# april9 sub

April 9, 2024

```
[]: import torch
import torch.nn as nn
import numpy as np
import matplotlib.pyplot as plt
from sklearn.preprocessing import OneHotEncoder, StandardScaler
import pickle
from torch.utils.data import Dataset, DataLoader
from tqdm import tqdm
import os
from skimage import draw
import pandas as pd
```

### 1 Creating Dataset

### 1.1 Helper Functions

```
[]: # Directories
     csv_dir = "../../DATASET/csv"
     im_dir = "../../DATASET/rgb"
     # Get File Names
     def get_files(dir):
         return [f for f in os.listdir(dir) if os.path.isfile(os.path.join(dir, f))]
     # Get CSV Dataframes
     def get_csv_df(dir, dir_paths, idx):
         path = os.path.join(dir, dir_paths[idx])
         return pd.read_csv(path)
     # Get Image Data
     def get_im_data(dir, dir_paths, idx):
         path = os.path.join(dir, dir_paths[idx])
         return plt.imread(path)
     def crop_img(image, xmin, ymin, xmax, ymax):
         return image[ymin:ymax, xmin:xmax]
```

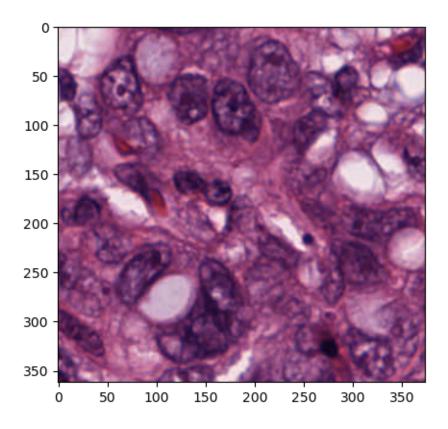
```
def get_xy(csv_df,idx):
   return csv_df[['coords_x', 'xmin', 'xmax', 'ymin', 'ymax', 'coords_y']].
 →iloc[idx].to_dict()
def cell_mask(img, x_cord, y_cord):
   if len(x cord) != len(y cord):
       raise ValueError("Length of x cord and y cord must be equal")
def get_nuc(img, csv, xshape, yshape, x_window = [70,100], y_window = [70,100]):
   num_nuc = len(csv)
   nucs_list = []
   for i in range(num_nuc):
       nuc = get_xy(csv, i)
       x_range = nuc['xmax'] - nuc['xmin']
       y_range = nuc['ymax'] - nuc['ymin']
       if (x_range < x_window[0] or x_range > x_window[1]) and (y_range <__
 continue
       x = np.array(nuc['coords_x'].split(",")).astype(int)
       y = np.array(nuc['coords_y'].split(",")).astype(int)
       im_h, im_w, im_c = img.shape
       mask = np.zeros((im_h, im_w, im_c), dtype=np.uint8)
       rr, cc = draw.polygon(y, x)
       try:
           mask[rr, cc,:] = 1
       except IndexError:
           continue
       del_back = np.multiply(mask, img)
       cropped_nuc = crop_img(del_back, nuc['xmin'], nuc['ymin'], nuc['xmax'],__

¬nuc['ymax'])
       blank_mask = np.zeros((xshape, yshape, 3))
       center_height = (blank_mask.shape[0] - cropped_nuc.shape[0]) // 2
       center_width = (blank_mask.shape[1] - cropped_nuc.shape[1]) // 2
       try:
           blank_mask[center_height:center_height + cropped_nuc.shape[0],__
 scenter_width:center_width + cropped_nuc.shape[1], :] = cropped_nuc
       except:
           continue
       nucs_list.append(blank_mask)
   return nucs_list
```

### 1.2 Get image

```
[]: csv_files = get_files(csv_dir)
   im_files = get_files(im_dir)
   im_files = get_files(im_dir)
   img_array = get_im_data(im_dir, im_files, 0)
   print(img_array.shape)
   plt.imshow(img_array)
   plt.show()
```

(362, 374, 3)



### 1.3 Boundary Regions from CSV files

```
[]: csv_df = get_csv_df(csv_dir, csv_files, 0)
csv_df
```

```
{\tt Unnamed: \ 0 \ raw\_classification \ main\_classification \ super\_classification \ \setminus \ number \ and \ number \ 
[]:
                                                                                                                                                                                                                                                                                           lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sTIL
                                                    1
                                                                                                                                                                                   1
                                                                                                                                                                                                                                                                                                                                                   tumor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor_any
                                                    2
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                                                    3
                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                   tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor_nonMitotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor_any
```

```
4
             4
                   apoptotic_body
                                                AMBIGUOUS
                                                                       AMBIGUOUS
5
             5
                        fibroblast
                                     nonTILnonMQ_stromal
                                                                 nonTIL_stromal
6
             6
                        lymphocyte
                                               lymphocyte
                                                                            sTIL
7
             7
                                                                       AMBIGUOUS
                         unlabeled
                                                AMBIGUOUS
             8
                         unlabeled
                                                AMBIGUOUS
                                                                       AMBIGUOUS
              xmin
                    ymin xmax
                                 ymax
       type
   polyline
0
                29
                      106
                             55
                                   135
  polyline
                      225
                                   280
               104
                            152
  polyline
                 0
                      278
                             72
                                   317
  polyline
                      237
3
                48
                             99
                                   296
4 polyline
               100
                      104
                            138
                                   136
5 polyline
               100
                      47
                            135
                                    88
6 polyline
               127
                      147
                            155
                                   180
7
  polyline
                            190
               163
                      285
                                   322
8 polyline
               258
                      289
                            280
                                   338
                                                coords_x \
0
                            47,29,35,45,53,55,53,51,47
   106,104,106,114,116,120,132,135,138,141,143,15...
1
2 0,0,5,8,20,27,46,51,55,69,71,72,71,67,64,56,37...
3 97,92,73,56,53,50,48,48,50,55,61,73,80,89,90,9...
4 138,137,132,126,124,101,100,100,104,113,125,13...
5 135,134,127,125,113,105,101,100,100,101,113,12...
6 148, 145, 138, 131, 129, 127, 127, 132, 140, 145, 150, 15...
7
   190,190,187,183,182,174,171,168,167,163,168,18...
         280,277,267,261,258,258,261,263,269,272,280
                                                coords_y
0
                  133, 106, 106, 109, 117, 123, 131, 135, 133
   269, 259, 251, 228, 226, 225, 225, 226, 228, 231, 236, 25...
1
2
   301,295,286,284,279,278,278,279,280,289,293,29...
   278, 296, 293, 280, 278, 272, 265, 263, 257, 241, 237, 23...
3
4
  121,131,136,136,135,121,116,112,107,104,104,10...
5
            84,88,88,86,77,68,62,59,51,47,51,64,77,84
  178, 180, 179, 175, 168, 162, 157, 152, 147, 148, 153, 15...
7
   293,297,310,321,322,322,321,320,314,291,285,28...
8
         297,338,332,317,309,300,293,289,289,290,297
```

### 1.4 Match Files with Corresponding Images

```
[]: matching_files = []
for csv in csv_files:
    for im in im_files:
        csv_d = os.path.splitext(csv)[0]
        im_d = os.path.splitext(im)[0]
        if csv_d == im_d:
```

```
matching_files.append((csv,im))
print("Number of matching files =", len(matching_files))
matching_files[0]
```

Number of matching files = 1337

### 1.5 Create Pickle Array

```
[]: csv_dir = "../../DATASET/csv"
     im_dir = "../../DATASET/rgb"
     csv_files = get_files(csv_dir)
     im_files = get_files(im_dir)
     im_save_dir = "../../DATASET/nuc"
     class_map = {'raw_classification':0, "main_classification":1,__
     ⇔'super_classification':2}
     org_class = class_map['super_classification']
     pickle array = []
     final_df = pd.DataFrame(columns=["file_name", 'raw_classification',_

¬"main_classification", 'super_classification'])
     iters = 0
     stop = 100
     for i, files in enumerate(matching files):
         csv_path = os.path.join(csv_dir, files[0])
         csv_df = pd.read_csv(csv_path)
         im_path = os.path.join(im_dir, files[1])
         img = plt.imread(im path)
         try:
             nucs = get_nuc(img, csv_df, xshape = 80, yshape = 80, x_window =__
      \hookrightarrow [25,75], y_window = [25,75])
         except IndexError:
             print(files)
             continue
         for j, nuc in enumerate(nucs):
             label_df = csv_df[['raw_classification', "main_classification", "
      ⇔'super_classification']].iloc[j]
             label = label_df.to_numpy()
```

```
if 'unlabeled' not in label and 'AMBIGUOUS' not in label and np.

omean(nuc) > 0:
    im_name = f"im_{iters}.png"
    pickle_lst = [nuc.transpose(2,0,1), label]
    pickle_array.append(pickle_lst)

len(pickle_array)
```

[]: 28130

#### 1.6 Create Dataset

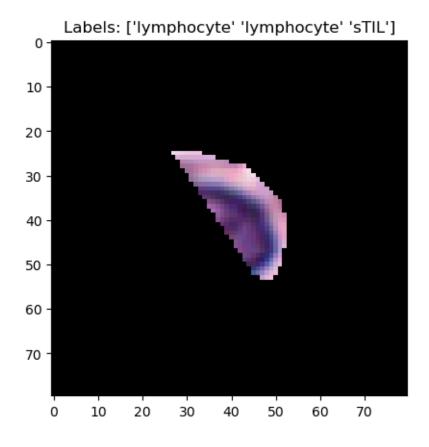
```
[]: pickle_path = os.path.join(im_save_dir, 'nuc_data.pkl')
with open(pickle_path, 'wb') as f:
    pickle.dump(pickle_array, f)
```

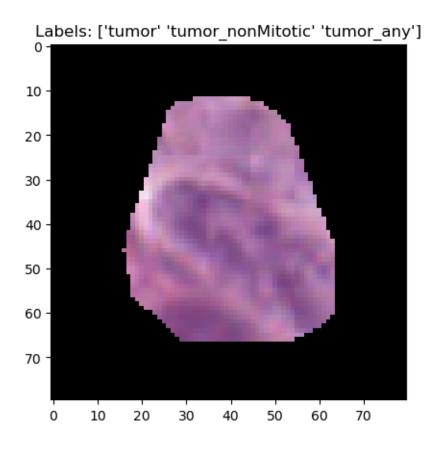
#### 1.7 Pickle Loader

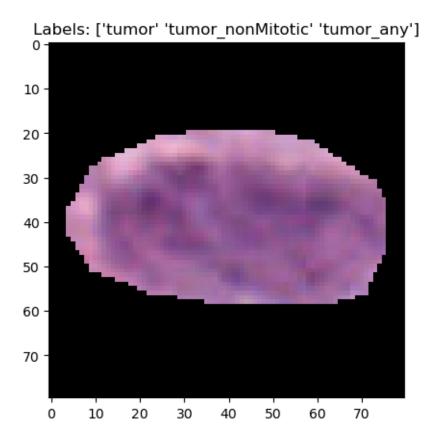
```
[]: def load_dataset(path):
    with open(path, 'rb') as f:
        data = pickle.load(f)
    return data
im_save_dir = "../../DATASET/nuc"
pickle_path = os.path.join(im_save_dir, 'nuc_data.pkl')
data = load_dataset(pickle_path)
```

## 2 Show Images and Labels

```
[]: for i in range(3):
    plt.title(f"Labels: {data[i][1]}")
    plt.imshow(data[i][0].transpose(1,2,0))
    plt.show()
```







### 3 Dataset Class

```
[]: class NuCLSDataset(Dataset):
         def __init__(self, X, y, mode='CNN', bkgd='black'):
             super().__init__()
             self.bkgd = bkgd
             padded_X = X
             if self.bkgd == 'black':
                 self.X = padded_X # just pad the input X's with black to the right_
      \rightarrow dimension
                 # print(f'Shape of padded X: {self.X.shape}')
             else: # change black pixels to average value fo pixels in the cropped ⊔
      ⇒image
                 for i in range(padded_X.shape[0]):
                     im = padded_X[i].transpose(1,2,0)
                     non_black_pixels = im[im.sum(axis=2) > 0]
                     average_color = np.mean(non_black_pixels, axis=0)
                     mask = np.all(im == [0, 0, 0], axis=-1)
                     im[mask] = average_color.astype(float)
                     padded_X[i] = im.transpose(2,0,1)
```

```
self.X = padded_X

self.X = torch.tensor(self.X, dtype=torch.float)
self.y = torch.tensor(y, dtype=torch.float)
self.mode = mode

def __len__(self):
    return len(self.y)

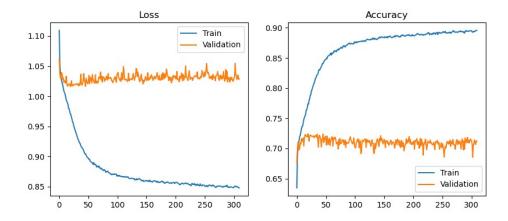
def __getitem__(self, idx):
    if self.mode == 'CNN':
        return self.X[idx], self.y[idx] # CNN returns index, for logreguereturns flttened image
else:
    return self.X[idx].reshape(-1), self.y[idx]
```

### 4 Basic CNN network

```
[]: class Cell_CNN(nn.Module):
         def __init__(self, num_classes=4):
             super().__init__()
             # conv
             self.conv1 = nn.Conv2d(3,100, kernel_size=5, stride=1)
             self.conv2 = nn.Conv2d(100,200, kernel_size=5, stride = 2, padding=1)
             self.conv3 = nn.Conv2d(200,300, kernel_size=5, stride = 2, padding=1)
             # pool
             self.pool1 = nn.MaxPool2d(kernel_size=3, stride=2)
             self.pool2 = nn.MaxPool2d(kernel_size=3, stride=2)
             self.pool3 = nn.MaxPool2d(kernel_size=3, stride=2)
             # activation function
             self.relu = nn.ReLU()
             self.softmax = nn.Softmax(dim=-1)
             # dropout layer
             self.dropout = nn.Dropout(0.8)
             # batch normalization
             self.bn1 = nn.BatchNorm2d(100)
             self.bn2 = nn.BatchNorm2d(200)
             self.bn3 = nn.BatchNorm2d(300)
             # flatten
```

```
self.flatten = nn.Flatten()
        # fully connected layer
        fcconst = 300
        self.fc1 = nn.Linear(fcconst, fcconst)
        self.fc2 = nn.Linear(fcconst, num_classes)
   def forward(self, x):
        x = self.relu(self.bn1(self.conv1(x)))
        x = self.pool1(x)
       x = self.relu(self.bn2(self.conv2(x)))
       x = self.pool2(x)
       x = self.relu(self.bn3(self.conv3(x)))
       x = self.pool3(x)
        x = self.flatten(x)
        x = self.fc1(x)
        x = self.relu(x)
        x = self.dropout(x)
        x = self.fc2(x)
       x = self.softmax(x)
                 # do not apply softmax
       return x
# model = Cell_CNN()
```

## 5 First Results from Training a Basic CNN structure



### 6 Densenet

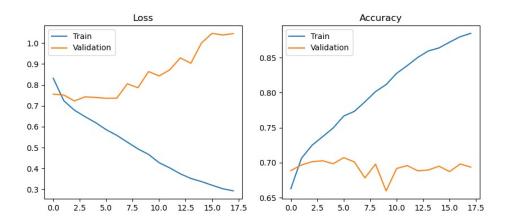
```
[]: from torchvision import models
class DenseNet(nn.Module):
    def __init__(self, num_classes=4):
```

```
super(DenseNet, self).__init__()
self.densenet = models.densenet121(pretrained=False)

num_features = self.densenet.classifier.in_features
self.densenet.classifier = nn.Linear(num_features, num_classes)

def forward(self, x):
    x = self.densenet(x)
    return x
# densenet = DenseNet()
```

# 7 First Results form PyTorch Default Class of DenseNet before our implementation



### 8 Trainer Class

```
class Trainer:

def __init__(self, model, opt_method, learning_rate, batch_size, epoch, 12):
    self.device = (
        "cuda"
        if torch.cuda.is_available()
        else "mps"
        if torch.backends.mps.is_available()
        else "cpu")
    self.model = model.to(self.device)

if opt_method == "adam":
        self.optimizer = torch.optim.Adam(model.parameters(),__
        elearning_rate, weight_decay=12)
        else:
```

```
raise NotImplementedError("This optimization is not supported")
      self.epoch = epoch
      self.batch_size = batch_size
  def train(self, train_data, val_data, early_stop=True, verbose=True, u
→draw_curve=True):
      train_loader = DataLoader(train_data, batch_size=self.batch_size,_
⇔shuffle=True)
      train_loss_list, train_acc_list = [], []
      val_loss_list, val_acc_list = [], []
      weights = self.model.state_dict()
      lowest_val_loss = np.inf
      loss_func = nn.CrossEntropyLoss()
      for n in tqdm(range(self.epoch), leave=False):
           self.model.train()
           epoch_loss, epoch_acc = 0.0, 0.0
           for X_batch, y_batch in train_loader:
               X_batch, y_batch = X_batch.to(self.device), y_batch.to(self.
⊸device)
               batch_importance = y_batch.shape[0] / len(train_data)
               y pred = self.model(X batch)
               batch_loss = loss_func(y_pred, y_batch)
               self.optimizer.zero_grad()
               batch loss.backward()
               self.optimizer.step()
               epoch_loss += batch_loss.detach().cpu().item() *__
⇒batch_importance
               batch_acc = torch.sum(torch.argmax(y_pred, axis=-1) == torch.
→argmax(y_batch, axis=-1)) / y_batch.shape[0]
               epoch_acc += batch_acc.detach().cpu().item() * batch_importance
           train_loss_list.append(epoch_loss)
           train_acc_list.append(epoch_acc)
           val_loss, val_acc = self.evaluate(val_data)
           val_loss_list.append(val_loss)
           val_acc_list.append(val_acc)
           if early_stop:
               if val_loss < lowest_val_loss:</pre>
                   lowest_val_loss = val_loss
                   weights = self.model.state_dict()
      if draw_curve:
           x_axis = np.arange(self.epoch)
```

```
fig, axes = plt.subplots(1, 2, figsize=(10, 4))
          axes[0].plot(x_axis, train_loss_list, label="Train")
          axes[0].plot(x_axis, val_loss_list, label="Validation")
          axes[0].set_title("Loss")
          axes[0].legend()
          axes[1].plot(x_axis, train_acc_list, label='Train')
          axes[1].plot(x_axis, val_acc_list, label='Validation')
          axes[1].set_title("Accuracy")
          axes[1].legend()
      if early stop:
          self.model.load_state_dict(weights)
      return {
          "train_loss_list": train_loss_list,
          "train_acc_list": train_acc_list,
          "val_loss_list": val_loss_list,
          "val_acc_list": val_acc_list,
      }
  def evaluate(self, data, print_acc=False):
      self.model.eval()
      loader = DataLoader(data, batch_size=self.batch_size, shuffle=True)
      loss func = nn.CrossEntropyLoss()
      acc, loss = 0.0, 0.0
      for X batch, y batch in loader:
          with torch.no_grad():
              X_batch, y_batch = X_batch.to(self.device), y_batch.to(self.
→device)
              batch_importance = y_batch.shape[0] / len(data)
              y_pred = self.model(X_batch)
              batch_loss = loss_func(y_pred, y_batch)
              batch_acc = torch.sum(torch.argmax(y_pred, axis=-1) == torch.
→argmax(y_batch, axis=-1)) / y_batch.shape[0]
              acc += batch_acc.detach().cpu().item() * batch_importance
              loss += batch_loss.detach().cpu().item() * batch_importance
      if print_acc:
          print(f"Accuracy: {acc:.3f}")
      return loss, acc
```

### 9 Load Dataset

```
encoder = OneHotEncoder()
y = encoder.fit_transform(y.reshape(-1,1)).toarray()
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, shuffle=True)

train_data = NuCLSDataset(X=X_train, y=y_train, mode='CNN', bkgd='avg')
test_data = NuCLSDataset(X=X_test, y=y_test, mode='CNN', bkgd='avg')
X.shape, y.shape
```

[]: ((28130, 3, 80, 80), (28130, 4))

### 10 Train Networks

```
[]: # dense_raw = DenseNet(num_classes=4)
# basic_cnn = Cell_CNN(num_classes=4)
# trainer = Trainer(dense_raw, "adam", 1e-4, 128, 2, 1e-5)
# trainer.train(train_data, test_data)
```

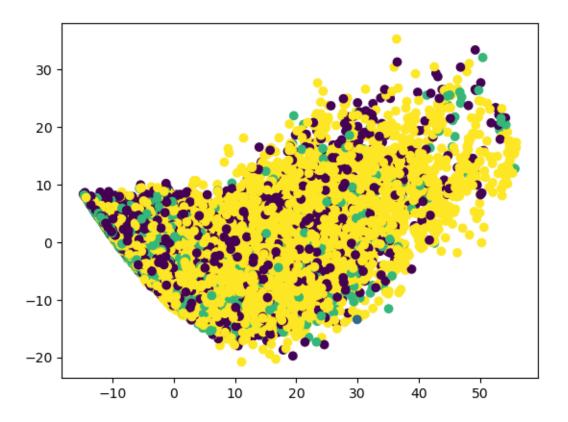
# 11 PCA and K Means Clustering

```
[]: X = np.array([data[i][0] for i in range(len(data))])
y = np.array([data[i][1][2] for i in range(len(data))])
print(X)
print(y)
```

```
[]: from sklearn.decomposition import PCA
  pca = PCA(n_components=0.95)
  X_pca = pca.fit_transform(X.reshape(-1, 80*80*3))
  print(X_pca)
```

### 11.1 PCA True Labels

```
[]: pc1 = X_pca[:,0]
pc2 = X_pca[:,1]
y_encoded = encoder.fit_transform(y.reshape(-1,1)).toarray()
y_labels = np.argmax(y_encoded, axis=-1)
plt.scatter(pc1, pc2, c=y_labels)
plt.show()
```



```
[]: from sklearn.cluster import KMeans
num_clusters = 4

kmeans = KMeans(n_clusters=num_clusters)
kmeans.fit(X_pca)

labels = kmeans.labels_
[]: y_train_true_labs = y
```

0.3680412371134021

## 11.2 K-Means Clustered

[]: plt.scatter(pc1, pc2, c=labels)

[]: <matplotlib.collections.PathCollection at 0x17708de10>

