

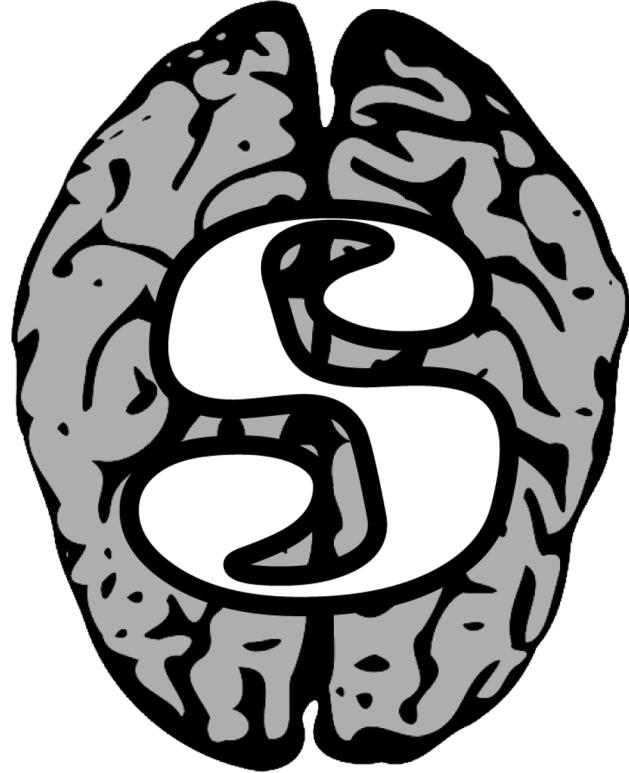


## SMART INDIA HACKATHON 2019

Team – Hexa-Codie,  
Team code – R8,  
Problem statement code – RC3

Team Leader: Swati Kanchan

Team Members: Swati Kanchan, Lokesh Nandanwar, Pradum Kumar, Saivaraprasad Bolloju, Purnima, Harsh Dokania



A Software for brain-MRI segmentation

# Segware

Health Care & Biomedical Devices

# Abstract

---

The idea is to develop a simple software for segmenting various crucial regions of a human brain from the MRIs. Inspired by the very recent achievements of deep concatenated and residual neural networks in medical imaging on account of dominance over the traditional method which was possible with the advent of efficient Graphics Processing Unit(GPU) - accelerated networks, our proposal will be based on 2 pre-trained DNNs, one for brain MRI segmentation of brain fluids, and another one for tumors. The python libraries PyQt and PyQtGraph will be used for developing the GUI and visualizing the brain MRI images.

# What is Segware

---

Segware consists of two parts:

- ❖ **Core Logic:** Data loader, Data pre-processing, Deep learning model, segmentation prediction and result visualization will be some of the modules.
- ❖ **PyQtGUI:** It contains UI options for loading the 3D MRI data of modalities T1, T2, T1c, FLAIR and IR, visualizing it in various plane views of brain (transverse, coronal and sagittal) with other controls for zooming in and out, dragging, contrast, etc. It also has feature to view data slice-wise with “next” and “preview” buttons along with a slider to comfortably set the values in all the 3 planes. The segmented data can then be saved for future reference.

# Segmentation of:

---

- ❖ Brain Tumour
- ❖ Cortical gray matter
- ❖ Basal ganglia
- ❖ White matter lesions
- ❖ White matter
- ❖ Cerebrospinal fluid in the extracerebral space
- ❖ Ventricles
- ❖ Cerebellum
- ❖ Brain stem

# Features of Segware

---

## Functional Features:

1. MRI File Support of several modalities (.nii, .mha)
2. Input visualization
3. Pre-processing
4. Deep learning algorithm support
5. Output visualization

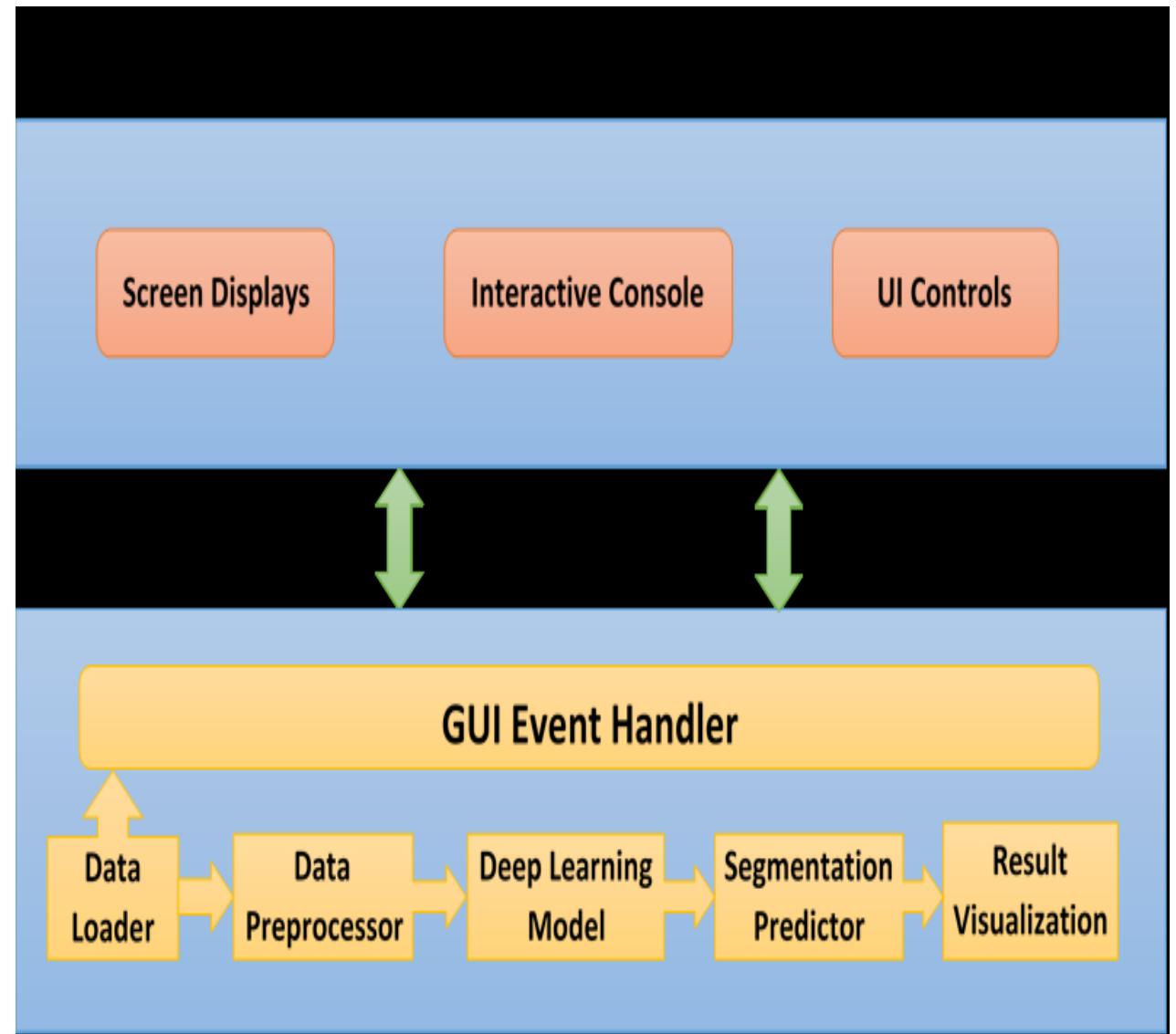
# Features of Segware (...continued)

---

## **Non-functional Features:**

1. Input/output responsiveness
2. Runtime stability
3. Help and support documentation
4. Ease of use
5. Cross-OS compatibility

# System Architecture / Use Case Diagram



# Development Phases:

---

- ❖ **Phase 1:** Training the DNN models on standard datasets. (This is one of the show stopper due to time and resource limitations. So we propose to use one of our pre-trained models for tumor segmentation.)
- ❖ **Phase 2:** PyQt5 GUI development
- ❖ **Phase 3:** Creating modules for GUI event handlers
- ❖ **Phase 4:** Adding more controls and features to GUI application
- ❖ **Phase 5:** Final testing, validation and bug fixing
- ❖ **Phase 6:** Making installer, deploying and packaging of application file for submission
- ❖ **Phase 7:** Final presentation

# Technology stack used

---

- **Python 3**
- **GUI:** PyQt , a python library.
- **Data loader:** MedPy library will be used to load MRI data.
- **Data preprocessing techniques:** Mean-centering, normalization and N4ITK bias-field correction. NumPy and SimpleITK libraries will be used.

# Technology stack used

---

- **Deep learning model:** Below are the deep learning models from our research projects (For more details please see to point number 4 in showstopper)
- **Tumor segmentation:** modified LinkNet or m-LinkNet will be used which is already trained on BraTS'15 dataset.
- **Brain Fluids segmentation:** IResUnet model will be used here. This was trained on MRBrainS dataset of neonatal brains.
- **Segmentation Predictor:** Keras with Tensorflow backend will be used as the framework for segmentation by the above models.
- **Result visualization:** PyQtGraph is the library used for visualizing MRI data.

# Backend

---

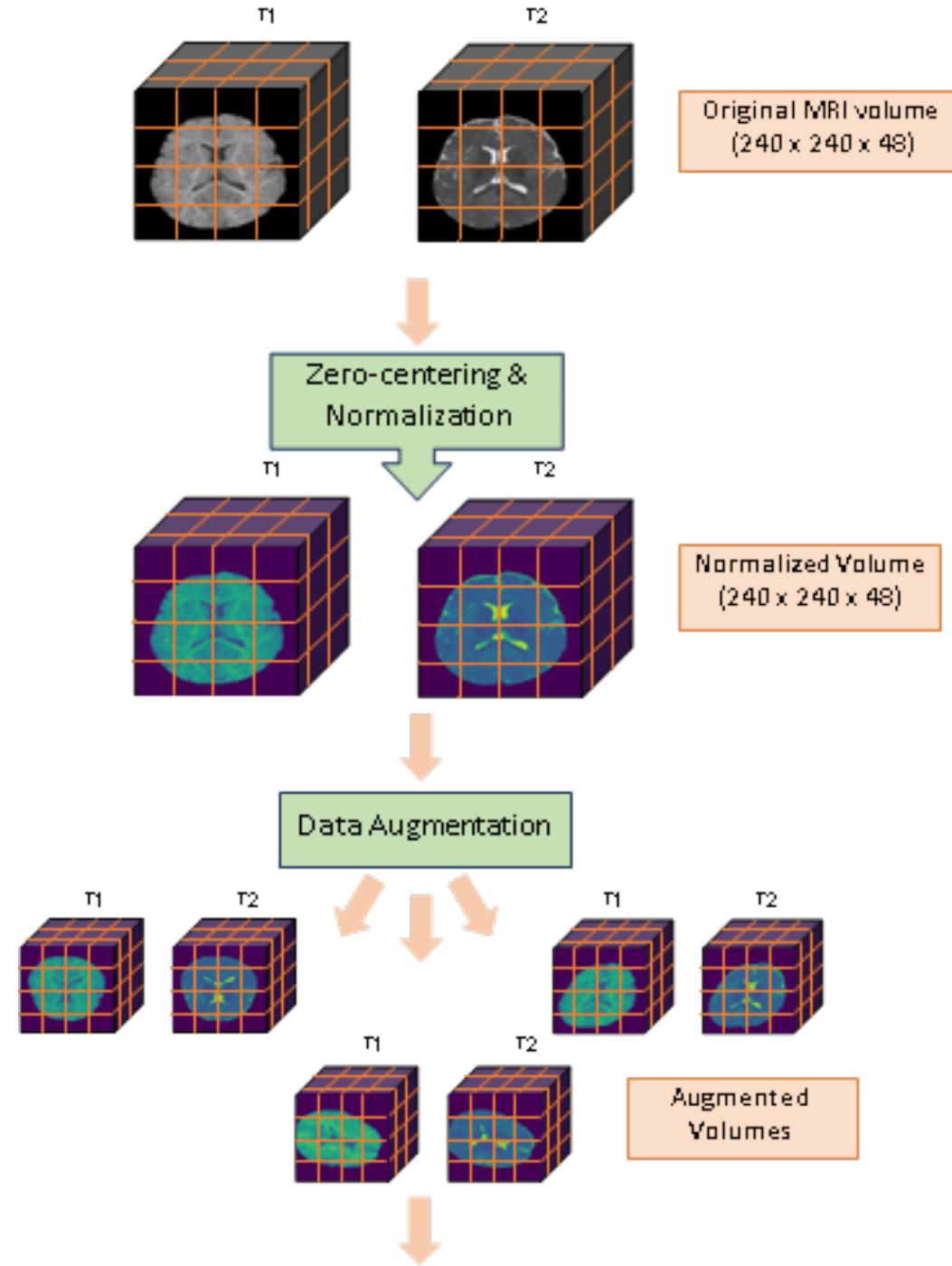
# Models

---

Brain Fluids Segmentation – **IResUnet CNN Model**

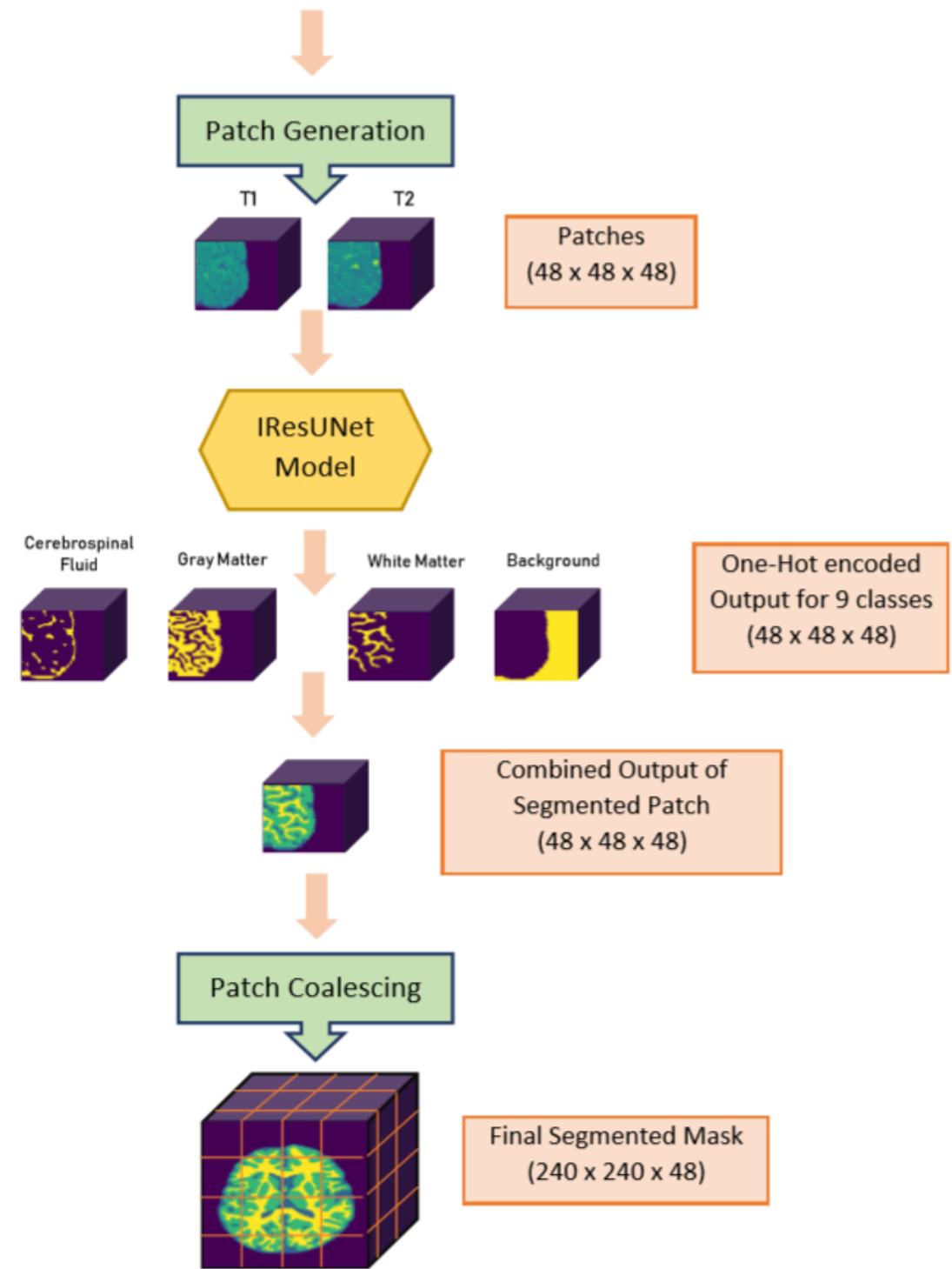
Brain Tumor Segmentation – **mLinknet CNN Model**

# Brain Fluids Segmentation – IResUnet – block diagram

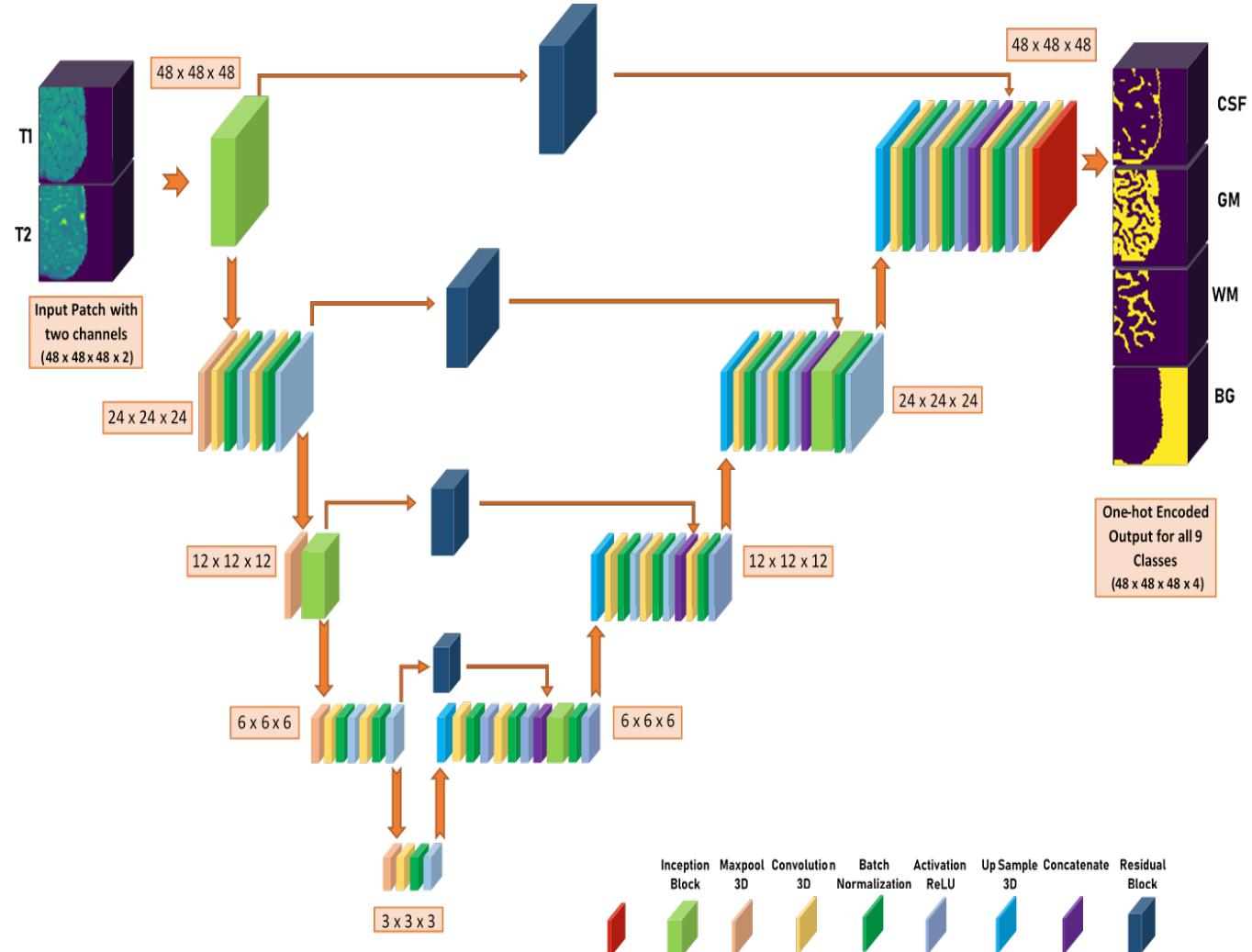


# Brain Fluids Segmentation – IResUNet – block diagram

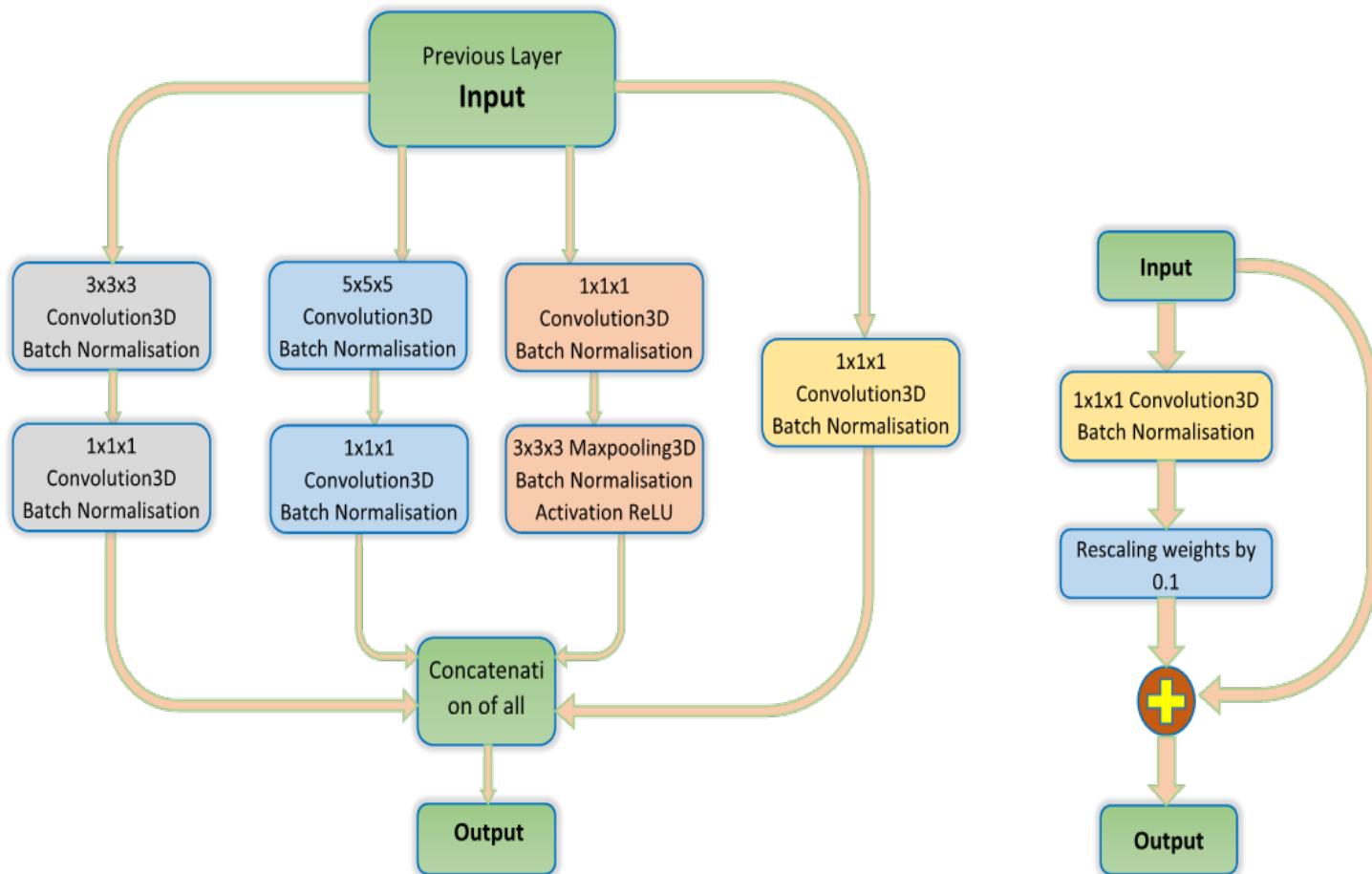
(...continued)



# Architecture



# Inception and Residual Block (Modified)

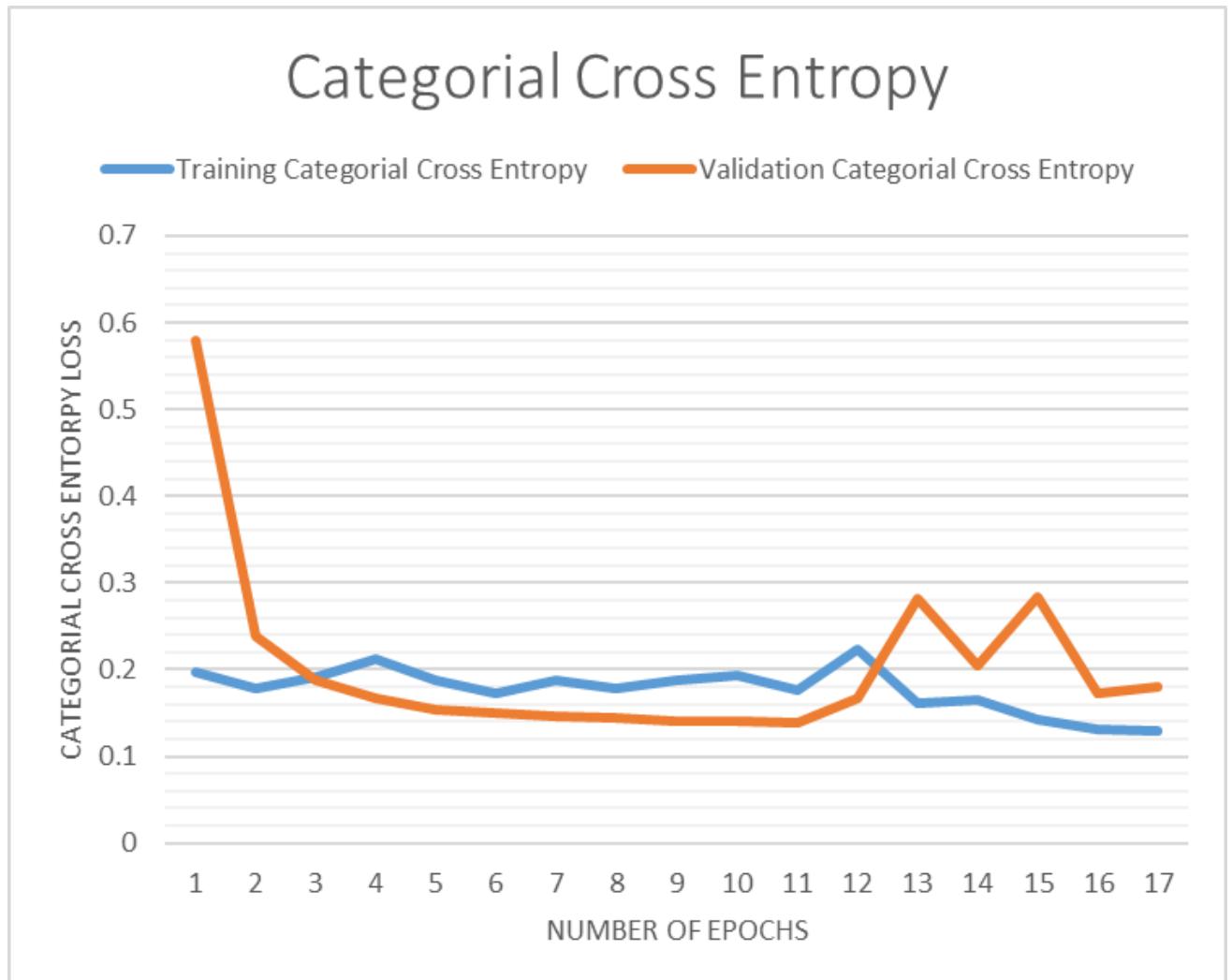


# Novelty

---

- ❖ Influenced by U-net3D, this work aims to overcome some of its shortcomings.
- ❖ To prevent the vanishing effect of feature maps in deep networks and to increase the flexibility in choosing the various kernel sizes, we replaced the skip connections with residual modules and upgraded some layers by incorporating inception layers.
- ❖ Selection of the input dimension by segregating the MRI volume into smaller 3D patches significantly reduced the training time as well as the number of learning parameters.

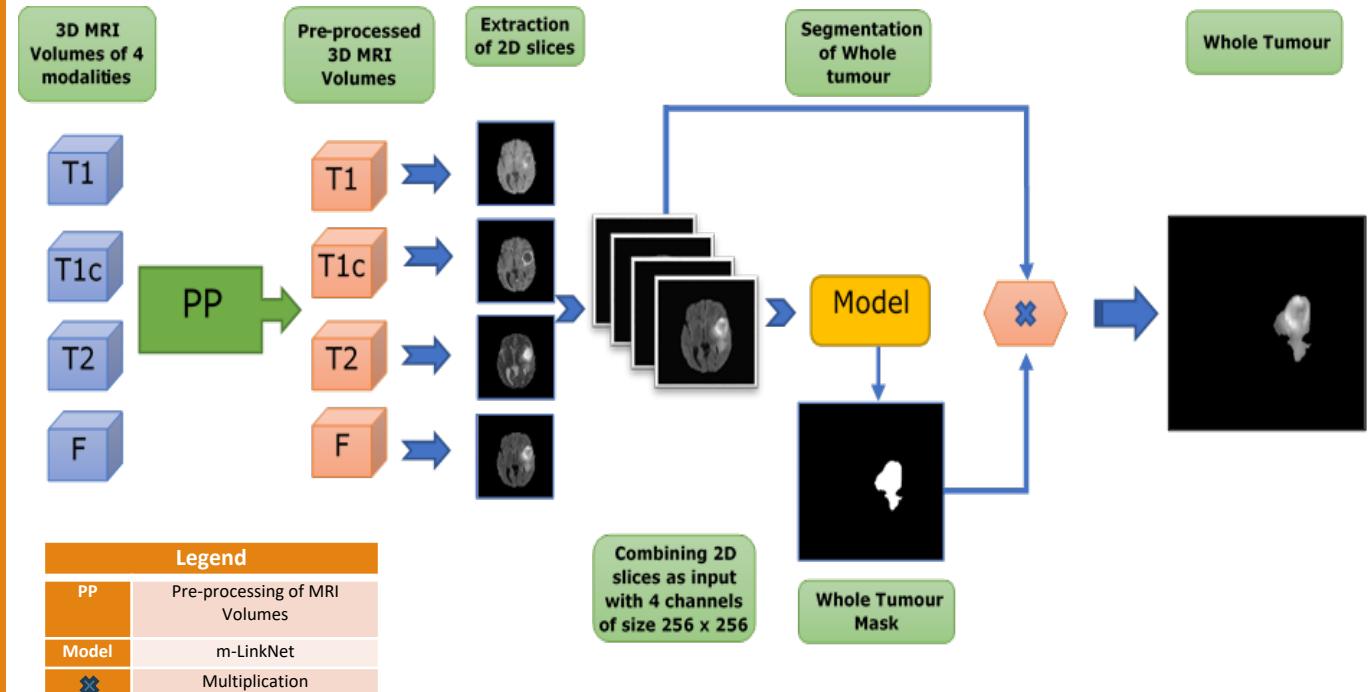
# Training and Validation Plots of Cross-entropy



# Results

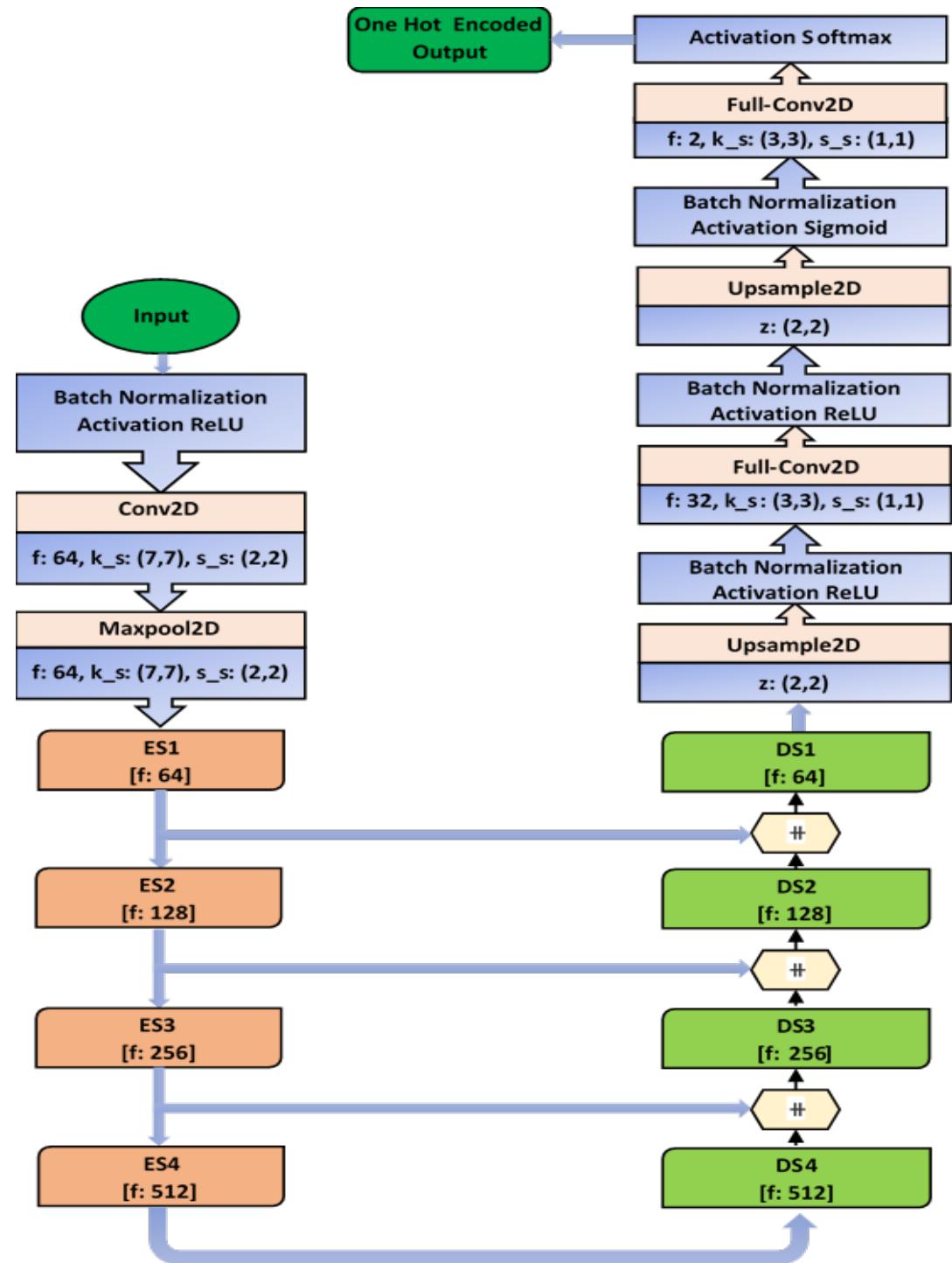
Class	Dice-score
Cortical gray matter	<b>.8171</b>
Basal ganglia	<b>.7001</b>
White matter	<b>.8043</b>
White matter lesions	<b>.8746</b>
Cerebrospinal fluid in the extra cerebral space	<b>.8031</b>
Ventricles	<b>.9224</b>
Cerebellum	<b>.8944</b>
Brain stem	<b>.8461</b>

# Brain Tumor Segmentation – mLinknet – Block diagram



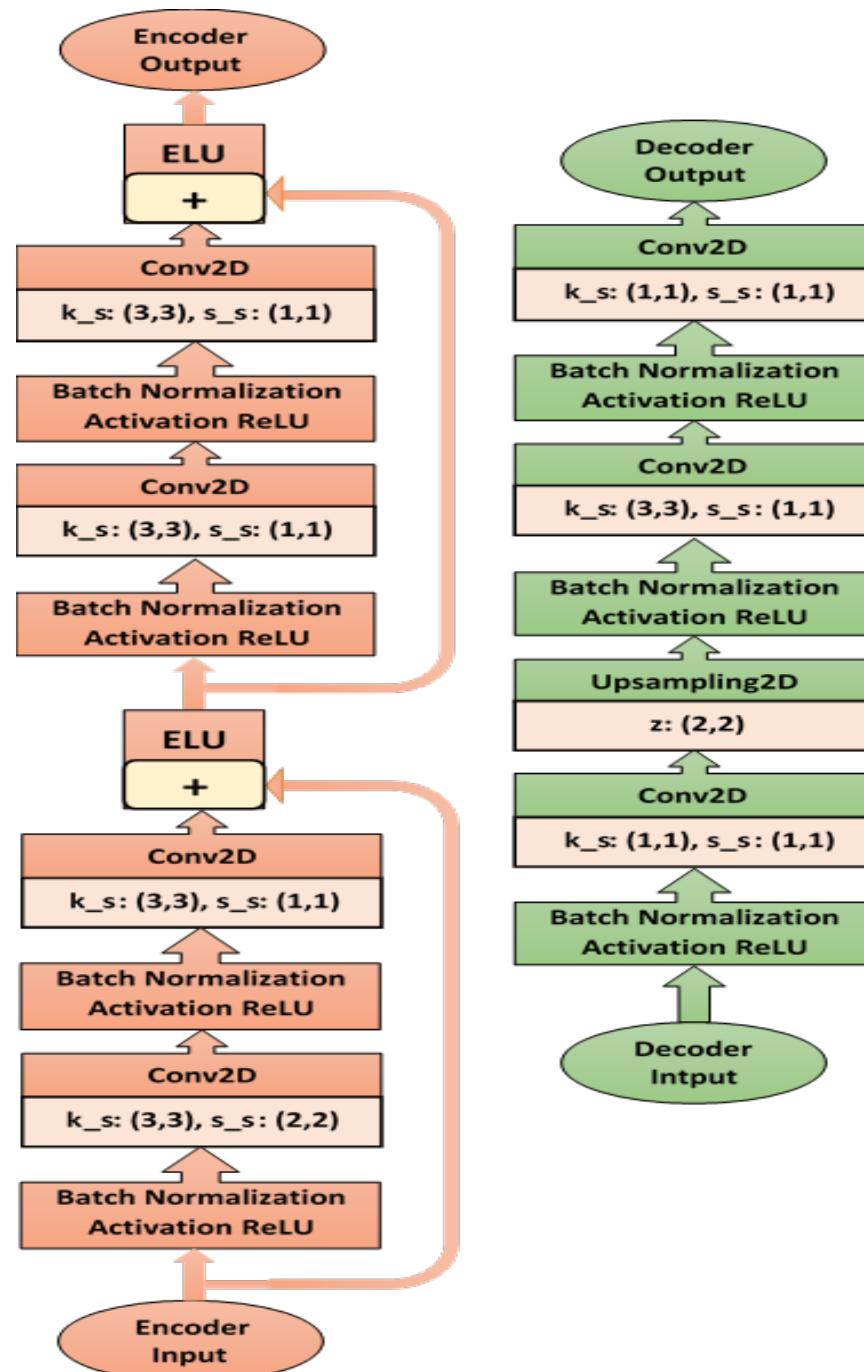
# Architecture

Legend	
f	Number of Filters
k_s	Kernel size
s_s	Strides
z	Up sampling size
#	Concatenate
Full-Conv2D	Fully connected convolution 2D
Conv2D	Convolution 2D
ES	Encoder segment
DS	Decoder segment



# Encoder- Decoder Segments

Legend	
$f$	Number of Filters
$k_s$	Kernel size
$s_s$	Strides
$z$	Up sampling size
$\#$	Concatenate
Full-Conv2D	Fully connected convolution 2D
Conv2D	Convolution 2D
ES	Encoder segment
DS	Decoder segment

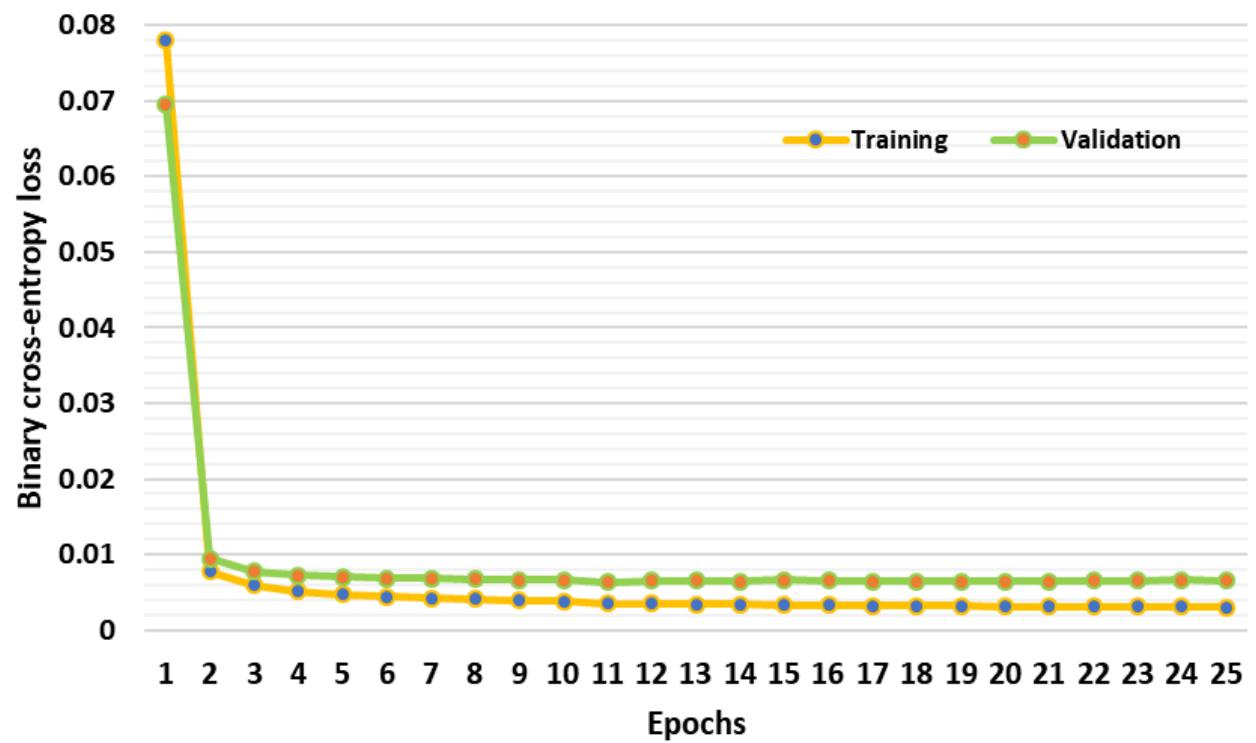


# Novelty

---

- ❖ Removal of blank data helped us reducing the training time
- ❖ Batch Normalization
- ❖ Concatenate layers instead of Add layers
- ❖ Softmax in final layer to get probabilistic output which further helped to evaluate Categorical cross-entropy.
- ❖ Changed Filter size in Encoder and Decoder segments to match our inputs and outputs
- ❖ Dropouts with probability 0.2 after each segment to prevent overfitting

# Training and Validation Plots of Cross-entropy



# Results

	DSC	Tanimoto Coefficent	Sensitivity	Precision
Tumor	<b>0.9405</b>	<b>0.8877</b>	<b>0.9315</b>	<b>0.9498</b>

# GUI

---

Choose Modality:

 T1 T2 T1c FLAIR IR

Set Slice Number:

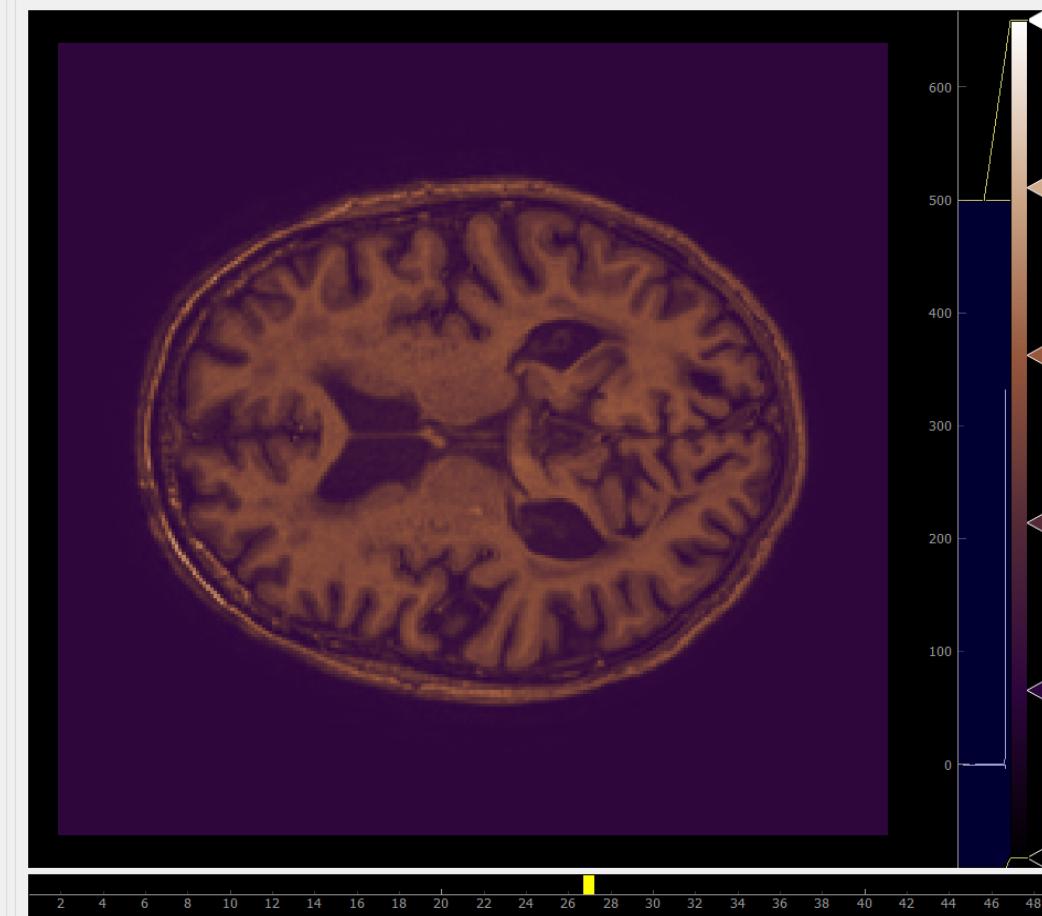
Current Slice : 

26

Choose Dimensionality:

 Transverse Sagittal Coronal

MRI View



^ ⌂ ⌂ ENG 01:34 PM

# The Graphical User Interface

# Features of Segware

---

- **The software contains two major sections:**

- Menu Bar and toolbar
- Layout(containing control unit and PyQtgraph)

- **MenuBar:**

- It contains FileMenu, HelpMenu. Under file menu we have :
  - View – to load and view T1, T2, T1c, Flair and IR data
  - Segment
  - Save segmented MRI and Mask
  - Exit
  - Open last closed
  - Open recently closed files

# Features of Segware

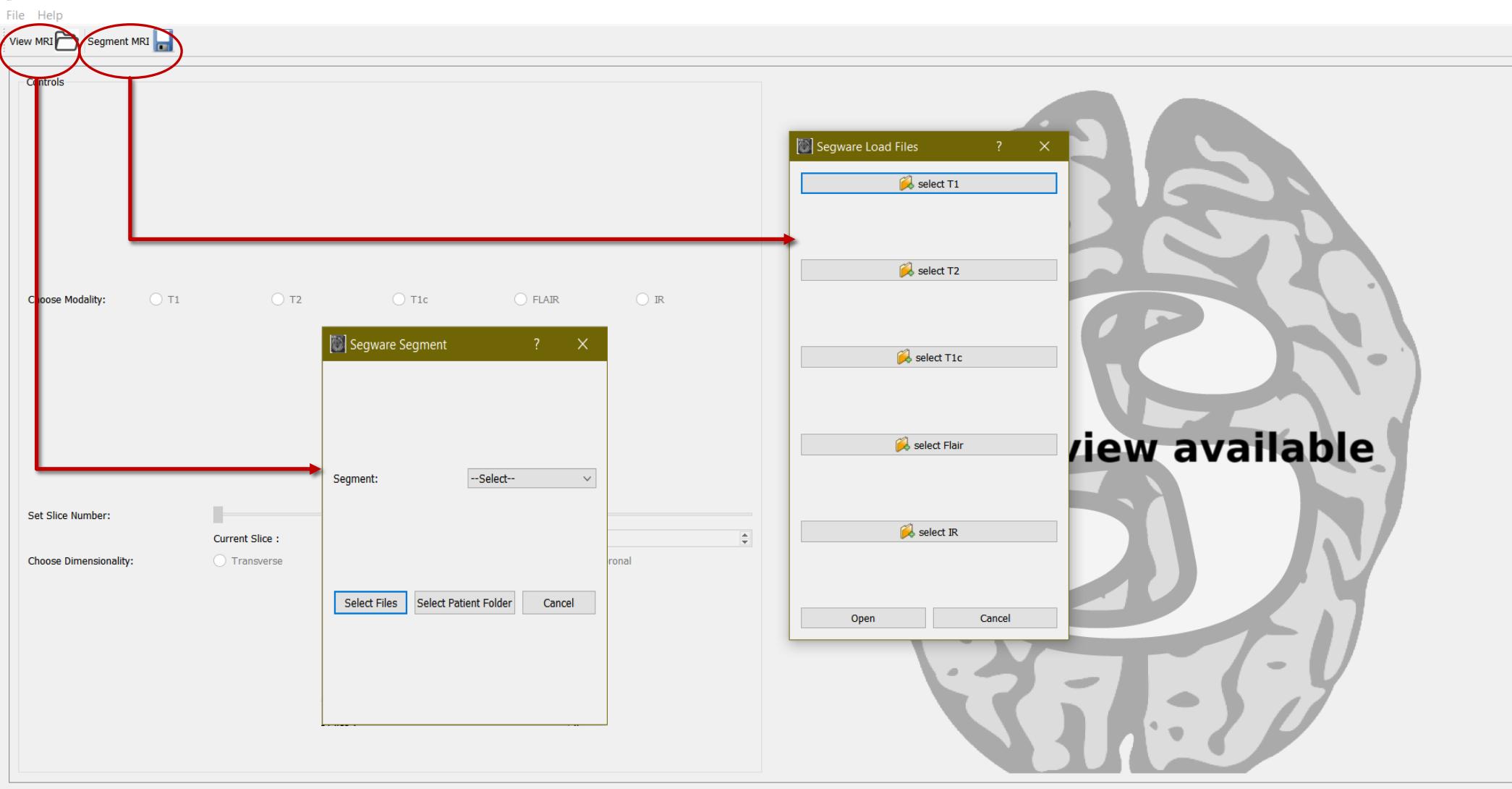
---

- **HelpMenu:**

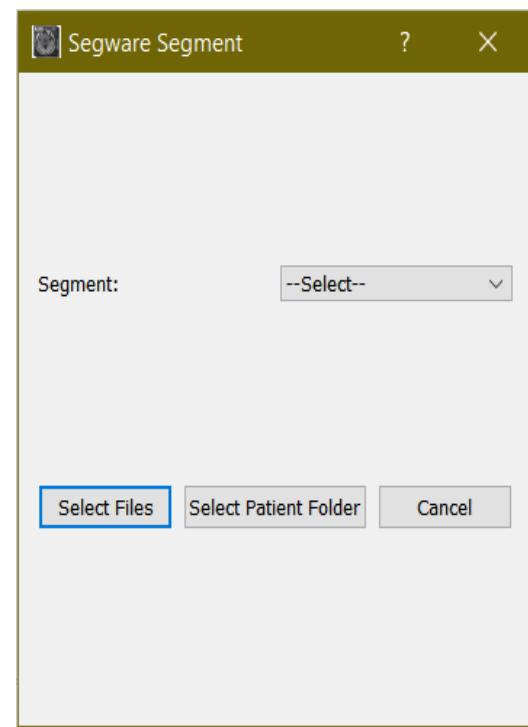
- About -contains software information
- Tutorial-It contains tutorial for using the software for user reference

- **Layout:** It contains the controls to perform various operations like

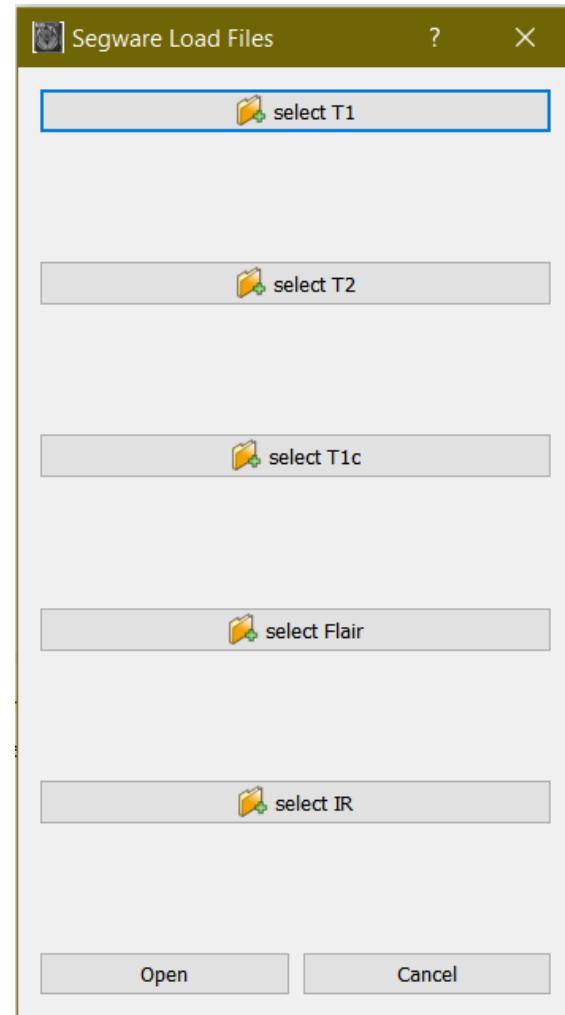
- Choose modality ,
- Slider to set slide number,
- Choose Dimensionality i.e Transverse,Saggital,Coronal



## TOOLBAR



SEGMENT TOOL



VIEW TOOL

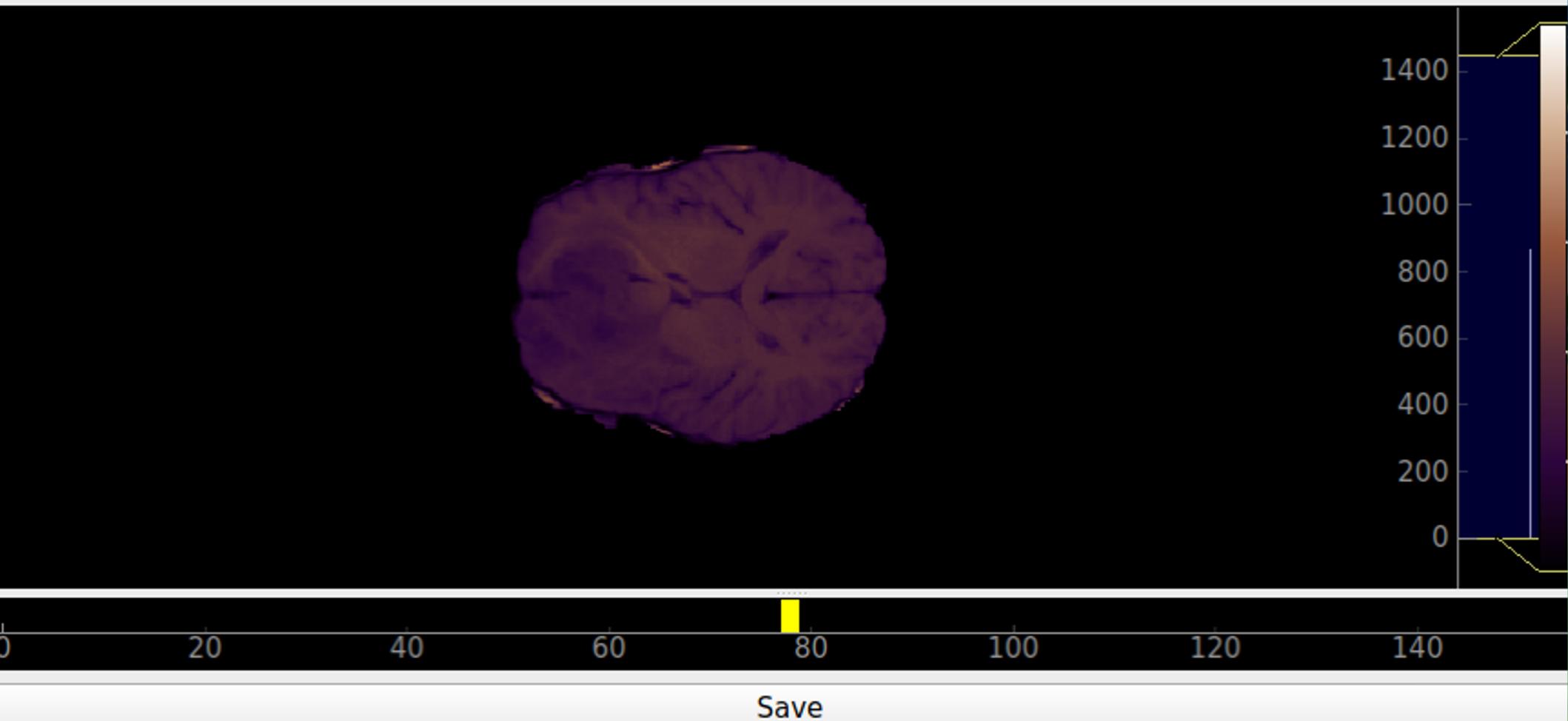
# CONTROLS

- MRI view: it is used to load and view t1,t2,t1c,flair,ir

- Mask view: It displays the mask view after performing segmentation .

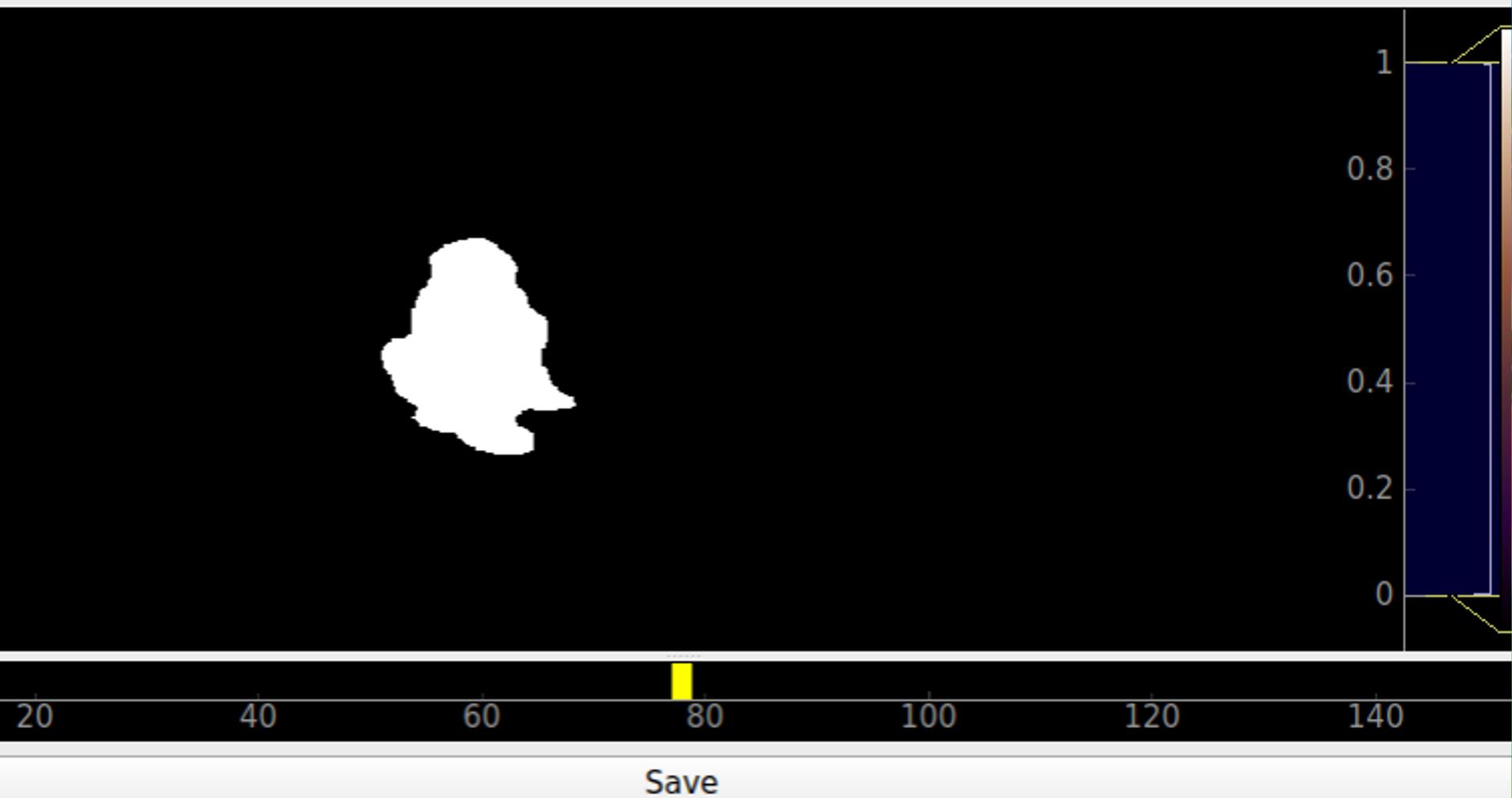
- Segmental view :It displays the segmentation view which is the product of MRI view and mask view





MRI View

Mask View



Mask View



Segmented View

# Dependencies/ Show stopper

---

1. The BraTS'15 dataset, the standard tumor segmentation dataset contain all the 4 modalities, i.e. T1, T2, T1c and FLAIR, and MRBrains dataset , the standard CSF-GM-WM segmentation for brains contain data only 3 modalities, i.e. T1, FLAIR-T2 and IR. Therefore we will require a more uniform dataset of human brains. For now, these datasets can be used for the application. Once the uniform dataset with ground truth is available, a new model can be trained and deployed for industrial use.
2. The BraTS dataset contain MRI which are skull-stripped and of size **256 x 256 x 144** whereas MRBrains dataset is not skull-stripped and of size **240 x 240 x 48**. Hence the MRIs should be of uniform dimensions and skull-stripped.
3. Training of models require high-end GPUs for fast computations and time of about 2-3 days.

# Thank you!!!

---