*You are currently looking at **version 1.3** of this notebook. To download notebooks and datafiles, as well as get help on Jupyter notebooks in the Coursera platform, visit the Jupyter Notebook FAQ (https://www.coursera.org/learn/python-machine-learning/resources/bANLa) course resource.*

Assignment 1 - Introduction to Machine Learning

For this assignment, you will be using the Breast Cancer Wisconsin (Diagnostic) Database to create a classifier that can help diagnose patients. First, read through the description of the dataset (below).

In [ ]:
```
import numpy as np
import pandas as pd
from sklearn.datasets import load_breast_cancer

cancer = load_breast_cancer()

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

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

In [8]:
```
cancer.keys()
```

Out[8]:
```
dict_keys(['feature_names', 'DESCR', 'data', 'target', 'target_names'])
```

Question 0 (Example)

How many features does the breast cancer dataset have?

This function should return an integer.

In [9]:
```
# You should write your whole answer within the function provided. The autograder will call
# this function and compare the return value against the correct solution value
def answer_zero():
    # This function returns the number of features of the breast cancer dataset, which is an i
    # The assignment question description will tell you the general format the autograder is e
    return len(cancer['feature_names'])

# You can examine what your function returns by calling it in the cell. If you have questions
# about the assignment formats, check out the discussion forums for any FAQs
answer_zero()
```

Out[9]:
```
30
```

Question 1

Scikit-learn works with lists, numpy arrays, scipy-sparse matrices, and pandas DataFrames, so converting the dataset to a DataFrame is not necessary for training this model. Using a DataFrame does however help make many things easier such as munging data, so let's practice creating a classifier with a pandas DataFrame.

Convert the sklearn.dataset `cancer` to a DataFrame.

This function should return a `(569, 31)` DataFrame with

columns =

```
['mean radius', 'mean texture', 'mean perimeter', 'mean area',
'mean smoothness', 'mean compactness', 'mean concavity',
'mean concave points', 'mean symmetry', 'mean fractal dimension',
'radius error', 'texture error', 'perimeter error', 'area error',
'smoothness error', 'compactness error', 'concavity error',
'concave points error', 'symmetry error', 'fractal dimension error',
'worst radius', 'worst texture', 'worst perimeter', 'worst area',
'worst smoothness', 'worst compactness', 'worst concavity',
'worst concave points', 'worst symmetry', 'worst fractal dimension',
'target']
```

and index =

```
RangeIndex(start=0, stop=569, step=1)
```

In [10]:
```
def answer_one():

    # Your code here
    df = pd.DataFrame(cancer.data, columns = cancer.feature_names)
    df['target'] = cancer.target

    return df


answer_one()
```

Out[10]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	...
0	17.990	10.38	122.80	1001.0	0.11840	0.27760	0.300100	0.147100	0.2419	0.07871	...
1	20.570	17.77	132.90	1326.0	0.08474	0.07864	0.086900	0.070170	0.1812	0.05667	...
2	19.690	21.25	130.00	1203.0	0.10960	0.15990	0.197400	0.127900	0.2069	0.05999	...
3	11.420	20.38	77.58	386.1	0.14250	0.28390	0.241400	0.105200	0.2597	0.09744	...
4	20.290	14.34	135.10	1297.0	0.10030	0.13280	0.198000	0.104300	0.1809	0.05883	...
5	12.450	15.70	82.57	477.1	0.12780	0.17000	0.157800	0.080890	0.2087	0.07613	...
6	18.250	19.98	119.60	1040.0	0.09463	0.10900	0.112700	0.074000	0.1794	0.05742	...
7	13.710	20.83	90.20	577.9	0.11890	0.16450	0.093660	0.059850	0.2196	0.07451	...
8	13.000	21.82	87.50	519.8	0.12730	0.19320	0.185900	0.093530	0.2350	0.07389	...
9	12.460	24.04	83.97	475.9	0.11860	0.23960	0.227300	0.085430	0.2030	0.08243	...
10	16.020	23.24	102.70	797.8	0.08206	0.06669	0.032990	0.033230	0.1528	0.05697	...
11	15.780	17.89	103.60	781.0	0.09710	0.12920	0.099540	0.066060	0.1842	0.06082	...
12	19.170	24.80	132.40	1123.0	0.09740	0.24580	0.206500	0.111800	0.2397	0.07800	...
13	15.850	23.95	103.70	782.7	0.08401	0.10020	0.099380	0.053640	0.1847	0.05338	...
14	13.730	22.61	93.60	578.3	0.11310	0.22930	0.212800	0.080250	0.2069	0.07682	...
15	14.540	27.54	96.73	658.8	0.11390	0.15950	0.163900	0.073640	0.2303	0.07077	...
16	14.680	20.13	94.74	684.5	0.09867	0.07200	0.073950	0.052590	0.1586	0.05922	...
17	16.130	20.68	108.10	798.8	0.11700	0.20220	0.172200	0.102800	0.2164	0.07356	...
18	19.810	22.15	130.00	1260.0	0.09831	0.10270	0.147900	0.094980	0.1582	0.05395	...
19	13.540	14.36	87.46	566.3	0.09779	0.08129	0.066640	0.047810	0.1885	0.05766	...
20	13.080	15.71	85.63	520.0	0.10750	0.12700	0.045680	0.031100	0.1967	0.06811	...
21	9.504	12.44	60.34	273.9	0.10240	0.06492	0.029560	0.020760	0.1815	0.06905	...
22	15.340	14.26	102.50	704.4	0.10730	0.21350	0.207700	0.097560	0.2521	0.07032	...
23	21.160	23.04	137.20	1404.0	0.09428	0.10220	0.109700	0.086320	0.1769	0.05278	...
24	16.650	21.38	110.00	904.6	0.11210	0.14570	0.152500	0.091700	0.1995	0.06330	...
25	17.140	16.40	116.00	912.7	0.11860	0.22760	0.222900	0.140100	0.3040	0.07413	...
26	14.580	21.53	97.41	644.8	0.10540	0.18680	0.142500	0.087830	0.2252	0.06924	...
27	18.610	20.25	122.10	1094.0	0.09440	0.10660	0.149000	0.077310	0.1697	0.05699	...
28	15.300	25.27	102.40	732.4	0.10820	0.16970	0.168300	0.087510	0.1926	0.06540	...
29	17.570	15.05	115.00	955.1	0.09847	0.11570	0.098750	0.079530	0.1739	0.06149	...
...	...	...	...	...	...	...	...	...	...	...	...
539	7.691	25.44	48.34	170.4	0.08668	0.11990	0.092520	0.013640	0.2037	0.07751	...
540	11.540	14.44	74.65	402.9	0.09984	0.11200	0.067370	0.025940	0.1818	0.06782	...
541	14.470	24.99	95.81	656.4	0.08837	0.12300	0.100900	0.038900	0.1872	0.06341	...
542	14.740	25.42	94.70	668.6	0.08275	0.07214	0.041050	0.030270	0.1840	0.05680	...

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	...
543	13.210	28.06	84.88	538.4	0.08671	0.06877	0.029870	0.032750	0.1628	0.05781	...
544	13.870	20.70	89.77	584.8	0.09578	0.10180	0.036880	0.023690	0.1620	0.06688	...
545	13.620	23.23	87.19	573.2	0.09246	0.06747	0.029740	0.024430	0.1664	0.05801	...
546	10.320	16.35	65.31	324.9	0.09434	0.04994	0.010120	0.005495	0.1885	0.06201	...
547	10.260	16.58	65.85	320.8	0.08877	0.08066	0.043580	0.024380	0.1669	0.06714	...
548	9.683	19.34	61.05	285.7	0.08491	0.05030	0.023370	0.009615	0.1580	0.06235	...
549	10.820	24.21	68.89	361.6	0.08192	0.06602	0.015480	0.008160	0.1976	0.06328	...
550	10.860	21.48	68.51	360.5	0.07431	0.04227	0.000000	0.000000	0.1661	0.05948	...
551	11.130	22.44	71.49	378.4	0.09566	0.08194	0.048240	0.022570	0.2030	0.06552	...
552	12.770	29.43	81.35	507.9	0.08276	0.04234	0.019970	0.014990	0.1539	0.05637	...
553	9.333	21.94	59.01	264.0	0.09240	0.05605	0.039960	0.012820	0.1692	0.06576	...
554	12.880	28.92	82.50	514.3	0.08123	0.05824	0.061950	0.023430	0.1566	0.05708	...
555	10.290	27.61	65.67	321.4	0.09030	0.07658	0.059990	0.027380	0.1593	0.06127	...
556	10.160	19.59	64.73	311.7	0.10030	0.07504	0.005025	0.011160	0.1791	0.06331	...
557	9.423	27.88	59.26	271.3	0.08123	0.04971	0.000000	0.000000	0.1742	0.06059	...
558	14.590	22.68	96.39	657.1	0.08473	0.13300	0.102900	0.037360	0.1454	0.06147	...
559	11.510	23.93	74.52	403.5	0.09261	0.10210	0.111200	0.041050	0.1388	0.06570	...
560	14.050	27.15	91.38	600.4	0.09929	0.11260	0.044620	0.043040	0.1537	0.06171	...
561	11.200	29.37	70.67	386.0	0.07449	0.03558	0.000000	0.000000	0.1060	0.05502	...
562	15.220	30.62	103.40	716.9	0.10480	0.20870	0.255000	0.094290	0.2128	0.07152	...
563	20.920	25.09	143.00	1347.0	0.10990	0.22360	0.317400	0.147400	0.2149	0.06879	...
564	21.560	22.39	142.00	1479.0	0.11100	0.11590	0.243900	0.138900	0.1726	0.05623	...
565	20.130	28.25	131.20	1261.0	0.09780	0.10340	0.144000	0.097910	0.1752	0.05533	...
566	16.600	28.08	108.30	858.1	0.08455	0.10230	0.092510	0.053020	0.1590	0.05648	...
567	20.600	29.33	140.10	1265.0	0.11780	0.27700	0.351400	0.152000	0.2397	0.07016	...
568	7.760	24.54	47.92	181.0	0.05263	0.04362	0.000000	0.000000	0.1587	0.05884	...

569 rows × 31 columns

Question 2

What is the class distribution? (i.e. how many instances of `malignant` (encoded 0) and how many `benign` (encoded 1)?)

This function should return a Series named `target` *of length 2 with integer values and index* = `['malignant', 'benign']`

In [27]:
```
def answer_two():
    cancerdf = answer_one()
    ans = pd.Series([212,357],name='target',index=['malignant','benign'])

    return ans

answer_two()
```

Out[27]:
```
malignant    212
benign       357
Name: target, dtype: int64
```

Question 3

Split the DataFrame into `X` (the data) and `y` (the labels).

This function should return a tuple of length 2: `(X, y)`*, where*

- `X`*, a pandas DataFrame, has shape* `(569, 30)`
- `y`*, a pandas Series, has shape* `(569,)`.

In [28]:
```
def answer_three():
    cancerdf = answer_one()

    X = cancerdf
    y = cancerdf.pop('target')

    return X, y
```

Question 4

Using `train_test_split`, split `X` and `y` into training and test sets `(X_train, X_test, y_train, and y_test)`.

Set the random number generator state to 0 using `random_state=0` to make sure your results match the autograder!

This function should return a tuple of length 4: `(X_train, X_test, y_train, y_test)`*, where*

- `X_train` *has shape* `(426, 30)`
- `X_test` *has shape* `(143, 30)`
- `y_train` *has shape* `(426,)`
- `y_test` *has shape* `(143,)`

In [29]:
```
from sklearn.model_selection import train_test_split

def answer_four():
    X, y = answer_three()

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

    return X_train, X_test, y_train, y_test
X_train, X_test, y_train, y_test = answer_four()
```

Question 5

Using KNeighborsClassifier, fit a k-nearest neighbors (knn) classifier with `X_train`, `y_train` and using one nearest neighbor (`n_neighbors = 1`).

This function should return a `sklearn.neighbors.classification.KNeighborsClassifier`.

In [30]:
```
from sklearn.neighbors import KNeighborsClassifier

def answer_five():
    X_train, X_test, y_train, y_test = answer_four()

    knn = KNeighborsClassifier(n_neighbors=1)
    knn.fit(X_train, y_train)

    return knn
```

Question 6

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

Hint: You can use `cancerdf.mean()[:-1].values.reshape(1, -1)` which gets the mean value for each feature, ignores the target column, and reshapes the data from 1 dimension to 2 (necessary for the precict method of KNeighborsClassifier).

This function should return a numpy array either `array([ 0.])` *or* `array([ 1.])`

In [31]:
```
def answer_six():
    cancerdf = answer_one()
    means = cancerdf.mean()[:-1].values.reshape(1, -1)
    knn = answer_five()

    return knn.preditc(means)
    means
```

Question 7

Using your knn classifier, predict the class labels for the test set `X_test`.

This function should return a numpy array with shape `(143,)` and values either `0.0` or `1.0`.

In [32]:
```
def answer_seven():
    X_train, X_test, y_train, y_test = answer_four()
    knn = answer_five()

    return knn.predict(X_test)
```

Question 8

Find the score (mean accuracy) of your knn classifier using `X_test` and `y_test`.

This function should return a float between 0 and 1

In [33]:
```
def answer_eight():
    X_train, X_test, y_train, y_test = answer_four()
    knn = answer_five()

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

Optional plot

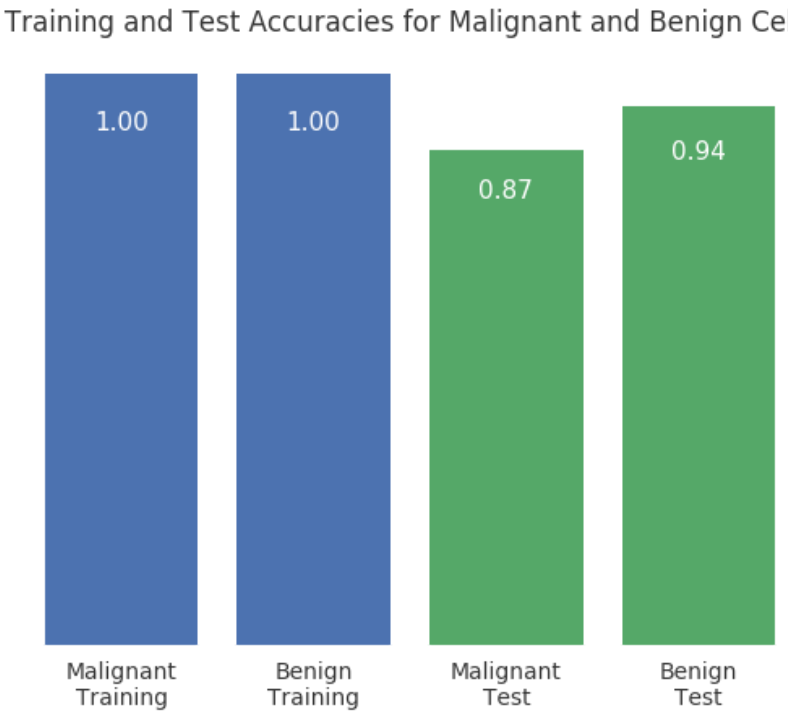
Try using the plotting function below to visualize the differet predicition scores between training and test sets, as well as malignant and benign cells.

In [34]:
```
def accuracy_plot():
    import matplotlib.pyplot as plt

    %matplotlib notebook

    X_train, X_test, y_train, y_test = answer_four()

    # 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]
    mal_test_y = y_test[y_test==0]
    ben_test_X = X_test[y_test==1]
    ben_test_y = y_test[y_test==1]

    knn = answer_five()

    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,
                    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', labelbo

    # 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', 'Beni
    plt.title('Training and Test Accuracies for Malignant and Benign Cells', alpha=0.8)
```

Uncomment the plotting function to see the visualization.

Comment out the plotting function when submitting your notebook for grading.

In [35]:
```
#accuracy_plot()
```



In [ ]:
```

```