University of Moratuwa
Department of Electronic and Telecommunication Engineering
EN3160 - Image Processing and Machine Vision
Semester 5

Project Report
Brain Tumor Segmentation
Group Enigma

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This report is submitted as a partial fulfillment of the module EN3160 - Image Processing and Machine Vision

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1 Outline of the Problem

A brain tumor is an abnormal mass of tissue in which cells grow and reproduce uncontrollably, seemingly unrestricted by the processes that govern normal cells. Although there are over 150 distinct types of brain tumors known to exist, primary and metastatic brain tumors are the two main categories.

Tumors that arise from the brain's tissues or the brain's surrounding tissues are referred to as primary brain tumors. Primary tumors can be classified as benign or malignant, glial which are made up of glial cells or non-glial which are formed on or in the brain's structures, such as nerves, blood vessels, and glands. Tumors that originate in other parts of the body (such the breast or lungs) then spread to the brain, typically through the bloodstream are called metastatic tumors.

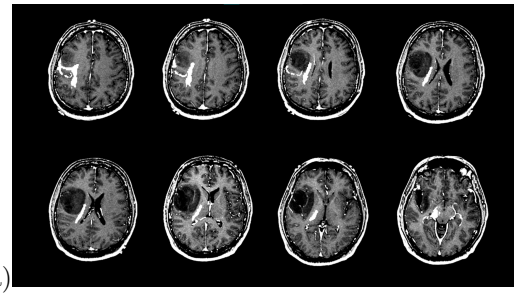
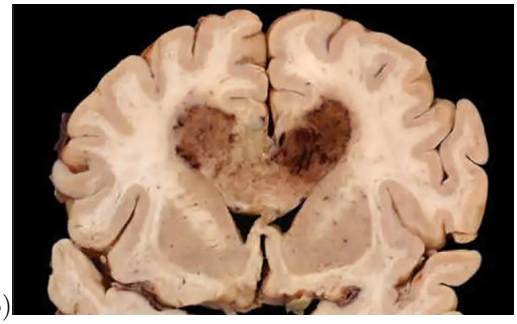
(a)  (b) 

Figure 1: (a) Growth of Brain Tumor (b) Actual Image of a Tumor

Types of brain tumors include

- Gliomas: These are tumors that originate in the glial cells, which provide support and protection to nerve cells. Gliomas are the most common primary brain tumors and are classified into subtypes based on the specific glial cell involved. Some common glioma types include:
  - Glioblastoma (GBM): An aggressive and malignant form of glioma.
  - Astrocytoma: Arising from astrocytes, a type of glial cell.
  - Oligodendroglioma: Originating in oligodendrocytes, another type of glial cell.
  - Ependymoma: Developing from ependymal cells lining the ventricles of the brain and the central canal of the spinal cord.
- Meningiomas: These tumors develop in the meninges, the protective layers surrounding the brain and spinal cord. Most meningiomas are benign, slow-growing tumors
- Pituitary Tumors: These tumors form in the pituitary gland, which is a small gland located at the base of the brain. Pituitary tumors can be benign or, in rare cases, malignant.

- Medulloblastomas: These are malignant tumors that typically occur in the cerebellum, often in children.
- Schwannomas: Also known as vestibular schwannomas or acoustic neuromas, these tumors develop from Schwann cells and primarily affect the nerves responsible for hearing and balance.
- Hemangioblastomas: These are usually benign tumors that form in blood vessels of the brain, spinal cord, or retina.
- Pineal Region Tumors: Pineal region tumors develop in or around the pineal gland and can include pineocytomas and pineoblastomas.
- Chordomas: Chordomas are slow-growing tumors that develop from remnants of the notochord, a structure in early development that is replaced by the spine.

An estimated 150,000 individuals annually, or almost one in four cancer patients, get brain metastases from their malignancies. It is estimated that up to 40 percent of lung cancer patients will experience brain tumor metastases. Patients with these malignancies used to have extremely poor prognoses, with normal survival rates of only a few weeks.

2 Existing Solutions

Brain tumors can be diagnosed using several methods.

- **Clinical assessment:** A thorough clinical assessment conducted by a healthcare professional is done. The medical history of the patient is examined, taking into account any neurological symptoms, any family history of brain tumors, and other pertinent health data. In order to evaluate neurological function and search for any symptoms or indicators that can point to a brain tumor, a physical examination is also performed.
- **Medical imaging:** The following imaging methods are most frequently employed:
  - Magnetic Resonance Imaging (MRI): MRI scans are a highly useful tool for evaluating the size, location, and features of brain tumors because they produce detailed pictures of the brain. Certain cancers may be made more visible with the application of contrast agents.
  - Computed Tomography (CT) Scan: Cross-sectional pictures of the brain can occasionally be obtained using CT scans. Because they may identify certain types of cancers and bleeding sooner than MRI scans, they are very helpful in emergency circumstances.
  - Positron Emission Tomography (PET) scans: PET scans may distinguish between healthy and tumorous brain tissue and are used to evaluate metabolic activity in the brain.
- **Biopsy:** In some cases, a biopsy may be required to determine its type and grade. A biopsy involves the removal of a small tissue sample from the tumor for microscopic examination by a pathologist. This can help determine if the tumor is benign or malignant and provide information on its specific type and characteristics.

Out of the above methods, medical imaging plays a key role in identifying brain tumors and with the development of deep learning based systems in medical imaging, identifying brain tumors out of the healthy tissues in the brain has become much easier. There are several reasons why deep learning based methods are highly effective in brain tumor identification.

- Feature Learning: Convolutional neural networks (CNNs), in particular, are deep learning models that can automatically extract pertinent features from the input. This is especially crucial for medical imaging, where the intricacy of the data makes human feature engineering difficult. Intricate characteristics in the photos that are essential for tumor segmentation can be captured by CNNs since they can learn hierarchical representations of the image.
- Information about Space: CNNs are made to identify spatial relationships in the data. The context and position of structures in medical imaging are sometimes just as significant as their individual features. Accurate tumor identification and segmentation depend on deep learning models' ability to concurrently take into account local and global spatial information.

- Hierarchical Representations: Deep learning models are able to capture hierarchical information because of their numerous layers. Their ability to identify low-level characteristics, such as edges and textures, progressively advances to high-level characteristics, such as tumor borders and forms. This enables them to discern minute variations between tumor and healthy tissues.
- Scalability: The scalability of deep learning models is quite high. They are appropriate for a variety of imaging modalities, including MRI, CT, and PET scans, since they can handle both 2D and 3D medical picture data. By changing the number of layers and filters, its design may also be tailored to varied issue difficulties.

3 Proposed Solution

Although deep learning based solutions give more accurate segmentation results, there are a few issues in those solution.

- Brain imaging results are skewed because tumors are tiny in relation to the rest of the brain. Because of this categorization, training a deep model frequently results in low true positive rates, and existing networks become skewed towards the one over-represented class.
- Restricted medical imaging datasets with annotations are a major difficulty. Accurate tumor annotations must be obtained from big and varied datasets in order to train deep learning models. The quality of the data, including noise and image resolution, can also affect how well the model performs.
- Deep learning models are often seen as "black boxes," making it challenging for clinicians to trust and interpret their results. Developing techniques for model's interpretation ability in medical imaging is an active area of research.
- Deterministic segmentation is frequently provided by deep learning algorithms. But it's crucial to quantify and communicate forecast uncertainty, particularly when the model can be confused about the tumor borders. Estimating uncertainty is essential to clinical decision support.
- Most of the deep learning techniques are complex in structure which are time consuming when running. They need more resources to run as well.

The proposed method of brain tumor segmentation is a deep learning technique which has the following architecture. It is following the UNET architecture but built in a custom manner.

```
Layer (type)                 Output Shape              Param No.     Connected to
==================================================================================================

input_1 (InputLayer)         [(None, 128, 128, 1       0             []
                             28, 3)]
conv3d (Conv3D)              (None, 128, 128, 12       1312          ['input_1[0][0]']
                             8, 16)
dropout (Dropout)            (None, 128, 128, 12       0             ['conv3d[0][0]']
                             8, 16)
conv3d_1 (Conv3D)            (None, 128, 128, 12       6928          ['dropout[0][0]']
                             8, 16)
max_pooling3d (MaxPooling3D)  (None, 64, 64, 64,       0             ['conv3d_1[0][0]']
                             16)

conv3d_2 (Conv3D)            (None, 64, 64, 64,        13856         ['max_pooling3d[0][0]']
                             32)
dropout_1 (Dropout)          (None, 64, 64, 64,        0             ['conv3d_2[0][0]']
                             32)
conv3d_3 (Conv3D)            (None, 64, 64, 64,        27680         ['dropout_1[0][0]']
                             32)
max_pooling3d_1 (MaxPooling3D)  (None, 32, 32, 32,     0             ['conv3d_3[0][0]']
                             32)
conv3d_4 (Conv3D)            (None, 32, 32, 32,        55360         ['max_pooling3d_1[0][0]']
                             64)
dropout_2 (Dropout)          (None, 32, 32, 32,        0             ['conv3d_4[0][0]']
                             64)
conv3d_5 (Conv3D)            (None, 32, 32, 32,        110656        ['dropout_2[0][0]']
                             64)
max_pooling3d_2 (MaxPooling3D)  (None, 16, 16, 16,     0             ['conv3d_5[0][0]']
                             64)
conv3d_6 (Conv3D)            (None, 16, 16, 16,        221312        ['max_pooling3d_2[0][0]']
```

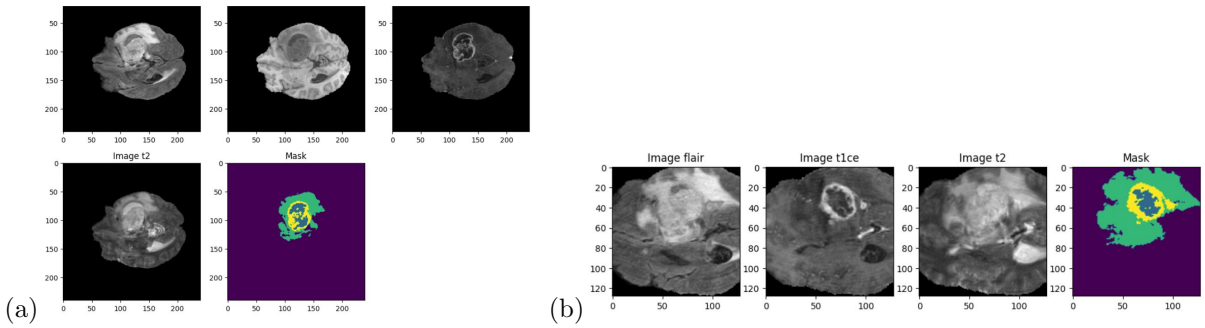
```
                                128)
 dropout_3 (Dropout)            (None, 16, 16, 16,   0           ['conv3d_6[0][0]']
                                128)
 conv3d_7 (Conv3D)              (None, 16, 16, 16,   442496      ['dropout_3[0][0]']
                                128)
 max_pooling3d_3 (MaxPooling3D)  (None, 8, 8, 8, 128  0          ['conv3d_7[0][0]']
                                )
 conv3d_8 (Conv3D)              (None, 8, 8, 8, 256  884992      ['max_pooling3d_3[0][0]']
                                )
 dropout_4 (Dropout)            (None, 8, 8, 8, 256  0           ['conv3d_8[0][0]']
                                )
 conv3d_9 (Conv3D)              (None, 8, 8, 8, 256  1769728     ['dropout_4[0][0]']
                                )
 conv3d_transpose (Conv3DTransp  (None, 16, 16, 16,   262272     ['conv3d_9[0][0]']
 ose)                           128)
 concatenate (Concatenate)      (None, 16, 16, 16,   0           ['conv3d_transpose[0][0]',
                                256)                              'conv3d_7[0][0]']

 conv3d_10 (Conv3D)             (None, 16, 16, 16,   884864      ['concatenate[0][0]']
                                128)
 dropout_5 (Dropout)            (None, 16, 16, 16,   0           ['conv3d_10[0][0]']
                                128)
 conv3d_11 (Conv3D)             (None, 16, 16, 16,   442496      ['dropout_5[0][0]']
                                128)
 conv3d_transpose_1 (Conv3DTran  (None, 32, 32, 32,   65600      ['conv3d_11[0][0]']
 spose)                         64)
 concatenate_1 (Concatenate)    (None, 32, 32, 32,   0           ['conv3d_transpose_1[0][0]'
                                                                  ,
                                128)                              'conv3d_5[0][0]']

 conv3d_12 (Conv3D)             (None, 32, 32, 32,   221248      ['concatenate_1[0][0]']
                                64)
 dropout_6 (Dropout)            (None, 32, 32, 32,   0           ['conv3d_12[0][0]']
                                64)
 conv3d_13 (Conv3D)             (None, 32, 32, 32,   110656      ['dropout_6[0][0]']
                                64)
 conv3d_transpose_2 (Conv3DTran  (None, 64, 64, 64,   16416      ['conv3d_13[0][0]']
 spose)                         32)
 concatenate_2 (Concatenate)    (None, 64, 64, 64,   0           ['conv3d_transpose_2[0][0]'
                                                                  ,
                                64)                               'conv3d_3[0][0]']

 conv3d_14 (Conv3D)             (None, 64, 64, 64,   55328       ['concatenate_2[0][0]']
                                32)
 dropout_7 (Dropout)            (None, 64, 64, 64,   0           ['conv3d_14[0][0]']
                                32)
 conv3d_15 (Conv3D)             (None, 64, 64, 64,   27680       ['dropout_7[0][0]']
                                32)
 conv3d_transpose_3 (Conv3DTran  (None, 128, 128, 12  4112       ['conv3d_15[0][0]']
 spose)                         8, 16)
 concatenate_3 (Concatenate)    (None, 128, 128, 12  0           ['conv3d_transpose_3[0][0]'
                                                                  ,
                                8, 32)                            'conv3d_1[0][0]']

 conv3d_16 (Conv3D)             (None, 128, 128, 12  13840       ['concatenate_3[0][0]']
                                8, 16)
 dropout_8 (Dropout)            (None, 128, 128, 12  0           ['conv3d_16[0][0]']
                                8, 16)
 conv3d_17 (Conv3D)             (None, 128, 128, 12  6928        ['dropout_8[0][0]']
                                8, 16)
 conv3d_18 (Conv3D)             (None, 128, 128, 12  68          ['conv3d_17[0][0]']
                                8, 4)
==================================================================================================

Total params: 5,645,828
Trainable params: 5,645,828
Non-trainable params: 0
```

The dataset used to train the model will be the **BraTS2020 Dataset** which contains images and the masks obtained by pre-processing techniques of the following MRI sequences.

- FLAIR (Fluid Attenuated Inversion Recovery): Particularly sensitive to the presence of cerebrospinal fluid which helps in highlighting pathological structures like edema (swelling) and lesions.

- T1CE (T1-Contrast Enhanced): Which is acquired after the administration of a contrast agent, such as Gadolinium and highlights areas of abnormal blood-brain barrier permeability.
- T2 (T2-Weighted): Helps in visualizing brain structures, including white matter, gray matter, and cerebrospinal fluid.
- T1 (T1-Weighted): Can show the location and shape of brain tumors and their relationship to surrounding healthy brain tissue

The images are rescaled and reshaped so the model can be efficiently trained in a shorter period of time.

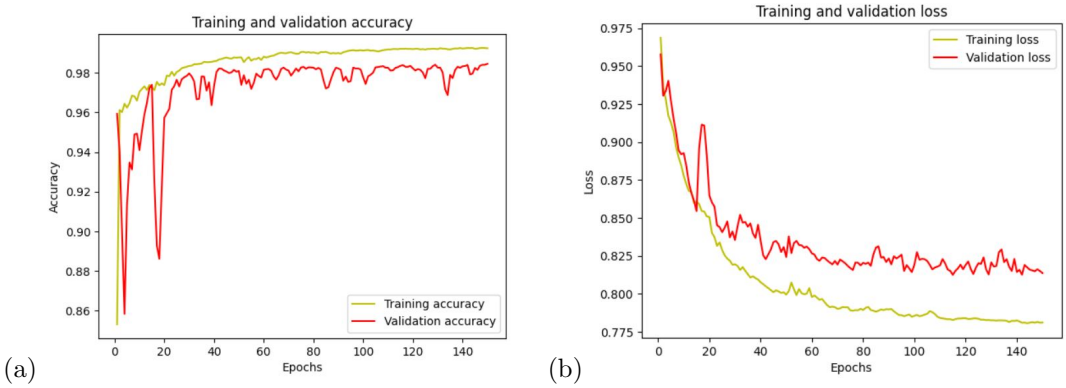


(a) (b)

Figure 2: (a) Images in Dataset (b) Images After Scaling

4 Results of the Proposed Model

The accuracy curve and the loss curve of the model after training are as follows.



(a) (b)

Figure 3: (a)Accuracy Curve (b) Loss Curve

With a **learning rate of 0.0001**, Adam optimizer as the optimizer and for 150 epochs, a mean Intersection over Union (IoU) of 0.62480104 was obtained after training the model.

Statistics of the last 5 epochs are as follows.

Epoch	Total loss	Training accuracy	Validation loss	Validation accuracy
145	0.779566	0.992780	0.811695	0.981929
146	0.779813	0.992710	0.815256	0.979983
147	0.780497	0.992482	0.812269	0.983043
148	0.779631	0.992876	0.813647	0.980607
149	0.779179	0.992947	0.809900	0.983940
150	0.779523	0.992787	0.810380	0.984409

Figure 4: For the last 5 Epochs

The outputs of the model for 5 random test image are as follows.

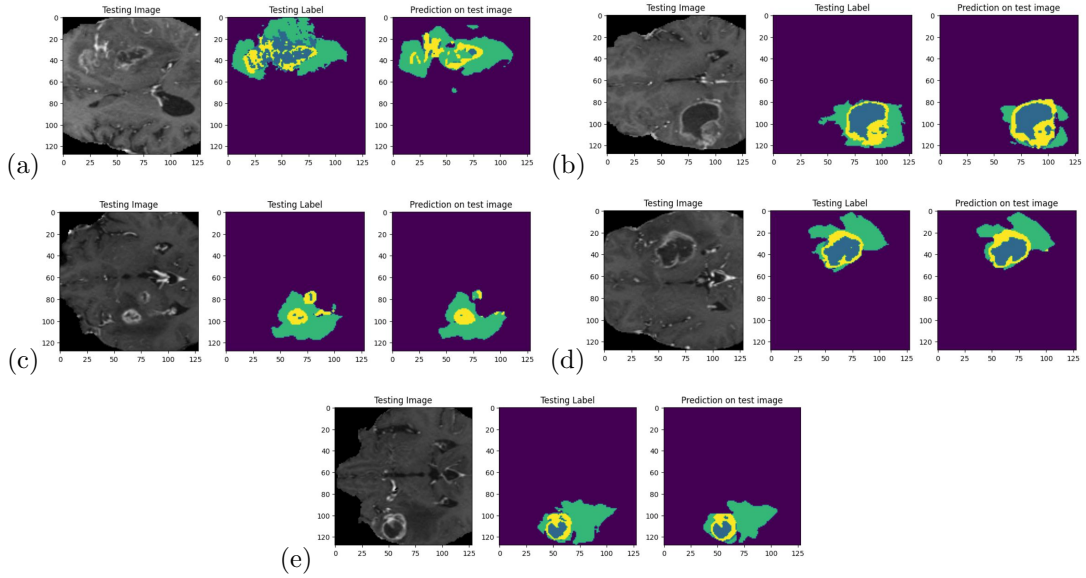


Figure 5: Actual Vs Predicted

5 Discussion

- When training the model, the loss in training the model is calculated as follows.

  $TotalLoss = DiceLoss + (1 * FocalLoss)$

  where the focal loss encourages the model to focus on challenging examples, leading to better performance in cases with class imbalance and the dice loss calculates the intersection and union of the predicted and ground truth binary masks. The loss is calculated in each training step.

  Since the accuracy of training is high in many training steps, the model is well trained and may robust for new data.

```
#Define loss metrics to be used for training
wt0, wt1, wt2, wt3 = 0.25,0.25,0.25,0.25
dice_loss = sm.losses.DiceLoss(class_weights=np.array([wt0, wt1, wt2, wt3])
)
focal_loss = sm.losses.CategoricalFocalLoss()
total_loss = dice_loss + (1 * focal_loss)

metrics = ['accuracy', sm.metrics.IOUScore(threshold=0.5)]

```

- Although the dataset contains 300 images in each category, because of the GPU and output storage constraint in Kaggle for the free account, only 120 images from each set will be considered in training. The model can be a scalable one with proper GPU access to train the model.

- The Intersection over Union (IoU) score which quantifies the degree of overlap between two regions or masks, typically a predicted mask and a ground truth mask is a common evaluation metric used in image segmentation. The mean IoU score is less in the proposed model, compared to a good model which has a score of 0.82. The reason is the dataset is not used in its maximum capacity.

- The model can be further developed to identify which type of brain tumor is detected since there are many types of brain tumors. Classification can also be done on top of this model.

- The model can be easily explained to a medical professional and the opinion from the medical professional can also be easily obtained which is an advantage compared with other models.

6 Acknowledgements

- NVIDIA TESLA P100 GPU by Kaggle

7 Code of the Model

Click here to access the code of the model for further reference.

8 References

- American Association of Neurological Surgeons - Brain Tumors - Click here.
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- Dataset Click here

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