

# Brain Structure Segmentation Using Multiple Deep Networks and Label Fusion

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## 1 Data Preprocessing

**Data normalization** A patient-wise normalization of the image intensities was performed both during training and testing. For the scan of each patient, the mean value and standard deviation were calculated based on intensities of all voxels. Then each image volume was normalized to zero mean and unit standard deviation.

**Data augmentation** Rotation, shearing, scaling along horizontal direction (x-scaling), and scaling along vertical direction (y-scaling) were employed for data augmentation. After data augmentation, a four times larger training dataset was obtained.

## 2 Methodology

### 2.1 Combination of modalities

We employ multi-sequence data including T1-weighted (T1), T1-weighted inversion recovery (T1-IR) and FLAIR which captures complementary information of different brain structures. In clinical practice, the combination of FLAIR and T1 is beneficial for segmenting white matter lesions while the combination of T1 and T1-IR is helpful for annotating cerebrospinal fluid. We feed different combinations of modalities for multiple networks.

### 2.2 Multiple deep networks

We employed two Dilated Residual U-Nets (DRUNet) and one normal U-Net for segmenting different labels. DRUNet was originally proposed in [1] for nerve head tissues segmentation in optical coherence tomography images. DRUNET exploits the inherent advantages of the U-Net skip connections [4], residual learning [2] and dilated convolutions [5] capture rich context information of different brain structures. Since not all the labels were annotated in the same modalities, i.e., white matter lesions were annotated on the FLAIR scan and the outer border of the CSF was segmented using both the T1-weighted scan and the T1-weighted

inversion recovery scan, we employed a multi-stage approach to segment different tissues from coarse to fine using different combinations of input modalities.

Firstly, coarse segmentation including eight brain tissues was performed using FLAIR and T1-weighted modalities by DRUNet (model 1). Secondly, CSF was independently segmented using T1 and T1-IR modalities by DRUNet (model 2). Thirdly, since segmentation of white matter lesions is a very challenging task, we used the pre-trained model of the winning method in MICCAI WMH challenge [3] (model 3) to perform segmentation independently. Finally we fused the multi-stage segmentation results.

### 2.3 Label fusion

We believe that the independent networks for specific labels which either employ complementary modalities or pre-trained model on extra dataset would outperform the DRUNET in the first stage. For CSF, the labels generated by model 1 and model 2 were fused by a union operation. For white matter lesions, since they are in small volume, thus are sensitive to simple union operation, the labels generated by model 3 were completely taken for the final segmentation. Firstly, the prediction label of *white matter lesions* by model 1 was set to the *white matter* and fused with the label generated by model 3.

### 2.4 Ensemble model

To improve the robustness of our model, an ensemble method was employed for segmentation. Five DRUNet models for model 1 and model 2 respectively with the same architecture were trained with shuffled batches. Then when given a new testing subject, each subject will be segmented based on the averaged probability maps by the ensemble model.

## References

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