White matter hyperintensities segmentation using UNet with highlighted foreground

Gilsoon Park, Jinwoo Hong, Jong-Min Lee*

Department of Biomedical Engineering, Hanyang University, Seoul, South Korea
* ljm@hanyang.ac.kr

1. Data and preprocessing

The training images consist of 60 subjects and are acquired from different three protocols, Utrecht, Singapore, and AmsterdamGE3T. To train our method, we used preprocessed training images, bias field corrected FLAIR images and bias field corrected T1 images registered with FLAIR images, and white matter hyperintensities label images.

The non-brain regions of T1 images were extracted using ROBEX [1] and the brain masks resulting from the ROBEX were used to extract the non-brain regions of FLAIR images. The intensities from the lower 5% to the upper 95% of T1 and FLAIR images then did gaussian normalization in brain mask region. Finally, all images cropped to 200x200 size in the axial plane. The data preprocessing also are applied to test data.

2. Methods

Data augmentation

Random affine transform (rotation, shearing, scaling, and translation) and flipping were employed for online data augmentation. The augmented data and original data were used for training at a ratio of 3:1.

Model

We used 2D UNet [2] as our basic model. The convolutional layers of our model consist of 3x3 or 5x5 convolution, batch normalization [3], and ELU activation function [4], excepted final convolutional layer consisting of 1x1 convolution and softmax function.

Highlighted foreground

We added a highlighted foreground information to decoder path of basic 2D UNet (Fig. 2). The highlighted foreground information was generated using max-pooling of original foreground information (Fig. 1). It is a label image with a higher percentage of foreground than the original label image, causing additional losses and helps to make training more effective. During testing, the highlighted foreground information is not used for segmentation result.

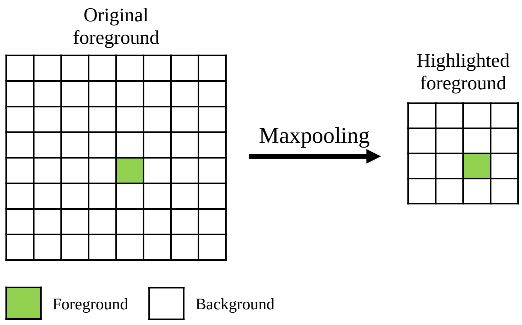

Fig. 1: Illustration of a highlighted foreground.

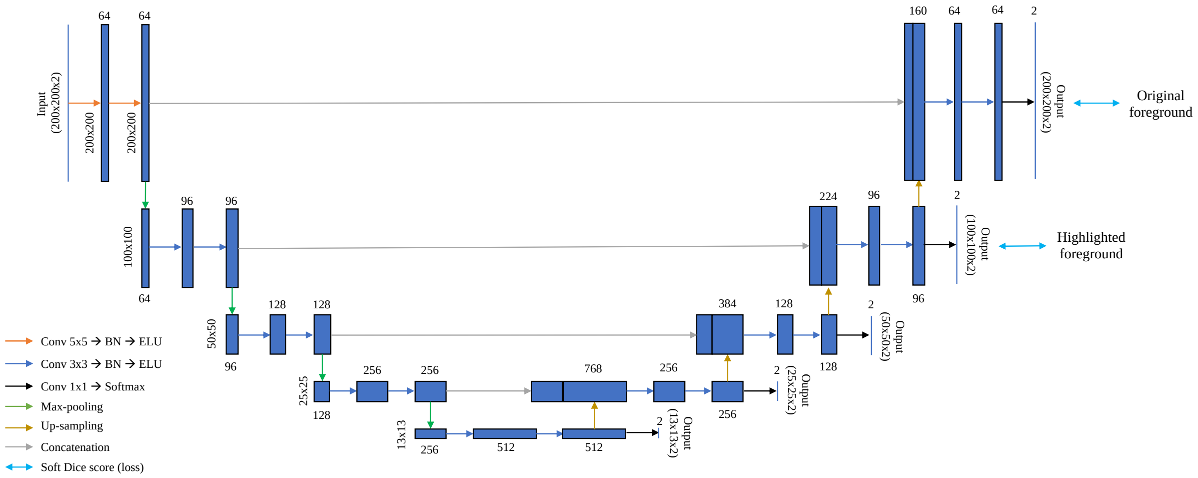

Fig. 2: Illustration of the UNet with a highlighted foreground.

3. Postprocessing

We aggregated the segmentation results from passing original and flipped data (x-axis, y-axis, and x, y-axis) through each of five models with the same architecture, but different initialization and batch. A 0.5 threshold was applied to the aggregated segmentation result for final segmentation result.

Reference

1. Iglesias, J.E., et al., *Robust brain extraction across datasets and comparison with publicly available methods*. IEEE transactions on medical imaging, 2011. **30**(9): p. 1617-1634.
2. Ronneberger, O., P. Fischer, and T. Brox. *U-net: Convolutional networks for biomedical image segmentation*. in *International Conference on Medical image computing and computer-assisted intervention*. 2015. Springer.
3. Ioffe, S. and C. Szegedy, *Batch normalization: Accelerating deep network training by reducing internal covariate shift*. arXiv preprint arXiv:1502.03167, 2015.
4. Clevert, D.-A., T. Unterthiner, and S. Hochreiter, *Fast and accurate deep network learning by exponential linear units (elus)*. arXiv preprint arXiv:1511.07289, 2015.