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Subject: Machine Learning

Class: BE Computer 1

Assignment 2:

Problem Statement:

Search a Medical related dataset

1. Download the dataset
2. Perform pre-processing on the dataset
3. Use this dataset to build a Naive Bayes Classifier
4. Use this dataset to build a Decision Tree Classifier
5. Compare the results and comment

Tool used:

Jupyter Notebook(Python).

Dataset:

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. The class has values that classify the tumor into "Malign" or "Benign"

Implementation:

Below attached is the converted notebook file with output for both the classifiers.

Conclusion:

Test data set performance of both the models are:

1. Decision Tree: 95.8%
2. Naive Bayes: 95.3%

In [14]:

```
from sklearn.datasets import load_breast_cancer
from sklearn.tree import DecisionTreeClassifier          #Decision Tree
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.tree import export_graphviz
import matplotlib.pyplot as plt
from sklearn.metrics import classification_report
from sklearn import metrics
from sklearn.naive_bayes import GaussianNB              #Naive Bayes
import numpy as np
import graphviz
%matplotlib inline
```

In [15]:

```
#Load the breast cancer data and few EDA  
cancer = load_breast_cancer()  
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 perimete
```

```
r)
```

```
- 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 thre
```

```
e
```

```
largest values) of these features were computed for each image,
```

```
resulting in 30 features. For instance, field 3 is Mean Radius, f
```

```
ield
```

```
13 is Radius SE, field 23 is Worst Radius.
```

```
- class:
```

```
- WDBC-Malignant
```

```
- WDBC-Benign
```

```
:Summary Statistics:
```

```
=====
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.

In [16]:

```
print(cancer.feature_names)
```

```
['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']
```

In [17]:

```
print(cancer.target_names)
```

```
['malignant' 'benign']
```

In [18]:

```
cancer.data
```

Out[18]:

```
array([[1.799e+01, 1.038e+01, 1.228e+02, ..., 2.654e-01, 4.601e-01,
        1.189e-01],
       [2.057e+01, 1.777e+01, 1.329e+02, ..., 1.860e-01, 2.750e-01,
        8.902e-02],
       [1.969e+01, 2.125e+01, 1.300e+02, ..., 2.430e-01, 3.613e-01,
        8.758e-02],
       ...,
       [1.660e+01, 2.808e+01, 1.083e+02, ..., 1.418e-01, 2.218e-01,
        7.820e-02],
       [2.060e+01, 2.933e+01, 1.401e+02, ..., 2.650e-01, 4.087e-01,
        1.240e-01],
       [7.760e+00, 2.454e+01, 4.792e+01, ..., 0.000e+00, 2.871e-01,
        7.039e-02]])
```

In [19]:

```
type(cancer.data)
cancer.data.shape
```

Out[19]:

```
(569, 30)
```

DECISION TREE

In [20]:

```

X_train, X_test, y_train, y_test = train_test_split(cancer.data, cancer.target, random_
state=42)

training_accuracy = []
test_accuracy = []

max_dep = range(1,15)

for md in max_dep:
    tree = DecisionTreeClassifier(max_depth=md,random_state=0)
    tree.fit(X_train,y_train)
    training_accuracy.append(tree.score(X_train, y_train))
    test_accuracy.append(tree.score(X_test, y_test))

plt.plot(max_dep,training_accuracy, label='Accuracy of the training set')
plt.ylabel('Accuracy')
plt.xlabel('Max Depth')
plt.legend()

# By having larger max_depth (>5), we overfit the model into training data, so the accu
racy for training set become
# but the accuracy for test set decrease

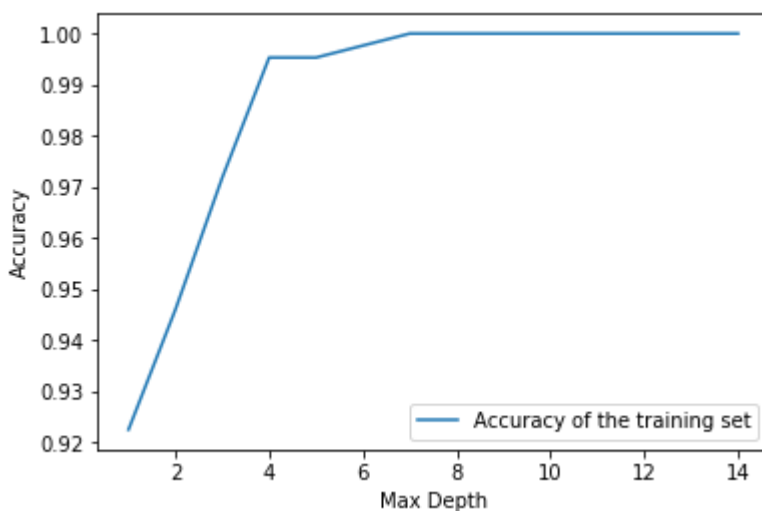
# other parameters than can work with:
# - min_samples_leaf, max_sample_leaf
# - max_leaf_node

# by looking at plot, best result accurs when max_depth is 3

```

Out[20]:

<matplotlib.legend.Legend at 0x7f4c7aec48d0>



In [21]:

```
tree = DecisionTreeClassifier(max_depth=3, random_state=0)
tree.fit(X_train, y_train)
```

Out[21]:

```
DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=3,
                        max_features=None, max_leaf_nodes=None,
                        min_impurity_decrease=0.0, min_impurity_split=None,
                        min_samples_leaf=1, min_samples_split=2,
                        min_weight_fraction_leaf=0.0, presort=False, random_state=0,
                        splitter='best')
```

In [22]:

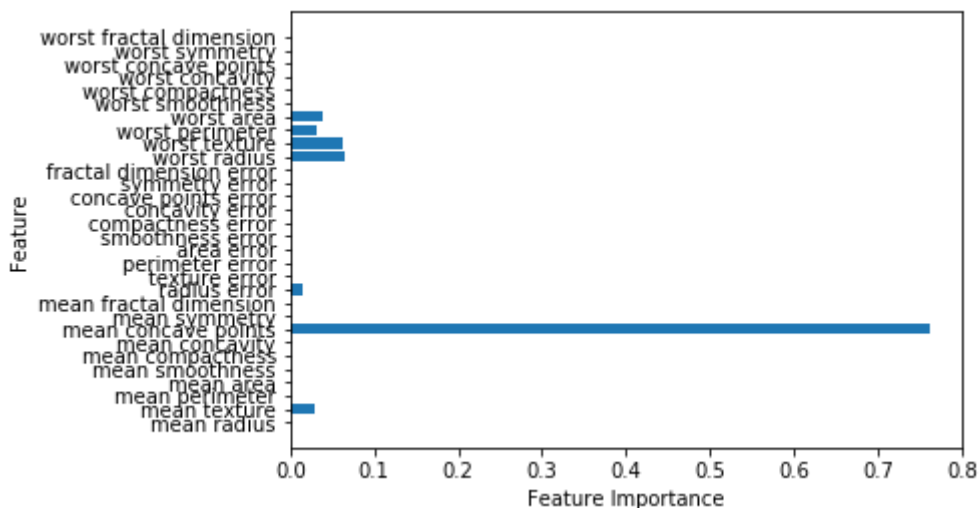
```
print('Training accuracy : {}'.format(tree.score(X_train, y_train)))
print('Testing accuracy : {}'.format(tree.score(X_test, y_test)))
```

Training accuracy : 0.971830985915

Testing accuracy : 0.958041958042

In [23]:

```
#Feature Importance
n_feature = cancer.data.shape[1]
plt.barh(range(n_feature), tree.feature_importances_, align='center')
plt.yticks(np.arange(n_feature), cancer.feature_names)
plt.xlabel('Feature Importance')
plt.ylabel('Feature')
plt.show()
```



Naive Bayes

In [24]:

```

X_train, X_test, y_train, y_test = train_test_split(cancer.data, cancer.target, test_size=0.3, random_state=109)

classifier = GaussianNB()
naive_bayes_model = classifier.fit(X_train, y_train)
y_true, y_pred = y_test, naive_bayes_model.predict(X_test)

print(classification_report(y_true, y_pred))
print("Accuracy:", metrics.accuracy_score(y_test, y_pred))
print("Precision:", metrics.precision_score(y_test, y_pred))
print("Recall:", metrics.recall_score(y_test, y_pred))

print(metrics.confusion_matrix(y_test, y_pred))

```

	precision	recall	f1-score	support
0	0.97	0.90	0.93	63
1	0.95	0.98	0.96	108
micro avg	0.95	0.95	0.95	171
macro avg	0.96	0.94	0.95	171
weighted avg	0.95	0.95	0.95	171

```

('Accuracy:', 0.9532163742690059)
('Precision:', 0.9464285714285714)
('Recall:', 0.9814814814814815)
[[ 57  6]
 [ 2 106]]

```

In []: