

WMH segmentation challenge at MICCAI 2017: Brief description of the method

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The given data were 2D multi-slice FLAIR image and 3D T1-weighted image that were registered onto the FLAIR space and all imaging data were corrected for magnetic field bias. The white matter hyperintensity (WMH) regions were segmented as follows using FSL, AFNI, and MATLAB.

1. Preprocessing step

The skull of the T1-weighted and FLAIR images were stripped by spatially warping and applying the Montreal Neurological Institute (MNI) brain mask onto the T1-weighted data. The skull stripped T1-weighted data was segmented into gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF). WM mask was refined to reduce misclassified voxel due to intensity similarity between WMH and GM using following procedures. The partial volume effect (PVE) of CSF mask was removed from the FLAIR data. In addition, the CSF PVE mask was skeletonized and dilated, and then removed from the FLAIR data. Ventricle mask was extracted using region growing method in each slice and then we subtracted the eroded ventricle mask from the dilated ventricle mask for the final ventricle mask. This step was performed to detect periventricular WMHs that were located near the ventricle. The refined WM mask of the FLAIR data was eroded and intensity normalization was performed with mean value of 1,000.

2. Detection step

The potential periventricular and deep WMHs were detected separately. The periventricular WMH voxels were detected by thresholding the WM of the FLAIR data with 1.4 times of the mean intensity of FLAIR. The detected voxels were clustered and region growing was performed using seeds that were from potential WMH clusters with size larger than 100 voxels. Region growing terminated when the boundary met a voxel with intensity value lower than 1.3 times of the mean FLAIR intensity. Maximum of 3 mm in Euclidean distance was allowed for the region growing step. The deep WMH voxels were detected by thresholding the WM of the FLAIR data with 1.3 times of the mean FLAIR intensity and the region growing was performed using seeds of every voxel except the detected periventricular WMHs. If the size of the region grown cluster exceeds 1,000 voxels, then it was considered as periventricular WMH and removed.

3. Classification step

We constructed random forest model to classify true and false WMHs to account for possible

false positive of the previous step. The classification step was performed on the periventricular and deep WMHs separately. A total of 238 features (19 texture and 100 multi-layer features per imaging modality, and the volume of the potential WMH clusters) were extracted from the dilated potential WMH clusters in intensity normalized FLAIR and T1 data. The texture features were calculated using voxel intensities and they were max, min, media, mean, variance, energy, standard deviation, root mean square, range, interquartile range, entropy, uniformity, and percentile of 2.5, 25, 50, 75, and 97.5. The multi-layer features were extracted by constructing an architecture similar to the convolutional neural network. It was composed of two convolutional layers, two max pooling layers, and one fully connected layer. Patches of two different sizes (15×15 and 7×7) were used. In the first convolutional layer, 25 2D filters of average, disk, Gaussian, log of Gaussian, Laplacian, prewitt, sobel, and motion filters with different hyper-parameters were applied and in the next max pooling layer, the patches were down-sampled with kernel size of two. In the second convolutional layer, 10 3D filters of average, ellipsoid, Gaussian, log of Gaussian with different hyper-parameters were used and then subsequently max pooling was applied with size of two. Finally, $3 \times 3 \times 10$ and $1 \times 1 \times 10$ imaging patches were obtained and they were vectorized in the fully connected layer. The potential WMH clusters (periventricular and deep separately) were divided into training and test sets with ratio of 8:2. The random forest model was constructed using the training set and validated using the test set. We performed the training and test steps using randomly selected training sets until we achieve the test accuracy over 95% for periventricular WMHs and 90% for deep WMHs. The classified periventricular and deep WMH clusters were merged into the one single image and it was considered as our final result.