Yolo 8 Brain Tumor Detect final

December 9, 2023

1 Introduction

The rapid evolution of medical imaging technologies has brought about transformative changes in the healthcare landscape. Among its many applications, one of the most crucial is the identification and classification of brain tumors. This complex task is paramount for healthcare professionals to determine appropriate treatment strategies and ultimately influence patient outcomes. The Brain Tumor Classification project aspires to harness state-of-the-art technologies and machine learning techniques to elevate the accuracy and efficiency of brain tumor diagnosis.

Brain tumors, whether benign or malignant, necessitate accurate and timely identification for effective medical intervention. Magnetic resonance imaging (MRI) scans, offering detailed visualization of internal brain structures, have emerged as indispensable tools for detecting abnormalities. This project is centered around crafting a robust classification system that analyzes MRI images. The project aims to automate the classification process by employing advanced machine learning algorithms, reducing reliance on manual interpretation and potentially expediting the diagnostic timeline.

The primary objectives of the Brain Tumor Classification project encompass achieving enhanced diagnostic accuracy through machine learning models, expediting the diagnosis process for time efficiency, and providing insights into tumor characteristics for personalized treatment planning. The exploration and implementation of advanced technologies, such as deep learning and image analysis, are critical to ensuring precision and reliability in tumor classification. The project also emphasizes seamless integration with existing healthcare systems and addresses ethical considerations surrounding patient privacy, data security, and the responsible use of artificial intelligence in the medical domain. In essence, the project stands at the intersection of medical science and technological innovation, with a mission to contribute to advancing neuroimaging and enhancing patient outcomes in the challenging domain of brain tumor diagnosis and classification.

2 Dataset

2.0.1 About the Selected Brain Tumor Image Detection Dataset

Data Source:

Subset of RSNA-MICCAI Brain Tumor Radiogenomic Classification dataset 400 images from the RSNA-MICCAI Brain Tumor Radiogenomic Classification dataset JPGs exported at their native size and separated by plane (Axial, Coronal, and Sagittal) and made available in Kaggle.

Key Features and Enhancements: 1. Manual Annotation: Tumors are hand-labeled using https://makesense.ai and bounding box coordinates and MGMT positive labels 2. Image Nor-

malization and Resizing: Original image sizes included 512x512, 256x512, 448x512 all which were multiples of 32 and so were handled with Yolo libraries with stride size 32

Dataset for demostration purposes It is important to note that although the source dataset which was released by the by the Radiological Society of North America (RSNA) in partnership with the American Society of Neuroradiology (ASNR) and the Medical Image Computing and Computer Assisted Interventions (MICCAI) Society as part of a brain tumor detection and classification using multi-parametric magnetic resonance imaging (mpMRI) scans, the annotated dataset used in our project has not been peer reviewed and so its use case should be only incldued as a proof of concept for demonstration purposes only. To move this project from proof of concept to production, one would need to anotate this images by a qualified health profesional and have them peer reviewed which is beyond the scope of this program.

Availability: Researchers and practitioners can access this dataset on Kaggle, providing a valuable resource for developing, testing, and validating machine learning models in the critical field of brain tumor classification.

2.1 Data Download

```
[1]: # import zipfile

# with zipfile.ZipFile('Brain_Tumors_256_by_256.zip', 'r') as zip_ref:

# zip_ref.extractall('Brain_Tumors_256_by_256')
```

```
[2]: # import zipfile

# with zipfile.ZipFile('Brain_Tumor_400_Images.zip', 'r') as zip_ref:

# zip_ref.extractall('Brain_Tumor_400_Images')
```

3 Data Processing

3.1 Preprocess the dataset

The Tumor detection dataset, initially consisting of labeled and unlabeled images and also consisting of only two segments, train and test was processed and organized into training, testing, and validation subsets with a ratio of 70:15:15 respectively

```
new_label_dir = os.path.join(base_dir, 'labels')
for folder in subfolders:
    os.makedirs(os.path.join(new_image_dir, folder), exist_ok=True)
    os.makedirs(os.path.join(new_label_dir, folder), exist_ok=True)
# Function to move files with renaming to avoid conflicts
def move_files(src_dir_img, src_dir_lbl, dest_img_dir,__
 dest_lbl_dir,class_prefix):
   files = os.listdir(src_dir_img)
   total_files = len(files)
    # creating indices for train:test:val => 70:15:15 distribution
   train_indices = np.arange(0,int(0.7*total_files))
   test_indices = np.arange(int(0.7*total_files),int(0.85*total_files))
   val_indices = np.arange(int(0.85*total_files),total_files)
   for i in np.arange(total_files):
       new_filename = f"{class_prefix}_{files[i]}"
        if i in train indices:
            shutil.move(os.path.join(src_dir_img, files[i]), os.path.

→join(dest_img_dir, 'train', new_filename))
            if os.path.exists(os.path.join(src_dir_lbl, files[i].replace('.
 →jpg', '.txt'))): # check if label file exists
                shutil.move(os.path.join(src_dir_lbl, files[i].replace('.jpg',__
 -'.txt')), os.path.join(dest_lbl_dir, 'train', new_filename.replace('.jpg', '.

stxt')))
        elif i in test indices:
            shutil.move(os.path.join(src_dir_img, files[i]), os.path.
 →join(dest_img_dir, 'test', new_filename))
            if os.path.exists(os.path.join(src_dir_lbl, files[i].replace('.
 →jpg', '.txt'))): # check if label file exists
                shutil.move(os.path.join(src_dir_lbl, files[i].replace('.jpg',__
 -'.txt')), os.path.join(dest_lbl_dir, 'test', new_filename.replace('.jpg', '.
 ⇔txt')))
        elif i in val indices:
            shutil.move(os.path.join(src_dir_img, files[i]), os.path.
 →join(dest_img_dir, 'validation', new_filename))
            if os.path.exists(os.path.join(src_dir_lbl, files[i].replace('.
 →jpg', '.txt'))): # check if label file exists
                shutil.move(os.path.join(src_dir_lbl, files[i].replace('.jpg',__
 -'.txt')), os.path.join(dest_lbl_dir, 'validation', new_filename.replace('.
 # Move and rename files from each class
```

```
for class_name in classes:
    for subfolder in ['train','test']: # for each of the original train/test_
    subfolders
    image_src = os.path.join(base_dir, class_name, 'images', subfolder)
    label_src = os.path.join(base_dir, class_name, 'labels', subfolder)

    move_files(image_src, label_src, new_image_dir, new_label_dir,_
    sclass_name)

print("Files successfully moved and organized into train and test sets.")
```

```
import os
import matplotlib.pyplot as plt
import cv2
import pandas as pd

# Directory paths
base_dir = 'Brain_Tumor_400_Images'
train_image_dir = os.path.join(base_dir,'images/train')
test_image_dir = os.path.join(base_dir,'images/test')
validation_image_dir = os.path.join(base_dir,'images/validation')

train_label_dir = os.path.join(base_dir,'labels/train')
test_label_dir = os.path.join(base_dir,'labels/test')
validation_label_dir = os.path.join(base_dir,'labels/test')
validation_label_dir = os.path.join(base_dir,'labels/validation')

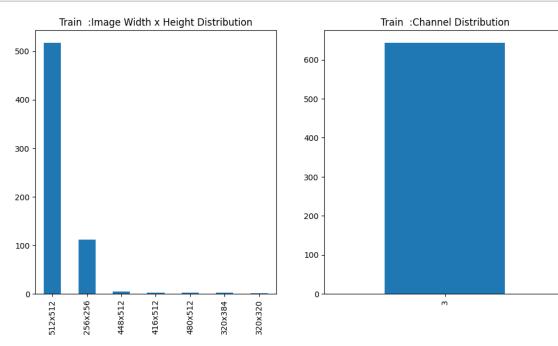
dataset = [(train_image_dir,"Train ",train_label_dir),(test_image_dir,"Test_u____,",test_label_dir),(validation_image_dir,"Validation ", validation_label_dir)]
```

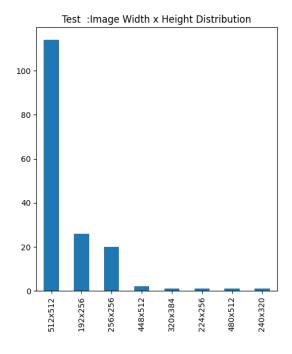
3.1.1 Visualize with a histogram with count distribution of images with different a) combination widthxheights and channels

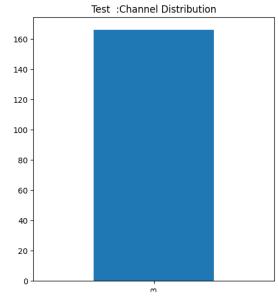
```
# Plotting histograms for width x height and channel distribution
plt.figure(figsize=(12,6))
plt.subplot(1,2,1)
df_sizes['WidthxHeight'].value_counts().plot(kind='bar')
plt.title(name +' : Image Width x Height Distribution')

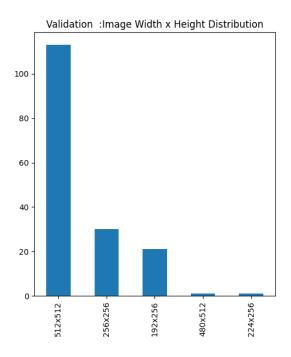
plt.subplot(1,2,2)
pd.Series(channels_count).value_counts().plot(kind='bar')
plt.title(name +' :Channel Distribution')

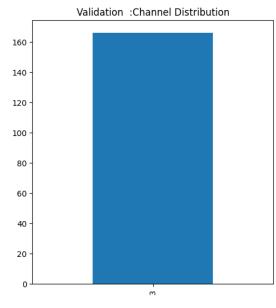
for dir, name, _ in dataset:
    visualize_histogram(dir, name)
```











3.1.2 Count all images that have missing lables and width xheights combination less less than 256×256

```
[50]: def count_missing_labels(images_directory, labels_directory):
          image_files_set = {file.split('.')[0] for file in os.
       →listdir(images_directory)}
          label_files_set = {file.split('.')[0] for file in os.
       →listdir(labels_directory)}
          missing_labels = image_files_set.difference(label_files_set)
          return len(missing_labels), len(image_files_set)
      def count_small_images(image_directory, threshold=(256,256)):
          count = 0
          for filename in os.listdir(image_directory):
              if filename.endswith('.png') or filename.endswith('.jpg'):
                  image_path = os.path.join(image_directory, filename)
                  img = cv2.imread(image_path)
                  height, width, _ = img.shape
                  if width < threshold[0] or height < threshold[1]:</pre>
                      count += 1
          return count
      for images_dir, name, labels_dir in dataset:
          missing count, total count=count missing labels (images dir, labels dir)
          print(f"Total {name} images: {total_count}, {name} Images without labels:
       →{missing count}")
      for images_dir, name, labels_dir in dataset:
          small_img_count=count_small_images(images_dir)
          print(f"{name} Images with size less than 256x256: {small img count}")
     Total Train images: 644, Train Images without labels: 1
     Total Test images: 166, Test Images without labels: 0
     Total Validation images: 166, Validation Images without labels: 0
     Train Images with size less than 256x256: 0
     Test Images with size less than 256x256: 28
```

3.1.3 Delete images that have missing lables

Validation Images with size less than 256x256: 22

```
print(os.path.join(images_directory, file+".jpg"))
    os.remove(os.path.join(images_directory, file+".jpg"))
for images_dir, name, labels_dir in dataset:
    delete_no_label_images(images_dir, labels_dir)
```

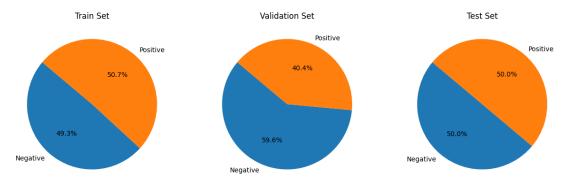
3.1.4 Delete images with dimentions less than 256x256

3.1.5 Verify the distribution of the datasets

```
[52]: import os
      import matplotlib.pyplot as plt
      def count_labels(directory):
          positive_count = 0
          negative_count = 0
          # Traverse through all files in the directory
          for filename in os.listdir(directory):
              if filename.endswith(".txt"):
                  filepath = os.path.join(directory, filename)
                  with open(filepath, 'r') as file:
                      line = file.readline()
                      label = line.split(' ')[0]
                      if label == '1':
                          positive_count += 1
                      elif label == '0':
                          negative_count += 1
```

```
return positive_count, negative_count
base_dir = 'Brain_Tumor_400_Images'
# Directories to traverse
dirs = ['train', 'validation', 'test']
data = {'train': [], 'validation': [], 'test': []}
# Count labels in each directory
for dir in dirs:
   pos, neg = count_labels(os.path.join(base_dir, 'labels', dir))
   data[dir] = [neg, pos]
# Plotting as pie charts
fig, axs = plt.subplots(1, len(dirs), figsize=(15, 5))
for i, dir in enumerate(dirs):
   axs[i].pie(data[dir], labels=['Negative', 'Positive'], autopct='%1.1f%%', __
 ⇔startangle=140)
   axs[i].set_title(f'{dir.capitalize()} Set')
plt.suptitle('Distribution of Positive and Negative Labels Across Datasets')
plt.show()
```

Distribution of Positive and Negative Labels Across Datasets



4 Detection

4.1 Random Print images from the Kaggle Dataset

```
[8]: import cv2
     import matplotlib.pyplot as plt
     import os
     import random
     def draw_bounding_box(img, labels, class_name):
         Function to draw bounding box and add class name on the image.
         for label in labels:
             # Parse label
             class_id, x_center, y_center, width, height = map(float, label.split())
             # Convert to pixel coordinates
             x_center = x_center * img.shape[1]
             y_center = y_center * img.shape[0]
             width = width * img.shape[1]
             height = height * img.shape[0]
             # Calculate minimum pixel coordinates
             x_min = int(x_center - width / 2)
             y_min = int(y_center - height / 2)
             # Determine class name based on class_id
             class_name = "tumor" if class_id == 1 else "no_tumor"
             # Draw bounding box and add class name
             cv2.rectangle(img, (x_min, y_min), (int(x_min + width), int(y_min +_u
      ⇔height)), (255, 0, 0), 2)
             cv2.putText(img, class_name, (x_min, y_min - 10), cv2.
      →FONT_HERSHEY_SIMPLEX, 0.5, (255, 0, 0), 2)
         return img
     # Directory paths
     base_dir = 'Brain_Tumor_400_Images'
     image_dir = os.path.join(base_dir,'images/train')
     label_dir = os.path.join(base_dir, 'labels/train')
     # Get random image files
     image_files = os.listdir(image_dir)
     random_images = random.sample(image_files, 9)
```

```
# Set up plot
fig, axes = plt.subplots(3, 3, figsize=(15, 15))
axes = axes.ravel()
for i, img_file in enumerate(random_images):
    # Paths for image and label
    image_path = os.path.join(image_dir, img_file)
    label_path = os.path.join(label_dir, img_file.replace('.jpg', '.txt'))
    try:
        # Load image and labels
        img = cv2.imread(image_path)
        if img is None:
            print(f"Image not loaded properly: {img_file}")
            continue
        # Get the dimensions of the image and print them
        height, width, _ = img.shape
        print(f"The image {img_file} is {width} pixels wide and {height} pixels⊔
 ⇔high.")
        img = cv2.cvtColor(img, cv2.COLOR_BGR2RGB)
        try:
            with open(label_path, 'r') as f:
                labels = f.readlines()
        except Exception as e:
            print(f"Error reading label file: {label_path}")
            continue
        # Draw bounding box
        if labels:
            img_with_boxes = draw_bounding_box(img, labels, "")
           # Display the image
            axes[i].imshow(img_with_boxes)
            axes[i].axis('off')
        else:
            print(f"No label found for: {img_file}")
    except Exception as e:
       print(f"Error loading image or drawing bounding box for: {img_file}")
       continue
plt.tight_layout()
```

plt.show()

The image axial_t1wce_2_class_00130_78.jpg is 256 pixels wide and 256 pixels high.

The image axial_t1wce_2_class_00111_110.jpg is 256 pixels wide and 256 pixels high.

The image sagittal_t1wce_2_class_00077_166.jpg is 512 pixels wide and 512 pixels high.

The image coronal_t1wce_2_class_88 (3).jpg is 512 pixels wide and 512 pixels high.

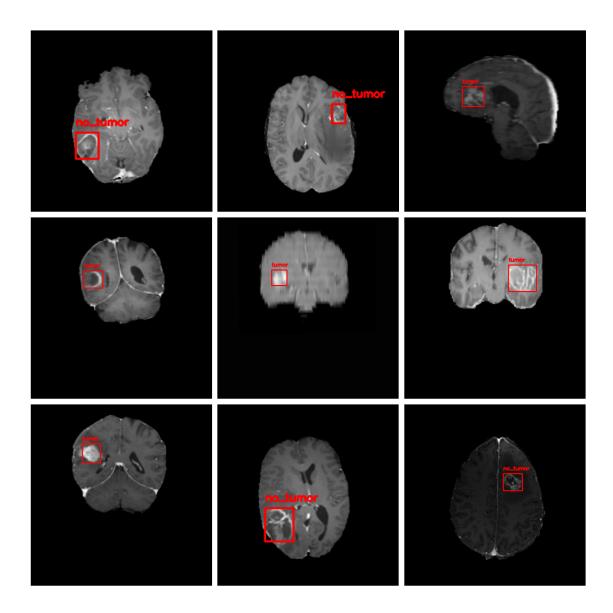
The image coronal_t1wce_2_class_74 (10).jpg is 512 pixels wide and 512 pixels high.

The image coronal_t1wce_2_class_74 (11).jpg is 512 pixels wide and 512 pixels high.

The image coronal_t1wce_2_class_87 (4).jpg is 512 pixels wide and 512 pixels high.

The image axial_t1wce_2_class_00130_100.jpg is 256 pixels wide and 256 pixels high.

The image axial_t1wce_2_class_00053_263.jpg is 512 pixels wide and 512 pixels high.



5 Training YOLO v8 for Tumor Detection

Developed by Ultralytics, YOLOv8 represents an advancement in state-of-the-art object detection and image segmentation models, released on January 10, 2023. It demonstrates superior speed and accuracy over other single-stage detectors like MobileNetSSDv2, primarily due to its ability to handle both object identification and classification in a single network pass. One of the key aspects of how YOLO operates is through image resizing which allows it to detect objects at different scales effectively.

```
[9]: from ultralytics import YOLO
#!wget https://github.com/ultralytics/assets/releases/download/v0.0.0/

⇔yolov8l-oiv7.pt .
```

```
#!wget https://github.com/ultralytics/assets/releases/download/v0.0.0/
yolov8x-oiv7.pt .

#!wget https://github.com/ultralytics/assets/releases/download/v0.0.0/
yolov8m-oiv7.pt .
```

5.0.1 Choice of YOLOv8m Medium trained on Open Image v7

We decided to employ the YOLOv8m medium checkpoints trained on Open Image V7 for our project. We made this choice based on several factors. Firstly, Open Image V7 has a larger number of pre-trained classes (600) compared to COCO's 80 pre-trained classes, providing a wider scope for detection and classification tasks in our data set. Secondly, comparing the performance metrics of YOLOv8m between both models, we observed that although there were differences in mAPval values and speed parameters between both versions, we expected that the benefits from using a more diverse dataset (Open Image V7), would outweigh any potential disadvantages. The dataset was trained on the medium checkpoint with 26.2M parameters for 20 epochs

```
[23]: model = YOLO('yolov8x-oiv7.pt') # load a pretrained model (recommended for_u straining)

results = model.train(data='combined.yaml', epochs=30, imgsz=640)
```

New https://pypi.org/project/ultralytics/8.0.225 available Update with 'pip

install -U ultralytics' Ultralytics YOLOv8.0.221 Python-3.9.18 torch-2.1.1+cu121 CUDA:0 (NVIDIA L4, 22488MiB) engine/trainer: task=detect, mode=train, model=yolov8x-oiv7.pt, data=combined.yaml, epochs=30, patience=50, batch=16, imgsz=640, save=True, save period=-1, cache=False, device=None, workers=8, project=None, name=train44, exist_ok=False, pretrained=True, optimizer=auto, verbose=True, seed=0, deterministic=True, single_cls=False, rect=False, cos_lr=False, close_mosaic=10, resume=False, amp=True, fraction=1.0, profile=False, freeze=None, overlap_mask=True, mask_ratio=4, dropout=0.0, val=True, split=val, save_json=False, save_hybrid=False, conf=None, iou=0.7, max_det=300, half=False, dnn=False, plots=True, source=None, vid_stride=1, stream_buffer=False, visualize=False, augment=False, agnostic_nms=False, classes=None, retina_masks=False, show=False, save_frames=False, save_txt=False, save_conf=False, save_crop=False, show_labels=True, show_conf=True, show_boxes=True, line_width=None, format=torchscript, keras=False, optimize=False, int8=False, dynamic=False, simplify=False, opset=None, workspace=4, nms=False, lr0=0.01, lrf=0.01, momentum=0.937, weight_decay=0.0005, warmup_epochs=3.0, warmup_momentum=0.8, warmup_bias_lr=0.1, box=7.5, cls=0.5, dfl=1.5, pose=12.0, kobj=1.0, label_smoothing=0.0, nbs=64, hsv_h=0.015, hsv_s=0.7, hsv_v=0.4, degrees=0.0, translate=0.1, scale=0.5, shear=0.0, perspective=0.0, flipud=0.0, fliplr=0.5, mosaic=1.0, mixup=0.0, copy_paste=0.0, cfg=None, tracker=botsort.yaml, save_dir=runs/detect/train44 Overriding model.yaml nc=601 with nc=2

from n params module

```
arguments
                                     ultralytics.nn.modules.conv.Conv
  0
                     -1 1
                                2320
[3, 80, 3, 2]
                              115520 ultralytics.nn.modules.conv.Conv
                     -1 1
[80, 160, 3, 2]
                     -1 3
                              436800 ultralytics.nn.modules.block.C2f
[160, 160, 3, True]
                     -1 1
                              461440 ultralytics.nn.modules.conv.Conv
[160, 320, 3, 2]
                             3281920 ultralytics.nn.modules.block.C2f
                     -1 6
[320, 320, 6, True]
                             1844480 ultralytics.nn.modules.conv.Conv
                     -1 1
[320, 640, 3, 2]
                            13117440 ultralytics.nn.modules.block.C2f
                     -1 6
[640, 640, 6, True]
                     -1 1
                             3687680 ultralytics.nn.modules.conv.Conv
[640, 640, 3, 2]
                     -1 3
                             6969600 ultralytics.nn.modules.block.C2f
[640, 640, 3, True]
                     -1 1
                             1025920 ultralytics.nn.modules.block.SPPF
[640, 640, 5]
                                    torch.nn.modules.upsampling.Upsample
10
                     -1 1
[None, 2, 'nearest']
                                   0 ultralytics.nn.modules.conv.Concat
11
                [-1, 6]
                        1
[1]
                     -1 3
                             7379200 ultralytics.nn.modules.block.C2f
12
[1280, 640, 3]
13
                     -1 1
                                   0 torch.nn.modules.upsampling.Upsample
[None, 2, 'nearest']
14
                [-1, 4]
                                   0 ultralytics.nn.modules.conv.Concat
                         1
[1]
15
                     -1 3
                             1948800 ultralytics.nn.modules.block.C2f
[960, 320, 3]
                     -1 1
                              922240 ultralytics.nn.modules.conv.Conv
[320, 320, 3, 2]
17
               [-1, 12] 1
                                   0 ultralytics.nn.modules.conv.Concat
[1]
18
                     -1 3
                             7174400 ultralytics.nn.modules.block.C2f
[960, 640, 3]
                             3687680 ultralytics.nn.modules.conv.Conv
19
                     -1 1
[640, 640, 3, 2]
20
                                   0 ultralytics.nn.modules.conv.Concat
                [-1, 9]
                       1
[1]
                             7379200 ultralytics.nn.modules.block.C2f
21
                     -1 3
[1280, 640, 3]
22
           [15, 18, 21] 1
                             8719894 ultralytics.nn.modules.head.Detect
[2, [320, 640, 640]]
YOLOv8x summary: 365 layers, 68154534 parameters, 68154518 gradients, 258.1
```

GFLOPs

Transferred 589/595 items from pretrained weights TensorBoard: Start with 'tensorboard --logdir runs/detect/train44', view at http://localhost:6006/ Freezing layer 'model.22.dfl.conv.weight' AMP: running Automatic Mixed Precision (AMP) checks with YOLOv8n... AMP: checks passed train: Scanning /home/jupyter/msaaiall/Vision/module7/Brain_Tumor_400_Images/labels/train.cache... 643 images, 0 | 643/643 [00:00<?, ?it/s] backgrounds, 0 corrupt: 100% val: Scanning /home/jupyter/msaaiall/Vision/module7/Brain_Tumor_400_Images/labels/validation.cache... 166 images, 0 backgrounds, 0 corrupt: 100% | 166/166 [00:00<?, ?it/s] Plotting labels to runs/detect/train44/labels.jpg... optimizer: 'optimizer=auto' found, ignoring 'lr0=0.01' and 'momentum=0.937' and determining best 'optimizer', 'lr0' and 'momentum' automatically... optimizer: AdamW(lr=0.001667, momentum=0.9) with parameter groups 97 weight(decay=0.0), 104 weight(decay=0.0005), 103 bias(decay=0.0) Image sizes 640 train, 640 val Using 8 dataloader workers Logging results to runs/detect/train44 Starting training for 30 epochs... Epoch box_loss cls_loss GPU_mem dfl_loss Instances Size 4.002 1/30 1.458 1.526 13.1G 640: | 41/41 [00:28<00:00, 1.46it/s] 100%| mAP50 Class Images Instances Box(P | 6/6 [00:02<00:00, 2.46it/s] mAP50-95): 100%| 176 0 0 all 166 0 0 Epoch GPU_mem box_loss cls_loss dfl loss Instances Size 2/30 1.363 1.52 7 640: 13.6G 1.811 100%| | 41/41 [00:27<00:00, 1.49it/s] Class Images Instances Box(P mAP50 mAP50-95): 100%| | 6/6 [00:02<00:00, 2.32it/s] 0 all 166 176 0 0 0

Epoch	GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
3/30 100% 4		1.413 27<00:00, 1		1.583	3	640:
mAP50-95): 10		Images 6/6 [00:02<			R	mAP50
	all	166	176	0	0	0
0						
Epoch	GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
4/30 100% 4		1.446 27<00:00, 1		1.571	4	640:
mAP50-95): 10	Class	Images	Instances		R	mAP50
4.99e-05	all	166	176	0.00437	0.00472	0.000117
Epoch	GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
5/30 100% 4		1.36		1.539	4	640:
mAP50-95): 10	Class	Images	Instances		R	mAP50
					0.0284	0.0139
0.00662						
-	_	_	_	_	Instances	
6/30 100% 4	1/41 [00:2	27<00:00, 1	.50it/s]		2	640:
mAP50-95): 10		Images 6/6 [00:02<			R	mAP50
0.00662	all	166	176	0.109	0.0284	0.0139
3.0002						

cls_loss

dfl_loss Instances

Size

Epoch

GPU_mem

box_loss

7/30 13.6G 1.318 1.504 1.495 100% 41/41 [00:27<00:00, 1.50it/s]	4	640:
Class Images Instances Box(P mAP50-95): 100% 6/6 [00:03<00:00, 1.98it/s]	R	mAP50
all 166 176 0.447 0.249	0.569	0.386
Epoch GPU_mem box_loss cls_loss dfl_loss	Instances	Size
8/30 13.6G 1.219 1.409 1.419 100% 41/41 [00:27<00:00, 1.50it/s]	6	640:
Class Images Instances Box(P mAP50-95): 100% 6/6 [00:03<00:00, 1.98it/s]	R	mAP50
all 166 176 0.445 0.292	0.656	0.44
Epoch GPU_mem box_loss cls_loss dfl_loss	Instances	Size
9/30 13.6G 1.2 1.356 1.417 100% 41/41 [00:27<00:00, 1.50it/s]	5	640:
Class Images Instances Box(P mAP50-95): 100% 6/6 [00:03<00:00, 1.96it/s]	R	mAP50
all 166 176 0.42 0.224	0.521	0.346
Epoch GPU_mem box_loss cls_loss dfl_loss	Instances	Size
10/30 13.6G 1.219 1.364 1.412 100% 41/41 [00:27<00:00, 1.50it/s]	3	640:
Class Images Instances Box(P mAP50-95): 100% 6/6 [00:03<00:00, 1.97it/s]	R	mAP50
all 166 176 0.433 0.291	0.708	0.44
Epoch GPU_mem box_loss cls_loss dfl_loss	Instances	Size
11/30 13.6G 1.207 1.386 1.417 100% 41/41 [00:27<00:00, 1.50it/s]	3	640:
Class Images Instances Box(P mAP50-95): 100% 6/6 [00:03<00:00, 1.98it/s]	R	mAP50

0.319)	all	166	176	0.423	0.706	0.473
	12/30 41)-95): 100	13.6G /41 [00:27 Class % 6	1.176 7<00:00, 1 Images 6/6 [00:03<	1.317 .50it/s] Instances 00:00, 1.9	1.386 Box(P 8it/s]	Instances 5 R 0.82	640: mAP50
	13/30 41 0-95): 100	13.6G /41 [00:27 Class % 6	1.195 7<00:00, 1 Images 5/6 [00:03<	1.322	1.396 Box(P 8it/s]	R	
	14/30 41)-95): 100	13.6G /41 [00:27 Class % 6	1.077 7<00:00, 1 Images 6/6 [00:03<	1.233 .50it/s] Instances 00:00, 1.9	1.303 Box(P 8it/s]	Instances 2 R 0.783	640: mAP50
	15/30 41 0-95): 100	13.6G /41 [00:27 Class % 6	1.105 '<00:00, 1 Images 6/6 [00:03<	1.239 .50it/s] Instances 00:00, 1.9	1.336 Box(P 8it/s]	Instances 4 R 0.798	640: mAP50

Epoch	GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
16/30 100% 4:		1.084		1.309	12	640:
mAP50-95): 100	Class	Images	Instances		R	mAP50
0.254	all	166	176	0.451	0.768	0.495
0.354						
	ap					a.
Epoch	GPU_mem	box_loss	cls_loss	dil_loss	Instances	Size
17/30 100% 4:		1.101 7<00:00, 1		1.329	6	640:
mAP50-95): 100		_			R	mAP50
	all	166	176	0.447	0.793	0.489
0.36						
Epoch	GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
18/30 100% 4:		1.099			5	640:
					R	mAP50
mAP50-95): 100)%	6/6 [00:03<	00:00, 1.9	7it/s]		
	all	166	176	0.463	0.767	0.497
0.358						
Epoch	GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
		1.11		1.321	4	640:
100% 4.	Class		Instances	Box(P	R	mAP50
mAP50-95): 100)%	6/6 [00:03<	00:00, 1.9	8it/s]		
	all	166	176	0.478	0.755	0.511
0.374						
Epoch	GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size

20/30 13.5G 1.033 1.149 1.267 100% 41/41 [00:27<00:00, 1.50it/s]	6	640:
Class Images Instances Box(P mAP50-95): 100% 6/6 [00:03<00:00, 1.98it/s]	R	mAP50
all 166 176 0.453 0.339	0.784	0.475
Closing dataloader mosaic		
Epoch GPU_mem box_loss cls_loss dfl_loss	Instances	Size
21/30 13.6G 1.022 1.2 1.359 100% 41/41 [00:27<00:00, 1.47it/s]	3	640:
Class Images Instances Box(P mAP50-95): 100% 6/6 [00:03<00:00, 1.98it/s]	R	mAP50
all 166 176 0.463	0.876	0.513
0.373		
	.	g.·
Epoch GPU_mem box_loss cls_loss dfl_loss		
22/30 13.6G 0.9933 1.138 1.361 100% 41/41 [00:27<00:00, 1.50it/s]		640:
Class Images Instances Box(P mAP50-95): 100% 6/6 [00:03<00:00, 1.98it/s]	R	mAP50
all 166 176 0.479 0.367	0.891	0.505
Epoch GPU_mem box_loss cls_loss dfl_loss	Instances	Size
23/30 13.6G 1.01 1.147 1.352	4	640:
100% 41/41 [00:27<00:00, 1.49it/s] Class Images Instances Box(P	R	mAP50
mAP50-95): 100% 6/6 [00:03<00:00, 1.96it/s]	16	mar 50
	0.818	0.525
0.388		
Epoch GPU_mem box_loss cls_loss dfl_loss	Instances	Size
-	3	640:
100% 41/41 [00:27<00:00, 1.50it/s]		

Class mAP50-95): 100%	Images 6/6 [00:03<			R	mAP50
all 0.374	166	176	0.451	0.872	0.513
Epoch GPU_mem	box loss	cls loss	dfl loss	Instances	Size
25/30 13.6G					640:
100% 41/41 [00:	27<00:00,	l.50it/s]			
Class mAP50-95): 100%	Images 6/6 [00:03<			R	mAP50
	166	176	0.445	0.882	0.506
0.372					
Epoch GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
26/30 13.6G 100% 41/41 [00:			1.264	3	640:
Class mAP50-95): 100%	Images			R	mAP50
	166			0 021	0 400
0.36	100	170	0.449	0.031	0.492
Epoch GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
27/30 13.6G	0.9071	1.046	1.267	3	640:
100% 41/41 [00:	27<00:00, 1 Images		Pow (D	R	mAP50
mAP50-95): 100%	_			r.	MAPSO
all	166	176	0.465	0.862	0.52
0.392					
Epoch GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
	0.8819		1.276	3	640:
100% 41/41 [00:	27<00:00, 1 Images		Box(P	R	mAP50
mAP50-95): 100%	_			10	

0.376	all	166	176	0.461	0.869	0.503
Epoch	GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
29/30 100% 4	13.6G 1/41 [00:27			1.215	3	640:
mAP50-95): 10		Images 8/6 [00:03<0			R	mAP50
0.399	all	166	176	0.467	0.888	0.521
Epoch	GPU_mem	box_loss	cls_loss	dfl_loss	Instances	Size
30/30 100% 4	13.6G			1.217	3	640:
mAP50-95): 10	Class	Images	Instances		R	mAP50
0.391	all	166	176	0.458	0.91	0.517

30 epochs completed in 0.356 hours.

Optimizer stripped from runs/detect/train44/weights/last.pt, 136.7MB Optimizer stripped from runs/detect/train44/weights/best.pt, 136.7MB

Validating runs/detect/train44/weights/best.pt...

Ultralytics YOLOv8.0.221 Python-3.9.18 torch-2.1.1+cu121 CUDA:0 (NVIDIA L4, 22488MiB)

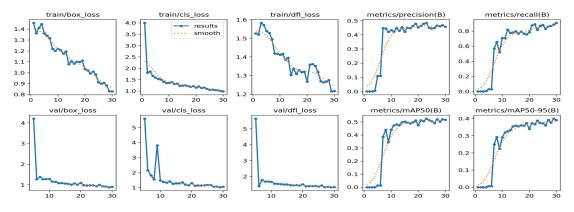
YOLOv8x summary (fused): 268 layers, 68125494 parameters, 0 gradients, 257.4 GFLOPs

mAP50-95):	Class	Images 6/6 [00:03<	Instances	Box(P 63it/s]	R	mAP50
0.398	all	166	176	0.465	0.887	0.519
	positive	166	106	0.565	0.93	0.64
0.483	negative	166	70	0.366	0.843	0.399
0.314						

Speed: 0.2ms preprocess, 13.7ms inference, 0.0ms loss, 0.7ms postprocess per image

Results saved to runs/detect/train44

```
[31]: run = "44"
      from PIL import Image
      from IPython.display import display
      width=2000
      height=int(width*.35)
      # Open the image file
      img = Image.open(f'runs/detect/train{run}/results.png')
      # Convert the image to RGB mode
      img_rgb = img.convert("RGB")
      # Specify the new size
      new_size = (width, int(height)) # Replace 'width' and 'height' with desired_
       \rightarrow values
      # Resize the image
      resized_img = img_rgb.resize(new_size)
      # Display the resized image in the notebook
      display(resized_img)
```



```
[25]: from PIL import Image
  from IPython.display import display, HTML

def display_images_side_by_side(run, filenames, width=2000):
    height = int(width * 0.7)
    images = []

# Load and resize each image
  for filename in filenames:
    img = Image.open(f'runs/detect/train{run}/{filename}').convert("RGB")
    resized_img = img.resize((width, height))
```

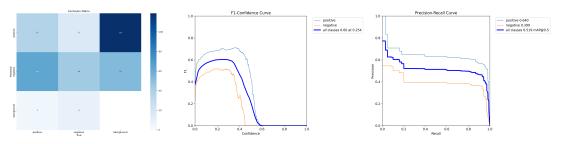
```
images.append(resized_img)

# Create a new blank image with enough width to contain all the images
total_width = width * len(images)
combined_img = Image.new('RGB', (total_width, height))

# Paste each image into the combined image
x_offset = 0
for img in images:
    combined_img.paste(img, (x_offset, 0))
    x_offset += width

# Display the combined image
display(combined_img)

filenames = ["confusion_matrix.png", "F1_curve.png", "PR_curve.png"]
display_images_side_by_side(run, filenames)
```



Results

Based on the confusion matrix, the accuracy of the model is approximately 23.28%. This means that about 23.28% of all predictions made by the model are correct. The relatively low accuracy suggests that the model might be struggling to correctly classify instances, especially considering the high number of misclassifications involving the background class. It might be beneficial to review the model's parameters, the data it was trained on, or consider other modeling approaches to improve performance.

5.1 Testing the model with the 256x256 Tumor Classification dataset

```
[29]: model = YOLO(f'runs/detect/train{run}/weights/best.pt')

import os
import random
import numpy as np
from PIL import Image
import matplotlib.pyplot as plt
```

```
validation_base_dir = 'Brain_Tumor_400_Images/images'
validation_classes = ['validation']
def predict_random_samples(model, validation_base_dir, classes, img_height):
    # Adjust the figure size based on the desired height for each image
   fig_width = 10  # you can change this as needed
   fig_height = img_height * 2 # 2 rows of images
   fig, axs = plt.subplots(2, 2, figsize=(fig_width, fig_height))
   for i in range(2):
       for j in range(2):
            # Randomly select class
            selected_class = random.choice(classes)
            # Get list of all image files for selected class
            image_files = os.listdir(os.path.join(validation_base_dir,__
 ⇔selected_class))
            # Randomly select two image files
            selected_images = random.sample(image_files, 2)
            for img_file in selected_images:
                img_path = os.path.join(validation_base_dir, selected_class,__
 →img_file)
                # Run prediction on each image and plot results
                result = model(img_path, save_txt=True, save_conf=True)
                for r in result:
                    im_array = r.plot() # plot a BGR numpy array of predictions
                    im = Image.fromarray(im_array[..., ::-1]) # Convert to RGB_
 →PIL image
                    axs[i, j].imshow(np.array(im))
                    axs[i, j].set_title(selected_class) # add title to plot
   plt.tight_layout()
   plt.show()
# Example usage
img_height = 10  # Set the desired height for each image
predict_random_samples(model, validation_base_dir, validation_classes,_
 →img height)
```

image 1/1 /home/jupyter/msaai-all/Vision/module7/Brain_Tumor_400_Images/images/v
alidation/axial_t1wce_2_class_00352_93.jpg: 640x480 1 positive, 14.8ms
Speed: 1.8ms preprocess, 14.8ms inference, 2.2ms postprocess per image at shape

(1, 3, 640, 480)

Results saved to runs/detect/predict31

1 label saved to runs/detect/predict31/labels

image 1/1 /home/jupyter/msaai-all/Vision/module7/Brain_Tumor_400_Images/images/v
alidation/axial_t1wce_2_class_00095_176.jpg: 640x640 1 positive, 1 negative,
16.5ms

Speed: 2.4ms preprocess, 16.5ms inference, 2.1ms postprocess per image at shape (1, 3, 640, 640)

Results saved to runs/detect/predict31

2 labels saved to runs/detect/predict31/labels

image 1/1 /home/jupyter/msaai-all/Vision/module7/Brain_Tumor_400_Images/images/v
alidation/coronal_t1wce_2_class_44.jpg: 640x640 1 positive, 14.8ms

Speed: 2.6ms preprocess, 14.8ms inference, 2.0ms postprocess per image at shape (1, 3, 640, 640)

Results saved to runs/detect/predict31

3 labels saved to runs/detect/predict31/labels

image 1/1 /home/jupyter/msaai-all/Vision/module7/Brain_Tumor_400_Images/images/v
alidation/coronal_t1wce_2_class_58 (4).jpg: 640x640 1 positive, 14.8ms

Speed: 2.6ms preprocess, 14.8ms inference, 2.1ms postprocess per image at shape (1, 3, 640, 640)

Results saved to runs/detect/predict31

4 labels saved to runs/detect/predict31/labels

image 1/1 /home/jupyter/msaai-all/Vision/module7/Brain_Tumor_400_Images/images/v
alidation/coronal_t1wce_2_class_83 (4).jpg: 640x640 1 positive, 14.8ms

Speed: 2.5ms preprocess, 14.8ms inference, 2.1ms postprocess per image at shape (1, 3, 640, 640)

Results saved to runs/detect/predict31

5 labels saved to runs/detect/predict31/labels

image 1/1 /home/jupyter/msaai-all/Vision/module7/Brain_Tumor_400_Images/images/v
alidation/axial_t1wce_2_class_00263_116.jpg: 640x480 1 positive, 1 negative,
15.1ms

Speed: 1.6ms preprocess, 15.1ms inference, 2.1ms postprocess per image at shape (1, 3, 640, 480)

Results saved to ${\tt runs/detect/predict31}$

6 labels saved to runs/detect/predict31/labels

image 1/1 /home/jupyter/msaai-all/Vision/module7/Brain_Tumor_400_Images/images/v
alidation/sagittal_t1wce_2_class_00162_122.jpg: 640x640 1 positive, 15.9ms

Speed: 2.5ms preprocess, 15.9ms inference, 2.0ms postprocess per image at shape (1, 3, 640, 640)

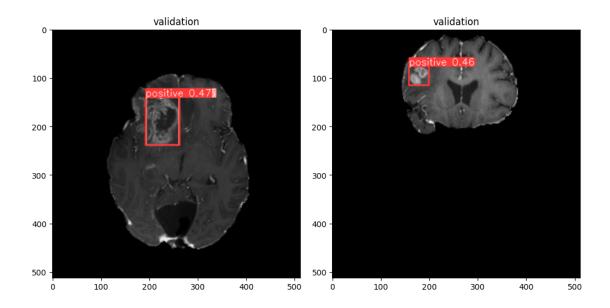
Results saved to runs/detect/predict31

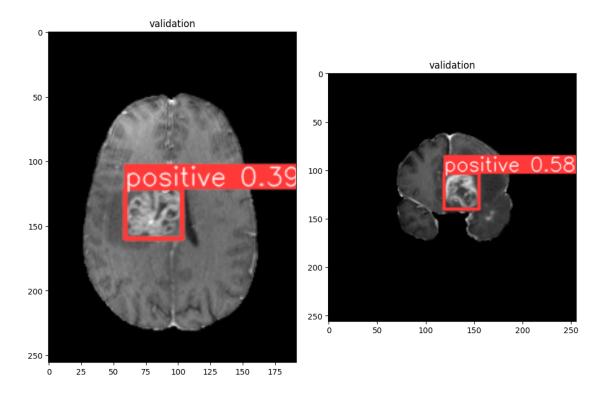
7 labels saved to runs/detect/predict31/labels

image 1/1 /home/jupyter/msaai-all/Vision/module7/Brain_Tumor_400_Images/images/v
alidation/coronal_t1wce_2_class_106 (2).jpg: 640x640 1 positive, 14.8ms
Speed: 2.3ms preprocess, 14.8ms inference, 2.1ms postprocess per image at shape
(1, 3, 640, 640)

Results saved to ${\tt runs/detect/predict31}$

8 labels saved to runs/detect/predict31/labels





6 Conclusion

In conclusion, our project demonstrated the feasibility of constructing a two-stage machine learning pipeline for brain tumor analysis. We successfully tested the pipeline on a classification dataset comprising glioma, meningioma, normal, and pituitary tumor images. The results, while limited by the lack of medical review and peer-reviewed annotations, highlight the potential of this approach in assisting medical professionals by classifying and localizing brain tumors. However, for clinical application, a dataset annotated by healthcare professionals and subjected to peer review is essential. Our work serves primarily as a proof of concept, underscoring the need for rigorous validation before deployment in a medical setting.

7 References

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