Automatic segmentation of gray matter multiple sclerosis lesions on FLAIR and DIR images

E. Veronese[1], E. Grisan[1], M. Calabrese[2], A. Favaretto[2], P. Gallo[2], D. Seppi[2], F. Rinaldi[2], I. Mattisi[2], and A. Bertoldo[1]
[1]Department of Information Engineering, University of Padova, Padova, Italy, [2]University Hospital of Padova

Introduction

Multiple Sclerosis (MS) is a chronic inflammatory demyelinating disease of the central nervous system. Although it is traditionally associated to white matter (WM) impairment, several studies [1,2] have recently demonstrated that a large amount of the distinctive MS lesions involve the grey matter (GM) as well. GM lesions are usually classified as pure intracortical or mixed GM-WM lesions. They have been demonstrated to play a major role in the physical and cognitive disability and in the disease progression [3]. That being so, identifying them is clearly fundamental, but manual detection in MRI sequences is always time consuming, error prone and operator dependent. An automatic algorithm for lesions detection in double inversion recovery (DIR) sequences has recently been proposed [4]. We present an algorithm that improves it, using fluid attenuated inverse recovery (FLAIR) and DIR sequences to increase the sensitivity while diminishing the number of false positives.

Materials and Methods

46 patients affected by Relapsing Remitting Multiple Sclerosis (RRMS) underwent MRI examination including FLAIR sequence (repetition time (TR)=10000 ms, echo time (TE)=120 ms, inversion time (TI)=2500 ms, 50 contiguous axial slices with a thickness = 3 mm, a matrix size=288x288) and DIR sequence (TR = 15631 ms, TE = 25 ms, TI = 3400 ms, 50 contiguous axial slices with a thickness = 3 mm, a matrix size = 256x256), acquired using a 1.5T machine (Achieva, Philips Medical Systems, Best, The Netherlands) with 33 mT/m power gradient, using a 16 channel head coil.

To provide the ground truth, MS lesions were manually outlined by an experienced neurologist, who was blinded to the results of our automatic method. He was asked to manually segment MS GM lesions in DIR images with the additional information provided by the visual inspection of the corresponding FLAIR and T1-weighted images.

After the coregistration of FLAIR on DIR sequence, using SPM8 [5], a skull-stripped version of the brain on each axial slice is computed. The three tissues (WM, GM and CSF) are segmented by means of two coupled level-sets, exploiting the information both of the FLAIR and of the DIR volumes. Then, on each axial slice, we evaluate a gray level threshold on a tessellation of square regions, obtaining a space variant local threshold that is able to capture locally hyperintense voxels while rejecting bias and low frequency variations. The thresholded image provides a number of regions representing candidate MS lesions. The appearance of these candidate regions is then analysed in order to keep the true positives and discard the non-lesions. In particular, we consider as lesions those regions that satisfy two conditions evaluated on the DIR data: a high contrast with respect to the surrounding tissues, and the presence of voxels brighter than the mean of the GM in that slice. The mean of the GM is multiplied by a factor that depends on the region of the brain we are analyzing: we know that, for instance, voxels in the region corresponding to the superior sagittal sinus are usually brighter, due to the blood that flows in the vessels located in this region of the cranium and that generates a hyperintense MR signal; in such regions our algorithm will be more restrictive.

Results and Discussion

A comparison between the automatic and manual segmentation performed by one experienced observer has been performed. For the 46 patients, a total of 455 GM lesions were manually detected. 4 patients presented no GM lesions. The percentage of lesions correctly detected in the remaining 42 patients is shown in Fig. 2: remarkably, in 32 of the 42 patients, all lesions have been detected, providing a sensitivity of 100%. The resulting mean sensitivity reaches the 98.2%. Besides, a very high correlation (r=0.98) can be found between the total number and the automatically detected lesions per patient (Fig. 3).

The technique is thus able to automatically segment GM lesions on FLAIR and DIR sequences with a high sensitivity, avoiding the intra/interobserver variability typical of manual detection. Moreover, the combined use of the two sequences and the exploitation of their specific characteristics, i.e. the cerebrospinal fluid (CSF) attenuation in FLAIR and the GM enhancement in DIR, makes it able to accurately segment the three tissues (WM, GM and CSF) and to correctly identify both intracortical and mixed GM-WM lesions. It is also worth noting that both the brain extraction and the tissues segmentation do not make use of any anatomical a priori information (i.e., we do not exploit image registration on brain atlases.

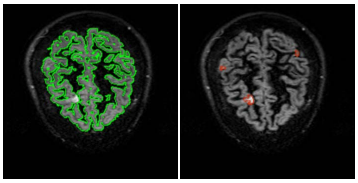

Figure 1 Left: obtained GM segmentation, superimposed to DIR image. Right: in red, GM obtained lesions, superimposed to DIR image.

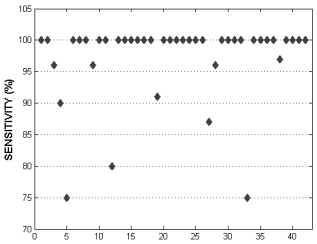

Figure 2 (Left) Percentage of correctly detected GM lesions for each of the 42 patients.

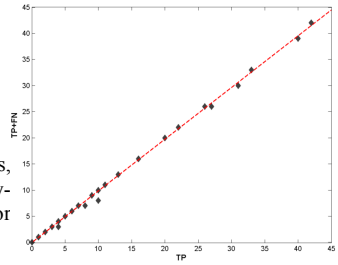

Figure 3 (Right) On x-axis, number of true positive; on y-axis, number of true lesions for each of the 46 patients.

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