A fully unsupervised method for spinal cord lesion segmentation in Multiple Sclerosis

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Synopsis

The presence of focal lesions in the spinal cord is an important diagnostic criteria for Multiple Sclerosis (MS). Accurate estimation of lesion volume is important for monitoring disease progression over time. However, manual and automated lesion segmentation for volume estimation remain challenging, since these rely either on the skills of the rater or the automated criteria set within the algorithms, respectively. In this work, we present an adaptation, to the spinal cord, of a fully unsupervised hierarchical model selection framework that automatically detects abnormality tissue patterns in the spinal cord without any pathological a priori knowledge.

Introduction

Spinal cord (SC) lesions are present in most Multiple Sclerosis (MS) patients; therefore, SC MRI has been included in the diagnostic criteria of MS [1]. Recently, several algorithms have been developed to segment MS lesions in the brain [2]. However, similar approaches are not yet available for SC. Analysis of SC MRI is challenging due to the small SC dimension, the large slice thicknesses due to a high in plane resolution, the grey matter shape, subject motion and artifacts [3,4]. In this work, we present an extension of a fully unsupervised hierarchical model selection framework [5] applied to the spinal cord, to automatically detect abnormality tissue patterns in the SC without any pathological a priori knowledge.

Methods

We analysed 22 patients with MS (13 females) with visible lesions in the SC, [2 clinically-isolated syndrome (CIS), 5 relapsing-remitting (RRMS), 8 secondary-progressive (SPMS) and 7 primary progressive (PPMS)] – with mean disease duration 16.5±13.1 years and median EDSS of 6.5 (range 1-7.5). All patients underwent a 3T MR scan (Philips Achieva) which included 3D-FFE and PSIR sequences [6], both acquired at a 0.5x0.5mm^2 in plane resolution and 5mm slice thickness. All sequences had the center of the volume positioned at the C2-3 intervertebral disc. Lesions were manually segmented over PSIR images by a rater using JIM v6 (Xinapse Systems, UK) and binarised to provide a ground truth (GT). The proposed lesion detection preprocessing pipeline is described hereafter. First, we corrected for motion between PSIR and 3DFFE; second, we used [7] to compute a white and grey matter (WM/GM) spinal cord segmentation. Third, WM, GM and cerebrospinal fluid (CSF) priors from the PAM50 atlas [8] were propagated into the subject native space using Spinal Cord Toolbox [9]. Fourth, all volumes were isotropically resampled using the NiftyReg software package. Then, using the subject specific mask and priors, a Gaussian mixture model with an adaptive number of components separating inliers and outliers, was obtained following a similar model as the one described in [5], with GM and WM combined in one single class to account for the limited contrast between tissues. In this probabilistic framework, we sample models according to [5] in order to find a mixture model that balances model fit and complexity. Finally, after the model selection process has converged, a post-processing step was applied to select candidate lesion voxels according to the distribution of the healthy appearing tissue, followed by a slice-by-slice morphological correction step used to remove spurious segmentations. Figure 1 illustrates the steps of the method. To assess the performance of the proposed method, we computed median and interquartile range (IQR) for different metrics including mean surface distance in mm (MSD), Dice score coefficient (DSC), sensitivity, specificity, accuracy and volume difference (VD) expressed in percentages between the obtained segmentation and the GT in the original acquisition space.

Results

Figure 2 shows a qualitative assessment of the results. A quantitative assessment showed a 80% ($p<0.05$) correlation between the automated lesion volumes and the GT (see Figure 3) with a median [IQR] VD of 46.2 [17.9;71.2]. Our unsupervised method obtained a median [IQR] DSC=41.6 [30.9;60.2] and MSD of 1.70 [0.87 2.43], when we compared to GT, see Figure 4. Finally, we also observed a median [IQR] sensitivity of 0.50 [0.25;0.71], specificity of 99.99 [99.99;100.0] and accuracy of 99.99 [99.98;100.0], all in percentages.

Discussion

The qualitative assessment of the results highlighted the good performance of the proposed method (Figure 2). Nonetheless, we observed a few spurious voxels in the spinal cord rim, and quantitative results suggested that disagreement between ground truth and automated methods occurred at the lesion borders. The volumes were found to correlate with the GT ($p<0.05$). Phenotypes with higher volume loads, especially SPMS (see Figure 3), resulted in better overall performance. Given the volume of lesions compared to the overall image volume, sensitivity ratios were found to be high.

Conclusions

In this work, we have demonstrated the feasibility of automatically segmenting MS spinal cord lesions using a fully unsupervised approach based on a Bayesian model selection. The proposed method tends to extend lesions in the cord rim when compared to the ground truth, with volumes being highly correlated. The main advantage of this technique is that it works without any pathological a priori knowledge or training dataset, potentially making its extension to other pathologies straightforward. Future work will focus on improving the biologically plausibility of the model, computing a subject-specific CSF, WM, GM and rim mask, and test the performance of the proposed method in other neurological conditions such as SC injury

and myelopathy.

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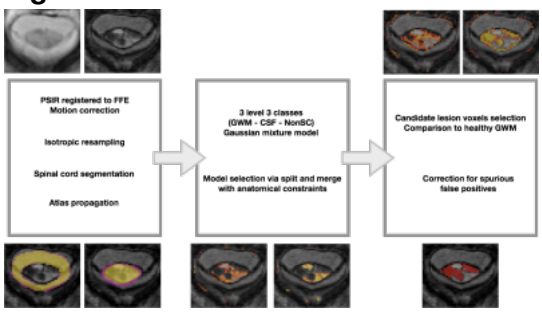
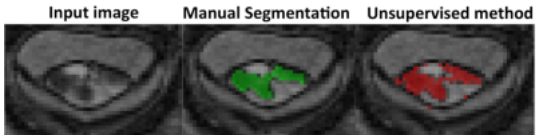
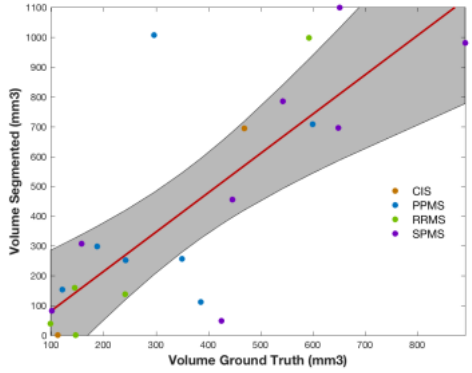
Figures



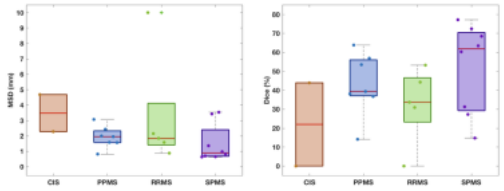
Schema representing the core steps of the presented framework with intermediate outputs



From left to right, PSIR input image, overlaid manual segmentation (green), segmentation results by the proposed unsupervised method (red)



Graph showing the correlation between the ground truth and the obtained lesion volumes in mm3 (blue line, and in grey the 95% CI). Each dot represents a subject and the dot's color is the MS phenotype of each subject



Mean Surface Distance in mm (smaller means better) and Dice score coefficient (bigger means better) per phenotype, each dot represents the obtained result for each individual subject..