LUNG CANCER DETECTION USING YOLOV8 (Classification)

import os

import shutil

import random

from sklearn.model\_selection import train\_test\_split

# Define paths to your folders

data\_folders = ['Bengin cases', 'Malignant cases', 'Normal cases']

source\_directory = r'/content/drive/MyDrive/The IQ-OTHNCCD lung cancer dataset'

destination\_directory = r'/content/drive/MyDrive/The IQ-OTHNCCD lung cancer dataset'

# Define ratios for train, validation, and test sets

train\_ratio = 0.7

val\_ratio = 0.15

test\_ratio = 0.15

# Create destination directories for train, validation, and test sets

for folder in ['train', 'val', 'test']:

    for subfolder in data\_folders:

        os.makedirs(os.path.join(destination\_directory, folder, subfolder), exist\_ok=True)

# Split data into train, validation, and test sets for each folder

for folder in data\_folders:

    files = os.listdir(os.path.normpath(os.path.join(source\_directory, folder)))

    random.shuffle(files)

    train\_files, test\_val\_files = train\_test\_split(files, test\_size=(val\_ratio + test\_ratio), random\_state=42)

    val\_files, test\_files = train\_test\_split(test\_val\_files, test\_size=test\_ratio/(test\_ratio + val\_ratio), random\_state=42)

    # Move files to their respective directories

    for file in train\_files:

        shutil.move(os.path.join(source\_directory, folder, file), os.path.join(destination\_directory, 'train', folder))

    for file in val\_files:

        shutil.move(os.path.join(source\_directory, folder, file), os.path.join(destination\_directory, 'val', folder))

    for file in test\_files:

        shutil.move(os.path.join(source\_directory, folder, file), os.path.join(destination\_directory, 'test', folder))

print("Data split successfully.")

!nvidia-smi

import os

HOME = os.getcwd()

print(HOME)

!pip install ultralytics==8.0.196

from IPython import display

display.clear\_output()

import ultralytics

ultralytics.checks()

from ultralytics import YOLO

from IPython.display import display, Image

from google.colab import drive

drive.mount('/content/drive')

!yolo task=classify mode=train model='yolov8n-cls.pt' data='/content/drive/MyDrive/gdrive' epochs=100

!yolo task=classify mode=val split=test batch=1 model=runs/classify/train/weights/best.pt data='/content/drive/MyDrive/gdrive'

!yolo task=classify mode=predict save\_txt=True model=runs/classify/train/weights/best.pt conf=0.25 save=True source=/content/Bengin-case-29-\_jpg.rf.f9afac9e3fc492fc975e6bca98a9ebae.jpg

with open('/content/runs/classify/predict/labels/Bengin-case-29-\_jpg.rf.f9afac9e3fc492fc975e6bca98a9ebae.txt', 'r') as f:

    text = f.read()

print(text)

# Define the path to your text file

file\_path = '/content/runs/classify/predict3/labels/Normal-case-106-\_jpg.rf.6d8694cf4f7f25734e421f073cad92d1.txt'

# Initialize an empty list to store the lines

lines = []

# Open the file and read its content

with open(file\_path, 'r') as file:

    # Read each line and append it to the list

    for line in file:

        lines.append(line.strip())  # strip() removes leading and trailing whitespace

for i in lines:

  myString = i

  myList = myString.split(' ')

  length=len(myList)

  for j in range(length):

    if j==0:

      val=float(myList[j])

      if val>0.00:

        val\_1=myList[j+1]

        if val\_1=='Bengin' or val\_1=='Malignant':

          print('cancerous')

        elif val\_1=='Normal':

          print('Non cancerous')

    break

# Define the path to your text file

file\_path = '/content/runs/classify/predict2/labels/Malignant-case-154-\_jpg.rf.3cbfa978555e05727a27099627b41331.txt'

# Initialize an empty list to store the lines

lines = []

# Open the file and read its content

with open(file\_path, 'r') as file:

    # Read each line and append it to the list

    for line in file:

        lines.append(line.strip())  # strip() removes leading and trailing whitespace

for i in lines:

  myString = i

  myList = myString.split(' ')

  length=len(myList)

  for j in range(length):

    if j==0:

      val=float(myList[j])

      if val>0.00:

        val\_1=myList[j+1]

        if val\_1=='Bengin' or val\_1=='Malignant':

          print('cancerous')

        elif val\_1=='Normal':

          print('Non cancerous')

    break

# Define the path to your text file

file\_path = '/content/runs/classify/predict/labels/Bengin-case-29-\_jpg.rf.f9afac9e3fc492fc975e6bca98a9ebae.txt'

# Initialize an empty list to store the lines

lines = []

# Open the file and read its content

with open(file\_path, 'r') as file:

    # Read each line and append it to the list

    for line in file:

        lines.append(line.strip())  # strip() removes leading and trailing whitespace

for i in lines:

  myString = i

  myList = myString.split(' ')

  length=len(myList)

  for j in range(length):

    if j==0:

      val=float(myList[j])

      if val>0.00:

        val\_1=myList[j+1]

        if val\_1=='Bengin' or val\_1=='Malignant':

          print('cancerous')

        elif val\_1=='Normal':

          print('Non cancerous')

    break

!yolo task=classify mode=predict save\_txt=True show\_labels=True model=runs/classify/train/weights/best.pt conf=0.25 save=True source=/content/Malignant-case-154-\_jpg.rf.3cbfa978555e05727a27099627b41331.jpg

!yolo task=classify mode=predict save\_txt=True model=runs/classify/train/weights/best.pt conf=0.25 save=True source=/content/Normal-case-106-\_jpg.rf.6d8694cf4f7f25734e421f073cad92d1.jpg

Image(filename =f'/content/runs/classify/train/results.png',width=640)

Image(filename =f'/content/runs/classify/train/confusion\_matrix.png',width=640)

Image(filename =f'/content/runs/classify/val/confusion\_matrix.png',width=640)

Image(filename =f'/content/runs/classify/predict3/Normal-case-106-\_jpg.rf.6d8694cf4f7f25734e421f073cad92d1.jpg',width=640)

Image(filename =f'/content/runs/classify/predict/Bengin-case-29-\_jpg.rf.f9afac9e3fc492fc975e6bca98a9ebae.jpg',width=640)