Ada Boost

May 18, 2022

1 Adaptive Boosting (AdaBoost) for classification with Python

Estimated time needed: 45 minutes

1.1 Objectives

After completing this lab you will be able to:

- Understand that AdaBoost is a linear combination of weak classifiers
- Apply AdaBoost
- Understand Hyperparameters selection in AdaBoost

In this notebook, you will learn AdaBoost, short for Adaptive Boosting, is a classification algorithm; AdaBoost is actually part of a family of Boosting algorithms. Like Bagging and Random Forest (RF), AdaBoost combines the outputs of many classifiers into an ensemble, but there are some differences. In both Bagging and RF, each classifier in the ensemble is powerful but prone to overfitting. As Bagging or RF aggregate more and more classifiers, they reduce overfitting.

With AdaBoost, each Classifier usually has performance slightly better than random. This is referred to as a weak learner or weak classifier. AdaBoost combines these classifiers to get a strong classifier. Unlike Bagging and Random Forest, in AdaBoost, adding more learners can cause overfitting. As a result, AdaBoost requires Hyperparameter tuning, taking more time to train. One advantage of AdaBoost is that each classifier is smaller, so predictions are faster.

In AdaBoost, the strong classifier H(x) is a linear combination of T weak classifiers $h_t(x)$ and α_t as shown in (1). Although each classifier $h_t(x)$ appears independent, the α_t contains information about the error of classifiers from $h_1(x), ..., h_t - 1(x)$. As we add more classifiers, the training accuracy gets larger. What's not so apparent in (1) is that during the training process, the values of that training sample are modified for $h_t(x)$. For a more in depth look at the theory behind Adaboost, check out The Elements of Statistical Learning Data Mining, Inference, and Prediction.

$$H(x) = \operatorname{sign}(\sum_{t} t = 1^{T} \alpha_{t} h_{t}(x))$$
 [1]

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<a href="https://#RFvsBag">What's the difference between RF and Bagging </a><a href="https://#Example">Cancer Data Example
```

<a href="https://practice/?utm_medium=Exinfluencer&utm_source=Exinfluencer&utm_content</pre>

Let's first import the required libraries:

```
[1]: import pandas as pd
  import pylab as plt
  import numpy as np
  import scipy.optimize as opt
  from sklearn import preprocessing
  %matplotlib inline
  import matplotlib.pyplot as plt
  from sklearn import metrics
  from tqdm import tqdm
```

/home/jupyterlab/conda/envs/python/lib/python3.7/sitepackages/sklearn/utils/validation.py:37: DeprecationWarning: distutils Version
classes are deprecated. Use packaging.version instead.

LARGE_SPARSE_SUPPORTED = LooseVersion(scipy_version) >= '0.14.0'

Ignore error warnings

```
[2]: import warnings warnings.filterwarnings('ignore')
```

This function will calculate the accuracy of the training and testing data given a model.

This function calculates the average accuracy of differnt learning rates on training and test data

```
#Iterate through different number of Learning rate and average out the
\neg results
  for n in tqdm(range(times)):
      X_train, X_test, y_train, y_test = train_test_split( X, y, test_size=0.
⇒3)
      for n_estimators in N_estimators:
          for j,lr in enumerate(Learning_rate_):
              model =
-AdaBoostClassifier(n_estimators=n_estimators+1,random_state=0,learning_rate=lr)
              model.fit(X_train,y_train)
               Accuracy=get_accuracy(X_train, X_test, y_train, y_test, model)
              train_acc[n,j,n_estimators-1] = Accuracy['trian Accuracy']
              test_acc[n,j,n_estimators-1] = Accuracy['test Accuracy']
  fig, ax1 = plt.subplots()
  mean_test=test_acc.mean(axis=0)
  mean_train=train_acc.mean(axis=0)
  ax2 = ax1.twinx()
  for j,(lr,line) in enumerate(zip(Learning_rate_,lines_array)):
      ax1.plot(mean_train[j,:],linestyle = line,color='b',label="Learning_"
→rate "+str(lr))
      ax2.plot(mean_test[j,:],linestyle = line, color='r',label=str(lr))
  ax1.set_ylabel('Training accuracy',color='b')
  ax1.legend()
  ax2.set_ylabel('Testing accuracy', color='r')
  ax2.legend()
  plt.show()
```

1.1.1 About the dataset

We will use a telecommunications dataset for predicting customer churn. This is a historical customer dataset where each row represents one customer. The data is relatively easy to understand, and you may uncover insights you can use immediately. Typically, it is less expensive to keep customers than to acquire new ones, so the focus of this analysis is to predict the customers who will stay with the company.

This data set provides information to help you predict what behavior will help you to retain customers. You can analyze all relevant customer data and develop focused customer retention programs.

The dataset includes information about:

- Customers who left within the last month the column is called Churn
- Services that each customer has signed up for phone, multiple lines, internet, online security, online backup, device protection, tech support, and streaming TV and movies
- Customer account information how long they have been a customer, contract, payment method, paperless billing, monthly charges, and total charges
- Demographic info about customers gender, age range, and if they have partners and dependents

Load Data From CSV File

```
[5]: churn_df = pd.read_csv("https://cf-courses-data.s3.us.cloud-object-storage.

appdomain.cloud/IBMDeveloperSkillsNetwork-ML0101EN-SkillsNetwork/labs/

Module%203/data/ChurnData.csv")

churn_df.head()
```

| [5]: | tenure | age | address | income | ed | employ | equip | callcard | wireless | \ |
|------|---------|------|----------|---------|--------|---------|--------|------------|-----------|---|
| 0 | 11.0 | 33.0 | 7.0 | 136.0 | 5.0 | 5.0 | 0.0 | 1.0 | 1.0 | |
| 1 | 33.0 | 33.0 | 12.0 | 33.0 | 2.0 | 0.0 | 0.0 | 0.0 | 0.0 | |
| 2 | 23.0 | 30.0 | 9.0 | 30.0 | 1.0 | 2.0 | 0.0 | 0.0 | 0.0 | |
| 3 | 38.0 | 35.0 | 5.0 | 76.0 | 2.0 | 10.0 | 1.0 | 1.0 | 1.0 | |
| 4 | 7.0 | 35.0 | 14.0 | 80.0 | 2.0 | 15.0 | 0.0 | 1.0 | 0.0 | |
| | | | | | | | | | | |
| | longmon | n | ager int | ernet o | :allwa | it conf | er ebi | ll loglone | r logtoll | ١ |

| | longmon | pager | internet | callwait | confer | ebill | loglong | logtoll | \ |
|---|---------|-----------|----------|----------|--------|-------|---------|---------|---|
| 0 | 4.40 | 1.0 | 0.0 | 1.0 | 1.0 | 0.0 | 1.482 | 3.033 | |
| 1 | 9.45 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 2.246 | 3.240 | |
| 2 | 6.30 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 1.841 | 3.240 | |
| 3 | 6.05 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.800 | 3.807 | |
| 4 | 7.10 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 1.960 | 3.091 | |

| | lninc | custcat | churn |
|---|-------|---------|-------|
| 0 | 4.913 | 4.0 | 1.0 |
| 1 | 3.497 | 1.0 | 1.0 |
| 2 | 3.401 | 3.0 | 0.0 |
| 3 | 4.331 | 4.0 | 0.0 |
| 4 | 4.382 | 3.0 | 0.0 |

1.1.2 Data pre-processing and selection

Let's select some features for the modeling. Also, we change the target data type to be an integer, as it is a requirement by the skitlearn algorithm:

```
[6]: churn_df = churn_df[['tenure', 'age', 'address', 'income', 'ed', 'employ',
    churn_df['churn'] = churn_df['churn'].astype('int')
   churn_df.head()
```

| [6]: | tenure | age | address | income | ed | employ | equip | callcard | wireless | \ |
|------|--------|------|---------|--------|-----|--------|-------|----------|----------|---|
| 0 | 11.0 | 33.0 | 7.0 | 136.0 | 5.0 | 5.0 | 0.0 | 1.0 | 1.0 | |
| 1 | 33.0 | 33.0 | 12.0 | 33.0 | 2.0 | 0.0 | 0.0 | 0.0 | 0.0 | |
| 2 | 23.0 | 30.0 | 9.0 | 30.0 | 1.0 | 2.0 | 0.0 | 0.0 | 0.0 | |
| 3 | 38.0 | 35.0 | 5.0 | 76.0 | 2.0 | 10.0 | 1.0 | 1.0 | 1.0 | |
| 4 | 7 0 | 35 0 | 14 0 | 80 0 | 2.0 | 15.0 | 0.0 | 1 0 | 0.0 | |

```
0
          1
```

churn

1 1

2 0

3 0 4

0

1.1.3 Select Variables at Random

Like Bagging, RF uses an independent bootstrap sample from the training data. In addition, we select m variables at random out of all M possible variables. Let's do an example.

```
[7]: X=churn_df[['tenure', 'age', 'address', 'income', 'ed', 'employ', 'equip']]
```

there are 7 features

Train/Test dataset

Let's define X, and y for our dataset:

```
[8]: y = churn_df['churn']
     y.head()
```

- [8]: 0 1
 - 1 1
 - 2 0
 - 3 0
 - 4 0

Name: churn, dtype: int64

1.3 Train/Test dataset

We split our dataset into train and test set:

```
[9]: from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split( X, y, test_size=0.3,

Grandom_state=1)

print ('Train set', X_train.shape, y_train.shape)

print ('Test set', X_test.shape, y_test.shape)
```

```
Train set (140, 7) (140,)
Test set (60, 7) (60,)
```

1.4 AdaBoost

We can import the AdaBoost Classifier in Sklearn

```
[10]: from sklearn.ensemble import AdaBoostClassifier
```

The parameter n_estimators int is the maximum number of classifiers (default=50) at which boosting is stopped. If the results are perfect, the training procedure is stopped early.

```
[11]: n_estimators=5 random_state=0
```

We can create a AdaBoostClassifier object.

```
[12]: model = AdaBoostClassifier(n_estimators=n_estimators,random_state=random_state)
```

If the outputs were y-1 and 1, the form of the classifier would be:

```
H(x) = \operatorname{sign}(\alpha + 1h + 1(x) + \alpha + 2h + 2(x) + \alpha + 3h + 3(x) + \alpha + 4h + 4(x) + \alpha + 5h + 5(x))
```

We can fit the object finding all the α_t $h_t(x)$ and then make a prediction:

```
[13]: model.fit(X_train, y_train)
y_pred = model.predict(X_test)
y_pred
```

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

We can find the training and testing accuracy:

```
[14]: print(get_accuracy(X_train, X_test, y_train, y_test, model))
```

```
{'test Accuracy': 0.7666666666666667, 'trian Accuracy': 0.7642857142857142}
```

We see the base model is a Decision Tree. Since it only has one layer, it's called a stump:

[15]: model.base_estimator_

```
[15]: DecisionTreeClassifier(class weight=None, criterion='gini', max depth=1,
                  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=None,
                  splitter='best')
     We can output a list of the weak classifiers: h = 1(x), h = 2(x), h = 3(x), h = 4(x) and h = 5(x)
[16]: model.estimators
[16]: [DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=1,
                   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=209652396, splitter='best'),
       DecisionTreeClassifier(class weight=None, criterion='gini', max depth=1,
                   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=398764591, splitter='best'),
       DecisionTreeClassifier(class weight=None, criterion='gini', max_depth=1,
                   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=924231285, splitter='best'),
      DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=1,
                   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=1478610112, splitter='best'),
       DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=1,
                   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=441365315, splitter='best')]
```

We see the weak classifiers do not perform as well:

```
[17]: [ ("for weak classifiers {} the we get ".format(i+1),get_accuracy(X_train, ∪ → X_test, y_train, y_test, weak_classifiers)) for i,weak_classifiers in ∪ → enumerate(model.estimators_)]
```

We can increase the number of weak classifiers:

```
[18]: n_estimators=100 random_state=0
```

and then fit the model

```
[19]: model = AdaBoostClassifier(n_estimators=n_estimators,random_state=random_state)
model.fit(X_train, y_train)

#Predict the response for test dataset
y_pred = model.predict(X_test)
```

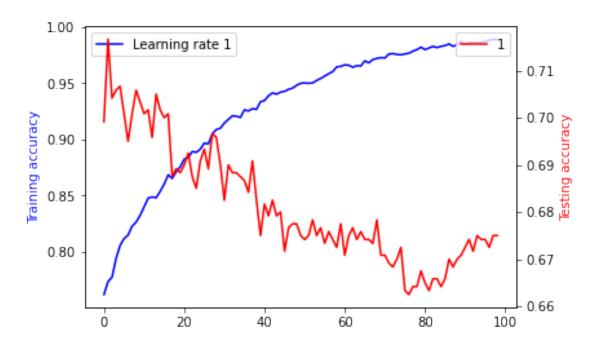
We obtain the training and testing accuracy:

```
[20]: print(get_accuracy(X_train, X_test, y_train, y_test, model))
```

We see that adding more weak classifiers causes overfitting. We can verify by plotting the training and test accuracy over the number of classifiers:

```
[21]: get_accuracy_bag(X,y,title="Training and Test Accuracy vs Weak_u Glassifiers",Learning_rate_=[1],times=20,xlabel='Number Estimators')
```

```
100% | 20/20 [03:11<00:00, 9.58s/it]
```



As you can see, as the number of classifiers increases so does the overfitting; the training accuracy increases and conversely, the testing accuracy decreases. One way to decrease overfitting is using the learning rate learning_rate with a default value of 1. This is a type of Regularization. For more detail on Regularization, check out here.

```
[22]: n_estimators=100
random_state=0
learning_rate=0.7
```

We can now train the model, make a prediction, and calculate the accuracy. We see that by increasing the learning rate the test accuracy has improved.

```
[23]: model =

AdaBoostClassifier(n_estimators=n_estimators,random_state=random_state,learning_rate=learni
model.fit(X_train, y_train)
y_pred = model.predict(X_test)
print(get_accuracy(X_train, X_test, y_train, y_test, model))
```

{'test Accuracy': 0.75, 'trian Accuracy': 0.95}

Compared to the previous results we see the model does better on the test data. We can try different learning rates using the method get_accuracy_bag. In this case, the learning rates are 0.2,0.4,0.6, and 1. As the learning rate goes down we see that the testing accuracy increases while conversely, the training accuracy decreases.

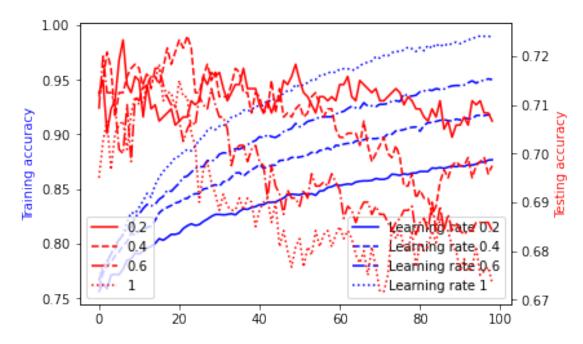
```
[24]:
```

```
get_accuracy_bag(X,y,title="Training and Test Accuracy vs Weak_\(\sigma\)

→Classifiers", Learning_rate_=[0.2,0.4,0.6,1], times=20, xlabel='Number_\(\sigma\)

→Estimators')
```

100% | 20/20 [12:53<00:00, 38.66s/it]



Another important parameter is algorithm with takes on the values SAMME, SAMME.R. The default is 'SAMME.R.' The SAMME.R algorithm typically converges faster than SAMME, achieving a lower test error with fewer boosting iterations. For more details, check. One issue is that SAMME.R can't be used all the time as we will need the Base classifier to generate the probability of belonging to each class.

1.5 Channing The Base Classifier

AdaBoost is usually performed with Decision Trees but we can use other base classifiers. However, if the classifier is too strong it will cause overfitting. Consider using the following Support Vector Machine (SVM) as the base classifier:

```
[25]: from sklearn.svm import SVC

[26]: base_estimator=SVC(kernel='rbf',gamma=1)
```

We see the SVM does extremely well:

```
[27]: base_estimator.fit(X_train, y_train)
print(get_accuracy(X_train, X_test, y_train, y_test, base_estimator))
```

```
{'test Accuracy': 0.766666666666667, 'trian Accuracy': 1.0}
```

The Base classifier for SVM can not generate the probability of belonging to each class. If you uncomment the following line of code you will get an error.

```
[]: #base_estimator.predict_proba(X_train)
```

Therefore the parameter algorithm must be 'SAMME'

We see the AdaBoost model does worse, this is similar to overfitting. In addition, SVM takes much longer to train than classification trees:

```
[30]: model.fit(X_train, y_train)

#Predict the response for test dataset
y_pred = model.predict(X_test)
print(get_accuracy(X_train, X_test, y_train, y_test, model))
```

{'test Accuracy': 0.7666666666666667, 'trian Accuracy': 0.6857142857142857}

We see that each tree in RF is less correlated than Bagging:

Cancer Data Example

The example is based on a dataset that is publicly available from the UCI Machine Learning Repository (Asuncion and Newman, 2007)[http://mlearn.ics.uci.edu/MLRepository.html]. The dataset consists of several hundred human cell sample records, each of which contains the values of a set of cell characteristics. The fields in each record are:

| Field name | Description |
|-------------|-----------------------------|
| ID | Clump thickness |
| Clump | Clump thickness |
| UnifSize | Uniformity of cell size |
| UnifShape | Uniformity of cell shape |
| MargAdh | Marginal adhesion |
| SingEpiSize | Single epithelial cell size |
| BareNuc | Bare nuclei |
| BlandChrom | Bland chromatin |
| NormNucl | Normal nucleoli |
| Mit | Mitoses |
| Class | Benign or malignant |

Let's load the dataset:

```
[31]: df = pd.read_csv("https://cf-courses-data.s3.us.cloud-object-storage.appdomain.
       →cloud/IBMDeveloperSkillsNetwork-ML0101EN-SkillsNetwork/labs/Module%203/data/
       ⇔cell_samples.csv")
      df.head()
[31]:
                         UnifSize UnifShape MargAdh SingEpiSize BareNuc
              ID
                  Clump
         1000025
                      5
                                1
                                           1
                                                                          1
                      5
                                           4
                                                                  7
      1 1002945
                                4
                                                     5
                                                                         10
      2 1015425
                      3
                                1
                                           1
                                                     1
                                                                  2
                                                                          2
      3 1016277
                      6
                                8
                                           8
                                                                          4
                                                     1
      4 1017023
                                1
                                           1
                                                     3
                                                                          1
                                    Class
         BlandChrom
                     NormNucl
                              Mit
      0
                  3
                                 1
                                        2
                            1
                  3
                            2
                                        2
      1
                                 1
                  3
      2
                            1
                                 1
                                        2
      3
                  3
                            7
                                 1
                                        2
      4
                  3
                                        2
                                 1
     Now lets remove rows that have a ? in the BareNuc column:
[32]: df= df[pd.to_numeric(df['BareNuc'], errors='coerce').notnull()]
     We obtain the features:
[33]: X = df[['Clump', 'UnifSize', 'UnifShape', 'MargAdh', 'SingEpiSize', 'BareNuc', |
       X.head()
                          UnifShape MargAdh SingEpiSize BareNuc BlandChrom \
[33]:
         Clump
                UnifSize
      0
             5
                       1
                                  1
                                           1
                                                         2
                                                                 1
                                                                             3
      1
             5
                       4
                                  4
                                           5
                                                         7
                                                                10
                                                                             3
      2
             3
                       1
                                  1
                                           1
                                                         2
                                                                 2
                                                                             3
                                                                 4
      3
             6
                       8
                                  8
                                           1
                                                         3
                                                                             3
```

NormNucl Mit
0 1 1
1 2 1
2 1 1
3 7 1
4 1 1

We obtain the class labels:

```
[34]: y=df['Class']
      y.head()
[34]: 0
           2
           2
      1
      2
           2
      3
           2
      4
           2
      Name: Class, dtype: int64
     We split the data into training and testing sets.
[35]: X_train, X_test, y_train, y_test = train_test_split( X, y, test_size=0.2,__
       →random_state=4)
      print ('Train set:', X train.shape, y train.shape)
      print ('Test set:', X_test.shape, y_test.shape)
     Train set: (546, 9) (546,)
     Test set: (137, 9) (137,)
     We use GridSearchCV to search over specified parameter values of the model.
[36]: from sklearn.model_selection import GridSearchCV
     We create a AdaBoost object and list the parameters using the method get params():
[37]: model = AdaBoostClassifier()
      model.get_params().keys()
[37]: dict_keys(['algorithm', 'base_estimator', 'learning_rate', 'n_estimators',
      'random_state'])
     We can use GridSearch for Exhaustive search over specified parameter values. We see many of
     the parameters are similar to Classification trees; let's try different parameters for learning rate,
     n_estimators, and algorithm.
[38]: param_grid = {'learning_rate': [0.1*(n+1) for n in range(10)],
                    'n_estimators' : [2*n+1 for n in range(10)],
                     'algorithm':['SAMME', 'SAMME.R']}
      param_grid
[38]: {'learning_rate': [0.1,
        0.2,
        0.30000000000000004,
        0.4,
        0.5,
        0.6000000000000001,
```

0.7000000000000001,

```
0.8,
0.9,
1.0],
'n_estimators': [1, 3, 5, 7, 9, 11, 13, 15, 17, 19],
'algorithm': ['SAMME', 'SAMME.R']}
```

We create the Grid Search object and fit it:

```
[39]: search = GridSearchCV(estimator=model, param_grid=param_grid,scoring='accuracy') search.fit(X_train, y_train)
```

We can see the best accuracy score of the searched parameters was $\sim 96\%$.

```
[40]: search.best_score_
```

[40]: 0.9652014652014652

The best parameter values are:

```
[41]: search.best_params_
```

```
[41]: {'algorithm': 'SAMME.R', 'learning rate': 0.2, 'n_estimators': 17}
```

We can calculate accuracy on the test data using the test data:

```
[42]: print(get_accuracy(X_train, X_test, y_train, y_test, search.best_estimator_))
```

```
{'test Accuracy': 0.9781021897810219, 'trian Accuracy': 0.9725274725274725}
```

Practice

Imagine that you are a medical researcher compiling data for a study. You have collected data about a set of patients, all of whom suffered from the same illness. During their course of treatment, each patient responded to one of 5 medications, Drug A, Drug B, Drug c, Drug x and y.

Part of your job is to build a model to find out which drug might be appropriate for a future patient with the same illness. The features of this dataset are Age, Sex, Blood Pressure, and the Cholesterol of the patients, and the target is the drug that each patient responded to.

It is a sample of multiclass classifier, and you can use the training part of the dataset to build a decision tree, and then use it to predict the class of a unknown patient, or to prescribe a drug to a

new patient.

```
[43]: df = pd.read_csv("https://cf-courses-data.s3.us.cloud-object-storage.appdomain.
       →cloud/IBMDeveloperSkillsNetwork-ML0101EN-SkillsNetwork/labs/Module%203/data/

drug200.csv", delimiter=",")

      df.head()
                      BP Cholesterol Na_to_K
[43]:
         Age Sex
                                                 Drug
                                        25.355 drugY
          23
               F
                    HIGH
                                 HIGH
      1
          47
               Μ
                     LOW
                                 HIGH
                                        13.093
                                                drugC
      2
          47
                     LOW
                                 HIGH
                                        10.114 drugC
               М
          28
      3
               F
                 NORMAL
                                 HIGH
                                         7.798
                                                drugX
      4
          61
               F
                                 HIGH
                                        18.043 drugY
                     LOW
     Let's create the X and y for our dataset:
[44]: X = df[['Age', 'Sex', 'BP', 'Cholesterol', 'Na to K']].values
      X[0:5]
[44]: array([[23, 'F', 'HIGH', 'HIGH', 25.355],
             [47, 'M', 'LOW', 'HIGH', 13.093],
             [47, 'M', 'LOW', 'HIGH', 10.114],
             [28, 'F', 'NORMAL', 'HIGH', 7.798],
             [61, 'F', 'LOW', 'HIGH', 18.043]], dtype=object)
[45]: y = df["Drug"]
      y[0:5]
[45]: 0
           drugY
      1
           drugC
      2
           drugC
      3
           drugX
      4
           drugY
      Name: Drug, dtype: object
     Now lets use a LabelEncoder to turn categorical features into numerical:
[46]: from sklearn import preprocessing
      le_sex = preprocessing.LabelEncoder()
      le_sex.fit(['F','M'])
      X[:,1] = le_sex.transform(X[:,1])
      le_BP = preprocessing.LabelEncoder()
      le_BP.fit([ 'LOW', 'NORMAL', 'HIGH'])
      X[:,2] = le_BP.transform(X[:,2])
```

```
le_Chol = preprocessing.LabelEncoder()
      le_Chol.fit([ 'NORMAL', 'HIGH'])
      X[:,3] = le\_Chol.transform(X[:,3])
      X[0:5]
[46]: array([[23, 0, 0, 0, 25.355],
             [47, 1, 1, 0, 13.093],
             [47, 1, 1, 0, 10.114],
             [28, 0, 2, 0, 7.798],
             [61, 0, 1, 0, 18.043]], dtype=object)
     Split the data into training and testing data with a 80/20 split.
[47]: X_train, X_test, y_train, y_test = train_test_split( X, y, test_size=0.2,__
       →random_state=4)
      print ('Train set:', X_train.shape, y_train.shape)
      print ('Test set:', X_test.shape, y_test.shape)
     Train set: (160, 5) (160,)
     Test set: (40, 5) (40,)
     We can use GridSearch for Exhaustive search over specified parameter values.
[48]: param grid = {'learning rate': [0.1*(n+1)] for n in range(10)],
                    'n_estimators' : [2*n+1 for n in range(10)],
                     'algorithm':['SAMME', 'SAMME.R']}
      param_grid
[48]: {'learning_rate': [0.1,
        0.2,
        0.30000000000000004,
        0.4,
        0.5,
        0.6000000000000001,
        0.7000000000000001,
        0.8,
        0.9,
        1.0],
       'n_estimators': [1, 3, 5, 7, 9, 11, 13, 15, 17, 19],
       'algorithm': ['SAMME', 'SAMME.R']}
     Create a AdaBoostClassifier object called model:
```

Click here for the solution

[49]: model = AdaBoostClassifier()

```
Create GridSearchCV object called search with the estimator set to model, param grid set to
     param grid, scoring set to accuracy, and cv set to 3 and Fit the GridSearchCV object to our
     X_train and y_train data.
[50]: search = GridSearchCV(estimator=model,
       →param_grid=param_grid,scoring='accuracy', cv=3)
      search.fit(X_train, y_train)
[50]: GridSearchCV(cv=3, error_score='raise-deprecating',
             estimator=AdaBoostClassifier(algorithm='SAMME.R', base_estimator=None,
                learning_rate=1.0, n_estimators=50, random_state=None),
             fit_params=None, iid='warn', n_jobs=None,
             param_grid={'learning_rate': [0.1, 0.2, 0.30000000000000004, 0.4, 0.5,
      0.60000000000001, 0.70000000000001, 0.8, 0.9, 1.0], 'n estimators': [1, 3,
      5, 7, 9, 11, 13, 15, 17, 19], 'algorithm': ['SAMME', 'SAMME.R']},
             pre_dispatch='2*n_jobs', refit=True, return_train_score='warn',
             scoring='accuracy', verbose=0)
     Click here for the solution
     search = GridSearchCV(estimator=model, param grid=param grid,scoring='accuracy', cv=3)
     search.fit(X_train, y_train)
     We can find the accuracy of the best model.
[51]: search.best_score_
[51]: 0.85
     We can find the best parameter values:
[52]: search.best_params_
[52]: {'algorithm': 'SAMME',
       'learning_rate': 0.30000000000000004,
       'n_estimators': 19}
     We can find the accuracy test data:
     Click here for the solution
     print(get accuracy(X train, X test, y train, y test, search.best estimator_))
[53]: print(get_accuracy(X_train, X_test, y_train, y_test, search.best_estimator_))
```

model = RandomForestClassifier()

{'test Accuracy': 0.775, 'trian Accuracy': 0.85}

1.5.1 Thank you for completing this lab!

1.6 Author

Joseph Santarcangelo

1.6.1 Other Contributors

1.7 Change Log

| Date (YYYY-MM-DD) | Versio | on Changed By | Change Description |
|-------------------|--------|---------------|-----------------------|
| 2020-11-27 | 0.1 | Joseph | Created Lab |
| | | Santarcangelo | Template |
| 2022-2-8 | 0.2 | Steve Hord | QA pass |
| ## | | | |

[]: