

Automatic WML segmentation and quantification using a machine learning approach

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Background:

Detection and quantification of white matter lesions (WML) is of great importance in many neurological disease processes. Manual delineation of WML is time-consuming and prone to user bias. A need for robust automated methods is therefore evident. Automated analysis is generally complicated partly by the lack of three-dimensional (3D) data acquisitions in a clinical setting, giving anisotropic voxels and poor spatial resolution in the slice direction. This is especially problematic for the standard WML sensitive fluid-attenuated inversion recovery (FLAIR) sequence, which is still commonly acquired as a multi-slice two-dimensional (2D) acquisition. A need for robust methods which also work for 2D acquisitions is therefore needed and in this work we present an automated framework for WML analysis using a machine learning approach with the overall aim to automatically segment, characterize and classify WMLs for use in subsequent statistical analysis of clinical data in various neurodegenerative disease groups.

Methods:

All image analysis was based on two classes of images; 2D FLAIR and 3D T1-weighted gradient echo (T1-w GRE). The FLAIR images were used to identify potential WMLs and the T1-w GRE images were used to include only white matter (WM) tissue into the analysis. The voxel size was $0.5 \times 0.5 \times 3.9 \text{ mm}^3$ and $1.35 \times 1.35 \times 1.2 \text{ mm}^3$, respectively for the FLAIR and the T1-w GRE sequences. The analysis pipeline was as follows:

1. Tissue segmentation and classification from the T1-w GRE images with the aim of a) reducing the analysis to WM for WML and b) classifying WML according to their position (periventricular WML, deep WML, brain lobe etc).
2. Co-registration of T1-w GRE and FLAIR using a rigid transformation with scaling (9-parameter transform, comprising each three dimensions of rotation, translation and scaling).
3. Segmentation of WML limited to the WM mask using a GENERATE and TEST method as outlined below:

GENERATE: Given that WMLs correspond to WM hyperintensities, the distribution of intensities for normal WM tissue was modelled by a Gaussian distribution (μ , σ) and a threshold was used to segment the upper-tail of the histogram distribution. The threshold was defined as $\mu + N * \sigma$, where N was defined experimentally from the results on the training data as a compromise between high true positive rates and low false negative rates (compared to the expert) A value of $N=2.5$ was used.

TEST: In order to reduce the amount of false positive WMLs, a classifier was defined that allows selection of only those lesions which corresponded to true WMLs as defined by the expert. To this end we defined a classifier using machine learning techniques that allows the classification of each lesion from a feature vector containing local (shape, size, intensity, etc.) and global (position, distance to borders, distance to ventricle, etc.) lesion information.

WM segmentation and tissue classification was performed using Freesurfer [1] and FLAIR-GRE image co-registration was performed in the BRAINSFit module of 3D-Slicer [2]. Training was performed in 15 patients selected from an ongoing study in patients with mild cognitive impairment (MCI) and chronic infarctions. Using the training base generated by the expert, a J.48 decision tree classifier was then estimated using tenfold cross-validation in the WEKA environment [3].

Results

The proposed method performed well with an overlap of 85.6% between automatic and expert detection. The total WML volume segmented by the automated method was 49% larger than the expert volume. Figure 1 shows a sample case of the resulting automated WML detection procedure.

Discussion / conclusions

We propose a method for automatic segmentation of WMLs with a high success rate in spite of sub-optimal 2D FLAIR images. The system characterizes each WML by a vector of 105 local and global features, which enabled robust segmentation. The fact that the automated method detected more lesions than the expert may be due to the improved sensitivity to subtle lesions offered by the model. Based on these results the method warrants further testing in ongoing studies in patients with neurodegenerative disease.

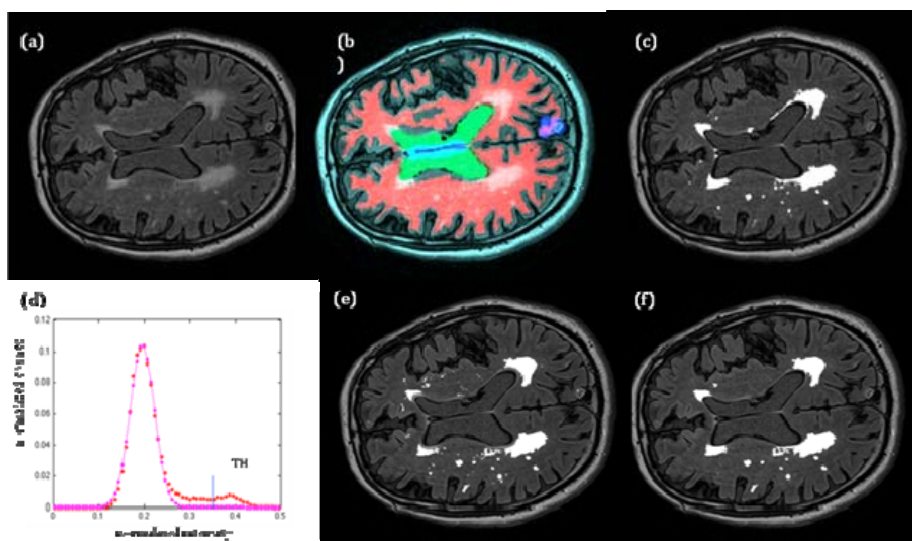


Fig. 1. WML segmentation. a) MRI FLAIR image; b) WM mask (red), ventricles (green), masked regions (blue); c) WML manually identified by an expert; d) approximation of the WM by a Gaussian distribution and threshold selected; e) segmentation obtained by the threshold; f) WML obtained by the classifier.

References

- [1] <http://www.slicer.org/>
- [2] Fischl B et al: Whole brain segmentation and automated labeling of neuroanatomical structures in the human brain. *Neuron*. 2002; 33(3):341-355.
- [3] Hall M et al: The WEKA Data Mining Software: An Update; *SIGKDD Explorations*, Volume 11, Issue 1 (2009).