

ML/DL

Code Review ML & DL

Chayanat Sangsawang 6110742035
Atdhasiri Sangchan 6110742084
Jirath Arnamnath 6110742175

01



01

Machine Learning

Overview

Feature Extraction
Machine Learning

augmentation

```
def augment(image):  
    image = tf.image.random_brightness(image, 0.1)  
    image = tf.image.random_contrast(image, 0.7, 1.3)  
  
    image = tf.image.random_hue(image, 0.005)  
    image = tf.image.random_saturation(image, 0.8, 1.3)  
  
    image = tf.image.adjust_gamma(image, 1)  
    image = tf.image.random_flip_left_right(image)  
    image = tf.image.random_flip_up_down(image)  
    return image
```

Feature Extraction

Picture preparation and Applying CLAHE

We need to convert pictures into size 256*256 and then apply CLAHE to every single picture and you can save it in temp file if you need to or just receive *bgr*

```
31 """**CLAHE**"""
32
33 def prepicture(bgr):
34     bgr = cv2.resize(bgr, (256, 256))
35     lab = cv2.cvtColor(bgr, cv2.COLOR_BGR2LAB)
36     lab_planes = cv2.split(lab)
37     clahe = cv2.createCLAHE(clipLimit=2.0, tileGridSize=(8,8))
38     lab_planes[0] = clahe.apply(lab_planes[0])
39     lab = cv2.merge(lab_planes)
40     bgr = cv2.cvtColor(lab, cv2.COLOR_LAB2BGR)
41     #save image to temp file
42     #cv2.imwrite('/content/drive/MyDrive/Dataset/temp/clahe-output.jpg', bgr)
43     return bgr
44
```

Feature Extraction

First order statistical(FoS)

We create fos by calculating the mean,std and so on.
Before using FoS you should use Greyscale for your image first

```
384 def fos(image):
385     ans = []
386     mean = np.mean(image)
387     ans.append(mean)
388     std = np.std(image)
389     ans.append(std)
390     var = np.var(image)
391     ans.append(var)
392     kurt = kurtosis(image, axis=None, fisher=True, bias=True)
393     ans.append(kurt)
394     sk = skew(image,axis=None)
395     ans.append(sk)
396     ent = entropy(image,axis=None)
397     ans.append(ent)
398     return ans
```

Feature Extraction

Cup and disc segmentation

We can segment the cup and disc using *cv2.split()* to split the picture into 3 colors (Abo - Blue , Ago-Green , Aro - Red) and we use Red for calculating treshold for disc and Green for calcualting treshold for cup then we creating Filter and histogram to plot graph if you want to see the result in histogram format

```
49 def segment_cd(image,plotHis,plotPic):
50     #PRE-PROCESSING AND SMOOTHING
51
52     Abo,Ago,Aro = cv2.split(image)  #splitting into 3 colors
53
54
55     Ar = Aro - Aro.mean()           #Preprocessing Red
56     Ar = Ar - Ar.mean() - Aro.std() #Preprocessing Red
57     Ar = Ar - Ar.mean() - Aro.std() #Preprocessing Red
58
59     Mr = Ar.mean()                  #Mean of preprocessed red
60     SDr = Ar.std()                   #SD of preprocessed red
61     Thr = 49.5 - 12 - Ar.std()       #OD Threshold
62
63
64     Ag = Ago - Ago.mean()           #Preprocessing Green
65     Ag = Ag - Ag.mean() - Ago.std() #Preprocessing Green
66
67     Mg = Ag.mean()                  #Mean of preprocessed green
68     SDg = Ag.std()                   #SD of preprocessed green
69     Thg = Ag.mean() + 2*Ag.std() + 49.5 + 12 #OC Threshold
70
71     filter = signal.gaussian(99, std=6) #Gaussian Window
72     filter=filter/sum(filter)
73
74     hist,bins = np.histogram(Ag.ravel(),256,[0,256])  #Histogram of preprocessed green channel
75     histr,binsr = np.histogram(Ar.ravel(),256,[0,256]) #Histogram of preprocessed red channel
76
77     smooth_hist_g=np.convolve(filter,hist)  #Histogram Smoothing Green
78     smooth_hist_r=np.convolve(filter,histr) #Histogram Smoothing Red
79
```

Feature Extraction

Plot histogram

this *plotHis* was set in *segment_cd()* 's parameter and if it's true it will plot you some graphs

```
80 if plotHis:
81     plt.subplot(2, 2, 1)
82     plt.plot(hist)
83     plt.title("Preprocessed Green Channel")
84
85     plt.subplot(2, 2, 2)
86     plt.plot(smooth_hist_g)
87     plt.title("Smoothed Histogram Green Channel")
88
89     plt.subplot(2, 2, 3)
90     plt.plot(histr)
91     plt.title("Preprocessed Red Channel")
92
93     plt.subplot(2, 2, 4)
94     plt.plot(smooth_hist_r)
95     plt.title("Smoothed Histogram Red Channel")
96
97     plt.show()
```

Feature Extraction

Applying Treshold and plot picture

First, it will create zero array(0 = black color) with the same size as the picture and check every pixel of the original picture and compare to it's threshold if that pixel has more value that it's threshold it will plot the zero array in the same location as white color (255 = white color) and if it lower it will plot zero. Do this with cup aswell.

and plotPic was set in *segment_cd()* 's parameter aswell so if it's true it will plot you the picture of segmented cup and disc

```
101 r,c = Ag.shape
102 Dd = np.zeros(shape=(r,c))
103 Dc = np.zeros(shape=(r,c))
104
105 for i in range(1,r):
106     for j in range(1,c):
107         if Ar[i,j]>Thr:
108             Dd[i,j]=255
109         else:
110             Dd[i,j]=0
111
112 for i in range(1,r):
113     for j in range(1,c):
114         if Ag[i,j]>Thg:
115             Dc[i,j]=1
116         else:
117             Dc[i,j]=0
118
119 #DISPLAYING SEGMENTED OPTIC DISK AND CUP
120 if plotPic:
121     plt.imshow(Dd, cmap = 'gray', interpolation = 'bicubic')
122     plt.axis("off")
123     plt.title("Optic Disk")
124     plt.show()
125
126     plt.imshow(Dc, cmap = 'gray', interpolation = 'bicubic')
127     plt.axis("off")
128     plt.title("Optic Cup")
129     plt.show()
130
```


Feature Extraction

Calculate cup-to-disc Ratio

Recieve to picture form *segment_cd()* and create clahe to apply with *morphologyEX()* to draw outline of the cup and disc and create contours out of cup's threshold and create ellipse to cover the area of cup and then use *cv2.boundingReact()* to get the final size of ellipse and then get max width and height to get *cup_diameter*

```
138 def cdr(cup,disc,plot):
139
140     clahe = cv2.createCLAHE(clipLimit=2.0, tileGridSize=(10,10))
141     #morphological closing and opening operations
142     R1 = cv2.morphologyEx(cup, cv2.MORPH_CLOSE, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(2,2)), iterations = 1)
143     r1 = cv2.morphologyEx(R1, cv2.MORPH_OPEN, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(7,7)), iterations = 1)
144     R2 = cv2.morphologyEx(r1, cv2.MORPH_CLOSE, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(1,21)), iterations = 1)
145     r2 = cv2.morphologyEx(R2, cv2.MORPH_OPEN, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(21,1)), iterations = 1)
146     R3 = cv2.morphologyEx(r2, cv2.MORPH_CLOSE, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(33,33)), iterations = 1)
147     r3 = cv2.morphologyEx(R3, cv2.MORPH_OPEN, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(43,43)), iterations = 1)
148
149     img = clahe.apply(r3)
150
151
152     ret,thresh = cv2.threshold(cup,127,255,0)
153     contours,hierarchy = cv2.findContours(thresh, cv2.RETR_EXTERNAL,cv2.CHAIN_APPROX_SIMPLE) #Get
154     cup_diameter = 0
155     largest_area = 0
156     el_cup = contours[0]
157     if len(contours) != 0:
158         for i in range(len(contours)):
159             if len(contours[i]) >= 5:
160                 area = cv2.contourArea(contours[i]) #Getting the contour with the largest area
161                 if (area>largest_area):
162                     largest_area=area
163                     index = i
164                     el_cup = cv2.fitEllipse(contours[i])
165
166     cv2.ellipse(img,el_cup,(140,60,150),3) #fitting ellipse with the largest area
167     x,y,w,h = cv2.boundingRect(contours[index]) #fitting a rectangle on the ellipse to get the length of major axis
168     cup_diameter = max(w,h) #major axis is the diameter
```

https://github.com/Atdhasiri/machineLearning/blob/main/ML/final_feature_extraction.py#L138-L168

Feature Extraction

```
170 #morphological closing and opening operations
171 R1 = cv2.morphologyEx(disc, cv2.MORPH_CLOSE, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(2,2)), iterations = 1)
172 r1 = cv2.morphologyEx(R1, cv2.MORPH_OPEN, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(7,7)), iterations = 1)
173 R2 = cv2.morphologyEx(r1, cv2.MORPH_CLOSE, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(1,21)), iterations = 1)
174 r2 = cv2.morphologyEx(R2, cv2.MORPH_OPEN, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(21,1)), iterations = 1)
175 R3 = cv2.morphologyEx(r2, cv2.MORPH_CLOSE, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(33,33)), iterations = 1)
176 r3 = cv2.morphologyEx(R3, cv2.MORPH_OPEN, cv2.getStructuringElement(cv2.MORPH_ELLIPSE,(43,43)), iterations = 1)
177
178 img2 = clahe.apply(r3)
179
180 ret,thresh = cv2.threshold(disc,127,255,0)
181 contours,hierarchy = cv2.findContours(thresh, cv2.RETR_EXTERNAL,cv2.CHAIN_APPROX_SIMPLE) #Getting all possible contours in the segmented image
182 disk_diameter = 0
183 largest_area = 0
184 el_disc = el_cup
185 if len(contours) != 0:
186     for i in range(len(contours)):
187         if len(contours[i]) >= 5:
188             area = cv2.contourArea(contours[i]) #Getting the contour with the largest area
189             if (area>largest_area):
190                 largest_area=area
191                 index = i
192                 el_disc = cv2.fitEllipse(contours[i])
193
194 cv2.ellipse(img2,el_disc,(140,60,150),3) #fitting ellipse with the largest area
195 x,y,w,h = cv2.boundingRect(contours[index]) #fitting a rectangle on the ellipse to get the length of major axis
196 disk_diameter = max(w,h) #major axis is the diameter
```

Calculate disk_diameter

Do the same thing as *cup_diameter*

Feature Extraction

Calculate MA

MA is one of the feature that can detect diabetic by checking swelling in the wall of a blood vessel
First, it will adjust gamma of the picture and calculate the microaneurysm and return the numpy of the result

```
219 def adjust_gamma(image, gamma=1.0):
220
221
222     table = np.array([((i / 255.0) ** gamma) * 255
223         for i in np.arange(0, 256)]).astype("uint8")
224
225     return cv2.LUT(image, table)
226 def extract_ma(image):
227     r,g,b=cv2.split(image)
228     comp=255-g
229     clahe = cv2.createCLAHE(clipLimit=5.0, tileGridSize=(8,8))
230     histe=clahe.apply(comp)
231     adjustImage = adjust_gamma(histe,gamma=3)
232     comp = 255-adjustImage
233     J = adjust_gamma(comp,gamma=4)
234     J = 255-J
235     J = adjust_gamma(J,gamma=4)
236
237     K=np.ones((11,11),np.float32)
238     L = cv2.filter2D(J,-1,K)
239
240     ret3,thresh2 = cv2.threshold(L,125,255,cv2.THRESH_BINARY|cv2.THRESH_OTSU)
241     kernel2=np.ones((9,9),np.uint8)
242     tophat = cv2.morphologyEx(thresh2, cv2.MORPH_TOPHAT, kernel2)
243     kernel3=np.ones((7,7),np.uint8)
244     opening = cv2.morphologyEx(tophat, cv2.MORPH_OPEN, kernel3)
245     return opening
```

Feature Extraction

```
249 def fast_glcm(img, vmin=0, vmax=255, nbit=8, kernel_size=5):
250     mi, ma = vmin, vmax
251     ks = kernel_size
252     h,w = img.shape
253
254     # digitize
255     bins = np.linspace(mi, ma+1, nbit+1)
256     gl1 = np.digitize(img, bins) - 1
257     gl2 = np.append(gl1[:,1:], gl1[:, -1:], axis=1)
258
259     # make glcm
260     glcm = np.zeros((nbit, nbit, h, w), dtype=np.uint8)
261     for i in range(nbit):
262         for j in range(nbit):
263             mask = ((gl1==i) & (gl2==j))
264             glcm[i,j, mask] = 1
265
266     kernel = np.ones((ks, ks), dtype=np.uint8)
267     for i in range(nbit):
268         for j in range(nbit):
269             glcm[i,j] = cv2.filter2D(glcm[i,j], -1, kernel)
270
271     glcm = glcm.astype(np.float32)
272     return glcm
```

Calculate GLCM

This function will create GLCM but first you need to change your picture into greyscale before using *fast_glcm()* and it will return numpy array as a result

Feature Extraction

```
275 def fast_glcmm_mean(img, vmin=0, vmax=255, nbit=8, ks=5):
276     '''
277     calc glcm mean
278     '''
279     h,w = img.shape
280     glcm = fast_glcmm(img, vmin, vmax, nbit, ks)
281     mean = np.zeros((h,w), dtype=np.float32)
282     for i in range(nbit):
283         for j in range(nbit):
284             mean += glcm[i,j] * i / (nbit)**2
285
286     return mean
287
288
289 def fast_glcmm_std(img, vmin=0, vmax=255, nbit=8, ks=5):
290     '''
291     calc glcm std
292     '''
293     h,w = img.shape
294     glcm = fast_glcmm(img, vmin, vmax, nbit, ks)
295     mean = np.zeros((h,w), dtype=np.float32)
296     for i in range(nbit):
297         for j in range(nbit):
298             mean += glcm[i,j] * i / (nbit)**2
299
300     std2 = np.zeros((h,w), dtype=np.float32)
301     for i in range(nbit):
302         for j in range(nbit):
303             std2 += (glcm[i,j] * i - mean)**2
304
305     std = np.sqrt(std2)
306     return std
```

Calculate GLCM using mean and std methods

the Mean method is using mean to calculate GLCM and the std method is using standard deviation to calculate GLCM

Feature Extraction

Calculate GLCM using contrast and dissimilarity methods

Contrast is measure of variation in intensity.

Dissimilarity is the measure of relationship between pairs with similar and different intensities, Higher is the value of dissi, more is the dissimilarity between the pairs of pixels

```
309 def fast_glcm_contrast(img, vmin=0, vmax=255, nbit=8, ks=5):
310     '''
311     calc glcm contrast
312     '''
313     h,w = img.shape
314     glcm = fast_glcm(img, vmin, vmax, nbit, ks)
315     cont = np.zeros((h,w), dtype=np.float32)
316     for i in range(nbit):
317         for j in range(nbit):
318             cont += glcm[i,j] * (i-j)**2
319
320     return cont
321
322
323 def fast_glcm_dissimilarity(img, vmin=0, vmax=255, nbit=8, ks=5):
324     '''
325     calc glcm dissimilarity
326     '''
327     h,w = img.shape
328     glcm = fast_glcm(img, vmin, vmax, nbit, ks)
329     diss = np.zeros((h,w), dtype=np.float32)
330     for i in range(nbit):
331         for j in range(nbit):
332             diss += glcm[i,j] * np.abs(i-j)
333
334     return diss
```

Feature Extraction

```
337 def fast_glcml_homogeneity(img, vmin=0, vmax=255, nbit=8, ks=5):
338     '''
339     calc glcm homogeneity
340     '''
341     h,w = img.shape
342     glcm = fast_glcml(img, vmin, vmax, nbit, ks)
343     homo = np.zeros((h,w), dtype=np.float32)
344     for i in range(nbit):
345         for j in range(nbit):
346             homo += glcm[i,j] / (1.+(i-j)**2)
347
348     return homo
349
350
351 def fast_glcml_ASM(img, vmin=0, vmax=255, nbit=8, ks=5):
352     '''
353     calc glcm asm, energy
354     '''
355     h,w = img.shape
356     glcm = fast_glcml(img, vmin, vmax, nbit, ks)
357     asm = np.zeros((h,w), dtype=np.float32)
358     for i in range(nbit):
359         for j in range(nbit):
360             asm += glcm[i,j]**2
361
362     ene = np.sqrt(asm)
363     return asm, ene
```

Calculate GLCM using homogeneity and ASM methods

Homogeneity is the metric used for analysis of homogeneity in an image.

Feature Extraction

```
366 def fast_glcmax(img, vmin=0, vmax=255, nbit=8, ks=5):
367     ...
368     calc glcm max
369     ...
370     glcm = fast_glcmax(img, vmin, vmax, nbit, ks)
371     max_ = np.max(glcmax, axis=(0,1))
372     return max_
373
374
375 def fast_glcmax_entropy(img, vmin=0, vmax=255, nbit=8, ks=5):
376     ...
377     calc glcm entropy
378     ...
379     glcm = fast_glcmax(img, vmin, vmax, nbit, ks)
380     pnorm = glcm / np.sum(glcmax, axis=(0,1)) + 1./ks**2
381     ent = np.sum(-pnorm * np.log(pnorm), axis=(0,1))
382     return ent
```

Calculate GLCM using Max and Entropy methods

Max method is to find the max value of neighbor

Entro is the measure of randomness or uncertainty

Machine learning

- create machine learning model

```
def create_model(model_name):  
    if(model_name == "svm"):  
        model = SVC(kernel='rbf',probability=True)  
        #kernel = {'linear', 'poly', 'rbf', 'sigmoid', 'precomputed'}  
    elif(model_name == "knn"):  
        model = KNeighborsClassifier(n_neighbors=5)  
    elif(model_name == "rf"):  
        model = RandomForestClassifier(n_estimators = 400, criterion = "gini")  
    return model
```

Machine learning

- Do 5-fold cross validation.
- separate data to train set and validate set.
- scaling feature.

```
for i ,(train_index, val_index) in enumerate(kf.split(X)):
```

```
    print("----- fold",i+1,"-----")
    X_train = sc.fit_transform(np.concatenate(X[train_index],axis=0))
    X_val = sc.transform(X[val_index][0])
    y_train = np.concatenate(y[train_index],axis=0)
    y_val = y[val_index][0]
```

Machine learning

- **Create model**
- **Do feature selection by important weight of specific model**
- **Apply those feature to classifier**
- **change model to be one vs rest**
- **train the model**

```
print("training model")

model_algorithm = create_model("rf")
clf = Pipeline([
    ('feature_selection', SelectFromModel(model_algorithm)),
    ('classification', model_algorithm)
])
model = OneVsRestClassifier(model_algorithm)
model.fit(X_train, y_train)

print("train finished")
```

Machine learning

- **select best model of all fold by compare sum of micro average AUC and macro average AUC**

```
if roc_auc["micro"]+roc_auc["macro"] > best_sum_average_AUC:
    best_sum_average_AUC = roc_auc["micro"]+roc_auc["macro"]
    best_sum_3class_AUC = roc_auc[0] + roc_auc[1] + roc_auc[2]
    bestModel = model
    bestFold = i+1
elif roc_auc["micro"]+roc_auc["macro"] == best_sum_average_AUC and best_sum_3class_AUC < roc_auc[0] + roc_auc[1] + roc_auc[2]:
    best_sum_average_AUC = roc_auc["micro"]+roc_auc["macro"]
    best_sum_3class_AUC = roc_auc[0] + roc_auc[1] + roc_auc[2]
    bestModel = model
    bestFold = i+1
```

Machine learning

- **plot mean ROC curve and calculate SD**

```
mean_tpr = np.mean(interp_tpr_all_fold, axis=0)
mean_tpr[-1] = 1.0
mean_auc = auc(mean_fpr, mean_tpr)
std_auc = np.std(aucs)

std_tpr = np.std(interp_tpr_all_fold, axis=0)
tprs_upper = np.minimum(mean_tpr + std_tpr, 1)
tprs_lower = np.maximum(mean_tpr - std_tpr, 0)
plt.show()

plt.figure()
plt.plot(mean_fpr, mean_tpr, color='b',
         label=r'Mean ROC (AUC = %0.2f $\pm$ %0.2f)' % (mean_auc, std_auc),
         lw=2)

for i in range(5):
    plt.plot(fprs[i], tprs[i], label='micro-average ROC curve of fold{} (area = {:.0.2f})'.format(i+1, aucs[i]), alpha=.5)

plt.plot([0, 1], [0, 1], 'k--', lw=lw)
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Mean ROC of all fold')
plt.legend(loc="lower right")
plt.show()
```

02



Deep Learning

Overview

Convert Image
Deep Learning

Convert Image

Save picture in numpy

This function will create .npy file in the path that you define

```
23 def save_to_numpy(imgs,label,path,filename):
24     np.save(os.path.join(path, filename + '.npy'), imgs)
25     np.save(os.path.join(path, filename + '_label' + '.npy'), label)
26     print('Numpy files have been saved')
```

Convert Image

Declaration

Declare the Classes and Fold that you have and create temp array for x (data) and temp array for y (label) and the real x and y. I created temp because I will create nested array which mean len(x) will answer 5 (Fold) and in each it will contain pictures

```
31 classes = ['Glaucoma', 'Normal', 'Other']
32 num_folders = ['1','2','3','4','5']
33 temp_x = []
34 temp_y = []
35 x=[]
36 y=[]
```


Convert Image

```
37 for k in range(len(num_folders)):
38     for i in range(len(classes)):
39         images_lst = os.listdir('/content/drive/MyDrive/Dataset/Train/' + classes[i] + '/Fold-' + num_folders[k])
40         #print(images_lst)
41         count = 0
42
43         for j in images_lst:
44             count += 1
45             if count == 2:
46                 break
47             print('\n' + j + ' ----> ', count, '/', len(images_lst))
48             print('class : ' + classes[i])
49             print('fold : ' + num_folders[k])
50             img = cv2.imread('/content/drive/MyDrive/Dataset/Train/' + classes[i] + '/Fold-' + num_folders[k]+'/' + j)
51             img = cv2.resize(img, (256, 256))
52             temp_x.append(np.array(img))
53             temp_y.append(i)
54
55         x.append(temp_x)
56         temp_x = []
57         y.append(temp_y)
58         temp_y = []
59
60     #save to .npy
61
62     #output_path = '/content/drive/MyDrive/Dataset/np_data/'
63     #save_to_numpy(x,y,output_path,'Train')
64     print('-----')
65     print('done')
```

Loop for every pictures in Train

It will loop every Fold that you have and then every Classes that you have and then it will resize the image to 256*256 and append to temp_x first and temp_y will appen the number of class

After the finished a Fold the temp_x and temp_y will append to real x and y to add a nested array and do this to another Fold

Convert Image

```
72 classes = ['Glaucoma', 'Normal', 'Other']
73 #num_folders = ['1','2','3','4','5']
74 #temp_x = []
75 #temp_y = []
76 x=[]
77 y=[]
78
79 for i in range(len(classes)):
80     images_lst = os.listdir('/content/drive/MyDrive/Dataset/Test/' + classes[i])
81     #print(images_lst)
82     count = 0
83
84     for j in images_lst:
85         count += 1
86         print('\n' + j + ' ----> ', count, '/', len(images_lst))
87         print('class : ' + classes[i])
88         #print('fold : ' + num_folders[k])
89         img = cv2.imread('/content/drive/MyDrive/Dataset/Test/' + classes[i] + '/' + j)
90         img = cv2.resize(img, (256, 256))
91         x.append(np.array(img))
92         if classes[i] == 'Glaucoma':
93             y.append('0')
94             print('Y appended : 0')
95         elif classes[i] == 'Normal':
96             y.append('1')
97             print('Y appended : 1')
98         else:
99             y.append('2')
100             print('Y appended : 2')
101
102
103 #save to .npy
104
105 #output_path = '/content/drive/MyDrive/Dataset/np_data/'
106 #save_to_numpy(x,y,output_path,'test folder not the training')
107 print('-----')
108 print('done')
```

Loop for every pictures in Test Folder

For dataset Test we don't have Fold so we just loop every pictures and add it directly to the x(data) array and y(label) array

Deep learning

- **load data**

```
X = np.load("/content/drive/MyDrive/Colab Notebooks/Dataset/np_data/Train.npy",allow_pickle=True)
y = np.load("/content/drive/MyDrive/Colab Notebooks/Dataset/np_data/TRAIN_label.npy",allow_pickle=True)

X_test = np.load("/content/drive/MyDrive/Colab Notebooks/Dataset/np_data/test.npy",allow_pickle=True)
y_test = np.load("/content/drive/MyDrive/Colab Notebooks/Dataset/np_data/test_label.npy",allow_pickle=True)

X = np.array([np.array(fold) for fold in X])
y = np.array([np.array(fold) for fold in y])
X_test = np.array(X_test)
y_test = np.array(y_test)
```

Deep learning

- **create model**

```
def build_model(base_model_name):

    print('Creating Model : {}'.format(base_model_name.upper()))
    if base_model_name == 'DenseNet121' :
        init_model = DenseNet121(input_shape= (height, width ,3), include_top=False, weights='imagenet', pooling='avg')
        x = init_model.output
        out_layer = Dense(num_output, activation="softmax")(x)
        model = Model(init_model.input, out_layer)
    elif base_model_name == 'ResNet101V2' :
        init_model = ResNet101V2(input_shape= (height, width ,3), include_top=False, weights='imagenet', pooling='avg')
        x = init_model.output
        out_layer = Dense(num_output, activation="softmax")(x)
        model = Model(init_model.input, out_layer)
    else :
        sys.exit("Model Not Support")
    return model
```

Deep learning

- create early stop function to early stop training if validation loss not decrease for 10 epochs
- create reduce learning rate function to reduce learning rate if validation loss not decrease for 7 epochs

```
earlyStopping = EarlyStopping(monitor='val_loss', patience=10, verbose=0, mode='min')  
  
reduce_lr_loss = ReduceLROnPlateau(monitor='val_loss', factor=0.1, patience=7, verbose=1, epsilon=1e-4, mode='min')
```

Deep learning

- Create and compile model
- apply optimizer(adam) and loss algorithm

```
• model_name = "DenseNet121"
  model = build_model(model_name)
  #model.summary()

• #class_weights = get_class_weights(y_train[train_idx])
  model.compile(optimizer=optimizers['adam'], loss='categorical_crossentropy', metrics=['accuracy'])
```

Deep learning

- **save weight at the best epoch(focus on val_loss)**

```
checkpoint_path = "/content/drive/MyDrive/Colab Notebooks/Dataset/weight/{}-weights_fold-{}.hdf5".format(model_name,i+1)
mcp_save = ModelCheckpoint(checkpoint_path, save_best_only=True, monitor='val_loss', mode='min',save_weights_only=True)

```

Deep learning

```
history = model.fit(X_train,y_train,
                    steps_per_epoch = (len(X_train) / batch_size ),
                    epochs = 50,
                    validation_data=(X_val, y_val),
                    callbacks=[earlyStopping, mcp_save, reduce_lr_loss]
                    )
```

- **train model**

Deep learning

- **select best model of all fold by compare sum of micro average AUC and macro average AUC**

```
if roc_auc["micro"]+roc_auc["macro"] > best_sum_average_AUC:
    best_sum_average_AUC = roc_auc["micro"]+roc_auc["macro"]
    best_sum_3class_AUC = roc_auc[0] + roc_auc[1] + roc_auc[2]
    bestModel = model
    bestFold = i+1
elif roc_auc["micro"]+roc_auc["macro"] == best_sum_average_AUC and best_sum_3class_AUC < roc_auc[0] + roc_auc[1] + roc_auc[2]:
    best_sum_average_AUC = roc_auc["micro"]+roc_auc["macro"]
    best_sum_3class_AUC = roc_auc[0] + roc_auc[1] + roc_auc[2]
    bestModel = model
    bestFold = i+1
```

Evaluation

```
def calculateFprTprAuc(binary_y_test, y_score):
    # Compute ROC curve and ROC area for each class
    fpr = dict()
    tpr = dict()
    roc_auc = dict()
    for i in range(n_classes):
        fpr[i], tpr[i], _ = roc_curve(binary_y_test[:, i], y_score[:, i])
        roc_auc[i] = auc(fpr[i], tpr[i])

    # Compute micro-average ROC curve and ROC area
    fpr["micro"], tpr["micro"], _ = roc_curve(binary_y_test.ravel(), y_score.ravel())
    roc_auc["micro"] = auc(fpr["micro"], tpr["micro"])
    return fpr, tpr, roc_auc
```

**Calculate FPR TPR and AUC
score of each classes and micro
average**

Evaluation

calculate macro average and Plot ROC curve of each classes(One vs Rest) and plot micro average and macro average of them

```
def plotROC(fpr,tpr,roc_auc,title):
    #aggregate all false positive rates
    all_fpr = np.unique(np.concatenate([fpr[i] for i in range(n_classes)]))

    #interpolate all ROC curves
    mean_tpr = np.zeros_like(all_fpr)
    for i in range(n_classes):
        mean_tpr += interp(all_fpr, fpr[i], tpr[i])

    #average tpr and compute AUC
    mean_tpr /= n_classes

    fpr["macro"] = all_fpr
    tpr["macro"] = mean_tpr
    roc_auc["macro"] = auc(fpr["macro"], tpr["macro"])

    # Plot all ROC curves
    plt.figure()
    plt.plot(fpr["micro"], tpr["micro"],
             label='micro-average ROC curve (area = {0:0.2f})'
                  ''.format(roc_auc["micro"]),
             color='deeppink', linestyle=':', linewidth=4)

    plt.plot(fpr["macro"], tpr["macro"],
             label='macro-average ROC curve (area = {0:0.2f})'
                  ''.format(roc_auc["macro"]),
             color='navy', linestyle=':', linewidth=4)

    colors = cycle(['aqua', 'darkorange', 'cornflowerblue'])
    for i, color in zip(range(n_classes), colors):
        plt.plot(fpr[i], tpr[i], color=color, lw=lw,
                 label='ROC curve of {0} (area = {1:0.2f})'
                      ''.format(classes_list[i], roc_auc[i]))

    plt.plot([0, 1], [0, 1], 'k--', lw=lw)
    plt.xlim([0.0, 1.0])
```

Evaluation

```
1 def plot_confusion_matrix(y_true, y_pred, classes,  
|                           title=None,  
|                           cmap=plt.cm.Blues):  
  
    np.set_printoptions(precision=2)  
  
    if not title:  
        title = 'Normalized confusion matrix'  
  
    # Compute confusion matrix  
    cm = confusion_matrix(y_true, y_pred)  
    # Only use the labels that appear in the data  
    classes = classes[unique_labels(y_true, y_pred)]  
  
    cm_normalize = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]  
    print("Normalized confusion matrix")  
  
    #print(cm)  
  
    fig, ax = plt.subplots()  
    im = ax.imshow(cm_normalize, interpolation='nearest', cmap=cmap)  
    ax.figure.colorbar(im, ax=ax)  
    # We want to show all ticks...  
    ax.set(xticks=np.arange(cm_normalize.shape[1]),  
          yticks=np.arange(cm_normalize.shape[0]),  
          # ... and label them with the respective list entries  
          xticklabels=classes, yticklabels=classes,  
          title=title,  
          ylabel='True label',  
          xlabel='Predicted label')
```

Plot 3 classes confusion metrix with normalization(percentage)

2

```
# Rotate the tick labels and set their alignment.  
plt.setp(ax.get_xticklabels(), rotation=45, ha="right",  
         rotation_mode="anchor")  
  
# Loop over data dimensions and create text annotations.  
fmt = '.2f' #if normalize else 'd'  
thresh = cm_normalize.max() / 2.  
for i in range(cm_normalize.shape[0]):  
    for j in range(cm_normalize.shape[1]):  
        ax.text(j, i, "{:.2%}\n({:d})".format(cm_normalize[i, j], cm[i, j]),  
                ha="center", va="center",  
                color="white" if cm_normalize[i, j] > thresh else "black")  
fig.tight_layout()  
#plt.xlim(-0.5, len(np.unique(y))-0.5)  
#plt.ylim(len(np.unique(y))-0.5, -0.5)  
plt.show()
```

1. <https://github.com/Atdhasiri/machineLearning/blob/main/DL/Deep%20learning.py#L118-L150>

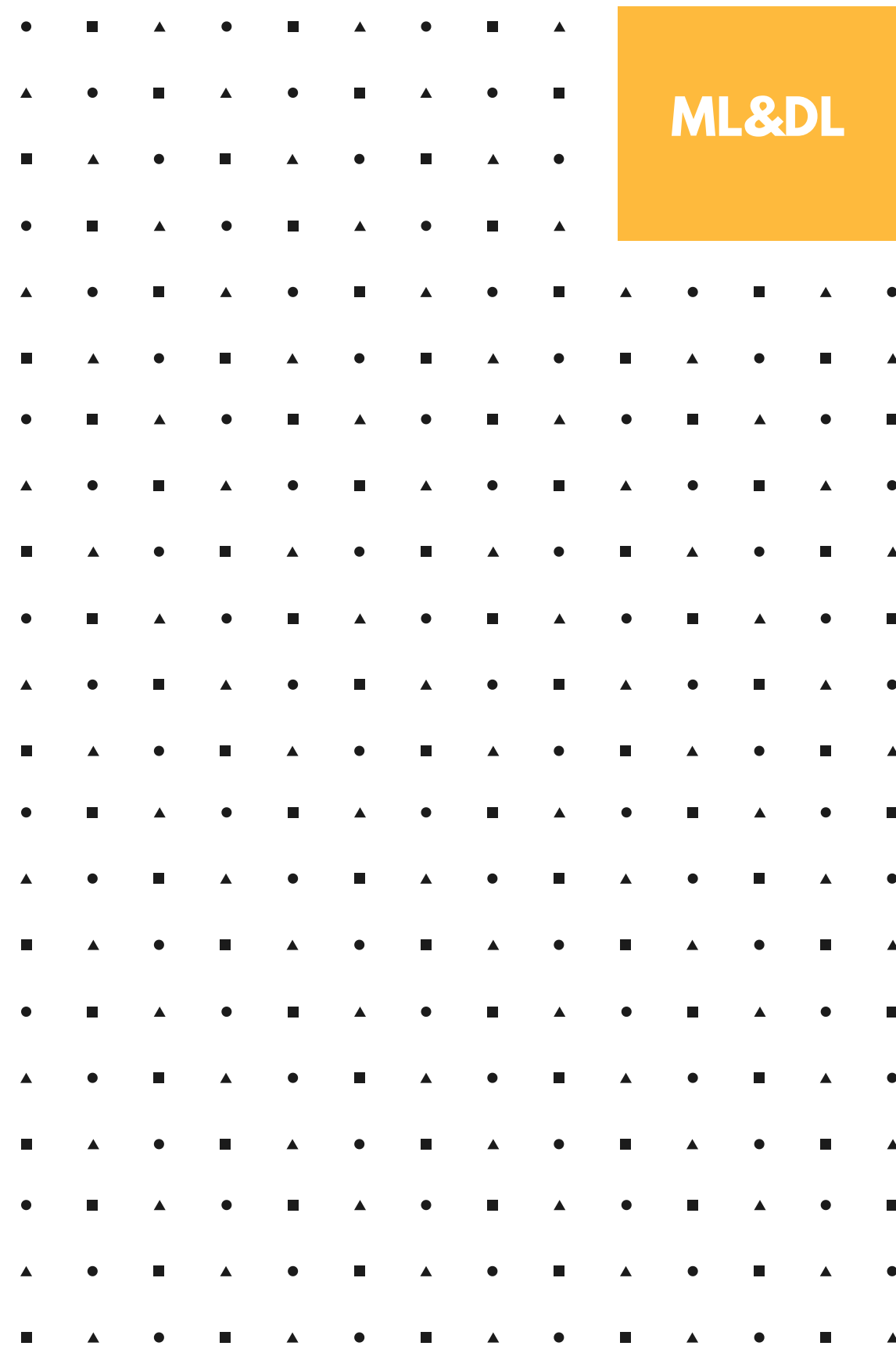
2. <https://github.com/Atdhasiri/machineLearning/blob/main/DL/Deep%20learning.py#L153-L167>

Evaluation

Calculate and print sensitivity , specificity and etc. by the value from confusion matrix

```
# Sensitivity, hit rate, recall, or true positive rate
TPR = TP/(TP+FN)
# Specificity or true negative rate
TNR = TN/(TN+FP)
# Precision or positive predictive value
PPV = TP/(TP+FP)
# Negative predictive value
NPV = TN/(TN+FN)
# Fall out or false positive rate
FPR = FP/(FP+TN)
# False negative rate
FNR = FN/(TP+FN)
# False discovery rate
FDR = FP/(TP+FP)
# F1-score
F1 = 2*((PPV*TPR)/(PPV+TPR))
# Overall accuracy
ACC = (TP+TN)/(TP+FP+FN+TN)

print("="*60)
print("{:<26} | {:>8} {:>8} {:>8}".format("value", "Glaucoma", "Normal", "Other"))
print("="*60)
print("{:<26} | {:>8.2f} {:>8.2f} {:>8.2f}".format("Sensitivity(TPR)", TPR[0], TPR[1], TPR[2]))
print("{:<26} | {:>8.2f} {:>8.2f} {:>8.2f}".format("Specificity(TNR)", TNR[0], TNR[1], TNR[2]))
print("{:<26} | {:>8.2f} {:>8.2f} {:>8.2f}".format("Precision(PPV)", PPV[0], PPV[1], PPV[2]))
print("{:<26} | {:>8.2f} {:>8.2f} {:>8.2f}".format("Negative predictive value", NPV[0], NPV[1], NPV[2]))
print("{:<26} | {:>8.2f} {:>8.2f} {:>8.2f}".format("False positive rate", FPR[0], FPR[1], FPR[2]))
print("{:<26} | {:>8.2f} {:>8.2f} {:>8.2f}".format("False negative rate", FNR[0], FNR[1], FNR[2]))
print("{:<26} | {:>8.2f} {:>8.2f} {:>8.2f}".format("False discovery rate", FDR[0], FDR[1], FDR[2]))
print("{:<26} | {:>8.2f} {:>8.2f} {:>8.2f}".format("F1-score", F1[0], F1[1], F1[2]))
print("{:<26} | {:>8.2f} {:>8.2f} {:>8.2f}".format("Overall accuracy", ACC[0], ACC[1], ACC[2]))
```



Thanks for
attending!