

Automated tissue segmentation of MR brain images in the presence of white matter lesions

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Abstract

Over the last few years, the increasing interest in brain tissue volume measurements on clinical settings has lead to the development of a wide number of automated tissue segmentation methods. However, white matter lesions are known to reduce the accuracy of automated tissue segmentation methods, which requires manual annotation of the lesions and refilling them before segmentation, which is tedious and time-consuming. Here, we propose a new, fully automated T1-w/FLAIR tissue segmentation approach designed to deal with images in the presence of WM lesions. This approach integrates a robust partial volume tissue segmentation with WM outlier rejection and filling, combining intensity and probabilistic and morphological prior maps. We evaluate the accuracy of this method on the MRBrainS13 tissue segmentation challenge database, and also on a set of Multiple Sclerosis (MS) patient images. On both databases, we validate the performance of our method with other state-of-the-art techniques. On the MRBrainS13 data, the presented approach was the best unsupervised ranked method of the challenge (7th position) and clearly outperformed the other unsupervised pipelines such as *FAST* and *SPM12*. On MS data, the differences in tissue segmentation between the images segmented with our method and the same images where manual expert annotations were used to refill lesions on T1-w images before segmentation were lower or similar to the best state-of-the-art pipeline incorporating automated lesion segmentation and filling. Our results show that the proposed pipeline quantitatively improved the accuracy of tissue segmentation while it achieved very competitive results on MS images. A public version of this approach is available to download for the neuro-imaging community.

Keywords: Brain, MRI, multiple sclerosis, automatic tissue segmentation, white matter lesions

1. Introduction

Brain tissue volume based on Magnetic Resonance Imaging (MRI) is increasingly being used in clinical settings to assess brain volume in different neurological dis-

eases such as Multiple Sclerosis (MS) (Giorgio and De Stefano, 2013). In MS, several studies have analyzed the histopathological changes in patients with respect to the progress of the disease, showing that the percentage of change in brain volume tends to correlate with worsening conditions (Pérez-Miralles et al., 2013; Soriano et al., 2014). However, manual segmentation of brain tissue is both challenging and time-consuming because of the large number of MRI slices for each patient that make up the three-dimensional information, and the

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inherent intra/inter-observer variability of manually segmented scans (Cabezas et al., 2011). The development of automated MS tissue segmentation methods that can segment large quantities of MRI data, do not suffer from intra/inter-observer variability and specific changes of the brain such as MS associated lesions and brain atrophy, is still an active research field

There are various brain tissue segmentation methods that have been used in MS so far. General purpose intensity based methods combining intensity and a priori statistical anatomic information such as FAST (Zhang et al., 2001) or SPM (Ashburner and Friston, 2005) are widely used nowadays. However, tissue abnormalities found in MS image patients such as White Matter (WM) lesions reduce the accuracy of these techniques (Chard et al., 2010; Battaglini et al., 2012) usually causing an overestimation of Gray Matter (GM) tissue not only by the effect of hypointense WM lesion voxels classified as GM, but also by the effect of these lesion voxels on normal-appearing tissue (Valverde et al., 2015b). In these cases, in-painting lesions on the T1-weighted image (T1-w) with signal intensities of the normal-appearing WM before tissue segmentation may be used to reduce the effects of the WM lesions on tissue segmentation (Chard et al., 2010; Battaglini et al., 2012; Valverde et al., 2014). However, MS lesions have to be delineated manually first, which may be a tedious, challenging and time-consuming task depending on the characteristics of the image (Lladó et al., 2012).

Regarding this issue, a wide number of automated lesion segmentation techniques have been proposed during the last years (Lladó et al., 2012; García-Lorenzo et al., 2013). Most of them integrate other imaging modalities such as T2-weighted, Proton Density (PD) and Fluid Attenuated Inverse Recovery (FLAIR), as these modalities present a high contrast between tissue and lesions (Lladó et al., 2012). More recent techniques include supervised learning classifiers based on a spatial decision forest (Geremia et al., 2011), statistical methods (Sweeney et al., 2013), patch-based models (Guizard et al., 2015) or adaptive dictionary learning methods (Deshpande et al., 2015). Furthermore, different unsupervised learning techniques make use of probabilistic models to separate WM lesions from normal-appearing tissue by considering lesions as an outlier class (Harmouche et al., 2015; Tomas-Fernandez and Warfield, 2015; Jain et al., 2015). Also, other unsu-

pervised techniques make use of the signal intensity of lesions on FLAIR to threshold regions with similar intensity to WM lesions, adding afterwards various post-processing steps to automatically classify these regions as either WM lesions or normal-appearing tissue (Schmidt et al., 2012; Roura et al., 2015). In contrast, there are fewer studies that have focused on tissue segmentation of MS images containing lesions. Those include non-supervised techniques combining intensity, anatomical and morphological maps (Nakamura and Fisher, 2009; Shiee et al., 2010), or supervised methods such as statistical classifiers (Datta and Narayana, 2013), atlas based nearest-neighbor methods (De Boer et al., 2009) and sparse dictionary learning approaches (Roy et al., 2015).

The increasing amount of published studies regarding automated WM lesion segmentation may be due to the particular need of a quantitative analysis of focal MS lesions in individual and temporal studies (Lladó et al., 2012). Recent studies in MS (Chard et al., 2010; Gelineau-Morel et al., 2012; Ceccarelli et al., 2012; Pérez-Miralles et al., 2013; Popescu et al., 2014; Magon et al., 2014; Valverde et al., 2015b) indicate a certain tendency to the use of widely validated segmentation tools such as Siena (Smith et al., 2002), FAST (Zhang et al., 2001) or SPM (Ashburner and Friston, 2005) in combination with automated lesion segmentation and/or lesion-filling approaches, although their application in clinical practice is still not generalized (Giorgio and De Stefano, 2013).

In this paper, we present the Multiple Sclerosis Segmentation pipeline (*MSSEG*), a novel, multi-channel method designed to segment GM, WM and cerebro-spinal fluid (CSF) tissues in images of MS patients. This method was motivated by our previous analysis of the effects of tissue segmentation on MS images (Valverde et al., 2015b), the role of lesion-filling (Valverde et al., 2014), and its combination with automated lesion segmentation on tissue segmentation (Valverde et al., 2015b). Similar to the work of Nakamura and Fisher (2009) and Shiee et al. (2010), our approach uses a combination of intensity and anatomical and morphological prior maps to guide the tissue segmentation. However, here the tissue segmentation is based on a robust, partial volume segmentation where WM outliers are estimated and refilled before the segmentation using a multi-channel post-processing algorithm. This post-processing algorithm

was partially inspired by the MS lesion segmentation algorithm proposed by Roura et al. (2015), but here we integrate multi-channel support, partial volume segmentation, spatial context, and prior anatomical and morphological atlases. In order to perform quantitative and qualitative evaluations of our approach, we analyze its accuracy with the MRBrainS13 challenge database, which includes manual tissue annotations, and also with a set of MS patient images with different lesion burdens. We quantitatively compare the performance of our approach with different state-of-the-art techniques that also competed in the MRBrainS13 challenge and/or have been used in recent MS studies. Furthermore, we also analyze the differences in the performance of our approach when using only T1-w or when using the multi-channel approach that includes T1-w and FLAIR. The *MSSEG* method is currently available for downloading at our research group webpage (<http://atc.udg.edu/nic/msseg>).

2. Methods

The proposed brain tissue segmentation method is composed of five different processes: registration of a statistical atlas into the T1-w space (Sec. 2.2), tissue estimation (Sec. 2.3), detection and re-assignment of lesion candidates to T1-w (Sec. 2.4), tissue re-estimation, and partial volume re-assignment of tissue maps into CSF, GM and WM (Sec. 2.5). The overall schema of the pipeline is depicted in figure 1. We describe each step in detail in the following subsections.

2.1. Notation

To describe our approach, we employ the following notations. T and F denote the input images T1-w and FLAIR, respectively. P^c denotes a probabilistic tissue atlas of a particular class $c = \{csf, csfgm, gm, gmwm, wm\}$. S^{st} denotes a morphological brain atlas of a particular parcellated structure st . For each of the above images, T_j, F_j, P_j^c and S_j^{st} denote an observation at a voxel $j \in \Omega$, Ω being the image domain.

2.2. Tissue prior registration

The MNI-ICBM 152 2009a Nonlinear T1-w average structural template image¹ was first affine registered to the native T1-w image space based on a block matching approach (Ourselin et al., 2002), and then non-rigid registered with a fast free-form deformation method (Modat et al., 2010), both using the Nifty Reg package². Transformation parameters obtained were then used to resample the available MNI CSF, GM and WM tissue priors to the T1-w space. The resampled probabilistic tissue maps P_{csf}^c, P_{gm}^c and P_{wm}^c were extended to build intermediate partial volumes P_{csfgm}^c as ($P_{csf}^c \geq 0.5 \cap P_{gm}^c \geq 0.5$) and P_{gmwm}^c as ($P_{gm}^c \geq 0.5 \cap P_{wm}^c \geq 0.5$) and taking the mean value of the two input atlases.

Also, a morphological brain structure atlas was first parcellated on the original MNI atlas using the hierarchical algorithm proposed by Pohl et al. (2007) on EM-Segmenter³, and then manually refined for the selected structures. The resulting atlas (S^{st}) consisted of useful structures for tissue segmentation such as cortical GM (S^{Cortex}), ventricles ($S^{Ventricle}$), basal ganglia (S^{Basal}) and brainstem ($S^{Brainstem}$). The same transformation parameters were also used to resample the morphological atlas to the T1-w space.

2.3. Tissue estimation

Brain tissue was estimated following a robust fuzzy-clustering approach similar to the one proposed in Pham (2001), as this method provides a straightforward implementation, fairly robust behavior including spatial context information, applicability to multichannel data, and the ability to model uncertainty within the data (Pham, 2001). In our approach, we designed the method to segment 5 classes in order to preserve the differences in signal intensity between local regions of the brain and lesion candidates better. We also extended the spatial penalizing weights by incorporating the probabilistic tissue priors in the segmentation process, similar to Shiee et al. (2010). Hence, we modified the objective function proposed by

¹<http://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152NLin2009>

²<http://cmictig.cs.ucl.ac.uk/wiki/index.php/NiftyReg>

³<https://www.slicer.org/slicerWiki/index.php/EMSegmenter-Overview>

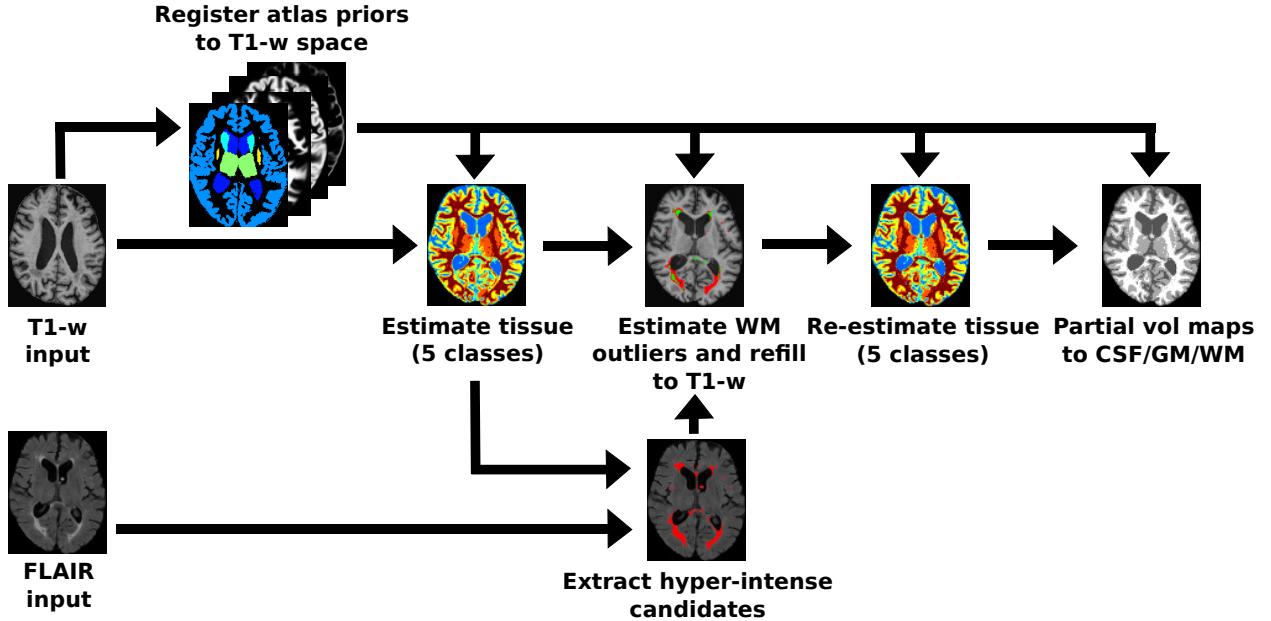


Figure 1: The proposed method *MSSEG* consists of five different steps: 1) Three statistical *a-priori* tissue atlases (CSF, GM and WM) and a brain structure atlas are first registered into the patient space (Sec. 2.2) and then used to 2) guide the tissue segmentation of the input T1-w image (Sec. 2.3). 3) Then, the same output segmentation is employed to detect and reassign candidate regions into WM based on the registered *a-priori* and hyper-intense FLAIR maps if available (Sec. 2.4). The voxel intensities of candidate regions on T1-w are then refilled with normal-appearance WM intensities and 4) The tissue is re-estimated (Sec. 2.3). 5) Finally, intermediate volume maps are reassigned into CSF, GM and WM using both neighbor and spatial prior information (Sec. 2.5).

Pham (2001) in order to incorporate also prior-atlas information as follows:

$$\begin{aligned}
 J_{MSSEG} = & \sum_{j \in \Omega} \sum_{k=1}^C u_{jk}^q \|T_j - v_k\|^2 + \\
 & + \frac{\beta}{2} \sum_{j \in \Omega} \sum_{k=1}^C u_{jk}^q \sum_{l \in N_j^w} \sum_{m \in M_k} u_{lm}^q + \\
 & + \frac{\gamma}{2} \sum_{j \in \Omega} \sum_{k=1}^C u_{jk}^q \sum_{l \in N_j^w} \sum_{m \in M_k} P_l^k
 \end{aligned} \quad (1)$$

where $\{k \in C \mid C = \{csf, csfgm, gm, gmwm, wm\}\}$, u_{jk} denotes the membership probability of each voxel j for a particular class, v_k are the cluster signal intensity centers of each class, N_j^w is the set of two-dimensional (2D) $(2w + 1)^2$ or three-dimensional (3D) $(2w + 1)^3$ neighbors centered on the voxel j , and $M_k = \{1, \dots, C\} \setminus \{k\}$. This approach depends on four parameters to adjust the membership functions: the weighting parameter q that controls the degree of fuzziness, the spatial constraint parameter β that controls the amount of neighbor information added, the prior belief parameter γ used to control the amount of prior atlas information about each tissue, and finally the window radius of neighbors w .

Similar to the work of Pham (2001), an iterative algorithm to minimize (1) was derived by evaluating the centroids and functions that satisfy a zero gradient condition as follows:

Algorithm 1 Tissue estimation

- 1: Obtain the initial estimates of the centroids for each class $k = \{1, \dots, C\}$:

$$v_k = \frac{1}{n} \sum_{j \in \Omega} (T_j^k \mid P_j^k \geq 0.5) \quad n = |(T_j^k \mid P_j^k \geq 0.5)|$$
 - 2: Compute the membership functions u_{jk}
 - 3: Compute the new centroids:

$$v_k = \frac{\sum_{j \in \Omega} u_{jk}^q T_j}{\sum_{j \in \Omega} u_{jk}^q} \quad k = \{1, \dots, C\}$$
 - 4: Repeat steps 2 and 3 until convergence
-

Initial centroids v_k were estimated for each class C by taking the mean signal intensity of the voxels on the T1-w image with prior-tissue probability $P_j^k \geq 0.5$. The membership function u_{jk} was also adapted to incorporate prior-atlas information and computed as follows:

$$u_{jk} = \frac{(\|T_j - v_k\|^2 + \beta \sum_{l \in N_j} \sum_{m \in M_k} u_{lm}^q + \gamma \sum_{l \in N_j} \sum_{m \in M_k} P_l^m)^{-1/(q-1)}}{\sum_{i=1}^C (\|T_j - v_i\|^2 + \beta \sum_{l \in N_j} \sum_{m \in M_i} u_{lm}^q + \gamma \sum_{l \in N_j} \sum_{m \in M_k} P_l^m)^{-1/(q-1)}} \quad (2)$$

The five class tissue segmentation mask SEG_j was computed by assigning to each voxel the class with the maximum membership as follows:

$$SEG_j = \arg \max_k u_{jk} \quad \forall j \in \Omega \quad (3)$$

The parameters q , γ and w can be tuned manually to increase the performance of the method, but were set to default values $q = 2$, $\gamma = 0.1$ and $w = 1$ with 2D that worked well in the majority of cases. In contrast, the β parameter depends on the brightness of the image, the deviation of the signal intensities of voxel class members with respect to their centroid value, and image noise (Pham, 2001). Hence, choosing a proper value for the β parameter is important to obtain an optimal or near-optimal performance. In our implementation, we automated the β parameter by fitting a function of the optimal empirical selection of the parameter with respect to different levels of noise. To do this, we iteratively estimated the sub-optimal β parameter of 10 images of the Brainweb dataset⁴ that included different noise level (1-9%) and ground-truth annotations. For each image, we also computed the noise level using the Fast Noise Variance method proposed by Immerkær (1996). Then, the correspondent β parameters and noise levels were used to fit a polynomial function to interpolate the β parameter. For all the evaluated images in this paper, we have automatically approximated the β as a function $B(x)$ of their noise level x as $B(x) = 0.0011x^4 - 0.0015x^3 + 0.0074x^2 - 0.001x + 0.05$.

2.4. Reassign WM outliers to T1-w

In a three class tissue segmentation approach, lesion regions are usually classified as either GM or WM, given the hypointense signal intensity profile of WM lesions. In some cases, this impedes differentiating them from surrounding GM and WM. In contrast, by creating the intermediate classes *CSFGM* and *GMWM*, new local clusters of voxels with similar signal intensities are delimited, increasing the chances of WM lesion regions being differentiated from normal-appearing GM and WM. Following this assumption, we estimated the WM lesion regions by analyzing all the local regions not initially segmented as

WM based on their prior probability and spatial connection to WM.

First, different binary segmentation masks M^c were computed for each of the classes $c = \{gmwm, gm, csfgm\}$. For each mask, all 2D regions of connected components were computed using a flood-fill algorithm with a 4-connected neighborhood. We define the set of all 4-connected p regions given an input binary image as follows:

$$R_p^T \leftarrow \oplus(M^c, n), \quad p = \{1, \dots, |R_p^T|\}$$

where the operator \oplus refers to the connected components function and n is the number of connected neighbors.

Secondly, a map of hyperintense region candidates was computed on the FLAIR image following the same strategy shown in Roura et al. (2015). The binary mask M^{GM} was first used to compute the intensity distribution on the FLAIR image, where GM is typically hyperintense with respect to CSF and WM, and WM lesions are considered hyperintense outliers to GM. The mean and standard deviation of the GM distribution was computed using the full-width at half maximum (FWHM) of the main peak of a generated histogram. Then, an initial map of hyperintense regions voxels, H^{FLAIR} , was determined by thresholding the FLAIR image F as follows:

$$H_j^{FLAIR} = \begin{cases} 1 & \text{if } F_j > \mu + \alpha\sigma \\ 0 & \text{otherwise} \end{cases} \quad \forall j \in \Omega \quad (4)$$

where μ and σ were the mean and standard deviation respectively, of the GM distribution as computed using the FWHM, and α was a weighting parameter that scaled the minimum signal intensity of outliers. The binary mask H^{FLAIR} was then used to group the candidate voxels into connected regions using the same method proposed before:

$$R_t^F \leftarrow \oplus(H^{FLAIR}, n), \quad t = \{1, \dots, |R_t^F|\}$$

where n was set to 3D connected elements ($n = 6$) in order to reduce the amount of 2D false positive regions such as hyperintense sub-arachnoid tissue.

Given the computed binary masks for each tissue M^{gmwm} , M^{gm} and M^{csfgm} , the map of hyperintense voxels on FLAIR H^{FLAIR} , and its connected components R_t^F ,

⁴<http://brainweb.bic.mni.mcgill.ca/brainweb/>

we used an iterative algorithm to estimate the regions with high a probability of belonging to WM. Lesion filling of selected regions was integrated in the same algorithm. Figure 2 shows in detail each step of the algorithm. Regions with no overlapping cortical GM on the morphological prior S_s^{CORTEX} were only processed if a matched region was also hyperintense in FLAIR, in order to reduce the amount of false positive regions such as isolated cortical GM segmented regions. Regions not touching cortical GM were filtered based on their prior probability of belonging to WM and their distance to surrounding WM. If half of the voxels of a region had a prior probability of belonging to WM and the region was connected to actual WM, the region was also added to the WM class, and those voxels were refilled as normal-appearing WM into the original T1-w image T using the same implementation proposed in Valverde et al. (2014). Note that classes were visited from *gmwm* to *csfgm* in order to add new belief of the actual WM and use it to filter the next region.

If the FLAIR modality is not available, H^{FLAIR} is automatically set to zero, disabling the evaluation of R^H regions and henceforth forcing the method to evaluate the next T1 region R_p^T . If FLAIR is used, all the regions that were discarded in the first part of the algorithm or overlapped the cortex, were filtered according to their spatial attributes in the FLAIR image. Each discarded region R_q^T in the segmented mask SEG was matched with a particular region in FLAIR R_t^H based on their overlap ($R_t^H \mid t = \arg \max(|R_t^H \cap R_q^T|)$). Then, matched regions where half of their surrounding neighbors were actually classified as *gmwm* or *wm* were also added to the WM class and T1-w was filled. In all cases, we referred to the neighboring voxels of a region N_S as the neighbors with one voxel of distance from the region's boundaries.

2.5. Partial volume maps

Once the WM outliers were reassigned to T1-w, the resulting refilled image was used to segment the brain tissue following the same method described in Sec. 2.3. Afterwards, partial volume maps (*csfgm*) and (*gmwm*) were reassigned to each of the three main classes CSF, GM and WM following a region-wise approach.

Local 2D regions with similar intensities that were classified as *csfgm* and *gmwm* were estimated using the same connected component algorithm described before. The

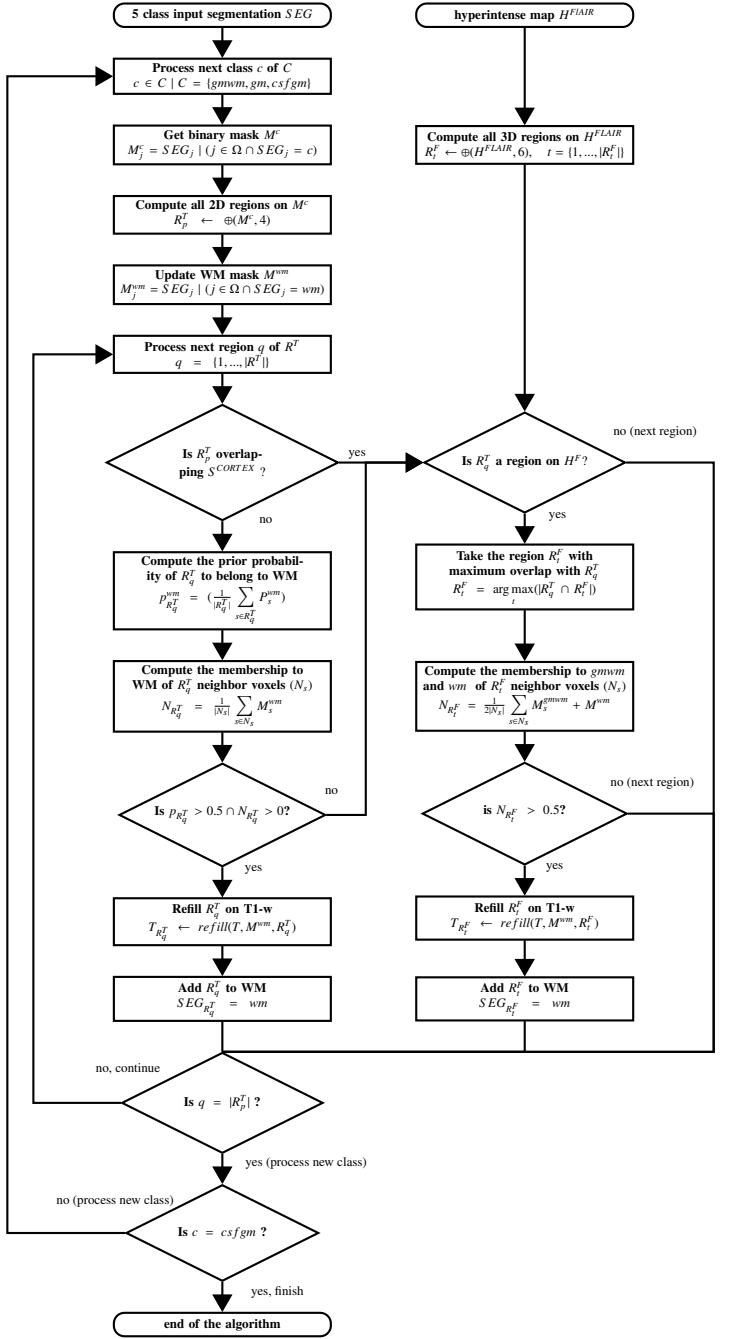


Figure 2: Proposed algorithm to estimate and refill outlier candidate regions into T1-w. The algorithm takes the 5 class T1-w segmentation and the hyper-intensity map H^{FLAIR} if available as inputs. Connected regions of voxels with similar intensities are filtered based on their spatial location probability in tissue and morphological prior atlases. Selected regions are then refilled in the original T1-w image.

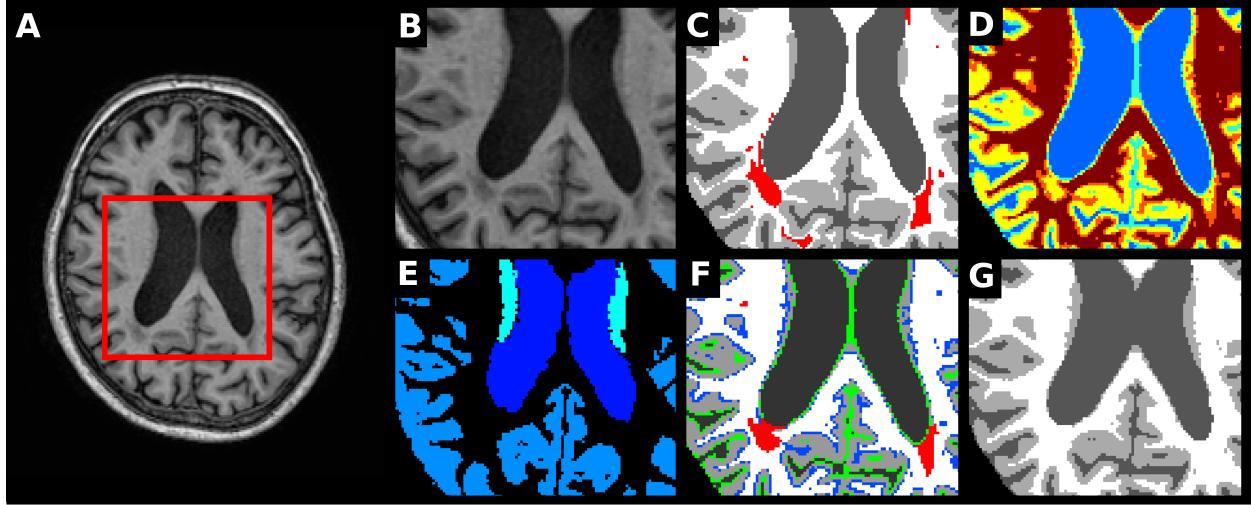


Figure 3: Partial volume assignment during tissue segmentation (Sec. 2.5). A) Original T1-w image. B) Detailed view of the T1-w image. C) Tissue ground-truth with WM lesions highlighted in red. D) Initial 5 class tissue segmentation where *csf*, *csfgm*, *gm*, *gmwm* and *wm* tissues are depicted in blue, cyan, yellow, orange and red, respectively (see Sec. 2.3). E) Morphological brain tissue atlas with parcellated GM regions and ventricles. F) Partial volume *csfgm* and *gmwm* regions (depicted in green and blue, respectively). Previously estimated lesion candidates are depicted in red (see Sec. 2.4). 2D regions with half of their voxels overlapping with the morphological atlas are reassigned to the correspondent tissue. The rest of the voxels are reassigned to the neighboring pure class with the most similar signal intensity. G) Final tissue segmentation with partial tissue volume maps re-estimated as CSF (dark gray), GM (light gray) and WM (white).

structural brain atlas S was then used to reassign regions where at least half of their voxels overlapped with certain structures as follows:

$$SEG_{R_p} = \begin{cases} CSF & \text{if } \left(\frac{1}{|R_p|} \sum_{s \in R_p} S_s^{VENT} \right) > 0.5 \\ GM & \text{if } \left(\frac{1}{2|R_p|} \sum_{s \in R_p} S_s^{CORTEX} + S_s^{BASAL} \right) > 0.5 \\ WM & \text{if } \left(\frac{1}{|R_p|} \sum_{s \in R_p} S_s^{BRAINSTEM} \right) > 0.5 \end{cases} \quad (5)$$

for all the regions $p = \{1, \dots, |R_p|\}$. The voxels not reassigned previously were reclassified by adding them to the surrounding pure class with the most similar intensity as follows:

$$SEG_j = \arg \min_c \left| T_j - \frac{1}{|N_j|} \sum_{s=1}^{|N_j|} (T_s \mid SEG_s = c) \right| \quad (6)$$

for pure classes $c = \{csf, gm, wm\}$ and partial volume voxels $j = \{\forall j \in \Omega \mid SEG_j = csfgm \cup gmwm\}$. The radius for neighbor voxels was set to 6 in two dimensions. Figure 3 depicts the partial volume re-assigment process for one particular T1-w image.

3. Experiments

3.1. MRBrainS database

3.1.1. Data

The available public MRBrainS 2013 database⁵ consisted of 20 scans with varying degrees of brain atrophy and white matter lesions. These scans were acquired on a 3.0T Philips Achieva MR scanner at the University Medical Center Utrecht (The Netherlands) with the following sequences: 3D T1-w (TR: 7.9ms, TE: 4.5ms), T1-Inverse Recovery (TR: 4416ms, TE: 15ms, and TI: 400ms), and T2-weighted/FLAIR (TR: 11000ms, TE: 125ms, and TI: 2800 ms). Each of the scans was co-registered (Klein et al., 2010) and intensity-corrected (Ashburner and Friston, 2005) before releasing the data. The T1, T1-IR, and T2/FLAIR voxel size was $(0.96 \times 0.96 \times 3.00 \text{ mm}^3)$ after registration (Vincken et al., 2015).

Three experts manually delineated each of the 20 scans into CSF, GM and WM and these annotations were used as the reference standard for the evaluation framework (Vincken et al., 2015). Extended manual annotation containing various brain structures and white matter lesions for 5 scans were provided for training while the remaining 15 scans were blind and had to be skull-stripped and segmented into CSF, GM and WM by participating teams.

⁵ Available for downloading at: <http://mrbrains13.isi.uu.nl/>

3.1.2. Evaluation:

The segmentation results had to be submitted online for external evaluation based on the following scores for the CSF, GM and WM tissues (c):

- Dice similarity coefficient (DSC_c) (Dice, 1945) between the manual tissue segmentation (GT_c) and the computed segmentation (SEG_c) masks:

$$DSC_c = \frac{2 |SEG_c \cap GT_c|}{|SEG_c| + |GT_c|} \times 100 \quad (7)$$

- The modified Hausdorff distance (95th percentile) (Huttenlocher et al., 1993) between the manual tissue segmentation (GT_c) points p' and the computed segmentation points p in (SEG_c) masks:

$$h_c^{95} = \max_{p \in SEG_c} \min_{p' \in GT_c} |p - p'| \quad (8)$$

- The absolute difference in tissue volume (AVD_c) between manual tissue segmentation (GT_c) and the computed segmentation (SEG_c) masks:

$$AVD_c = \left\| \frac{|SEG_c| - |GT_c|}{|GT_c|} \right\| \quad (9)$$

In order to evaluate the performance of our method, we submitted two different segmentation sets; one using either only the T1-w sequences, and the other using both T1-w and FLAIR images. We validated the performance by comparing our scores with those of other submitted segmentation pipelines.

3.1.3. Parameter settings

The skull stripping of the input images was performed using a similar approach to other methods participating in the challenge (Jog et al., 2013; Oproeck et al., 2013; Rajchl et al., 2015). The 5 training images were non-rigidly registered to the image space of each of the T1-w (Modat et al., 2010), and the brainmask was generated by a simple voting of the registered masks. Afterwards, each mask was refined in the T1-IR image by thresholding hyperintense voxels.

All the parameters of our tissue segmentation method were set to default values ($q = 2, \gamma = 0.1, w = 1$). The β parameter was computed automatically as described in Section 2.3. The α parameter that scaled the minimum signal intensity on the H^F mask was set to $\alpha = 3$.

3.2. MS database

3.2.1. Data

This non-public database of images was composed of 24 images of clinically isolated syndrome (CIS) patients acquired with a 3T Siemens MR scanner (Trio Tim, Siemens, Germany) with a 12-channel phased-array head coil (data from Hospital Vall D'Hebron, Barcelona, Spain). The following pulse sequences were obtained: 1) transverse proton density and T2-weighted fast spin-echo (TR=2500 ms, TE=16-91 ms, voxel size=0.78×0.78×3mm³); 2) transverse fast T2-FLAIR (TR=9000ms, TE=93ms, TI=2500ms, flip angle=120°, voxel size=0.49×0.49×3mm³); and 3) sagittal 3D T1 magnetization prepared rapid gradient-echo (MPRAGE) (TR=2300 ms, TE=2 ms; flip angle=9°; voxel size=1×1×1.2mm³). For each scan, T1-w and FLAIR images were first skull-stripped using BET (Smith, 2002) and then intensity-corrected using the N3 method (Sled et al., 1998). Finally, FLAIR images were co-registered into the T1-w space and then re-aligned into the MNI space using SPM12 co-registration tools with the normalized mutual information as the objective function and tri-linear interpolation with no wrapping (Ashburner and Friston, 2005). White matter lesion masks were semi-automatically delineated from FLAIR using JIM software⁶ by a trained technician at the hospital center. The mean lesion volume was 4.30 ± 4.84 ml (range 0.1-18.3 ml).

3.2.2. Evaluation

Expert manual annotations of tissues were not available for this database. As validated in previous MS studies (Battaglini et al., 2012; Valverde et al., 2015b,c), WM lesions in original T1-w scans were first refilled with signal intensities similar to normal-appearing WM using the SLF lesion filling method (Valverde et al., 2014). Then, both the original and the refilled images were segmented into CSF, GM and WM tissues using our proposed approach. The performance of our tissue segmentation method was evaluated by computing the absolute difference in tissue volume (AVD_c) between the images segmented containing lesions and the same images where WM lesions were refilled before the tissue segmentation:

⁶Xinapse Systems, <http://www.xinapse.com/home.php>

$$AVD_c = \left\| \frac{|SEG_c| - |GT_c^{fill}|}{|GT_c^{fill}|} \right\| \times 100 \quad (10)$$

where SEG_c refers to the output segmentation masks of the segmented images containing lesions, and GT_c^{fill} refers to the output tissue segmentation masks of images where lesions were filled before segmentation and considered as ground-truth.

Several works (DellOglio et al., 2014; Valverde et al., 2015c) have already shown that part of the actual error in tissue segmentation may be partially masked by opposite directions in the differences in total and normal-appearing tissue. In order to add an additional measure estimator of the actual error in tissue segmentation that will not be biased by these differences, we also compared, for each tissue, the percentage of mis-classified voxels PMC_c between the original SEG_c and the expert filled GT_c^{fill} masks:

$$PMC_c = \frac{|\overline{SEG}_c \cap GT_c^{fill}|}{|GT_c^{fill}|} \times 100 \quad (11)$$

In order to analyze the benefits of using FLAIR images in the proposed approach, we evaluated the performance of our method using only a T1-w image first, and then using both T1-w and FLAIR. We then validated it with two other automated pipelines widely used in brain tissue segmentation, FAST (Zhang et al., 2001) (version FSL 5.0) and SPM (Ashburner and Friston, 2005) (version SPM12 rev 6225), using either original images or after estimating lesions using the automated approach SLS proposed by Roura et al. (2015). With images where lesions were automatically segmented, estimated lesion masks were then filled with the same SLF method (Valverde et al., 2014) before tissue segmentation. Similar to our approach, we considered the tissue segmentation masks of the experts refilled T1-w images segmented with FAST and SPM12 as the ground-truth for each method. Table 1 summarizes each of the evaluated pipelines and the corresponding process followed to segment the MS images.

3.2.3. Parameter settings

The BET skull-stripping process was optimized as proposed by Popescu et al. (2012) without removing CSF from the brainmask. N3 was run with optimized parameters by reducing the smoothing distance parameter to 30–50 mm (Boyce et al., 2008; Zheng et al., 2009).

Table 1: Summary of evaluated pipelines and processes used on the MS data. On the *FAST only T1* and *SPM12 only T1* pipelines, images were segmented containing lesions without any prior automated lesion segmentation. On the *FAST + SLS* and *SPM12 + SLS* pipelines, WM lesions were automatically segmented using the SLS approach (Roura et al., 2015) and estimated lesion masks were afterwards filled using the SLF method (Valverde et al., 2014). On our proposed pipeline, using *MSSEG only T1* and *MSSEG T1 + FLAIR*, lesion segmentation and filling was part of the same segmentation method. Manual lesion annotations were used to refill T1-w images on *FAST GT*, *SPM12 GT* and *MSSEG GT* pipelines before segmenting the images using *FAST*, *SPM12* and *MSSEG*, respectively. AVD_c and PMC_c scores were then computed between pipelines 1 vs 3, 2 vs 3, 4 vs 6, 5 vs 6, 7 vs 9 and 8 vs 9.

Pipeline	Modality	Lesion seg.	Lesion filling	Tissue seg.
1. FAST only T1	T1	<i>none</i>	<i>none</i>	FAST
2. FAST + SLS	T1, FLAIR	SLS (FLAIR)	SLF	FAST
3. FAST GT	T1	<i>expert manual</i>	SLF	FAST
4. SPM12 only T1	T1	<i>none</i>	<i>none</i>	SPM12
5. SPM12 + SLS	T1, FLAIR	SLS (FLAIR)	SLF	SPM12
6. SPM12 GT	T1	<i>expert manual</i>	SLF	SPM12
7. MSSEG only T1	T1	<i>internal</i>	<i>internal</i>	MSSEG
8. MSSEG T1 + FLAIR	T1, FLAIR	<i>internal</i>	<i>internal</i>	MSSEG
9. MSSEG GT	T1	<i>expert manual</i>	SLF	MSSEG

The SLF lesion filling method was run with default parameters in all experiments. In the FAST and SPM12 images, where we estimated lesion masks automatically, the lesion segmentation method SLS was optimized for 3.0T data identically as shown in Roura et al. (2015).

All the parameters of our proposed method were fixed to default values ($q = 2, \gamma = 0.1, w = 1$) as done in the MRBrainS13 database. The β parameter was computed automatically. The α parameter that scaled the minimum signal intensity on the H^F mask was set again to $\alpha = 3$.

3.3. Statistical significance

The statistical significance of the performance between methods was computed by running a series of permutation tests (Menke and Martinez, 2004; Klein et al., 2009; Diez et al., 2014) between the differences in the scores obtained by each method. These tests allowed us to analyze the fraction of times that a particular method with the lowest score was significantly better than the other methods with $p\text{-value} \leq 0.05$. The methods were then ranked into three different levels according to the difference between the mean score of the best method $\mu_o \pm \sigma_o$ and the distance with respect to the mean scores of the rest of the methods. Hence, Rank 1 contained methods with mean scores of $(\mu_o - \sigma_o, \mu_o]$, Rank 2 contained those with mean scores of $(\mu_o - 2\sigma_o, \mu_o - \sigma_o]$ and Rank 3 those in the interval $(\mu_o - 3\sigma_o, \mu_o - 2\sigma_o]$ (Klein et al., 2009; Diez et al.,

2014; Valverde et al., 2015a). For all the tests, we set the number of comparisons between each pair of methods to $N = 1000$.

3.4. Implementation details

The proposed pipeline was entirely developed in MATLAB (v2014a, The Mathworks Inc, US), except for the registration process that was run using the available NiftyReg package (Ourselin et al., 2002; Modat et al., 2010). The method was configured to run either in CPU or GPU. Experiments were carried out on a GNU/Linux machine with a single Intel core i7 processor at 3.4 Ghz (Intel Corp, US), and a NVIDIA K40 with 12GB of RAM (NVIDIA, US). The average execution time for the proposed method including registration and tissue segmentation was 8 minutes running on the CPU core. Execution time on the GPU was approximately 2 minutes, reducing the execution time on the CPU processor by four times.

4. Results

4.1. MRBrainS13 dataset

Table 2 shows the mean DSC_c , h_c^{95} and AVD_c scores obtained by our proposed method. We compare our scores with other non-supervised strategies that also participated in the challenge, such as FAST, SPM12, or VBM12⁷, and also with respect to the best ranked method proposed by Stollenga and Byeon (2015). The overall ranking of the methods also included the combined brain (GM + WM) and intracranial (CSF + GM + WM) volumes, which are not shown in the table for simplicity⁸. At the time of submitting our results in the online application, our approach, using both T1 and FLAIR (*MSSEG T1+FLAIR*), was the best unsupervised method in the challenge (*7th* position overall 31 participants), and its accuracy was very competitive in comparison with several supervised methods that were explicitly trained for the challenge. When using only the T1-w modality (*MSSEG only T1*), our method was ranked in the *10th* position, but still clearly out-performed *FAST* (*21th* position), and *SPM12* using

FLAIR+T1 (*17th* position), the T1-IR modality (*18th* position), and the T1-w modality (*20th* position).

Figure 4 illustrates the different steps performed by our approach. After registering the probabilistic atlases into the subject space (Fig.4 panels E to H), tissue was estimated from the T1-w into 5 different classes (Fig.4 panel I). Then, WM outliers were estimated in the T1-w image by analyzing all the regions not initially segmented as WM with a high probability of belonging to WM based on its spatial local probability and prior tissue information (red regions depicted in Fig.4 panel J). If FLAIR was also provided, lesion candidates were analyzed as well based on their signal intensity in the FLAIR image and their spatial local probability of belonging to WM (green regions depicted in Fig.4 panel J). Afterwards, the lesion candidate regions were refilled in the T1-w image with signal intensities similar to the WM, the refilled T1-w image was re-estimated again and CSFGM and GMWM volumes were reassigned to the three main classes (Fig.4 panels K and L).

4.2. MS data

Table 3 (a) depicts the mean % of absolute differences in the CSF, GM and WM volume (AVD_c) for each of the methods evaluated after segmenting the 24 3T images. Table 3 (b) shows the mean % of mis-classified CSF, GM and WM voxels (PMC_c) for each method.

Methods were ranked based on their scores after running the permutation tests. Table 4 shows the ranking of each method evaluated for the AVD_c (Table 4 (a)) and PMC_c scores (Table 4 (b)), respectively. The differences in tissue volume were the lowest when the methods also used the FLAIR image to estimate the WM outliers. Our proposed approach reported competitive results and again was categorized in the first rank of methods for all tissues. Methods using only T1 yielded a significantly higher difference in GM and WM volumes and were ranked in the second and third group. The proposed approach, using only T1-w, was significantly better than the other methods in terms of the % of miss-classified GM and WM voxels, but its performance was worse for WM and was ranked in the second group for WM. As shown in Table 4 (a), the % of miss-classified WM voxels was significantly lower in both *FAST+SLS* and our proposed method *MSSEG T1+FLAIR* when compared with the rest of the evaluated pipelines.

⁷<http://www.neuro.uni-jena.de/>

⁸Overall ranking of methods for all the measurements can be consulted at <http://mrbrains13.isi.uu.nl/results.php>

Table 2: Segmentation results on the 15 test images of the MRBrainS challenge. Mean DSC_c , h_c^{95} and AVD_c scores for CSF, GM and WM tissue are shown for our proposed method when using only the T1-w modality (*MSSEG only T1*) and when using the T1-w and FLAIR modalities (*MSSEG T1+FLAIR*). The obtained values are compared with the best approach at the time of writing this paper (Stollenga and Byeon, 2015), and also with other unsupervised techniques that also participated in the challenge such as *FAST*, *SPM12* and *VBM12*. The overall ranking of the methods in the challenge is shown in the last column.

Method	DSC_c			h_c^{95}			AVD_c			Rank
	CSF	GM	WM	CSF	GM	WM	CSF	GM	WM	
Best method	83.72 ± 2.63	84.82 ± 1.37	88.33 ± 0.89	2.14 ± 0.36	1.70 ± 0.01	2.08 ± 0.33	7.09 ± 4.01	6.77 ± 3.28	7.05 ± 5.22	1
FAST only T1	69.95 ± 2.81	78.66 ± 2.24	85.98 ± 2.58	3.41 ± 0.25	4.35 ± 1.13	3.65 ± 0.85	11.83 ± 10.38	8.65 ± 6.34	11.47 ± 6.24	21
SPM12 only T1	70.69 ± 3.75	80.34 ± 2.37	85.58 ± 1.73	5.34 ± 1.47	2.93 ± 0.25	3.06 ± 0.08	23.24 ± 16.04	6.95 ± 6.57	5.99 ± 3.95	20
SPM12 T1+FLAIR	74.03 ± 3.42	81.17 ± 2.24	86.03 ± 1.48	4.59 ± 0.61	2.90 ± 0.15	3.00 ± 0.07	10.07 ± 4.86	10.59 ± 8.34	5.21 ± 3.88	17
SPM12 T1-iR	78.25 ± 3.78	79.41 ± 2.15	83.54 ± 2.14	4.01 ± 0.63	3.01 ± 0.29	3.60 ± 0.27	10.47 ± 5.69	7.23 ± 6.50	6.34 ± 4.61	18
VBM12	74.56 ± 2.70	82.29 ± 1.49	87.95 ± 1.71	3.03 ± 0.14	3.20 ± 0.32	2.32 ± 0.42	6.80 ± 4.57	5.91 ± 3.91	6.06 ± 4.42	8
MSSEG only T1	80.18 ± 2.67	82.06 ± 1.68	87.05 ± 1.46	2.81 ± 0.21	3.33 ± 0.21	2.91 ± 0.42	7.18 ± 3.33	6.15 ± 3.51	6.20 ± 5.45	10
MSSEG T1+FLAIR	80.16 ± 2.67	82.20 ± 1.60	87.33 ± 1.35	2.81 ± 0.21	3.18 ± 0.15	2.88 ± 0.39	7.21 ± 3.31	5.99 ± 3.43	5.95 ± 5.44	7

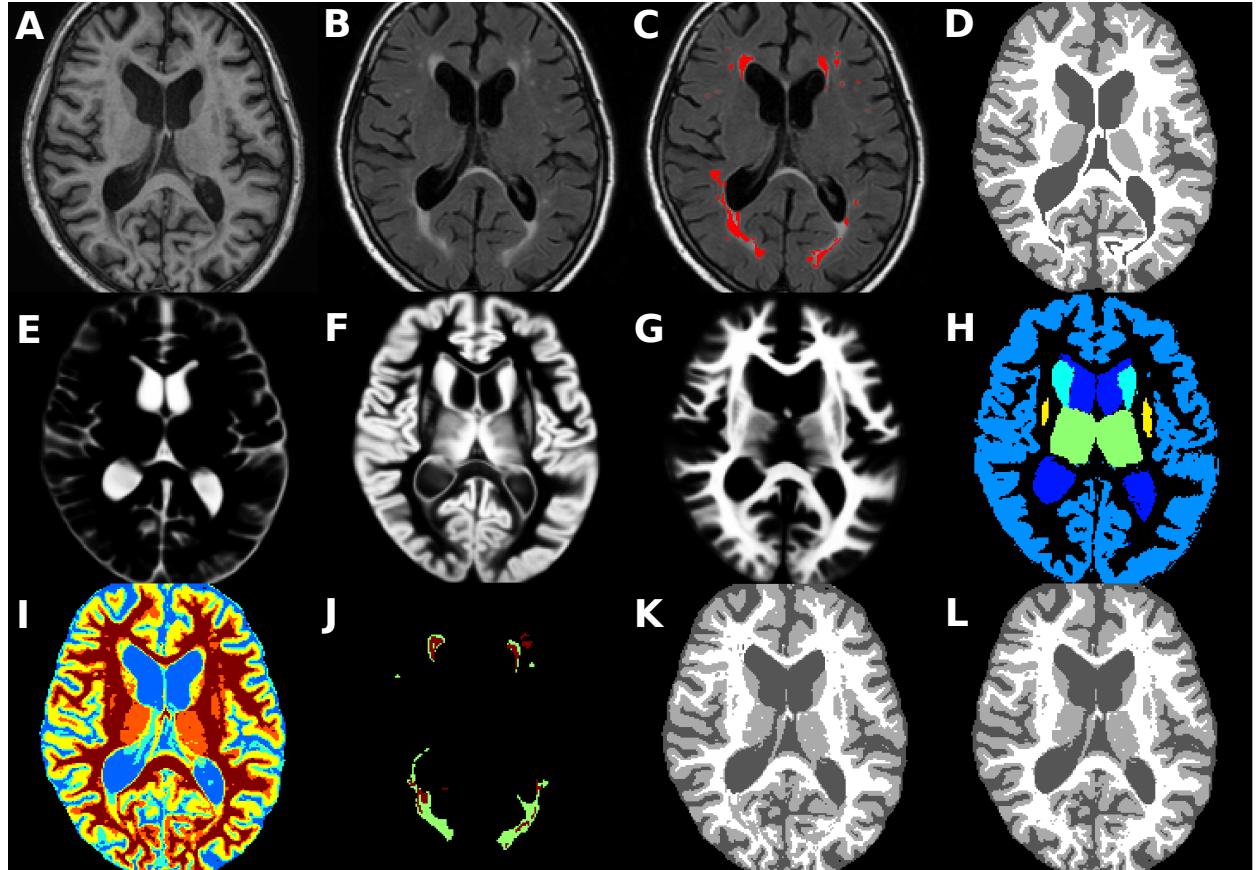


Figure 4: Automated tissue segmentation of the *MSSEG* method on the *second subject* of the training set of the MRBrainS13 database. A) Original T1-w image. B) Original FLAIR image. C) FLAIR image with manual annotated WM lesions depicted in red. D) Provided ground-truth for training purposes. Registered CSF, GM and WM prior atlas to the subject space (E, F and G, respectively). H) Morphological brain structural atlas registered to the subject space. I) First partial volume segmentation with *csf* depicted in blue, *csfgm* in cyan, *gm* in yellow, *gmwm* in orange and *wm* in red. J) Obtained WM outliers extracted from either T1-w (depicted in red) and FLAIR (depicted in green). K) Final tissue segmentation using only the T1-w image, with CSF depicted in dark gray, GM in light gray and WM in white. L) Final tissue segmentation when using both T1 and the FLAIR images.

Table 3: Mean % of absolute difference in the CSF, GM and WM volume between the 24 3T tissue masks where expert annotations were refilled before segmentation and the same images segmented including white matter lesions. For each method, the reported values are the mean and standard deviation $\mu \pm \sigma$ for the (a) AVD_c and (b) PMC_c scores obtained along the entire database.

(a) Differences in AVD_c			
Method	Dif CSF (%)	Dif GM (%)	Dif WM (%)
FAST only T1	0.07 ± 0.13	0.33 ± 0.45	0.42 ± 0.56
FAST + SLS	0.04 ± 0.07	0.08 ± 0.12	0.11 ± 0.16
SPM12 only T1	0.31 ± 0.46	0.27 ± 0.45	0.56 ± 0.69
SPM12 + SLS	0.22 ± 0.22	0.13 ± 0.23	0.20 ± 0.32
MSSEG only T1	0.13 ± 0.20	0.21 ± 0.26	0.42 ± 0.54
MSSEG T1+FLAIR	0.04 ± 0.05	0.06 ± 0.05	0.13 ± 0.11

(b) Differences in PMC_c			
Method	CSF (%)	GM (%)	WM (%)
FAST only T1	0.08 ± 0.11	0.09 ± 0.12	0.53 ± 0.69
FAST + SLS	0.06 ± 0.06	0.14 ± 0.16	0.25 ± 0.30
SPM12 only T1	0.16 ± 0.32	0.25 ± 0.33	0.73 ± 0.86
SPM12 + SLS	0.22 ± 0.31	0.24 ± 0.29	0.41 ± 0.43
MSSEG only T1	0.02 ± 0.03	0.03 ± 0.05	0.46 ± 0.58
MSSEG T1+FLAIR	0.04 ± 0.04	0.14 ± 0.13	0.27 ± 0.29

4.2.1. WM outlier rejection

Finally, we evaluated the performance of the proposed WM outlier rejection algorithm with respect to the other pipelines. A traditional comparison of the number of true-positive and false-positive WM lesion voxels for each pipeline is not appropriate here, given that our approach only processed WM lesion candidates that were not initially classified as WM. In contrast, the error in the expected WM lesion volume segmented can be a good indicator of the performance of each method segmenting WM lesions as WM. Figure 5 shows the % of absolute difference in WM lesion volumes for each of the evaluated pipelines and their correspondent GT_c^{fill} images. As expected, these methods yielded the lowest differences in WM lesion volume when they also used the FLAIR modality to estimate WM lesions. The *MSSEG+FLAIR* showed the lowest differences in WM lesion volume of all methods evaluated.

5. Discussion

In this paper we have presented a new, automated brain tissue segmentation pipeline for MS patient images that

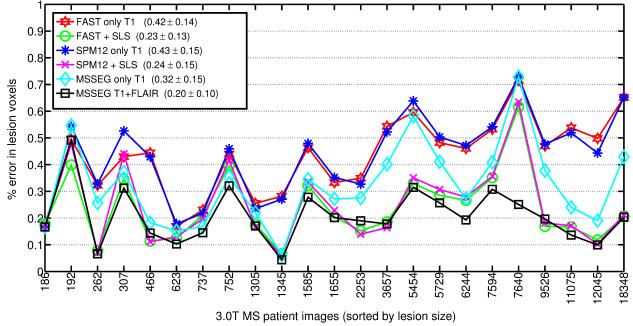


Figure 5: % of absolute difference in WM lesion volume for each of the pipelines evaluated with the 3T MS database. Figure legends also show the mean and standard deviation $\mu \pm \sigma$ for the entire set of images. Images are sorted by lesion size (number of lesion voxels).

combines multi-channel intensities, anatomical and morphological prior maps at different levels to estimate brain tissue in the presence of WM lesions. The current method integrates a WM outlier estimation and refilling algorithm that is applied intermediately in order to reduce the effect of WM lesions on tissue segmentation. As shown by the results, the proposed technique yields competitive and consistent results in both general and MS specific databases without parameter tweaking. Furthermore, although we did not explicitly analyze the execution times of each of the evaluated algorithms, the proposed method takes advantage of new affordable processors such as GPUs that reduce up to four times the execution time to register and segment tissue when compared with general purpose CPUs.

The MRBrainS challenge permitted us to evaluate the efficacy of our method and to validate it with other state-of-the-art tissue segmentation methods. Although the challenge was not focused on the MS disease, the methods were evaluated by comparing them with respect to manual expert annotations of tissues and WM lesions, which provided a quantitative measure of the accuracy of the method. The overall results showed that supervised methods obtained the best results in the challenge, taking advantage of the inherent capability to fit the database characteristics. At the time of writing this paper, *MSSEG T1+FLAIR* was ranked in 7th position out of 31 participants, being the best non-supervised strategy followed by the VBM12 approach. As shown by the differences in

Table 4: Permutation tests results for evaluated methods on the 3T MS database. (a) Final rank based on the absolute % difference in CSF, GM and WM volume between methods. (b) Final rank based on % of miss-classified CSF, GM and WM voxels between methods. Reported values are mean and standard deviation (μ_o, σ_o) of the fraction of times when each method produces significant p-values ($p \leq 0.05$). Positive values indicate that in average, the method out-performed the other methods in pair-wise significant tests. Negative values indicate the contrary. Rank 1: $(\mu_o - \sigma_o, \mu_o)$, Rank 2: $(\mu_o - 2\sigma_o, \mu_o - \sigma)$, Rank 3 $(\mu_o - 3\sigma_o, \mu_o - 2\sigma_o)$. All permutation tests were run with 1000 random iterations.

(a) Evaluated methods ranked by the absolute % of CSF, GM and WM volume of 3T data.						
Rank	Method (CSF)	$\mu \pm \sigma$	Method (GM)	$\mu \pm \sigma$	Method (WM)	$\mu \pm \sigma$
Rank 1	MSSEG T1+FLAIR	0.5 ± 0.55	MSSEG T1+FLAIR	0.5 ± 0.55	FAST + SLS	0.67 ± 0.52
	FAST only T1	0.5 ± 0.55	FAST + SLS	0.5 ± 0.55	MSSEG T1+FLAIR	0.5 ± 0.55
	FAST + SLS	0.5 ± 0.55	SPM12 + SLS	0.33 ± 0.52		
Rank 2	MSSEG only T1	-0.43 ± 0.64	MSSEG only T1	-0.17 ± 0.75	SPM12 + SLS	0.14 ± 0.72
	SPM12 + SLS	-0.5 ± 0.55	SPM12 only T1	-0.5 ± 0.55	FAST only T1	-0.24 ± 0.62
	SPM12 only T1	-0.57 ± 0.5				
Rank 3			FAST only T1	-0.67 ± 0.52	MSSEG only T1	-0.47 ± 0.52
					SPM12 only T1	-0.59 ± 0.49

(b) Evaluated methods ranked by the absolute % of miss-classified CSF, GM and WM of 3T data.						
Rank	Method (CSF)	$\mu \pm \sigma$	Method (GM)	$\mu \pm \sigma$	Method (WM)	$\mu \pm \sigma$
Rank 1	MSSEG only T1	0.83 ± 0.41	MSSEG only T1	0.83 ± 0.41	MSSEG T1+FLAIR	0.67 ± 0.52
	MSSEG T1+FLAIR	0.44 ± 0.8	FAST only T1	0.5 ± 0.84	FAST + SLS	0.67 ± 0.52
Rank 2					SPM12 + SLS	-0.17 ± 0.75
					MSSEG only T1	-0.17 ± 0.75
					FAST only T1	-0.17 ± 0.75
Rank 3	FAST + SLS	0 ± 0.89	FAST + SLS	-0.17 ± 0.75	SPM12 only T1	-0.83 ± 0.41
	SPM12 only T1	-0.27 ± 0.43	MSSEG T1+FLAIR	-0.17 ± 0.75		
	FAST only T1	-0.33 ± 0.82	SPM12 only T1	-0.33 ± 0.52		
	SPM12 + SLS	-0.67 ± 0.52	SPM12 + SLS	-0.66 ± 0.51		

each of the scores obtained, the FLAIR modality appeared useful to improve the accuracy of the method when compared with the *MSSEG T1*, which was ranked 10th. The performance of the *MSSEG* was superior with all tissues when compared to general purpose methods such as *FAST* (ranked 21th) and *SPM12* (best ranked 17th), even if they used both image modalities. However, the final method ranking should be taken with care, given the differences in the skull-stripping processes between methods. Differences in the boundaries of the estimated skull masks may be behind the remarkable differences in CSF among methods, altering also the intra-cranial cavity measurements and consequently the overall score of each of the methods.

In MS data, the performance of our method was similar or better to the best pipeline incorporating a state-of-the-art method for lesion segmentation and filling, validating its overall capability to reduce the effects of WM lesions on tissue segmentation. The *MSSEG T1+FLAIR* and *FAST+SLS* were ranked in the first group of methods with error differences in tissue volume below 0.15% in all

the tissues. Pipelines using only T1-w showed a similar or lower % of miss-classified CSF and GM voxels than those using both FLAIR and T1-w. In contrast, the % of miss-classified WM voxels (Table 4 (a)) and the differences in the reassigned lesion volume (Fig. 5) were significantly higher on the former, showing that these methods tended to overestimate GM and underestimate WM caused by the effect of WM lesions. In this aspect, our results are consistent with previous studies that also analyzed the effects of WM lesions on tissue segmentation (Battaglini et al., 2012; Gelineau-Morel et al., 2012; Valverde et al., 2015b,c).

Differences in the AVD_c between the *MSSEG T1+FLAIR* and the *MSSEG only T1* on the MRBrains13 data were similar to those reported in MS data, showing that, in general, the inclusion of the FLAIR modality reduced the overall error in tissue volume on all the analyzed databases. On MS data, the % of miss-classified CSF and GM voxels was significantly lower on the *MSSEG only T1*, but significantly higher in WM, evidencing that *MSSEG only T1* tended to overestimate

WM, while the error in the *MSSEG T1+FLAIR* was similar in both GM and WM. In addition, the results show that the % difference in the total WM and lesion volume was significantly lower on the *MSSEG T1+FLAIR* in comparison with the *MSSEG only T1*. Hence, we would recommend using both the T1-w and FLAIR modalities when possible. However, the accuracy of the *MSSEG only T1* pipeline was still superior to the *FAST* and *SPM12* when compared with the ground-truth annotations of the MRBrainS13 database. This suggests that at least with the available data, the improvement in tissue segmentation was not only caused by the addition of the FLAIR modality, but also by the combination of intensity and the anatomical and morphological priors.

This study, however, has some limitations. The lack of a database consisting of MS images with manual annotations on the tissue, limits our analysis to the differences in the tissue volume with respect to images where expert lesion annotations were lesion filled before tissue segmentation. However, the previous analysis in prior studies proved to be effective in evaluating the effects of WM lesions on tissue segmentation (Battaglini et al., 2012; Valverde et al., 2015b,c). Furthermore, the mean lesion sizes of the MS cohorts do not allow us to investigate better the performance of the proposed method in the presence of images with higher lesion loads. As a future work, we believe that an additional study on MS with manual annotated tissue masks and higher lesion loads would be helpful not only to analyze the benefits of the proposed algorithm with MS images, but also to investigate the benefits of adding other image channels such as T2 or PD. Furthermore, although the method was designed for cross-sectional data, we are sensible to the fact that the current approach could be benefited by the possibility of evaluating longitudinal changes in the tissue volume.

6. Conclusion

In this paper, we have proposed the Multiple Sclerosis SEGmentation pipeline (*MSSEG*), a new MRI brain tissue segmentation method designed to deal with MS patient images containing lesions. Our proposed approach incorporates robust partial volume tissue segmentation with outlier rejection and filling, combining intensity and

probabilistic and morphological prior maps in a novel way. When combining T1-w and FLAIR modalities, our method has shown very competitive results with the MRBrainS13 database, ranked in 7th position out of 31 participant strategies and being the best non-supervised approach so far. With MS data, differences in the tissue volume were lower or similar to the best available pipeline composed of the *FAST* and a state-of-the-art method for lesion segmentation and filling. In all the experiments, the inclusion of the FLAIR modality into the proposed method reduced the effect of WM lesions on the tissue segmentation, which suggests that this modality should be used when available. In conclusion, our results show that, at least with the presented data, the *MSSEG* improves the measurement of brain tissue volume in images containing WM lesions. Hence, we strongly believe that the neuro-image community can benefit from its use in future settings.

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