X_train = np.array(X_train) 100%| 826/826 [00:01<00:00, 552.14it/s] 822/822 [00:01<00:00, 636.57it/s] 100%| 395/395 [00:00<00:00, 633.63it/s] 100%| | 827/827 [00:01<00:00, 546.27it/s] In [23]: for label in labels: testPath = os.path.join('brain_tumor/test',label) for file in tqdm(os.listdir(testPath)): image = cv2.imread(os.path.join(testPath, file),0) image = cv2.resize(image, (image_size, image_size)) X_test.append(image) Y_test.append(label) $X_{\text{test}} = \text{np.array}(X_{\text{test}})$ 100%| 100/100 [00:00<00:00, 557.82it/s] 115/115 [00:00<00:00, 460.54it/s] 100%| 100% 105/105 [00:00<00:00, 836.35it/s] 100%| | 74/74 [00:00<00:00, 139.26it/s] X_train, Y_train = shuffle(X_train, Y_train, random_state=28) In [25]: $y_train_ = []$ for i in Y_train: y_train_.append(labels.index(i)) $Y_{train} = y_{train}$ Y_train = tf.keras.utils.to_categorical(Y_train) y_test_ **=** [] for i in Y_test: y_test_.append(labels.index(i)) Y_test = y_test_ Y_test = tf.keras.utils.to_categorical(Y_test) In [26]: model=Sequential() model.add(Conv2D(16, kernel_size=(3, 3),activation='relu',input_shape=(200,200,1),padding='same')) model.add(MaxPooling2D(pool_size=2)) model.add(Conv2D(32, kernel_size=(3, 3), activation='relu', padding='same')) model.add(MaxPooling2D(pool_size=2)) model.add(Conv2D(64, kernel_size=(3, 3), activation='relu', padding='same')) model.add(MaxPooling2D(pool_size=2)) model.add(Flatten()) model.add(Dense(32, activation='relu')) model.add(BatchNormalization()) model.add(Dense(16, activation='relu')) model.add(BatchNormalization()) model.add(Dense(4, activation='softmax')) model.summary() Model: "sequential_1"

dense_3 (Dense) (None, 32) batch_normalization_2 (Batc (None, 32) hNormalization) dense_4 (Dense) (None, 16) batch_normalization_3 (Batc (None, 16) hNormalization) dense_5 (Dense) (None, 4) ______ Total params: 1,304,116 Trainable params: 1,304,020 Non-trainable params: 96 In [27]: X_train, X_val, Y_train, Y_val = train_test_split(X_train, Y_train, test_size=0.2, random_state=28) X_train.shape, X_test.shape ((2296, 200, 200), (394, 200, 200)) model.compile(loss='categorical_crossentropy', optimizer='Adam', metrics=['accuracy']) In [29]: CNN = model.fit(X_train, Y_train, batch_size=32, validation_data=(X_val, Y_val),epochs=10) Epoch 1/10 Epoch 2/10 Epoch 3/10 Epoch 4/10 Epoch 5/10 Epoch 6/10 Epoch 7/10 Epoch 8/10 Epoch 9/10 Epoch 10/10 In [30]: plt.plot(CNN.history['loss'], label='train loss') plt.plot(CNN.history['val_loss'], label='val loss') plt.legend() plt.show() plt.savefig('LossVal_loss')

In [21]:

In [22]:

import numpy as np import pandas as pd

from tqdm import tqdm import tensorflow as tf

import numpy as np from glob import glob

 $X_{train} = []$ $Y_{train} = []$ $X_{test} = []$ Y_test = [] image_size=200

Layer (type)

conv2d_3 (Conv2D)

conv2d_4 (Conv2D)

conv2d_5 (Conv2D)

flatten_1 (Flatten)

2D)

Output Shape

max_pooling2d_3 (MaxPooling (None, 100, 100, 16)

max_pooling2d_4 (MaxPooling (None, 50, 50, 32)

max_pooling2d_5 (MaxPooling (None, 25, 25, 64)

(None, 200, 200, 16)

(None, 100, 100, 32)

(None, 50, 50, 64)

(None, 40000)

Param # ========

160

4640

18496

0

0

0

0

128

528

64

68

1280032

for label in labels:

from sklearn.utils import shuffle

import matplotlib.pyplot as plt

from keras.models import Model

from tensorflow.keras.preprocessing import image

from tensorflow.keras.models import Sequential

from keras.layers import Dense, Dropout, Flatten

from tensorflow.keras.layers import MaxPooling2D

for file in tqdm(os.listdir(trainPath)):

X_train.append(image) Y_train.append(label)

from sklearn.model_selection import train_test_split

from keras.layers.advanced_activations import LeakyReLU

trainPath = os.path.join('brain_tumor/train',label)

image = cv2.imread(os.path.join(trainPath, file),0) image = cv2.resize(image, (image_size, image_size))

from sklearn.metrics import classification_report,confusion_matrix

from tensorflow.keras.layers import Input, Lambda, Dense, Flatten, Conv2D, BatchNormalization

from tensorflow.keras.preprocessing.image import ImageDataGenerator,load_img

labels = ['glioma_tumor', 'meningioma_tumor', 'no_tumor', 'pituitary_tumor']

import os import cv2

plt.plot(CNN.history['accuracy'], label='train acc') plt.plot(CNN.history['val_accuracy'], label='val acc') plt.legend() plt.show() plt.savefig('AccVal_acc') 1.75 train loss val loss 1.50 1.25 1.00 0.75 0.50 0.25 0.00 2 1.0 train acc val acc 0.9 0.8 0.7 0.6 0.5 0.4

In [31]:

In [32]:

160 - 140 - 120 - 100 - 80 - 60 - 40 - 20 pituitary_tumor

2 <Figure size 432x288 with 0 Axes> y_test=np.argmax(Y_val,axis=1) y_pred = np.argmax(model.predict(X_val), axis=-1) cm = confusion_matrix(y_test, y_pred) plt.figure(figsize= (8,8)) plt.imshow(confusion_matrix(y_test, y_pred)) plt.xticks(np.arange(4), labels) plt.yticks(np.arange(4), labels) plt.colorbar() plt.show() print(cm) glioma_tumor meningioma_tumor no_tumor glioma_tumor meningioma_tumor no_tumor 0] 8] 3 0 169]] recall f1-score support precision

pituitary_tumor [[153 7 0 [10 141 10 4 6 59 3] 1 report = classification_report(y_test, y_pred) print(report) 0.93 160 0 0.91 0.96 0.90 169 1 0.83 0.87 2 0.86 0.82 0.84 72 3 0.94 0.96 173 0.98

0.91 574 accuracy macro avg 0.90 0.90 0.90 574 weighted avg 0.91 0.91 574

In [33]: from sklearn.metrics import mean_squared_error

MSE = mean_squared_error(y_test, y_pred) print ("MSE:{0}".format(MSE))

MSE:0.18292682926829268

In []:

In []: