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Subject: Machine Learning
Class: BE Computer 1

Assignment 3:
Problem Statement:

Search a COVID related dataset
1. Download the dataset
2. Perform Pre-processing on the dataset
3. Use this dataset to build a Naïve Bayes Classifier
4. Use this dataset to build a Decision Tree Classifier
5. Apply Ensemble to improve the accuracy.

Tool used:
Jupyter Notebook(Python).

Dataset:
The dataset consists of the test report of various medical tests of a set of people including haemoglobin, platelets etc. They are classified as covid positive or negative.

Implementation:
Below attached is the converted notebook file with output.

Conclusion:
Test data set performance of both the models are:
1. Naive Bayes: 72.0%
2. Ensemble NB:84.20%
3. Decision Tree: 87.50%
4. Random Forest:92.50%

In [27]:

```
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.pylab 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 pandas as pd
import graphviz
%matplotlib inline
```

In [2]:

```
df_covid=pd.read_csv('COVID-19_formatted_dataset.csv', index_col=0)
```

In [3]:

```
df_covid.head()
```

Out[3]:

	Patient age quantile	SARS-Cov-2 exam result	Hematocrit	Hemoglobin	Platelets	Mean platelet volume	Red blood Cells	Lymphocytes	Mean c h concentrati
1	17	negative	0.236515	-0.022340	-0.517413	0.010677	0.102004	0.318366	
8	1	negative	-1.571682	-0.774212	1.429667	-1.672222	-0.850035	-0.005738	
15	9	negative	-0.747693	-0.586244	-0.429480	-0.213711	-1.361315	-1.114514	
18	11	negative	0.991838	0.792188	0.072992	-0.550290	0.542763	0.045436	
22	9	negative	0.190738	-0.147652	-0.668155	1.020415	-0.127191	0.002791	

In [4]:

```
df_covid.shape
```

Out[4]:

```
(598, 16)
```

In [5]:

```
df_covid['SARS-Cov-2 exam result'] = df_covid['SARS-Cov-2 exam result'].map({'negative'
: 0, 'positive': 1})
```

In [6]:

```
df_covid['SARS-Cov-2 exam result']
```

Out[6]:

```
1       0
8       0
15      0
18      0
22      0
       ..
5602    0
5614    0
5615    0
5618    0
5643    1
Name: SARS-Cov-2 exam result, Length: 598, dtype: int64
```

In [7]:

```
X = df_covid.drop('SARS-Cov-2 exam result', axis =1).values
```

In [8]:

```
X.shape
```

Out[8]:

```
(598, 15)
```

In [9]:

```
Y = df_covid['SARS-Cov-2 exam result'].values
Y[:5]
```

Out[9]:

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

In [10]:

```
df= df_covid.values
type(df)
```

Out[10]:

```
numpy.ndarray
```

In [11]:

```
from sklearn.model_selection import train_test_split
```

In [12]:

```
X_train,X_test, Y_train,Y_test = train_test_split(X, Y, test_size=0.2, random_state=0)
```

In [13]:

```
Feature = list(df_covid.columns)

Feature.remove('SARS-Cov-2 exam result')

Feature
```

Out[13]:

```
['Patient age quantile',
 'Hematocrit',
 'Hemoglobin',
 'Platelets',
 'Mean platelet volume ',
 'Red blood Cells',
 'Lymphocytes',
 'Mean corpuscular hemoglobin concentration\xa0(MCHC)',
 'Leukocytes',
 'Basophils',
 'Mean corpuscular hemoglobin (MCH)',
 'Eosinophils',
 'Mean corpuscular volume (MCV)',
 'Monocytes',
 'Red blood cell distribution width (RDW)']
```

Naive Bayes

Generating model using GauusianNB

In [15]:

```
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score, confusion_matrix
```

In [16]:

```
naives_model = GaussianNB()
naives_model.fit(X_train,Y_train)
```

Out[16]:

```
GaussianNB(priors=None, var_smoothing=1e-09)
```

In [17]:

```
Y_hat = naives_model.predict(X_test)
Y_hat
```

Out[17]:

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

In [18]:

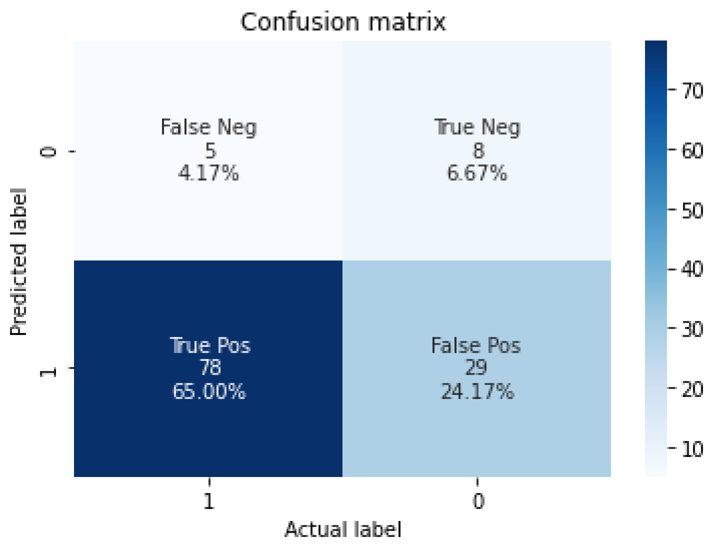
```
model_acc = accuracy_score(Y_test, Y_hat)
print('The accuracy of our naive model is: %0.2f'% model_acc)
```

```
The accuracy of our naive model is: 0.72
```

In [19]:

```
model_conf = confusion_matrix(Y_test, Y_hat)
model_conf
print('The accuracy of our confusion matrix is:\n', model_conf)
group_names = ['True Pos','False Pos','False Neg','True Neg']
group_counts = ["{0:0.0f}".format(value) for value in
                model_conf.flatten()]
group_percentages = ["{0:.2%}".format(value) for value in
                     model_conf.flatten()/np.sum(model_conf)]
labels = [f"{v1}\n{v2}\n{v3}" for v1, v2, v3 in
          zip(group_names,group_counts,group_percentages)]
labels = np.asarray(labels).reshape(2,2)
fig, ax = plt.subplots(figsize=(6,4))
sns.heatmap(model_conf, annot=labels, fmt='', cmap='Blues')
plt.xticks([0.5,1.5],labels=[1,0])
plt.yticks([0.5,1.5],labels=[1,0])
ax.set_ylim([0,2])
plt.title('Confusion matrix')
plt.xlabel('Actual label')
plt.ylabel('Predicted label')
plt.show()
```

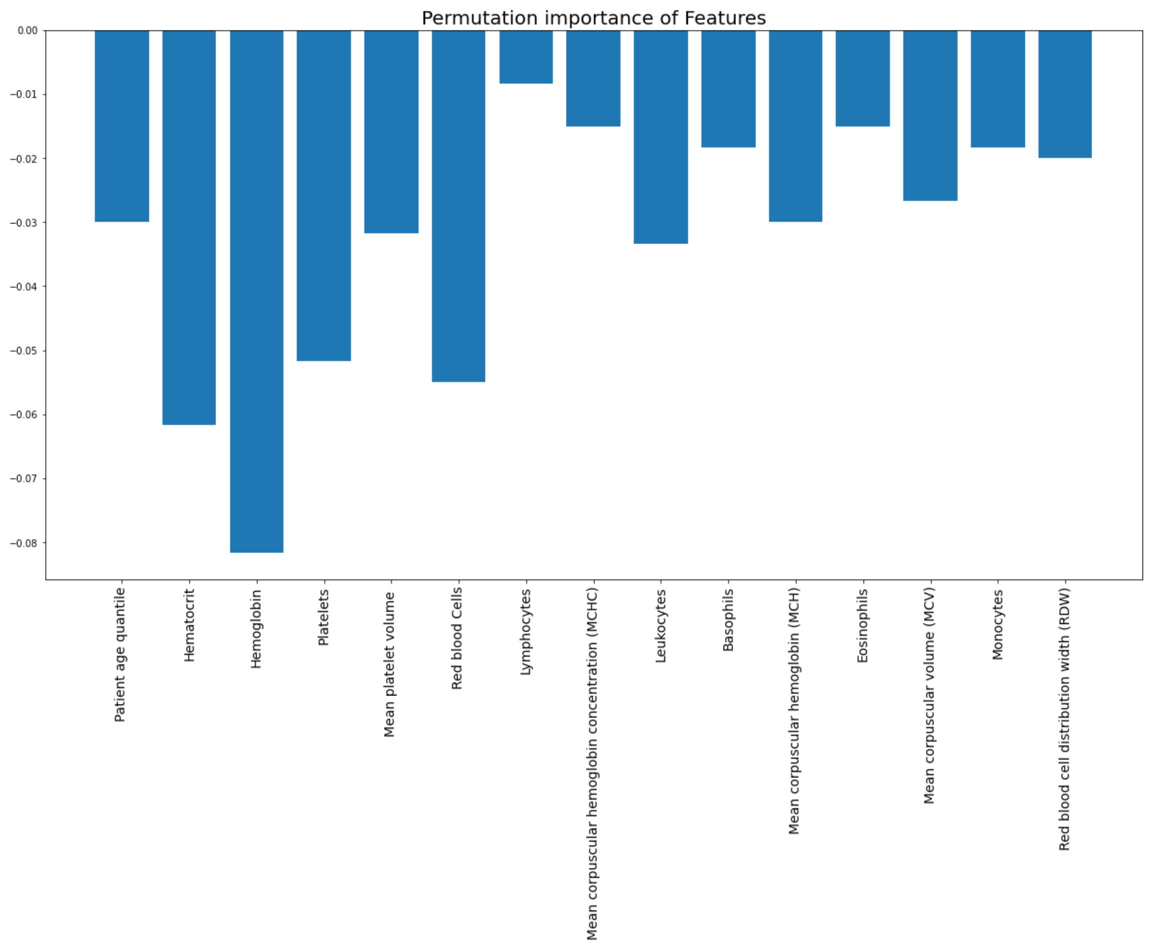
```
The accuracy of our confusion matrix is:
 [[78 29]
 [ 5  8]]
```



In [20]:

```
from matplotlib import pyplot
from sklearn.inspection import permutation_importance
imps = permutation_importance(naives_model, X_test, Y_test, scoring='accuracy')
imp = imps.importances_mean
for i,v in zip(Feature,imp):
    print('Feature:',i, 'Score: %.5f' % (v))
# plot feature importance
fig = plt.figure(figsize=(16,8))
ax = fig.add_axes([0,0,1,1])
ax.bar(Feature, imp)
plt.xticks(Feature, rotation='vertical', size=14)
plt.title("Permutation importance of Features", size=20)
plt.show()
```

```
Feature: Patient age quantile Score: -0.03000
Feature: Hematocrit Score: -0.06167
Feature: Hemoglobin Score: -0.08167
Feature: Platelets Score: -0.05167
Feature: Mean platelet volume  Score: -0.03167
Feature: Red blood Cells Score: -0.05500
Feature: Lymphocytes Score: -0.00833
Feature: Mean corpuscular hemoglobin concentration (MCHC) Score: -0.01500
Feature: Leukocytes Score: -0.03333
Feature: Basophils Score: -0.01833
Feature: Mean corpuscular hemoglobin (MCH) Score: -0.03000
Feature: Eosinophils Score: -0.01500
Feature: Mean corpuscular volume (MCV) Score: -0.02667
Feature: Monocytes Score: -0.01833
Feature: Red blood cell distribution width (RDW) Score: -0.02000
```



In [21]:

```
x = df_covid[['Leukocytes','Lymphocytes','Eosinophils','Red blood cell distribution wid
th (RDW)' ]].values
y = df_covid[['SARS-Cov-2 exam result']].values
```

In [22]:

```
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.2, random_state=0
)
print('x_train:',x_train.shape,'\ny_train:',y_train.shape)
print('x_test:',x_test.shape,'\ny_test:',y_test.shape)
```

```
x_train: (478, 4)
y_train: (478, 1)
x_test: (120, 4)
y_test: (120, 1)
```

In [23]:

```
naives_model_1 = GaussianNB()
naives_model_1.fit(x_train,y_train.ravel())
```

Out[23]:

```
GaussianNB(priors=None, var_smoothing=1e-09)
```

In [24]:

```
y_hat = naives_model_1.predict(x_test)
y_hat
```

Out[24]:

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

In [25]:

```
model_acc_1 = accuracy_score(y_test, y_hat)
print('The accuracy of our naive model is: %0.3f'% model_acc_1)
```

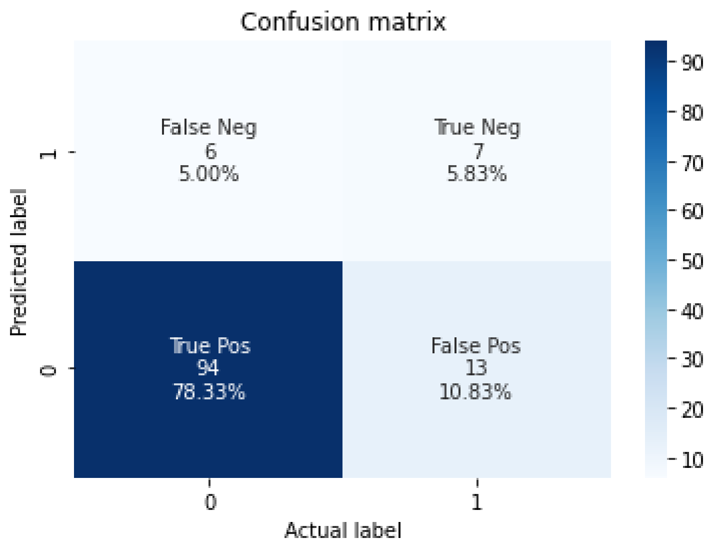
```
The accuracy of our naive model is: 0.842
```

In [26]:

```
model_conf_1 = confusion_matrix(y_test, y_hat)
print('The accuracy of our confusion matrix is:\n', model_conf_1)
plt.figure(figsize=(12,8))
group_names = ['True Pos','False Pos','False Neg','True Neg']
group_counts = ["{0:0.0f}".format(value) for value in
                model_conf_1.flatten()]
group_percentages = ["{0:.2%}".format(value) for value in
                     model_conf_1.flatten()/np.sum(model_conf_1)]
labels = [f"{v1}\n{v2}\n{v3}" for v1, v2, v3 in
          zip(group_names,group_counts,group_percentages)]
labels = np.asarray(labels).reshape(2,2)
fig, ax = plt.subplots(figsize=(6,4))
sns.heatmap(model_conf_1, annot=labels, fmt='', cmap='Blues')
ax.set_ylim([0,2])
plt.title('Confusion matrix')
plt.xlabel('Actual label')
plt.ylabel('Predicted label')
plt.show()
```

```
The accuracy of our confusion matrix is:
 [[94 13]
 [ 6  7]]

<Figure size 864x576 with 0 Axes>
```



In [29]:

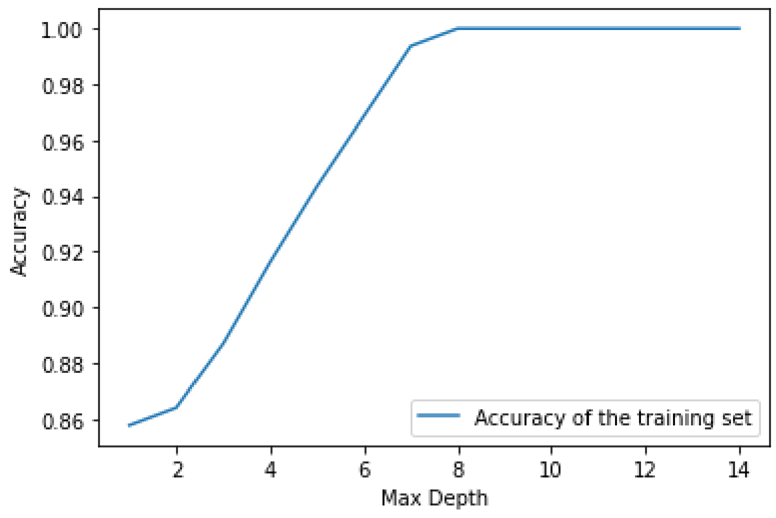
```
training_accuracy = []
test_accuracy = []
max_dep = range(1,15)

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()
```

Out[29]:

```
<matplotlib.legend.Legend at 0x7f166256f8d0>
```



In [30]:

```
tree = DecisionTreeClassifier(max_depth=8,random_state=0)
tree.fit(X_train,y_train)
```

Out[30]:

```
DecisionTreeClassifier(ccp_alpha=0.0, class_weight=None, criterion='gini',
                       max_depth=8, max_features=None, max_leaf_nodes=Non
e,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, presort='deprecated',
                       random_state=0, splitter='best')
```

In [33]:

```
tree.score(X_train, y_train)
```

Out[33]:

```
1.0
```

In [34]:

```
tree.score(X_test, y_test)
```

Out[34]:

```
0.875
```

In [36]:

```
from sklearn.ensemble import RandomForestClassifier
# creating a RF classifier
clf = RandomForestClassifier(n_estimators = 100)

# Training the model on the training dataset
# fit function is used to train the model using the training sets as parameters
clf.fit(X_train, y_train)

# performing predictions on the test dataset
y_pred = clf.predict(X_test)

# metrics are used to find accuracy or error
from sklearn import metrics
print()

# using metrics module for accuracy calculation
print("ACCURACY OF THE MODEL: ", metrics.accuracy_score(y_test, y_pred))
```

```
ACCURACY OF THE MODEL:  0.925

/usr/local/lib/python3.7/dist-packages/ipykernel_launcher.py:7: DataConver
sionWarning: A column-vector y was passed when a 1d array was expected. Pl
ease change the shape of y to (n_samples,), for example using ravel().
  import sys
```

In [ ]: