Bioinspired Inference System for Medical Image Segmentation

Hakima Zouaoui and Abdelouahab Moussaoui

Abstract In the present article, we propose a new approach for the segmentation of the MRI images of the Multiple Sclerosis which is an autoimmune inflammatory disease affecting the central nervous system. Clinical tracers are used nowadays for the diagnosis and the Inter-observer and intra-observer therapeutic assessment. However, those tracers are subjective and subject to a huge variability. The Magnetic Resonance Imaging (MRI) allows the visualization of the brain and it is widely used in the diagnosis and the follow-up of the patients suffering from MS. Aiming to automate a long and tedious process for the clinician, we propose the automatic segmentation of the MS lesions. Our algorithm of segmentation is composed of three stages: segmentation of the brain into regions using the algorithm FCM (Fuzzy C-Means) in order to obtain the characterization of the different healthy tissues (White matter, grey matter and cerebrospinal fluid (CSF)), the elimination of the atypical data (outliers) of the white matter by the optimization algorithm PSOBC (Particle Swarm Optimization-Based image Clustering), finally, the use of a Mamdani-type fuzzy model to extract the MS lesions among all the absurd data.

Keywords Multiple sclerosis · Magnetic resonance imaging · Segmentation · Fuzzy C-Means · Particle swarm optimization · Mamdani

1 Introduction

Multiple sclerosis (MS) is a chronic inflammatory demyelinating disease of the central nervous system. Magnetic resonance imaging (MRI) detects lesions in MS patients with high sensitivity but low specificity, and is used for diagnosis,

H. Zouaoui (✉) · A. Moussaoui
Computer Science Department, Ferhat Abbas University, Ain Taya, Algeria
e-mail: Hak-soraya@yahoo.fr

A. Moussaoui
e-mail: Moussaoui.abdel@gmail.com

S. Chikhi et al. (eds.), *Modelling and Implementation of Complex Systems*, Lecture Notes in Networks and Systems 1,
DOI 10.1007/978-3-319-33410-3_3

prognosis and as a surrogate marker in MS trials [1, 2]. In this article, we are interested in the brain MRI analysis within the context of following up the patients suffering from Multiple Sclerosis (MS).

The segmentation of various tissues and structures in medical images in a robust and efficient manner is of crucial significance in many applications, such as the identification of brain pathologies in Magnetic Resonance (MR) images [3]. The Magnetic Resonance Imaging (MRI) has widely contributed in the establishment of new knowledge about the Multiple sclerosis that allowed the clinicians to significantly improve effective therapeutic approaches. The Magnetic Resonance Imaging (MRI) is one of the complementary examinations in this disease's diagnosis approach. It plays also a key role in the patient's state follow-up and the quantification of a response after having taken medicines. So, the automatic extraction of quantifiers for the Multiple Sclerosis has many potential applications, in the clinical as well as pharmaceutical fields. On the other hand, reading those images is difficult due to the variability in size, contrast and lesions' localization.

The appearance of new lesions or the raising of ancient patches detected by MRI constitutes one of the acknowledged criteria for definitive diagnosis. If the MRI provides essential information on the appearance of lesions of the white substance (Multiple sclerosis), the evolution of the lesions and their consequences on the clinical state of the patient remain weakly correlated. This observation has underlined the concept of "the clinico-radiological paradox" [4]. Besides, the paradigm of a disease primarily inflammatory is contested at present by the hypothesis of a neurodegenerative pathogen which is reinforced by the observation, that the bouts do not influence the progression of an irreversible handicap. In fact, some recent histological works [5] have clearly shown that, besides focal inflammatory and demyelinating lesions disseminated in the white substance, there is a spread and progressive attack of the whole CNS, in both of the white substance of normal appearance and the grey substance, expressed in microscopic manner by the axonal loss and the tissue atrophy.

In this paper, we focus our studies on Brain MR imaging of the brain and we propose an automatic method of segmentation to detect the lesions of MS. Our algorithm of segmentation is composed of three stages: segmentation of the brain into regions using the algorithm FCM (Fuzzy C-Means) in order to obtain the characterization of the different healthy tissues (White matter, grey matter and cerebrospinal fluid (CSF)). In the second stage, we eliminate the atypical data of the white matter by the Optimization algorithm PSOBC (Particle Swarm Optimization-Based image Clustering). Finally in the third stage, a decision is made to use of a Mamdani-type fuzzy model composed of a group of fuzzy rules "if…. then" to extract the MS lesions among all the absurd data.

We present in the second section the related work. We will present the steps of the automatic method of segmentation of the proposed approach to detect the lesions of MS in the third section. The fourth section will present the results obtained on the MRI images. Finally, we will finish by a conclusion and future work in the fifth section.

2 Related Work

A variety of approaches to MS lesion segmentation have been proposed in the literature. Generally speaking, they can be classified into two groups: outlier-based and class- based methods.

In outlier-based methods [6–10], MS lesions are treated and detected as the outliers to the normal brain tissue distribution, which is usually modelled with a Finite Gaussian Mixture (FGM) of CSF, GM and WM classes. Van Leemput et al. [6] pioneered this approach. Under their framework, MR field inhomogeneities, parameters of the Gaussian distribution and membership are computed iteratively, with the contextual information being incorporated using a Markov random field. Observed intensity values whose Mahalanobis-distances exceed a predefined threshold are marked as lesions. The thresholds are empirically set in this work. Bricq et al. [11] applied neighborhood information during the inference process using a Hidden Markov Chain model and outliers were extracted using the Trimmed Likelihood Estimator (TLE) [12]. This approach was evaluated on real data including MS lesions using T1 and FLAIR MR images.

Class-based methods [13–18] model the lesions as an independent class to be extracted. In [14], a combination of intensity-based k-nearest neighbor classification (k-NN) and a template-driven segmentation (TDS+) was designed to segment different types of brain tissue. Lesions are modeled as one of the expected tissue types, and the class parameters are obtained through an operator supervised voxel sampling on two randomly selected scans. Since the manual training step is highly data-dependent, it is expected be conducted for each study or data set. A similar approach was proposed in [7]. The segmentation method determines for each voxel in the image the probability of being part of MS-lesion tissue, and the classification is conducted also based on K-NN algorithm. Voxel intensities and spatial information are integrated as discriminative features, and voxels are classified based on their proximity to the pre-classified samples in the feature space. It should be noted that manual or semiautomatic training is normally a required step in k-NN based methods, and the value of k (number of classes) has to be determined in advance, either interactively [14] or empirically [7].

One should note that in the class-based approaches [7, 14–16, 18], a training procedure, to either calibrate the classifier parameters or to choose the tissue class representatives, is normally required. In order to obtain desired segmentation results, the testing data sets are also expected to be highly similar to the training sets, ideally from the same group. Outlier-based models [6–10] relax the training requirement, but they usually subsume a thresholding step. Those thresholds, critical for segmentation performance and system reproducibility, usually require certain prior to be set up precisely, which are often difficult to be determined.

Image segmentation is the process of partitioning a digital image into non-overlapped homogeneous regions with respect to some characteristics, such as gray value, motion, texture, etc. Image segmentation is used in various applications like medical imaging, locating objects in satellite images, face recognition, traffic

control systems, and machine vision, etc. [19]. Several techniques for image segmentation have been proposed [20]. They can be classified into region based approaches [21, 22] and edge detection based approaches [23]. In the present work, we are focused on the region based approach using fuzzy clustering algorithm (soft clustering), instead of hard clustering strategies. In the latter, each data point is assigned to only one cluster, while in soft clustering each data point belongs to all clusters with different degrees of membership, thus taking a better account for poor contrast, overlapping regions, noises, and intensity inhomogeneities [24].

3 Proposed Approach

In classical methods, each voxel of the brain is assigned to one of four following classes: WM, GM, CSF, or MS lesions [10]. The Fig. 1 shows the processing sequence proposed for the segmentation of MS lesions. The images are noisy, the inhomogeneities are corrected and all images are registered in the same space. So, our segmentation algorithm can be decomposed into three main steps:

1. Segmentation of brain tissues into three classes (WM, GM, CSF)
2. Segmentation of the white matter to extract the atypical data
3. Decision-making

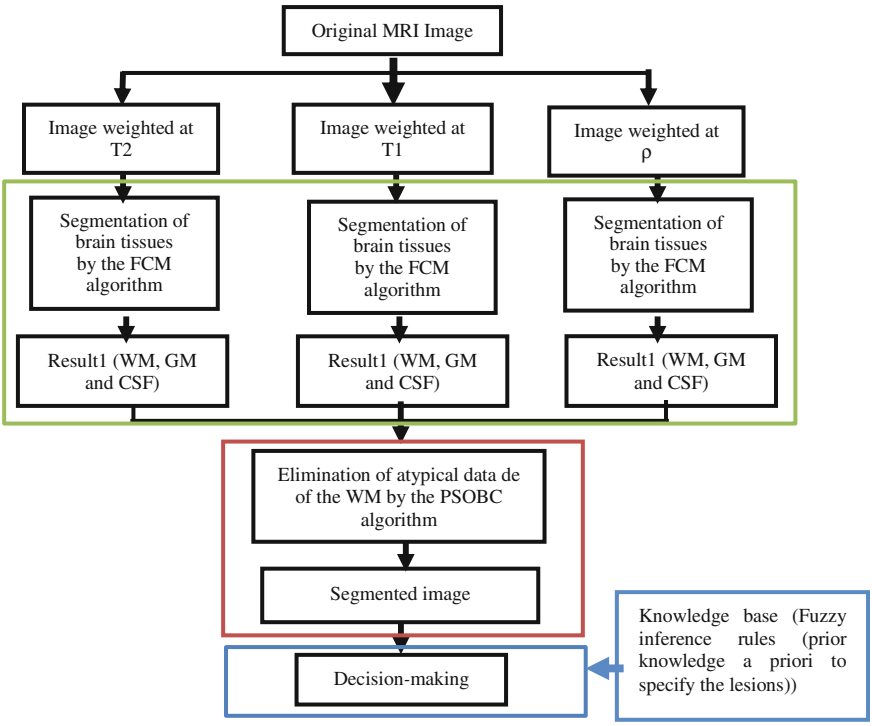

Fig. 1 General architecture of the steps of the automatic segmentation of MS lesions

3.1 Segmentation of the Brain Tissues

The segmentation of the brain tissues into different compartments (white matter (WM), gray matter (SG) and cerebrospinal fluid (CSF)) is a key step in our study. The outcome of this segmentation serves as the basis for implementing lesion-handling based strategies.

The first question we faced in order to achieve this task is whether a supervised or a non-supervised algorithm will be employed for this purpose.

The use of a supervised algorithm requires a learning database for each class and each patient, which restricts applicability of no such labelled data is fully available as reported in [25]. Given the context of our study, we have chosen a non-supervised based approach.

Fuzzy c-means algorithm

Motivation grounds. Motivated by its reported success in various fields, i.e., agricultural engineering, astronomy, chemistry, geology, image analysis, medical diagnosis [26, 27], its reduced complexity, easy implementation, especially for large data but also its blurring (integration degree of membership) [28], we advocate in this paper the use of fuzzy c-means (FCM) approach for clustering, which consisted in our case in separating the three classes (white matter (WM), gray matter (SG) and cerebrospinal fluid (CSF)). On the other hand, the FCM algorithm has been widely used for segmentation brain images, regardless of the modality and the type of acquisition (mono or multimodal) and many studies have been performed including imaging magnetic resonance [24, 29, 30].

Formulating of FCM algorithm. FCM is a fuzzy clustering method based on the minimization of a quadratic criterion where clusters are represented by their respective centers [31]. More specifically, for a set of data patterns $X = \{x_1, x_2, \ldots, x_N\}$ the fuzzy c-means clustering algorithm allows us to partition the data space, by calculating the centers of classes (c_i) and the membership matrix (U), by minimizing an objective function J with respect to these centers and membership degrees

$$J = \sum_{i=1}^{C} \sum_{j=1}^{N} \left(u_{ij}\right)^{m} d^2\left(x_j, c_i\right) \tag{1}$$

Under constraints:

$$\forall j \in [1, N]: \sum_{i=1}^{C} u_{ij} = 1 \; \forall i \in [1, C], \forall j \in [1, N]: u_{ij} \in [0, 1] \tag{2}$$

where

$U = [u_{ij}]_{C \times N}$ is the membership function matrix,

$d(x_j, c_i)$ is the metric which calculates the distance between the element x_j and the center of cluster c_i,

C is the number of clusters,

N is the number of data,
m is the degree of fuzziness ($m > 1$).

The problem of minimizing the objective function (1) under the constraints (2) is solved by converting the problem to an unconstrained one using the Lagrange multiplier. Both centers of classes and membership degrees cannot be found directly at the same time, so an alternating procedure is used. Firstly, the prototype of classes are fixed arbitrary to find the membership degrees, secondly, the membership degrees are fixed to find the centers corrected. These two steps are alternatively repeated until convergence is attained.

The fuzzy c-means clustering algorithm proceeds according to Algorithm 1.

Algorithm 1

Require: Set values for the number of clusters C, the degree of fuzziness $m>1$ and the error ε.

1: Initialize randomly the centers of clusters $c_i^{(0)}$.

2. k $\leftarrow$ 1

3. **repeat**

4. Calculate the membership matrix $U^{(k)}$ using the centers $C_i^{(k-1)}$:

$$u_{ij}^{(k)} \leftarrow \left[\sum_{I=1}^{C} \left(\frac{d\left(x_j, c_j^{(k-1)}\right)}{d\left(x_j, c_I^{(k-1)}\right)} \right)^{\frac{2}{(m-1)}} \right]^{-1}$$

5. Update the centers $c_i^{(k)}$ using $U^{(k)}$: $c_i^{(k)} \leftarrow \dfrac{\sum_{j=1}^{N} (u_{ij}^{(k)})^m .x_j}{\sum_{j=1}^{N} (u_{ij}^{(k)})^m}$

6. k $\leftarrow$ k+1

7. **until** $\left\| C_i^{(k)} - C_i^{(k+1)} \right\| \leq \varepsilon$

8. **Return** c_i the centers of clusters and the membership degrees u_{ij}

In image segmentation, x_i can represent the gray value of the ith pixel, N is the number of pixels of the image, C is the number of the regions (clusters), $d^2(x_i, c_j)$ is the Euclidean distance between the pixel x_i and the center c_j and u_{ij} is the membership degree of pixel x_i in the jth cluster.

3.2 Segmentation of the White Matter

Although it is not always correlated with the clinical disability as shown in other studies [32, 33], the load lesional constitutes the primary indicator of inflammatory phenomena. However, the infringement predominantly inflammatory present in the WM is probably in relationship with the mechanisms of degeneration and achievement, axonal. As well, the measurement of the load lesional informs us about the degree of achievement of the WM in the course of the disease.

Particle swarm optimization algorithm. The next stage in our methodology is the segmentation of the Multiple Sclerosis lesions. although the segmentation of the multiple sclerosis lesions provides an excellent contrast for the different tissues of the brain parenchyma (white matter, grey matter, CSF). The lesions of the multiple sclerosis are not always well contrasted and their segmentation has become more difficult due to the partial volume with the surrounding tissues. In order to elaborate a segmentation system which accommodates our large variety of images, we consider the segmentation as an optimization problem. The latter makes use of *particle swarm optimization (PSO) based algorithm.* This is motivated by: its simplicity and proven efficiency in similar other segmentation tasks as reported in [34]. Besides, its rapid convergence and ability to deal with high dimension dataset, which enable to fly around the solution space effectively, have been pointed out in [35, 36].

More formally, particle swarm optimization (PSO) is a population-based stochastic optimization algorithm proposed for the first time by Kennedy and Eberhart [37], inspired by bird flocking and fish schooling. The problem is tackled by considering a population (particles), where each particle is a potential solution to the problem. Initial positions and velocities of the particles are chosen randomly. In the commonly used standard PSO, each particle's position is updated at each iteration step according to its own personal best position and the best solution of the swarm. The evolution of the swarm is governed by the following equations:

$$V^{(k+1)} = w.V^{(k)} + c_1.rand_1.\left(Pbest^{(k)} - X^{(k)}\right) + c_2.rand_2.\left(Gbest^{(k)} - X^{(k)}\right) \quad (3)$$

$$X^{(k+1)} = X^{(k)} + V^{(k+1)} \quad (4)$$

where

X is the position of the particle,
V is the velocity of the particle,
W is the inertia weight,
Pbest is the best position of the particle,
Gbest is the global best position of the swarm,
$rand_1$, $rand_2$ are random values between 0 and 1,
c_1, c_2 are positive constants which determine the impact of the person al best solution and the global best solution on the search process, respectively,
k is the iteration number.

PSO-Based Image Clustering. In the context of clustering, a single particle represents the C cluster centroid vectors. That is, each particle x_i is constructed as follows:

$$X_i = (x_{i1}, \ldots, x_{ij}, \ldots, x_{iC}) \tag{5}$$

where x_{ij} refers to the j-th cluster centroid vector of the i-th particle in cluster *Cij*. Therefore, a swarm represents a number of candidate clustering's for the current data vectors. The fitness of particles is easily measured as the quantization error,

$$J_e = \frac{\sum_{j=1}^{C} \left[\sum_{\forall x_i \in C_j} d(x_i, c_j) \right] / N_j}{C} \tag{6}$$

where

$$d(x_i, c_j) = \sqrt{\sum_{k=1}^{N_d} (x_{ik} - c_{jk})^2} \tag{7}$$

And

- N_d denotes the input dimension, i.e. the number of parameters of each data vector
- N denotes the number of WM image pixels
- C denotes the number of cluster centroids (as provided by the user)
- x_i denotes the coordinates of pixel i
- c_j denote the means of cluster j.
- N_j is the number of pixels in C_j

The PSO based image clustering algorithm is summarized below

Algorithm 2

1. Initialize each particle to contain C randomly selected cluster means.
2. For t = 1 to t_{max} do
   (a) For each particle i do
   (b) For each pixel x_i
   - calculate $d(x_i, c_{ij})$ to all cluster centroids using equation (7)
   - assign x_i to cluster C_{ij} where
     $$d(x_i, c_{ij}) = \min_{\forall k=1,\ldots,C} \{d(x_i, c_{ik})\}$$
   - calculate the fitness using equation (6).

   (c) Update the global best and local best positions
   (d) Update the cluster centroids using equations (3) and (4).

where t_{max} is the maximum number of iterations.

3.3 Decision-Making

The last step consists in the decision-making concerning the belonging of a voxel of the white matter to a class of the MS disease. The MS lesions appear in hypo and hyper-signal in comparison to the WM according to the MRI methods. The weighted images in T2 and PD underline the myelin component in the lesions characterized by the edemas with hyper-intense appearance in comparison to the white matter. Furthermore, the method T1 underlines the irreversible destruction of the tissues with the appearance in the white matter of persistent "*black holes*" (Hypo-signal) [38]. For this purpose, we propose the use of the Mamdani's fuzzy inference process. This fuzzy model is composed of:

Fuzzification stage (Fig. 2). The system has two inputs, the weighting contrast of MRI and the type of the voxels' signal. And a signal of output which diagnose the Multiple Sclerosis disease.

The steps of *fuzzification* consist in setting the belonging functions, the steps of which are:

1 To set the *linguistic variables*
2 To set the fuzzy quantifiers (Number of the *linguistic values);*
3 To assign a digital signification to each fuzzy quantifier: *belonging function*

For the fuzzification of the contrast, we choose three fuzzy intervals and belonging functions of the Gaussian types. Figure 3 shows the fuzzy repartition of contrast input variable.

For the fuzzification of signal's type, we choose two fuzzy intervals and belonging functions of Gaussian types. Figure 4 shows the fuzzy repartition of the input variable of signal's type.

For the output variable, we choose three fuzzy intervals and Gaussian membership functions, which define predicates: *low, normal and high* of the MS disease in comparison to the white matter. Figure 5 shows the fuzzy repartition of the output variable of the decision of the MS disease.

Fuzzy rule base. In the view of intuitive interpretation of the input variables, some fuzzy rules can be set up manually, for instance:

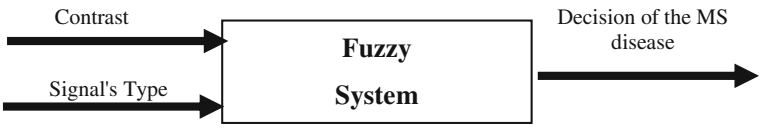

Fig. 2 Diagram of fuzzy system of the MS disease

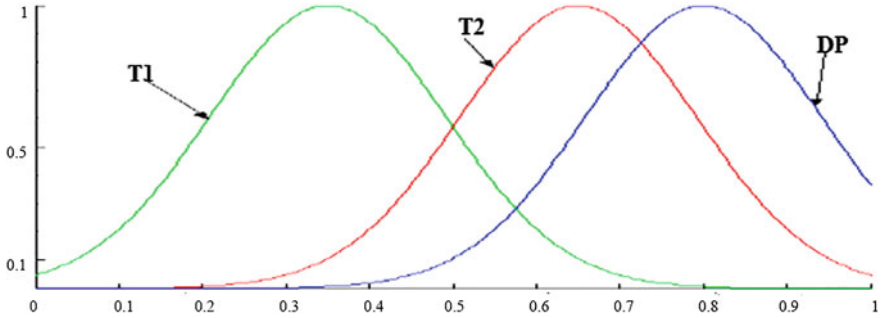

Fig. 3 Fuzzy repartition of contrast input variable

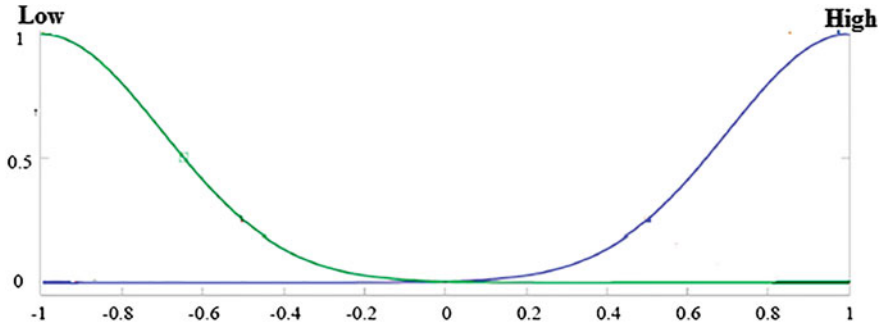

Fig. 4 Fuzzy repartition of input variable of signal's type

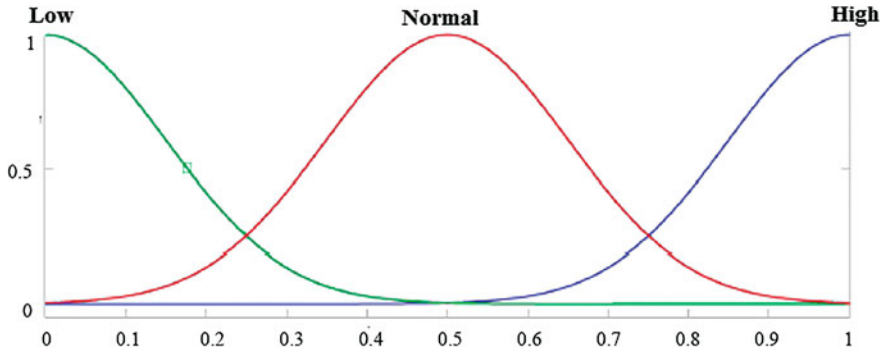

Fig. 5 Fuzzy repartition of the output variable giving the decision of the MS disease

Table 1 Fuzzy rule base

Signal/Sequence	T1	T2	PD
High	Low/Normal	High	High
Low	Low	High	High
High after injection of gadolinium	Normal	High	High

Here are ten examples of the rules' base represented in a linguistic form:

1. **If** [(the contrast weighted at T1) and (the zones are of high intensity)] **then** (the MS is low).
2. **If** [(the contrast weighted at T1) and (the zones are of high intensity)] **then** (the MS is normal in comparison to the white matter).
3. **If** [(the contrast weighted at T2) and (the zones are of high intensity)] **then** (the MS is high).
4. **If** [(the contrast weighted at PD) and (the zones are of high intensity)] **then** (the MS is high).
5. **If** [(the contrast weighted at T1) and (the zones are of low intensity)] **then** (the MS is low).
6. **If** [(the contrast weighted at T2) and (the zones are of low intensity)] **then** (the MS is high).
7. **If** [(the contrast weighted at PD) and (the zones are of low intensity)] **then** (the MS is high).
8. **If** [(the contrast weighted at T1) and (the zones are of high intensity after injection of gadolinium)] **then** (the MS is normal in comparison to the WM).
9. **If** [(the contrast weighted at T2) and (the zones are of high intensity after injection of gadolinium)] **then** (the MS is high).
10. **If** [(the contrast weighted at PD) and (the zones are of high intensity after injection of gadolinium)] **Then** (the MS is high).

Table 1 summarizes the set of exhibited fuzzy rules.

The selected inference method is Mamdani's method. Consequently, the operator is realized by the calculation of the minimum, whiles the operator OR is realized by the calculation of the maximum.

The *defuzzification* step is done using the method of calculating the center of attraction.

4 Results and Discussion

To validate the developed method, we relied on the BrainWeb database (http://www.bic.mni.mcgill.ca/brainweb/). This database was chosen as it is frequently used in the literature and thus allows providing an easier comparison with alternative methods proposed in literature.

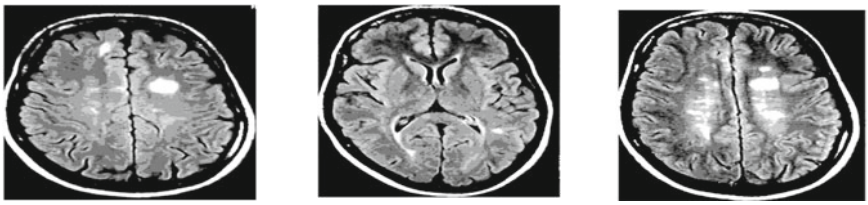

Fig. 6 Original Images

The actual images on which we worked were acquired as part of the collaboration between LSI laboratory (Laboratory Intelligent Systems: image and signal team) Ferhat Abbas University of Setif and LAMIH UMR CNRS 8201 (Laboratory of Industrial and Human Automation control, Mechanical engineering and Computer Science) University of Valenciennes Cedex 9 France (Figs. 5 and 6).

4.1 Analysis of the Results

It concerns the images weighted at T1, T2 and Proton density (Pd) for different old patients (Pixel size = 1 mm, matrix size 512 × 512). The images are in the form of DICOM (*Digital Imaging and Communications in Medicine*). The selection of the proposed noise on site BrainWeb is between 0 and 9 % and that of the heterogeneity of the setting values between 0 and 40 %. The brain segmentation was successfully applied on some real images, the results are shown in the following figures

Step 1: segmentation of tissues (WM, GM and CSF)

The Fig. 7 show the segmentation by the FCM algorithm for the T2 weighted image in order to obtain a characterization of the different healthy tissues (White matter, Grey matter and cerebrospinal fluid)

To compare the performance of these images, we compute different coefficients reflecting how well two segmented volumes match. We used different performance measures:

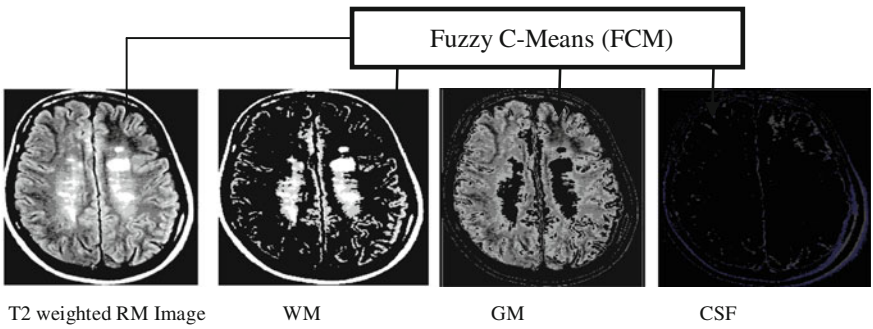

Fig. 7 Image T2 segmented by FCM

Table 2 Comparison of segmentation results

	T1		T2		PD	
	SI	*ovrl*	*SI*	*ovrl*	*SI*	*ovrl*
WM	0.93	0.90	0.96	0.93	0.83	0.76
GM	0.86	0.83	0.95	0.92	0.80	0.70
CSF	0.83	0.67	0.94	0.90	0.78	0.58

$$Overlap \quad (ovrl) = \frac{TP}{TP + FN + FP} \tag{8}$$

$$Similarity \quad (SI) = \frac{2.TP}{2.TP + FN + FP} \tag{9}$$

where TP and FP stand for true positive and false positive, which were defined as the number of voxels correctly and incorrectly classified as brain tissue by the automated algorithm. TN and FN stand for true negative and false negative, which were defined as the number of voxels correctly and incorrectly classified as non-brain tissue by the automated algorithm. The comparative results are presented in Table 2 below:

The results in Table 2 show a considerable improvement for all tissues using T2 than T1 and PD.

Step 2: segmentation of the white matter by PSOBC

The use of PSOBC allows us to eliminate the atypical data of the white matter for each image (T1, T2, PD) as exhibited in Fig. 8 for image T2.

Table 3 summarizes the segmentation outcome by PSOBC

The results obtained by PSOBC are very satisfactory and well confirm the validity of the algorithm, its ease of implementation gives it a substantial advantage. We have made an improvement in optimizing the white matter and atypical data (Table 4).

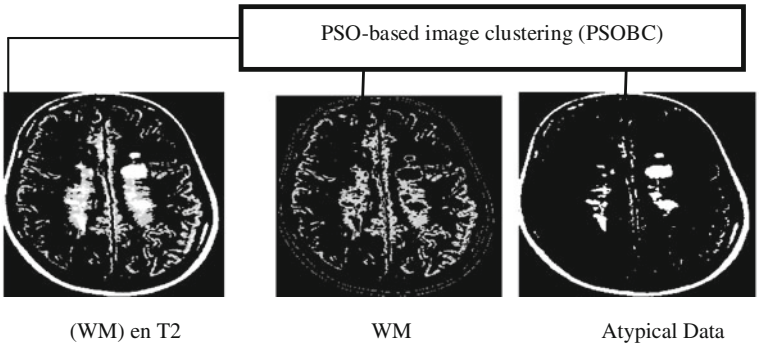

Fig. 8 WM of the image T2 segmented by PSOBC

Table 3 Comparative results

	T1		T2		PD	
	SI	*ovrl*	*SI*	*ovrl*	*SI*	*ovrl*
Atypical Data	0.92	0.93	0.97	0.94	0.95	0.93
WM	0.90	0.87	0.96	0.93	0.91	0.81

Table 4 Result of the defuzzification of the atypical data of the different sequences

	T1	T2	PD
MS lesions	MS is normal	SEP is high	SEP is normal

Step 3: **Decision-making**

However, in complex structure, we can not make a final decision because of the blur. For this, the selected inference method is Mamdani's method. Consequently, the operator is realized by the calculation of the minimum, whiles the operator OR is realized by the calculation of the maximum.

The following table presents the results of defuzzification:

The decision-making depends always on the expertise, the patient suffers from the multiple sclerosis and the MS lesions are detected in all the sequences by a normal or a high characterization.

4.2 Experimental Results

The Fig. 9 shows the results obtained after segmentation of the images (a) weighted T2 on axial plane. The images (b), (c), (d) and (e) are the results of segmentation realized by the expert, FCM, PSOBC and the approach successively proposed.

The results of each stage of the segmentation are presented on a sectional level (Fig. 6) in which the localization allows distinguishing three separated classes of the tissue:

- GM (Pallidum, Putamen, caudate nucleus, thalamus and cortex)
- WM (brain parenchyma).
- CSF (subarachnoid space, lateral ventricles and V3).

The interpretation of our results is done by an expert (hospital center of Ain Naadja Algiers) on simulated and real images. By analyzing the images of the Fig. 9, the expert has established the following statement:

- **Image (b)**: The interpretation of the classes is totally improved in relation to (FCM, PSOBC), we notice the distinction between the 03 classes of the brain and the class of the pathology SEP.
- **Image (c)**: The class CSF does not conform to the class of the original image. The lack of information about the small grooves (image (a)) and the poor

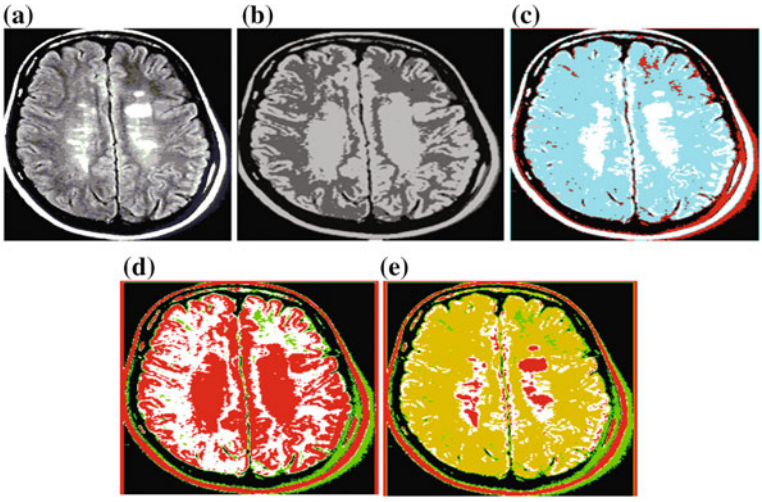

Fig. 9 Pathological image (**a**) and its segmentation gotten by (**b**) segmentation by the expert; **c** FCM; **d** PSOBC and **e** Proposed approaches

discrimination CSF/GM make that the segmented CSF class does not well represent the fluid distribution. The distributions of the WM and GM get closer to those given by the original image. The detection of the pathology is indicated according to the expert but the details are not well expressed.

- **Image (d)**: PSOBC is unsuitable in this segmentation in relation to the image (o).
- **Image (e)**: the proposed approach brings a great performance to the segmentation for the three classes and especially for the fourth one which is the pathology that specifies well the size and the details about this later.

We compare the T2 weighted RM Images between the segmentation by the segmentation realized by the expert, FCM and PSOBC for a given time of acquisition and the segmentation by the proposed approach.

The results of the Table 5 and the Fig. 10 underline the advantages of the proposed approach in comparison to the segmentation by FCM and PSOBC for all tissues CSF, WM, GM and MS lesions.

Table 5 Comparison of the results gotten by different algorithms

	GM (%)	CSF (%)	WM (%)	Lesions (%)
Segmentation by the expert	93	69	95	97
FCM	71	55,9	79.6	74
PSOBC	80,2	64	85	68
Proposed approach	88,7	66	90,5	95,8

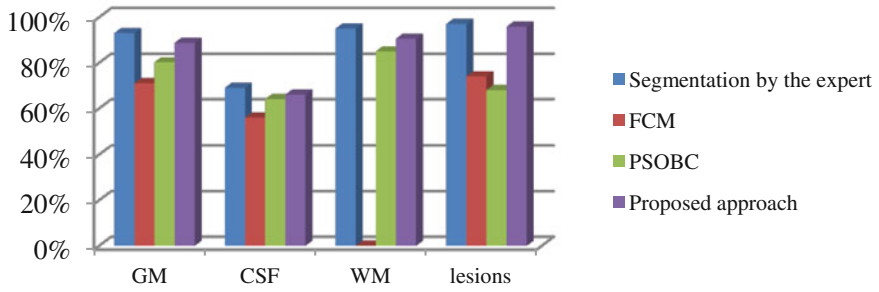

Fig. 10 Performance measures of the results gotten by different algorithms

5 Conclusion

In this article, we have proposed a new automatic approach of segmentation of the MS lesions' images. Two reasons explain their difficulties:

1. The first is that there is a very wide variety of abnormal tissues which are different in their size, shape, position and composition.
2. The second reason is that the datum issued from the MRI acquisition is sensitive to the noise background noise and to the sampling collection.

We have firstly split up the process of automatic segmentation of the MS lesions into three fundamental stages:

Firstly, we segmented the brain into regions by using the algorithm FCM (Fuzzy C-Means) in order to obtain the characterization of the different healthy tissues (White matter, Grey matter and cerebrospinal fluid (CSF). Secondly, we eliminated of the atypical data of the white matter by the optimization algorithm PSOBC (Particle Swarm Optimization -Based image Clustering). Finally, in the framework of our application on the MS disease, we used a Mamdani-type fuzzy model to make decision of the MS disease. We presented the results of our work consisting in the use of an algorithm for the segmentation if medical images in order to improve the quality of the MS lesions' detection. The good quality of our solutions depends on the fact that:

- It is a method totally automatic due to the modeling of the *prior* knowledge of the neuroradiology experts. the fuzzy theory is important for modeling the human knowledge using the mathematical functions and to solve the effect of the partial volume of the MRI.
- It satisfies the application's constraints due to the automaticity and the different final results which may be provided by the fuzzy 3D reconstruction.
- Its performance is better than the performance of the supervised method.
- It is a system based on fuzzy and optimization theory
- It is efficient on 2 types of tissues at least.

References

1. Miller, D.H.: Biomarkers and surrogate outcomes in neurodegenerative disease: lessons from multiple sclerosis. NeuroRX. **1**(2), 284–294 (2004)
2. Daniel, G.-L., Sylvain, P., Douglas, A., Louis, C., Christian, B.: Trimmed-likelihood estimation for focal lesions and tissue segmentation in multisequence MRI for multiple sclerosis. In: IEEE Transactions on Medical Imaging, Institute of Electrical and Electronics Engineers (IEEE) (2011)
3. Jason, E.H., Brian, N., Sunanda, M.: An information theoretic approach via IJM to segmenting MR images with MS lesions. In: IEEE 27th International Symposium on Computer-Based Medical Systems (2014)
4. Barkhof, F.: The clinico-radiological paradox in multiple sclerosis revisited. Current Opinion in Neurology, vol. 15, pp. 239–245. 3, (2002)
5. Lucchinetti, C.F., Parisi, J., Bruck, W.: The pathology of multiple sclerosis. Neurol. Clinics **23**, 77–105 (2005)
6. Van Leemput, K., Maes, F., Vandermeulen, D., Colchester, D., Suetens, P.: Automated segmentation of multiple sclerosis lesions by model outlier detection. IEEE TMI **20**(8), 677–689 (2001)
7. Anbeek, P., Vinchen, K.L., van Osch, M.J.P., Bisschops, R.H.C., van der Grond, J.: Probabilistic segmentation of white matter lesions in MR imaging. NeuroImage **21**, 1037–1044 (2004)
8. Souplet, J.C., Lebrun, C., Anyche, N., Malandain, G.: An Automatic Segmentation of T2-FLAIR Multiple Sclerosis Lesions. 3D Segmentation in the Clinic: A Grand Challenge II: MS lesion segmentation (2008)
9. Dugas-Phocion, G., Gonzalez, M.A., Lebrun, C., Chanalet, S., Bensa, C., Malandain, G., Ayache, N.: Hierarchical Segmentation of Multiple Sclerosis Lesions Multi-Sequence MRI. ISBI'08
10. Garcia-Lorenzo, D., Prima, S., Morrissey, S.P., Barillot, C.: A Robust Expectation-Maximization Algorithm for Multiple Sclerosis Lesion Segmentation. Segmentation in the Clinic: A Grand Challenge II: lesion segmentation (2008)
11. Bricq, S., Collet, Ch., Armspach, JP.: Markovian segmentation of 3D brain MRI to detect multiple sclerosis lesions. In: IEEE international conference on image processing, ICIP'2008, pp. 733–736 (2008)
12. Neykov, N., Neytchev, P.: A robust alternative of the of the Maximum Likelihood Estimator. COMPSTAT—Short Communications. Dubrovnik, Yugoslavia, pp. 99–100 (1990)
13. Prastawa, M., Guido G.: Automatic MS Lesion Segmentation by Outlier Detection and Information Theoretic Region Partitioning. 3D Segmentation in the Clinic: A Grand Challenge II: MS lesion segmentation (2008)
14. Wu, Y., Warfield, S.K., Tan, I.L., Wessl III, W.M., Meier, D.S., Van Schijndel, R.A., Barkhof, F., Guttmann, C.: Automated segmentation of multiple sclerosis lesion subtype with multichannel MRI. NeuroImage **32**, 1025–1215 (2006)
15. Tu, Z., Narr, K., Dinov, I., Dollar, P., Thompson, P., Toga, A.: Brain anatomical structure parsing by hybrid discriminative/generative models. IEEE TMI (2008)
16. Morra, J. Tu, Z., Toga, A., Thompson, P.: Automatic Segmentation of MS Lesions Using a Contextual Model for the MICCAI Grand Challenge. 3D Segmentation in the Clinic: A Grand Challenge II: MS lesion segmentation (2008)
17. Anbeek, P., Vinchen K.L.. Viergever, M.A.: Antomated MS-Lesion Segmentation by K-Nearest Neighbor Classification. 3D Segmentation in the Clinic: A Grand Challenge II: MS lesion segmentation (2008)
18. Bazin, P.L., Pham, D.L.: Statistical and topological atlas based brain image segmentation. MICCAI (2007)
19. Christ, M., Parvathi, R.M.S.: Magnetic resonance brain image segmentation, intern. J. VLSI Design Commun. Syst. **3**, 121–133 (2012)

20. Dey, V., Zhang, Y., Zhong, M.: A review on image segmentation techniques with remote sensing perspective. In: Wagner, W., Szekely, B. (eds.) ISPRS TC VII Symposuim-100 Years ISPRS, vol. XXXVII, pp. 31–42, Vienna, Austria (2011)
21. Ciesielski, K.C., Udupa, J.K.: Region-based segmentation: fuzzy connectedness graph cut and related algorithms. In: Deserno, T.M. (ed.), Biomedical Image Pressing, Biological and Medical Physics, Biomedical Engineering. Springer, Berlin, Heidelberg, pp. 251–278 (2011)
22. Nakib, A., Oulhadj, H., Siarry, P.: A thresholding method based on two dimensional fractional differentiation. Image Vis. Comput. **27**, 1343–1357 (2009)
23. Papari, G., Petkov, N.: Edge and line oriented contour detection. State of the art. Image Vis. Comput. **29**, 79–103 (2011)
24. Benaichouche, A.N., Oulhadj, H., Siarry, P.: Improved spatial fuzzyc-means clustering for image segmentation using PSO initialization, Mahalanobis distance and post-segmentation correction. Digit. Signal Proc. **23**, 1390–1400 (2013)
25. Bezdek, J., Hall, l., Clarke. L.: Review of MR image segmentation techniques using pattern recognition. Med. Phys. **20**, 1033–1048, 1993
26. Ghosh, S., Kumar, S.: Comparative analysis of K-means and fuzzy C-means algorithms. Int. J. Adv. Comput. Sci. Appl. **4**(4) (2013)
27. Tejwant, S., Manish, M.: Performance comparison of fuzzy C means with respect to other clustering algorithm. Int. J. Adv. Res. Comput. Sci. Softw. Eng. **4**(5) (2014)
28. Bezdek, J.C.: Fuzzy mathematics in pattern classification. Ph.D dissertation, Cornell University, Ithaca, NY, 1973
29. Zouaoui, H., Moussaoui, A.: Clustering par Fusion Floue de Données Appliqué à la Segmentation d'Images IRM Cérébrales. CIIA, vol. 547 von CEUR Workshop Proceedings, CEUR-WS.org (2009)
30. Premalatha. K., Natarajan, A.M.: A New approach for data clustering based on PSO with local search. Comput. Inform. Sci. **1**(4) (2008)
31. Clark, M., Hall, L., Goldgof, D., Clark, L., Velthuizen R., and Silbiger, M.: MRI segmentation using fuzzy clustering techniques. IEEE Eng. Med. Biol. 730–742 (1994)
32. Filippi, M, et al.: Correlations between changes in disability and T2 weighted brain MRI activity in multiple sclerosis. A follow-up study. 2, Neurology, **45**, 255–260 (1995)
33. Barkhof, F.: MRI in multiple sclerosis: correlation with expanded disability status scale (EDSS). Multiple Sclerosis **5**, 283–286 (1999)
34. El Dor, A., Lepagnot, J., Nakib, A., Siarry, P.:PSO-2S optimization algorithm for brain MRI segmentation. In: Genetic and Evolutionary Computing, pp. 13–22. Springer (2014)
35. Selvi, V., Umarani, Dr. R.: Comparative analysis of ant colony and particle swarm optimization techniques. Int. J. Comput. Appl. (0975–8887) **5**(4) (2010)
36. Shi, Y., Eberhart, R.C.: Empirical study of particle swarm optimization, vol. 3, pp. 1945–1950 (1999)
37. Kennedy, J., Eberhart, R.: Particle swarm optimization. In: Proceedings IEEE International Conference on Neural Networks, vol. 4, pp. 1942–1948. Perth, Australia (1995)
38. Aït-Ali, L.S., Prima, S., Edan, G., Barillot. C.: Longitudinal segmentation of MS lesions in multimodal brain MRI. In: 15éme Congrès Francophone AFRIF/AFIA de Reconnaissance des Formes et Intelligence Artificielle (RFIA), Tours, France, Janvier (2006)