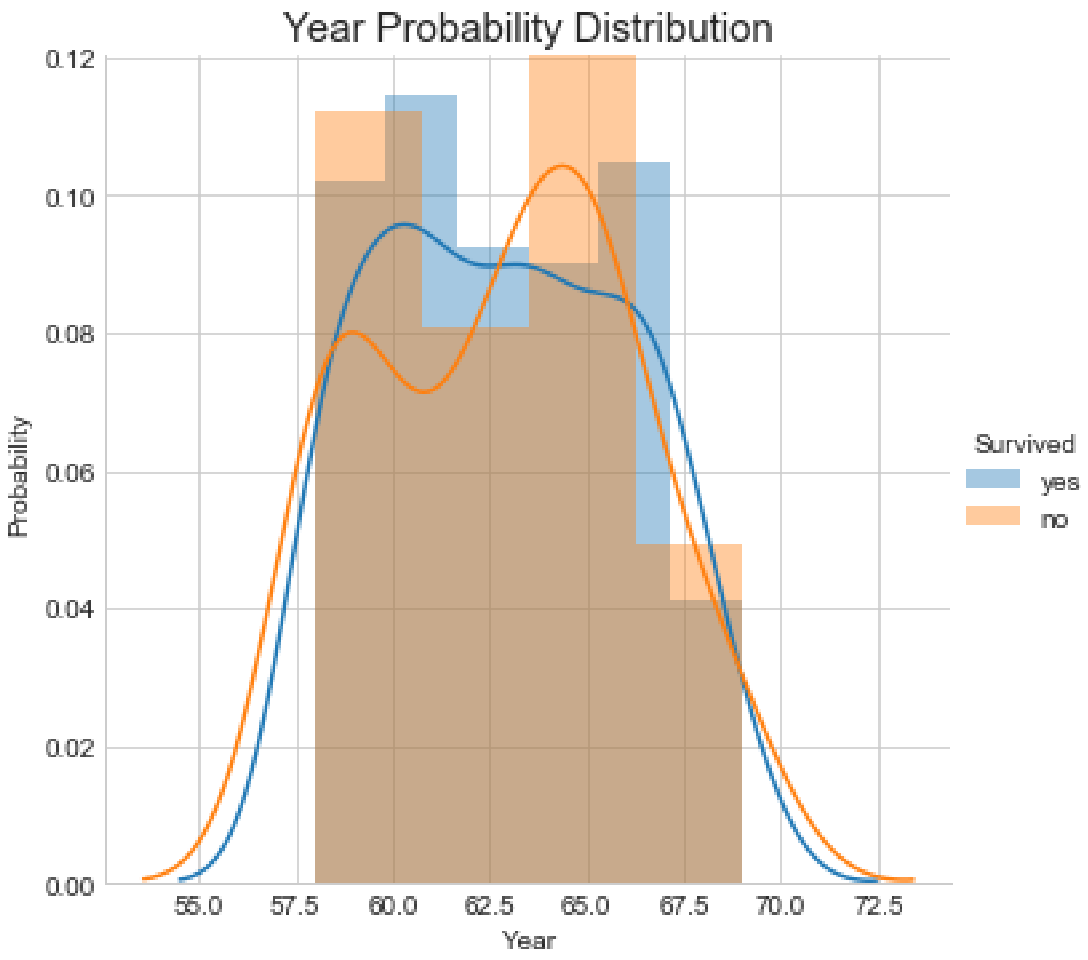
Univariate Analysis is conducted **to find out whether any single feature in the dataset is enough to build a model** to identify whether a patient would survive or not.

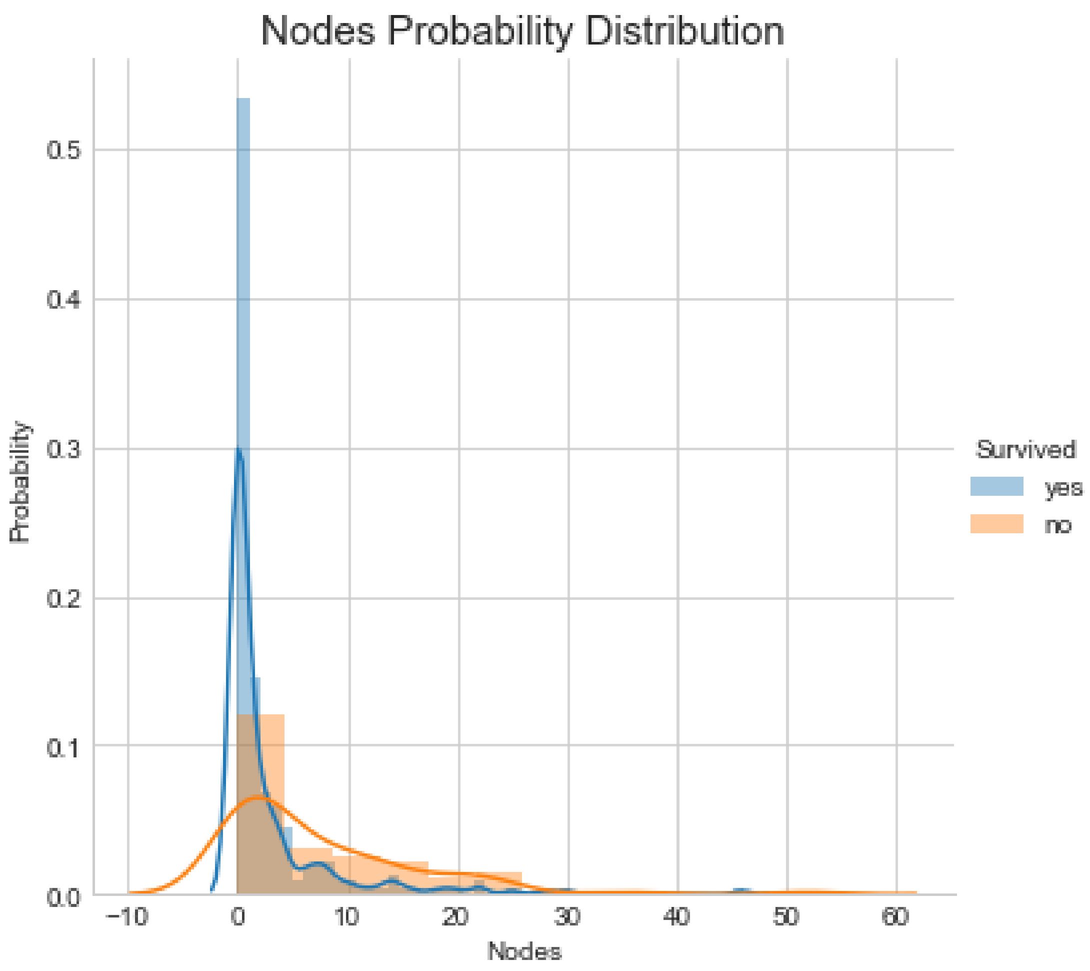
3.1 3.1 Probability Distribution Function (PDF)

```
In [50]: # Plot PDF of each feature

         for col in haberman.columns[:-1]:
             sns.FacetGrid(haberman, hue="Survived", size=5) \
                .map(sns.distplot, col) \
                .add_legend();
             plt.title(col+' Probability Distribution',fontsize=15)
             plt.ylabel('Probability')
             plt.show();
```


Age Probability Distribution
Probability
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
20
30
40
50
60
70
80
90
100
Age
Survived
yes
no


Year Probability Distribution
Probability
Year
0.00
0.02
0.04
0.06
0.08
0.10
0.12
55.0
57.5
60.0
62.5
65.0
67.5
70.0
72.5
Survived
yes
no



3.2 3.2 Cumulative Distribution Function (CDF)

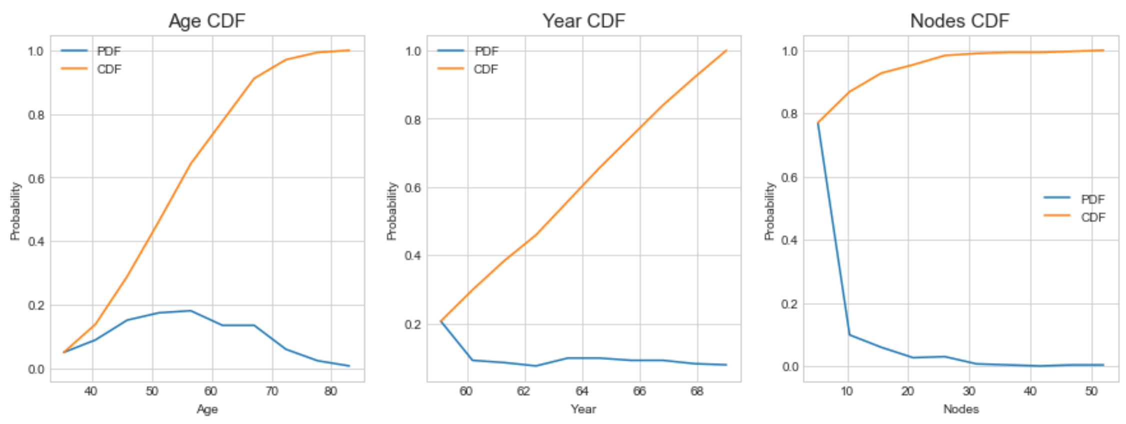
```
In [51]: # You can get the success percentage directly from CDF given one x value.
         # Such information is not available from PDF directly

         plt.figure(figsize=(15,5))

         for idx, col in enumerate(haberman.columns[:-1]):
             counts, bin_edges = np.histogram(haberman[col], bins=10,
                                              density = True)
             pdf = counts/(sum(counts))
             cdf = np.cumsum(pdf)

             plt.subplot(1, 3, idx+1)
             plt.plot(bin_edges[1:],pdf, label='PDF')
             plt.plot(bin_edges[1:],cdf, label='CDF')
             plt.title(col + " CDF",fontsize=15)
```

```
        plt.xlabel(col)
        plt.ylabel('Probability')
        plt.legend()
```

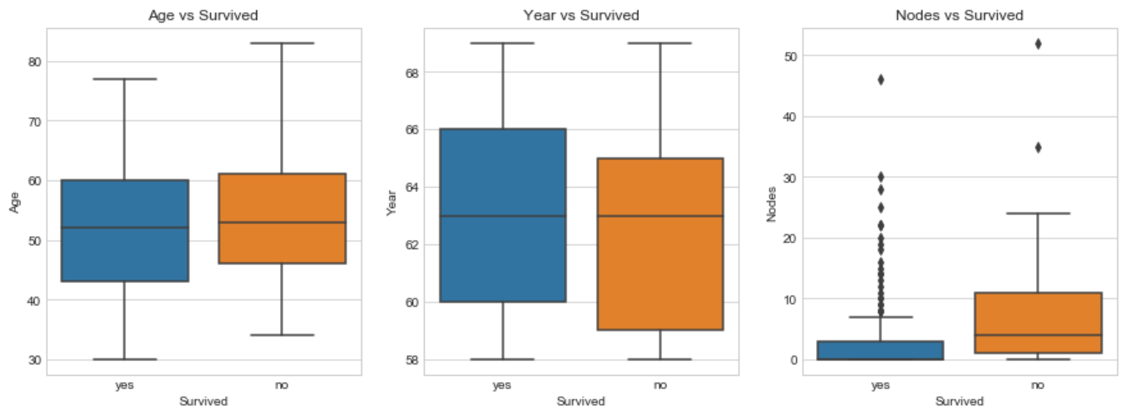


3.3 3.3 Box Plots

```
In [52]: #Box-plot with whiskers: another method of visualizing the
         #1-D scatter plot more intuitively.

         fig, axes = plt.subplots(1, 3, figsize=(15, 5))

         for idx, col in enumerate(haberman.columns[:-1]):
             sns.boxplot(x='Survived',y=col, data=haberman,
                         ax=axes[idx]).set_title(col+' vs Survived')
         plt.show()
```



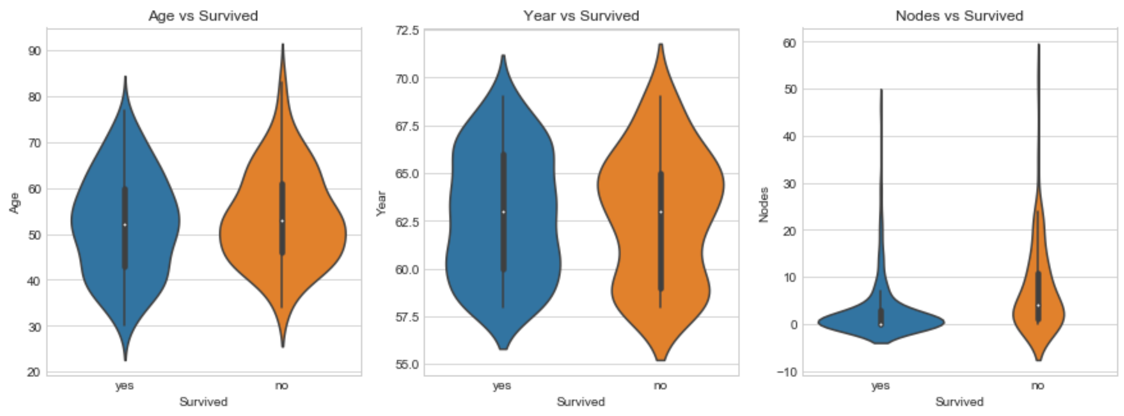
3.4 3.4 Violin Plot

```
In [53]: # 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

         fig, axes = plt.subplots(1, 3, figsize=(15, 5))

         for idx, col in enumerate(haberman.columns[:-1]):
             sns.violinplot(x="Survived", y=col, data=haberman, size=8, ax=axes[idx]) \
             .set_title(col+' vs Survived')
         plt.show()
```

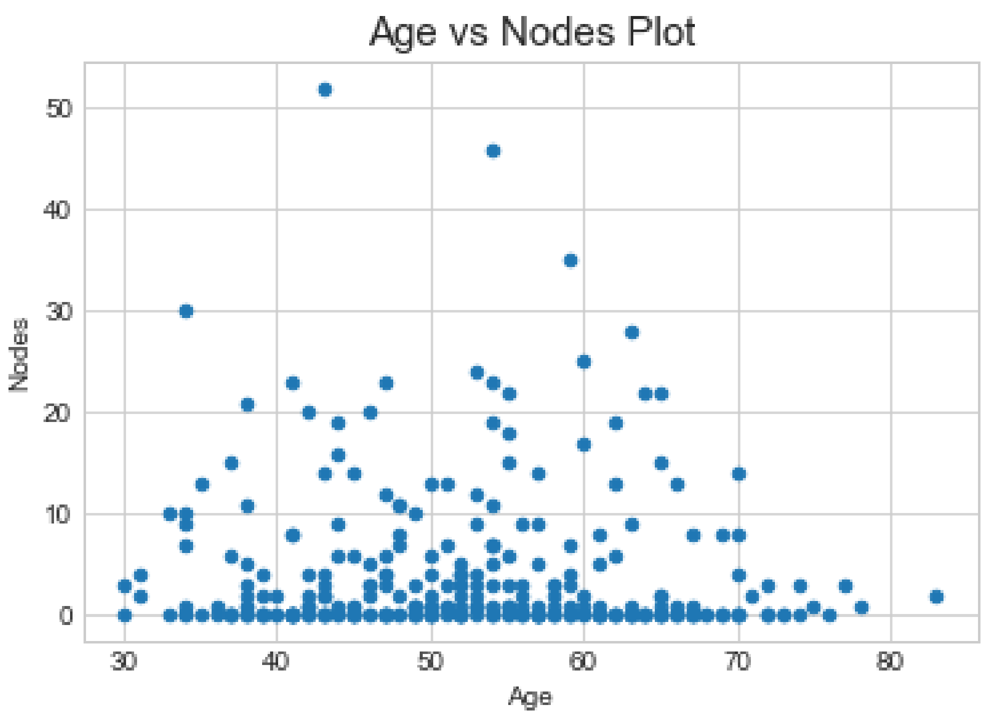


4 Multi-variate Analysis

4.1 3.1 2-D Scatter Plot

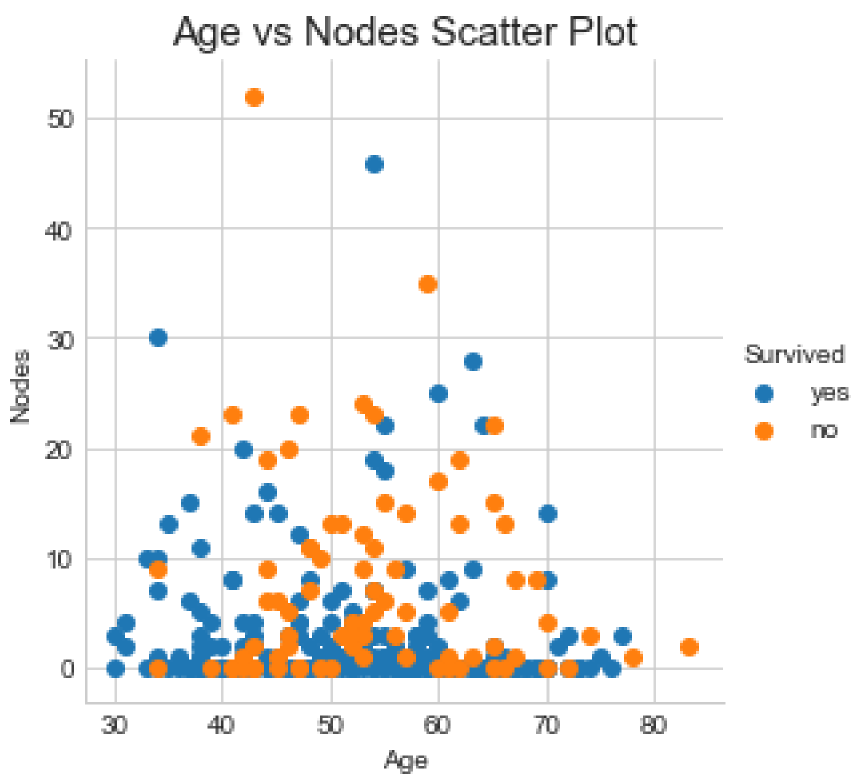
```
In [54]: #2-D scatter plot:
         #plot 2 features (chosen intuitively) that can  impact surivability

         haberman.plot(kind='scatter', x='Age', y='Nodes')
         plt.title("Age vs Nodes Plot",fontsize=15)
         plt.xlabel('Age')
         plt.ylabel('Nodes')
         plt.show()
         #cant make much sense of data.
         #Will try color the points by class label (survived or not).
```



```
In [55]: # 2-D Scatter plot with color-coding for each class: survived or not
         sns.set_style("whitegrid");
         sns.FacetGrid(haberman, hue="Survived", size=4) \
            .map(plt.scatter, "Age", "Nodes") \
            .add_legend();
         plt.title('Age vs Nodes Scatter Plot',fontsize=15)
         plt.show();

         # The orange and blue data points are not easily separable.
         # Considerable overlap is there. We will try multiple 2-D scatter
         # plots for each combination of features using pair plot.
```



4.2 1.3 Pair Plot

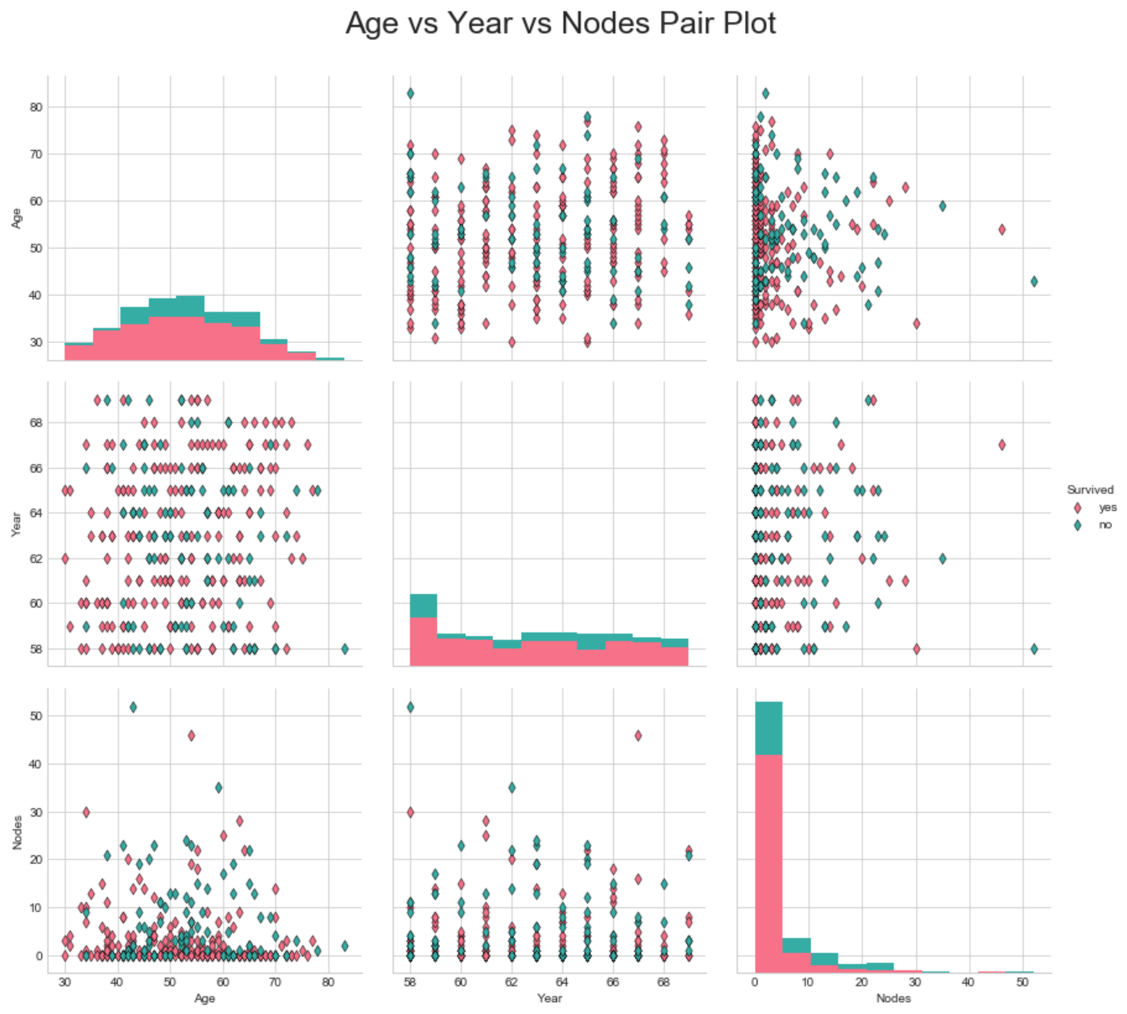
```
In [56]: # Pairwise scatter plot: Pair-Plot:
         # To estimate which combination of features are the
         # best among to get maximum classification.
         # NOTE: the diagnol elements are PDFs for each feature.

         # plt.close();
         # sns.set_style("whitegrid");
         # sns.pairplot(haberman[:-1], hue="Survived", size=4)
         # plt.title()
         # plt.show()

         g = sns.pairplot(haberman, hue='Survived',
                          palette='husl', markers='d', size=4, plot_kws=
             {
             "s":40,
             "alpha":1.0,
             'lw':0.5,
             'edgecolor':'k'
             })
```

```
g.fig.subplots_adjust(top=0.92, bottom=0.08)
g.fig.suptitle('Age vs Year vs Nodes Pair Plot',fontsize=25)
```

```
Out[56]: Text(0.5,0.98,'Age vs Year vs Nodes Pair Plot')
```



5 Observations

5.1 High-Level Analysis

1. Haberman is an **imbalanced dataset** with 224 survived patients & 81 otherwise
2. To make haberman balanced, either under-sample positive class or over-sample negative class. In imbalanced sets, classification algorithms like KNN will favour majority class.
3. **25% of patients dont have any positive lymph node, 50% patients have <=1** and 75% have <= 4 positive lymph nodes. Maximum number of lymph nodes = 52 seems very rare.
4. **50% of patients are in 44-61 age group**, though age ranges from 30 to 83.
5. Haberman **doesnt have missing values**, hence data imputation is not required.

5.2 Univariate Analysis

1. PDF: The number of positive lymph nodes are **highly dense between 0-5**
2. CDF: **Nearly 80%** of positive lymph nodes are **less than 5**
3. Box-Plot: Patients who were **treated in later years had higher chances of survival.**
4. Box-Plot: Patients with **higher # of positive lymph nodes has much less chances of survival.**
5. Violin-Plot: Same conclusions as in Box Plot.

5.3 Multi-variate Analysis & Conclusion

1. **With given features**, survived & non-survived patient data points show **overlapping behaviour.** It is difficult to predict survivability with good accuracy as the data is **not clearly separable.**
2. Among the pair plots, **'Year of Operation vs Lymph Nodes' plot provides better seperation.**
3. 'Age vs Lymph' Nodes plot could also be used for classification.