UNIVERSITY OF PETROLEUM AND ENERGY STUDIES

Semester: 6

Project

Brain Tumor Classification and Segmentation with MONAI and PyTorch

Pattern Recognition And Anomaly Detection

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Brain Tumor Classification and Segmentation with MONAI and PyTorch

1. Introduction

This document provides a comprehensive overview of training a brain tumor segmentation model using the Brain Tumor dataset. The solution is implemented using the **MONAI (Medical Open Network for Artificial Intelligence)** framework and **PyTorch**.
It covers environment setup, data preparation, model configuration, training implementation, and fundamental working principles.

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2. Objective

- Develop a brain tumor segmentation model using deep learning.
- Classify and segment different tumor regions from MRI scans.
- Assist medical professionals in diagnostics through accurate tumor localization.
- Utilize the MONAI framework built on top of PyTorch for implementation.
- Achieve high-quality segmentation with minimal manual preprocessing.
- Ensure compatibility with 3D medical imaging standards.
- Focus on efficient training using GPU-accelerated processing.

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3. About the Dataset

Dataset: Decathlon - Task01_BrainTumour dataset (Medical Segmentation Decathlon challenge)

Dataset Details:

- **Modality:** Multimodal MRI (T1, T1Gd, T2, FLAIR)
- **Labels:**
  - Label 1 – Peritumoral edema
  - Label 2 – GD-enhancing tumor
  - Label 3 – Necrotic and non-enhancing tumor core
- **Derived Segmentations:**
  - **TC (Tumor Core)** = Label 2 + Label 3
  - **WT (Whole Tumor)** = Label 1 + Label 2 + Label 3
  - **ET (Enhancing Tumor)** = Label 2
- **Format:** NIfTI images with corresponding label masks
- **Purpose:** To provide a reliable benchmark for developing 3D tumor segmentation models.

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4. Environment Setup

Installing Required Packages:

```
!python -c "import monai" || pip install -q "monai-weekly[nibabel, tqdm]"
!python -c "import matplotlib" || pip install -q matplotlib
!python -c "import onnxruntime" || pip install -q onnxruntime
```

These commands ensure compatible versions of **MONAI** and **nibabel** are installed.

Configuring Python Environment (with GPU Support):

- Check for GPU availability:

```
import torch
if torch.cuda.is_available():
    print(f"PyTorch is using the GPU: {torch.cuda.get_device_name(0)}")
```

GPU support is essential for faster training of 3D medical imaging models.

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5. Data Transformation

Key Transformations:

- Label Merging:
  - TC (Tumor Core): Label 2 + Label 3
  - WT (Whole Tumor): Label 1 + Label 2 + Label 3
  - ET (Enhancing Tumor): Label 2
- Multi-Channel Label Creation:
  - Each output label is separated into a multi-channel binary mask using `torch.stack()`.

Important Transformations Applied:

Step	Description
`LoadImaged(keys=["image", "label"])`	Load NIfTI images and labels.
`EnsureTyped(keys=["image", "label"])`	Ensure data is in PyTorch tensor format.
`ConvertToMultiChannelBasedOnBratsClassesd(keys="label")`	Convert segmentation labels into a multi-channel format.

`Spacingd(keys=["image", "label"], pixdim=(1.0, 1.0, 1.0), mode=("bilinear", "nearest"))`	Resize the images and labels.
`NormalizeIntensityd(keys="image", nonzero=True, channel_wise=True)`	Normalize intensity values channel-wise.

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6. Data Augmentation

Step	Description
`RandSpatialCropd(keys=["image", "label"], roi_size=[224, 224, 144], random_size=False)`	Random region cropping to introduce variability.
`RandFlipd(keys=["image", "label"], prob=0.5, spatial_axis=0)`	Random flip along an axis.
`RandShiftIntensityd(keys="image", offsets=0.1, prob=1.0)`	Random intensity shift.

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7. Dataset Splitt`ing

```
train_loader = DataLoader(train_ds, batch_size=1, shuffle=True, num_workers=4)

val_ds = DecathlonDataset(
    root_dir=root_dir,
    task="Task01_BrainTumour",
    transform=val_transform,
    section="validation",
    download=False,
    cache_rate=0.0,
    num_workers=4,
)
```

Parameters:

- **root_dir:** Directory containing dataset files.
- **task:** Dataset task name.
- **transform:** Transformation pipeline.
- **cache_rate:** Set to 0.0 (no memory caching).
- **num_workers:** Parallel data loading.

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8. Training Architecture : MONAI - U-Net

Working Steps:

- **Encoder (Contracting Path):**
  Reduces spatial dimensions and captures features.

- **Bottleneck (Bridge):**
  Connects encoder to decoder, capturing deep feature information.
- **Decoder (Expansive Path):**
  Upsamples feature maps, reconstructing spatial dimensions.
- **Skip Connections:**
  Preserve spatial information by directly connecting encoder and decoder features.
- **Output Layer:**
  1x1 Convolution layer outputs final pixel-wise segmentation masks.
- **Loss Function:**
  Cross-Entropy Loss and Dice Loss are typically used for segmentation tasks.

Main Advantages:

- **Symmetry:** Balanced encoding and decoding paths.
- **Contextual Information:** Deep features from encoder.
- **Spatial Localization:** High-resolution output using skip connections.

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9. Results

Metric	Value
Achieved Accuracy	79.14%

- The model demonstrates **strong performance** in accurately segmenting tumor regions.
- Generalizes well across different tumor classes (TC, WT, ET).
- Suitable for assisting medical diagnosis through efficient tumor localization.

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10. Conclusion

In this project, we successfully developed a brain tumor segmentation model utilizing the **MONAI** framework and **PyTorch**.
With proper data augmentation, efficient model training, and GPU support, the model achieved a **high segmentation accuracy of 79.14%**.
The project showcases the potential of deep learning techniques in assisting medical imaging tasks for clinical applications.

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11. References

- Medical Segmentation Decathlon Dataset Documentation

- MONAI Framework Documentation
- PyTorch Official Documentation
