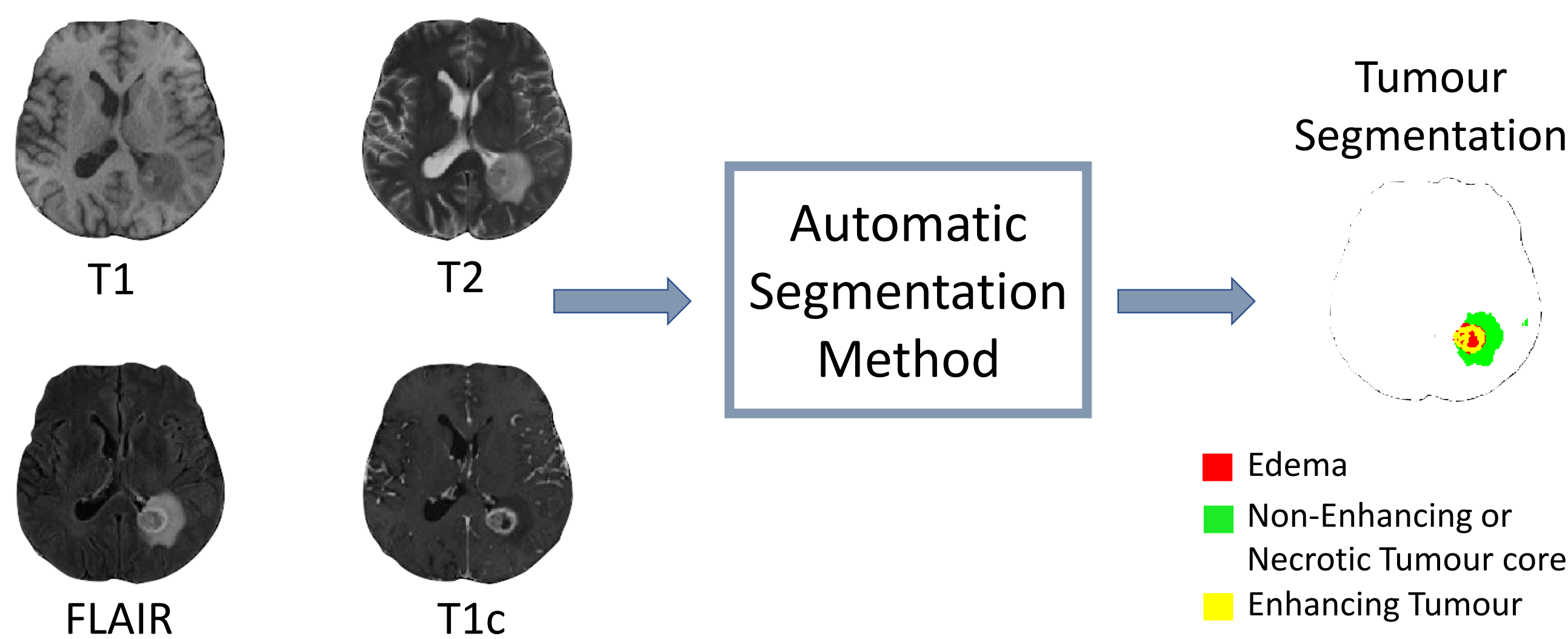
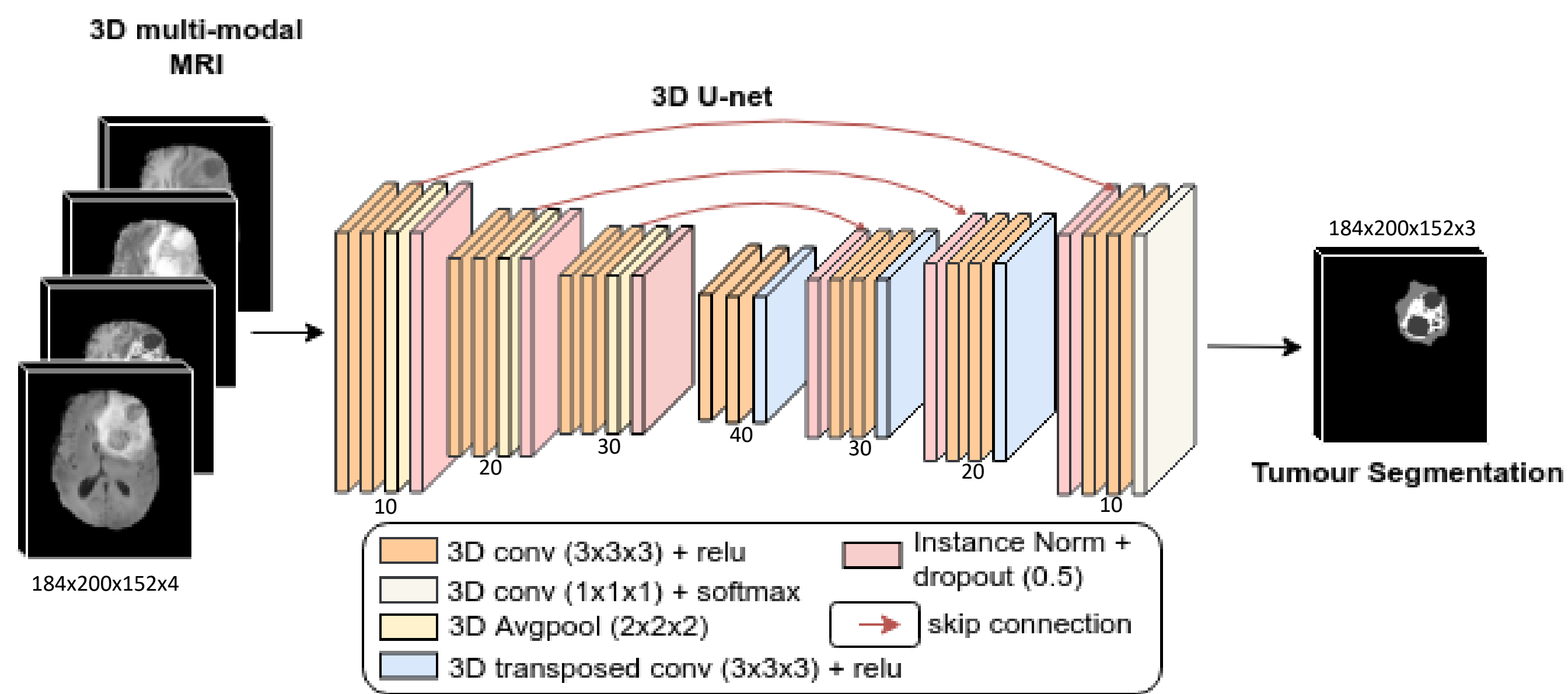


## Introduction



- Automatic segmentation algorithms can be useful for faster and reliable tumour delineation.
- Automatic brain tumor segmentation is a challenging task due to the wide variety of tumor locations, sizes, and shapes
- Various machine learning approaches for automatic tumour segmentation
  - Context-sensitive Random Forrest [1]
  - Multilevel Markov Random Field [2]
  - Multi-scale 3D CNN with Conditional Random Field [3]
  - Boundary Aware Fully Convolutional Neural Network [4]

## Method



### Architecture Details:

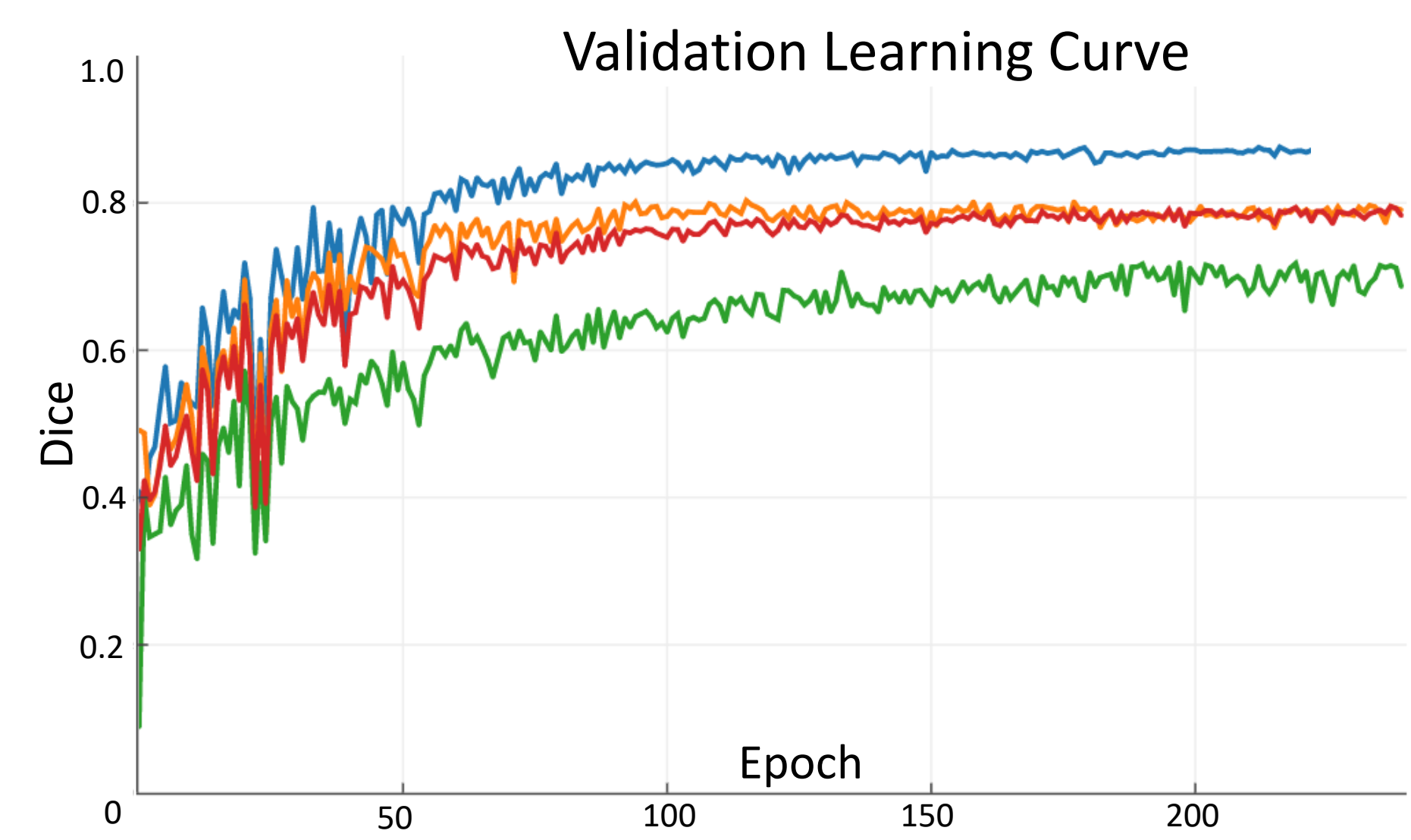
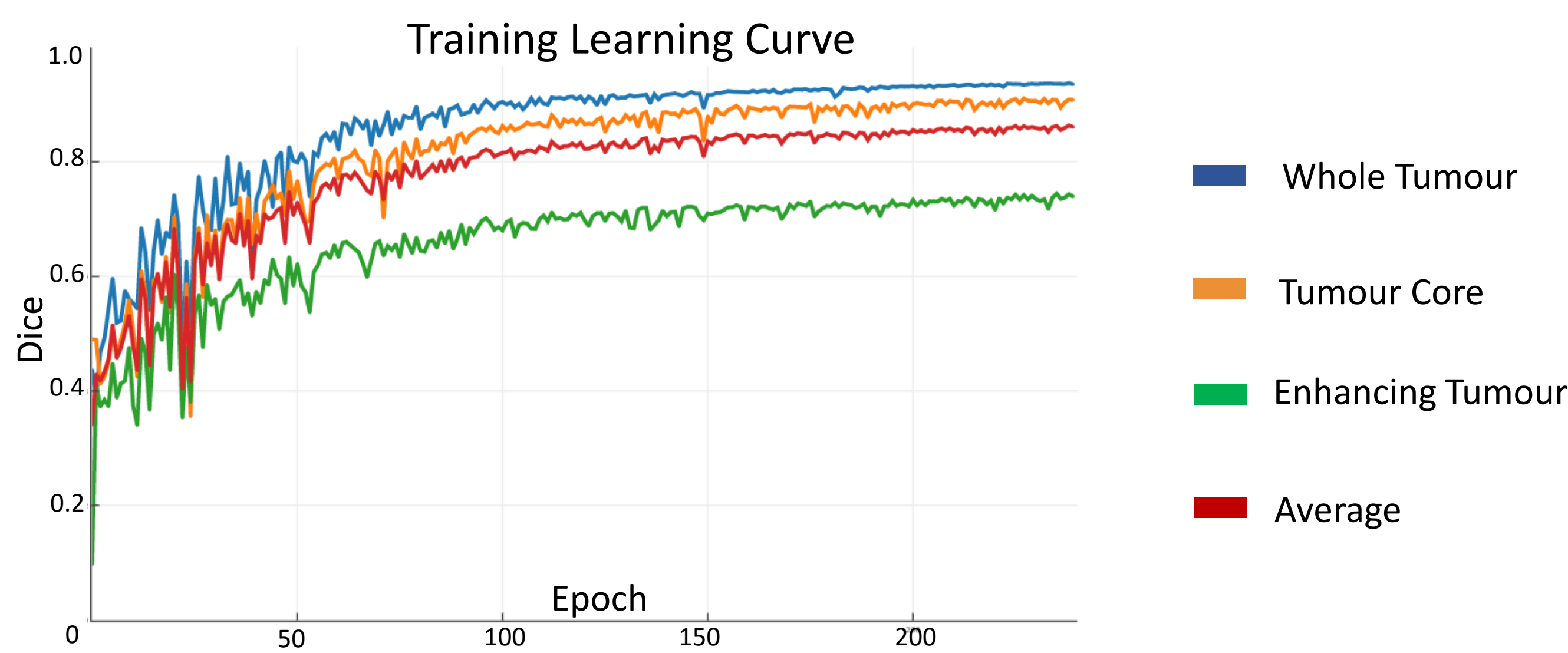
- 4 resolution step 3D U-net [5]
- Use of AvgPooling instead of MaxPooling for downsampling.
- Use of Transposed convolution for upsampling.
- Use of Instance-Norm and Dropout after each step
- Categorical Cross-Entropy (CCE) with curriculum class weight as loss function
- Pre-processing: Intensity Standardization using the mean and standard deviation over the masked region of a given MR image

## Quantitative Results

	Dice			Sensitivity			Specificity			Hausdorff-95		
	ET	WT	TC	ET	WT	TC	ET	WT	TC	ET	WT	TC
Mean	0.690	0.888	0.793	0.774	0.880	0.802	0.998	0.995	0.996	7.251	6.600	7.941
StdDev	0.294	0.094	0.206	0.245	0.118	0.210	0.004	0.006	0.007	13.318	11.215	11.805
Median	0.817	0.918	0.876	0.861	0.913	0.879	0.999	0.996	0.999	2.237	3.606	4.062
25quantile	0.641	0.878	0.748	0.709	0.850	0.723	0.997	0.994	0.996	1.414	2.236	2.236
75quantile	0.878	0.941	0.926	0.935	0.958	0.942	0.999	0.998	0.999	5.385	6.557	9.327

	Dice			Sensitivity			Specificity			Hausdorff-95		
	ET	WT	TC	ET	WT	TC	ET	WT	TC	ET	WT	TC
Mean	0.788	0.909	0.825	0.824	0.911	0.811	0.998	0.995	0.998	3.520	4.923	8.316
StdDev	0.233	0.059	0.179	0.222	0.082	0.212	0.004	0.004	0.002	4.992	8.154	13.521
Median	0.869	0.921	0.902	0.893	0.933	0.901	0.999	0.996	0.999	1.732	2.914	3.240
25quantile	0.809	0.894	0.773	0.824	0.880	0.711	0.998	0.994	0.998	1.414	2.000	2.000
75quantile	0.911	0.951	0.945	0.942	0.964	0.958	0.999	0.998	0.999	3.000	4.970	8.658

Challenge Metric Statistics: 5-Fold Cross-Validation on BraTS 2018 Training Set (Left) and BraTS 2018 Validation Set (Right). Results are specified for enhancing tumor (ET ■), whole tumor ( WT ■ ■ ■ ), and tumor core ( TC ■ )



Training (Left) and Validation (Right) Dice Scores as a function of number of epochs for one of the five cross-validation fold.

## Qualitative Results

T1c	Expert Segmentation	Predicted Segmentation	T1c	Expert Segmentation	Predicted Segmentation	T1c	Predicted Segmentation	T1c	Predicted Segmentation	T1c	Predicted Segmentation
TCIA02_300			TCIA10_241			MDA_1018		TCIA02_230		KLHD_930	
CBICA_AAG			TCIA13_654			UAB_3499		TCIA10_609		UAB_3460	
2013_1			2013_0			WashU_W053		CBICA_BLK		WashU_S025	
BraTS 2018 Training Dataset HGG case			BraTS 2018 Training Dataset LGG case			BraTS 2018 Validation Dataset			BraTS 2018 Test Dataset		

Reference:  
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