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A Classifier Based on Superpixels and Markov Random Fields for Multiple Sclerosis Lesions on Magnetic Resonance Images

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Abstract— **In this work we present a methodology for lesion detection in Magnetic Resonance Imaging (MRI). Many physicians rely on brain images for the diagnosis of neuropathologies such as Multiple Sclerosis (MS). Unfortunately, in Mexico, not all public health institutions have access to commercial imaging software. For this reason, physicians are interested in the development of tools that could partially replace commercial software, for instance, for the detection of brain lesions. The proposed method uses the Simple Linear Iterative Clustering method (SLIC) in order to reduce the number of variables, followed by a Gauss Markov Measure Field (GMMF) model to perform the classification. In literature, these methods have demonstrated many advantages such as: computational efficiency, border preservation and accuracy. Results obtained with the proposed method are promising and confirm these benefits.**

Key words— **Markov measure fields, Multiple sclerosis, MRI, Superpixels**

I. Introduction

The human body is a complex organism whose function has been largely studied throughout history; with the brain being the organ that many people considers the most striking. Almost any corporal functions are governed by the brain; however, there are many brain-related phenomena that neuroscience is still unable to explain. Unfortunately, like many organs in the human body, the brain can suffer degenerative changes due to aging, diseases or injuries. Neurodegenerative diseases cause alterations not only in the lifestyle of the person affected but they may also affect the dynamic of the people with whom the patient interacts.

Multiple sclerosis (MS) is a neurodegenerative disease that affects the myelin sheath of the axons that insulates the electric impulse signals that are transmitted between neurons [1,2]. Some principal symptoms and signs are: weakness, depression, monocular blindness, dysphagia and ataxia. The symptomatology depends of the affected zone. To this day, physicians cannot fully explain under which conditions a person can acquire this disease. Usually, the diagnosis is based on the presence of some of these symptoms and confirmed by medical imaging techniques such as Magnetic Resonance Imaging (MRI) or a Computer Tomography [3]. MS is the second neurodegenerative disease in incidence rate in young adults (20 to 40 years old), with epilepsy being the first. This means that these diseases affect many people during their most productive phase. MS produces lesions in the white matter which appear as hyper-intense spots in a T2 MRI. The number and size of these spots allow the physician to diagnose and follow the evolution of the disease. However, detecting, counting and measuring these regions is a time-consuming task. For this reason, it is interesting to develop automated methods for the segmentation of MS lesions.

In this paper, an algorithm is proposed for the segmentation of MS lesions in MRI images. The algorithm is based on segmentation in superpixels followed by a classification stage using Markov Random Fields. The methodology is presented in Section II, followed by preliminary results in Section III. Finally, some conclusions are presented in Section IV.

II. Methodology

The proposed method is based on performing an over-segmentation in superpixels using the Simple Linear Iterative Clustering (SLIC) algorithm [4], and then classifying each superpixel using a Gauss Markov Measure Field model [7]. This methodology is applied in two stages: in the first stage, the goal is to segment the whole brain in order to remove the skull and other structures. In the second stage, segmentation is applied only to the brain region to detect the MS lesions. Figure 1 shows the main steps of the process and the details are described below.

A. Oversegmentation in superpixels

Many image segmentation algorithms attempt to assign a class label to each pixel, depending on its characteristics (intensity, color, etc.) and, possibly, those of its neighbors. Recently, it has been proposed to group similar pixels in spatially-compact clusters so that all pixels in a cluster can be treated as one single super-pixel [4-6]. Such methods can often reduce the number of unknown variables (e.g., class labels) that must be computed for certain tasks. Another advantage of using these methods is that super-pixels aim to preserve borders in the images.

In the proposed method, a popular method for super-pixel clustering, called SLIC, is applied [4]. This method is based on the K-means algorithm and merges pixels in clusters using a measure that combines distance and intensity. The main advantage of SLIC, in comparison with K-means, is that the search space is reduced, significantly decreasing the execution time.

The algorithm works as follows: let $I(\vec{r})$ be an image defined over a lattice L (that is, $\vec{r} \in L$) and K the desired number of super-pixels into which the input image will be segmented. Each super-pixel will be denoted by $S_k = [C_k, D_k]$, for $k = 1, \dots, K$, where C_k is the average intensity of the super-pixel and $D_k = [x_k, y_k] \in \mathbb{R}^2$ is its geometric

center (note that D_k does not necessarily belong to L). In the case of MRI images, one may assume that C_k is a real number. Cluster centers are initialized in a regular hexagonal grid in L, and their average intensities C_k are initialized as the pixel intensity at D_k. For each super-pixel, a square neighborhood of size $2M \times 2M$, with $M = \sqrt{|L|/K}$, and centered at D_k is defined in order to reduce the search space of the K-means method; that is, only pixels within the neighborhood of a given super-pixel can be assigned to it. Each pixel $\vec{r} \in L$ will be assigned to the neighboring super-pixel that minimizes the combined distance

$$\delta_k(\vec{r}) = \sqrt{d_c(\vec{r},k) + \gamma d_e(\vec{r},k)}, \quad (1)$$

where

$$d_c(\vec{r},k) = \frac{1}{m^2}\,\|I(\vec{r}) - C_k\|^2 \quad (2)$$

measures the difference in intensities,

$$d_e(\vec{r},k) = \frac{1}{M^2}\,\|\vec{r} - D_k\|^2 \quad (3)$$

measures the spatial distance and m is the dynamic range of the data and γ is a hyperparameter that weights the importance between terms.

Once each pixel has been assigned to a cluster, each cluster C_k and D_k is updated with the intensity and position averages of all pixels belonging to the cluster, and the process is iterated (re-assign pixels to clusters and so on). In our experience, the algorithm converges in 10 iterations. Figure 1b exemplifies the SLIC method applied to the image in Figure 1a with $K = 972$ and $\gamma = 0.1$. Note how the borders of the super-pixels adhere to the borders between different structures. This algorithm also returns an image $l(\overrightarrow{r})$ which represents the index of the super-pixel to which pixel $\vec{r}$ belongs.

B. Super-pixel fragmentation and fusion

Depending on the input image and the value of γ, it is possible for SLIC to produce super-pixels that are spatially fragmented. These clusters have unconventional neighborhoods that may bias a classifier based on Markov fields. For this reason, a connected components algorithm [8] is used to re-label all the fragments as individual super-pixels, effectively increasing the actual number of super-pixels. On the other hand, to reduce the effects of noise, super-pixels whose area is smaller than 3% of the average area (given by $\bar{A} = |L|/K$) are merged with the most similar neighboring cluster (in terms of average intensity), reducing the number of actual super-pixels. Figure 1c shows a zoomed region where small clusters are merged with neighboring super-pixels. In fusion process from 2014 regions found with connected component process to 1285 regions for all regions with area of 3% or less merged.

C. Segmentation of the brain region

It is well known that MS lesions are located in the white matter. On the other hand, other structures in the MRI image, such as the skull, may also show high intensity values that may confound a classifier. For this reason it is useful to isolate the brain area from the MRI image. One way to achieve this segmentation is by classifying each super-pixel according to its average intensity and that of its neighbors. This can be done, for instance, by estimating the probability $p_j(k)$ that super-pixel S_k belongs to class j, for each $k = 1, \ldots, K$ and $j = 1, \ldots, C$, using a Gauss Markov Measure Field (GMMF) model [7]. Under this model, the probabilities are obtained by minimizing, for each class j, the energy function $U_j(p_j)$ given by:

$$U(p_j) = \sum_{S_k} \left(p_j(k) - g_j(k)\right)^2 + \lambda \sum_k \sum_{r \in N_k} \left(p_j(k) - p_j(r)\right)^2.$$

The first term in Eq. 5 represents the normalized likelihood between the k-th super-pixel and the j-th class given by $g_j(k) = v_j(k) / \sum_j v_j(k)$, where $v_j(k)$ is the likelihood function. For instance, if each class has a Gaussian distribution with mean μ_j and variance ${\sigma_j}^2$, the likelihood can be modeled as

$$v_j(k) = \exp\left\{-\kappa \left\|C_k - \mu_j\right\|^2 / 2{\sigma_j}^2\right\}, \quad (7)$$

where κ is a hyper-parameter which controls the overall variance of all classes.

The second term in Eq. 5 is a regularization term that promotes the similarity between pairs of neighboring super-pixels. For each super-pixel S_k, one can obtain the set of its neighboring super-pixels N_k by inspecting the label image $l(\overrightarrow{r})$. The hyper-parameter λ controls the balance between both terms of the energy function, and therefore determines the granularity of the results.

To minimize Eq. 5, one can calculate its derivative (with respect to each $p_j(k)$ and equal it to zero to obtain a linear equation system, which can solved iteratively by the Gauss–Seidel method. The equation which updates each $p_j(k)$ is thus given by:

$$p_j(k) = \frac{g_j(k) + \lambda \sum_{r \in N_k} p_j(r)}{1 + \lambda |N_k|}. \quad (8)$$

A Gauss-Seidel iteration consists in updating $p_j(k)$ for all k and all j. In our experience, the process converges in 5 to 10 iterations. After convergence, the class c_k assigned to the k-th super-pixel is obtained as $c_k = \arg\min_j \{p_j(k)\}$.

It is also possible to update the means μ_j and variances ${\sigma_j}^2$ for all classes according to the up-to-date classification after each Gauss-Seidel iteration. From the GMMF segmentation, a binary mask is obtained where the value for each pixel in the mask is 1 if the pixel belongs to a super-pixel whose class corresponds to the brain region, or zero otherwise. Since there are other structures outside of the brain with similar gray levels, a connected components algorithm is applied to the mask to isolate the largest component, which corresponds to the brain. Finally, a hole-filling algorithm [9] is used to obtain the full brain mask. The result of this process is shown in Figure 1e.

D. Lesion Segmentation

Once the brain region has been isolated, a linear tone transfer function is applied to the image so that the first and last percentiles of the pixels are saturated to the lowest (0) and highest (255) intensity values, respectively. This increases the uniformity of the intensity values in the lesions. The segmentation process (SLIC+fusion+GMMF) is applied once more to the intensity-adjusted brain region in order to detect the lesions in the brain (Figures 1f and 1g); in this case, the resolution of the segmentation is increased by using a larger number super-pixels and a lower value for λ. Once again, a binary mask is obtained to indicate which pixels are part of a lesion (i.e., those that belong to the highest-intensity classes), and the connected components is applied to the mask to label each lesion and obtain their area and eccentricity. Finally, potential lesions are filtered according to their area and eccentricity in order to discard those regions that are either too small or too eccentric to be considered as true lesions. Figure 1h shows the final result where the reported lesions were marked in red.

III. Preliminary Results

Additional experiments were performed using one axial and one sagittal MRI images, and the results are shown in Figure 2. The parameters for both tests were the following: $K = 1000$ SLIC clusters, $\gamma = 0.1$, λ=0.1, κ=0.1, and $\mu = [5, 20, 30, 40, 50, 100]$ for the first stage (segmentation of the brain region). For the second stage (segmentation of the lesions), we used $K = 5000$ SLIC clusters and $\mu = [0, 70, 150, 200, 230, 250]$ for the axial image and $\mu = [0, 170, 190, 210, 230, 250]$ for the sagittal image. The lesions correspond to classes μ_5 and μ_6 since some lesions are less bright than others.

IV. Conclusion

A methodology for the segmentation of Multiple Sclerosis lesions in MRI images was presented. The proposed method is based on super-pixels and Markov Measure Fields. The results achieved during the preliminary experiments are promising since most lesions can be found; however, some false positive structures were also found in regions that possibly correspond to gray matter. The proposed method is also computationally efficient and easy to implement. Future work will focus in a 3D implementation of the algorithm and an heuristic to estimate the initial class parameters.

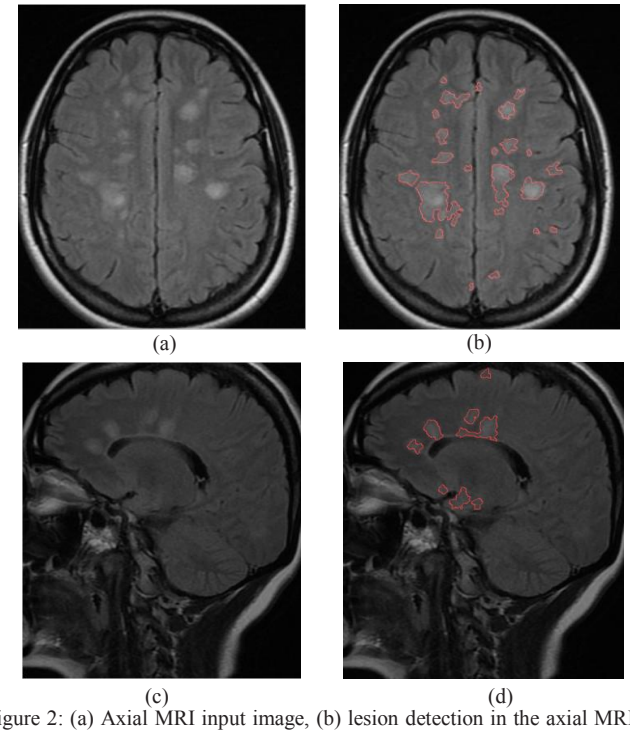

Figure 2: (a) Axial MRI input image, (b) lesion detection in the axial MRI image, (c) Sagittal MRI input image, (d) lesion detection in the sagittal MRI image.

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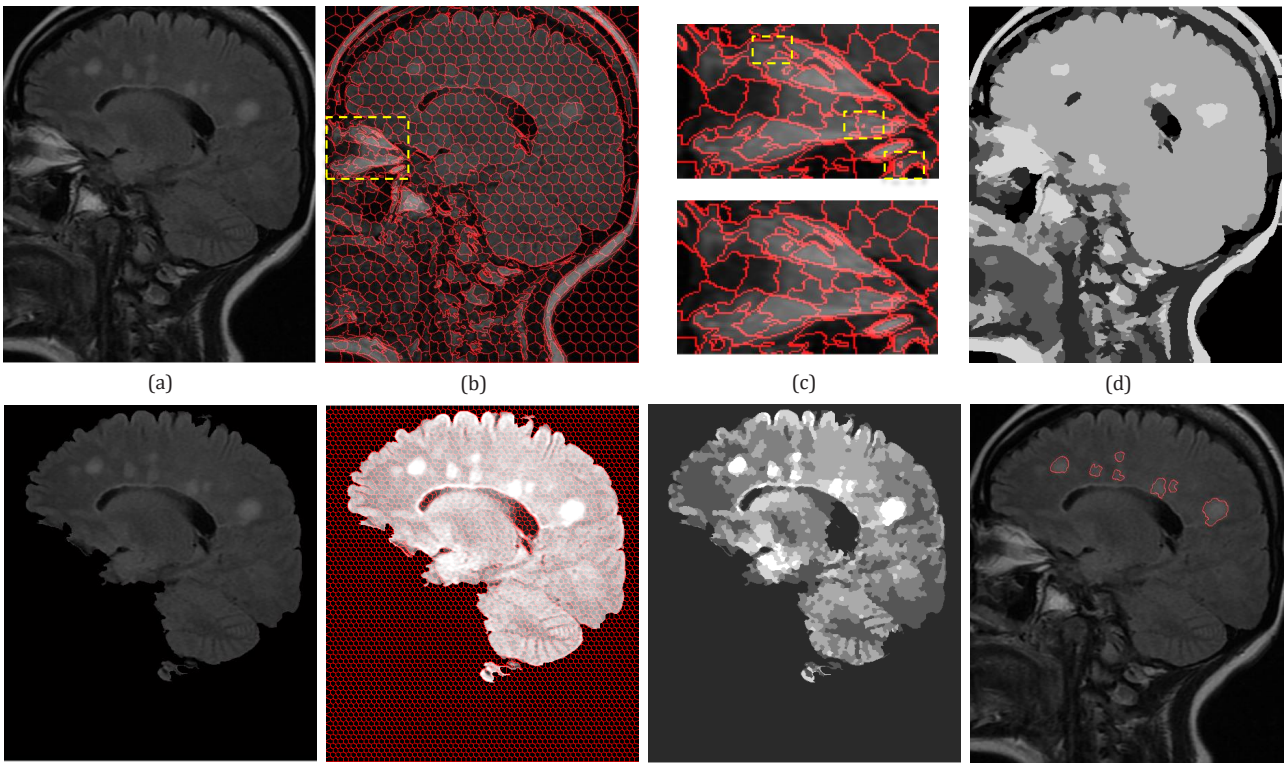

Figure 1: Complete process for detection of lesions in the brain. (a) Sagittal MRI input image of 520x459 pixels, (b) image segmented in superpixels with γ=0.1 and 1000 desired clusters (resulting in $K = 972$ clusters), (c) Zoomed region where small clusters are shown (top), result of the fusion process where small regions were merged (bottom)., (d) Result of GMMF segmentation with 10 iterations, $\lambda = 0.1$ and $k = 0.1$, (e) Isolated brain area, (f) Segmentation of the intensity-adjusted brain region in 5000 super-pixels, resulting in $K = 5453$ clusters after connected component were found, (g) GMMF segmentation of the brain region, (h) final result detecting 7 lesions in the white matter with eccentricity less that 0.9 and area of at least 80 pixels.