National College of Ireland

Configuration Manual for Advancing Biomedical Image Segmentation of Lower-Grade Gliomas using Transfer Learning

MSc Research Project
Msc in Data analytics

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MSc Project Submission Sheet

School of Computing

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Configuration Manual for Advancing Biomedical Image Segmentation of Lower-Grade Gliomas using Transfer Learning

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1. Introduction

This configuration manual provides detailed instructions for setting up and running the model used in the research titled "Advancing Biomedical Image Segmentation of Lower-Grade Gliomas using Transfer Learning" using the Swin Transformer model for tumor segmentation in MRI images of lower-grade gliomas (LGGs).

The manual includes software requirements, hardware configurations, and step-by-step guidance on how to prepare the environment, dataset, and model for training, validation, and testing.

2. Prerequisites

Before you start, make sure you have the following:

2.1. Hardware Requirements

- GPU: A machine with at least one NVIDIA GPU (e.g., GTX 1080 or better) is highly recommended for training deep learning models.
- RAM: Minimum 16 GB RAM.
- Storage: SSD with at least 50 GB of free space for storing datasets and models.

2.2. Software Requirements

- Operating System: Linux (Ubuntu 18.04 or later), Windows (with WSL2), or macOS.
- Python: Version 3.8 or later.
- CUDA and cuDNN: For GPU acceleration (Optional, but recommended for faster training).
- Libraries and Frameworks:
  - TensorFlow or PyTorch (depending on which framework is used for implementation)
  - transformers library (from Hugging Face, for using transformer models)
  - scikit-learn
  - matplotlib, seaborn (for plotting and visualization)
  - opencv-python, Pillow (for image processing)
  - SimpleITK, nibabel (for handling medical imaging formats like MRI scans)

3. Dataset Configuration

3.1. Dataset Overview

The dataset used for training and evaluation in this project is the LGG-MRI dataset, which consists of MRI scans of patients with lower-grade gliomas along with their corresponding tumor masks.

- Format: TIFF images and binary segmentation masks.
- Size: 256x256 pixel images.

3.2. Dataset Setup

Download the Dataset:

- The dataset can be downloaded from Kaggle or other public repositories.

```
# Collects paths of all images in the specified directory
all_image_paths = []

for dirname in os.listdir(dataset_path):
    if os.path.isdir(os.path.join(dataset_path, dirname)):

        for filename in os.listdir(os.path.join(dataset_path, dirname)):
            # Only the files with ',tif' format should be added to the 'paths' list
            if filename.endswith('.tif'):
                all_image_paths.append(dataset_path+'/'+dirname+'/'+filename)

len(all_image_paths), all_image_paths[:25:1]
```

- Make sure the images and masks are organized in directories as follows:

```
(7858,
 ['dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_8_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_9_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_2_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_3_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_20_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_9.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_15_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_14_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_8.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_16.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_18_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_19_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_17.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_15.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_14.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_12_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_13_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_10.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_11.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_13.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_5_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_4_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_12.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_16_mask.tif',
  'dataset/lgg-mri-segmentation/kaggle_3m/TCGA_CS_6667_20011105/TCGA_CS_6667_20011105_17_mask.tif'])
```

Data Preprocessing:

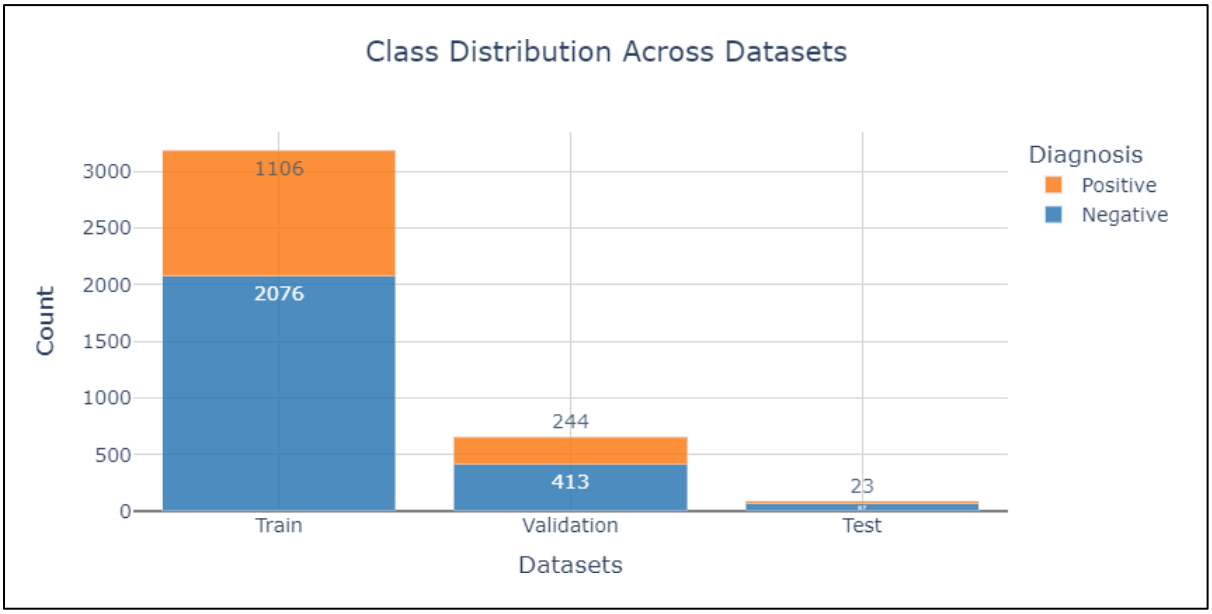
- Resize images to a consistent size (e.g., 256x256 pixels).

```python
# Processes the image
def decode_and_resize_image(img_path):
    # Reading '.tiff' format image
    img = tf.io.read_file(img_path)
    with tf.io.gfile.GFile(img_path, 'rb') as f:
        img = Image.open(f)
        img = np.array(img)
    img = tf.convert_to_tensor(img, dtype=tf.float32)
    img = tf.image.resize(img, IMAGE_SIZE, preserve_aspect_ratio=True)

    # Normalizing the image to the range [0, 1]
    img = img / 255.0

    return img
```

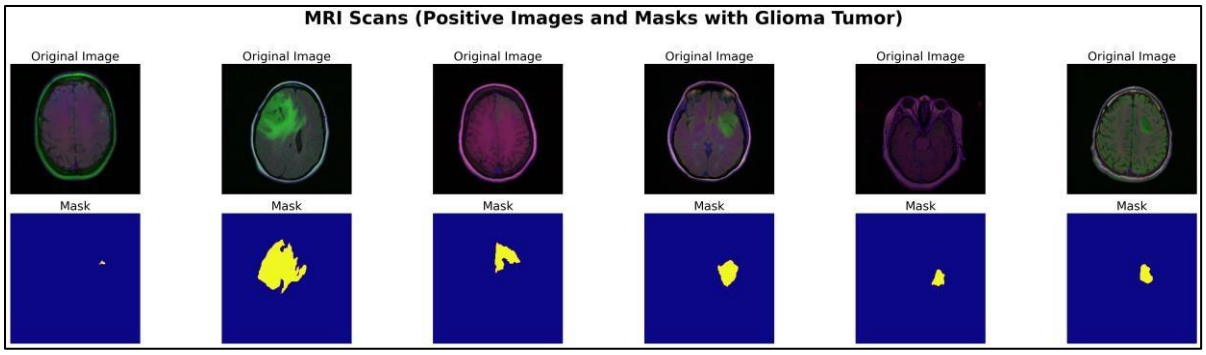
- Normalize pixel values (e.g., scale between 0 and 1).

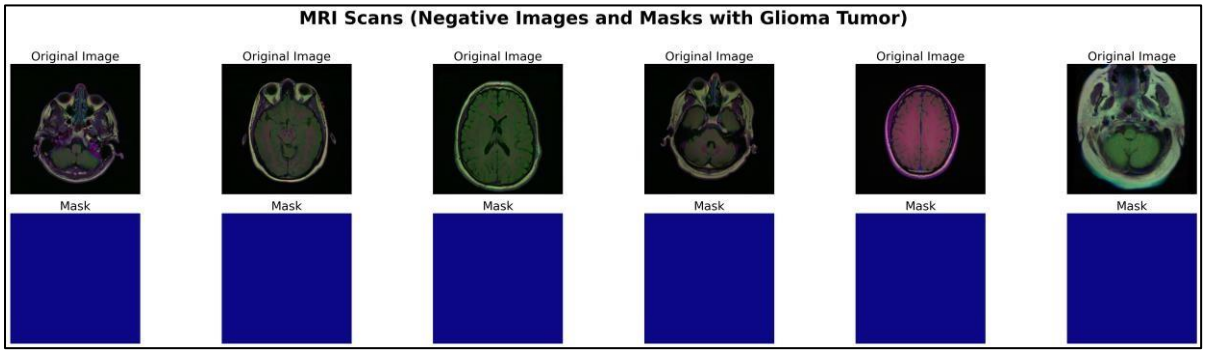
```python
# Processes the mask
def decode_and_resize_mask(mask_path):
    # Reading '.tiff' format masks
    mask = tf.io.read_file(mask_path)
    with tf.io.gfile.GFile(mask_path, 'rb') as f:
        mask = Image.open(f)
        mask = np.array(mask)
    mask = tf.convert_to_tensor(mask, dtype=tf.float32)
    mask = np.expand_dims(mask, axis=-1)
    mask = tf.image.resize(mask, IMAGE_SIZE, method='nearest', preserve_aspect_ratio=True)
    grayscale_mask = tf.reduce_mean(mask, axis=-1, keepdims=True)

    # Normalizing the mask to the range [0, 1]
    grayscale_mask = grayscale_mask / 255.0

    return grayscale_mask
```

- Split the dataset into training (70%), validation (15%), and test (15%) sets.



- Apply data augmentation (e.g., random rotations, zooming, flipping) to increase the diversity of the training set.






```
# Display the some value attributes of training dataset
train_data.head()
```

Python

	ID	Image	Mask	Diagnosis
812	TCGA_DU_5853_19950823_8	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_DU...	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_DU...	0
1550	TCGA_DU_5871_19941206_15	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_DU...	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_DU...	0
2228	TCGA_DU_8163_19961119_21	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_DU...	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_DU...	0
1108	TCGA_DU_7304_19930325_11	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_DU...	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_DU...	0
3728	TCGA_HT_7881_19981015_52	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_HT...	dataset/lgg-mri-segmentation/kaggle_3m/TCGA_HT...	0

4. Defining the Segmentation Model for Lower-Grade Glioma Segmentation through Transfer Learning

4.1. Load Pretrained Swin Transformer

The Swin Transformer model is available in the transformers library by Hugging Face. You can use a pretrained Swin Transformer model fine-tuned for image segmentation tasks.

4.2. Model Customization

To use the pretrained Swin Transformer for segmentation, modify the model architecture to include a final convolutional layer for pixel-wise classification:

4.3. Freezing Layers for Transfer Learning
Fine-tune only the later layers to adapt the model for medical imaging tasks:

```
# Building the Segmentation model
def build_segmentation_model(input_shape=(256, 256, 3)):
    inputs = layers.Input(shape=input_shape)

    # Use pre-trained Swin Transformer model layer (classification task)
    layer = SwinForImageClassification.from_pretrained("microsoft/swin-base-patch4-window7-224")

    # Convolutional layers
    x = layers.Conv2D(32, (3, 3), padding='same', activation='relu')(inputs)
    x = layers.MaxPooling2D(pool_size=(2, 2))(x)

    x = layers.Conv2D(64, (3, 3), padding='same', activation='relu')(x)
    x = layers.MaxPooling2D(pool_size=(2, 2))(x)

    x = layers.Conv2D(128, (3, 3), padding='same', activation='relu')(x)
    x = layers.MaxPooling2D(pool_size=(2, 2))(x)

    # Flatten the output for dense layers
    x = layers.Flatten()(x)
    x = layers.Dense(256, activation='relu')(x)
    x = layers.Dense(128, activation='relu')(x)

    # Output layer with a dense layer
    outputs = layers.Dense(input_shape[0] * input_shape[1], activation='sigmoid')(x)

    # Reshape output to match the input dimensions
    outputs = layers.Reshape((input_shape[0], input_shape[1], 1))(outputs)

    # Creating the model
    model = models.Model(inputs, outputs)

    return model

# Instantiate the model
model = build_segmentation_model()

# Compile the model
model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

# Summary of the model
model.summary()
```

5. Training Configuration for Segmentation Model

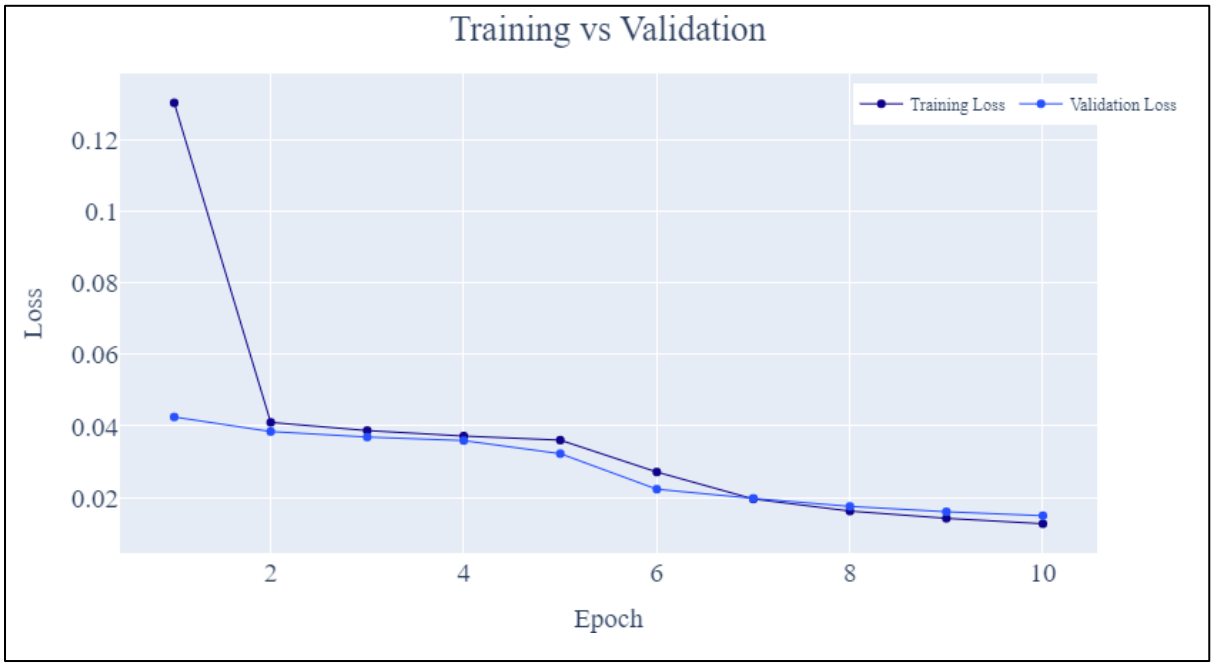
5.1. Hyperparameters
Adjust the following hyperparameters based on your system and dataset:

- Learning Rate: 0.001 (for Adam optimizer)
- Epochs: 10 (adjust based on convergence)
- Optimizer: Adam

- Loss Function: Binary Cross-Entropy for segmentation

```
# Training the model
history = model.fit(train_dataset, validation_data=validation_dataset,
                    epochs=10)
```

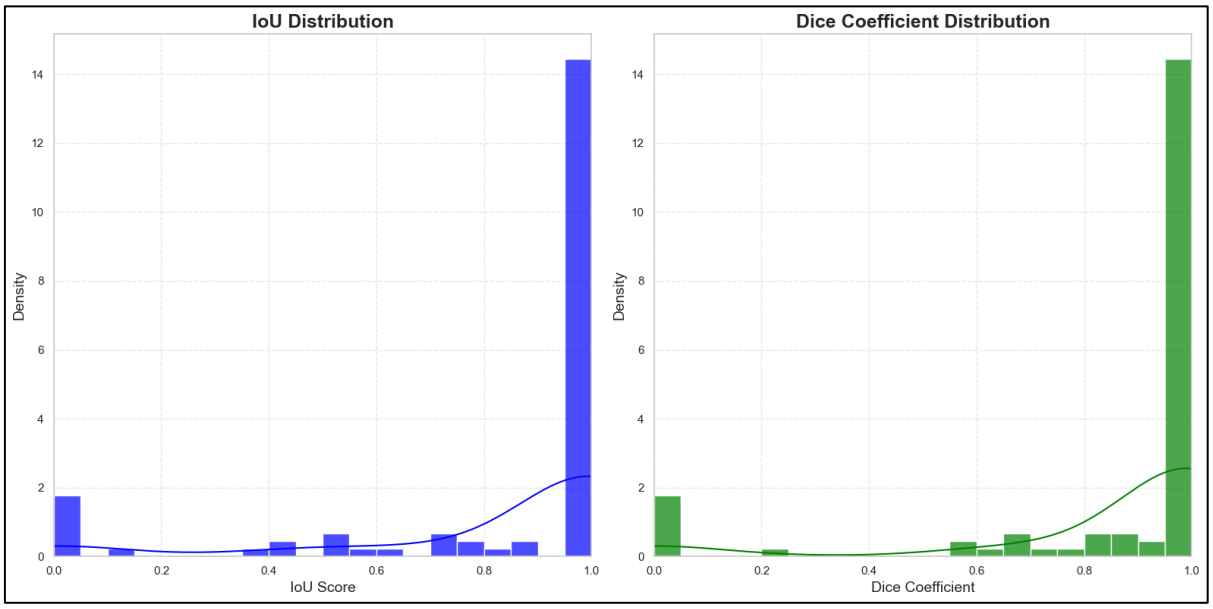
```
Epoch 1/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 81s 1s/step - accuracy: 0.9049 - loss: 0.2625 - val_accuracy: 0.9897 - val_loss: 0.0425
Epoch 2/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 99s 1s/step - accuracy: 0.9898 - loss: 0.0417 - val_accuracy: 0.9897 - val_loss: 0.0384
Epoch 3/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 98s 1s/step - accuracy: 0.9898 - loss: 0.0387 - val_accuracy: 0.9897 - val_loss: 0.0369
Epoch 4/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 114s 2s/step - accuracy: 0.9900 - loss: 0.0366 - val_accuracy: 0.9897 - val_loss: 0.0359
Epoch 5/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 101s 1s/step - accuracy: 0.9897 - loss: 0.0361 - val_accuracy: 0.9900 - val_loss: 0.0322
Epoch 6/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 116s 2s/step - accuracy: 0.9910 - loss: 0.0294 - val_accuracy: 0.9920 - val_loss: 0.0223
Epoch 7/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 108s 2s/step - accuracy: 0.9928 - loss: 0.0204 - val_accuracy: 0.9928 - val_loss: 0.0197
Epoch 8/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 110s 2s/step - accuracy: 0.9939 - loss: 0.0169 - val_accuracy: 0.9935 - val_loss: 0.0175
Epoch 9/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 107s 2s/step - accuracy: 0.9945 - loss: 0.0150 - val_accuracy: 0.9940 - val_loss: 0.0160
Epoch 10/10
71/71 ━━━━━━━━━━━━━━━━━━━━ 121s 2s/step - accuracy: 0.9949 - loss: 0.0133 - val_accuracy: 0.9943 - val_loss: 0.0149
```

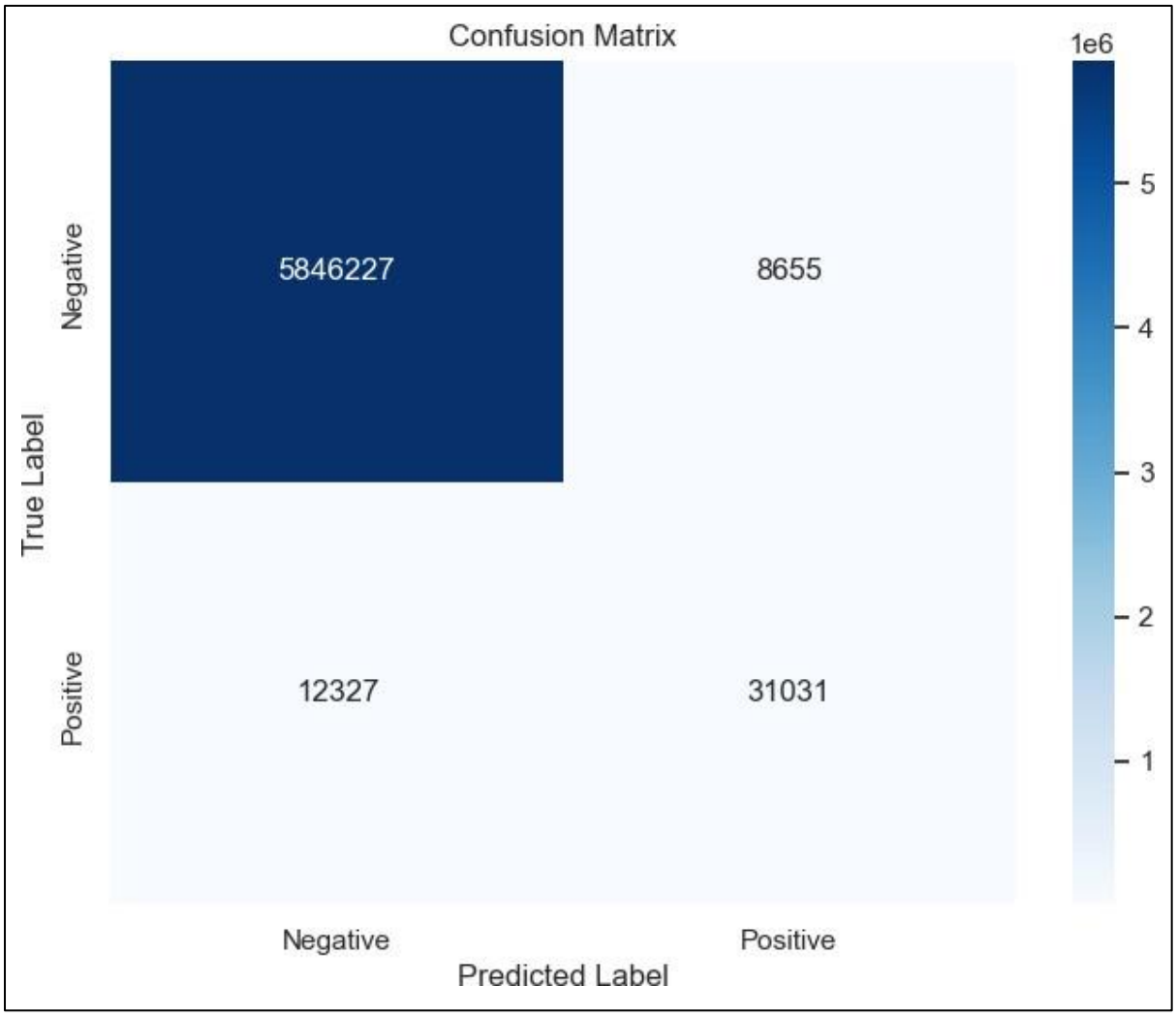


6. Evaluation Configuration

6.1. Segmentation Metrics

Evaluate the model using metrics like IoU, Dice Similarity Coefficient (DSC), and Confusion Matrix:


IoU Distribution
Density
IoU Score
0.0
0.2
0.4
0.6
0.8
1.0
0
2
4
6
8
10
12
14
Dice Coefficient Distribution
Density
Dice Coefficient


Confusion Matrix
1e6
5
4
3
2
1
True Label
Negative
Positive
5846227
8655
12327
31031
Negative
Positive
Predicted Label

```
Classification Report:
              precision    recall  f1-score   support

    Negative       1.00      1.00      1.00   5854882
    Positive       0.78      0.72      0.75     43358

    accuracy                           1.00   5898240
   macro avg       0.89      0.86      0.87   5898240
weighted avg       1.00      1.00      1.00   5898240
```

Conclusion

This manual provides the necessary steps to configure and run the segmentation model for lower-grade gliomas using a Swin Transformer-based architecture with transfer learning. By following this guide, users can replicate the results of this study or adapt the approach for their own medical imaging tasks.

References

Python: https://www.python.org
Dataset Source: https://www.kaggle.com/datasets/mateuszbuda/lgg-mri-segmentation