```
!pip install imutils
```

```
Requirement already satisfied: imutils in /opt/conda/lib/python3.6/site-packages (0.5.3)
```

```
# This Python 3 environment comes with many helpful analytics libraries installed
# It is defined by the kaggle/python docker image: https://github.com/kaggle/docker-pyth
# For example, here's several helpful packages to load in

import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)

# Input data files are available in the "../input/" directory.
# For example, running this (by clicking run or pressing Shift+Enter) will list all file

import os

from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.applications import VGG16
from tensorflow.keras.layers import AveragePooling2D
from tensorflow.keras.layers import Dropout
from tensorflow.keras.layers import Flatten
from tensorflow.keras.layers import Dense
from tensorflow.keras.layers import Input
from tensorflow.keras.models import Model
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.utils import to_categorical
from sklearn.preprocessing import label_binarize
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
from imutils import paths
import matplotlib.pyplot as plt
import numpy as np
import argparse
import cv2
import os
import pandas as pd
import shutil
import random
from sklearn.cluster import KMeans
from sklearn import metrics
from scipy.spatial.distance import cdist

# Any results you write to the current directory are saved as output.
```

BUILD DATASET

```
dataset_path = './dataset'
```

```
samples = 25
```

```
covid_dataset_path = '../input/covid-chest-xray'
```

```

%%bash
rm -rf dataset
mkdir -p dataset/covid
mkdir -p dataset/normal


```

```
# construct the path to the metadata CSV file and load it
csvPath = os.path.sep.join([covid_dataset_path, "metadata.csv"])
df = pd.read_csv(csvPath)

# loop over the rows of the COVID-19 data frame
for (i, row) in df.iterrows():
    # if (1) the current case is not COVID-19 or (2) this is not
    # a 'PA' view, then ignore the row
    if row["finding"] != "COVID-19" or row["view"] != "PA":
        continue

    # build the path to the input image file
    imagePath = os.path.sep.join([covid_dataset_path, "images", row["filename"]])

    # if the input image file does not exist (there are some errors in
    # the COVID-19 metadeta file), ignore the row
    if not os.path.exists(imagePath):
        continue

    # extract the filename from the image path and then construct the
    # path to the copied image file
    filename = row["filename"].split(os.path.sep)[-1]
    outputPath = os.path.sep.join([f"{dataset_path}/covid", filename])

    # copy the image
    shutil.copy2(imagePath, outputPath)
```

BUILD NORMAL XRAY DATASET

```
pneumonia_dataset_path ='../input/chest-xray-pneumonia/chest_xray'
```

```
basePath = os.path.sep.join([pneumonia_dataset_path, "train", "NORMAL"])
imagePaths = list(paths.list_images(basePath))

```

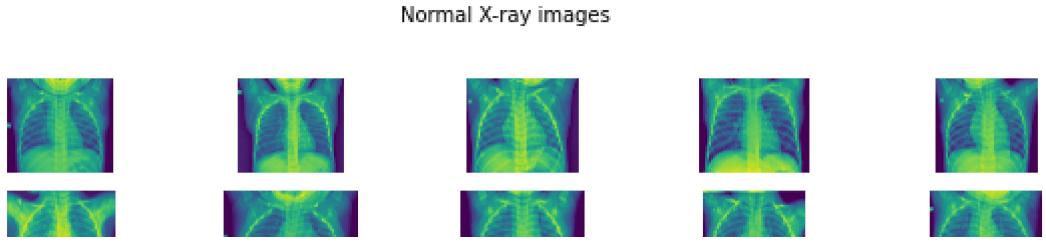
```
# randomly sample the image paths
random.seed(42)
random.shuffle(imagePaths)
imagePaths = imagePaths[:samples]

# loop over the image paths
for (i, imagePath) in enumerate(imagePaths):
    # extract the filename from the image path and then construct the
    # path to the copied image file
    filename = imagePath.split(os.path.sep)[-1]
    outputPath = os.path.sep.join([f"{dataset_path}/normal", filename])

    # copy the image
    shutil.copy2(imagePath, outputPath)
```

PLOT THE XRAYs

```
#helper functions to plot them in a grid
def ceildiv(a, b):
    return -(-a // b)

def plots_from_files(imspaths, figsize=(10,5), rows=1, titles=None, maintitle=None):
    """Plot the images in a grid"""
    f = plt.figure(figsize=figsize)
    if maintitle is not None: plt.suptitle(maintitle, fontsize=10)
    for i in range(len(imspaths)):
        sp = f.add_subplot(rows, ceildiv(len(imspaths), rows), i+1)
        sp.axis('Off')
        if titles is not None: sp.set_title(titles[i], fontsize=16)
        img = plt.imread(imspaths[i])
        plt.imshow(img)
```

```
normal_images = list(paths.list_images(f"{dataset_path}/normal"))
covid_images = list(paths.list_images(f"{dataset_path}/covid"))
```

```
plots_from_files(normal_images, rows=5, maintitle="Normal X-ray images")
```




```
plots_from_files(covid_images, rows=5, maintitle="Covid-19 X-ray images")
```

DATA PREPROCESSING

```
# grab the list of images in our dataset directory, then initialize
# the list of data (i.e., images) and class images
print("[INFO] loading images...")
imagePaths = list(paths.list_images(dataset_path))
data = []
labels = []
# loop over the image paths
for imagePath in imagePaths:
    # extract the class label from the filename
    label = imagePath.split(os.path.sep)[-2]
    # load the image, swap color channels, and resize it to be a fixed
    # 224x224 pixels while ignoring aspect ratio
    image = cv2.imread(imagePath)
    image = cv2.cvtColor(image, cv2.COLOR_BGR2RGB)
    image = cv2.resize(image, (224, 224))
    # update the data and labels lists, respectively
    data.append(image)
    labels.append(label)
# convert the data and labels to NumPy arrays while scaling the pixel
# intensities to the range [0, 1]
data = np.array(data) / 255.0
labels = np.array(labels)
```

```
labels = np.array(labels)
```

```
[INFO] loading images...
```

```
# perform one-hot encoding on the labels
lb = label_binarize(labels, classes=['covid','normal'])
#labels = lb.fit_transform(labels)
labels = to_categorical(lb)

# partition the data into training and testing splits using 80% of
# the data for training and the remaining 20% for testing
(trainX, testX, trainY, testY) = train_test_split(data, labels, test_size=0.20, stratify
# initialize the training data augmentation object
trainAug = ImageDataGenerator(rotation_range=15, fill_mode="nearest")
```

DEFINING THE MODEL

```
# initialize the initial learning rate, number of epochs to train for,
# and batch size
INIT_LR = 1e-3
EPOCHS = 20
BS = 8
```

```
baseModel = VGG16(weights="imagenet", include_top=False,input_tensor=Input(shape=(224, 2

# construct the head of the model that will be placed on top of the
# the base model
headModel = baseModel.output
headModel = AveragePooling2D(pool_size=(4, 4))(headModel)
headModel = Flatten(name="flatten")(headModel)
headModel = Dense(64, activation="relu")(headModel)
headModel = Dropout(0.5)(headModel)
headModel = Dense(2, activation="softmax")(headModel)

# place the head FC model on top of the base model (this will become
# the actual model we will train)
model = Model(inputs=baseModel.input, outputs=headModel)

# loop over all layers in the base model and freeze them so they will
# *not* be updated during the first training process
for layer in baseModel.layers:
    layer.trainable = False
```

```
Downloading data from https://github.com/fchollet/deep-learning-models/releases/download
58892288/58889256 [==============================] - 3s 0us/step
```

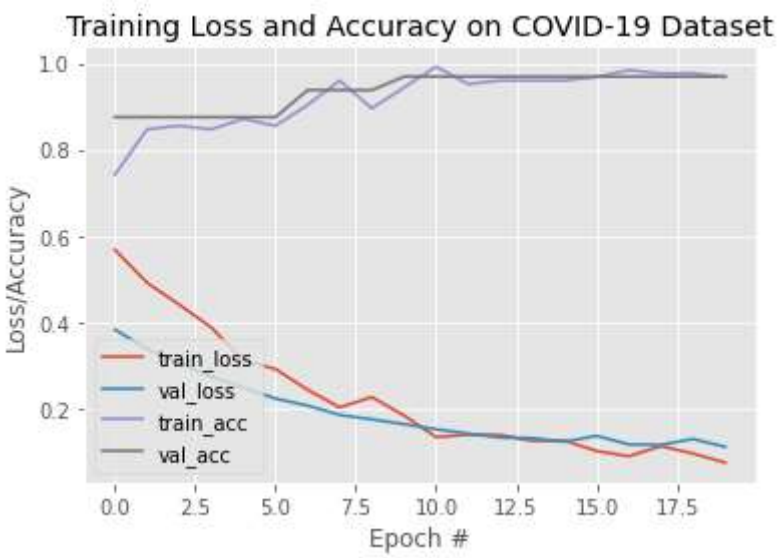
TRAINING

```
# compile our model
print("[INFO] compiling model...")
opt = Adam(lr=INIT_LR, decay=INIT_LR / EPOCHS)
model.compile(loss="binary_crossentropy", optimizer=opt,
metrics=["accuracy"])

# train the head of the network
print("[INFO] training head...")
H = model.fit_generator(trainAug.flow(trainX, trainY, batch_size=BS),steps_per_epoch=len
validation_steps=len(testX) // BS,
epochs=EPOCHS)
```

```
[INFO] compiling model...
[INFO] training head...
Train for 16 steps, validate on 34 samples
Epoch 1/20
16/16 [==============================] - 6s 405ms/step - loss: 0.5853 - accuracy: 0.7419
Epoch 2/20
16/16 [==============================] - 2s 98ms/step - loss: 0.5004 - accuracy: 0.8468
Epoch 3/20
16/16 [==============================] - 2s 98ms/step - loss: 0.4570 - accuracy: 0.8548
Epoch 4/20
16/16 [==============================] - 2s 94ms/step - loss: 0.3877 - accuracy: 0.8468
Epoch 5/20
16/16 [==============================] - 2s 98ms/step - loss: 0.3176 - accuracy: 0.8710
Epoch 6/20
16/16 [==============================] - 2s 102ms/step - loss: 0.2922 - accuracy: 0.8548
Epoch 7/20
16/16 [==============================] - 1s 93ms/step - loss: 0.2476 - accuracy: 0.9032
Epoch 8/20
16/16 [==============================] - 1s 92ms/step - loss: 0.2005 - accuracy: 0.9597
Epoch 9/20
16/16 [==============================] - 2s 94ms/step - loss: 0.2265 - accuracy: 0.8952
Epoch 10/20
16/16 [==============================] - 1s 92ms/step - loss: 0.1835 - accuracy: 0.9435
Epoch 11/20
16/16 [==============================] - 2s 94ms/step - loss: 0.1345 - accuracy: 0.9919
Epoch 12/20
16/16 [==============================] - 2s 94ms/step - loss: 0.1411 - accuracy: 0.9516
Epoch 13/20
16/16 [==============================] - 2s 105ms/step - loss: 0.1385 - accuracy: 0.9597
Epoch 14/20
16/16 [==============================] - 1s 93ms/step - loss: 0.1290 - accuracy: 0.9597
Epoch 15/20
16/16 [==============================] - 1s 93ms/step - loss: 0.1246 - accuracy: 0.9597
Epoch 16/20
16/16 [==============================] - 2s 94ms/step - loss: 0.1005 - accuracy: 0.9677
Epoch 17/20
16/16 [==============================] - 2s 94ms/step - loss: 0.0919 - accuracy: 0.9839
Epoch 18/20
16/16 [==============================] - 2s 94ms/step - loss: 0.1128 - accuracy: 0.9758
Epoch 19/20
16/16 [==============================] - 2s 98ms/step - loss: 0.0965 - accuracy: 0.9766
Epoch 20/20
16/16 [==============================] - 2s 110ms/step - loss: 0.0748 - accuracy: 0.9677
```

PLOT TRAINING METRICS

```
# plot the training loss and accuracy
N = EPOCHS
plt.style.use("ggplot")
plt.figure()
plt.plot(np.arange(0, N), H.history["loss"], label="train_loss")
plt.plot(np.arange(0, N), H.history["val_loss"], label="val_loss")
plt.plot(np.arange(0, N), H.history["accuracy"], label="train_acc")
plt.plot(np.arange(0, N), H.history["val_accuracy"], label="val_acc")
plt.title("Training Loss and Accuracy on COVID-19 Dataset")
plt.xlabel("Epoch #")
plt.ylabel("Loss/Accuracy")
plt.legend(loc="lower left")
plt.savefig("plot.png")
```



Part2: Analyzing each individual XRAYs****

in this section two tasks have been performed in an attempt to compare a normal chest XRAY with th deeper level

1. image clustering: to cluster the xrays into optimal level of clusters a. maybe, this culd help us cr semantic segmentation tasks(supervised approach) b. one common features of a covid19 xray chose unsupervised clustering approach is to differentiate the opaque part of the chest from th determining if the person might need a ventilator in near future.
2. bit plane slicing: this is a technique that is normally used in image compression. but this simple edges and boundaries. this information might be useful when compared with normal xray

for testing purposes, i tried both the tasks on a sample image. but thais can be done on all the images

for clustering, optimal value of clusters (k) has to be determined. this has been done using the elbow

```
#k_opt gives the optimal value of k.
def find_optimal_k(img):
    image = cv2.imread(img)
    # reshape the image to a 2D array of pixels and 3 color values (RGB)
    pixel_values = image.reshape((-1, 3))
    # convert to float
    pixel_values = np.float32(pixel_values)
    distortions = []
    inertias = []
    mapping1 = {}
    mapping2 = {}
    K = range(1,20)
    for k in K:
        #Building and fitting the model
        kmeanModel = KMeans(n_clusters=k).fit(pixel_values)
        kmeanModel.fit(pixel_values)
        distortions.append(sum(np.min(cdist(pixel_values, kmeanModel.cluster_centers_, '
        inertias.append(kmeanModel.inertia_)
        mapping1[k] = sum(np.min(cdist(pixel_values, kmeanModel.cluster_centers_, 'eucli
        mapping2[k] = kmeanModel.inertia_
        #find the optimal value of k
        # the approximate value of k is where the dip occurs
        #here, i have taken the dip to occur at that point where the distortion values s
    for i in K:
        if(mapping1[i] - mapping1[i+1]) <=2:
            k_opt = i
            break
    for key,val in mapping1.items():
        print(str(key)+' : '+str(val))


    plt.plot(K, distortions, 'bx-')
    plt.xlabel('Values of K')
    plt.ylabel('Distortion')
    plt.title('The Elbow Method using Distortion')
    plt.show()

    return k_opt

```

visualize clusters vs distortions. the optimal value of k occurs approximately at the dip

kmeans method

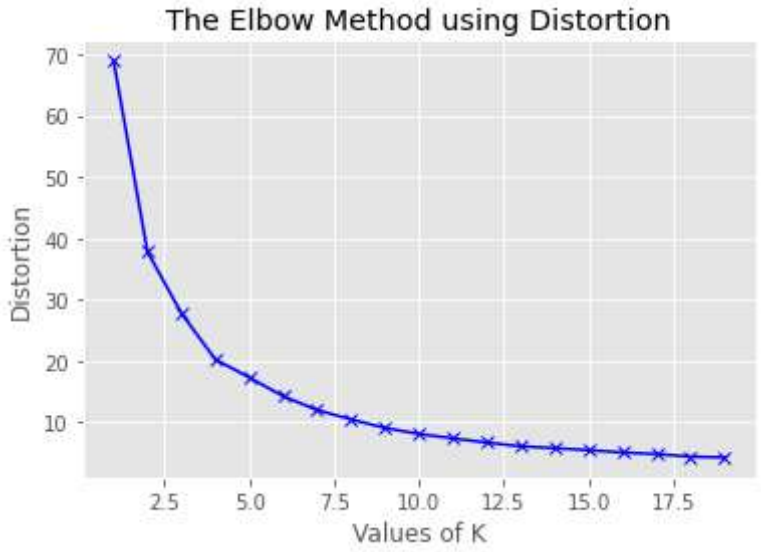
```
def kmeans_seg(img,k_opt):
    image = cv2.imread(img)
    # reshape the image to a 2D array of pixels and 3 color values (RGB)
    pixel_values = image.reshape((-1, 3))
    # convert to float
    pixel_values = np.float32(pixel_values)
    print(pixel_values.shape)
    # define stopping criteria
    criteria = (cv2.TERM_CRITERIA_EPS + cv2.TERM_CRITERIA_MAX_ITER, 100, 0.2)
    # number of clusters (K)
    k = k_opt
    _, labels, (centers) = cv2.kmeans(pixel_values, k, None, criteria, 10, cv2.KMEANS_RA
    # convert back to 8 bit values
    centers1 = np.uint8(centers)
    # flatten the labels array
    labels1 = labels.flatten()
    # convert all pixels to the color of the centroids
    segmented_image = centers1[labels1.flatten()]
    # reshape back to the original image dimension
    segmented_image1 = segmented_image.reshape(image.shape)
    # show the image
    plt.title('clustered xray')
    plt.imshow(segmented_image1)
    plt.show()
    plt.title('original xray')
    plt.imshow(image)
    plt.show()

```

testing it on a sample image

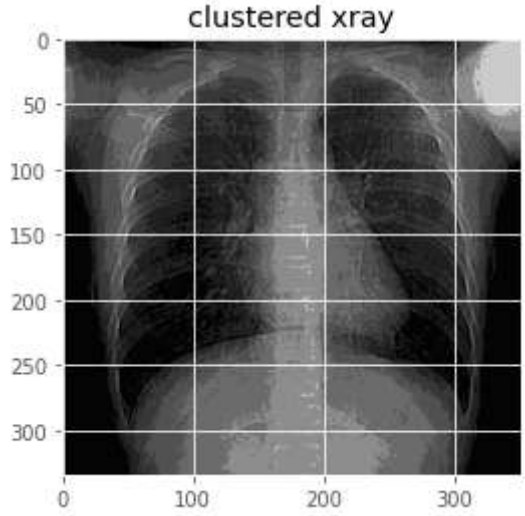
clustering on covid19 xray

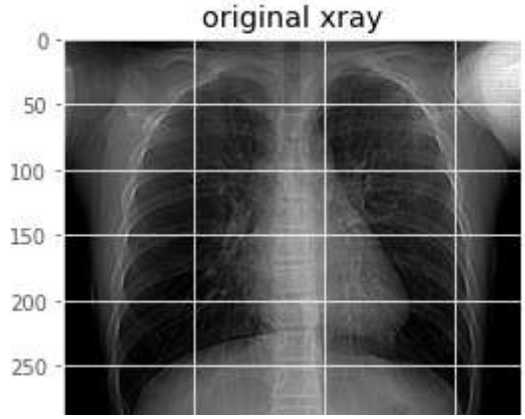
```
k_opt = find_optimal_k(covid_images[1])
kmeans_seg(covid_images[1],k_opt)

```

```
10 : 8.131232199432984
11 : 7.414758910007666
12 : 6.7336300126474935
13 : 6.121610478074323
14 : 5.823086398547219
15 : 5.484543315546248
16 : 5.115858229504767
17 : 4.86228753304588
18 : 4.442332423618841
19 : 4.307823580599332
```




```
(117568, 3)
```





clustering on normal xray

```
k_opt1 = find_optimal_k(normal_images[1])
kmeans_seg(normal_images[1],k_opt1)
```

```
def bit_plane_slicing(img):
    #read the image in grayscale
    image = cv2.imread(img,0)
    lst = []
    for i in range(image.shape[0]):
        for j in range(image.shape[1]):
            lst.append(np.binary_repr(image[i][j] ,width=8)) # width = no. of bits

    # We have a list of strings where each string represents binary pixel value. To extr
    # Multiply with 2^(n-1) and reshape to reconstruct the bit image.
    eight_bit_img = (np.array([int(i[0]) for i in lst],dtype = np.uint8) * 128).reshape(
    seven_bit_img = (np.array([int(i[1]) for i in lst],dtype = np.uint8) * 64).reshape(i
    six_bit_img = (np.array([int(i[2]) for i in lst],dtype = np.uint8) * 32).reshape(ima
    five_bit_img = (np.array([int(i[3]) for i in lst],dtype = np.uint8) * 16).reshape(im
    four_bit_img = (np.array([int(i[4]) for i in lst],dtype = np.uint8) * 8).reshape(ima
    three_bit_img = (np.array([int(i[5]) for i in lst],dtype = np.uint8) * 4).reshape(im
    two_bit_img = (np.array([int(i[6]) for i in lst],dtype = np.uint8) * 2).reshape(imag
    one_bit_img = (np.array([int(i[7]) for i in lst],dtype = np.uint8) * 1).reshape(imag

    fig = plt.figure(figsize = (16,8))
    fig,a =  plt.subplots(2,4)
    fig. tight_layout(pad=50)

    a[0][0].imshow(eight_bit_img)
    a[0][0].set_title('eight bit slice')
    a[0][1].imshow(seven_bit_img)
    a[0][1].set_title('seven bit slice')
    a[0][2].imshow(six_bit_img)
    a[0][2].set_title('six bit slice')
    a[0][3].imshow(five_bit_img)
    a[0][3].set_title('five bit slice')
    a[1][0].imshow(four_bit_img)
    a[1][0].set_title('four bit slice')
    a[1][1].imshow(three_bit_img)
    a[1][1].set_title('three bit slice')
    a[1][2].imshow(two_bit_img)
    a[1][2].set_title('two bit slice')
    a[1][3].imshow(one_bit_img)
    a[1][3].set_title('one bit slice')
```

testing it on a sample image

bit plane slicing of covid19 xrays

```
1   bit_plane_slicing(covid_images[1])
```

```
1   bit_plane_slicing(normal_images[1])
```