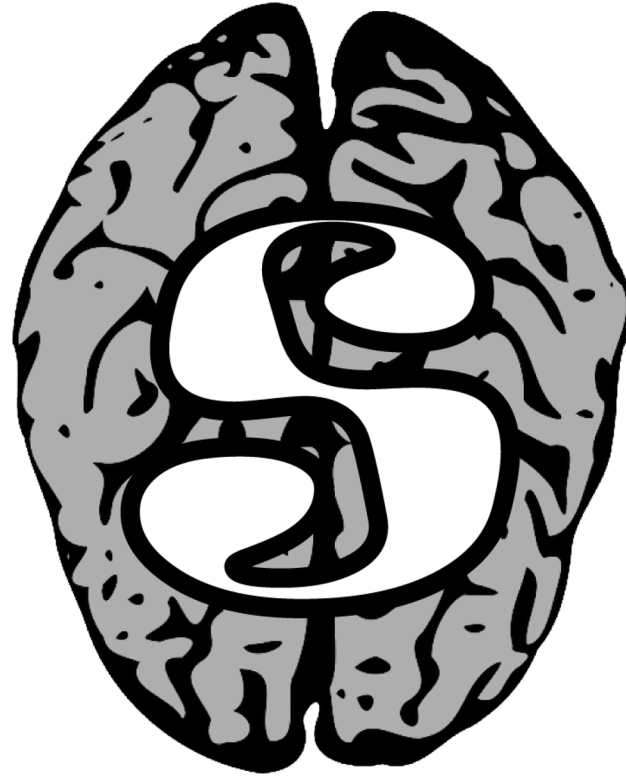




**SMART INDIA
HACKATHON
2019**

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

Team Leader: Swati Kanchan
Team Members: Swati Kanchan, Lokesh Nandanwar, Pradum
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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:

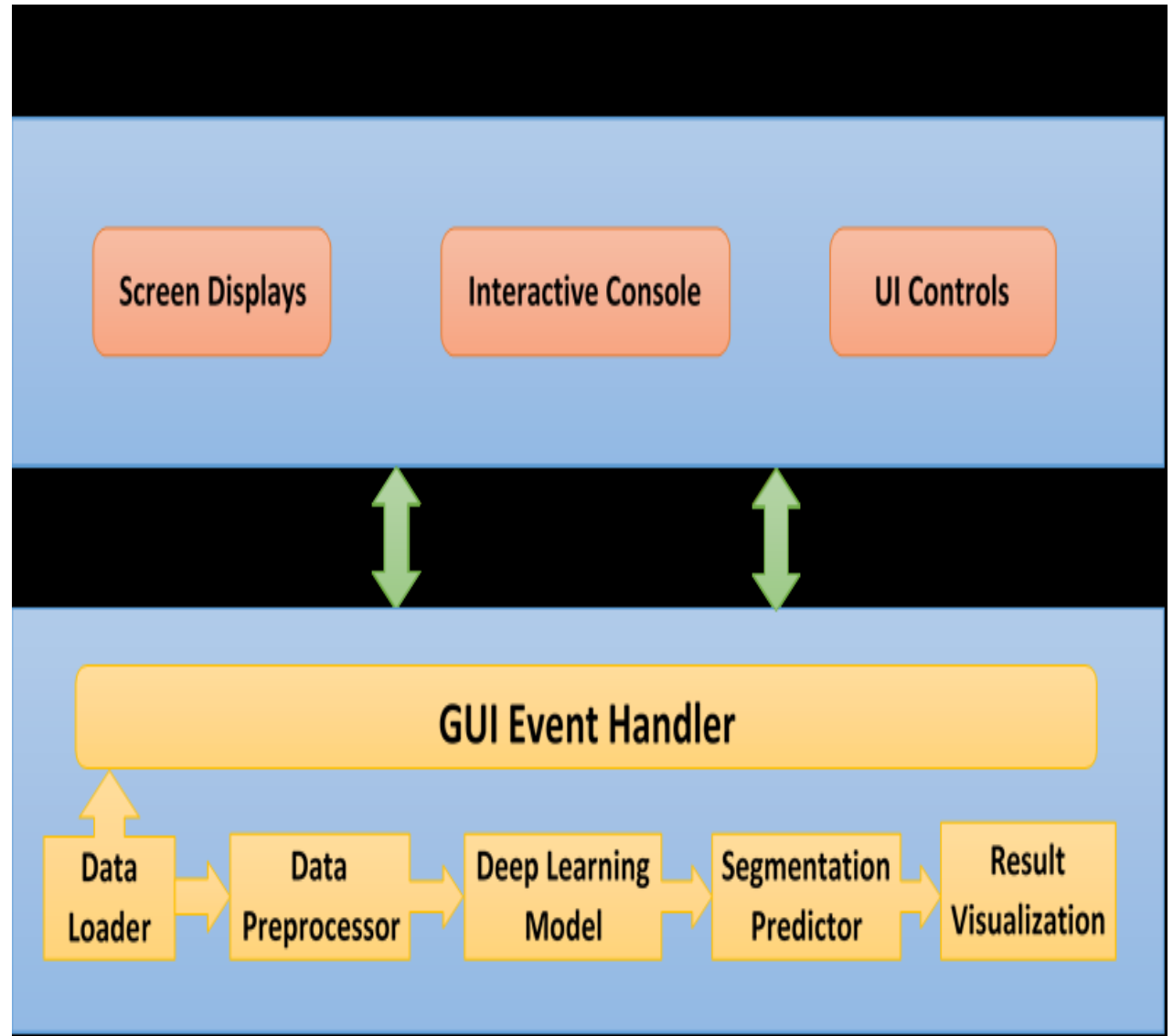
1. MRI File Support of several modalities (.nii, .mha)
2. Input visualization
3. Pre-processing
4. Deep learning algorithm support
5. Output visualization

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 show-stopper)
- **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.

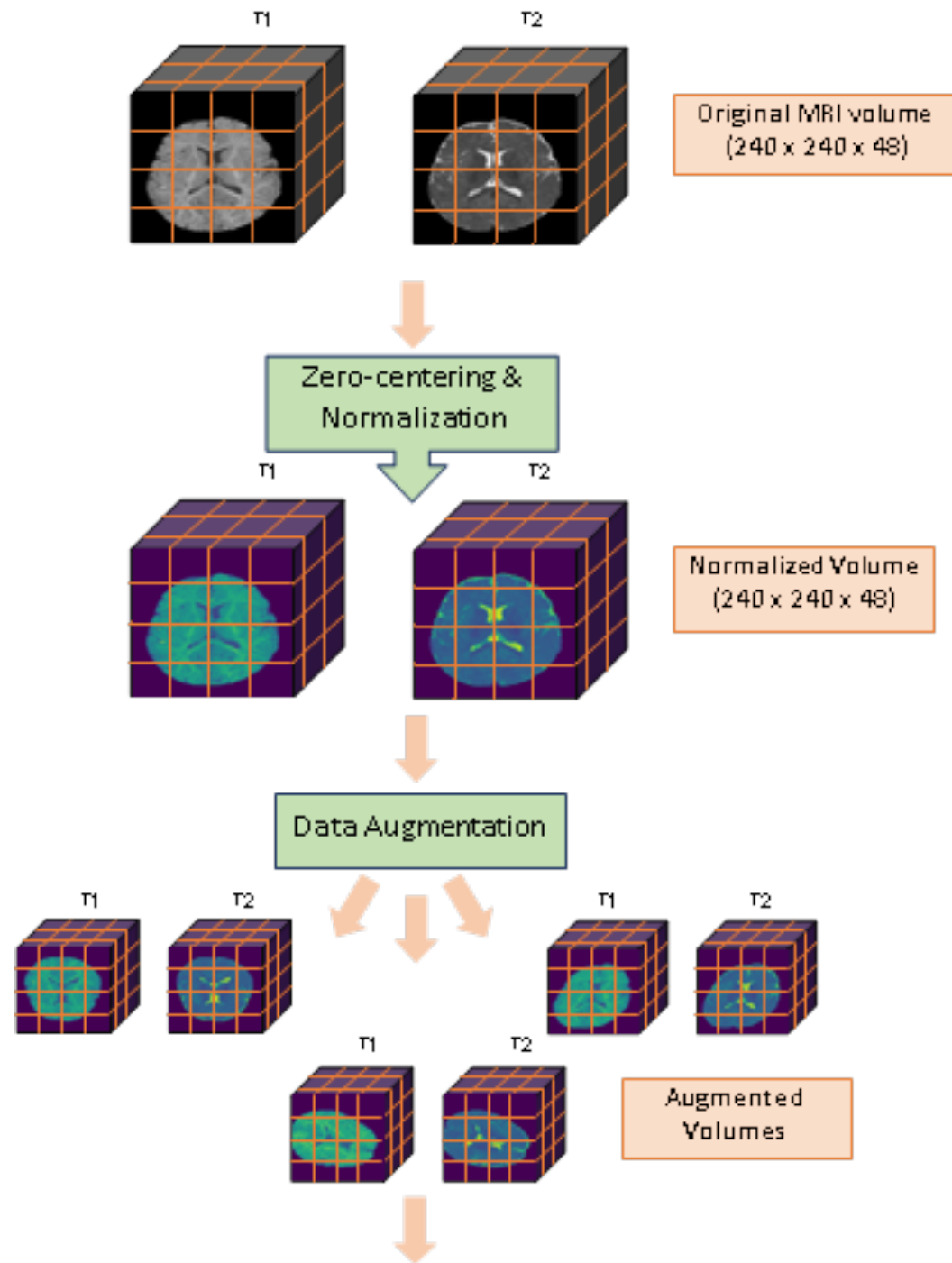
Backend

Models

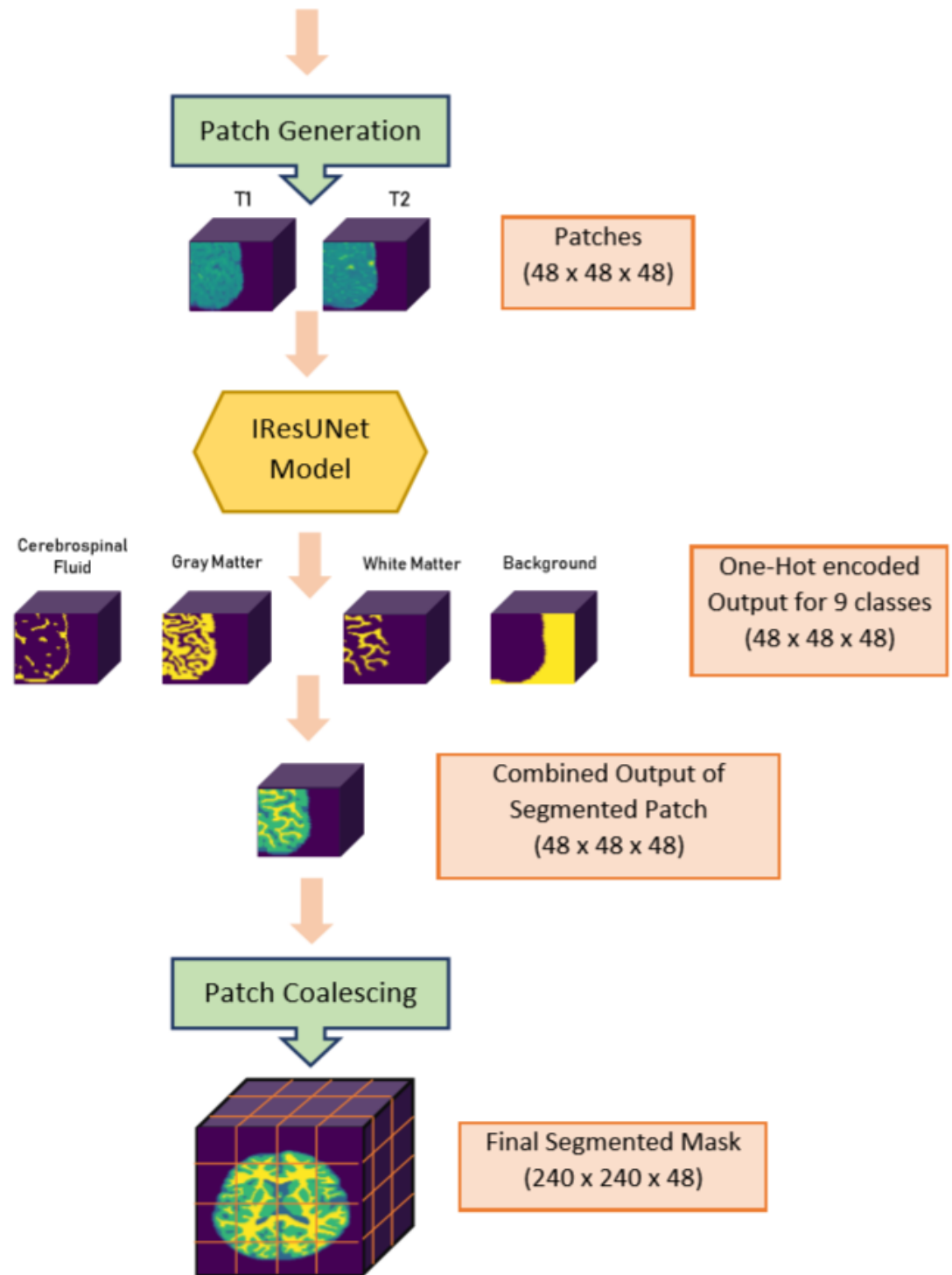
Brain Fluids Segmentation – **IResUnet CNN Model**

Brain Tumor Segmentation – **mLinknet CNN Model**

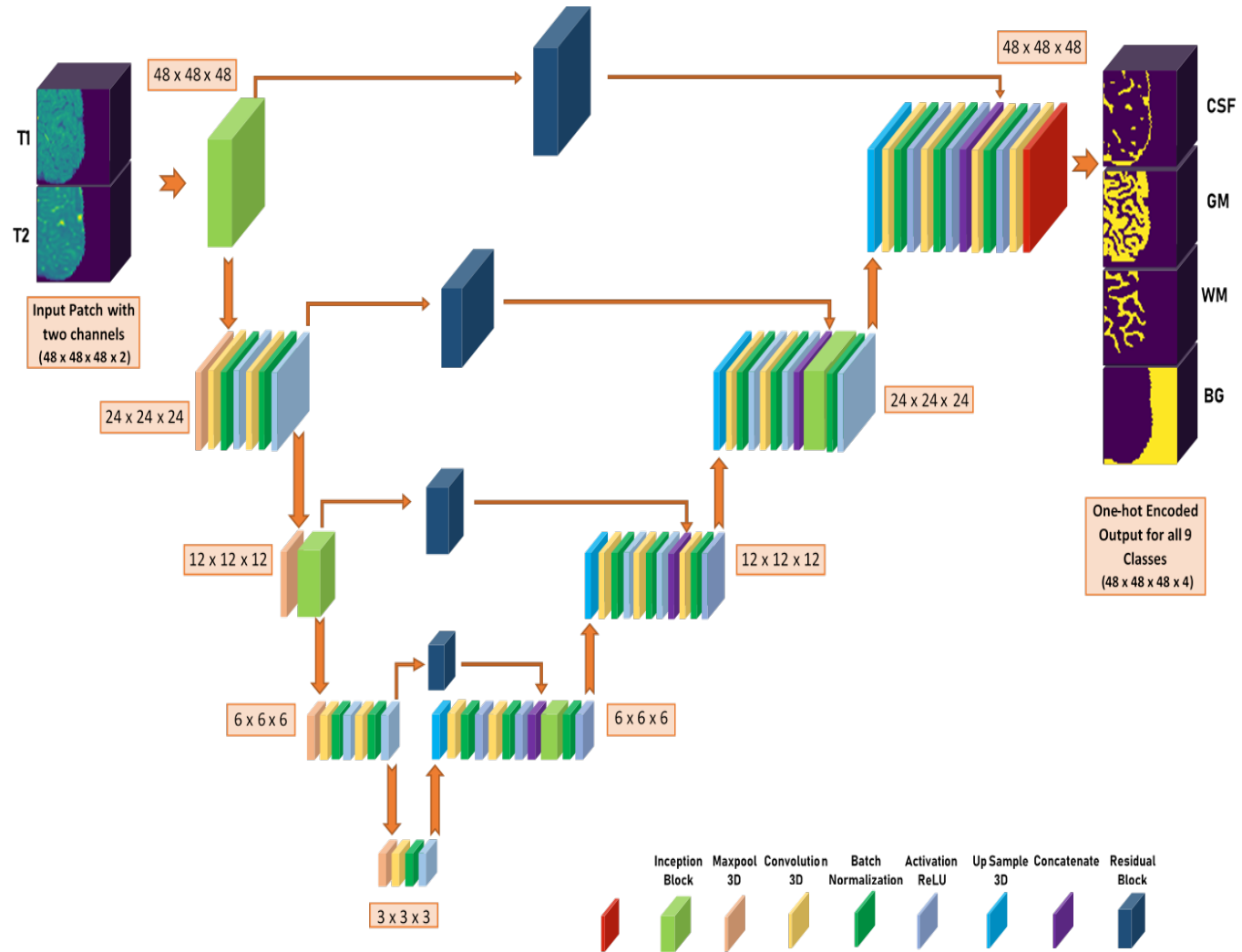
Brain Fluids Segmentation – IResUnet – block diagram



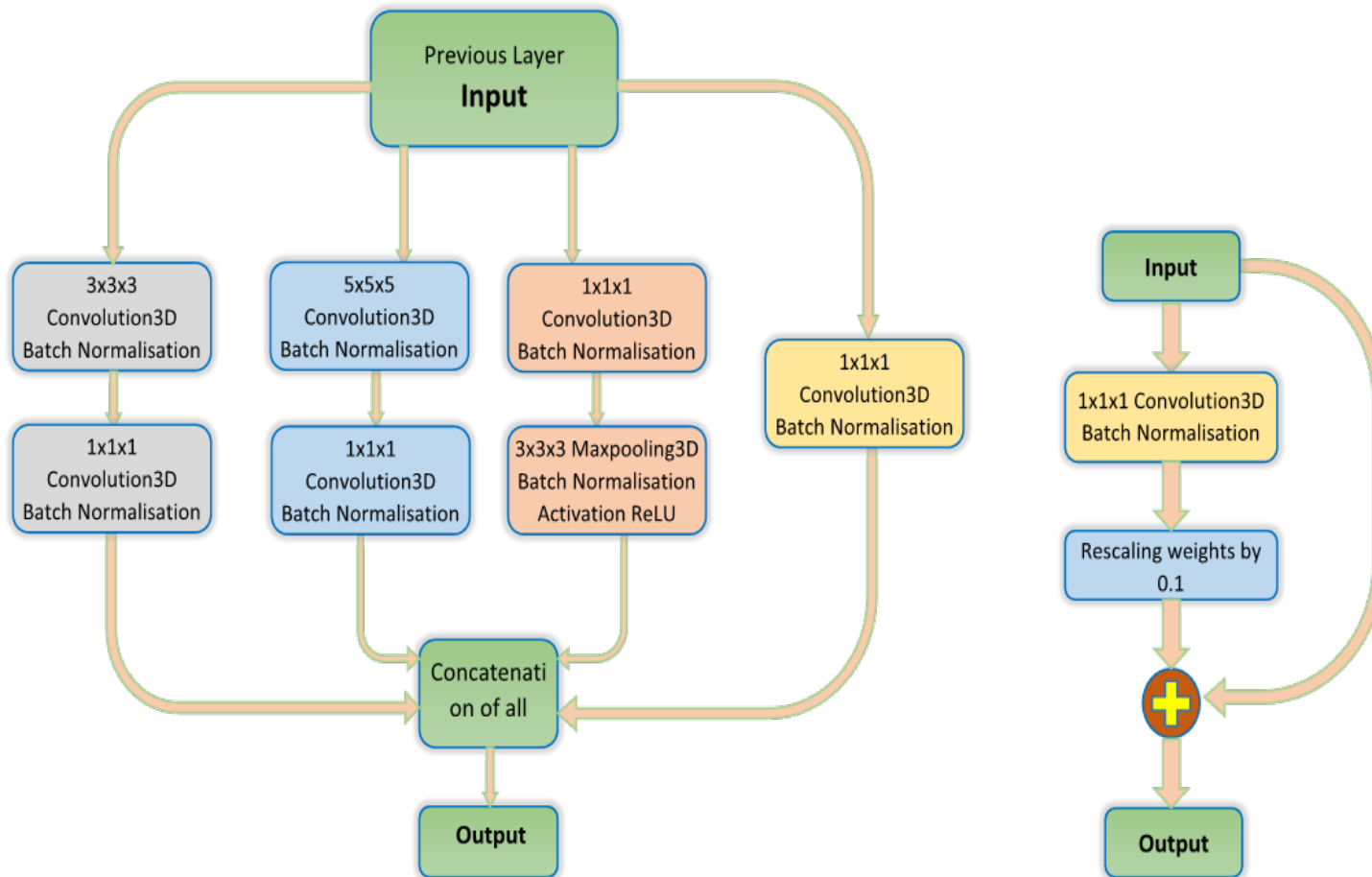
Brain Fluids Segmentation – IResUnet – block diagram (...continued)



Architecture



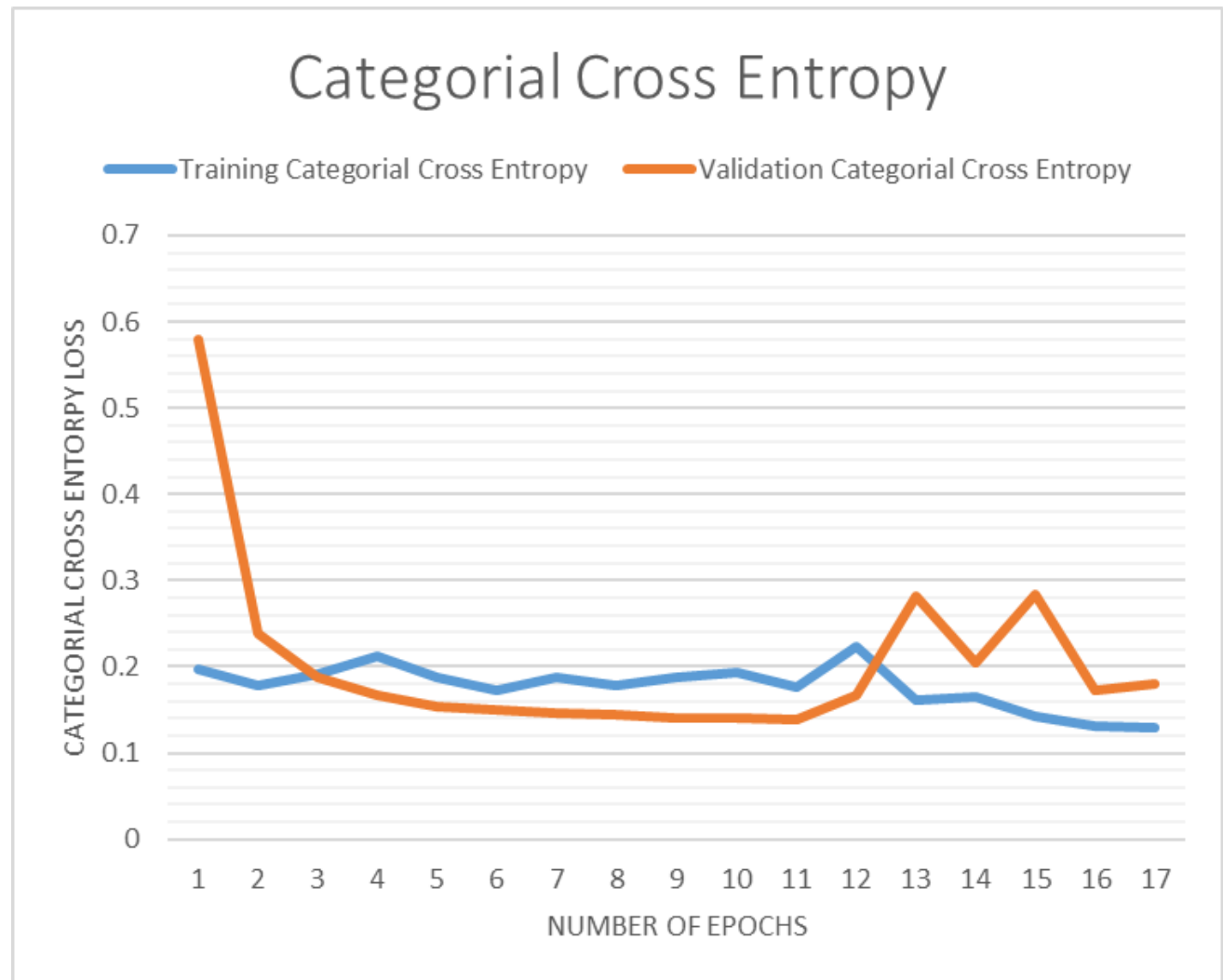
Inception and Residual Block (Modified)



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.

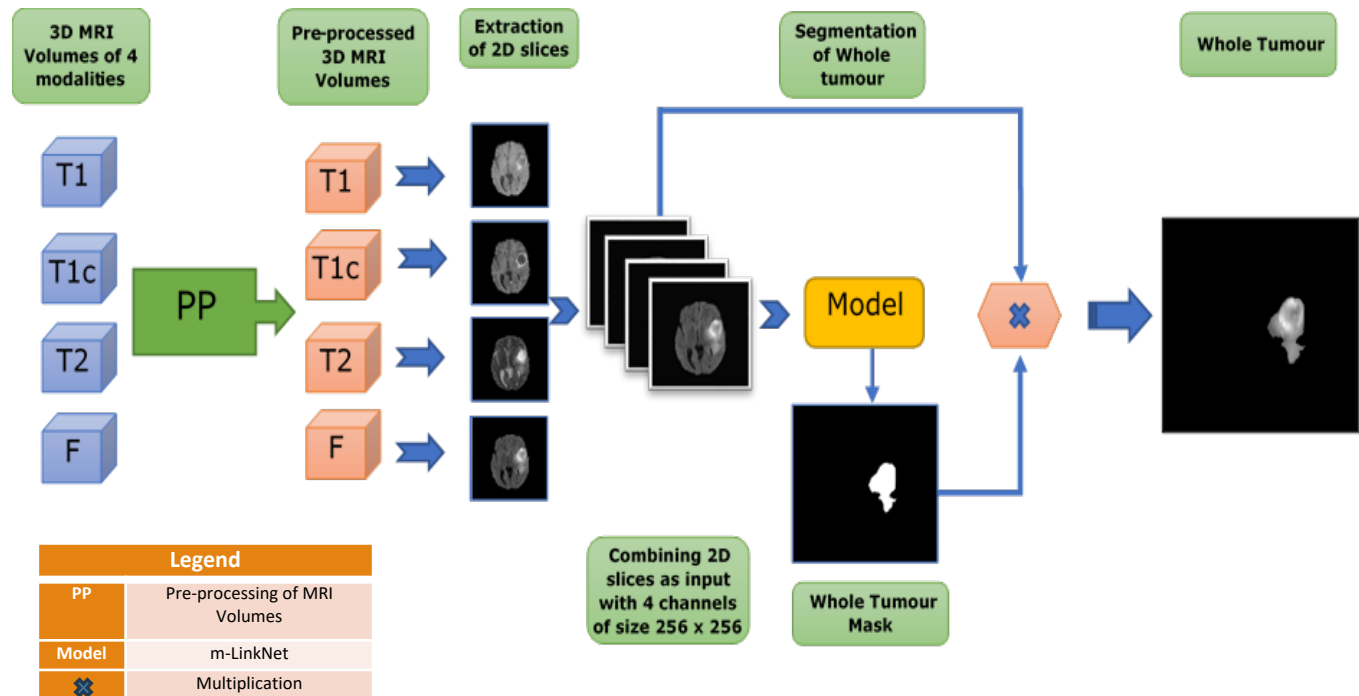
Training and Validation Plots of Cross-entropy



Results

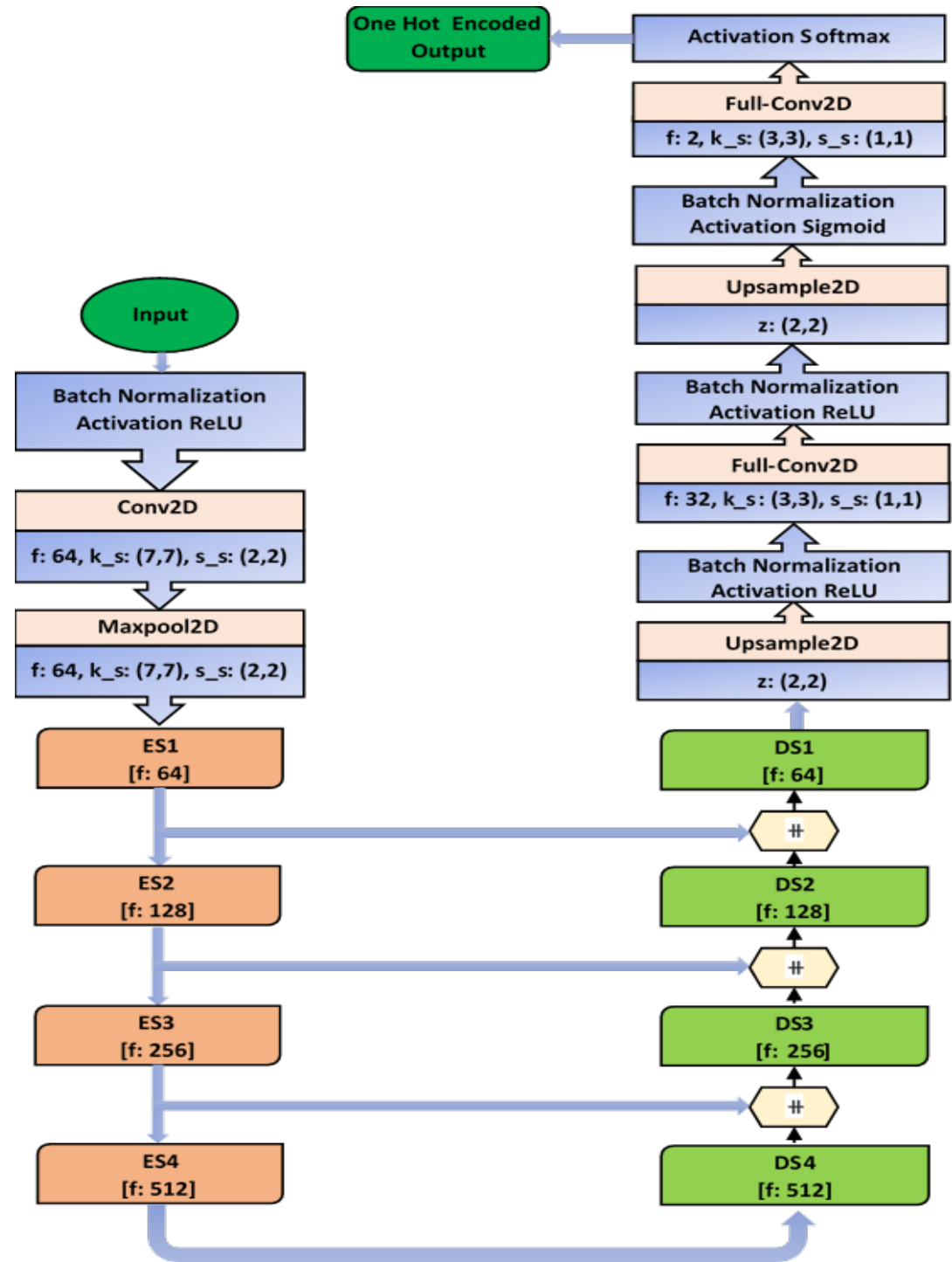
Class	Dice-score
Cortical gray matter	.8171
Basal ganglia	.7001
White matter	.8043
White matter lesions	.8746
Cerebrospinal fluid in the extra cerebral space	.8031
Ventricles	.9224
Cerebellum	.8944
Brain stem	.8461

Brain Tumor Segmentation – mLinknet – Block diagram



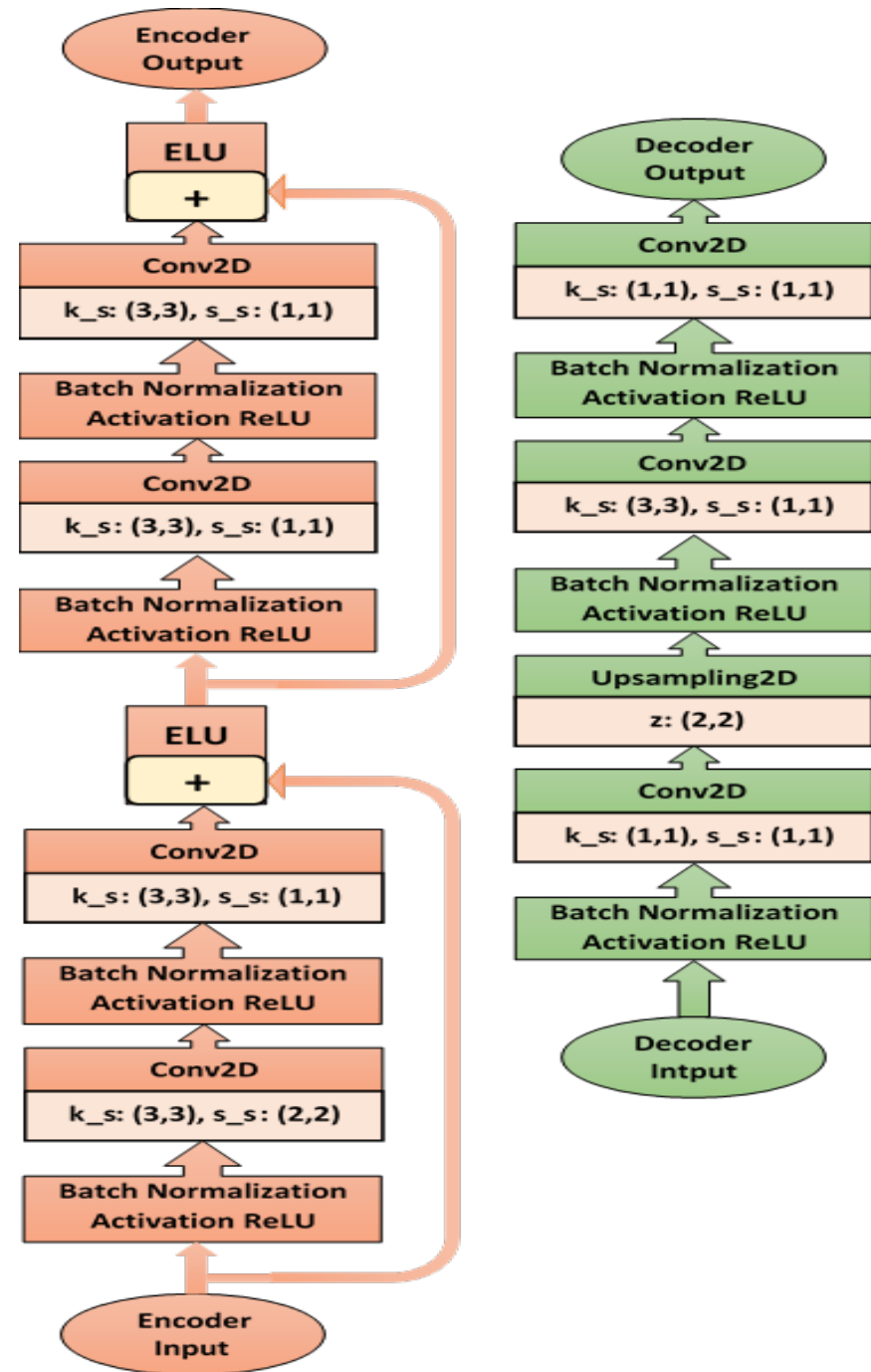
Architecture

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

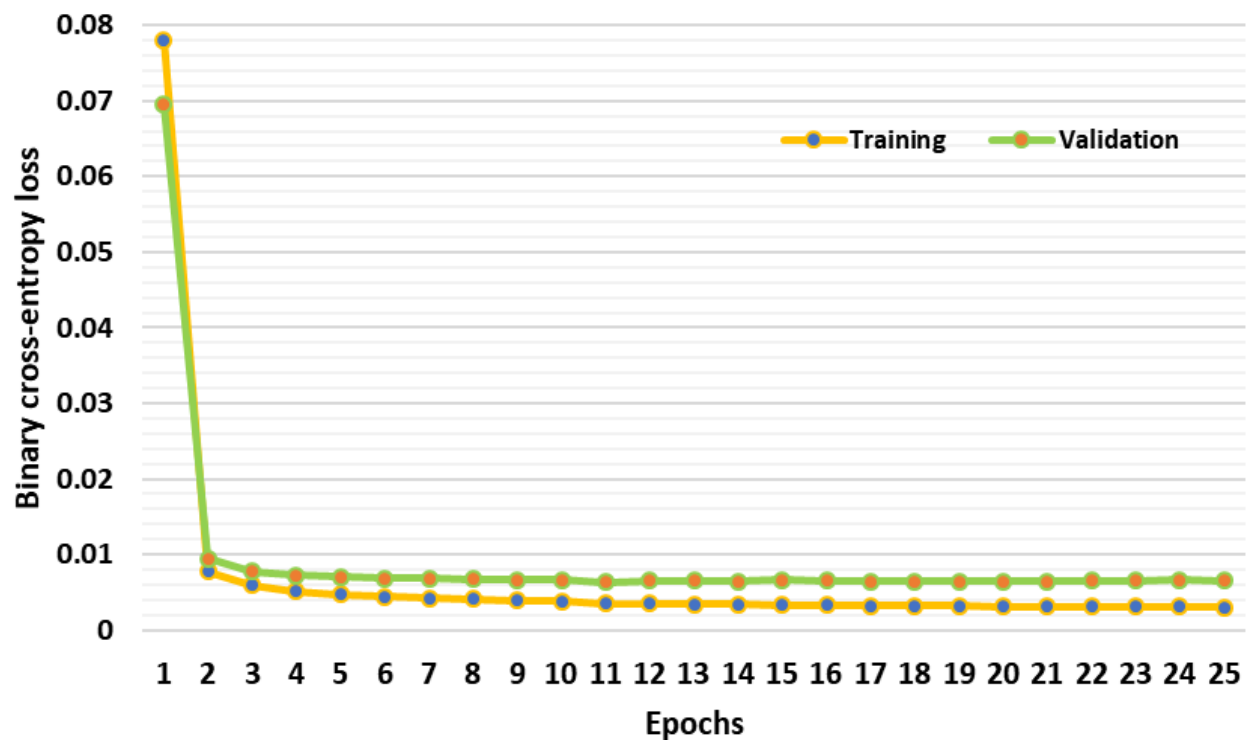
Legend	
f	Number of Filters
k_s	Kernel size
s_s	Strides
z	Up sampling size
⊕	Concatenate
Full-Conv2D	Fully connected convolution 2D
Conv2D	Convolution 2D
ES	Encoder segment
DS	Decoder segment



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

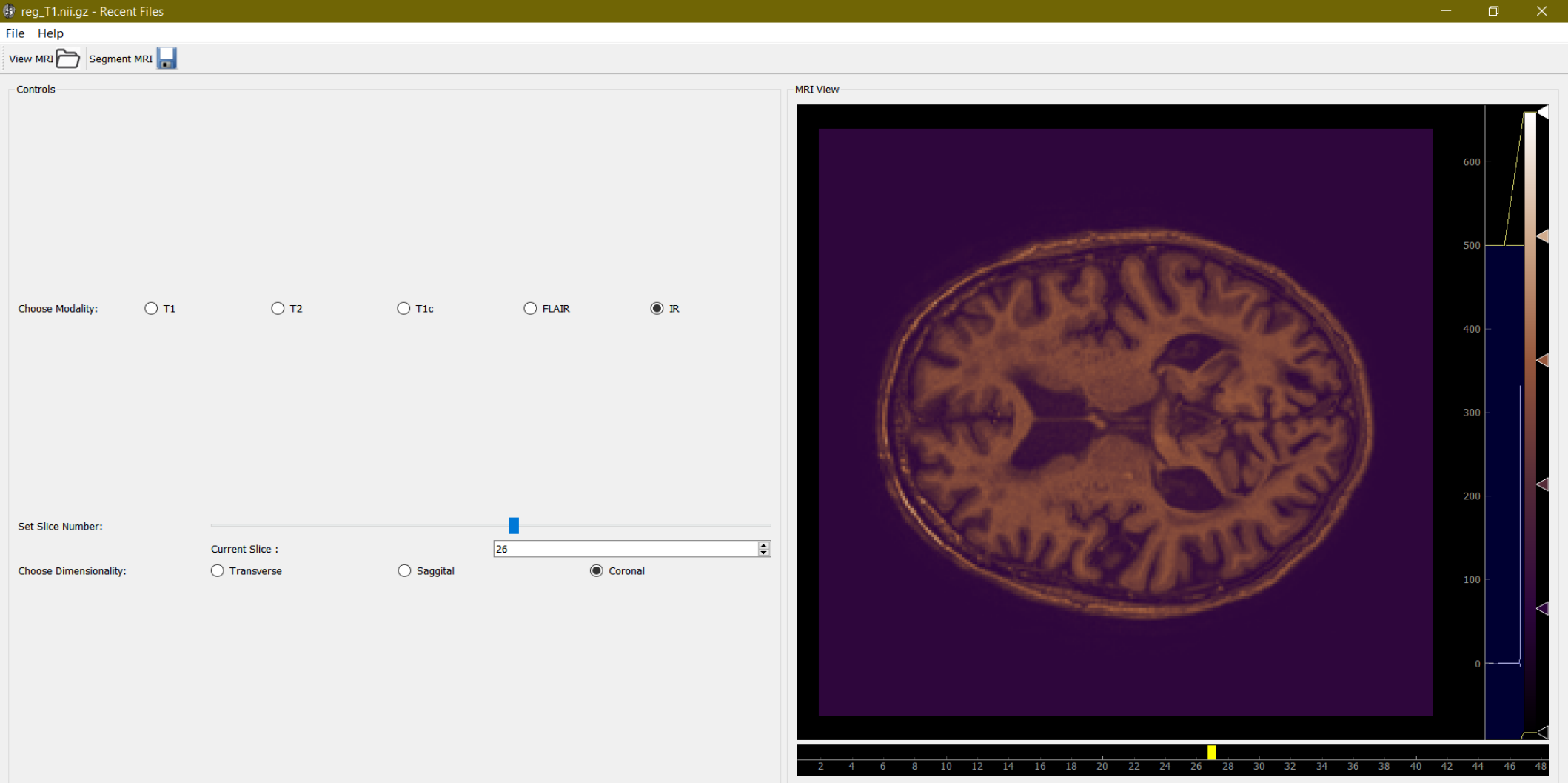
Training and Validation Plots of Cross-entropy



Results

	DSC	Tanimoto Coefficient	Sensitivity	Precision
Tumor	0.9405	0.8877	0.9315	0.9498

GUI



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

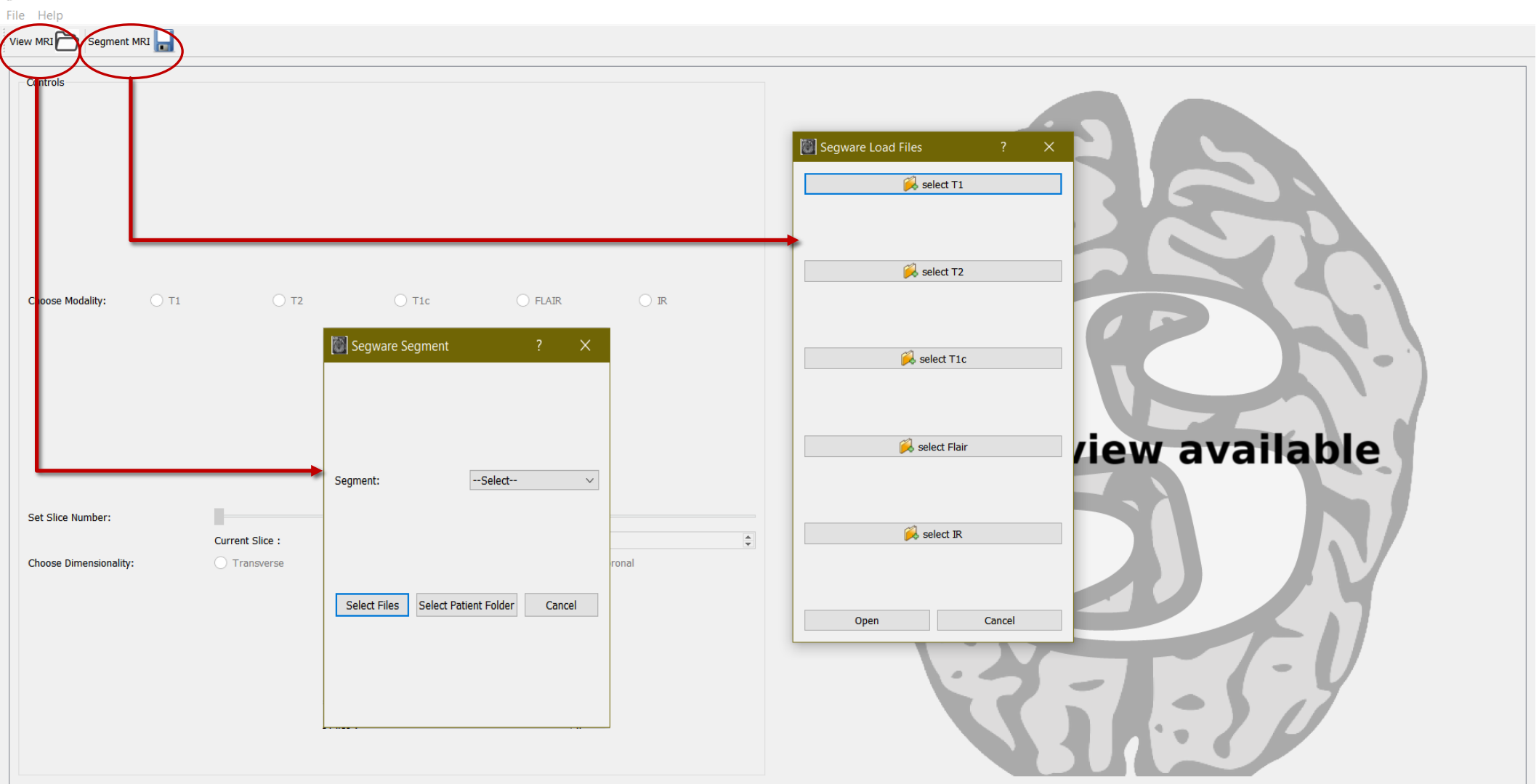
Features of Segware

- **HelpMenu:**

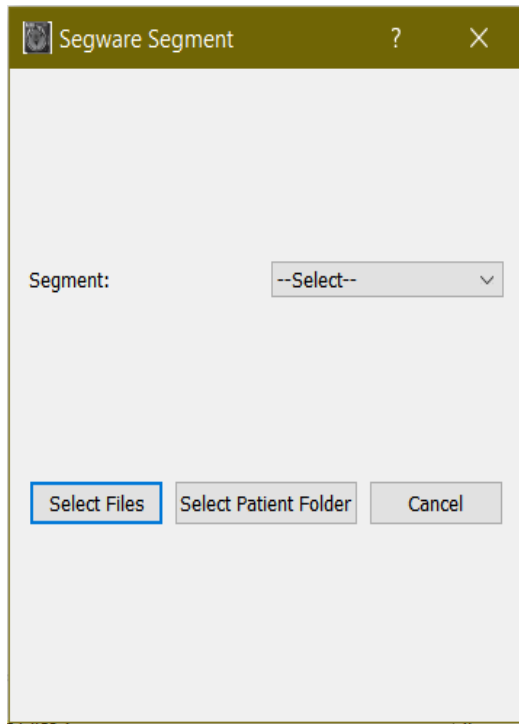
- About -contains software information
- Tutorial-It contains tutorial for using the software for user reference

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

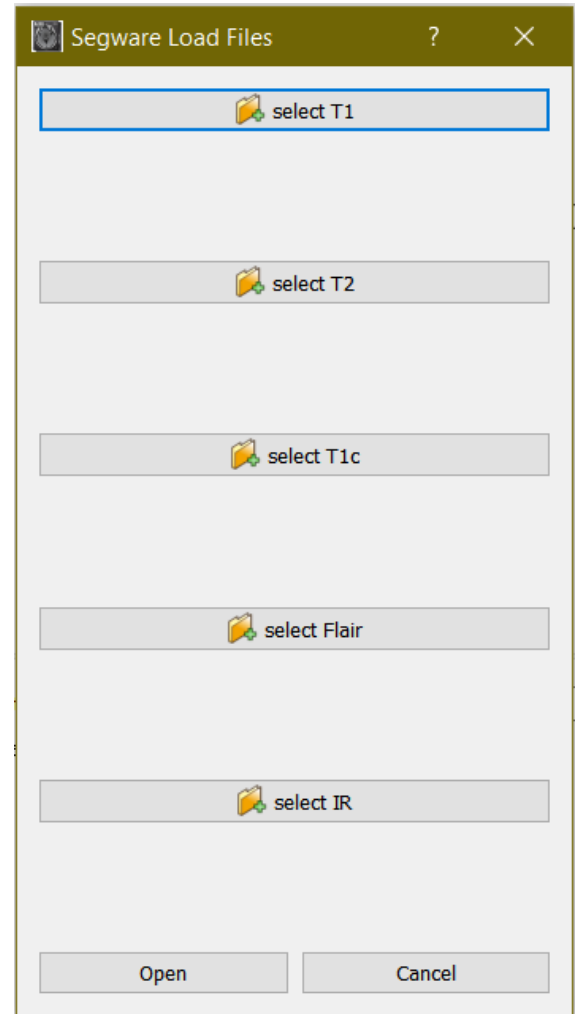
- Choose modality ,
- Slider to set slide number,
- Choose Dimensionality i.e Transverse,Saggital,Coronal



TOOLBAR



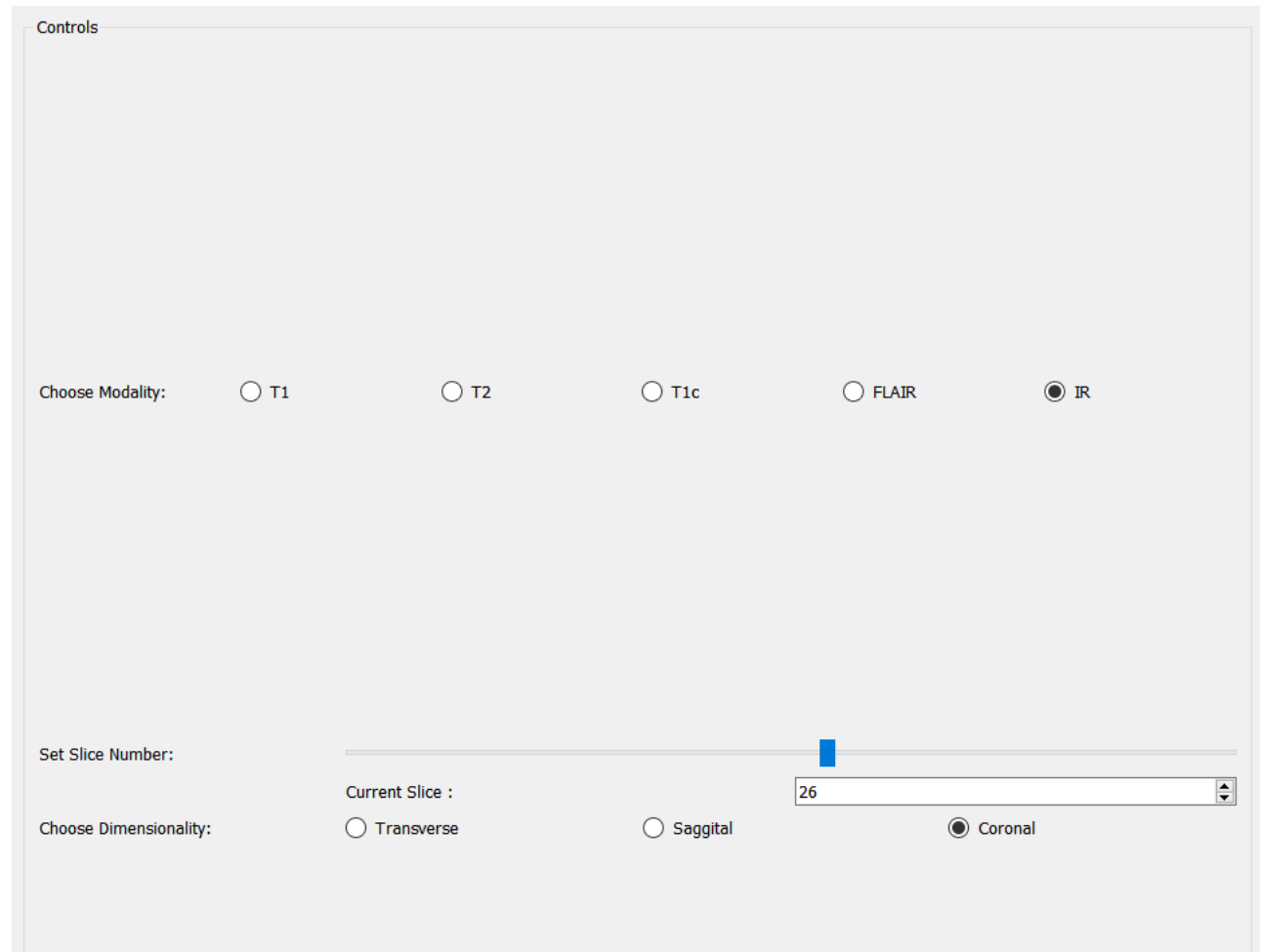
SEGMENT TOOL

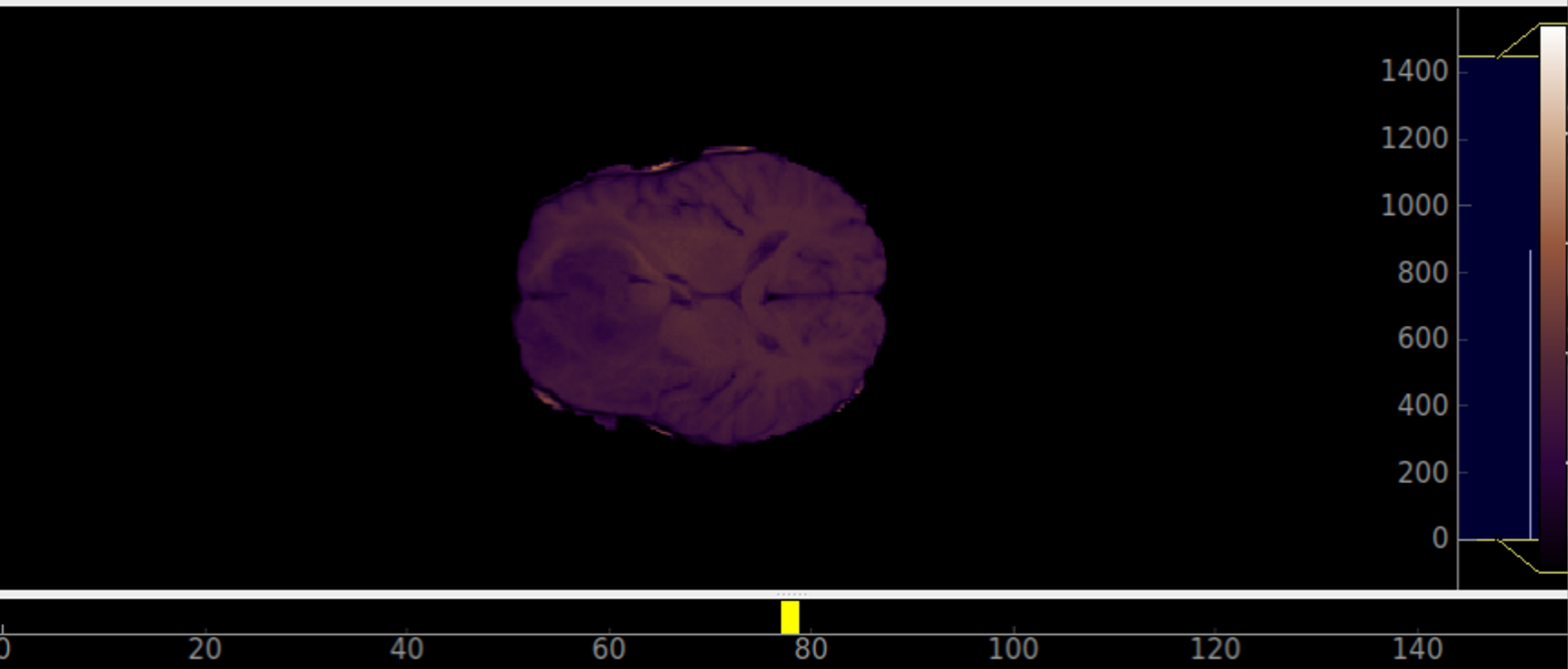


VIEW TOOL

CONTROLS

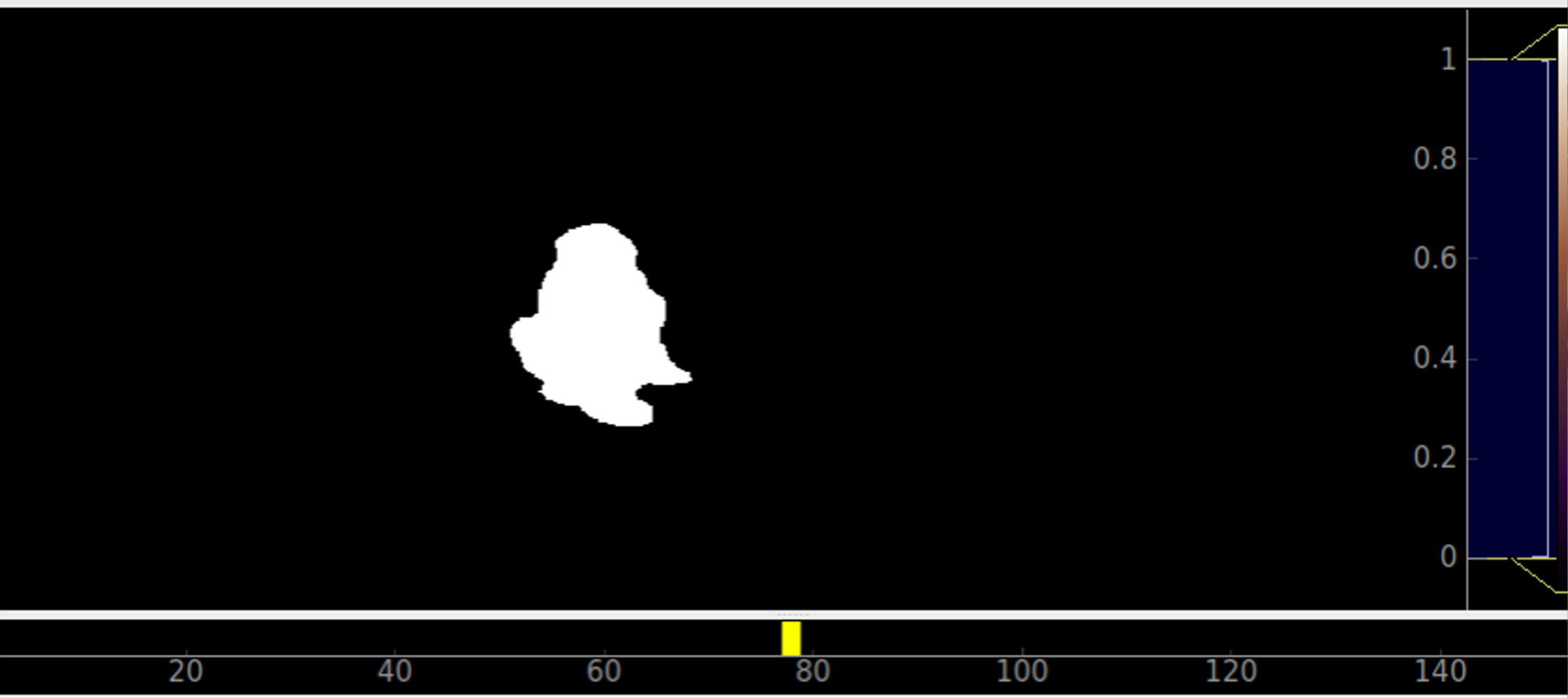
- MRI view: it is used to load and view t1,t2,t1c,flair,ir
- Mask view: It displays the mask view after performing segmentation .
- Segmental view :It displays the segmentation view which is the product of MRI view and mask view





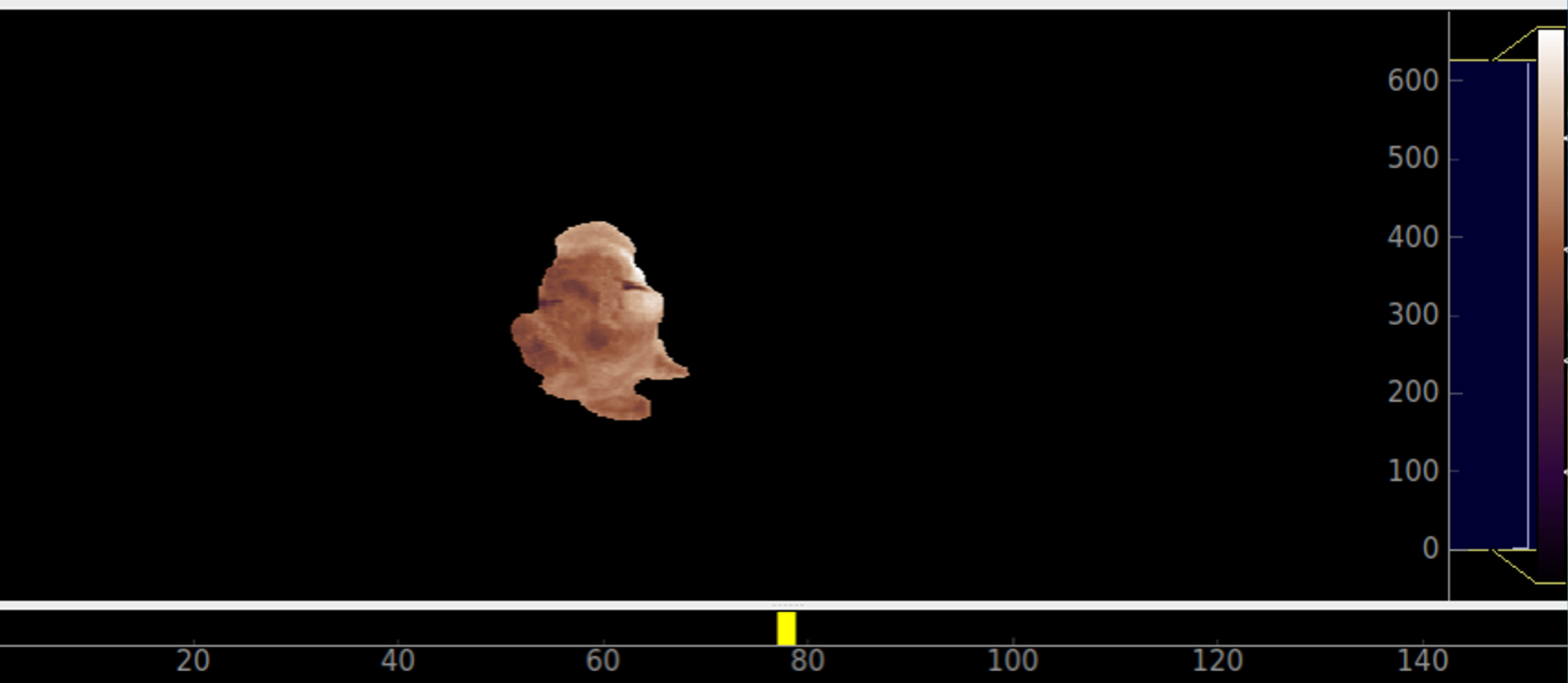
Save

MRI View



Save

Mask View



Save

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!!!
