Short thesis for the degree of Doctor of Philosophy (PhD)

MS lesion detection via machine learning algorithm based on converting 3D to 2D MRI images by using value of binary pattern classification and computational methods

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1. Introduction

In the twenty first century, there have been various scientific discoveries which have helped in addressing some of the fundamental health issues. Specifically, the discovery of machines which are able to assess the internal conditions of individuals, has been a significant boost in the medical field. Multiple Sclerosis (MS) is a demyelinating disease in which the insulating covers of nerve cells in the brain and spinal cord are damaged. This damage disrupts the ability of the nervous system's parts in various forms to transmit signals, therefore results a wide range of symptoms including physical, mental and psychiatric problems. In this regard, most of the researchers have focused on improving the classification of brain lesions, especially those from MS, which is a relatively difficult task, using different algorithms, but mainly in determining the edge. However, the absence of learning methods have caused complexity and difficulties for having accurate results in the previous works. Therefore, this need motivated us to use various tools of learning methods with a focus on Cellular Learning Automata (CLA) to achieve more accurate results in detection of MS lesions.

Cellular Learning Automata (CLA) is a hybrid model of two, Learning Automata and Cellular Automata, which is a simple

discrete system that can exhibit complex calculations and behavior through simple and local rules. In this study, we aim to propose a new combinational algorithm using Support Vector Machine (SVM) used for classification and cellular learning automata (CLA) to increase the accuracy of MS lesion detection. The objective is to create artificial models using support vector machines (SVM) to classify MS and normal brain MRI images, analyze the effectiveness of these models and their potential to use them in multiple sclerosis (MS) diagnosis. In order to develop such combination method, we start with simple learning methods such as k-means to find MS lesion.

The research was carried out in four stages, respectively, the algorithms are as follows; a) Semi-automatic method and use of K-Means, b) Automatic MS Segmentation Approach Based on Cellular Learning Automata, c) MS Segmentation Approach based on SVM, CLA and K-Means, d) Accurate Simulated Database, 3D MRI to 2D Images, using value of Binary Pattern Classification for MS Detection. The algorithms consist of pre-processing parts, detecting MS-hemispheres, feature extraction, classification and post-processing. In the pre-processing section, the brightness intensity of the normalized images and the brain region are first extracted. Then, to reduce the computational volume, the lesions are diagnosed. The proposed

approach can be considered as a supplementary or superior method for other methods such as Graph Cuts (GC), fuzzy c-means, mean-shift, k-Nearest Neighbor (KNN). We try to see the benefits of having a 3D database but to use 2D vectors only for better comparison and more accurate results. Support vector machines (SVM) can be a useful tool during the multiple sclerosis (MS) disease diagnosis process, however to be able to make better assumptions, more tests are needed.

1.1. Brain MRI images

MRI is one of the successful technologies in the field of medical imaging that has made significant improvements in the quality and speed of imaging in recent years. The waves used in MRI are radio and magnetic waves that do not harm the body. In this way the patient is placed in a very strong magnetic field. This field causes the protons to rotate round that axis (known as precession), so that any proton at any moment in time will be pointing in some direction in the XY plane. These are the protons of atoms in all body tissues (especially the protons in the nucleus of the water molecule) along the lines of the MRI magnetic field. Certain radio waves are then transmitted to the patient's body. These pulsed waves cause the axis of the protons to rotate slightly. At the end of the radio pulse, the axis of the proton rotates again along the lines of the magnetic field. This

reversal generates a new radio wave (electromagnetic) [1]. Secondary radio waves emitted from individual protons are then received by the MRI receivers and transmitted to the computer. The received waves are quickly analyzed and then images are made based on these analyses. An MRI computer identifies what areas of the body have emitted the most radio waves. The higher the intensity of the incoming wave, the higher the proton density at that point and because the most abundant atom in the body is the hydrogen atom in the water molecule, so it has more water wherever more radio waves are sent back. MRI can be used to lower the left (coronal), the upper (axial) and even in the direction of oblique imaging [2]. The signal strength generated by MRI depends on the two factors of proton density which are T1 and T2 relaxation times. T1 is the time when 63% of the longitudinal magnetic moment of a proton, after excitation, returns from perpendicular to the field parallel to the magnetic field. T2 is the period or time when the transverse magnetic moment of a proton drops to 37% of its initial value after excitation. In each context this time period is different. For example, at 1.5 Tesla, the T1 constant is 260 milliseconds for fat tissue and 920 milliseconds for gray matter. Most pathological processes increase their T1 and T2 relaxation time and, therefore, have a lower (darker) signal in T1-weighted images and higher signal in T2-Wighted images compared to

surrounding natural tissues. Depending on what type of pulse sequence is selected, and how parameters such as repetition time (TE) and reflection time (TR) are determined (Fig. 1-1), the contrast with T1 and T2 can be illustrated and the ability of MRI to be determined. This is the special property. For example, in one image the fat is light and the other is dark [3, 4].

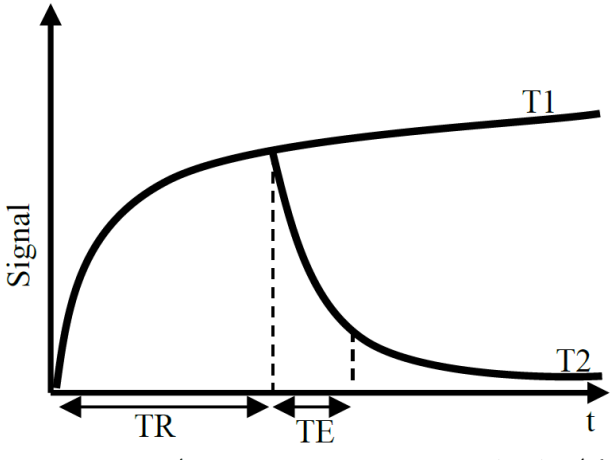

Figure 1-1: TR and TE in MRI Image [3, 4]

Each image slice is coded by the phase and frequency of the received waves on the Y and X axes, respectively. Magnetic fields need to be changed to perform encoding, which is produced at any given moment by superconducting magnets. The information received is entered into a data space called k

space and is eventually transformed into image-based instantaneous transformations. Signals received by MRI systems contain a great deal of information that can be used to extract the physical and chemical information of the body or tissue in question. According to the desired information the MRI system is programmed and finally the imaging is presented in one of the following ways or combined methods. MRI images have different sequences, e.g. the one of most common ones is the multi-echo gradient recalled echo (GRE), which is produced by a single RF pulse in conjunction with a gradient reversal. The GRE formation is illustrated schematically [5]. Common techniques used to diagnose MS include T1-W, T2-W, PD-W, and FLAIR[1] images, which are described in the following sections below [6].

1.2. Segmentation MRI images for the diagnosis of MS

The task of white matter cells is to carry signals between the gray matter areas and other parts of the body, where they are processed, and the peripheral nervous system seldom engages. These white matter lesions are visible on conventional MRI images. MS shows itself on MRI in the form of numerous

[1] Fluid-Attenuated Inversion Recovery

rounds, elliptical white spots on the white matter of the brain, so-called plaque. Due to the non-invasive MRI monitoring, this technique has been used extensively for clinical and investigational researches of MS. It is difficult to accurately identify and diagnose MS lesions in MRI images, and segmentation may be error-prone. An accurate alternative to brain segmentation is computer segmentation, which can be done more accurately and in a shorter time for the physician. In fact, segmentation of an image is the separation of the image into different regions so that the pixels of each region share a specific property (which can belong to an object). The most important feature in segmenting a single image is the color intensity of the image in a color image (the color components of that image). The edges of the image and its texture are also important features in the segmentation [7]. The purpose of segmentation is to break down an image into different fragments and to facilitate its analysis. Image segmentation is usually done to find an object or a series of borders (lines, curves, etc.) more precisely in images. Image segmentation is the process of assigning a label to each pixel of an image, so that pixels with similar labels have similar properties [8, 9]. For several reasons, segmentation of MRI images faces problems that have not been fully resolved, first of all, that data acquisition is always subject to problems. In other words, the

taken images are subject to various damaging factors such as noise, non-uniformity of brightness, and so on. This is especially true for MRI images, which essentially use magnetic fields with high non-linear properties.

The second reason is that, tissue segmentation (especially soft tissue) is fundamentally self-operative with uncertainty. There is generally no definite boundary for the regions of each tissue and consequently no definitive answer for their segmentation. This difficulty is not only limited to automated methods. In semi- automated methods, human experts may also have doubts about the segmentation of these images. It may even be possible for an expert to differentiate a picture in different ways [10, 11].

1.3. Clustering and the Unsupervised Learning

Clustering is an unsupervised learning algorithm and a common technique for data analysis that is widely used in image segmentation, bioinformatics, pattern recognition, statistics, and so on. In fact, data is clustered into meaningful groups or clusters. The contents of each cluster are called clustering features that are similar and yet not identical to other objects in other clusters. Such algorithms are used in large datasets and in cases where there are many data attributes. This method of grouping-similar-documents is based on their content so that

documents that have similar properties and features will be grouped together. The purpose of clustering is to place similar documents in one cluster so that they are different from those in the other clusters. The most important algorithms used for clustering are the K-means algorithm. The difference between clustering and classification is that at the beginning of the computation, the clusters are not known and not predefined. In other words, it is not clear in advance the clustering of the groups, and it is also unclear as to which grouping properties [12, 13].

1.4. Supervised learning and classification

SVM2 is one of the most supervised learning methods used for classification and regression and can be said to be one of the most accurate and robust data mining algorithms. The support vector machine approach is that in the training phase, it tries to select the decision boundary in such a way as to maximize its minimum distance to any of the categories concerned. In this method, it is attempted to implement a system of minimum capacity, or better yet, a system of minimum complexity to obtain class boundaries. As a result, SVM can accurately estimate system boundaries using less training data

[2] Support vector machines

than competitors, without compromising system generalizability. The support vector machine algorithm falls into the category of pattern recognition algorithms and can be used wherever it is necessary to identify patterns or classify objects in specific classes. In the reference [14] to classify benign or malignant tumors, support vector machine classification is used. In the reference [14, 15] an SVM classification method based on the features, extracted by the dual complex wavelet transform was proposed, but they believed that it would perform better in other approaches. In order to improve the classification speed in SVM, reference [16, 17], a textured energy criterion law of images is considered.

2. Proposed method

The most important and widely used algorithm in clustering is the K-means algorithm, which is one of the partitioning methods where each cluster is represented by its mean objects (cluster center). This algorithm works well when the clusters are separated into compact clouds. This method is effective for relatively large databases, but often results in a local optimization. One of the disadvantages of the method is to determine the number of clusters that must be known in advance and no efficient method has been provided. It is also not suitable for detecting clusters with complex shapes. Another major

disadvantage of this approach is its sensitivity to remote data. These data easily change centers and may not produce the desired results [18].

2.1 Unsupervised learning system and K-means method

In the K-means algorithm, *K* first randomly selects a member (where *K* is the number of clusters) and considers them as the centers of the clusters. The remaining *N* - *K* members are then allocated to the nearest cluster. After the allocation of all members, the cluster centers are recalculated, and the members are allocated to the clusters according to the new centers, which will continue until the cluster centers remain constant with no change. In other words, if we have data sets of *n* data points $(x_1, \dots x_n)$ and number of *k* clusters $(C_1, \dots, C_k), k \leq n$, the K-means goal is to minimize the mean squared of the similarity interval $\|x_j - c_i\|^2$ [19]:

$$Min \sum_{i=1}^{k} \sum_{x_j \in C_i} \|x_j - c_i\|^2 \qquad (2\text{-}1)$$

In Eq. (4-1), to find the centers of the *K* cluster, the Euclidean mean squared distance must be minimized, between a data point and the nearest cluster center. The K-means algorithm provides an easy way to implement an approximate solution of the

equation. The reasons for the utility of the K-means method are its ease, simplicity, scalability, convergence speed and consistency with sparse data. The K-means clustering algorithm can be considered as a slope or descending gradient method. Cluster centers begin and regularly update cluster centers in order to reduce the objective function in the equation K-means always converges to the minimum location. To avoid such computations, we can trace all of our data elements at wider intervals for the value as shown in simplified Pseudo Algorithm and block diagram (Figure 2-1). (Figure 2-2), as follows [20]:

Define constant WIDTH

*Define intervals li = li * WIDTH, (i+1) * WIDTH and tag them with value i * WIDTH*

Mark the entire data set to be visited

For each point to be visited

Compute e = min (dpci - dpcw) where Cw is the center of the winner (closest) cluster and Ci, i=1..k, l≠w stands for all other centroids

*Map all points with i * WIDTH <e < (i+1) * WIDTH to interval i * WIDTH where i is a positive integer*

Compute new centroids Cj, where j=1..k and their maximum deviation D = max(|CjCj'|)

*Update ij's tag by subtracting 2 * D (points owned by this interval got closer to the edge by 2 * D)*

Pick up all points inside intervals whose tag is less or equal to 0, and go to 4 to revisit them

Figure 2-1: Simplified Pseudo Algorithm

Algorithm group points with values so that we can execute it for the whole group instead of visiting each data element and controlling it against the distance near the edge and their boundary. The key to all optimization is in compatibility performance. Wide compatibility has a great impact on optimization. If the value of the width is low, then the number of intervals increases and therefore workload for checking and controlling and updating the intervals in each iteration can be significantly increased. If the value is too wide, the number of points increases for each distance, and although the number of intervals decreases. The absence and loss of execution is obvious when the long distances are re-marked. It is easily noticeable and clear to see that the quality of the final clustering will not be affected by the proposed optimization. In each iteration, clustering and sorting are exactly the same as if standard k-means were used [16].

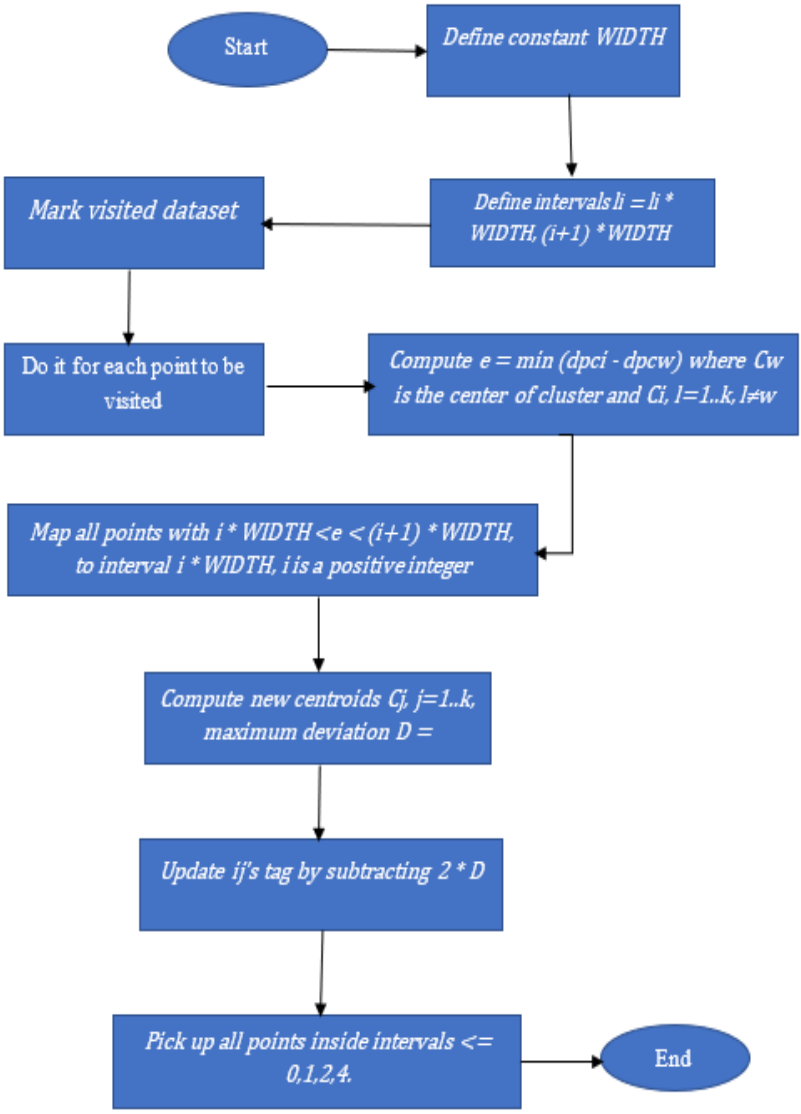

Figure 2-2: Simplified Pseudo Algorithm block diagram [15]

2.2 Automatic MS Segmentation Approach Based on Cellular Learning Automata

In recent years, MS plaque detection based on color has attracted the attention of the many scholars for its low computational complexity. Most of these methods have a high error rate for not considering the texture of the lesion. In this paper, a novel method to detect MS lesions is proposed. This method combines the image information in the gray area and texture, detects the skin area by using Cellular Learning Automata (CLA) [17, 18, 21].

Cellular Learning Automata (CLA), the combination of Cellular Automata (CA) and Learning Automata (LA), is preferable to both CA and LA individually. Unlike CA or LA, CLA tries to learn optimal actions and it can improve the learning capability by using a set of learning automata that interact with each other. In addition, CLA can optimize outside standard sequential processes mapping real world solutions more accurately. Firstly, the candidate lesion regions are detected through defining a threshold, and then these regions are assigned to a texture analyzing system. The output of texture analyzing system is the probability rate of being lesion for each pixel. Then this probable mapping is given to a CLA. By using neighborhood relations and texture information, CLA

converges to a steady state representing the final output of the proposed system. The proposed algorithm is shown in Fig. (2-3), proposed Pseudo algorithm is shown in Fig. (2-4) and Flowchart of the proposed algorithm in Fig. (2-5) [22]:

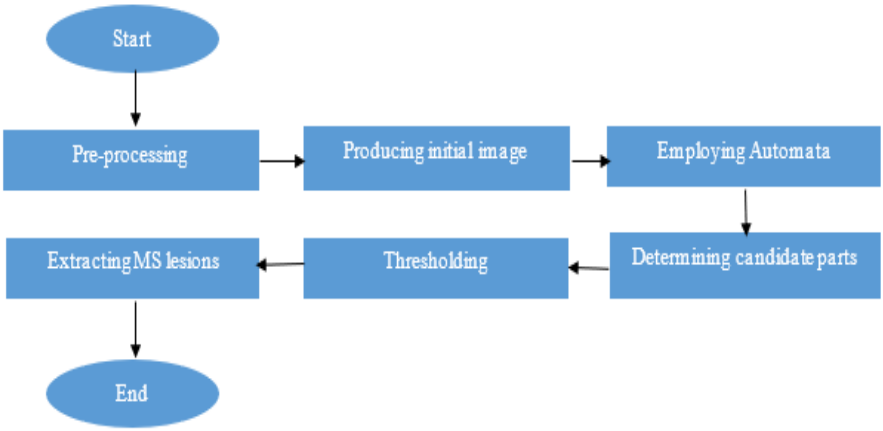

Figure 2-3: Block diagram illustrating the proposed CLA algorithm [15]

```
Function (plaque detection function using cellular learning
automata) Establish an associative CLA.
Initialize the state of cells in CLA.
for each cell j in the CLA do
Let x be a data sample from the data   set, give x to cell j
Let i be the class of data x
Cell j selects an action αj
 if Cell j is in row i then
  if αj = 1 AND half or more neighbors of cell j selects action 1
then
   Reward the selected action of LA in the cell j
    else
     Penalize the selected action of LA in the cell j
  end if
    else
  if αj = -1 AND half or more neighbors of cell j selects action -
1 then
  Penalize the selected action of LA in the cell j
    else
   Reward the selected action of LA in the cell j
   end if
 end if
end for
```

Figure 2-4- The Pseudo algorithm of the proposed CLA algorithm [15]

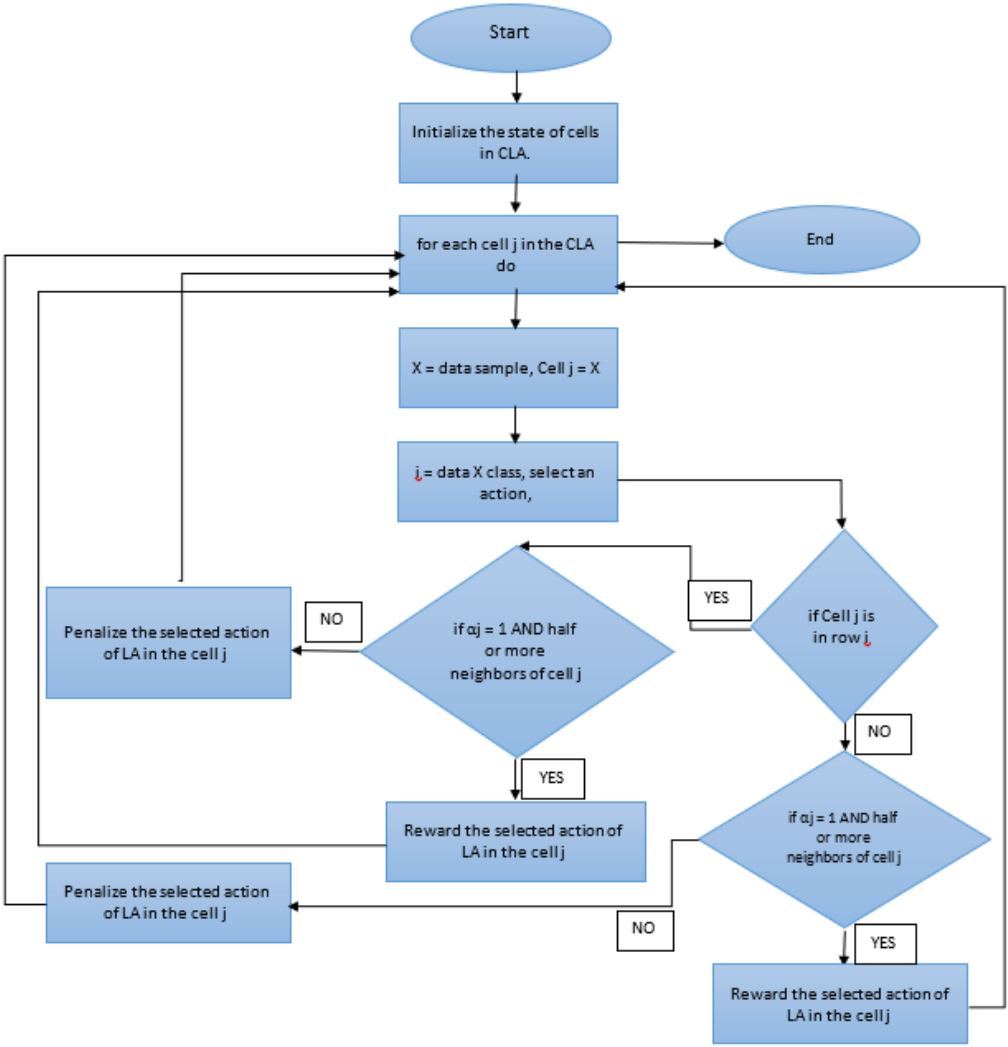

Figure 2-5- Block diagram of the proposed algorithm

2.3 Result

The proposed algorithm is benchmarked on 10 benchmark function [23]. And then to verify results, the results are compared with three above optimization algorithms (GWO, particle swarm optimization (PSO) [24] and Biogeography-based optimization (BBO) [25]). The results are shown in the following.

Table 2-6: Result of benchmark functions in number of iteration 200 and 72 Images and repetition time of 18

Function	Simulated Database,	GWO	PSO	BBO
Sphere	0	0	0.064355	0.045546
Chung Reynolds	0	0	0	0.063455
Schwefel 2/22	0	0.049545	0.035231	0.902745
Schwefel 2/21	0.939634	0.015366	0.104434	0.223567
Cube	0	0.094653	0.873244	0.083556
Dixon & Price	0.891556	0.034444	0.742324	0.075743
Griewank	0.948567	0.743433	0.047651	0.124456
Rosenbrock	0.910545	0.022655	0.107431	0.144677
Ackley	0.084238	0.872762	0.752764	0.934357
Rastrigin	0.915251	0.094749	0.774321	0.873534
Brown	0.075231	0.030769	0.060328	0.053567

2.4 Results of Simulated Database, 3D MRI to 2D Images

The first step of this section was to determine the appropriate dataset for the machine learning algorithms. For this more source can be appropriated, for instance the dataset used in the below mentioned MS MRI Lesion Segmentation research. This dataset is the MRI results of 38 MS patients. The disadvantage of this dataset is that it does not contain normal brain MRI images and additional data about the MS severity of the patients [16]. The most common use of SVM is binary pattern classification. To resolve this, One-Against-One (1A1) and One-Against-All (1AA) are commonly used techniques. The 1AA divides the N class dataset into N two-class cases, while 1A1 approach creates a model for each pair of classes so N(N-1)/2 models are built. In these methods every classification method gives one vote to one class and the final class is determined by the votes. Weights can be involved too in the voting process. For building the model MATLAB® fitcsvm function was used with linear kernel function with standardized predictor data. With each method 10 runs were done, in each run 30% of the dataset (23 images) was selected randomly and used for model testing. The analysis of the results is different, it depends on the model used for training [16].

Table 2-7- Example result of One-Against-All classification [16]

Expected	Normal2All	MildMS2All	ModerateMS2All	SevereMS2All	2AllResult
normal	normal	all	all	all	normal
normal	normal	all	all	all	normal
normal	normal	all	all	all	normal
normal	all	mild_ms	all	severe_ms	more_results
normal	normal	all	all	all	normal
normal	normal	all	all	all	normal
normal	normal	all	all	all	normal
normal	normal	all	all	severe_ms	more_results
mild_ms	normal	all	all	all	normal
mild_ms	all	all	all	all	all
mild_ms	normal	all	all	all	normal
mild_ms	normal	all	all	all	normal
mild_ms	all	mild_ms	all	all	mild_ms
moderate_ms	all	all	moderate_ms	all	moderate_ms
moderate_ms	all	all	all	severe_ms	severe_ms
moderate_ms	all	all	moderate_ms	all	moderate_ms
moderate_ms	all	all	moderate_ms	all	moderate_ms
moderate_ms	all	all	moderate_ms	all	moderate_ms
moderate_ms	all	all	moderate_ms	all	moderate_ms
moderate_ms	all	all	moderate_ms	all	moderate_ms
severe_ms	all	all	all	severe_ms	severe_ms
severe_ms	all	all	all	severe_ms	severe_ms
severe_ms	normal	all	all	all	normal

Table 2-8- Example result of One-Against-One classification [16]

Expected	Normal2 MildMS	Normal2 ModerateMS	Normal2 SevereMS	MildMS2 ModerateMS	MildMS2 SevereMS	ModerateMS 2 SevereMS	2OneResult
normal	normal	normal	normal	moderate_ms	severe_ms	severe_ms	normal
normal	normal	normal	normal	mild_ms	mild_ms	severe_ms	normal
normal	normal	normal	normal	mild_ms	severe_ms	severe_ms	normal
normal	mild_ms	normal	severe_ms	mild_ms	severe_ms	severe_ms	severe_ms
normal	normal	normal	normal	mild_ms	mild_ms	severe_ms	normal
normal	normal	normal	normal	mild_ms	mild_ms	severe_ms	normal
normal	normal	normal	normal	mild_ms	mild_ms	severe_ms	normal
normal	normal	normal	severe_ms	mild_ms	severe_ms	severe_ms	severe_ms
mild_ms	normal	normal	normal	moderate_ms	mild_ms	severe_ms	normal
mild_ms	normal	normal	severe_ms	mild_ms	severe_ms	severe_ms	severe_ms
mild_ms	normal	normal	normal	moderate_ms	mild_ms	severe_ms	normal
mild_ms	normal	normal	normal	moderate_ms	mild_ms	severe_ms	normal
mild_ms	mild_ms	normal	normal	mild_ms	mild_ms	severe_ms	mild_ms
moderate_ms	normal	moderate_ms	severe_ms	moderate_ms	severe_ms	moderate_ms	moderate_ms
moderate_ms	normal	normal	severe_ms	mild_ms	severe_ms	severe_ms	severe_ms
moderate_ms	normal	moderate_ms	severe_ms	moderate_ms	severe_ms	moderate_ms	moderate_ms
moderate_ms	normal	moderate_ms	severe_ms	moderate_ms	severe_ms	moderate_ms	moderate_ms
moderate_ms	normal	moderate_ms	severe_ms	moderate_ms	severe_ms	moderate_ms	moderate_ms
moderate_ms	normal	moderate_ms	severe_ms	moderate_ms	severe_ms	moderate_ms	moderate_ms
moderate_ms	normal	moderate_ms	severe_ms	moderate_ms	severe_ms	moderate_ms	moderate_ms
severe_ms	normal	normal	severe_ms	mild_ms	severe_ms	severe_ms	severe_ms
severe_ms	normal	normal	severe_ms	moderate_ms	severe_ms	severe_ms	severe_ms
severe_ms	normal	normal	normal	moderate_ms	severe_ms	severe_ms	normal

Table 2-9- Overall results for SVM using 1AA and 1A1 technique [16]

ID	2AllResult Accuracy	2OneResult Accuracy	2AllMore Result	2OneMore Result	2AllNo Result	2OneNo Result	Differences
1	0.739130435	0.739130435	1	0	0	0	0.130434783
2	0.826086957	0.826086957	0	0	1	0	0.043478261
3	0.739130435	0.739130435	0	0	0	0	0
4	0.913043478	0.913043478	0	0	0	0	0
5	0.826086957	0.782608696	2	0	2	0	0.391304348
6	0.826086957	0.826086957	1	0	2	0	0.130434783
7	0.782608696	0.826086957	0	0	0	0	0.043478261
8	0.52173913	0.434782609	2	7	9	0	0.565217391
9	0.956521739	0.913043478	0	0	0	0	0.086956522
10	0.652173913	0.652173913	2	0	1	0	0.130434783
AVG	0.77826087	0.765217391	0,8	0,7	1,5	0	**0.152173913**

To summarize the efficiency of the two techniques of SVM according to the result of the 10 runs (Table 5-8), the 1AA (2AllResult) reached a slightly better average accuracy than 1A1 (2OneResult) and average Dice similarity coefficient (DSC) for 1A1 (2OneResult) is 0.739.

In all cases the accuracy of the 1A1 approach was the same or worse than the 1AA method. The average accuracy of the 1AA model is slightly worse compared to the previous model, however the 1A1 model produced a slightly better result. For

the 2AllResult (the accuracy of the 1AA models), the previous average accuracy of the models was 0.77826087 while for 2OneResult (the accuracy of the 1A1 models) models was 0.765217391. This was not explained in the previous study, but the system would have been the following:

- 1AA method is used for the primary decision.
- if 1AA resulted in more results, the more severe result should be used.
- if 1AA resulted in no results, the 1A1 result should be used.
- if 1A1 has more results, the more severe should be used.

This rule should be rejected, because of the 1A1 has produced a slightly better result compared to the 1AA method and because no sample got more results in this case, so using such a technique wouldn't improve the overall results. For SVM, a different kernel function can be tested to examine the method efficiency [17].

Table 2-10- SVM results using linear kernel function [17]

ID	2All Result	2One Result	2AllMore Result	2OneMore Result	2AllNo Result	2OneNo Result	Differences	ST. DEV
1	0.739130435	0.652173913	0	0	6	0	0.391304	0.061488
2	0.739130435	0.782608696	0	0	6	0	0.26087	0.030744
3	0.695652174	0.739130435	0	0	7	0	0.304348	0.030744
4	0.826086957	0.826086957	0	0	4	0	0.173913	0
5	0.782608696	0.782608696	0	0	5	0	0.26087	0
6	0.739130435	0.782608696	0	0	6	0	0.26087	0.030744
7	0.739130435	0.739130435	0	0	6	0	0.26087	0
8	0.695652174	0.75	0	0	7	0	0.304348	0.03843
9	0.782608696	0.826086957	0	0	5	0	0.217391	0.030744
10	0.695652174	0.782608696	0	0	7	0	0.304348	0.061488
AVG	**0.743478261**	**0.766304348**	**0**	**0**	**5.9**	**0**	**0.273913**	**0.01614**

Table 5-10- SVM results using rbf kernel function

ID	2All Result	2One Result	2AllMore Result	2OneMore Result	2AllNo Result	2OneNo Result	Differences	ST. DEV
1	0.739130435	0.782608696	0	0	6	0	0.260869565	0.030744
2	0.739130435	0.782608696	0	0	6	0	0.260869565	0.030744
3	0.695652174	0.739130435	0	0	7	0	0.304347826	0.030744
4	0.826086957	0.826086957	0	0	4	0	0.173913043	0
5	0.782608696	0.826086957	0	0	5	0	0.217391304	0.030744
6	0.739130435	0.739130435	0	0	6	0	0.260869565	0
7	0.739130435	0.739130435	0	0	6	0	0.260869565	0
8	0.695652174	0.782608696	0	0	7	0	0.304347826	0.061488
9	0.782608696	0.826086957	0	0	5	0	0.217391304	0.030744
10	0.695652174	0.739130435	0	0	7	0	0.304347826	0.030744
AVG	**0.743478261**	**0.778260870**	**0**	**0**	**5.9**	**0**	**0.256521739**	0.024595

This kernel function is the radial basis function (rbf) and the result can be seen in (Table 5-10). Comparison of the results of different MS lesion detection methods is shown in Figure (5-11), and the results show that integrated SVM, K-Means and CLA method (DSC=0.948) has better results than DSC = 0.891 from previous research [15-17].

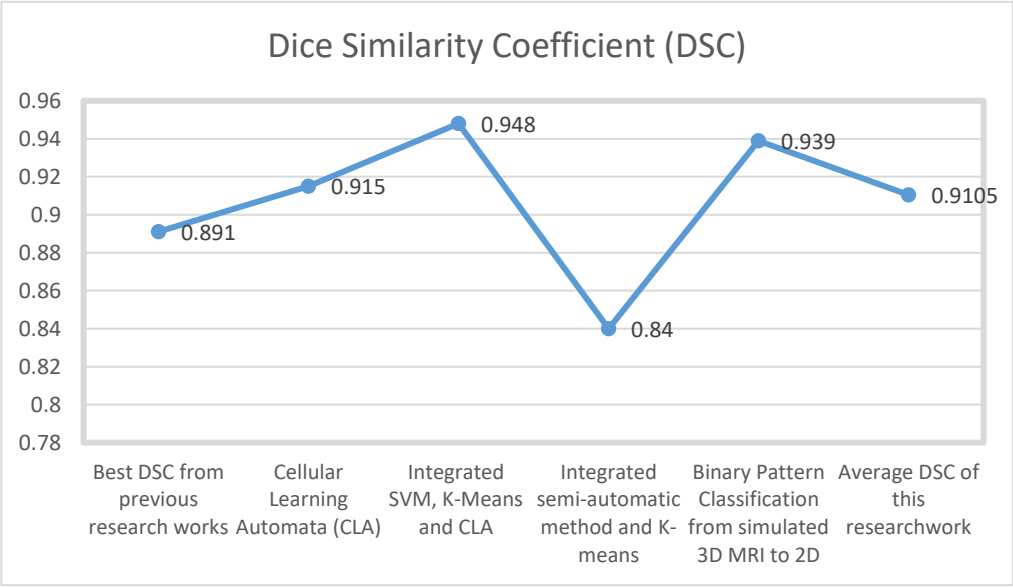

Figure 5-11- Comparison of accuracy of different methods for diagnosing MS

3. Suggestion and future works

This dissertation practices the research of SVM used for classification and CLA, then it expands the research to other method such as k-NN and ANN and at that point compares the results of them. 3D images can be converted into 2D and by considering machine learning techniques and SVM tools. Our main focus in this study was on suggesting a novel machine learning and classification algorithm to improve MS detection in MRI images and to improve the performance of computational methods. Some issues related to MS lesion detection and available algorithm, their advantage and disadvantages need further research and have not been addressed in this thesis.

A) Design a mechanism for deep, layered and fast learning
B) Design of medical decision support system

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List of other publications

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