The re-evaluation of Brain Tumor Segmentation using Cascaded Anisotropic Convolutional Neural Network

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Introduction

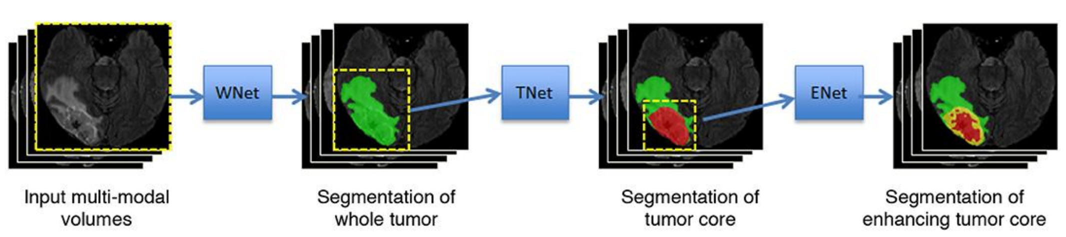
Conditional Random Field (CRF) is a discriminative statistical modelling method that is used when the class labels for different inputs are not independent. In some cases of the image segmentation, the class label for the pixel depends on the label of its neighboring pixels as well. Besides, we would like to introduce Dice Coefficient and Dice Loss. Dice Coefficient is essentially a measure of overlap between two samples. This measure ranges from 0 to 1 where a Dice coefficient of 1 denotes perfect and complete overlap, while the dice loss=1-dice coefficient.

Objectives

We intended to further improve the segmentation performance of the brain tumor segmentation, in order to get rid of some noise in the results. We thought about using CRF as a post-process method to address this issue. We want to use it to eliminate some falsely segmented pixel areas occurred mostly in some tumor strips. Besides, we are also considering using the dice loss in the PyTorch implementation and using it to evaluate how the segmentation results are different after CRF and before CRF.

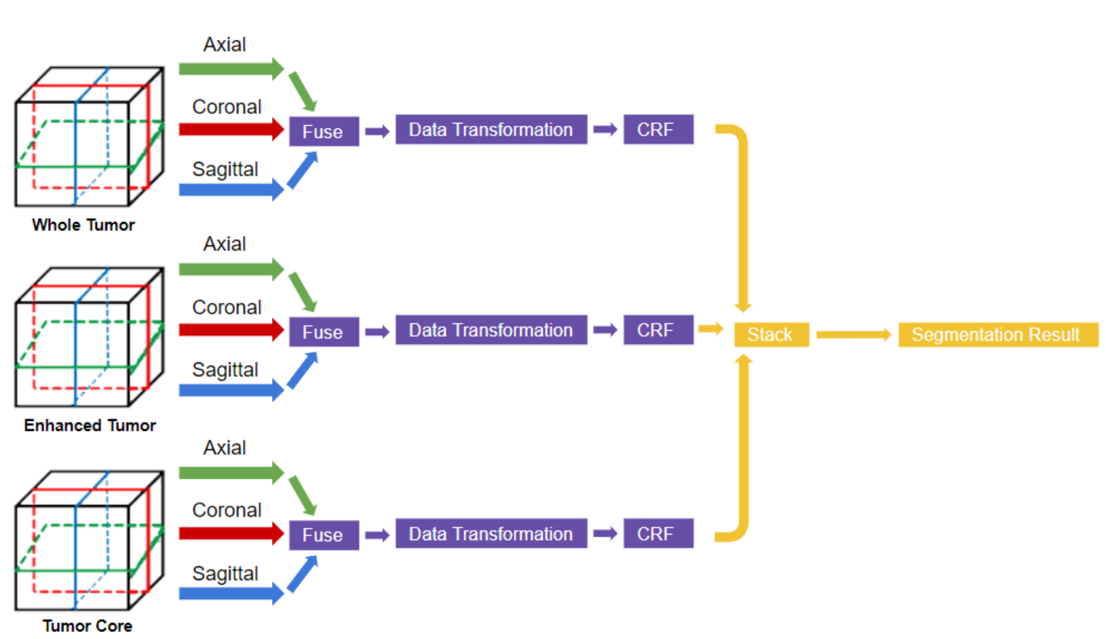
Methods and Personal Contributions

1. I converted most of the TensorFlow blocks and workflow into the PyTorch based codes:
   A. Eliminate the session mechanism and rewrote the training workflow
   B. Added the weight initialization scripts using Xavier initializer.
   C. Added the PyTorch model saver/loader using state_dict.
   D. Changed the Conv2dBlock structure to solve the unmatched shapes between the original implementation and the revised one.



2. I implemented an initial version of the new Dice Loss that is more compatible to our project, using a third-party dice loss package, along with the data pre-processing function.

3. I implemented the CRF post-processing method using segcrf and some logics related to its data transformation processes.



Methods & Results

I ran the evaluation in two scenarios. First, I only tested the whole tumor with 20 testing images. Second, I tested all types with the complete testing dataset. It turned out that while running with small testing set, the means are small and the standard deviations are high.

	Enhanced Tumor	Whole Tumor	Tumor Core
Mean	0.3598	0.5058	0.2007
Standard Deviation	0.3906	0.2632	0.3073

FIGURE 1: 20 testing set, no crf

	Enhanced Tumor	Whole Tumor	Tumor Core
Mean	0.3002	0.5445	0.2244
Standard Deviation	0.3648	0.2467	0.3046

FIGURE 2: 20 testing set, with crf

	Enhanced Tumor	Whole Tumor	Tumor Core
Mean	0.7831	0.8739	0.7748
Standard Deviation	0.2215	0.1319	0.2700

FIGURE 4: Original, All testing set, no crf

	Enhanced Tumor	Whole Tumor	Tumor Core
Mean	0.6575	0.8979	0.7983
Standard Deviation	0.2861	0.1034	0.2255

FIGURE 3: All testing set, no crf

	Enhanced Tumor	Whole Tumor	Tumor Core
Mean	0.7065	0.8845	0.8230
Standard Deviation	0.2704	0.1131	0.2083

FIGURE 4: All testing set, with crf

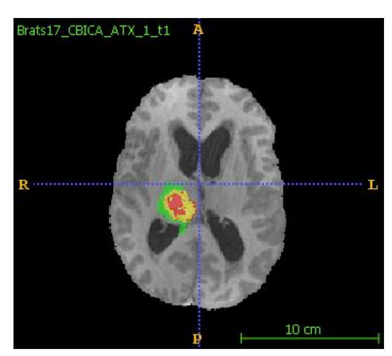


FIGURE 5: Ground Truth - Axial

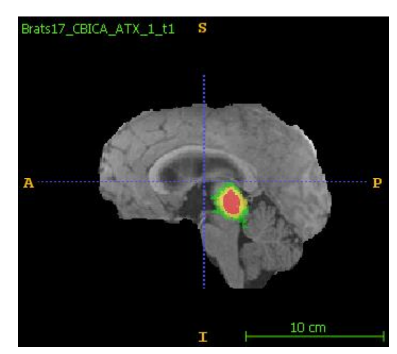


FIGURE 6: Ground Truth - Coronal

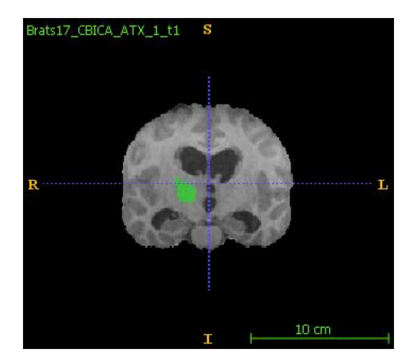


FIGURE 7: Ground Truth -Sagittal

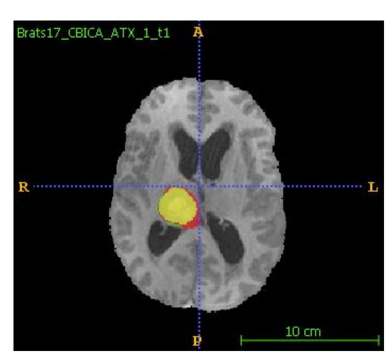


FIGURE 8: No CRF - Axial

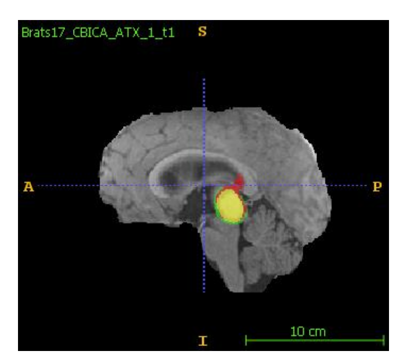


FIGURE 9: No CRF - Coronal

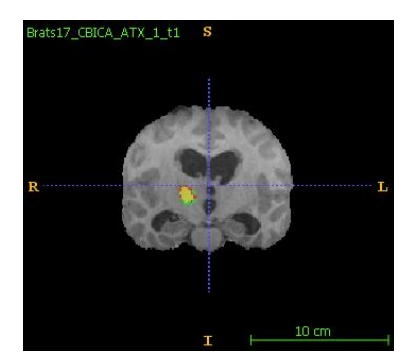


FIGURE 10: No CRF - Sagittal

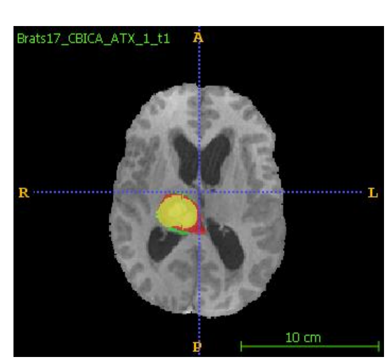


FIGURE 11: CRF - Axial

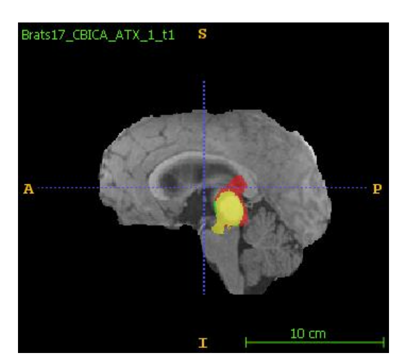


FIGURE 12: CRF - Coronal

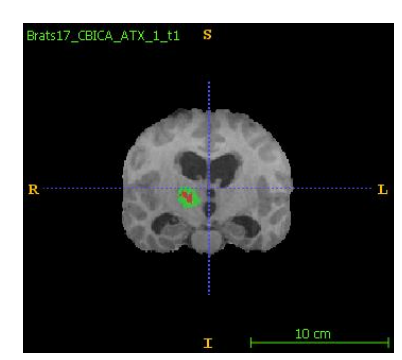


FIGURE 13: CRF - Sagittal

Conclusion

With the revision to a new PyTorch implementation, the complex variable initialization and session mechanism in TensorFlow are eliminated and the original gradient descent process are reengineered, from the dice loss to cross-entropy loss, due to the non-differentiability of some mathematical components in the PyTorch implementation. Dice loss becomes the evaluation method only.

CRF is achieved and works as the post-process to get more spatially regularized segmentation, in which the noisy segmented pixels are corrected or eliminated, and the general dice score means are increased with less deviation. It is suggested from the experiment that the CRF may have a minor negative impact on the segmentation performance in the whole tumors, while it largely increases the accuracy of other parts.

References

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