EDA ON HABERMAN DATASET

- Haberman Dataset is collection of of patients who had undergone surgery for breast cancer.
- The data collection is between 1958 and 1970 at the University of Chicago's Billings Hospital.
- Main objective is explore data on what caueses(features) the patinet can survive or die (1 -yes or 2 die)

In [1]:

```
# numpy for computations
import numpy as np
# pandas - for data anlaysis
import pandas as pd
# seaborn - for data visuvalization
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:

```
# Loading haberman.csv file into pandas dataFrame
haberman_df = pd.read_csv('haberman.csv')
```

In [3]:

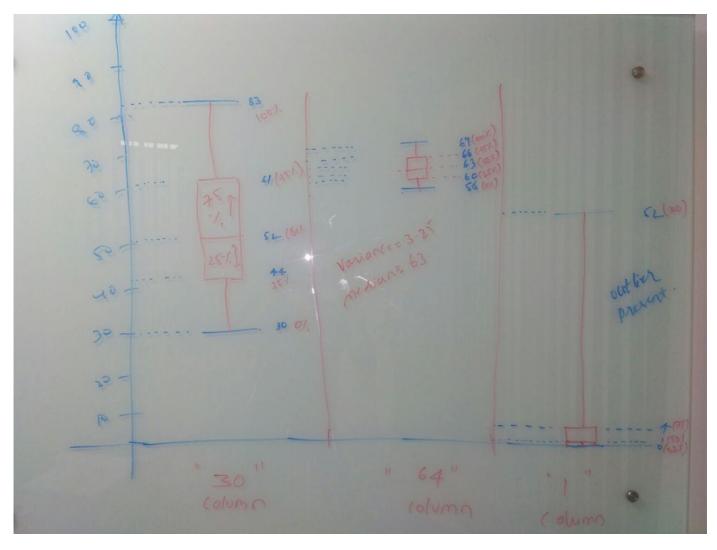
```
#colleting the information regarding the data '''
info()
1. Projecting there are 305 rows and 4 colomns(30,64,1,1.1)
2. There are no empty cells in the dataframe
3. Index column start from 0 and end at 304
haberman_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 305 entries, 0 to 304
Data columns (total 4 columns):
30     305 non-null int64
64     305 non-null int64
1     305 non-null int64
1.1     305 non-null int64
dtypes: int64(4)
memory usage: 9.7 KB
```

In [4]:

Out[4]:

	30	64	1	1.1
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 [5]:

```
''' I found there is large data imbalance as we see below nearly 25% of 2-values ar haberman_df['1.1'].value_counts(normalize=True)
```

Out[5]:

0.734426
 0.265574

Name: 1.1, dtype: float64

In [6]:

```
"" Renaming the columns name
   - As there is no describition for the csv file in kaggle, naming columns as fea
   - On google search i found cloumns are named as :
        feature_1 as age,
        feature_2 as year_of_treatment,
        feature_3 as positive_lymph_nodes,
        feature_4 as survival_status_after_5_years

#NOTE: To make difference and more understanding i am using my own names for cloumn
haberman_df = haberman_df.rename(columns={"30": "feature_1", "64": "feature_2","1":
haberman_df
```

Out[6]:

	feature_1	feature_2	feature_3	labels
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
300	75	62	1	1
301	76	67	0	1
302	77	65	3	1
303	78	65	1	2
304	83	58	2	2

305 rows × 4 columns

In [7]:

```
''' Mapping the labels (target classes)
    - 1- success & 2- failure

haberman_df['labels']= haberman_df['labels'].map({1:'yes', 2:'no'})
haberman_df
```

Out[7]:

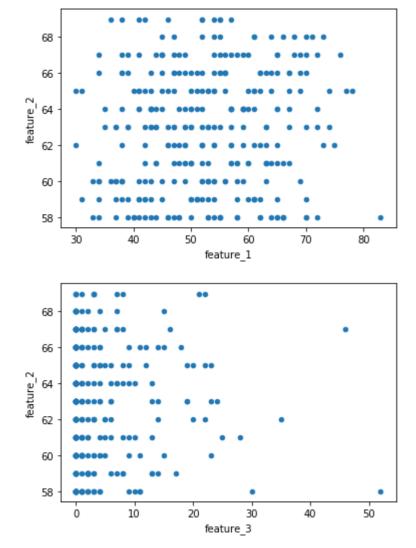
	feature_1	feature_2	feature_3	labels
0	30	62	3	yes
1	30	65	0	yes
2	31	59	2	yes
3	31	65	4	yes
4	33	58	10	yes
300	75	62	1	yes
301	76	67	0	yes
302	77	65	3	yes
303	78	65	1	no
304	83	58	2	no

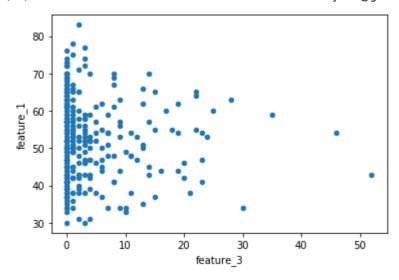
305 rows × 4 columns

In [8]:

```
# Univariate Analysis
''' - Its has to see difference between the features, but we can the range and data
    from feature-1, feature-2& feature-3'''
haberman_df.plot(kind='scatter', x='feature_1', y='feature_2');
plt.show()
haberman_df.plot(kind='scatter', x='feature_3', y='feature_2');
plt.show()
haberman_df.plot(kind='scatter', x='feature_3', y='feature_1');
plt.show()

#In below plots we can observer:
    - min range of the data
    - max range of data
    - dense points of data, how to varies from feature to feature
'''
```





Out[8]:

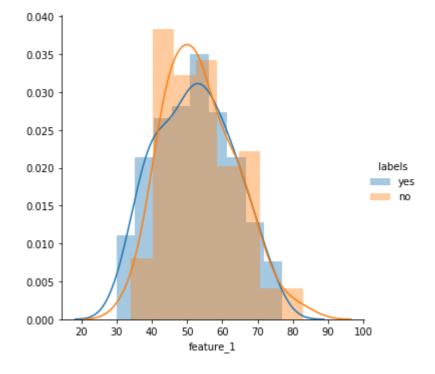
'\n - min range of the data\n - max range of data\n - dense p oints of data, how to varies from feature to feature\n'

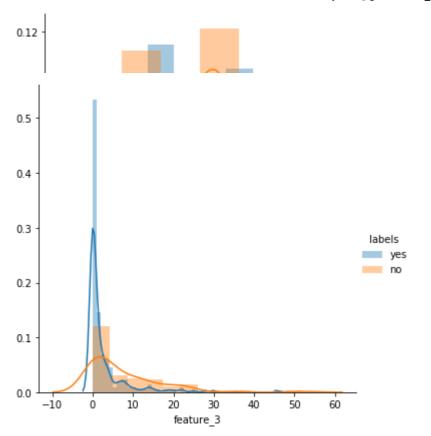
In [9]:

```
''' - Adding colour to each feature is done by FacetGrid - distplot'''
#Looping through all features except the lables (target classes)
for feature_indx, feature in enumerate(list(haberman_df.columns)[:-1]):
    haberman_fg = sns.FacetGrid(haberman_df, hue='labels', size=5)
    haberman_fg.map(sns.distplot, feature).add_legend()
    plt.show()
''' By observing the below plots:
    - Histogram indication of data points range on y-axis and features value on x-a
    - we can see the smooth curve of histogram which PDF (propability distributuon
    - Clear indication is there is not clear or approximate differenation of labels
    - There is data-imbalance as show in the image above
    - By removing the outliers and data balancing we can over come
    - In feature_3 there is large histogram difference projects the indication of o
    - By seeing the PDF in all features we compare labels differance
```

/home/trinath/.local/lib/python3.6/site-packages/seaborn/axisgrid.py:2 30: UserWarning: The `size` paramter has been renamed to `height`; ple ase update your code.

warnings.warn(msg, UserWarning)





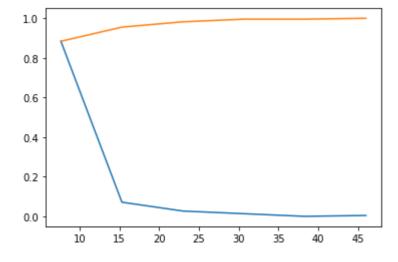
Out[9]:

'By observing the below plots:\n - Histogram indication of data po ints range on y-axis and features value on x-axies\n - we can see t he smooth curve of histogram which PDF (propability distributuon funct ion) for lables yes and no\n - Clear indication is there is not cle ar or approximate differenation of labels of each feature\n - There is data-imbalance as show in the image above\n - By removing the outliers and data balancing we can over come\n - In feature_3 there is large histogram difference projects the indication of outlier\n - By seeing the PDF in all features we compare labels difference \n'

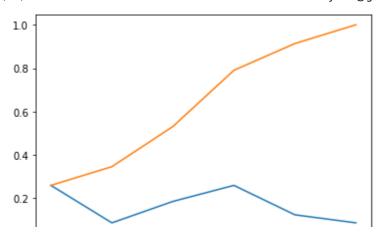
In [10]:

```
Below is CDF - which projects the differentiation of PDF
    - here i am taking "feature_3" as to visuvalize, because of above plots
    - yes - there is one specific point projecting high (10-15), and other are norm
    (by removing outiers we can increase chance of wining)
    - for no lables its not like that - but un-uniform values as there, i obser (60
#here i am using the bin size of 6, if reauired can based on range we want to focu
cdf_lables_yes = haberman_df.loc[haberman_df["labels"] == "yes"];
cdf labels no = haberman df.loc[haberman df["labels"] == "no"];
counts, bin edges = np.histogram(cdf lables yes['feature 3'], bins=6,density = True
# yes labels
'''the pdf line which starts with high value in range (5-15) and normal from range(
haberman pdf = counts/(sum(counts))
haberman cdf = np.cumsum(haberman pdf)
print(haberman pdf);
print(haberman cdf)
plt.plot(bin edges[1:],haberman pdf)
plt.plot(bin edges[1:], haberman cdf)
plt.show();
# no labels
''' the pdf line diffreent from yes lables, which has more ups and downs as showed
counts, bin edges = np.histogram(cdf labels no['feature 2'], bins=6, density = True
haberman pdf = counts/(sum(counts))
print(haberman pdf);
print(bin edges)
haberman cdf = np.cumsum(haberman pdf)
plt.plot(bin edges[1:],haberman pdf)
plt.plot(bin edges[1:], haberman cdf)
plt.show();
[0.88392857 0.07142857 0.02678571 0.01339286 0.
                                                        0.004464291
```

```
[0.88392857 0.95535714 0.98214286 0.99553571 0.99553571 1.
```



```
[0.25925926 0.08641975 0.18518519 0.25925926 0.12345679 0.08641975]
[58.
             59.83333333 61.66666667 63.5
                                                  65.33333333 67.166666
67
            ]
69.
```



In [11]:

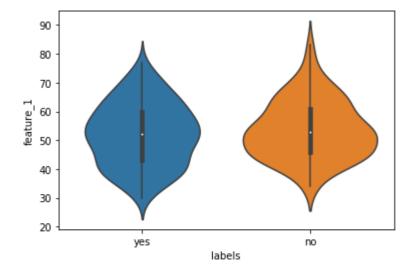
```
''' 3d -scatter plots '''
# sns.boxplot(x='labels',y='feature 1', data=haberman df)
# plt.show()
fig, axes = plt.subplots(1, 3, figsize=(15, 5))
for idx, feature in enumerate(list(haberman df.columns)[:-1]):
    sns.boxplot( x='labels', y=feature, data=haberman df, ax=axes[idx])
plt.show()
    - very clear projection of labels range for each feature in a single shot
    - As feature 1 and feature 2 more than 50% lables(1 & 2) lies in smae range whe
  80
                            68
                                                      40
  70
                            66
feature_1
                           64 ا<mark>ل</mark>
  50
                                                      20
  40
                                                      10
                            60
             labels
                                       labels
```

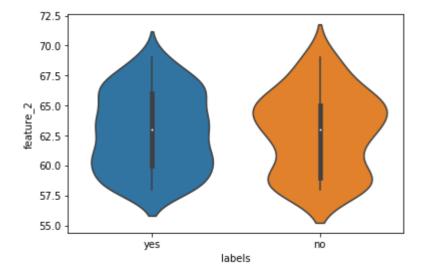
Out[11]:

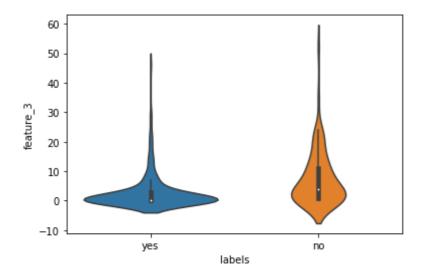
' - very clear projection of labels range for each feature in a single shot\n - As feature_1 and feature_2 more than 50% lables(1 & 2) lie s in smae range where as for the feature_3 (2 lables are higher) we c an see major difference.\n'

In [12]:

```
''' The combination of box and smooth histogram clear plots are represented below in
sns.violinplot(x='labels',y='feature_1', data=haberman_df)
plt.show()
sns.violinplot(x='labels',y='feature_2', data=haberman_df)
plt.show()
sns.violinplot(x='labels',y='feature_3', data=haberman_df)
plt.show()
'''
1. In feature_2 58.5 to 62 if we observe carefully yes label have more wide and
2. From feature_3 also we observe the yes labels wide range than no lables rang
```







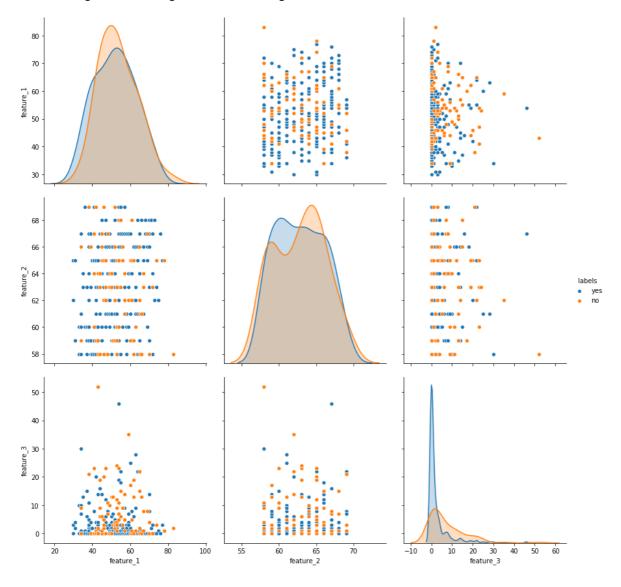
Out[12]:

'.\n 1. In feature_2 58.5 to 62 if we observe carefully yes label have more wide and no lable has less wide\n 2. From feature_3 also we observe the yes labels wide range than no lables range at the star $t.\n'$

In [13]:

/home/trinath/.local/lib/python3.6/site-packages/seaborn/axisgrid.py:2 065: UserWarning: The `size` parameter has been renamed to `height`; p leaes update your code.

warnings.warn(msg, UserWarning)



Out[13]:

' \n - feature_1 has range from 30 to 82 where as median as 52 \n - And most of my feautures are clearly represented as shown in the image\n'

,,,

- Apart from iris dataset haberman can not class on single feature (To obta in more win chances).
- feature_2 and features_3 projected more inofrmation for classifing lables(yes | no) rather than feature 1
- I am able to plot my own projection using the in-built functions as info, describe
- As shown in the image if we do more data-balance and removing of outliers if helps in more predicting the lables with higher accuracy

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