1. Import Libraries/Dataset (0 mark) A. Import the required libraries and the dataset (use Google Drive if required). B. Check the GPU available (recommended- use free GPU provided by Google Colab). How do Deep Learning Networks distinguish between healthy and unhealthy lungs? Most deep neural network applied to the task of pneumonia diagnosis have been adapted from natural image classification. Since natural image classification models have a large number of parameters as well as high hardware requirements, which makes them prone to overfitting and harder to deploy in mobile settings (Fourcade & Khonsari, 2019). Convolutional Neural Networks are a common form of deep networks for classification tasks. CNNs have extensive learning capacity and can infer the nature of an input image without any prior knowledge, which makes them a suitable method for image classification (Toraman, Alakus, & Turkoglu, 2020). CNNs make use of the following three properties: 1. First: units in each layer receive inputs from the previous units which are located in a small neighborhood. This way, elementary features such as edges and corners can be extracted. Then these features will be combined in next layers to detect higher order features. 2. Second: important property is the concept of shared weights, which means similar feature detectors are used for the entire image. 3. Third: CNNs usually have several sub-sampling layers. These layers are based on the fact that the precise location of the features are not only beneficial, but also harmful, because this information tends to vary for different instances (Yadav & Jadhav, 2019). #libraries import numpy as np import pandas as pd import random # folder import os # Imports packages to view data import cv2 from glob import glob import matplotlib.pyplot as plt from PIL import Image from google.colab.patches import cv2 imshow from prettytable import PrettyTable import matplotlib.pyplot as plt %matplotlib inline import seaborn as sns plt.rc('image', cmap='gray') from sklearn.preprocessing import LabelEncoder from sklearn.model selection import train test split #tensorflow and keras import tensorflow as tf from tensorflow import keras from tensorflow.keras.models import Sequential from tensorflow.keras.layers import Activation, Dense, Flatten, BatchNormalization, Conv2D, MaxPool2D from tensorflow.keras.optimizers import Adam from tensorflow.keras.metrics import categorical crossentropy from tensorflow.keras import layers from tensorflow.keras.preprocessing.image import ImageDataGenerator, load img from tensorflow.keras.models import Sequential from tensorflow.keras.layers import Conv2D, MaxPooling2D from tensorflow.keras.layers import Activation, Dropout, Flatten, Dense from tensorflow.keras import backend as K from tensorflow.keras.callbacks import EarlyStopping, ReduceLROnPlateau, ModelCheckpoint from tensorflow.keras.regularizers import 12 #google drive from google.colab import drive drive.mount('/content/drive') Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", for ce remount=True). print(tf.__version__) 2.7.0 In [40]: train data dir = "/content/drive/My Drive/Colab Notebooks/chest xray/train" val data dir = "/content/drive/My Drive/Colab Notebooks/chest xray/val" test data dir = "/content/drive/My Drive/Colab Notebooks/chest xray/test" In [4]: !ls "/content/drive/My Drive/Colab Notebooks/chest xray" test train val **Exploratory Data Analysis** 1. Data Visualization and augmentation (1 mark) A. Plot at least two samples from each class of the dataset (use matplotlib/seaborn/any other library). In [41]: # Set up folders for normal cases and pneumonia cases wihtin our train data train_n = train_data_dir + '/NORMAL/' train_p = train_data_dir + '/PNEUMONIA/' # Random normal picture from train set print(f"Normal X-Rays From Validation Set: {len(os.listdir(train_n))} ") print(f"PNEUMONIA X-Rays From Validation Set: {len(os.listdir(train p))} ") Normal X-Rays From Validation Set: 1342 PNEUMONIA X-Rays From Validation Set: 3876 In [14]: ## Select 10 normal pictures norm pic = os.listdir(train n)[25:35] # for 10 images only we are showing norm pic Out[14]: ['IM-0546-0001.jpeg', 'IM-0534-0001.jpeg', 'IM-0539-0001-0001.jpeg', 'IM-0533-0001-0002.jpeg', 'IM-0545-0001-0001.jpeg', 'IM-0542-0001.jpeg', 'IM-0551-0001-0001.jpeg', 'IM-0548-0001.jpeg', 'IM-0535-0001.jpeg' 'IM-0545-0001-0002.jpeg'] norm pic address = [train n + pic for pic in norm pic] norm pic address Out[15]: ['/content/drive/My Drive/Colab Notebooks/chest xray/train/NORMAL/IM-0546-0001.jpeg', '/content/drive/My Drive/Colab Notebooks/chest xray/train/NORMAL/IM-0534-0001.jpeg', '/content/drive/My Drive/Colab Notebooks/chest_xray/train/NORMAL/IM-0539-0001-0001.jpeg', $\verb|'/content/drive/My Drive/Colab Notebooks/chest_xray/train/NORMAL/IM-0533-0001-0002.jpeg'|,$ $\verb|'/content/drive/My Drive/Colab Notebooks/chest_xray/train/NORMAL/IM-0545-0001-0001.jpeg'|,$ '/content/drive/My Drive/Colab Notebooks/chest xray/train/NORMAL/IM-0542-0001.jpeg', '/content/drive/My Drive/Colab Notebooks/chest_xray/train/NORMAL/IM-0551-0001-0001.jpeg', '/content/drive/My Drive/Colab Notebooks/chest xray/train/NORMAL/IM-0548-0001.jpeg', '/content/drive/My Drive/Colab Notebooks/chest xray/train/NORMAL/IM-0535-0001.jpeg', '/content/drive/My Drive/Colab Notebooks/chest xray/train/NORMAL/IM-0545-0001-0002.jpeg'] print(f"Pneumonia X-Rays From Validation Set: {len(os.listdir(train p))} ") Pneumonia X-Rays From Validation Set: 3876 ## Select 10 Pneumonia pictures pneumonia pic = os.listdir(train p)[40:50] pneumonia address = [train p + pic for pic in pneumonia pic] for i in range (0,10): # Load the images norm img = Image.open(norm pic address[i]) pneumonia_img = Image.open(pneumonia_address[i]) #Let's plt these images ## plot normal picture f = plt.figure(figsize= (10,6)) a1 = f.add subplot(1,2,1)img_plot = plt.imshow(norm_img) a1.set_title(f'Normal {norm_pic[i]}') ## plot pneumonia picture a2 = f.add subplot(1, 2, 2)img_plot = plt.imshow(pneumonia_img) a2.set_title(f'Pneumonia {pneumonia_pic[i]}') Normal IM-0546-0001.jpeg 0 Pneumonia person500 virus 1009.jpeg 200 100 400 200 600 300 800 400 1000 500 1200 1400 200 400 600 800 1000 1250 1500 1750 0 Normal IM-0534-0001.jpeg 0 Pneumonia person525 bacteria 2218.jpeg 200 100 400 200 600 300 400 800 500 1000 600 1200 0 200 400 600 800 750 500 1000 1250 Normal IM-0539-0001-0001.jpeg 0 Pneumonia person52_bacteria_251.jpeg 200 400 200 600 400 800 600 1000 1200 800 1400 1000 1600 400 600 800 1000 1200 1400 500 1000 1500 2000 Normal IM-0533-0001-0002.jpeg Pneumonia person551_bacteria_2310.jpeg 200 400 200 400 800 1000 600 1200 800 1400 800 1000 200 400 1250 250 500 750 1000 1500 1750 Normal IM-0545-0001-0001.jpeg 0 Pneumonia person548_bacteria_2301.jpeg 200 100 400 200 600 300 800 400 1000 500 1200 600 1400 200 400 600 800 1000 1250 1500 1750 500 750 Pneumonia person523_virus_1043.jpeg Normal IM-0542-0001.jpeg 0 200 200 400 400 600 600 800 1000 800 1200 1000 1400 1000 1250 1500 1750 Normal IM-0551-0001-0001.jpeg Pneumonia person508_bacteria_2143.jpeg 0 200 200 400 400 600 800 600 1000 800 1200 200 400 600 800 1000 500 750 1000 1250 1500 0 Normal IM-0548-0001.jpeg Pneumonia person504 bacteria 2130.jpeg 0 200 100 200 400 300 600 400 800 500 1000 400 600 1000 1000 1250 1500 1750 750 Pneumonia person498_bacteria_2102.jpeg Normal IM-0535-0001.jpeg 0 200 200 400 600 600 800 800 1000 1000 600 800 1000 1200 1400 1000 1200 1400 400 600 800 Normal IM-0545-0001-0002.jpeg Pneumonia person53 bacteria 252.jpeg 200 200 400 600 400 800 600 1000 1200 800 1400 750 1000 1250 1500 1750 500 1. Data Visualization and augmentation (1 mark) A. Apply rotation and height shift augmentation (rotation_range, height_shift_range) to the dataset separately. Print the augmented image and the original image for each class and each augmentation. In [24]: # Specify the Column Names while initializing the Table mytable = PrettyTable(["Method", "Setting"], title = "Settings for the image augmentation.") # Add rows mytable.add row(["Rescale", "1/255"]) mytable.add row(["Rotation Range", "30 degrees"]) mytable.add row(["Shear Range", "0.2"]) mytable.add_row(["Zoom Range", "0.2"]) mytable.add row(["Samplewise std normalization", "True"]) mytable.add row(["Height Shift", "0.2"]) mytable.add_row(["Width Shift", "0.2"]) mytable.add row(["Horizontal Flip", "True"]) print(mytable) Settings for the image augmentation. Method | Setting Rescale | 1/255 | 30 degrees | Rotation Range Shear Range | 0.2 Zoom Range | 0.2 Samplewise std normalization | True Height Shift | 0.2 Width Shift | 0.2 Horizontal Flip | True Create a data augmentor data_augmentor = ImageDataGenerator(samplewise_center=True, # set each sample mean to 0 rescale=1./255, # rescale rotation_range = 30, # randomly rotate images in the range (degrees, 0 to 180) shear_range=0.2, # Randomly shear image zoom_range = 0.2, # Randomly zoom image samplewise_std_normalization=True, # divide each input by its std validation_split=0.2, height_shift_range = 0.2, # randomly shift images horizontally (fraction of total height) width_shift_range = 0.2, # randomly shift images horizontally (fraction of total width) horizontal_flip = True) # randomly flip images data augmentor = ImageDataGenerator(samplewise center=True, rescale=1./255, shear range=0.2, zoom range = 0.2,samplewise std normalization=True, validation split=0.2) # Set hyperparameters target size = (128,128) target dims = (128, 128, 3) # add channel for RGB n batch size = 32 1. Data Visualization and augmentation (1 mark) A. Bring the train and test data in the required format # Create datasets train generator = data augmentor.flow from directory(train data dir, target size=target size, subset='training val_generator = data_augmentor.flow_from_directory(train_data_dir, target_size=target_size, subset='validation', test_generator = data_augmentor.flow_from_directory(test_data_dir, target_size=target_size,batch_size= 1,class] Found 4173 images belonging to 2 classes. Found 1043 images belonging to 2 classes. Found 624 images belonging to 2 classes. 1. Data Visualization and augmentation (1 mark) A. Print the shapes of train and test data train generator.image shape Out[38]: (128, 128, 3) In [39]: test_generator.image_shape Out[39]: (128, 128, 3) 1. Model Building (0.2*5 = 1 mark)The Architecture Our architecture for the CNN has been inspired by the article from Stephan and colleagues (2019) and Yadav and Sjadav (2019). Their neural network architectures were specifically designed for pneumonia image classification tasks. The proposed architecture consists of the convolution, max-pooling, and classification layers combined together. We will now dive into each component and why we chose them. 1. Model Building (0.2*5 = 1 mark)A. Sequential Model layers- Use AT LEAST 3 hidden layers with appropriate input for each. Choose the best number for hidden units and give reasons. B. Add L2 regularization to all the layers. C. Add one layer of dropout at the appropriate position and give reasons. D. Choose the appropriate activation function for all the layers. def initialize model(name): model = Sequential(name=name) model.add(layers.Conv2D(32, (3, 3), activation="relu", input shape=target dims, padding='same')) model.add(layers.MaxPool2D(pool size=(2, 2))) model.add(Dropout(0.1)) model.add(layers.Conv2D(64, (3, 3), activation="relu", padding='same')) model.add(layers.MaxPool2D(pool size=(2, 2))) model.add(Dropout(0.1)) model.add(layers.Conv2D(128, (3, 3), activation="relu", padding='same')) model.add(layers.MaxPool2D(pool size=(3, 3))) model.add(Dropout(0.1)) model.add(layers.Flatten()) model.add(layers.Dense(64, activation='relu')) model.add(Dropout(0.2)) model.add(layers.Dense(1, activation='sigmoid')) return model Dropout Dropout is used to prevent overfitting by temporarily "dropping" a neuron during training time at each iteration with probability p. Which means that all the inputs and outputs to this neuron will be disabled at the current iteration. The dropped-out neurons are resampled with probability p at every training step, so a dropped out neuron at one step can be active at the next one. The hyperparameter p is called the dropout-rate and we set it to 0.5, corresponding to 50% of the neurons being dropped out which is proposed as the best option for X-ray image classification (yadav & Jadhav, 2019). 1. Model Building (0.2*5 = 1 mark)A. Print the model summary. model = initialize model(name="basemodel") model.summary() Model: "basemodel" Output Shape Layer (type) Param # ______ conv2d (Conv2D) (None, 128, 128, 32) 896 max pooling2d (MaxPooling2D (None, 64, 64, 32) (None, 64, 64, 32) dropout (Dropout) 18496 conv2d 1 (Conv2D) (None, 64, 64, 64) max pooling2d 1 (MaxPooling (None, 32, 32, 64) dropout_1 (Dropout) (None, 32, 32, 64) conv2d 2 (Conv2D) (None, 32, 32, 128) 73856 max pooling2d 2 (MaxPooling (None, 10, 10, 128) dropout 2 (Dropout) (None, 10, 10, 128) (None, 12800) flatten (Flatten) (None, 64) dense (Dense) 819264 dropout 3 (Dropout) (None, 64) dense 1 (Dense) (None, 1) Total params: 912,577 Trainable params: 912,577 Non-trainable params: 0 1. Model Compilation (0.25 mark) A. Compile the model with the appropriate loss function. B. Use an appropriate optimizer. Give reasons for the choice of learning rate and its value. C. Use accuracy as a metric. def compile model(model): model.compile(optimizer="adam",loss='binary_crossentropy',metrics="binary_accuracy") return model Regularization In order to prevent our model to overtrain we implement the following regularization measures. In [34]: model baseline = initialize model(name="baseline") history baseline = compile model(model baseline) callback = [EarlyStopping(patience=5, monitor='val accuracy', restore best weights=True), ReduceLROnPlateau(monitor = 'val loss', patience = 2, factor=0.3, verbose=1), ModelCheckpoint("xray model v2.h5", save best only=True)] 1. Model Training (0.5 + 0.25 = 0.75 mark)A. Train the model for an appropriate number of epochs. Print the train and validation accuracy and loss for each epoch. Use the appropriate batch size. B. Plot the loss and accuracy history graphs for both train and validation set. Print the total time taken for training. history baseline = model baseline.fit(train generator, batch size=n batch size, validation data=val generator, shuffle=True, callbacks=callback) #,class weight=class weights) arly stopping conditioned on metric `val accuracy` which is not available. Available metrics are: loss, binary a ccuracy, val_loss, val_binary_accuracy 0.2502 - val_binary_accuracy: 0.8945 - lr: 0.0010 1. Model Evaluation (0.5 + 0.5 = 1 mark)A. Print the final train and validation loss and accuracy. Print confusion matrix and classification report for the validation dataset. Analyse and report the best and worst performing class. B. Print the two most incorrectly classified images for each class in the test dataset. scores = model baseline.evaluate(val generator) scores 33/33 [==============] - 27s 819ms/step - loss: 0.2688 - binary accuracy: 0.8840 [0.26881924271583557, 0.8839884996414185] Evaluate our model by looking at a graph In [42]: history frame = pd.DataFrame(history baseline.history) history_frame.loc[:, ['loss', 'val_loss']].plot() history frame.loc[:, ['binary accuracy', 'val binary accuracy']].plot(); 0.34 loss val loss 0.32 0.30 0.28 0.26 -0.04-0.020.00 0.02 0.04 binary_accuracy val_binary_accuracy 0.89 0.88 0.87 0.86 -0.04 -0.020.02 0.00 0.04 Hyperparameter Tuning- Build two more additional models by changing the following hyperparameters ONE at a time. Write the code for Model Building, Model Compilation, Model Training and Model Evaluation as given in the instructions above for each additional model. (1 + 1 = 2 marks1. Optimiser: Use a different optimizer with the appropriate LR value. 2. Network Depth: Change the number of hidden layers and hidden units for each layer. Write a comparison between each model and give reasons for the difference in results.