Original Article

Feature Selection in Order to Extract Multiple Sclerosis Lesions Automatically in 3D Brain Magnetic Resonance Images Using Combination of Support Vector Machine and Genetic Algorithm

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ABSTRACT

This paper presents a new feature selection approach for automatically extracting multiple sclerosis (MS) lesions in three-dimensional (3D) magnetic resonance (MR) images. Presented method is applicable to different types of MS lesions. In this method, T1, T2, and fluid attenuated inversion recovery (FLAIR) images are firstly preprocessed. In the next phase, effective features to extract MS lesions are selected by using a genetic algorithm (GA). The fitness function of the GA is the Similarity Index (SI) of a support vector machine (SVM) classifier. The results obtained on different types of lesions have been evaluated by comparison with manual segmentations. This algorithm is evaluated on 15 real 3D MR images using several measures. As a result, the SI between MS regions determined by the proposed method and radiologists was 87% on average. Experiments and comparisons with other methods show the effectiveness and the efficiency of the proposed approach.

Key words: *Classification, features selection, genetic algorithm, medical images, multiple sclerosis lesions, support vector machine*

INTRODUCTION

Multiple sclerosis (MS) is a progressive neurological disorder, which is caused by structural damages of axons and their myelin sheathes in the central nervous system. MS lesions present temporal changes in shape, location, and area among patients, and thus it is necessary for radiologists to accurately detect and evaluate MS lesions.[1] However, the accurate assessment of each lesion in magnetic resonance (MR) images would be a demanding and time-consuming task, and also a manual measurement could be subjective and have poor reproducibility. Therefore, a number of semi-automated or automated methods have been proposed for identifying and/or segmenting MS lesions in MR images.

Khayati *et al*.[2] proposed an approach for fully-automated segmentation of MS lesions in fluid attenuated inversion recovery (FLAIR) MR images. The proposed approach, based on a Bayesian classifier, utilizes the adaptive mixtures method (AMM) and Markov random field (MRF) model to obtain and upgrade the class conditional probability density function (CCPDF) and *a priori* probability of each class. A mean value equal to 0.75 was obtained for Similarity Index (SI).

Anbeek *et al*.[3] proposed a novel automatic approach for segmentation of the white matter (WM) lesions in MR images of brain. Their introduced algorithm uses different information, including voxel intensity and the spatial information, to classify voxels by a K-nearest neighbor (KNN) classifier. This technique assigns a probability to each voxel to be a part of WM lesion. The SI, then, is used for the determination of an optimal threshold on the probability map to segment the images. They showed the high accuracy of their approach, in comparison with other methods for similar task. Lorenzo *et al*.[4] suggested an approach that used the information from the proton density (PD), T2-weighted and FLAIR images. This strategy involved cerebrospinal fluid (CSF) and lesion classification using the Parzen window classifier. Image processing, morphological operations and ratio maps of PD and T2-weighted images are used for minimizing false positives. Contextual information is exploited for minimizing the false negative lesion classifications using hidden Markov random field expectation maximization (HMRF-EM) algorithm. Lesions

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are delineated using fuzzy connectivity. Prastawa *et al*.[5] presented a novel, fully-automatic segmentation method for MS lesions in brain MRI that combined outlier detection and region partitioning. The method was based on an atlas of healthy subjects and detected lesions as outliers, without the necessity to use training data with segmented lesions. Ardizzone *et al*.[6] presented a novel approach to detect multiple sclerosis (MS) lesions in T2-and PD-weighted MR images. The core of the proposed method is the use of the two channels fuzzy C-means (FCM) segmentation of data, where the classical FCM approach runs, at first, on two separate spectra. Then, the one-dimensional (1D) distributions of the clusters centers obtained by FCM are composed in the two-dimensionally, which is *a priori* imposed on the two-spectrum segmentation procedure. Admasu *et al*.[7] suggested a method that combined the strengths of the two existing techniques: Fuzzy connectedness and artificial neural networks. From the input MR brain image, the fuzzy connectedness algorithm was used to extract segments which were parts of CSF, WM, or gray matter (GM). Segments of the MR image which were not extracted as part of CSF, WM or GM were processed morphologically, and features were computed for each. These computed features were then fed to a trained artificial neural network, which decided whether a segment was a part of a lesion or not. Admiraal-Behloul *et al*.[8] suggested a fully-automatic segmentation method for quantifying WM hyper intensity in a large clinical trial on elderly patients. Their algorithm combined information from three different MR images including PD, T2-weigted, and FLAIR and FCM algorithm for clustering process. The approach demonstrated very high volumetric and spatial agreement with expert delineation.

In the previous algorithm suggested by the authors of this paper, an automatic approach was introduced for MS segmentation of brain, in MR-T1 and T2 images.[9] The proposed approach was based on a new clustering algorithm named Spatially Constrained Possibilistic Fuzzy C-means (SCPFCM). SCPFCM uses membership, typicality, and spatial information to cluster each voxel. The proposed method relies on an initial segmentation of MS lesions in T1- and T2-weighted images by applying SCPFCM algorithm, and the T1 image is then used as a mask and is compared with the T2 image.

The presented methods use a fixed number of features and the segmentation of different MS lesions are performed with these features. This paper presents a new method that uses dynamically a variable number of features. This approach can use different features for segmenting different MS lesions.

SUPPORT VECTOR MACHINE

The support vector machine (SVM) is a machine learning technique that facilitates linear and nonlinear binary classification. Given a sample, $S = \{(x_i, y_i)\}_{i=1}^{M}$ with $x_i \in X \subseteq R^N$ being a vector of N measurements, $y_i \in \{-1, +1\}$ the corresponding binary class label, and M denoting the number of observations, SVMs infer (learn) from the data of a functional model, $f_\Lambda(x) : X \infty \{-1, +1\}$. This enables estimation of the class membership of novel examples (i.e., observations not contained in *S*). The vector Λ includes the parameters of the classifier which are fitted on *S* in a model building stage (classifier training).

SVMs are inspired by the statistical learning theory.[10] To derive a classification model from *S*, they implement the concept of a maximal margin separation. That is, they strive to maximize the distance between examples that are closest to a linear-decision surface separating the two classes.[11] It can be shown that by maximizing this margin, a bind on the generalization error, i.e., the error on future data, is minimized.[10]

To construct a linear classifier with maximal margin, the norm of the corresponding hyperplane's weight vector, w, has to be minimized, subject to the constraint that training examples of each class reside on opposite sides of the separating surface [Figure 1].

With $y_i \in \{-1, +1\}$, this constraint can be formulated as:[12]

$$y_i(wx_i + b) \geq 1, \quad i = 1, ..., M \tag{1}$$

Examples which satisfy (1) with equality are called support vectors as they define the orientation of the resulting hyper plane. To account for misclassifications (i.e., examples violating (1)), the soft margin formulation[11] introduces continuous slack variables ξ_i. Hence, to build a maximal margin SVM classifier, the following convex quadratic programming problem has to be solved:

$$\begin{aligned} &\min 1/2\|w\|^2 + C\sum_i \xi_i \\ &s.t. y_i(wx_i + b) \geq 1 - \xi_i, \xi_i > 0 \forall i \end{aligned} \tag{2}$$

The primal decision variables w and b define the separating hyper plane so that the resulting classifier takes the form:

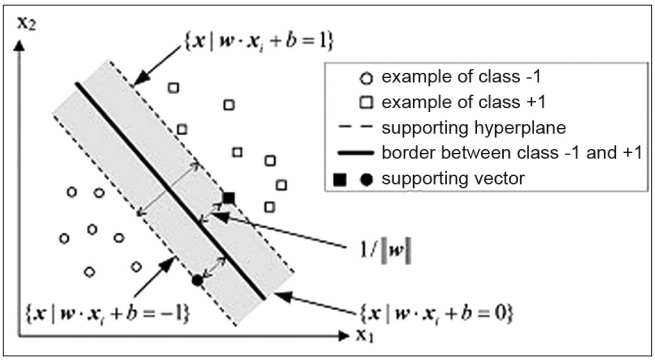

Figure 1: Linear separation of two classes − 1 and + 1 in two-dimensional (2D) space with a support vector machine classifier

$$f_{\Lambda=\{w,b\}}(x) = sign((w^*.x) + b^*), \quad (3)$$

where w* and b* represent the solution of (2).

To construct more general nonlinear decision surfaces, SVMs map the input data into a high-dimensional feature space via an *a priori* chosen mapping function Φ. Constructing a separating hyper plane in this feature space leads to a nonlinear decision boundary in the input space.[9] The capability of SVMs to disclose nonlinear relationships among input variables by projecting the data into a feature space of higher dimension has been demonstrated on several well-known benchmarking datasets.[13] For example, standard nonlinear classification tasks like the exclusive or (XOR) problem, the 2-spiral problem, or the classification of a chess board into black and white regions are solved with SVMs.[11,14,15]

The mapping of the data is accomplished implicitly to avoid resource intensive calculations in the transformed feature space. Consider the dual of (2), with α_i denoting the Lagrangian multipliers:[2-9]

$$L_D = \sum_{i=1}^{l} \alpha_i - \frac{1}{2} \sum_{i,j=1}^{l} \alpha_i \alpha_j y_i y_j (x_i.x_j)$$
$$s.t \quad \sum_{i=1}^{M} \alpha_i y_i = 0; \quad 0 \le \alpha_i \le C \quad \forall i = 1,...,M \quad (4)$$

GENETIC ALGORITHM

A genetic algorithm (GA) is a search heuristic that mimics the process of natural evolution. This heuristic is routinely used to generate useful solutions to optimize and search problems. GAs belong to the larger class of evolutionary algorithms (EA), which generate solutions to optimization problems using techniques inspired by natural evolution, such as inheritance, mutation, selection, and crossover.

In a GA, a population of strings (called chromosomes or the genotype of the genome), which encode candidate solutions (called individuals, creatures, or phenotypes) to an optimization problem, evolves toward better solutions. Traditionally, solutions are represented in binary as strings of 0s and 1s, but other encodings are also possible. The evolution usually starts from a population of randomly generated individuals and happens in generations. In each generation, the fitness of every individual in the population is evaluated, while multiple individuals are stochastically selected from the current population (based on their fitness), and modified (recombined and possibly randomly mutated) to form a new population. The new population is, then, used in the next iteration of the algorithm. Commonly, the algorithm terminates when either a maximum number of generations have been produced, or a satisfactory fitness level has been reached for the population. If the algorithm has terminated due to a maximum number of generations, a satisfactory solution may or may not be reached.[16]

PROPOSED METHOD

The proposed method in the first step preprocesses three-dimensional (3D) T1-weighted, T2-weighted, and FLAIR images of the patient. Then efficient features to extract MS lesions are chosen by using GA. In this step, fitness function is the accuracy of SVM classifier which classifies voxels of images into MS and Non-MS classes. Finally, one set of selected features by GA produce the best segmentation result of MS lesion in the patient image by SVM classifier. Figure 2 shows the block diagram of the presented method in general. The trained SVM classifier, with the selected features, is then used as a segmentation machine for extracting MS lesions in other images.

Preprocessing

Noises and non-uniformity of T1, T2, and FLAIR image are firstly removed by using common techniques. Then, FMRI Software Library (FSL) tools[17] are applied to register T1 and FLAIR images to T2 image by local–global technique. By applying a set of morphological operations, the surrounded area of brain is deleted.

Chromosomes

Chromosomes are coded in binary form in the GA. Each chromosome contains 27 genes and every gene is related to a feature. These features are the intensity of the voxel and eight neighbors of voxel in T1, T2, and FLAIR images. Each '0' gene in the chromosome shows that the related feature is not selected and each '1' gene indicates considering the feature in assessment [Figure 3].

Genetic Algorithm Operators

In the applied GA, the population number is five. Roulette wheel model, single-point crossing operator with 0.8 of crossover rate and mutation operator with 0.01 of mutation rate are used to select proper chromosomes to produce next generation.

SVM Classification

SVM classifier is here used to classify the voxels into MS and Non-MS classes. The SVM classifier is initially trained using a set of images that were manually segmented by a radiologist. With training images used, a set of effective features for MS lesions' extraction are selected. These features are then used to segment MS lesion in patient's image by trained SVM classifier.

Fitness Function

To evaluate each chromosome in the population, SI (Eq. 5) of SVM classifier is used. The SI of SVM classifier shows fitness function, maximization of which is our goal.

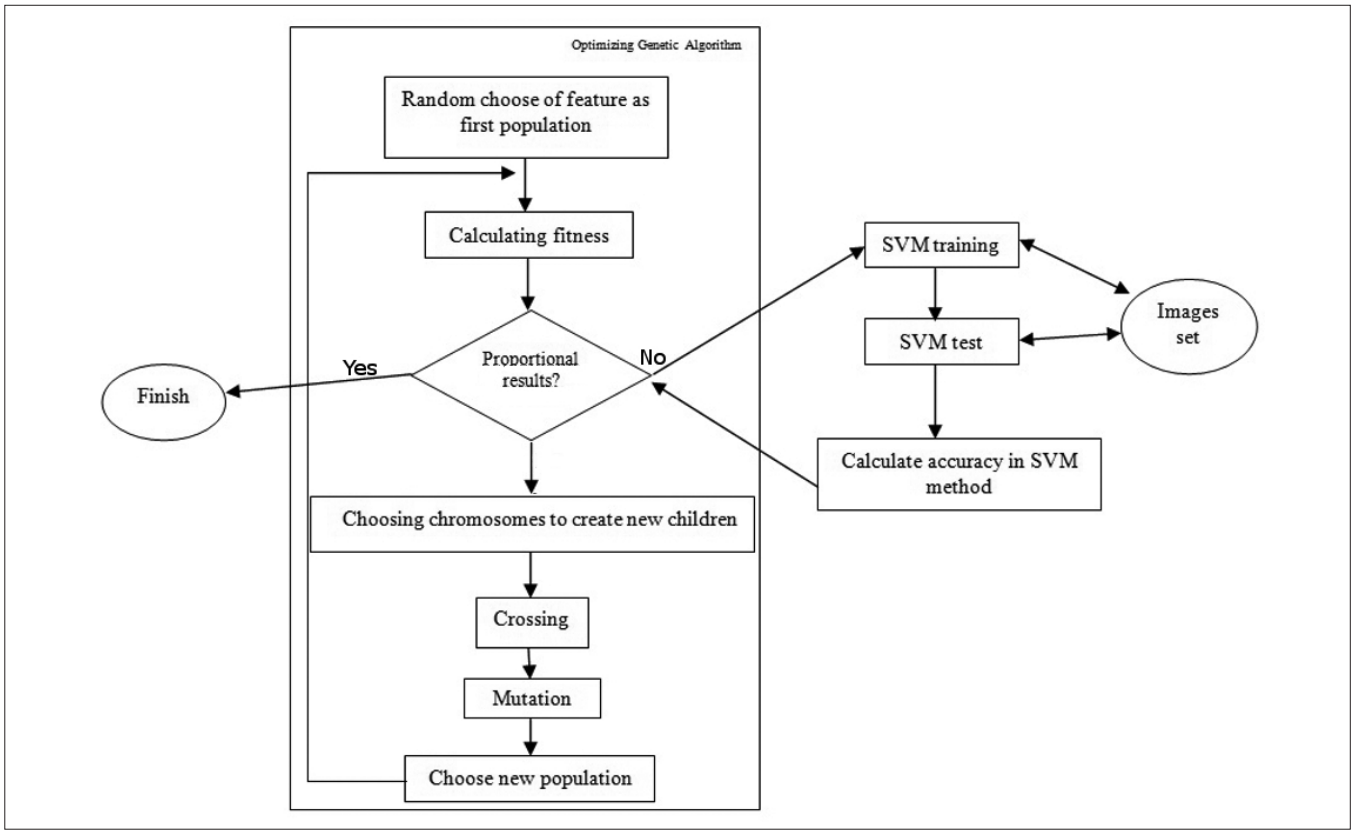

Figure 2: Overview of the proposed method based on combination of genetic algorithm and support vector machine method

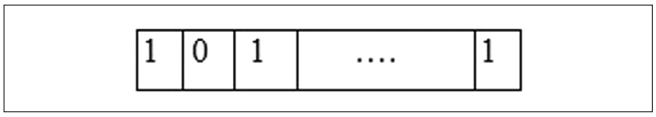

Figure 3: View of a chromosome

VERIFICATION AND RESULTS

MR Imaging

We exert the suggested method on real MR images of 15 patients taken from Imam Khomeini hospital. Images were selected in this study according to the revised McDonald criteria 2005.[18] The size of used images and the intensity of each 3D voxel are $256 \times 256 \times 25$ voxels and $0.97 \times 0.97 \times 4$ mm in order. The location and the size of lesion are different in these 15 patients. Five images are used to train the SVM classifier and ten images are applied as test images. To compare the segmentation of lesions for Patients with different lesion volumes (*LV*), three patient categories: patients with, small ($LV < 4$ cc), moderate (4 cc $< LV < 18$ cc), and large lesion ($LV > 18$ cc) load, in our selected slices, were composed.[8] Accordingly, 4 out of 10 reviewed patients have small lesion, 4 have medium lesion and 2 have large lesion.

Evaluation

Results of the lesion segmentation based on the proposed method are compared with those of gold standard. The SI,[19] overlap fraction (OF), and extra-fraction (EF),[19] are calculated for the selected slices. The SI is a criterion for the correctly classified lesion area relative to the total area of the lesions, in both the gold standard and in the segmented image. The OF and EF specify, respectively, the areas which have been correctly and falsely classified, as lesion areas relative to the lesion area in the gold standard.

$$SI = \frac{2TP}{2TP+FP+FN} \quad (5)$$

$$OF = \frac{TP}{TP+FN} \quad (6)$$

$$EF = \frac{FP}{TP+FN} \quad (7)$$

In these equations, TP stands for true positive voxels, FP for false positive voxels, and FN for false negative voxels. SI and OF for a good segmentation should be close to 1 and EF should be close to 0. Practically, a value for SI, more than 0.7, represents a very good segmentation in this field.[19]

RESULTS

Five images are used for training and 10 images for test.

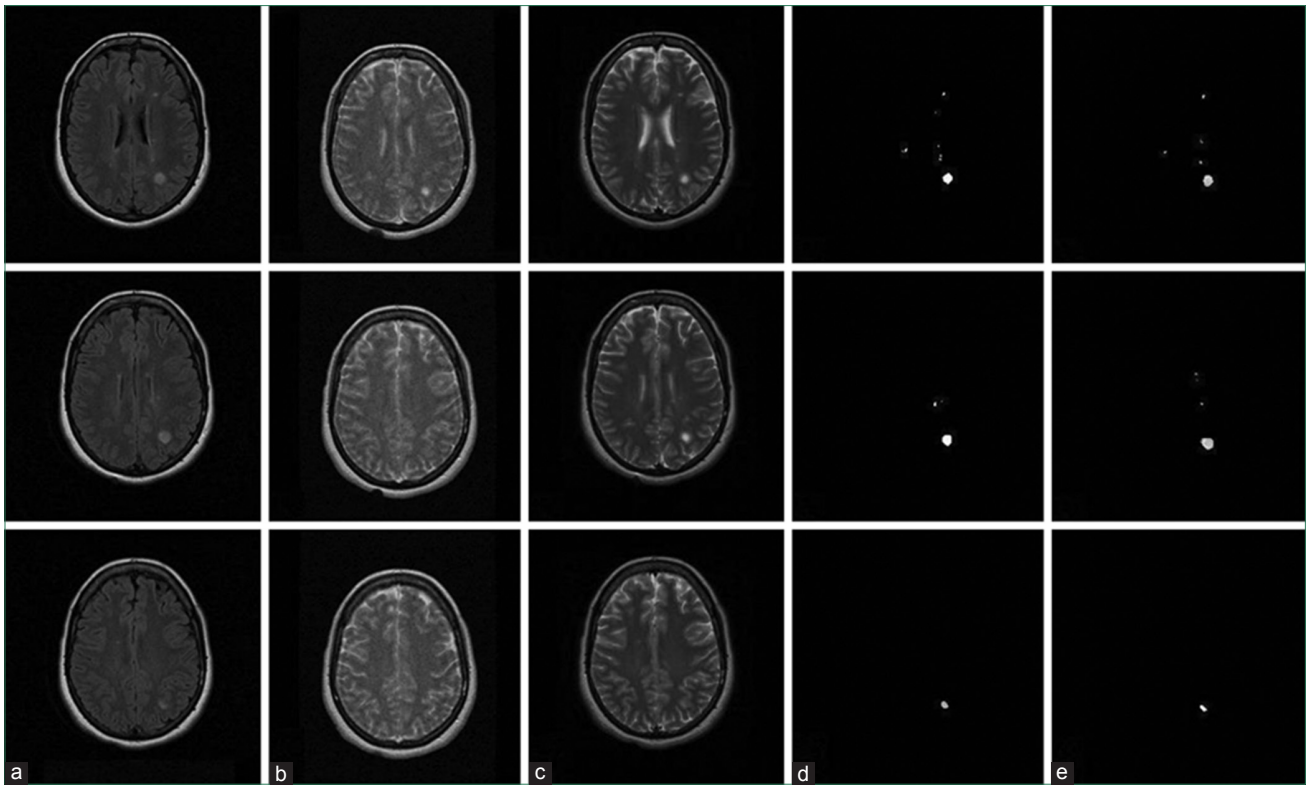

Figure 4: Segmentation of multiple sclerosis lesions in three slices of a real magnetic resonance (MR) images. (a) Original fluid attenuated inversion recovery image; (b) original T2 image; (c) original T1 image, (d) automatic segmentation of MS lesions by genetic algorithm–support vector machine method; (e) manual segmentation of MS lesions

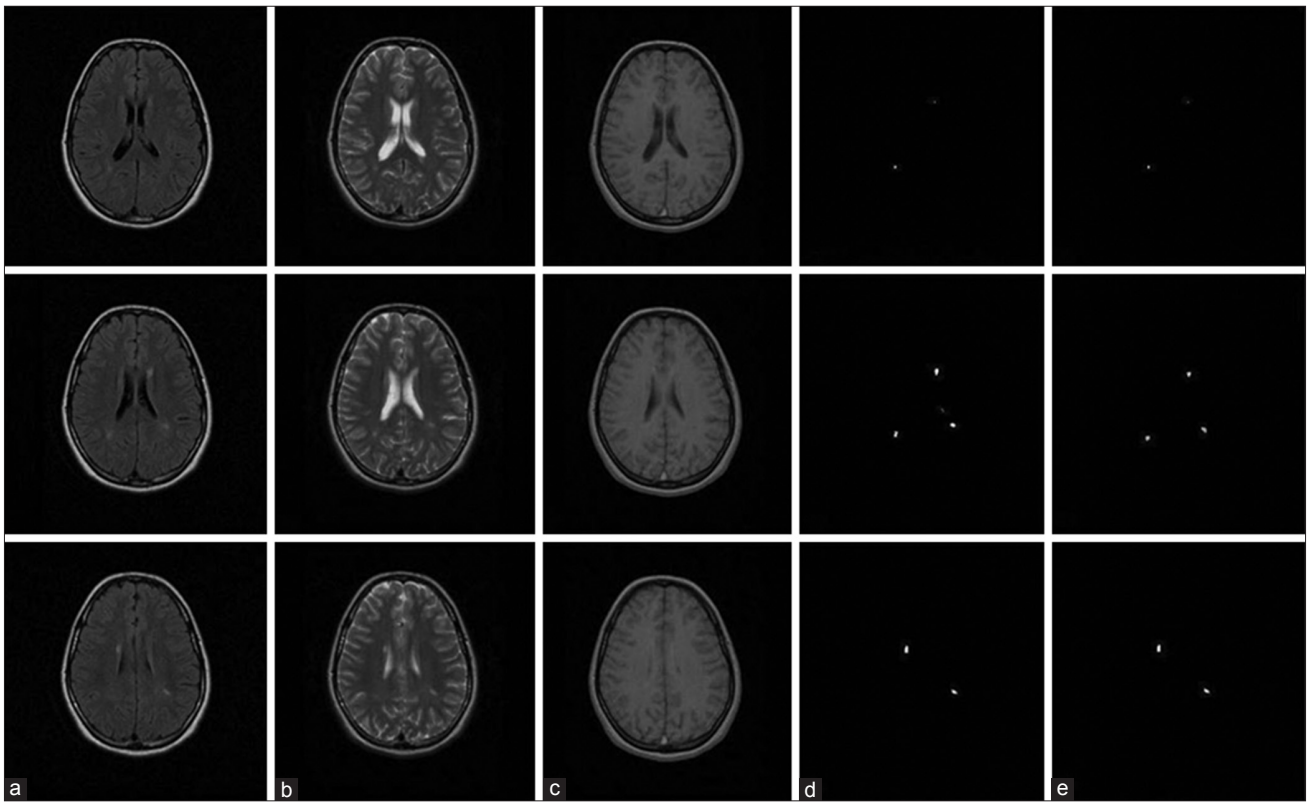

Figure 5: Segmentation of multiple sclerosis lesions in three slices of a real magnetic resonance images. (a) Original fluid attenuated inversion recovery image; (b) original T2 image; (c) original T1 image, (d) automatic segmentation of MS lesions by genetic algorithm–support vector machine method; (e) manual segmentation of MS lesions

Classification results in three and five slices of three real images into two classes of MS lesion and Non-MS lesion are shown in Figures 4-6. To evaluate results, all slices of MR images of 10 patients were classified by a radiologist. The output of every slice is a binary image in which the lesion is distinctive.

DISCUSSION

Compared with previous methods to extract MS lesions, our proposed method produces significantly better results. Images used in this method are the same as those of other methods based on imaging criteria.[18]

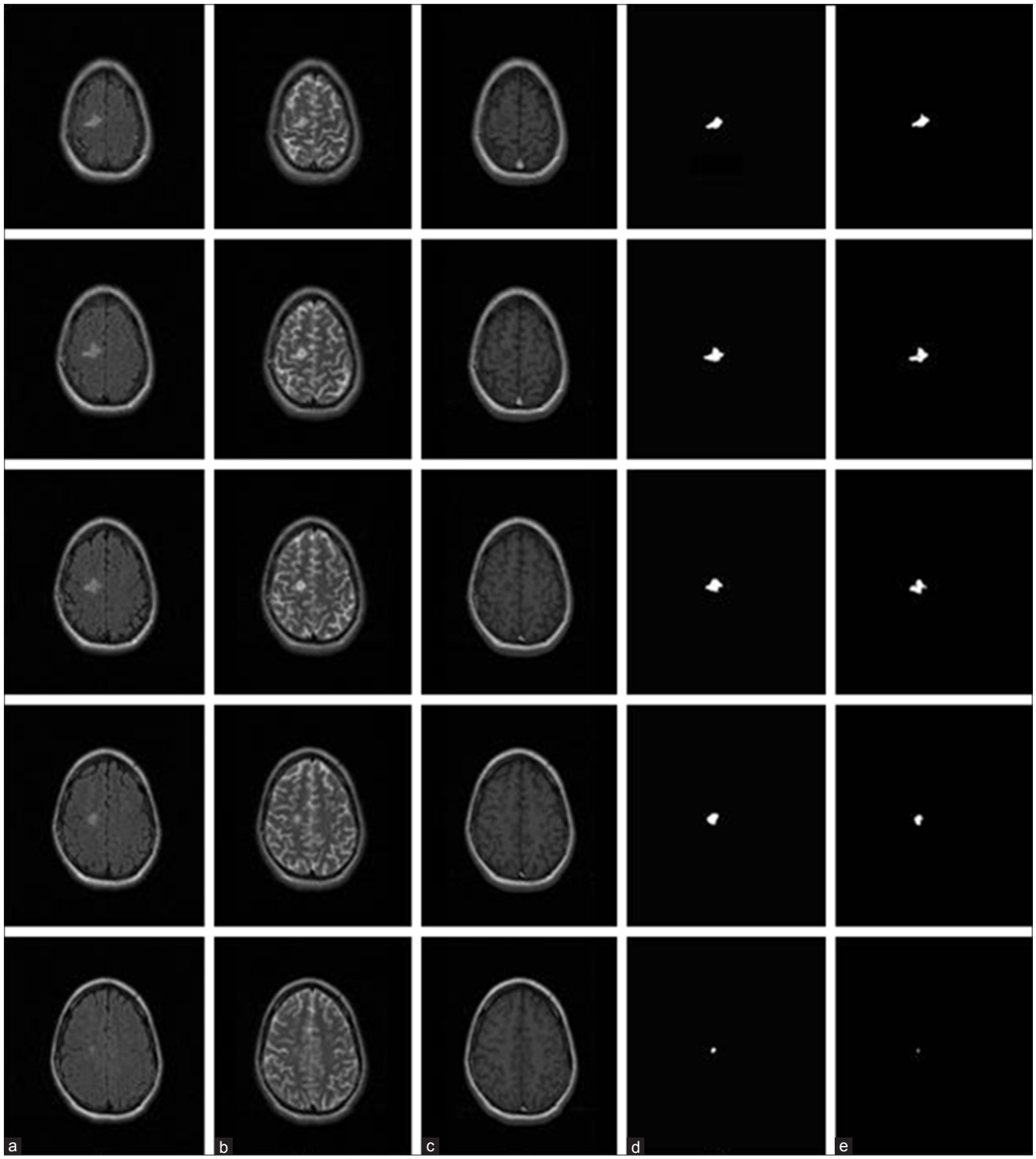

Figure 6: Segmentation of MS lesions in 5 slices of a real MR images. (a) Original FLAIR image; (b) Original T2 image; (c) Original T1 image, (d) Automatic segmentation of MS lesions by GA-SVM method; (e) Manual segmentation of MS lesions

Table 1: Comparison of similarity criteria of real magnetic resonance images which have been concluded genetic algorithm–support vector machine and spatially constrained possibilistic fuzzy C-means algorithms[9]

Algorithm	SI	OF	EF
GA – SVM	87.2	86.9	12.6
SCPFCM[9]	82.6	77.1	10.3

MR – Magnetic resonance; GA – SVM – Genetic algorithm – Support vector machine; SCPFCM – Spatially constrained possibilistic fuzzy C-means; SI – Similarity index; OF – Overlap fraction; EF – Extra-fraction

Table 2: Comparison of proposed method with the previous ones based on similarity index factor

	Khayati, *et al*.[2]	Admiraal-behloul *et al*.[8]	Anbeek *et al*.[3]	Khotanlou, *et al*.[9]	GA–SVM
Small lesion load	0.72	0.7	0.5	0.81	0.80
Moderate lesion load	0.75	0.75	0.75	0.82	0.89
Large lesion load	0.80	0.82	0.85	0.84	0.91
All patients	0.75	0.75	0.80	0.82	0.87

GA–SVM – Genetic algorithm–Support vector machine; SI – Similarity index

It is reminded that these researchers have used manual segmentation for the evaluation of their methods. We, too, used manual segmentation for evaluation. Therefore, comparison of our method with these methods is reasonable.

The quantitative results obtained with genetic algorithm–support vector machine (GA–SVM) and SCPFCM algorithms[9] are provided in Table 1. As it is seen in this table, the means of the calculated similarity criteria for the GA–SVM compared to SCPFCM increased about 4.6%, 9.8%, and 2.3% for SI, OF, and EF, respectively. Table 2 shows the results of several methods. Method,[2] and,[8] are statistical methods and method,[3] is a fuzzy method based on FCM algorithm. Method,[9] is another method presented by the author, based on SCPFCM algorithm and is tested and investigated on the same images. So the offered method is more efficient than the previous methods. The method works better than all the other except,[9] in medium and large lesions proposed method that have better results than the other methods compared with. As it is seen in the Table 2, the segmentation algorithm presented in this paper improves 12%, 12%, 7%, and 5%, the results reported by Khayati *et al*.,[2] Admiraal-Behloul *et al*.,[8] Anbeek *et al*.,[3] and Khotanlou *et al*.,[9] respectively.

CONCLUSION

We presented a new method to select features in order to extract MS lesions based on combination of GA and SVM classification method. This method was compared with the manual method and the results show that this method works better than other methods and is a good choice to find, and initially classify, MS lesions in MR images.

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