Boosting

Implementing Adaptive Boosting with a simple classifier

Assignment Contents:

EXPECTED TIME: 4 HRS

Overview

This assignment extends the w ork done in Assignment 6 w ith Random Forests.

Initially the assignment is theory heavy, both a simple classifier and an adaptive boosting model w ill be built from scratch. This w ill primarily involve creating `Python` implementations of the algorithms found in lectures, both this w eek and last w eek. As usual, pre-built versions of these algorithms w ill be demonstrated at the end of the lesson.
Building the algorithms from scratch help to ensure depth of theoretical know ledge before allow ing `Python` and its packages to handle the heavy lifting.

Activities in this Assignment

- Create a simple Classifier
  - Find potential splits in data
  - Find the best split according to entropy
  - Create binary predictions given a chosen split
- Create an Adaptive Boosting Algorithm
  - Create Weights
  - Calculate Epsilon and Alph
  - Update Weights
- Use Adaptive Boosting to Create Predictions on Census Data

Imports

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
```

Building a Simple Binary Tree Classifier

Below, pseudo-code for a simple binary tree classifier class is provided.

The structure of this pseudo-code mimics the structure of the `sklearn` classifiers in that it creates "fit" and "predict" methods.

```
class Simple_Binary(object):

    def __init__(self):
        pass

    def fit(self, X,y):
        """
            1. Find best split in X
                - According to entropy
            2. After finding split, assign:
                - self.col_idx
                - self.split_value
                - self.left_pred
                - self.right_pred
        """
        pass

    def predict(self, X):
        """
            1. Make predictions given values calculated
                in the `.fit(X,y)` method.
            2. return predictions as numpy array.
        """
        pass
```

Instead of building a class like `sklearn`, our `.fit()` and `.predict()` methods w ill be w ritten as independent `simple_binary_tree_fit()` and `simple_binary_tree_predict()` functions.

In `simple_binary_tree_fit`, **3 steps** must be accomplished:

1. Find all of the potential values for splitting.
2. Find the column and split_value that results in the low est entropy.
3. Given that "best split", determine w hich predictions should be made w hen data is "<=" and="" "="">" that split value.

The below provides framew ork for returning the column and split value that yeilds the low est entropy, and the predictions indicated by that split.

After correctly defining `find_splits()`, `ent_from_split()`, and `pred_from_split()` -- marked w ith " `### <------` " -- the `simple_binary_tree_fit()` function should w ork.

```
def simple_binary_tree_fit(X,y):
    """

    Positional arguments -
        X -- a numpy array of numeric observations:
            Assume rows are separate observations, columns are features
        y -- a numpy array of binary labels:
            *Assume labels are 1 for "True" and 0 for "False"*

    1. Find best split in X
        - According to entropy
    2. After finding split, return:
        - col_idx - index of column used to split data
        - split_value - value upon which data is split
        - left_pred - The prediction for observation <= split_value
        - right_pred - The prediciton for observation > split_value

    """

    # create variable "best_split" which will hold:
    # (col_number, split_value, entropy)
    best_split = (-1,-1,1)

    # loop through each column in X, keeping track of the column index.
    # # # Note, taking the transpose of X -- X.T -- yeilds columns in this "for" loop
    for col_idx, col in enumerate(X.T):

        # Find potential split values within column using `find_splits(col)`
        splits = find_splits(col) ### <------

        # For each split, calculate entropy
        for s in splits:
            ent = ent_from_split(col, s, y) ### <------

            # Check if calculated entropy is less than previous "best"
            if ent < best_split[2]:
                best_split = (col_idx, s, ent)

    # Now, the "best split" has been found.
    # create "left" and "right" predictions for the best_split
    # The "left" predictions is for when `observation` <= `split_value`
    # The "right" prediction is for when `observation` > `split_value`
    # Each prediction will either be 1 for "True" or 0 for "False"

    left_pred, right_pred = pred_from_split(X, y, *best_split[:2]) ### <------

    col_idx, split_value = best_split[:2]

    # return:
    # - the index of the column to split on.
    # - the value to split that column on
    # - the prediction for rows with observations in that column less than or equal to the split
    # - the prediction for rows with observations in that column greater than the split

    return col_idx, split_value, left_pred, right_pred
```

Question 1

Build the `find_splits()` method.

```
### GRADED
### Code a function called `find_splits`.
### ACCEPT a 1-dimensional numpy array as input.
### RETURN a numpy.array of "split values"

### "Split values" are the mid-points between the values in the sorted list of unique values.

### e.g., Input of np.array([1, 3, 2, 3, 4, 6])
### Yields a sorted-unique list of: np.array([1, 2, 3, 4, 6])
### Then the "splits" in between those values will be: np.array([1.5, 2.5, 3.5, 5])

### YOUR ANSWER BELOW

def find_splits(col):
    """
    Calculate and return all possible split values given a column of numeric data

    Positional argument:
        col -- a 1-dimensional numpy array, corresponding to a numeric
            predictor variable.

    Example:
        col = np.array([0.5, 1. , 3. , 2. , 3. , 3.5, 3.6, 4. , 4.5, 4.7])
        splits  = find_splits(col)
        print(splits) # --> np.array([0.75, 1.5, 2.5, 3.25, 3.55, 3.8, 4.25, 4.6])

    """


    # col = np.array([0.5, 1. , 3. , 2. , 3. , 3.5, 3.6, 4. , 4.5, 4.7])
    # Sort list of unique values
    srt = np.sort(np.unique(col))

    # srt = np.array([0.5 1.  2.  3.  3.5 3.6 4.  4.5 4.7])

    # Shift values by inserting value at begining, also deleting final value
    shift = np.delete(np.insert(srt,0,0), -1)
    # shift = np.array([0.  0.5 1.  2.  3.  3.5 3.6 4.  4.5])

    # Take the difference divided by two of the sorted and shifted list, and remove initial placeholder
    # Add to the sorted list with final element removed
    splits = np.delete(srt,-1) + np.delete((srt-shift)/2,0)

    # splits =
    # # np.delete(srt,-1) --> np.array([0.5 1.  2.  3.  3.5 3.6 4.  4.5])
    # # +
    # # np.delete((srt-shift)/2,0) -- > np.array([0.25 0.5  0.5  0.25 0.05 0.2  0.25 0.1 ])
    # # =
    # # np.array([0.75, 1.5, 2.5, 3.25, 3.55, 3.8, 4.25, 4.6])

    return splits
```

Equation for Entropy for binary classification at binary split:

The entropy at a node containing only tw o classes is calculated by:

$Entropy(node) = -p_{class1}log_2(p_{class1}) + -p_{class2}log_2(p_{class2})$

Suppose a node contains the observations [1,0,1,1]. Then:

$Entropy(node) = -p_{class1}log_2(p_{class1}) + -p_{class2}log_2(p_{class2})$

$\ = -.75log_2(.75) + -.25log_2(.25)$

$\ = .311 + .5$

$\ \approx .811$

This calculation is already programmed into the supplied `entropy()` function below.

```
def entropy(class1_n, class2_n):
    # If all of one category, log2(0) does not exist,
    # and entropy = 0
    if (class1_n == 0) or (class2_n == 0):
        return 0

    # Find total number of observations
    total = class1_n + class2_n

    # find proportion of both classes
    class1_proprtion = class1_n/total
    class2_proportion = class2_n/total

    # implement entropy function
    return  sum([-1 * prop * np.log2(prop)
                 for prop in [class1_proprtion, class2_proportion] ])

print(entropy(3,1))
```

The entropy of a split is:
$Entropy(split) = p_{node1} * Entropy(node1)+ p_{node2}* Entropy(node2)$

Where $p_{node}$ is the proportion of observations at that node

Suppose:
Node 1 contains the observations - [1,0,1,1]
Node 2 contains the observations - [0,0,0,1,1,0]

Then:
$Entropy(split) = p_{node1} * Entropy(node1)+ p_{node2}* Entropy(node2)$

$\ = .4 *Entropy(node1) + .6 * Entropy(node2)$

For our purposes, the tw o classes in each node w ill be defined by:

1. Observations w ith values less than or equal to the split value
2. Observations w ith values greater than the split value.

Question 2

```
### GRADED
### Code a function called `ent_from_split`
### ACCEPT three inputs:
### 1. A numpy array of values
### 2. A value on which to split the values in the first array, (into two groups; <= and >)
### 3. Labels for the observations corresponding to each value in the first array.
### ### Assume the labels are "0"s and "1"s

### RETURN the entropy resulting from that split: a float between 0 and 1.

### Feel free to use the `entropy()` function defined above
### YOUR ANSWER BELOW

def ent_from_split(col, split_value, labels):

    """
    Calculate the entropy of a split.

    Positional arguments:
        col -- a 1-dimensional numpy array, corresponding to a numeric
            predictor variable.
        split_value --  number, defining where the spliting should occur
        labels -- a 1-dimensional numpy array, corresponding to the class
            labels associated with the observations in `col`.
            assume they will be "0"s and "1"s
    Example:
        col = np.array([1,1,2,2,3,3,4])
        split = 2.5
        labels = np.array([0,1,0,0,1,0,1])

        ent = ent_from_split(col, split, labels)

        print(ent) # --> 0.8571428571428571

    """

    # Define entropy function
    def entropy(class1_n, class2_n):
        # If all of one category, log2(0) does not exist,
        # and entropy = 0
        if (class1_n == 0) or (class2_n == 0):
            return 0

        # Find total number of observations
        total = class1_n + class2_n

        # find proportion of both classes
        class1_proprtion = class1_n/total
        class2_proportion = class2_n/total

        # implement entropy function
        return  sum([-1 * prop * np.log2(prop)
                     for prop in [class1_proprtion, class2_proportion] ])

    # Helper function to find number in each class at each node.
    def node_classes(col, split_value, labels):
        # subset labels by observations that are <= / > the split value
        le_node = labels[col <= split_value]
        g_node = labels[col > split_value]

        # count members of each class at each node
        # c1 corresponds to "1's"
        # c2 corresponds to "0's
        le_c1 = np.count_nonzero(le_node)
        le_c2 = len(le_node) - le_c1

        g_c1 = np.count_nonzero(g_node)
        g_c2 = len(g_node) - g_c1

        return le_c1, le_c2, g_c1, g_c2

    # Find number in each class at both nodes
    le_c1, le_c2, g_c1, g_c2 = node_classes(col, split_value, labels)
    #print(le_c1, le_c2, g_c1, g_c2)
    # calculate proportion of total at each node
    total = len(col)
    p_g = (g_c1 + g_c2) / total
    p_le = (le_c1+ le_c2) / total

    # implement entropy calculation
    return (p_le * entropy(le_c1, le_c2)) + (p_g * entropy(g_c1, g_c2))
```

Question 3

Creating predictions from the observed majority class at each node.

```
### GRADED
### Code a function called `pred_from_split`
### ACCEPT four inputs:
### 1. a numpy array of observations
### 2. a numpy array of labels: 0's and 1's
### 3. a column index
### 4. a value to split that column specified by the index

### RETURN a tuple of (left_pred, right_pred) where:
### left_pred is the majority class of labels where observations are <= split_value
### right_pred is the majority class of labels where observations are > split_value

### If the split yeilds equal number of observations of each class in BOTH nodes,
### ### let both `left_pred` and `right_pred` be 1.
### If the split yeilds equal number of observations of each class in ONLY ONE node,
### ### predict the opposite of the other node. e.g.

### ### node 1    |   node 2
### ###  c1  | c2 |  c1 | c2
### ###  5  | 4   |  3  |  3

### The prediction for node 1 would be "class 1".
### Because of the equal numbers of each class in node 2,
### the prediction for node 2 would be the opposite of the node 1 prediction.
### e.g. the prediction for node 2 would be "class 2"

### YOUR ANSWER BELOW

def pred_from_split(X, y, col_idx, split_value):

    """
    Return predictions for the nodes defined by the given split.

    Positional argument:
        X -- a 2-dimensional numpy array of predictor variable observations.
            rows are observations, columns are features.
        y -- a 1-dimensional numpy array of labels, associated with observations
             in X.
        col_idx -- an integer index, such that X[:,col_idx] yeilds all the observations
            of a single feature.
        split_value -- a numeric split, such that the values of X[:,col_idx] that are
            <= split_value are in the left node. Those > split_value are in the right node.

    Example:
        X = np.array([[0.5, 3. ], [1.,  2. ], [3.,  0.5],
                      [2.,  3. ], [3.,  4. ]])

        y = np.array([ 1, 1, 0, 0, 1])

        col_idx = 0
        split_value = 1.5

        pred_at_nodes = pred_from_split(X, y, col_idx, split_value)
        print(pred_at_nodes) # --> (1, 0)

    """

    # Helper function to find number in each class at each node.
    def node_classes(col, split_value, labels):
        # subset labels by observations that are <= / > the split value
        le_node = labels[col <= split_value]
        g_node = labels[col > split_value]

        # count members of each class at each node
        # c1 corresponds to "1's"
        # c2 corresponds to "0's

        le_c1 = np.count_nonzero(le_node)
        le_c2 = len(le_node) - le_c1

        g_c1 = np.count_nonzero(g_node)
        g_c2 = len(g_node) - g_c1

        return le_c1, le_c2, g_c1, g_c2

    # Return count of each class at each node using helper function
    le_c1, le_c2, g_c1, g_c2 = node_classes(X[:,col_idx], split_value, y)

    # if more of class 1 than class 2, return True (1)
    # if more of class 2 than class 1, return False (0)
    # if equal number, return None

    def pred_for_node(cl1, cl2):
        if cl1 > cl2: return True
        elif cl1 < cl2: return False
        else: return None

    # Create intial predictions
    left = pred_for_node(le_c1,le_c2)
    right = pred_for_node(g_c1, g_c2)

    # Check predictions for ties
    # Check to see if one of the predictions came back as "None"
    if ((right == None) or (left == None)) and (right != left):

        if left == None:
            left = not right
        else:
            right = not left

    # Check to see if both predictions came back as "None"
    if (right == None) and (left == None):
        right = True; left = True

    # Convert predictions to integers, and return as tuple
    return (int(left), int(right))
```

Question 4

Creating Predictions

```
### GRADED
### Code a function called "simple_binary_tree_predict"
### ACCEPT five inputs:
### 1. A numpy array of observations
### 2. A column index
### 3. A value to split the column specified by the index
### 4/5. Two values, 1 or 0, denoting the predictions at left and right nodes

### RETURN a numpy array of predictions for each observation

### Predictions are created for each row in x:
### 1. For a row in X, find the value in the "col_idx" column
### 2. Compare to "split_value"
### 3. If <= "split_value", predict "left_pred"
### 4. Else predict "right_pred"

### YOUR ANSWER BELOW

def simple_binary_tree_predict(X, col_idx, split_value, left_pred, right_pred):
    """
    Create an array of predictions built from: observations in one column of X,
        a given split value, and given predictions for when observations
        are less-than-or-equal-to that split or greater-than that split value

    Positional arguments:
        X -- a 2-dimensional numpy array of predictor variable observations.
            rows are observations, columns are different features
        col_idx -- an integer index, such that X[:,col_idx] yeilds all the observations
            in a single feature.
        split_value -- a numeric split, such that the values of X[:,col_idx] that are
            <= split_value are in the left node, and those > are in the right node.
        left_pred -- class (0 or 1), that is predicted when observations
            are less-than-or-equal-to the split value
        right_pred -- class (0 or 1), that is predicted when observations
            are greater-than the split value

    Example:
        X = np.array([[0.5, 3. ], [1.,  2. ], [3.,  0.5],
                [2.,  3. ], [3.,  4. ]])
        col_idx = 0
        split_value = 1.5
        left_pred = 1
        right_pred = 0

        preds = simple_binary_tree_predict(X, col_idx, split_value, left_pred, right_pred)
        print(preds) #--> np.array([1,1,0,0,0])

    """

def simple_binary_tree_predict_T(X, col_idx, split_value, left_pred, right_pred):
    # take out column
    col = X[:,col_idx]

    # If both predictions are same, return all that prediction
    if left_pred == right_pred:
        preds = np.ones(len(col))
        preds *= int(left_pred)

    # Otherwise, predictions are different.
    # if left_pred ( == 1)
    # return 1's where col is <= split

    # otherwise, 1's where col is > split
    elif left_pred:
        preds = (col<= split_value)*1
    else:
        preds = (col >split_value)*1

    return preds
```

At this point, we have a functioning binary-tree classifier that can be fit on data, and then given that fit, make predictions on out-of-sample data.

However, our ultimate goal is creation of an Adaptive Boosting algorithm.

Our Adaptive Boosting algorithm's prediction for out of sample data will be:

$$f_{boost}(x_0) = sign(\sum_{t=1}^T\alpha_tf_t(X_0))$$

The alpha is equal to:
$$\alpha_t = \frac12ln(\frac{1-\epsilon_t}{\epsilon_t})$$

The Epsilon is equal to:

$$\epsilon_t = \sum_{i=1}^nw_t(i)\mathbb{1}{y_i\ne f_t(x_i)}$$

Where all weights starts at $\frac1n$

And weights update by:
$$w_{t+1}(i) = \frac{\hat{w}_{t+1}(i)}{\sum_j\hat{w}_{t+1}(j)}$$

Where:
$$\hat{w}_{t+1}(i) = w_t(i)e^{-\alpha_ty_if_t(x_i)}$$

While we could use the `simple_binary_tree` functions created above, in the interest of speed, we will use sklearn's `DecisionTreeClassifier` as a the simple predictor to boost.

The below gives a short example of using `DecisionTreeClassifier` that:

- Splits toy data in two
- Builds two Trees each on 1/2 of data
- Saves each tree with an associated "alpha" in a dictionary (As will be done in boosting)
- Creates predictions

```
### This helper function will return an instance of a `DecisionTreeClassifier` with
### our specifications - split on entropy, and grown to depth of 1.
from sklearn.tree import DecisionTreeClassifier

def simple_tree():
    return DecisionTreeClassifier(criterion = 'entropy', max_depth= 1)


### Our example dataset, inspired from lecture
pts = [[.5, 3,1],[1,2,1],[3,.5,-1],[2,3,-1],[3,4,1],
 [3.5,2.5,-1],[3.6,4.7,1],[4,4.2,1],[4.5,2,-1],[4.7,4.5,-1]]

df = pd.DataFrame(pts, columns = ['x','y','classification'])

# Plotting by category

b = df[df.classification ==1]
r = df[df.classification ==-1]
plt.figure(figsize = (4,4))
plt.scatter(b.x, b.y, color = 'b', marker="+", s = 400)
plt.scatter(r.x, r.y, color = 'r', marker = "o", s = 400)
plt.title("Categories Denoted by Color/Shape")
plt.show()


print("df:\n",df, "\n")

### split out X and y
X = df[['x','y']]

# Change from -1 and 1 to 0 and 1
y = np.array([1 if x == 1 else 0 for x in df['classification']])

### Split data in half
X1 = X.iloc[:len(X.index)//2, :]
X2 = X.iloc[len(X.index)//2:, :]

y1 = y[:len(y)//2]
y2 = y[len(X)//2:]


### Fit classifier to both sets of data, save to dictionary:
```

```
tree_dict = {}

tree1 = simple_tree()
tree1.fit(X1,y1)
print("threshold:", tree1.tree_.threshold[0], "feature:", tree1.tree_.feature[0])

### made up alpha, for example
alpha1 = .6
tree_dict[1] = (tree1, alpha1)

tree2 = simple_tree()
tree2.fit(X2,y2)
print("threshold:", tree2.tree_.threshold[0], "feature:" ,tree2.tree_.feature[0])

### made up alpha, again.
alpha2 = .35

tree_dict[2] = (tree2, alpha2)

### Create predictions using trees stored in dictionary
print("\ntree1 predictions on all elements:", tree_dict[1][0].predict(X))
print("tree2 predictions on all elements:", tree_dict[2][0].predict(X))

### Showing Ent
print("\nEntropy of different splits for observations 5-9")
print("Col 1, @ 3.35:", ent_from_split(X2.iloc[:,1].values,3.35, y2))
print("Col 0, # 4.25:", ent_from_split(X2.iloc[:,0].values, 4.25, y2))
```

Running the above cell a number of times, you might notice that the threshold and feature for `tree2` change.

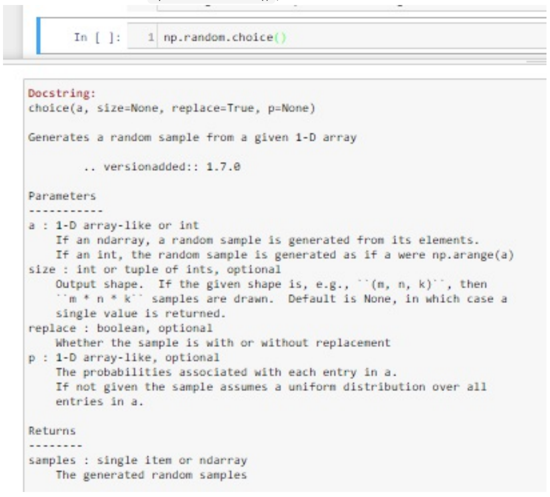
At the bottom of the cell, the entropy for tw o different splits is show n to be identical. This is unlikely to happen w ith "real" data.

Bootstrapping

Taking a bootstrap sample in adaptive boosting requires selecting observation w ith pre-defined probabilities.

Below offers an example of selecting random numbers w ith numpy given pre-defined probabilities.

This w ill be done w ith `np.random.choice()` , documentation below :



```
In [ ]:  np.random.choice()
```

```
Docstring:
choice(a, size=None, replace=True, p=None)

Generates a random sample from a given 1-D array

        .. versionadded:: 1.7.0

Parameters
-----------
a : 1-D array-like or int
    If an ndarray, a random sample is generated from its elements.
    If an int, the random sample is generated as if a were np.arange(a)
size : int or tuple of ints, optional
    Output shape.  If the given shape is, e.g., ``(m, n, k)``, then
    ``m * n * k`` samples are drawn.  Default is None, in which case a
    single value is returned.
replace : boolean, optional
    Whether the sample is with or without replacement
p : 1-D array-like, optional
    The probabilities associated with each entry in a.
    If not given the sample assumes a uniform distribution over all
    entries in a.

Returns
--------
samples : single item or ndarray
    The generated random samples
```

Try running the below cell a few times, to gain a sense of how `.choice()` w orks w hile passing a value for the `<p>` argument.

```
select_from = list(range(5))
print("selecting from:", select_from, "\n")

### Implement 1/n weights (which is the np.random.choice default)
### Also note:
### replace = True (default, used for boot-strapping)
### size = len(array) - This will be the sample size used in our algorithms.

print("Equal Weights:\n",
    np.random.choice(select_from,
                size = len(select_from),
                replace = True,
                p = np.array([.2,.2,.2,.2,.2,])
                )
)

### Now, using uneven weights

print("\nWeights of [.9,.05,.03,.02,0]:\n",
    np.random.choice(select_from,
                size = len(select_from),
                p = np.array([.9,.05,.03,.02,0]))
)
```

Building Adaptive Boosting

Below Gives the outline of the fitting process for the adaptive boosting algorithm.

Again, the functions next to " `###<------` " w ill be created in the exercises below. They include:

- `default_weights()`
- `calc_epsilon()`
- `calc_alpha()`
- `update_weights()`

```
def simple_adaboost_fit(X,y, n_estimators):
    """
    Positional arguments :
        X -- a numpy array of numeric observations:
            rows are observations, columns are features
        y -- a numpy array of binary labels:
            *Assume labels are 1 for "True" and 0 for "False"*
        estimator -- a model capable of binary classification, implementing
            the `.fit()` and `.predict()` methods.
        n_estimators -- The number of estimators to fit.

    Steps:
        1. Create probability weights for selection during boot-straping.
        2. Create boot-strap sample of observations according to weights
        3. Fit estimator model with boot-strap sample.
        4. Calculate model error: epsilon
        5. Calculate alpha to associate with model
        6. Re-calculate probability weights
        7. Repeat 2-6 unil creation of n_estimators models.

    """

    def simple_tree():
        return DecisionTreeClassifier(criterion = 'entropy', max_depth= 1)

    # Create default weights array where all are equal to 1/n
    weights = default_weights(len(y)) ### <------

    est_dict = {}
    for i in range(n_estimators):
        # Create bootstrap sample
        bs_X, bs_y = boot_strap_selection(X, y, weights)

        mod = simple_tree()
        mod.fit(bs_X, bs_y)

        # Note: Predicting on all values of X, NOT boot-strap
        preds = mod.predict(X)

        epsilon = calc_epsilon(y, preds, weights) ### <------
        alpha = calc_alpha(epsilon) ### <------

        # Note that the i+1-th model will be keyed to the int i,
        # and will store a tuple of the fit model and the alpha value
        est_dict[i] = (mod, alpha)

        weights = update_weights(weights, alpha, y, preds) ### <------

    return est_dict
```

Question 5

Creating vector of default w eights

```
### GRADED
### Code a function called 'default_weights
### ACCEPT a single integer, `n`,  as input
### RETURN default weights; a numpy array of lenth n, where each value is equal to 1/n

### YOUR ANSWER BELOW

def default_weights(n):
    """
    Create the default list of weights, a numpy array of length n
    with each value equal to 1/n

    Example:
        n = 10
        dw = default_weights(n)
        print(dw) #--> np.array([0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1])

    """
    return np.ones(n)*(1/n)
```

boot_strap_selection

Below, the "`boot_strap_selection`" algorithm is provided. The function creates a boot-strap sample given the passed-in w eights.

Example given

```
def boot_strap_selection(X, y, weights):
    """
    Create and return a boot-strapped sample of the given data,
    According to the provided weights.

    Positional Arguments:
        X -- a numpy array, corresponding to the matrix of x-observations
        y -- a numpy array, corresponding to a vector of y-labels
            All either 0 or 1
        weights -- a numpy array, corresponding to the rate at which the observations
            should be sampled for the boot-strap.

    Example:

        X = np.array([[1,1],[2,2],[3,3],[4,4],[5,5]])
        y = np.array([1,0,1,0,1])
        weights = np.array([.35,.1,.1,.35,.1])

        print(boot_strap_selection(X,y, weights))
        #-->(
            np.array([[4, 4],
                   [2, 2],
                   [4, 4],
                   [5, 5],
                   [5, 5]]),
            np.array([0, 0, 0, 1, 1]))
        ### Actual results will vary
    """

    # Take random sample of indicies, with replacement
    bss_indicies = np.random.choice(range(len(y)), size = len(y), p = weights)

    # Subset arrays with indicies
    return X[bss_indicies,:], y[bss_indicies]

### Example of use
X = np.array([[1,1],[2,2],[3,3],[4,4],[5,5]])
y = np.array([1,0,1,0,1])
weights = np.array([.35,.1,.1,.35,.1])

print(boot_strap_selection(X,y, weights))
```

Question 6

Calculating Epsilon

The Epsilon is equal to:
$$\epsilon_t = \sum_{i=1}^nw _t(i)\mathbb{1}{y_i\ne f_t(x_i)}$$

```
### GRADED
### Code a function called `calc_epsilon`
### ACCEPT three inputs:
### 1. The True labels
### 2. The Predicted labels
### 3. The current Weights

### RETURN the epsilon value, calculated according to the above equation.
### ### Will be a float between 0 and 1

### The epsilon is the sum of the weights where the true-label DOES NOT EQUAL the predicted-label

### YOUR ANSWER BELOW

def calc_epsilon(y_true, y_pred, weights):

    """
    Calculate the value of epsilon, given the above equation

    Positional Arguments:
        y_true -- An np.array of 1's and 0's corresponding to whether each observation is
            a member of class 1 or class 2
        y_pred -- An np.array of 1's and 0's corresponding to whether each observation was
            predicted to be a member of class 1 or class 2
        weights -- An np.array of floats corresponding to each observation's weight.
            All the weights will sum up to 1.

    Example:
        y_true = np.array([1,0,1,1,0])
        y_pred = np.array([0,0,0,1,0])
        weights = np.array([.4,.4,.1,.05,.05])

        ep = calc_epsilon(y_true, y_pred, weights)

        print(ep) # --> .5

    Assumptions:
        Assume both the true labels and the predictions are both all 0's and 1's.
    """

    # subset weights taking only values where y_true != y_pred
    # then sum
    return weights[y_true != y_pred].sum()
```

Question 7

Calculating alpha.

Alpha is equal to:
$$\alpha_t = \frac12ln(\frac{1-\epsilon_t}{\epsilon_t})$$

```
### GRADED
### Code a function called `calc_alpha`
### ACCEPT a non-negative float (epsilon) as input
### RETURN the alpha (float) calculated using the equation above.
### HOWEVER, if epsilon equals 0, return np.inf

### NB: np.log() calculates the natural log

### YOUR ANSWER BELOW

def calc_alpha(epsilon):
    """
    Calculate the alpha value given the epsilon observed from a model

    Positional Argument:
        epsilon -- The epsilon value calculated from a particular model
    Example:
        ep = .4
        alpha = calc_alpha(ep)
        print(alpha) # --> 0.2027325540540821
    """

    if epsilon == 0:
        return np.inf

    return .5 * np.log(((1-epsilon)/epsilon))
```

Question 8

Updating weights

To update weights:
$$w_{t+1}(i) = \frac{\hat{w}_{t+1}(i)}{\sum_j\hat{w}_{t+1}(j)}$$

Where:
$$\hat{w}_{t+1}(i) = w_t(i)e^{-\alpha_ty_if_t(x_i)}$$

```
### GRADED
### Code a function "update_weights"
### ACCEPT four inputs:
### 1. A numpy array of a weight vector
### 2. An alpha value (float)
### 3/4. numpy arrays of true labels and predicted labels vectors.

### NB: Labels will need to be converted from 0s and 1s to -1s and 1s

### RETURN an updated array of weights, according to equation above.

### YOUR ANSWER BELOW

def update_weights(weights, alpha, y_true, y_pred):
    """
    Create an updated vector of weights according to the above equations

    Positional Arguments:
        weights -- a 1-d numpy array of positive floats, corresponding to
            observation weights
        alpha -- a positive float
        y_true -- a 1-d numpy array of true labels, all 0s and 1s
        y_pred -- a 1-d numpy array of labels predicted by the last model;
             all 0s and 1s.

    Example:
        y_true = np.array([1,0,1,1,0])
        y_pred = np.array([0,0,1,1,1])
        weights = np.array([.4,.4,.1,.05,.05])
        alpha = 0.10033534773107562

        print(update_weights(weights, alpha, y_true, y_pred))
        #-->np.array([0.44444444 0.36363636 0.09090909 0.04545455 0.05555556])

    """

    # helper function to convert target of 1's and 0's to 1's and -1's
    def target_for_weight_update(y):
        toRet = y.copy()
        toRet[toRet == 0] = -1
        return toRet

    # convert predictions and actual labels to 1's and -1's
    y = target_for_weight_update(y_true)

    pred = target_for_weight_update(y_pred)
    #print("sol:", y[:10], pred[:10])
    # implement weight update equation
    weights = weights * np.e**(-alpha*y*pred)
    #print("sol:",-alpha*y*pred)
    # normalize weights by dividing by sum of all weights
    weights = weights / sum(weights)

    return weights
```

With the above functions created, the "`simple_adaboost_fit()`" method should work correctly.

`simple_adaboost_fit()` returns a dictionary where the keys are 0 through n-1 where n is the `n_estimators` from the function signature.

The values of the dictionaries are (model, alpha) where `model` is a `DecisionTreeClassifier`, and `alpha` is a float.

Question 9

Creating a Prediction from boosted trees

Our prediction will be:

$$f_{boost}(x_0) = sign(\sum_{t=1}^T\alpha_tf_t(X_0))$$

```
### GRADED
### Code a function called `predict`

### ACCEPT two inputs:
### 1. a 2-d numpy array of x-obervations
### 2. a dictionary that contains classifiers and alphas (described more below and above)

### Combine the models as in the manner described in the equation above
### to create predictions for the observations.
### RETURN a 1-d numpy array of observations (all 0s and 1s)

### YOUR ANSWER BELOW

def predict(X, est_dict):
    """
    Create a np.array list of predictions for all of the observations in x,
    according to the above equation.

    Positional Arguments:
        X -- a 2-d numpy array of X observations. Features in columns,
            observations in rows.
        est_dict -- a dictionary consists of keys 0 through n with tuples as values
            The tuples will be (<mod>, alpha), where alpha is a float, and
            <mod> is a sklearn DecisionTreeClassifier
    Example:

        ### Our example dataset, inspired from lecture
        pts = [[.5, 3,1],[1,2,1],[3,.5,0],[2,3,0],[3,4,1],
         [3.5,2.5,0],[3.6,4.7,1],[4,4.2,1],[4.5,2,0],[4.7,4.5,0]]

        df = pd.DataFrame(pts, columns = ['x','y','classification'])

        ### split out X and labels
        X = df[['x','y']]
        y = df['classification']
        ### Split data in half
        X1 = X.iloc[:len(X.index)//2, :]
        X2 = X.iloc[len(X.index)//2:, :]

        y1 = y[:len(y)//2]
        y2 = y[len(X)//2:]


        ### Fit classifiers to both sets of data, save to dictionary:

        ### Tree-creator helper function
        def simple_tree():
            return DecisionTreeClassifier(criterion = 'entropy', max_depth= 1)

        tree_dict = {}

        tree1 = simple_tree()
        tree1.fit(X1,y1)
        print("threshold:", tree1.tree_.threshold[0], "feature:", tree1.tree_.feature[0])

        ### made up alpha, for example
        alpha1 = .6
        tree_dict[1] = (tree1, alpha1)

        tree2 = simple_tree()
        tree2.fit(X2,y2)
        print("threshold:", tree2.tree_.threshold[0], "feature:" ,tree2.tree_.feature[0])

        ### made up alpha, again.
        alpha2 = .35
        tree_dict[2] = (tree2, alpha2)

        print(predict(X, tree_dict))
        #--> np.array([1., 1., 0., 0., 0., 0., 0., 0., 0., 0.])

        ###############################
        ### For Further Checking of your function:
        ### The sum of predictions from the two models should be:

        # If tree2 splits on feature 1:
        # np.array([ 0.25  0.25 -0.95 -0.95 -0.25 -0.95 -0.25 -0.25 -0.95 -0.25])

        # If tree2 splits on feature 0:
        # np.array([ 0.95  0.95 -0.25 -0.25 -0.25 -0.25 -0.25 -0.25 -0.95 -0.95])
        ###############################

    Assumptions:
        The models in the `est-dict` tuple will return 0s and 1s.
            HOWEVER, the prediction equation depends upon predictions
            of -1s and 1s.
            FINALLY, the returned predictions should be 0s and 1s.
    """

    fin_preds = np.zeros(X.shape[0])
    for k in est_dict:
        preds = est_dict[k][0].predict(X)
        preds[preds<1] = -1
        #print(preds, est_dict[k][1])
        preds = preds *est_dict[k][1]

        fin_preds += preds
        #print(fin_preds)

    fin_preds[fin_preds >= 0 ] = 1
    fin_preds[fin_preds <0] = 0

    return fin_preds
```

Census Data

This assignment will use the `Census Income Data` from the UCI Machine Learning Repository. A thorough description of the data and its features may be accessed either at the link above, or this text file.

In particular, this classification attempts to predict whether or not a particular census respondant has an income of more or less than $50,000.

The Data

```
col_names = [
"age", "workclass", "fnlwgt", "education",
"education-num", "marital-status", "occupation", "relationship",
"race", "sex", "capital-gain", "capital-loss", "hours-per-week",
"native-country", "income"
]

data_path = "../resource/asnlib/publicdata/adult.data"

data = pd.read_csv(data_path, header = None, names = col_names)
data.head()
```

Taking a subset of the data relevant to the prediction problem.

```
cols = ["age", "workclass", "education-num", "occupation", "sex", "hours-per-week", "income"]
data = data[cols]
data.head()
```

A quick look at the data:

```
data.describe(include = 'all')
```

```
plt.figure(figsize=(10,10))
for i, col in enumerate(data.drop("hours-per-week", axis = 1)):
    d = data[col].value_counts().sort_index()
    plt.bar(d.index, d)
    plt.xticks(rotation = 90)
    plt.title(col)
    plt.show()

plt.hist(data['hours-per-week'], bins = 20);
plt.title("Hours Per Week");
```

Question 10

```
### GRADED
### The target variable of income over/under $50k is _________
### 'a') mostly balanced
### 'b') unbalanced
### Assign character associated with your choice as string to ans1
### YOUR ANSWER BELOW

ans1 = 'b'
```

Preprocessing

The follow ing cells demonstrates the functions used in preprocessing, concluding w ith the division of data into a training and testing sets, that are then preprocessed.

Dummy Variables

In the creation of dummy variables, the most frequently occuring class w ill be dropped as a w ay of avoiding multicollinearity.

Thus, for `n` categories, `n-1` features w ill be created. Below demonstrates finding the most frequent category.

```
val_count = data['workclass'].value_counts()
print('All Value Counts:')
print(val_count)

top = val_count[0]
print("\nTop category:", top)
```

Question 11

```
### GRADED
### In the above, the top category is obtained by making a reference
### to the `.index` attribute.
### What would result from instead calling val_count[0]

### 'a') The observed frequency of that top term
### 'b') The result would be the same
### 'c') an error would be thrown: `.iloc[0]` is needed
### Assign the character associated with your choice as a string to ans1

### YOUR ANSWER BELOW
ans1 = 'a'
```

One Hot Encoder

Dummies w ill be created using `sklearn`'s `OneHotEncoder`. The follow ing cell demonstrates fitting and transforming data using the One Hot Encoder.

```
from sklearn.preprocessing import OneHotEncoder

ex_df = pd.DataFrame(
    np.array([['b', 'a', 'c', 'a', 'c',], ["z","y","y","y","z"]]).T,
    columns = ["beg","end"],
    index = range(500,505))

test_df = pd.DataFrame(
    np.array([["c","b"],["y","y"]]).T,
    columns = ["beg","end"],
    index = [56,72])

print("Initial DataFrame:")
print(ex_df)

print("\nTest df")
print(test_df)
```

```
# Instantiate OneHotEncoder
# sparse = False means data will not be stored in sparse matrix
ohe = OneHotEncoder(sparse = False)

# Fitting OHE with the "training" data
ohe.fit(ex_df)

# Transforming the "training" dat
tr_vals = ohe.transform(ex_df)

print("\nTransformed values")
print(tr_vals)

print("\nCategories")
print(ohe.categories_)

# Creating column names from `.categories_`
ohe_cats = np.concatenate(ohe.categories_)

# In creation of new df. Note the use of np.concatenate
final_df = pd.DataFrame(tr_vals, columns = ohe_cats)

print("\nFinal DataFrame")
print(final_df)

# Putting everything together to transform test data
print("\nTransformed test df")
print(pd.DataFrame(ohe.transform(test_df), columns= ohe_cats))
```

Question 12

```
### GRADED
### True or False:
### The OneHotEncoder preserves the index of a DataFrame

### Assign Boolean choice to ans1

### YOUR ANSWER BELOW

ans1 = False
```

LabelEncoder

`sklearn`'s `LabelEncoder` will be used to transform our income variable from strings to 0s and 1s.

Demonstrated below :

```
from sklearn.preprocessing import LabelEncoder

# Create target Series
target_train = pd.Series(np.random.choice(data['income'].unique(), size = 10))
target_test = pd.Series(np.random.choice(data['income'].unique(), size = 5))
print("Target Train Series")
print(target_train)

print("\nTarget Test Series")
print(target_test)
```

```
# Instantiate encoder
le = LabelEncoder()

# Fit with training data
le.fit(target_train)

# Transform training and test data
trans_train = le.transform(target_train)
trans_test = le.transform(target_test)

print("Transformed training values")
print(trans_train)

print("\nTransformed test values")
print(trans_test)

print("\nLabelEncoder `.classes_`")
print(le.classes_)
```

Define a custom preprocessing function

Using the processes demonstrated above, a function is created to preprocess the census data.

The function is then used to create a training and testing dataset

```
def preprocess_census(X_train, X_test, y_train, y_test):

    ### Hardcode variables which need categorical encoding
    to_encode = ["workclass", "occupation", "sex"]

    ### Find top categories in categorical columns
    ### Used for dropping majority class to prevent multi-colinearity
    top_categories = []

    for col in to_encode:
        top_categories.append(X_train[col].value_counts().index[0])

    ### Create and fit one-hot encoder for categoricals
    OHE = OneHotEncoder(sparse = False)
    OHE.fit(X_train[to_encode])

    ## Create and fit Label encoder for target
    LabEnc = LabelEncoder()
    LabEnc.fit(y_train)

    def create_encoded_df(X, to_encode = to_encode, OHE = OHE, top_categories = top_categories):
        # Return columns which need encoding.
        def return_encoded_cols(X, to_encode = to_encode, OHE = OHE, top_categories = top_categories):
            # Use onehotencoder to transform.
            # Use "categories" to name
            toRet = pd.DataFrame(OHE.transform(X[to_encode]), columns = np.concatenate(OHE.categories_))

            # Drop top_categories and return
            return toRet.drop(top_categories, axis = 1)

        # create encoded columns
        ret_cols = return_encoded_cols(X)

        # Drop columns that were encoded
        dr_enc = X.drop(to_encode, axis = 1)

        # Concatenate values
        # use index from original data
        # use combined column names
        return pd.DataFrame(np.concatenate([ret_cols.values, dr_enc.values],axis = 1),
                            index = dr_enc.index,
                            columns = list(ret_cols.columns) + list(dr_enc.columns))


    def encode_target(y, LabEnc = LabEnc):
        # Use label encoder, and supply with original index
        return pd.Series(LabEnc.transform(y), index= y.index)

    return create_encoded_df(X_train), create_encoded_df(X_test), encode_target(y_train), encode_target(y_test)
```

```
from sklearn.model_selection import train_test_split

# Create training and testing sets; preprocess them.
target = data['income']
predictors = data.drop("income", axis = 'columns')

X_train, X_test, y_train, y_test = preprocess_census(*train_test_split(predictors, target, test_size = .2))
```

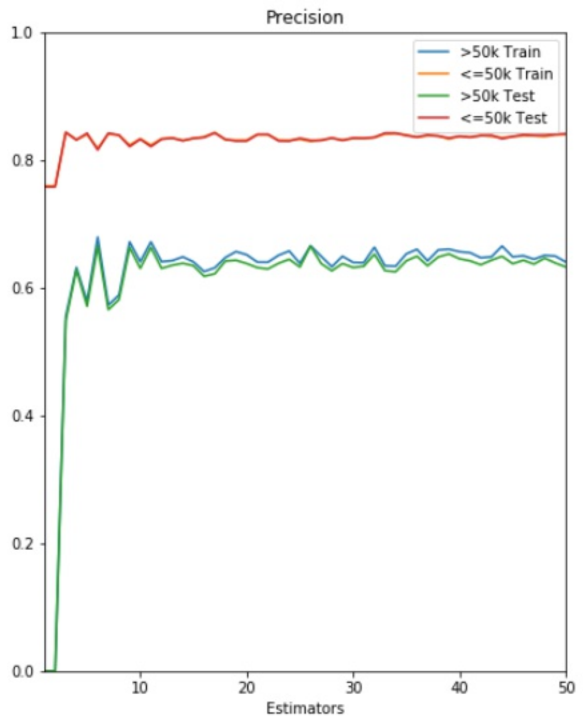
Fitting Models to Data

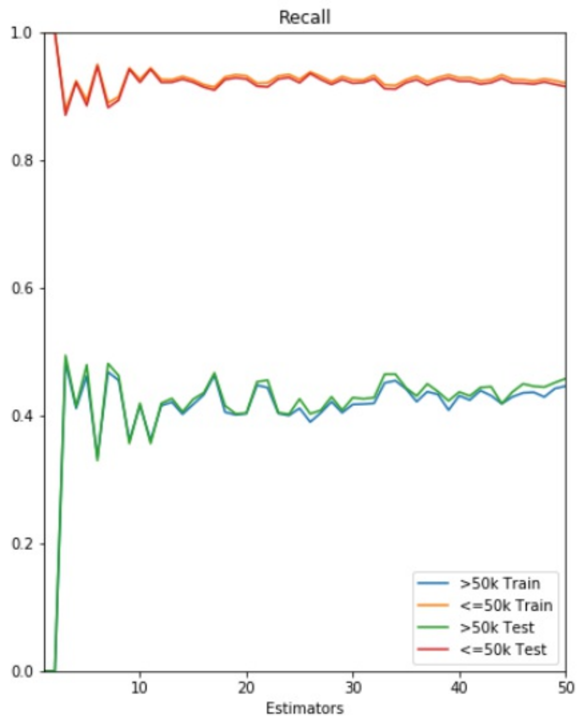
If the above functions are defined correctly, the follow ing cells should w ork; creating predictions from your adaptive-boosted model.

Try playing around w ith the number of estimators

```
from sklearn.metrics import classification_report
d = simple_adaboost_fit(X_train.values.copy(), y_train.values.copy(), 50)
preds = predict_T(X_test, d)
print(classification_report(y_test,preds))
```

This image gives an idea of how the precision and recall on both the training and test set changes as the number of estimators is changed.





`sklearn` Implementation of Adaptive Boosting

```
from sklearn.ensemble import AdaBoostClassifier, RandomForestClassifier

RF = RandomForestClassifier(n_estimators = 50)
RF.fit(X_train, y_train)

print("Random Forest:\n")
print(classification_report(y_test, RF.predict(X_test)))
ABC = AdaBoostClassifier(n_estimators = 50)
ABC.fit(X_train, y_train)
print("\nAdaBoost:\n")
print(classification_report(y_test, ABC.predict(X_test)))
```

You should find that the precision and recall of the your custom Adaptive Boosting are very similar to the `sklearn` adaboost.

Notice the higher precision of the AdaBoost compared to the Random Forest