Q2 DH tq

March 19, 2021

1 Question 2: DH algorithm (50 points)

In this question we are going to implemented the DH algorithm according to this paper:https://icml.cc/Conferences/2008/papers/324.pdf, in which we try to predict protein localization sites in Eukaryotic cells.

```
import copy
import warnings
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from numpy.random import choice
from scipy.cluster.hierarchy import linkage
from sklearn.datasets import make_blobs
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.linear_model import LogisticRegression
seed = 2021
warnings. filterwarnings("ignore")
```

1.1 2.0 Data loading and hierarchical clustering

DH algorithm is based on hierarchical clustering of the dataset, we will use the DH algorithm on this classification problem: Protein Localization Prediction, the first step is to load the dataset and conduct a hierarchical clustring using the **Scipy** package. This part has been implemented, read through the code to make sure you understand what is being done.

```
[2]: def load_data(seed = 2021):
    """ Loads "Protein Localizataion Prediction" data. Computes linkage from
    →hierarchical clustering.
    :returns X_train: data matrix 538x8
    :returns Y_train: true labels 538x1
    :returns X_test: data matrix 135x8
    :returns Y_test: true labels 135x1
    :returns T: 3 element tree
        T[0] = linkage matrix from hierarchical clustering. See https://docs.
    →scipy.org/doc/scipy/reference/generated/scipy.cluster.hierarchy.linkage.html
```

```
for details. If you are unfamiliar with hierarchical clustering \Box
 \rightarrowusing scipy, the following is another helpful resource (We won't use<sub>\square</sub>
 \hookrightarrow dendrograms
                here, but he gives a nice explanation of how to interpret the
 \hookrightarrow linkage matrix):
                https://joernhees.de/bloq/2015/08/26/
 \rightarrow scipy-hierarchical-clustering-and-dendrogram-tutorial/
        T[1] = An array denoting the size of each subtree rooted at node i, \sqcup
 \hookrightarrow where i indexes the array.
                ie. The number of all leaves in subtree rooted at node i (w_i in_\_
 \hookrightarrow the paper).
         T[2] = dict where keys are nodes and values are the node's parent
    df = pd.read_csv('./data/data.csv')
    np.unique(df.Label,return_counts = True)
    filter_class = ['MIT','NUC']
    mask = df.Label ==0
    for x in filter_class:
        mask = mask | (df.Label==x)
    df = df[mask]
    X = df.iloc[:,:8].to_numpy()
    y = df.Label.astype('category').cat.codes.to_numpy()
    X, X_test, y, y_test = train_test_split(X,y,test_size = 0.2, random_state = ___
 ⇒seed)
    n_{samples} = len(X)
    Z = linkage(X,method='ward')
    link = Z[:,:2].astype(int)
    subtree_sizes = np.zeros(link[-1,-1]+2)
    subtree_sizes[:n_samples] = 1
    parent = {}
    parent[2*(n_samples-1)] = -1 #set root node as 0
    for i in range(len(link)):
        left = link[i,0]
        right = link[i,1]
        current = i + n  samples
        subtree_sizes[current] = subtree_sizes[left] + subtree_sizes[right]
        parent[left] = current
        parent[right] = current
    T = [link,subtree_sizes,parent]
    return X.astype("float"), y, X_test, y_test, T
X_train, y_train, X_test, y_test, T = load_data()
```

```
[]: ## Logistic Regression
     lr = LogisticRegression()
     lr.fit(X_train, y_train)
     ## Random Forest
     N_{estimator_rf} = 20
     MAX_depth_rf = 6
     rf = RandomForestClassifier(n_estimators = N_estimator_rf,
                                 max_depth = MAX_depth_rf, random_state = seed)
     rf.fit(X_train, y_train)
     ## Gradient Boosting Decision Tree
     N_{estimator_gbdt} = 20
     gbdt_max_depth = 6
     gbdt = GradientBoostingClassifier(n estimators = N_estimator_gbdt,
                                      learning_rate = 0.1,
                                      max_depth = gbdt_max_depth,
                                      random_state = seed)
     gbdt.fit(X_train,y_train)
     ## 3-Layer fully connected NN
     import torch
     from torch.utils.data import Dataset
     from torch import optim
     from torch.utils.data import DataLoader, TensorDataset
     torch.manual seed(seed)
     class NNClassifier(object):
         def __init__(self,
                      feature_n,
                      class_n,
                      hidden_n = 30,
                      learning_rate = 4e-3,
                      weight_decay = 1e-5):
             self.model = torch.nn.Sequential(torch.nn.Linear(feature_n,hidden_n),
                                             torch.nn.SiLU(),
                                             torch.nn.Linear(hidden_n, hidden_n),
                                             torch.nn.SiLU(),
                                             torch.nn.Linear(hidden_n,class_n))
             self.model =self.model.cuda()
             self.lr = learning_rate
             self.wd = weight_decay
         def fit(self,X_train,y_train,epoches = 300,batch_size = 50):
             X_t = torch.from_numpy(X_train.astype(np.float32))
             y_t = torch.from_numpy(y_train.astype(np.int64))
             dataset = TensorDataset(X_t,y_t)
             loader = DataLoader(dataset,batch_size = batch_size,shuffle = True)
             loss_fn = torch.nn.CrossEntropyLoss(reduction = 'mean').cuda()
```

```
optimizer = optim.Adam(self.model.parameters(), lr=self.
 →lr,weight_decay=self.wd)
        loss_record = 0.0
        report_epoch = 50
        for epoch_i in range(epoches):
            for batch in loader:
                x_batch, y_batch = batch
                x_batch = x_batch.cuda()
                y_batch = y_batch.cuda()
                y_pred = self.model(x_batch)
                loss = loss_fn(y_pred,y_batch)
                self.model.zero_grad()
                loss.backward()
                optimizer.step()
                loss_record += loss.item()
            if epoch_i%report_epoch == report_epoch-1:
                print("[%d|%d] epoch loss:%.2f"%(epoch_i+1,epoches,loss_record/
→report_epoch))
                loss_record = 0.0
            if epoch_i>=epoches:
                break
    def score(self, X_test, y_test):
        X_test_tensor = torch.from_numpy(X_test.astype(np.float32))
        y_pred_test = self.model(X_test_tensor)
        y_output = torch.argmax(y_pred_test,axis = 1).numpy()
        return (y output == y test).mean()
nn = NNClassifier(feature_n = X_train.shape[1],class_n = len(np.
→unique(y_train)))
nn.fit(X_train,y_train)
## Accuracy of 4 classifiers.
print('Accuracy of logistic regression: \t{:.3f}'.format(lr.

¬score(X_test,y_test)))
print('Accuracy of random forest: \t\t{:.3f}'.format(rf.score(X_test,y_test)))
print('Accuracy of Gradient Boosting Decision Tree: \t\t{:.3f}'.format(gbdt.

¬score(X_test,y_test)))
print('Accuracy of Neural Network: \t\t{:.3f}'.format(nn.score(X_test,y_test)))
```

2 2.0.1 Supervised classification methods.

Following we provide several classifiers that can be used, choose your favourite one. To use the Neural Network classifier, you need to install pytorch.

2.0.1 Choose and initialize your classifier:

The classifier is going to be used in 2.2, the choose of classifier won't influence your grade

2.1 Implement the DH algorithm (Hierarchical Sampling for Active Learning). (30 points)

Please complete the functions to implement the DH algorithm and run the active learning algorithm on the training dataset. The utils functions has been implemented and attached in the homework folder, including update_empirical.py, best_pruning_and_labeling.py, assign_labels.py and get_leaves.py, please read them and finish the following functions to implement the DH algorithm.

```
[6]: from update_empirical import update_empirical from best_pruning_and_labeling import best_pruning_and_labeling from assign_labels import assign_labels from get_leaves import get_leaves
```

```
[27]: def compute_error(L,labels):
    """Compute the error

:param L: labeling of leaf nodes
:param labels: true labels of each node

:returns error: error of predictions"""

wrong = 0
wrong = (L[:len(labels)]!=labels).sum()
error = wrong/len(labels)
return error

def select_case_1(data,labels,T,budget,batch_size):
    """DH algorithm where we choose P proportional to the size of subtree_□
→rooted at each node
```

```
:param data: Data matrix 1200x8
   :param labels: true labels 1200x1
   :param T: 3 element tree
       T[0] = linkage matrix from hierarchical clustering. See https://docs.
→scipy.org/doc/scipy/reference/generated/scipy.cluster.hierarchy.linkage.html
               for details. If you are unfamiliar with hierarchical clustering.
\negusing scipy, the following is another helpful resource (We won't use\sqcup
\hookrightarrow dendrograms
               here, but he gives a nice explanation of how to interpret the
\hookrightarrow linkage matrix):
               https://joernhees.de/blog/2015/08/26/
\hookrightarrow scipy-hierarchical-clustering-and-dendrogram-tutorial/
       T[1] = An array denoting the size of each subtree rooted at node i, \sqcup
\rightarrow where i indexes the array.
               ie. The number of all children + grandchildren + \dots + the node_{\sqcup}
\hookrightarrow itself
       T[2] = dict where keys are nodes and values are the node's parent
   :param budget: Number of iterations to make
   :param batch_size: Number of queries per iteration"""
   n nodes = len(T[1]) #total nodes in T
   n_samples = len(data) #total samples in data
   L = np.zeros(n_nodes) #majority label
   p1 = np.zeros(n_nodes) #empirical label frequency (for label 1)
   n = np.zeros(n_nodes) #number of points sampled from each node
   error = [] #np.zeros(n_samples) #error at each round
   root = n nodes-1 #corresponds to index of root
   P = np.array([root])
   L[root] = 1
   for i in range(budget):
       selected_P = []
       for b in range(batch_size):
            #TODO: select a node from P proportional to the size of subtree_
→rooted at each node
            size_p = np.array([len(get_leaves([],v,T,n_samples)) / n_samples_u
→for v in P])
           probs = size_p / sum(size_p)
           select_node_index = np.random.choice(np.arange(len(P)), p=probs)
           select_node = P[select_node_index]
           selected_P.append(select_node)
```

```
##TODO: pick a random leaf node from subtree Tv and query its label
            leafs = get_leaves([],select_node,T,n_samples)
            z = np.random.choice(leafs)
            z_1 = labels[z]
            \#TODO: update empirical counts and probabilities for all nodes u on
\rightarrow path from z to v
            n, p1 = update empirical(n,p1,select node,z,z 1,T)
        for p in selected_P:
            #TODO: update admissible A and compute scores; find best pruning □
\rightarrow and labeling
            P_best, L_best = best_pruning_and_labeling(n,p1,p,T,n_samples)
            #TODO: update pruning P and labeling L
            P = np.array([node_ for node_ in P if node_ != p] + [node_ for_
→node_ in P_best])
            L[p] = L_best
        #TODO: temporarily assign labels to every leaf and compute error
        L_{temp} = L.copy()
        for i in range(len(P)):
            L_temp = assign_labels(L_temp,P[i],P[i],T,n_samples)
        error_i = compute_error(L[:n_samples],labels)
        error.append(error_i)
    for i in range(len(P)):
        L = assign_labels(L,P[i],P[i],T,n_samples)
    return L, np.array(error)
def select_case_2(data,labels,T,budget,batch_size):
    """DH algorithm where we choose P by biasing towards choosing nodes in \Box
→areas where the observed labels are less pure
    :param data: Data matrix 1200x8
    :param labels: true labels 284x1
    :param T: 3 element tree
        T[0] = linkage matrix from hierarchical clustering. See https://docs.
 →scipy.org/doc/scipy/reference/generated/scipy.cluster.hierarchy.linkage.html
               for details. If you are unfamiliar with hierarchical clustering
 \negusing scipy, the following is another helpful resource (We won't use\sqcup
\hookrightarrow dendrograms
               here, but he gives a nice explanation of how to interpret the \sqcup
\hookrightarrow linkage matrix):
```

```
https://joernhees.de/bloq/2015/08/26/
\hookrightarrow scipy-hierarchical-clustering-and-dendrogram-tutorial/
       T[1] = An array denoting the size of each subtree rooted at node i, \sqcup
\rightarrow where i indexes the array.
               ie. The number of all children + grandchildren + ... + the node_{\sqcup}
\hookrightarrow itself
       T[2] = dict where keys are nodes and values are the node's parent
   :param budget: Number of iterations to make
   :param batch_size: Number of queries per iteration"""
   n_nodes = len(T[1]) #total nodes in T
   n_samples = len(data) #total samples in data
   L = np.zeros(n_nodes,dtype = int) #majority label
   p1 = np.zeros(n_nodes) #empirical label frequency
   n = np.zeros(n_nodes) #number of points sampled from each node
   error = [] #np.zeros(n_samples) #error at each round
   root = n_nodes-1 #corresponds to index of root
   P = np.array([root])
   L[root] = 1
   for i in range(budget):
       selected_P = []
       for b in range(batch size):
            #TODO: select a node from P biasing towards choosing nodes in areasu
→where the observed labels are less pure
            size_p = np.array([len(get_leaves([],v,T,n_samples)) / n_samples_u
\rightarrowfor v in P])
           weights = size_p / sum(size_p)
           probs = weights
           for idx, prune in enumerate(P):
                lv = L[prune]
                if lv == 1:
                    pvlv = p1[prune]
                else:
                    pvlv = 1 - p1[prune]
                upper_pvlv = min(1, pvlv - (1 / (1e-12 + n[prune]) + \
                                             np.sqrt((pvlv * (1 - pvlv)) /__
\rightarrow (1e-12 + n[prune])))
                                 )
                probs[idx] = weights[idx] * (1 - upper_pvlv)
           if probs.sum() != 0:
                probs = probs / probs.sum()
```

```
else:
               probs = None
           select_node_index = np.random.choice(np.arange(len(P)), p=probs)
           select_node = P[select_node_index]
           selected_P.append(select_node)
           #TODO: pick a random leaf node from subtree Tv and query its label
           leafs = get_leaves([],select_node,T,n_samples)
           z = np.random.choice(leafs)
           z l = labels[z]
           #TODO: update empirical counts and probabilities for all nodes u on
\rightarrow path from z to v
           n, p1 = update_empirical(n,p1,select_node,z,z_1,T)
       for p in selected P:
           #TODO: update admissible A and compute scores; find best pruning □
\rightarrow and labeling
           P_best, L_best = best_pruning_and_labeling(n,p1,p,T,n_samples)
           #TODO: update pruning P and labeling L
           P = np.array([node_ for node_ in P if node_ != p] + [node_ for_
→node_ in P_best])
           L[p] = L_best
       #TODO: temporarily assign labels to every leaf and compute error
       L temp = L.copy()
       error_i = compute_error(L[:n_samples],labels)
       error.append(error_i)
   for i in range(len(P)):
       L = assign_labels(L,P[i],P[i],T,n_samples)
   return L, np.array(error)
```

2.2 Run the sample code (10 points)

Run the following sample code and compare the two figures.

```
[29]: def call_DH(part,clf,budget):

"""Main function to run all your code once complete. After you complete
select_case_1() and select_case_2(), this will run the DH algo for each
dataset and generate the plots you will submit within your write-up.

:param part: which part of the homework to run
:param clf: The classifier used to predcit on the dataset.
:param budget: The number of times that one can query a label from the

→oracle.

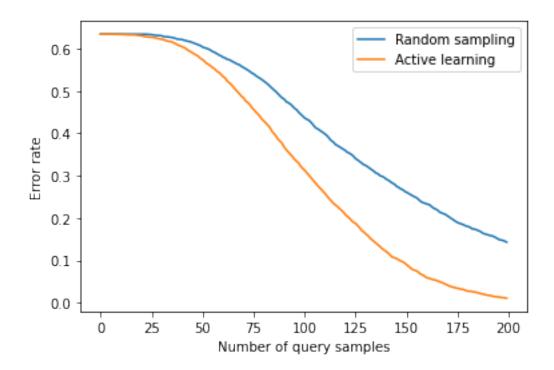
"""
```

```
part = part.lower()
   num_trials = 5
   batch_size = 10
   clf2 = copy.deepcopy(clf)
   axs = plt.subplot()
   if part == "b":
       print("Running part B")
       X_train, y_train, X_test, y_test, T = load_data()
       1 = np.zeros(budget)
       for i in range(num trials):
           print("Currently on iteration {}".format(i))
           L, error = select_case_1(X_train,y_train,T,budget,batch_size)
           1 += error
       1 /= num_trials
       ## TODO: train the classifier clf on the predicted label.
       #raise(NotImplementedError)
       clf.fit(X_train,L[:len(X_train)])
       print('Accuracy of classifier trained on random sampling dataset: \t{:.
→3f}'.format(clf.score(X_test,y_test)))
       axs.plot(np.arange(budget),1,label = "Random sampling")
   elif part == "c":
       print("Running part C")
       X_train, y_train, X_test, y_test, T = load_data()
       1 = np.zeros(budget)
       for i in range(num_trials):
           print("Currently on iteration {}".format(i))
           L, error = select_case_2(X_train,y_train,T,budget,batch_size)
           1 += error
       1 /= num_trials
       ## TODO: train the classifier clf2 on the predicted label.
       #raise(NotImplementedError)
       clf2.fit(X_train,L[:len(X_train)])
       print('Accuracy of classifier trained on active learning dataset: \t{:.
→3f}'.format(clf2.score(X_test,y_test)))
       axs.plot(np.arange(budget),1,label = "Active learning")
   else:
       print("Incorrect part provided. Either 'b', 'c', 'd', or 'e' expected")
   axs.set_xlabel("Number of query samples")
   axs.set_ylabel("Error rate")
   plt.legend()
```

```
plt.savefig("q2_2_bc.png")

BUDGET = 200 #You can change this number to a smaller one during testing.
for part in "bc":
    call_DH(part,classifier,BUDGET)
Running part B
Currently on iteration 0
```

```
Currently on iteration 0
Currently on iteration 1
Currently on iteration 2
Currently on iteration 3
Currently on iteration 4
[50|300] epoch loss:5.32
[100|300] epoch loss:5.18
[150|300] epoch loss:5.07
[200|300] epoch loss:5.00
[250|300] epoch loss:4.95
[300|300] epoch loss:4.90
Accuracy of classifier trained on random sampling dataset:
                                                                0.844
Running part C
Currently on iteration 0
Currently on iteration 1
Currently on iteration 2
Currently on iteration 3
Currently on iteration 4
[50|300] epoch loss:3.96
[100|300] epoch loss:3.76
[150|300] epoch loss:3.71
[200|300] epoch loss:3.64
[250|300] epoch loss:3.55
[300|300] epoch loss:3.49
Accuracy of classifier trained on active learning dataset:
                                                                0.867
```



2.3 Explain

From the figure we can see that the active learning approach can produce better error rate comparing to random sampling, indicating active learning can approximate more accurate lables than random sampling.

Additionally, the active learning also converge faster than random sampling and produce higher accuarcy at the test time.

- 2.4 2.3 Questions (10 points):
- 2.4.1 What is a "admissible pair" according to the paper (5 points)?
- 2.4.2 Please explain the sampling bias that is dealt with in the DH algorithm and why it would be a problem if we just query the unlabeled point which is closest to the decision boundary (5 points)?
- 2.5 1. "Admissible pair"

$$A_{v,l}(t) = True \iff (1 - p_{v,l}^{LB}(t)) < \beta min_{l' \neq l} (1 - p_{v,l'}^{UB}(t))$$

On the left, it means the max error if v is paired with l, and the right represents the min error if v pair with other labels l'. So we consider (v, l) to be admissible, i.e. we are confident abount assigning l to v when even the worst mistake we can make by assigning l to v is better than the best other assignment can produce.

2.6 2. Sampling bias

The initial random sample would be bias so methods that are based on the initial sample to partition the hypothesis space would be biased since some rare case could be overlooked. If we then follow the initial samples to query points around the boundary, then we will only get suboptimal solution and potentially ignore the true decision boundary.

On the other hand, if we incorporate clusters in the data, and query based on the agreement and the size within each cluster, it would avoid overlook any data cluster and hence reduce sampling bias when our budgets are limited.

[]: