Brain Tumors Segmentation(BraTS) with Deep Learning

Data Analyses

04.09.2020

Wai Po Kevin Teng, Xiongjun Wang

Dataset

- BraTS2015 Challenge dataset
- Multimodal MRI images (Flair, T1, T1c, T2)
- Associate with multi-labeled brain tumor (OT)

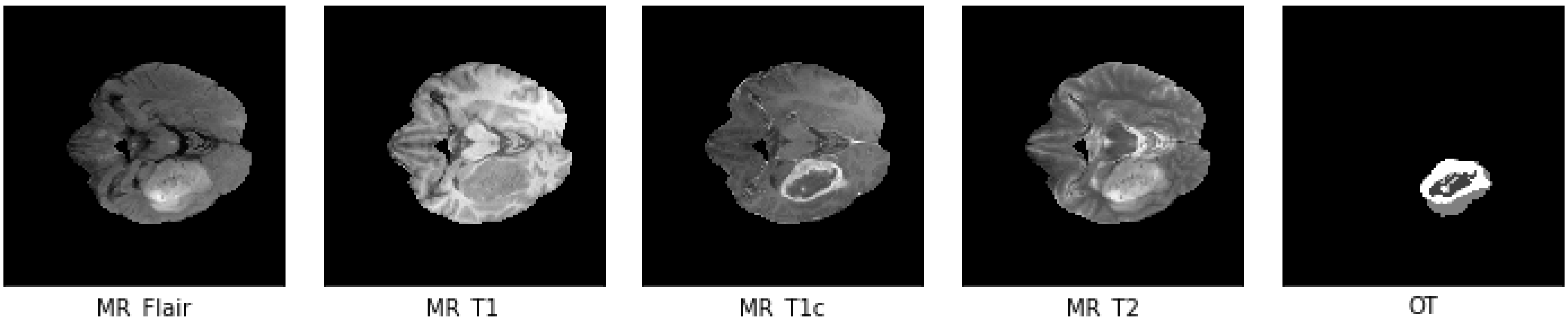
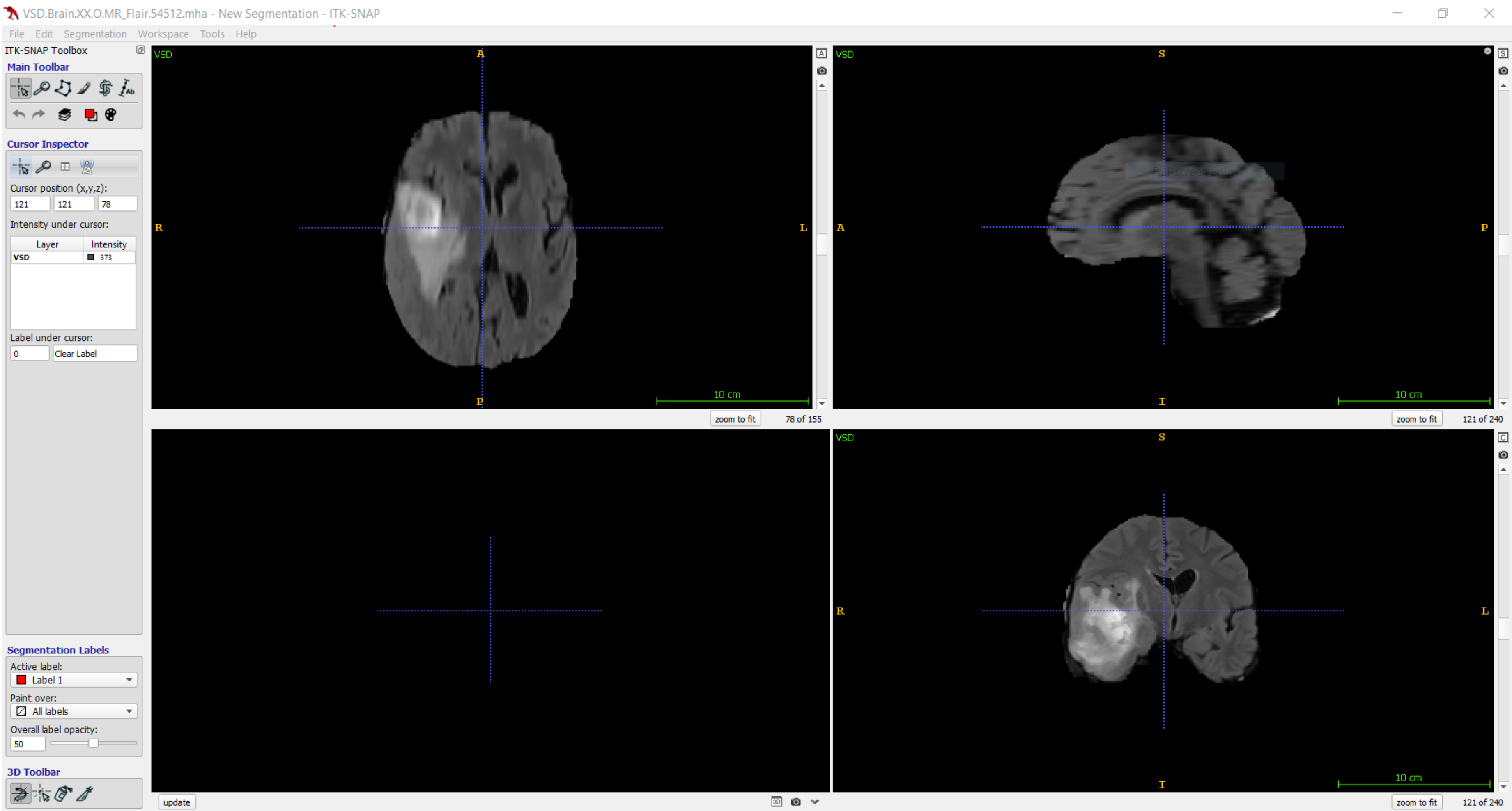


Fig. 1: Output slice of brain medical images from various mode

Criterion	Descriptions
File	A File has Multi-Modal MRI Data of one patient
File Format	.mha
Image Dimension	240(width) x 240(height) x 155(slices)
Image Mode	4 Multi-mode per patient

Software for Quick Analyses:



ITK-SNAP for visualizing .mha medical images

Multimodal MRI

Four MRI contrasts:

- **T1:** T1-weighted, native image, sagittal or axial 2D acquisition, with 1-6mm slice thickness
- **T1c:** T1-weighted, contrast-enhanced image, with 3D acquisition and 1mm isotropic voxel size for most patients
- **T2:** T2-weighted image, axial 2D acquisition, with 2-6mm slice thickness
- **FLAIR:** T2-weighted FLAIR image, axial, coronal, or sagittal 2D acquisition, 2-6mm slice thickness

Multi-labelled Brain Tumor

Four tumor tissue classes:

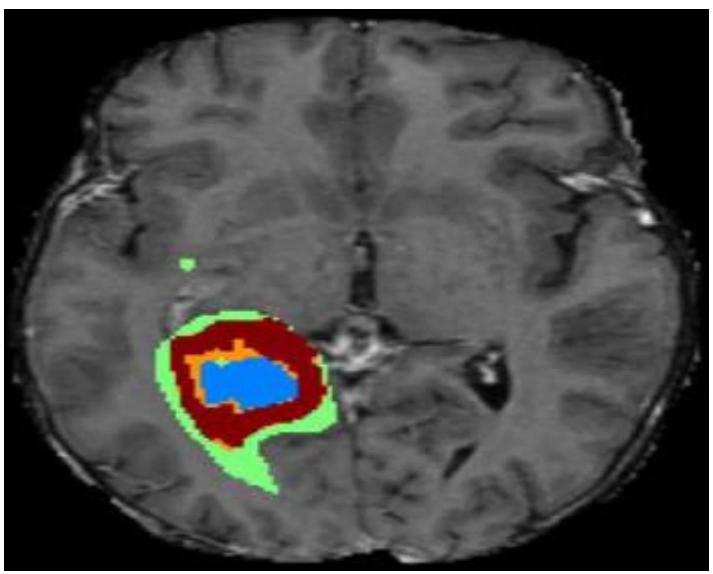
- *Edema*
- Necrosis
- Non-enhancing Tumor
- Enhancing Tumor

Complete Tumor

Core

Enhancing Tumor

Segmentation Task Evaluation



(left) Fig. 2: Schematic illustrations on the labelled tissue classes with color, where: *green* – edema, *blue* – necrosis, *orange* – non enhancing tumor, *dark red* – enhancing tumor (S.Pereira 2017) [1]

[1] S. Pereira, A. Oliveira, V. Alves and C. A. Silva, "On hierarchical brain tumor segmentation in MRI using fully convolutional neural networks: A preliminary study," 2017 IEEE 5th Portuguese Meeting on Bioengineering (ENBENG), Coimbra, 2017, pp. 1-4.

BraTS Dataset Tree Structure:

```
BRATS2015_Testing
 -> HGG_LGG
  --> brats_2013_pat0103_1
   ---> VSD.Brain.XX.O.MR_Flair.54193
   ---> VSD.Brain.XX.O.MR_T1.54194
   ---> VSD.Brain.XX.O.MR_T1c.54195
   ---> VSD.Brain.XX.O.MR_T2.54196
*Number of patients: 110

BRATS2015_Training
 -> HGG
  --> brats_2013_pat0001_1
   ---> VSD.Brain.XX.O.MR_Flair.54512
   ---> VSD.Brain.XX.O.MR_T1.54513
   ---> VSD.Brain.XX.O.MR_T1c.54514
   ---> VSD.Brain.XX.O.MR_T2.54515
   ---> VSD.Brain_3more.XX.O.OT.54517
*Number of patients: 220

 -> LGG
  --> brats_2013_pat0001_1
   ---> VSD.Brain.XX.O.MR_Flair.54632
   ---> VSD.Brain.XX.O.MR_T1.54633
   ---> VSD.Brain.XX.O.MR_T1c.54634
   ---> VSD.Brain.XX.O.MR_T2.54635
   ---> VSD.Brain_3more.XX.O.OT.54637
*Number of patients: 54


[Summary]
Total number of patients: 384
Total number of 2D images: 59520
  |_ Training: 42470
  |_ Testing: 17050
```

HGG: High Grade Gliomas

LGG: Low Grade Gliomas

Histogram Plots

*Medical image referred to Fig.1.

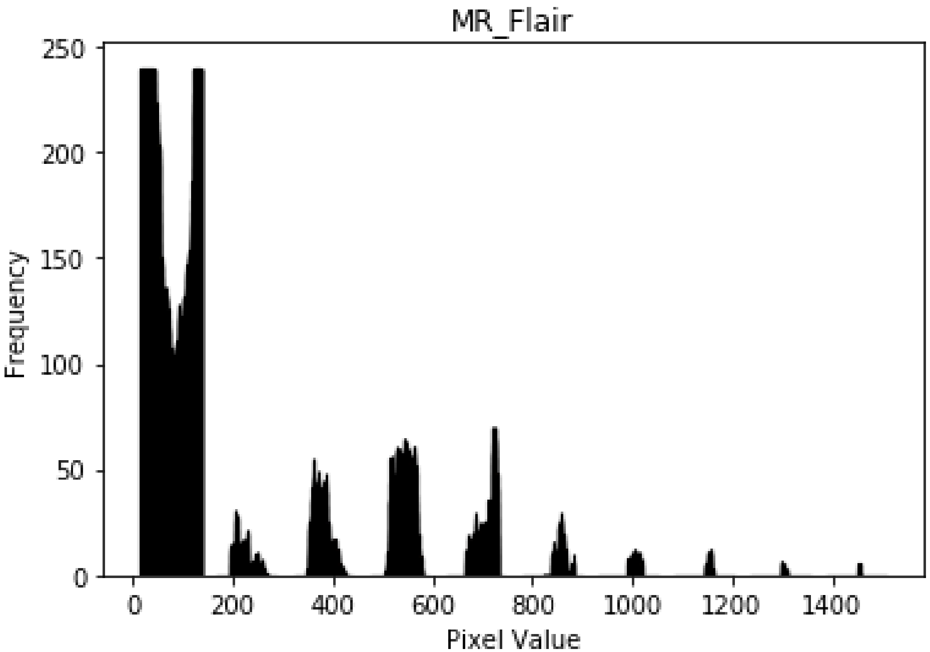


Image size: 240x240
Image slices: 155
Image max value: 1524
Image min value: 0
Mean value of image:146.48196180555556
Standard deviation of image:261.0431828653199

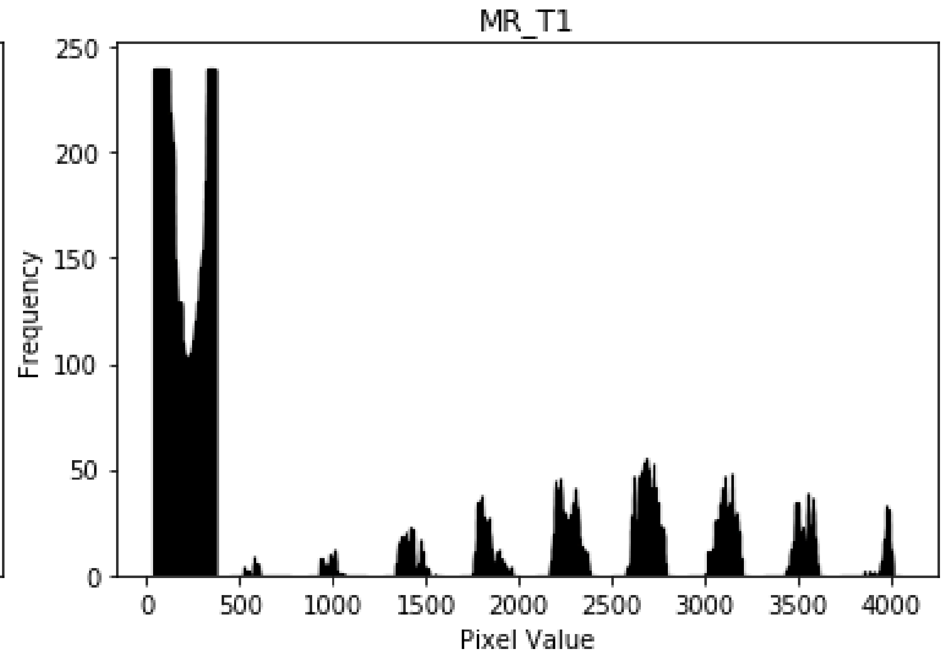


Image size: 240x240
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Image max value: 4090
Image min value: 0
Mean value of image:709.5326388888889
Standard deviation of image:1204.3953687131807

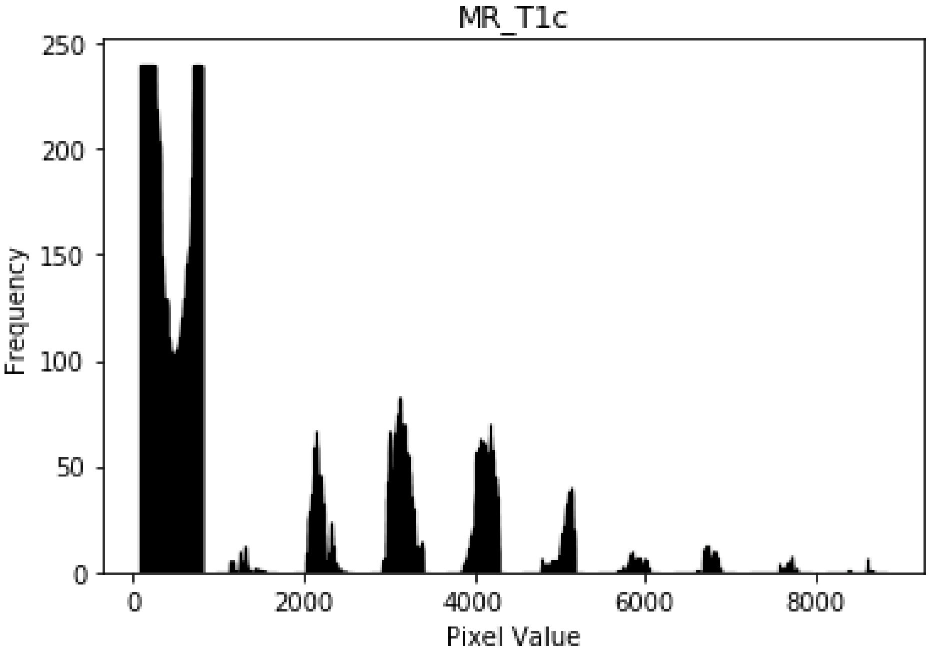


Image size: 240x240
Image slices: 155
Image max value: 8925
Image min value: 0
Mean value of image:973.6755555555555
Standard deviation of image:1677.0295555186333

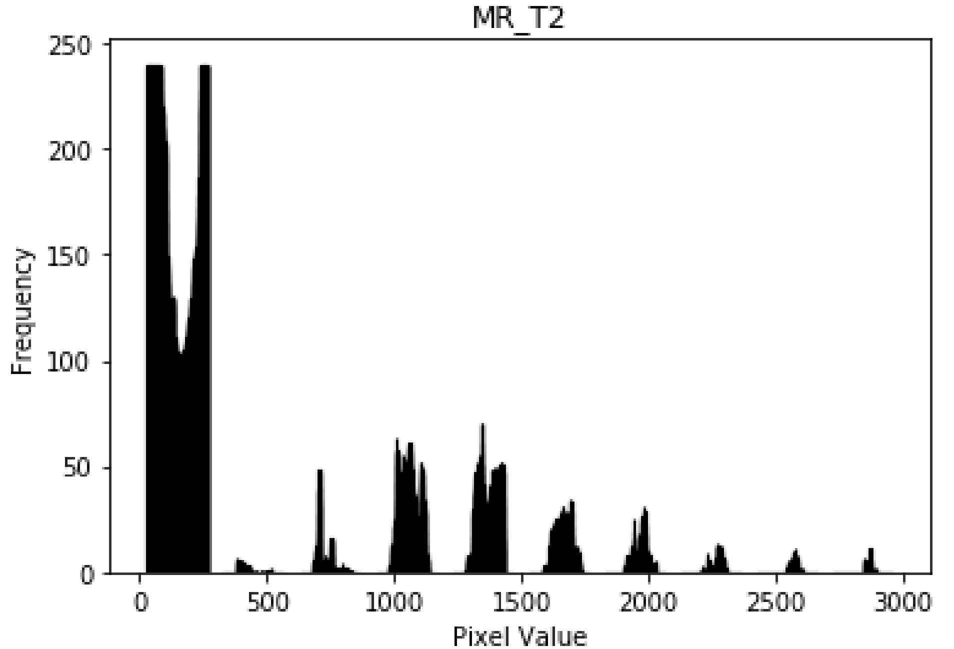
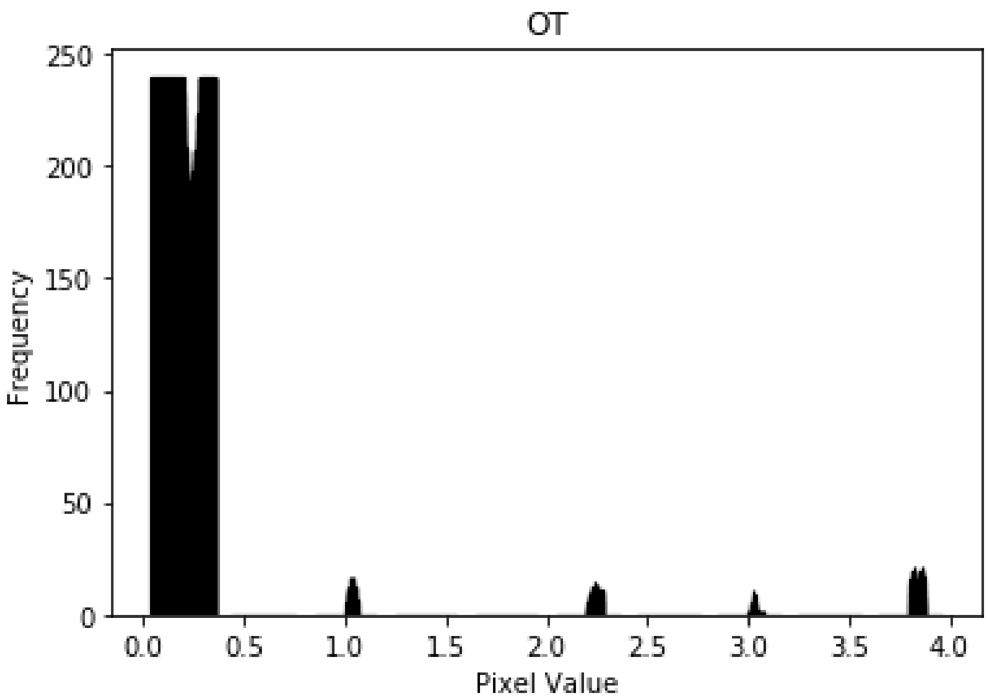


Image size: 240x240
Image slices: 155
Image max value: 2992
Image min value: 0
Mean value of image:362.8049826388889
Standard deviation of image:622.8808614343079

Ground Truth Distribution



Label Description:

1 – *Necrosis*

2 – *Edema*

3 – *Non-enhancing Tumor*

4 – E*nhancing Tumor*

0 – *Everything else*

(Menze et al. 2015)

Image size: 240x240
Image slices: 155
Image max value: 4
Image min value: 0

Image Pre-processing

1. **Min Max Normalization:**

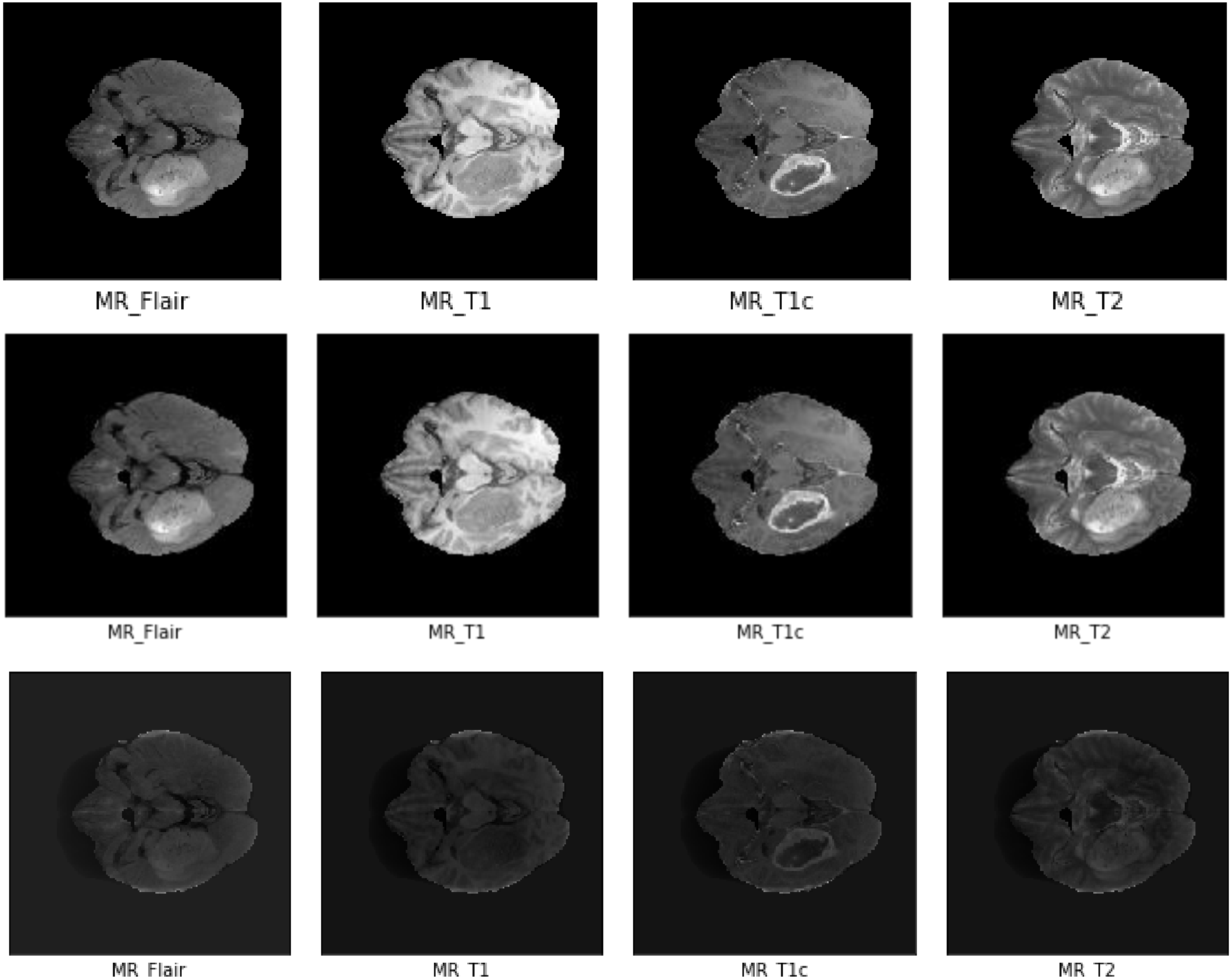
   Squash pixel intensity values to [0 , 1]

$$x_{norm} = \frac{x_i \; - \min(x_i)}{\max(x_i) - \min(x_i)}$$

2. Channel-Wise Standardization:

$$\mathrm{x_{std}} = \frac{x_i - \mu_{channel}}{\sigma_{channel}}$$

Plot Comparison

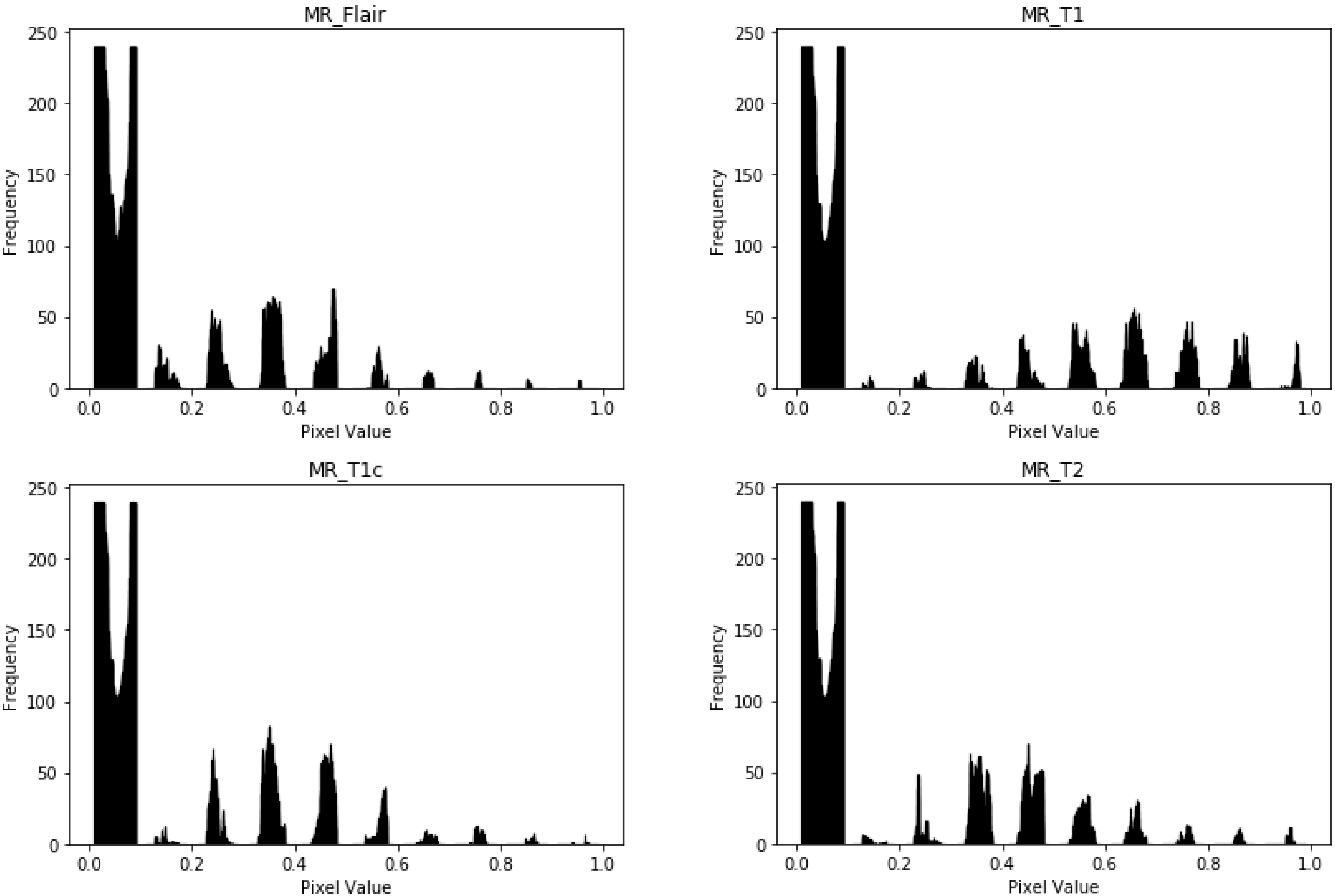


Original Dataset

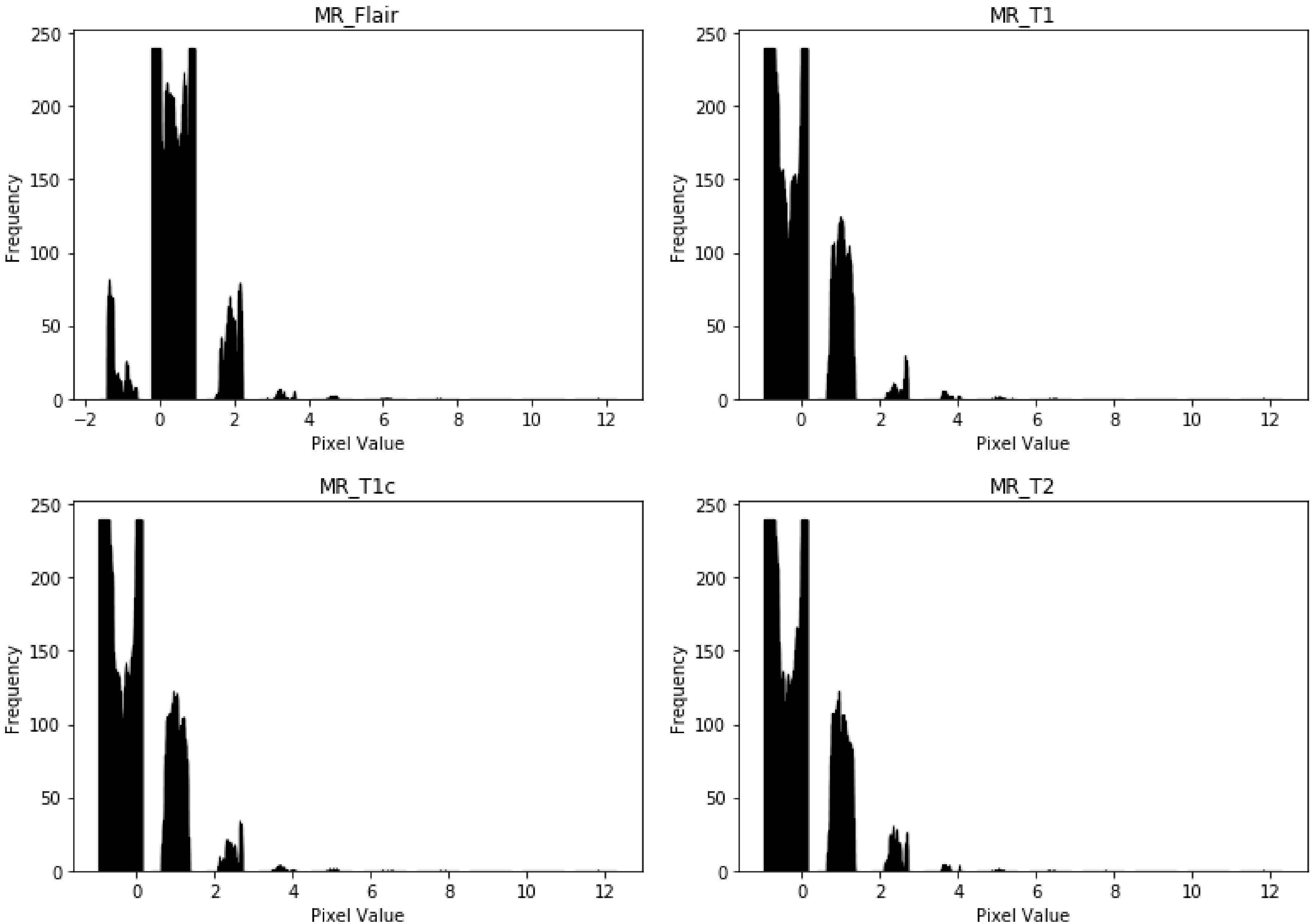
Min Max Norm

Channel wise Standardi-zation

Histograms (Min Max Norm.)



Histograms (Channel-wise Standardization)



Baseline Model

- Image Segmentation with U-Net (2D)

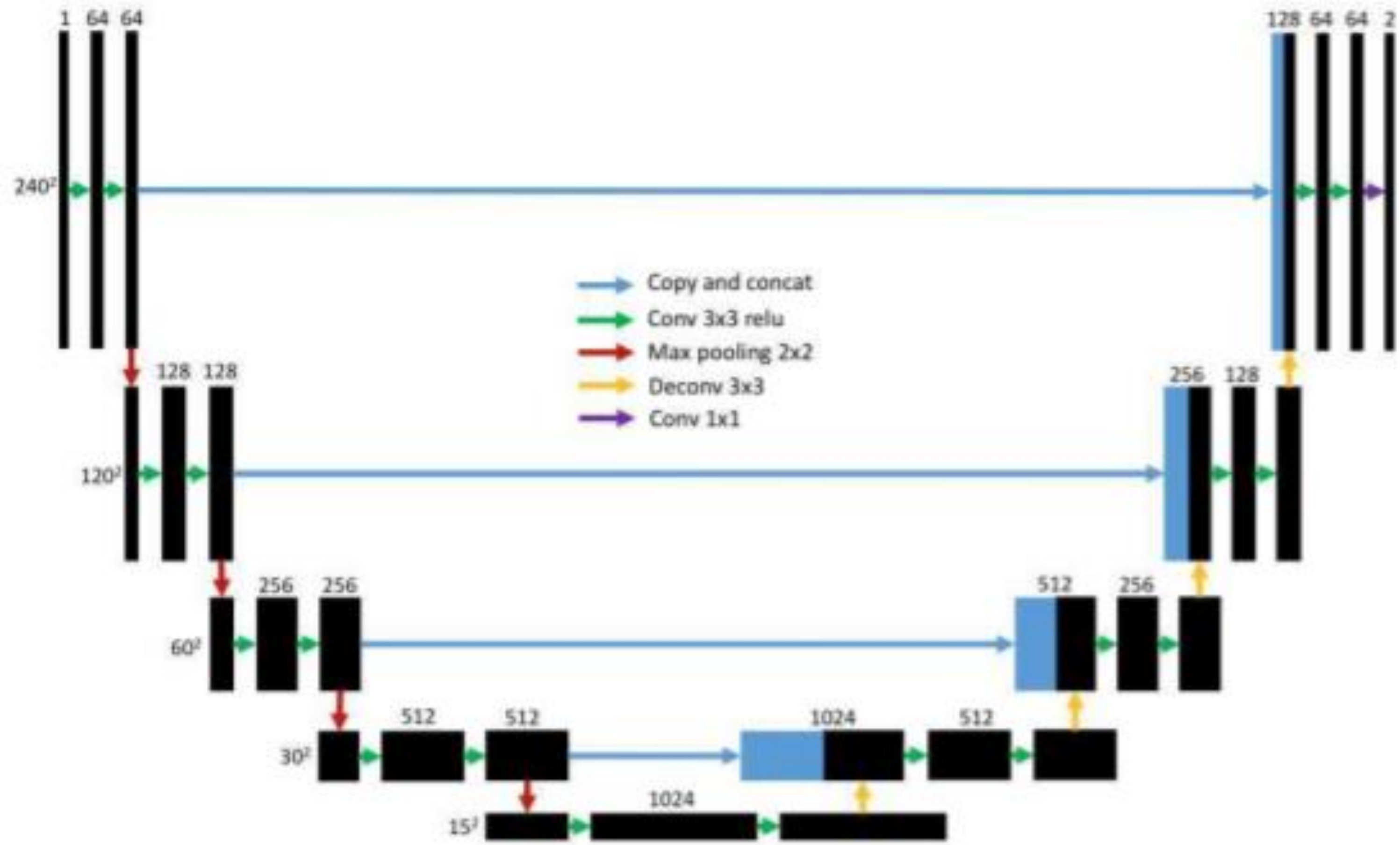


Fig. 3: Schematic U-Net Architecture for BraTS2015 Dataset *(H.Dong 2017)* [1]

[1]H.Dong, G.Yang, F.Liu, Y.Mo and Y.Guo, "Automatic Brain Tumor Detection and Segmentation Using U-Net Based Fully Convolutional Networks", Medical Image Understanding and Analysis, 2017.

Evaluation Metrics

- **Dice Coefficient** – Measurement for Union of Intersection (UOI) between the labelled tumor region and the segmented results from the model

$$DSC = \frac{2TP}{FP + 2TP + FN}$$

- **Sensitivity** – Evaluate the number of TP and FN

$$Sensitivity = \frac{TP}{TP + FN}$$

Where TP, FP and FN denote True Positive, False Positive and False Negative measurements, respectively

Results

- By H.Dong et. al. 2017

				DSC	
Method	**Data**	**Grade**	**Complete**	**Core**	**Enhancing**
	5 fold Cross Validation on	HGG	0.88	0.87	0.81
2D U-net	BraTS 2015	LGG	0.84	0.85	0.00
	Training Datasets	Combined	0.86	0.86	0.65

References

- Menze et al., The Multimodal Brain TumorImage Segmentation Benchmark (BRATS), IEEE Trans. Med. Imaging, 2015.
- Kistler et. al, The virtual skeleton database: an open access repository for biomedical research and collaboration. JMIR, 2013
- H.Dong, G.Yang, F.Liu, Y.Mo and Y.Guo, “Automatic Brain Tumor Detection and Segmentation Using U-Net Based Fully Convolutional Networks”, Medical Image Understanding and Analysis(MIUA), 2017.
- Paul A. Yushkevich, Joseph Piven, Heather Cody Hazlett, Rachel Gimpel Smith, Sean Ho, James C. Gee, and Guido Gerig. User-guided 3D active contour segmentation of anatomical structures: Significantly improved efficiency and reliability. *Neuroimage* 2006 Jul 1;31(3):1116-28
- S. Pereira, A. Oliveira, V. Alves and C. A. Silva, "On hierarchical brain tumor segmentation in MRI using fully convolutional neural networks: A preliminary study," 2017 IEEE 5th Portuguese Meeting on Bioengineering (ENBENG), Coimbra, 2017, pp. 1-4.

Thank You for Your Kind Attention!