CLASS ACTIVITY

a) To build and train a model using human cell records, and classify cells to whether the samples are benign or malignant, you are required to write 3 lines of codes in input (In[19]) to produce output in line Out[26] and plot graphs where necessary. The data set was downloaded from URL:
https://s3-api.us-geo.objectstorage.softlayer.net/cf-courses-data/CognitiveClass/ML0101ENv3/labs/cell_samples.csv

Importing Needed packages

In [19]:
```
# Write 3 lines of codes
# CODE STRAT HERE



# CODE END HERE
import pylab as pl
import scipy.optimize as opt
from sklearn import preprocessing
from sklearn.model_selection import train_test_split
%matplotlib inline
```

In [20]:
```
#Click here and press Shift+Enter
!wget -O cell_samples.csv https://s3-api.us-geo.objectstor
```

In [26]:
```
cell_df = pd.read_csv("cell_samples.csv")
cell_df.head()
```

Out[26]:

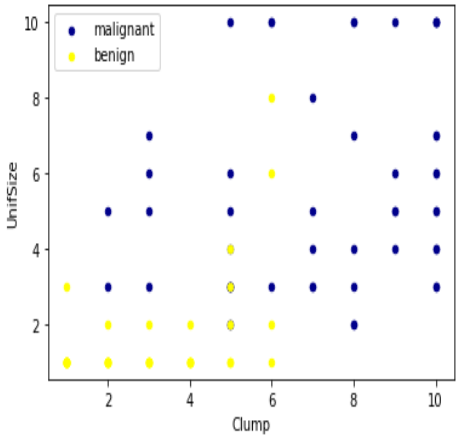
	ID	Clump	UnifSize	UnifShape	MargAdh	SingEpiSize	BareNuc	BlandChrom	NormNucl	Mit	Class
0	1000025	5	1	1	1	2	1	3	1	1	2
1	1002945	5	4	4	5	7	10	3	2	1	2
2	1015425	3	1	1	1	2	2	3	1	1	2
3	1016277	6	8	8	1	3	4	3	7	1	2
4	1017023	4	1	1	3	2	1	3	1	1	2

(**Hint.** Submit in the screen shot of your codes.) **(12 marks)**

b) Write the following codes to produce the graph below and explain the shape of the graph **(5 marks)**

In [34]:

```
ax = cell_df[cell_df['Class'] == 4][0:50].plot(kind='scatter', x='Clump', y='UnifSize', color='DarkBlue', label='malignant');
cell_df[cell_df['Class'] == 2][0:50].plot(kind='scatter', x='Clump', y='UnifSize', color='Yellow', label='benign', ax=ax);
plt.show()
```



Total 25 Marks