we will be using the Breast Cancer Wisconsin (Diagnostic) Database to create a classifier that can help diagnose patients.

importing necessary libraries

In [13]:

```
import numpy as np
import pandas as pd
from sklearn.datasets import load_breast_cancer
import matplotlib.pyplot as plt
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import train_test_split
%matplotlib notebook
```

Read the data

In [2]:

```
cancer = load_breast_cancer()

# Print the data set description
print(cancer.DESCR)
```

```
.. _breast_cancer_dataset:

Breast cancer wisconsin (diagnostic) dataset
--------------------------------------------

**Data Set Characteristics:**

    :Number of Instances: 569

    :Number of Attributes: 30 numeric, predictive attributes and the class

    :Attribute Information:
        - radius (mean of distances from center to points on the perimeter)
        - texture (standard deviation of gray-scale values)
        - perimeter
        - area
        - smoothness (local variation in radius lengths)
        - compactness (perimeter^2 / area - 1.0)
        - concavity (severity of concave portions of the contour)
        - concave points (number of concave portions of the contour)
        - symmetry
        - fractal dimension ("coastline approximation" - 1)

        The mean, standard error, and "worst" or largest (mean of the three
        largest values) of these features were computed for each image,
        resulting in 30 features.  For instance, field 3 is Mean Radius, field
        13 is Radius SE, field 23 is Worst Radius.

        - class:
                - WDBC-Malignant
                - WDBC-Benign

    :Summary Statistics:

    ===================================== ====== ======
                                           Min    Max
    ===================================== ====== ======
    radius (mean):                        6.981  28.11
    texture (mean):                       9.71   39.28
    perimeter (mean):                     43.79  188.5
    area (mean):                          143.5  2501.0
    smoothness (mean):                    0.053  0.163
    compactness (mean):                   0.019  0.345
    concavity (mean):                     0.0    0.427
    concave points (mean):                0.0    0.201
    symmetry (mean):                      0.106  0.304
```

```
    fractal dimension (mean):             0.05   0.097
    radius (standard error):              0.112  2.873
    texture (standard error):             0.36   4.885
    perimeter (standard error):           0.757  21.98
    area (standard error):                6.802  542.2
    smoothness (standard error):          0.002  0.031
    compactness (standard error):         0.002  0.135
    concavity (standard error):           0.0    0.396
    concave points (standard error):      0.0    0.053
    symmetry (standard error):            0.008  0.079
    fractal dimension (standard error):   0.001  0.03
    radius (worst):                       7.93   36.04
    texture (worst):                      12.02  49.54
    perimeter (worst):                    50.41  251.2
    area (worst):                         185.2  4254.0
    smoothness (worst):                   0.071  0.223
    compactness (worst):                  0.027  1.058
    concavity (worst):                    0.0    1.252
    concave points (worst):               0.0    0.291
    symmetry (worst):                     0.156  0.664
    fractal dimension (worst):            0.055  0.208
    ===================================== ====== ======

    :Missing Attribute Values: None

    :Class Distribution: 212 - Malignant, 357 - Benign

    :Creator:  Dr. William H. Wolberg, W. Nick Street, Olvi L. Mangasarian

    :Donor: Nick Street

    :Date: November, 1995

This is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.
https://goo.gl/U2Uwz2

Features are computed from a digitized image of a fine needle
aspirate (FNA) of a breast mass.  They describe
characteristics of the cell nuclei present in the image.

Separating plane described above was obtained using
Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree
Construction Via Linear Programming." Proceedings of the 4th
Midwest Artificial Intelligence and Cognitive Science Society,
pp. 97-101, 1992], a classification method which uses linear
programming to construct a decision tree.  Relevant features
were selected using an exhaustive search in the space of 1-4
features and 1-3 separating planes.

The actual linear program used to obtain the separating plane
in the 3-dimensional space is that described in:
[K. P. Bennett and O. L. Mangasarian: "Robust Linear
Programming Discrimination of Two Linearly Inseparable Sets",
Optimization Methods and Software 1, 1992, 23-34].

This database is also available through the UW CS ftp server:

ftp ftp.cs.wisc.edu
cd math-prog/cpo-dataset/machine-learn/WDBC/

.. topic:: References

   - W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction
     for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on
     Electronic Imaging: Science and Technology, volume 1905, pages 861-870,
     San Jose, CA, 1993.
   - O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and
     prognosis via linear programming. Operations Research, 43(4), pages 570-577,
     July-August 1995.
   - W.H. Wolberg, W.N. Street, and O.L. Mangasarian. Machine learning techniques
     to diagnose breast cancer from fine-needle aspirates. Cancer Letters 77 (1994)
     163-171.
```

The object returned by load_breast_cancer() is a scikit-learn Bunch object, which is similar to a dictionary.

In [3]:

```
cancer.keys()
```

Out[3]:

```
dict_keys(['data', 'target', 'target_names', 'DESCR', 'feature_names', 'filename'])
```

Total features does the breast cancer dataset have?

In [4]:

```
len(cancer['feature_names'])
```

Out[4]:

```
30
```

making Data Frame using the present data and target

In [7]:

```
data=pd.DataFrame(cancer.data,columns=cancer.feature_names)
target=pd.DataFrame(cancer.target,columns=['target'])

cancer_df = data.join(target)
cancer_df
```

Out[7]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	...	worst texture	worst perimeter
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.14710	0.2419	0.07871	...	17.33	184.60
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.07017	0.1812	0.05667	...	23.41	158.80
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.12790	0.2069	0.05999	...	25.53	152.50
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.10520	0.2597	0.09744	...	26.50	98.87
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.10430	0.1809	0.05883	...	16.67	152.20
...	...	...	...	...	...	...	...	...	...	...	...	...	...
564	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	0.1726	0.05623	...	26.40	166.10
565	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	0.1752	0.05533	...	38.25	155.00
566	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	0.1590	0.05648	...	34.12	126.70
567	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	0.2397	0.07016	...	39.42	184.60
568	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	0.1587	0.05884	...	30.37	59.16

569 rows × 31 columns

Count of Melignant and Benign

In [8]:

```
cancer_df.target.value_counts().rename({1: 'benign', 0 : 'maligant'},)
```

Out[8]:

```
benign      357
maligant    212
Name: target, dtype: int64
```

Spliting the Dataset into X and y using train_test_split method

In [16]:

```
X= cancer_df.iloc[:,:-1]
y= cancer_df.iloc[:,-1]

X_train, X_test, y_train, y_test = train_test_split(X,y, random_state=0)

# creating the k-nn classifier at k=1

clf=KNeighborsClassifier(n_neighbors=1,n_jobs=-1)

# fit the x_train and y_train to the knn classifier

clf.fit(X_train, y_train)
```

Out[16]:

```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=-1, n_neighbors=1, p=2,
                     weights='uniform')
```

Using knn classifier, predict the class label using the mean value for each feature.

In [17]:

```
means = cancer_df.mean()[:-1].values.reshape(1, -1)

result = clf.predict(means)
result
```

Out[17]:

```
array([1])
```

In [19]:

```
knn = clf

X_test_predict = knn.predict(X_test)
X_test_predict
```

Out[19]:

```
array([1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 0, 1, 0, 0, 0, 0, 1,
       1, 1, 0, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1,
       0, 0, 1, 1, 1, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 0, 0, 0, 1, 1, 0, 1,
       0, 0, 0, 1, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 0, 0, 0, 1, 0, 1, 1, 1,
       0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 1, 0, 1,
       1, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 0, 1,
       1, 1, 1, 1, 1, 0, 0, 1, 1, 1, 0])
```

score

In [20]:

```
score= knn.score(X_test, y_test)
score
```

Out[20]:

```
0.916083916083916
```

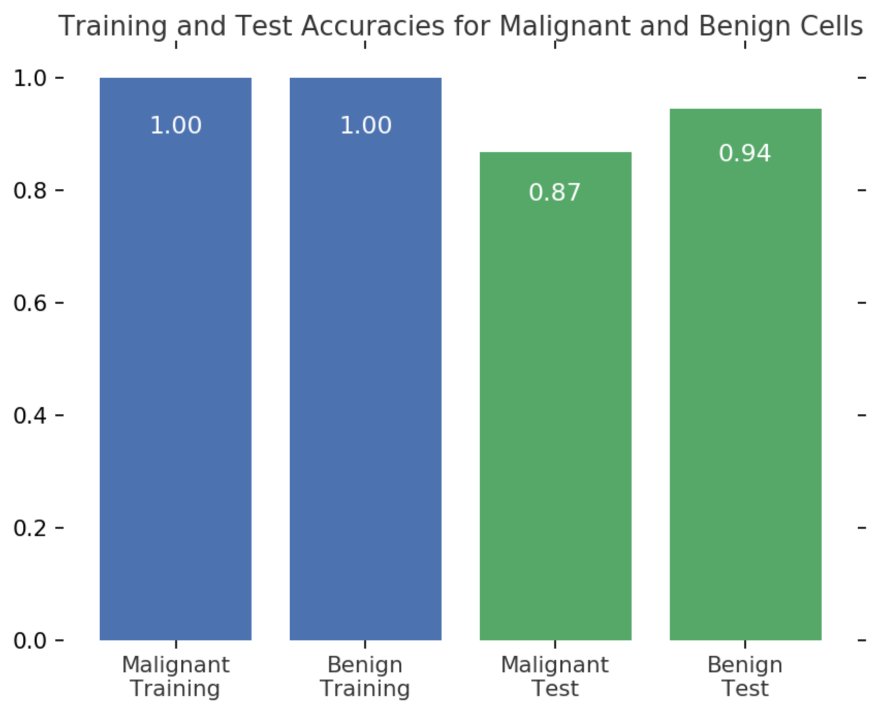
In [25]:

```
def accuracy_plot():

    # Find the training and testing accuracies by target value (i.e. malignant, benign)
    mal_train_X = X_train[y_train==0]
    mal_train_y = y_train[y_train==0]
    ben_train_X = X_train[y_train==1]
    ben_train_y = y_train[y_train==1]

    mal_test_X = X_test[y_test==0]
```

```python
    mal_test_y = y_test[y_test==0]
    ben_test_X = X_test[y_test==1]
    ben_test_y = y_test[y_test==1]

    scores = [knn.score(mal_train_X, mal_train_y), knn.score(ben_train_X, ben_train_y),
              knn.score(mal_test_X, mal_test_y), knn.score(ben_test_X, ben_test_y)]


    plt.figure()

    # Plot the scores as a bar chart
    bars = plt.bar(np.arange(4), scores, color=['#4c72b0','#4c72b0','#55a868','#55a868'])

    # directly label the score onto the bars
    for bar in bars:
        height = bar.get_height()
        plt.gca().text(bar.get_x() + bar.get_width()/2, height*.90, '{0:.{1}f}'.format(height, 2),
                     ha='center', color='w', fontsize=11)

    # remove all the ticks (both axes), and tick labels on the Y axis
    plt.tick_params(top='off', bottom='off', left='off', right='off', labelleft='off', labelbottom=
'on')

    # remove the frame of the chart
    for spine in plt.gca().spines.values():
        spine.set_visible(False)

    plt.xticks([0,1,2,3], ['Malignant\nTraining', 'Benign\nTraining', 'Malignant\nTest', 'Benign\nT
est'], alpha=0.8);
    plt.title('Training and Test Accuracies for Malignant and Benign Cells', alpha=0.8)
```

In [26]:

```python
accuracy_plot()
```



In [ ]: