Ensemble of Deep 2D and 3D Fully Convolutional Neural Network for Brain Tumor Segmentation

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Introduction

- Deep learning paradigms like Convolutional Neural Networks employed to learn features for pixel wise segmentation
- Ensemble of 2-D and 3-D Convolutional Networks were used to perform the task of segmentation
- Final prediction was attained by computing the Arithmetic Mean of all the posterior probabilities (4 different networks).
- Post-processing using Conditional Random Field and 3-D connected components

Network architecture

- The ensemble comprises of two 3-D networks viz BrainNet & 3-D Tiramisu and one 2-D network (2-D Tiramisu).
- BrainNet processes patches at multiple resolution and predicts the class associated to subset of voxels in the input patch (9^3), Fig 1.
- The 3-D and 2-D variant of the Tiramisu-77 in the ensemble differs only type of convolution, Fig 2 (b).
- Various building blocks for the network are shown in Fig 2 (a) and Fig 3

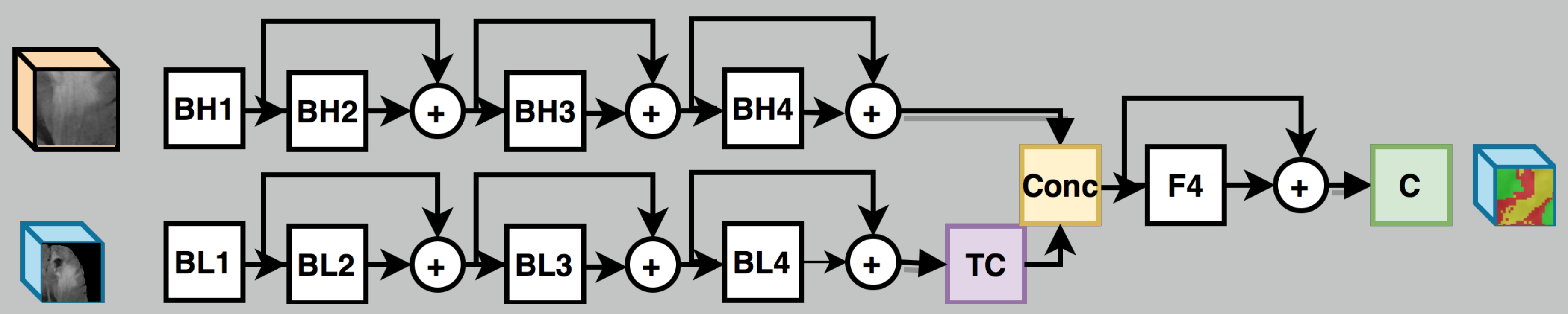
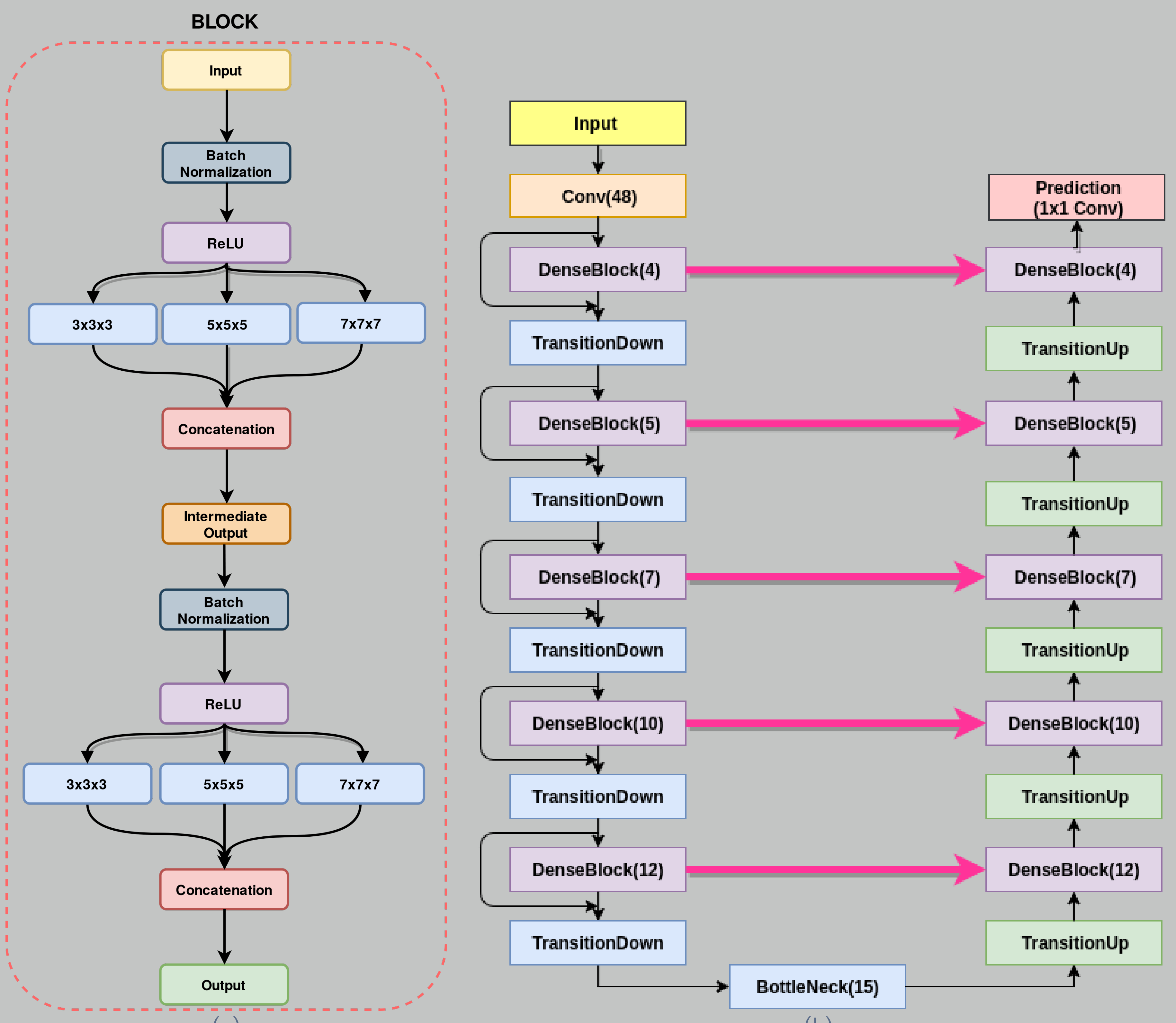
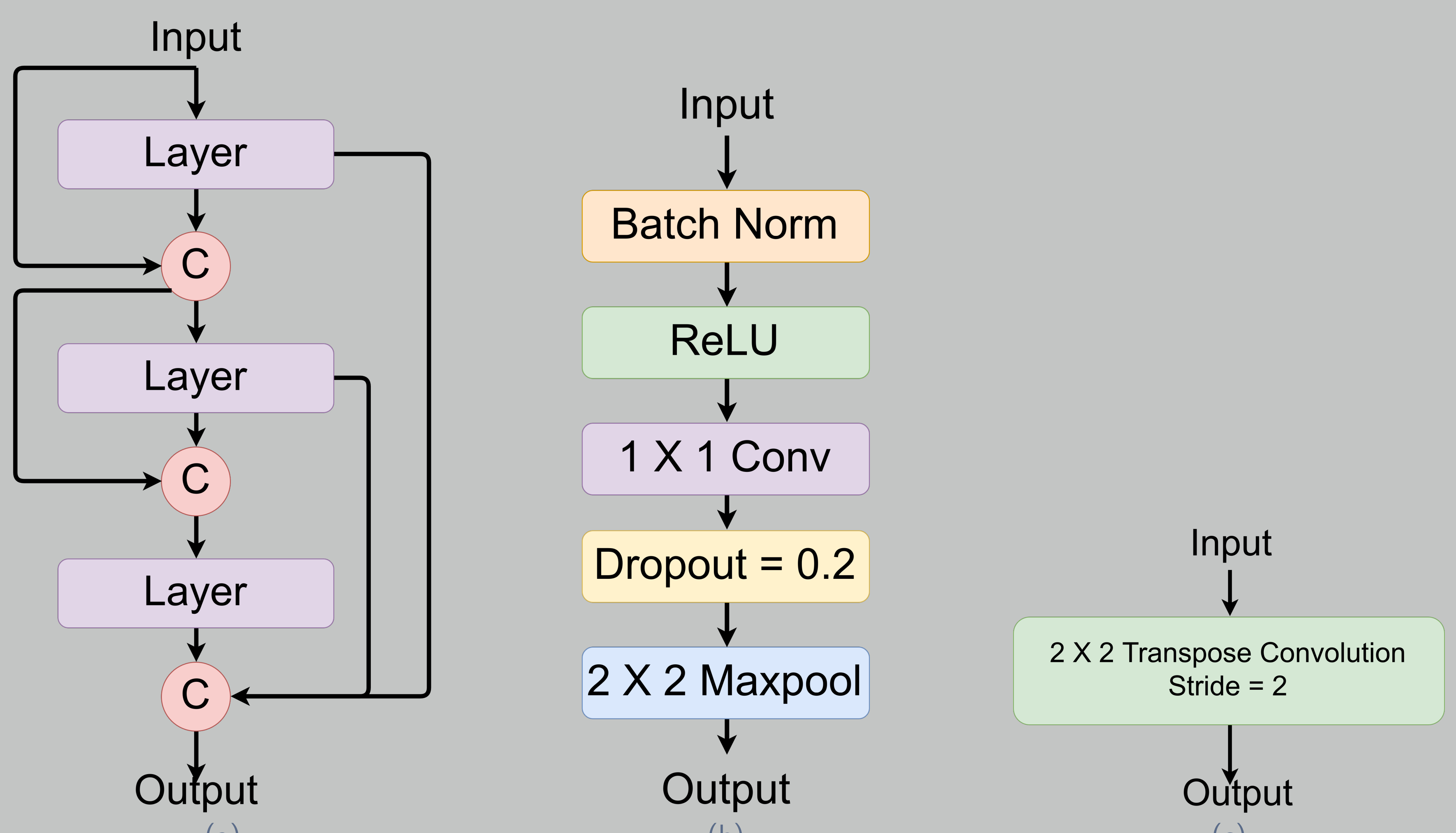


Figure: 3-D Fully Convolutional Neural network (BrainNet)



(a) (b)

Figure: a) BLOCK in 3-D network. b) 2-D 77 layer Tiramisu (FC-DenseNet77)



(a) (b) (c)

Figure: Blocks used in the model. a) Dense Block. b) Transition Down. c) Transition Up

Methods

- Pre-Processing and Data
  - Volume wise Z-score normalization used to reduce scan variation between patients
  - Stratified sampling was adopted for 3-D patch extraction (64x64x64) and (25x25x25 with 19x19x19)
  - 2-D Slices were taken along the axial direction (240*240 pixels) for training 2-D networks
- Training
  - 2D and 3D versions of Tiramisu model along with BrainNet models were used to perform segmentation
  - Weights initialized using Xavier initializer; trained using ADAM optimizer
  - All the networks were trained combined HGG + LGG data (200 patients in training set, 57 in validation)
  - Networks were trained using the combination of Weighted Cross Entropy and Dice Loss.
  - Training was done using batch size = 4 and initial learning rate of 0.0001 and decay factor of 0.1
- Post-processing
  - Dense CRF with Gaussian edge potentials was used to smoothen predictions
  - Network trained to detect Air, Brain and Lesion along with 3-D connected component analysis was used to reduce outliers

Results: Local Data

- On the local test data, the ensemble of all networks achieved whole tumor, tumor core and active tumor dice score of 0.91, 0.76, 0.75 respectively

Table: Results of local test data (n=30)

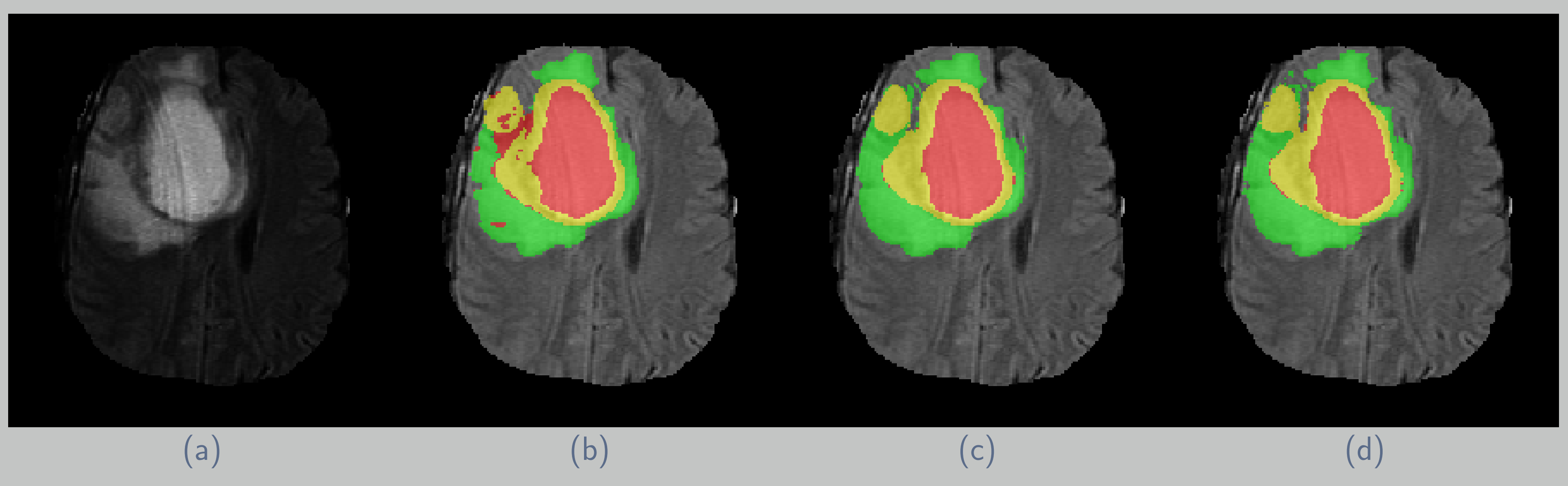
	Whole Tumor	Tumor Core	Active Tumor
Mean	0.91	0.76	0.75
Std	0.10	0.26	0.31
Median	0.92	0.92	0.86

- Proposed segmentation algorithm achieve whole tumor, tumor core and active tumor dice of 0.89, 0.76 and 0.76 respectively on BraTS 2018 validation data

Table: Results of BraTS 2018 validation data, (n= 66)

	Whole Tumor	Tumor Core	Active Tumor
Mean	0.89	0.76	0.76
Std	0.11	0.22	0.28
Median	0.88	0.82	0.83

Results: Figure



(a) (b) (c) (d)

Figure: (a) FLAIR, (b) Without Post-processing, (c) With Post-processing, (d) Ground truth. In images b, c and d, Green, Yellow & Red represent Edema, Enhancing Tumor and Necrosis present in the lesion.

Tools and Code Availability

- The networks were developed using Pytorch framework.
- Networks were trained and evaluated on Nvidia GTX Titan X and Tesla K40C GPUs.
- https://github.com/koriavinash1/Ensemble-of-Deep-2D-and-3D-Fully-Convolutional-Neural-Network-for-Brain-Tumor-Segmentation

References

1. Huang G, Liu Z, Weinberger KQ, van der Maaten L. "Densely connected convolutional networks". arXiv preprint arXiv:1608.06993. 2016 Aug 25.
2. Jégou S, Drozdzal M, Vazquez D, Romero A, Bengio Y. The one hundred layers tiramisu: Fully convolutional DenseNets for semantic segmentation. arXiv preprint arXiv:1611.09326. 2016 Nov 28.
3. Krhenbhl, Philipp, and Vladlen Koltun. "Efficient inference in fully connected crfs with gaussian edge potentials." Advances in neural information processing systems. 2011.
4. Kamnitsas, K., Ferrante, E., Parisot, S., Ledig, C., Nori, A.V., Criminisi, A., Rueckert, D. and Glocker, B., 2016, October. DeepMedic for brain tumor segmentation. In International Workshop on Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries (pp. 138-149). Springer, Cham.

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