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An Amend Implementation of Brain Tumor Detection Using Segmentation Based On Artificial Intelligence

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Abstract — **Implementation of a segmentation process of the MRI data with Artificial Intelligence is resented in this study to detect various tissues like white matter, gray matter, csf and tumor. The advantage of hierarchical self organizing map and clustering algorithms are used to classify the image layer by layer. The lowest level weight vector is achieved by the abstraction level. We have also achieved a higher value of tumor pixels by this approach. The computation speed of the proposed method is also studied. The multilayer segmentation results of the Soft Computing are shown to have interesting consequences from the viewpoint of clinical diagnosis.**

Soft computing technique shows that MRI brain tumor segmentation using SOM & Clustering Algorithm also perform more accurate one.

Keywords— **Image analysis, segmentation, SOM, K-means Clustering, Artificial Intelligence, tumor detection**

I. Introduction

Magnetic Resonance Imaging (MRI) is the state-of the- art medical imaging technology which allows cross sectional view of the body with unprecedented tissue contrast [1-2]. MRI plays an important role in assessing pathological conditions of the ankle, foot and brain. It has rapidly evolved into an accepted modality for medical imaging of disease processes in the musculoskeletal system, especially the foot and brain due to the use of non-ionizing radiation. MRI provides a digital representation of tissue characteristic that can be obtained in any tissue plane. The images produced by an MRI scanner are best described as slices through the brain. MRI has the added advantage of being able to produce images which slice through the brain in both horizontal and vertical planes.

Segmentation is an important process to extract information from complex medical images. Segmentation has wide application in medical field [3-4]. The main objective of the image segmentation is to partition an image into mutually exclusive and exhausted regions such that each region of interest is spatially contiguous and the pixels within the region are homogeneous with respect to a predefined criterion.

Widely used homogeneity criteria include values of intensity, texture, color, range, surface normal and surface curvatures. During the past many researchers in the field of medical imaging and soft computing have made significant survey in the field of image segmentation [5-8].

Image segmentation techniques can be classified as based on edge detection, region or surface growing, threshold level, classifier such as Hierarchical Self Organizing Map (HSOM), and feature vector clustering or vector quantization. Vector quantization has proved to be a very effective model for image segmentation process [9]. Vector quantization is a process of portioning an ndimensional vector space into M regions so as to optimize a criterion function when all the points in each region are approximated by the representation vector Xi associated with that region. There are two processes involved in the vector quantization: one is the training process which determines the set of codebook vector according to the probability of the input data, the other is the encoding process which assigns input vectors to the code book vectors. Vector quantization process has been implemented in terms of the competitive learning neural network (CLNN) [10]. Self Organizing Map (SOM) [11] is a member of the CLNNs and this can be the best choice when implementing vector quantization using neural network [11-16].

The importance of SOM for vector quantization is primarily due to the similarity between the competitive learning process employed in the SOM and the vector quantization procedure. It is not however, possible to determine a priori the correct number of regions M in the segmented image. This is the main limitation of the conventional SOM for image segmentation.

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The HSOM directly address the aforesaid shortcomings of the SOM.HSOM is the combination of self organization and topographic mapping technique. HSOM combine the idea of regarding the image segmentation process as one of data abstraction where the segmented image is the final domain independent abstraction of the input image. The hierarchical segmentation process for a hierarchical structure is called abstraction tree. The abstraction tree bears some resemblance to the major familiar quad tree data structure [17] used in the several image processing and image analysis algorithms. Clustering is the process of grouping a data set in a way that the similarity between data within a cluster is maximized while the similarity between data of different clusters is maximized [18] and is used for pattern recognition in image processing. To recognize a given pattern in an image various techniques have been utilized, but in general two broad categories of classifications have been made: unsupervised techniques and supervised techniques. In the unsupervised method, data items that are to be clustered are not pre-classified while in supervised clustering the data points are preclassified. One of the well-known unsupervised algorithms that can be applied to many applications, such as image segmentation [19], K-means Clustering [20] etc.

K-means algorithm is one of the popular clustering algorithms which are classified as constrained soft clustering algorithm. A soft clustering algorithm finds a soft partition of a given data set by which an element in the data set may partially belong to multiple clusters. Moreover, there is a constraint on the function that the membership degree of a point in all the clusters adds up to 1[21-22]. The researchers in this field have used SOM or HSOM or K-means separately as one of the tool for the image segmentation of MRI brain for the tumor analysis. In this Work, we propose a hybrid technique combining the advantages of HSOM and K-means and implemented for the MRI image segmentation process to detect various tissues like white matter, gray matter, cst and tumor.

Literature Review

Hierarchical Self Organizing Map (HSOM) A self-organizing map (SOM) or self-organizing feature map (SOFM) is a type of artificial neural network for unsupervised learning. SOMs operate in two modes: training and mapping, Training is a competitive process, also called vector quantization. Mapping automatically classifies a new input vector. Segmentation is an important process to extract information from complex medical images. Segmentation has wide application in medical field. The main objective of the image segmentation is to partition an image into mutually exclusive and exhausted regions such that each region of interest is spatially contiguous and the pixels within the region are homogeneous with respect to a predefined criterion. Widely used homogeneity criteria include values of intensity, texture, color, range, surface normal and surface curvatures. During the past many researchers in the field of medical imaging and soft computing have made significant survey in the field of image segmentation.

Vector quantization is a process of portioning ndimensional vector space into M regions so as to optimize a criterion function when all the points in each region are approximated by the representation vector Xi associated with that region. There are two processes involved in the vector quantization: one is the training process which determines the set of codebook vector according to the probability of the input data, the other is the encoding process which assigns input vectors to the code book vectors. Vector quantization process has been implemented in terms of the competitive learning neural network (CLNN).

Self Organizing Map (SOM) is a member of the CLNNs and this can be the best choice when implementing vector quantization using neural network. The importance of SOM for vector quantization is primarily due to the similarity between the competitive learning process employed in the SOM and the vector quantization procedure. The main shortcoming of the SOM is that the number of neural units in the competitive layer needs to be approximately equal to the number of regions desired in the segmented image. The HSOM directly address the aforesaid shortcomings of the SOM. HSOM is the combination of self organization and graphic mapping technique. The abstraction tree bears some resemblance to the major familiar quad tree data structure used in the several image processing and image analysis algorithms. In this work, we propose a hybrid technique combining the advantages of HSOM was implemented with Clustering Technique for the MRI image segmentation.

The HSOM is organized as pyramidal structure consisting of multiple layers where each layer resembles the single layer SOM. The detailed explanations and the structure of the HSOM were presented by S.M. Bhandarkar et.al. [2]. Learning process consists of sequential corrections of the vectors representing neurons. On every step of the learning process a random vector is chosen from the initial data set and then the best-matching (the most similar to it) neuron coefficient vector is identified. The winner is selected, which is the most similar to the input vector [23]. The distance between the vectors usually measured in the

Euclidean metric and is given by

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$$\left\| x - w_C \right\| = \min_i \{[x - \mathbf{w}_i]\} \qquad (1)$$

Where, x is the neuron, W_C is the winning neuron vector and W_i is the weight vector. The modified weight vector coefficients can be calculated by

$$\mathbf{W}_i(t+1) = \mathbf{W}_i(t) + h_{ci}(t) * \left[x(t) - \mathbf{W}(\mathbf{t})\right] \qquad (2)$$

Where t is the epoch number (discrete-time index), x (t) is the vector and is obtained by selecting a sample randomly for iteration t.

The function h_{ci} (t) is called neighbourhood function and it represents a non-increasing function of time and the distance between the winning neuron and its neighbours on the grid.

The function h_{ci} (t) consists of two parts: the proper distance function and the learning rate function and is given by

$$\mathbf{h}(t) = \mathbf{h}\left(\left\|r_c - r_i\right\|\right) * \mathbf{a}(t) \qquad (3)$$

Where, r determines neuron position on the grid. The result of neighborhood function h(t) is an initial cluster centre (centroid) for fuzzy c means algorithms. Cluster is a group of vectors with the distance between any two of them shorter than that between this group and the neighbouring ones.

Flow Diagram of Brain tumor Detection using Self Organizing map is shown in Figure Below

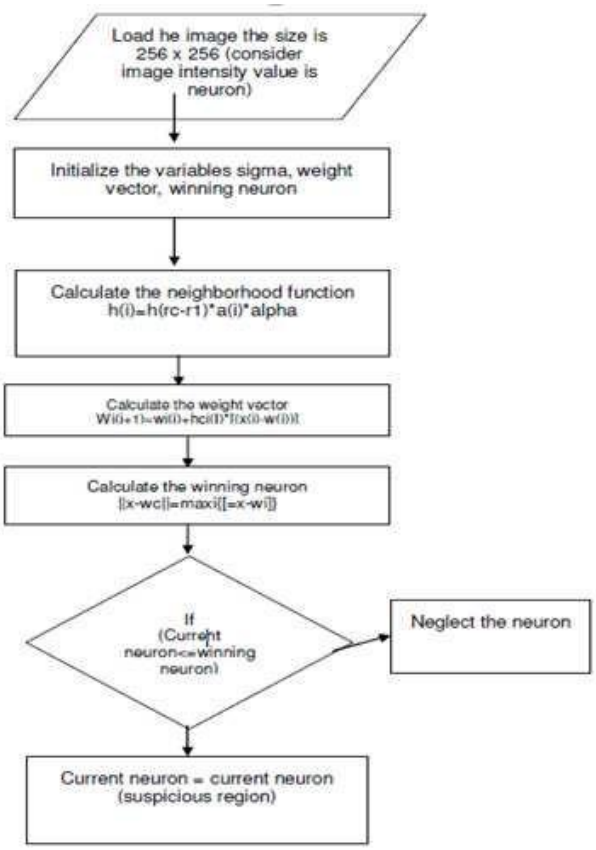

Figure1: Flowdiagram HSOM for detection of brain tumor

Component Declaration &Updated Formula

```
map=8; wx=0; wy=0; sigma=0.0;
update_lrate=0.99;  update_radius=map/3;
radius_decay=0.999;
Give These Input to selector file to find winner nueron
ny=0;nx=0;
        dy=0;dx=0;
        dis=0;gain=0.0;
for y=y1:y2      dy=y-wy;
ny=rem((y+map),map);
for x=x1:x2      dx=x-wx;
dis=sqrt(dx^2 +dy^2);
gain=update_lrate * exp(-
dis/(2 * update_radius));
for a=1:m
     mw(x,y,a)=mw(x,y,a)+gain          *(mw(wx,wy,a)-
mw(x,y,a));
end    end
end
```

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update_lrate=0.999/(0.999+(0.01*t));

update_radius=1.0+(update_radius1.0)*radius_decay;
i=i+1; end
smap=mw;

MRI Segmentation using Clustering Algorithm

Clustering is an unsupervised way of data grouping with a given measure of similarity. Clustering algorithms attempts to organize unlabeled feature vectors into clusters, such as samples within a cluster, that are more similar to each other than to samples belonging to different clusters, in which a validity measure is computed for each set of clusters. The number of clusters, which optimizes this measure, is the optimum number of clusters in the data set. The flowchart of the clustering approach is shown in Figure 1. The critical part of the clustering approach is choosing the additional cluster centre. [3, 4]One of the most common clustering methods is the K means algorithm. In its first step, initial mean vector iteration is arbitrarily specified for each of the K clusters. Each pixel of the training set is then assigned to the class of which the mean vector is closest to the pixel vector, forming the first set of decision boundaries. A new set of cluster mean vectors is then calculated from this classification, and the pixels are reassigned accordingly. In iterations, the K means will tend to gravitate toward concentrations of data in nearby regions of the feature space. The algorithm iterates until there is no significant change in pixel assignments. The criterion for terminating the iterative process can be defined in terms of the net mean migration from one to the next iteration.

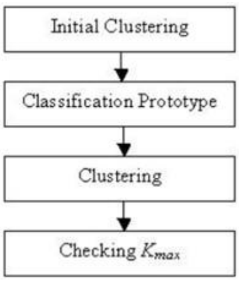

Figure2: Flowchart of the clustering approach

Following are the Clustering algorithm:

Step 1.Begin with a decision on the value of k = number of clusters

Step 2.Put any initial partition that classifies the data into k clusters. You may assign the training samples randomly, or systematically as the following:

• Take the first k training sample as single-element clusters • Assign each of the remaining (N-k) training samples to the cluster with the nearest centroid.

After each assignment, the centroid of the gaining cluster is recomputed.

Step 3.Take each sample in sequence and compute its distance from the centroid of each of the clusters. If a sample is not currently in the cluster with the closest centroid, switch this sample to that cluster and update the centroid of the cluster gaining the new sample and the cluster losing the sample.

Step 4.Repeat step 3 until convergence is achieved, that is until a pass through the training sample causes no new assignments.

The most common algorithm uses an iterative refinement technique. Due to its ubiquity it is often called the k-means algorithm; it is also referred to as Lloyd's algorithm, particularly in the computer science community. Given an initial set of k means $m_1(1)$… $m_k(1)$ (see below), the algorithm proceeds by alternating between two steps: Assignment step: Assign each observation to the cluster with the closest mean (i.e. partition the observations according to the Voronoi diagram generated by the means).

$$S_i^{(t)} = \{x_p : \|x_p - m_i^{(t)}\| \le \|x_p - m_j^{(t)}\| \ \forall\ 1 \le j \le k\}$$

Where each x_p of them is goes into exactly one $S_i^{(t)}$, even if it could go in two of them.

Update step: Calculate the new means to be the centroid of the observations in the cluster.

$$\mathbf{m}_i^{(t+1)} = \frac{1}{|S_i^{(t)}|} \sum_{\mathbf{x}_j \in S_i^{(t)}} \mathbf{x}_j$$

The algorithm is deemed to have converged when the assignments no longer change.

Commonly used initialization methods are Forgy and Random Partition. The Forgy method randomly chooses k observations from the data set and uses these as the initial means. The Random Partition method first randomly assigns a cluster to each observation and then proceeds to the Update step, thus computing the initial means to be the centroid of the cluster's randomly assigned points. The Forgy method tends to spread the initial means out, while Random Partition places all of them close to the centre of the data set. According to Hamerly et al., the Random Partition method is generally preferable for algorithms such as the k-harmonic means and fuzzy k-means. For expectation maximization and standard k-means algorithms, the Forgy method of initialization is preferable. As it is a heuristic algorithm, there is no guarantee that it will

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converge to the global optimum, and the result may depend on the initial clusters. As the algorithm is usually very fast, it is common to run it multiple times with different staring conditions. However, in the worst case, kmeans can be very slow to converge: in particular it has been shown that there exist certain point sets, even in 2 dimensions, on which k-means takes exponential time, which is 2^{Ω} (n), to converge. These point sets do not seem to arise in practice: this is corroborated by the fact that the smoothed running time of k-means is polynomial. The "assignment" step is also referred to as expectation step, the "update step" as maximization step, making this algorithm a variant of the generalized expectation-maximization algorithm.

II. RESULTS

Figure3: Original Image

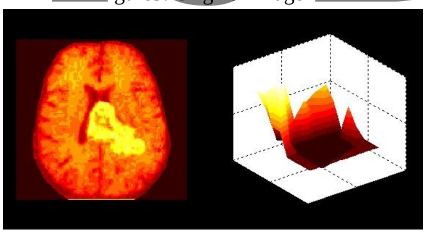

Figure4: Self Organizing Map is used in Original Image to classify data row by row

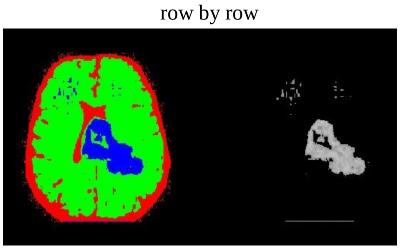

Figure5: Finally clustering algorithm (K-means clustering) is applied On Classified image to separate tumor region.

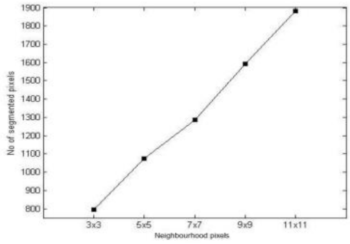

Figure6: Relationship between number of segmented pixel and neighbourhood pixels.

III. CONCLUSION

A Soft Computing & Clustering based segmentation process to detect brain tumor was implemented. We studied the performance of the MRI image in terms of weight vector, execution time and tumor pixels detected and compared the results with the existing ones. A layer by layer abstraction level with clustering technique was implemented to detect various tissues like white matter, gray matter, csf and tumor. We have achieved a higher value of detected tumor pixels than any other segmentation techniques. We have also achieved the weight vector value for this Approach is (6×6) with the additional input features. The weight vector value, the number of tumor will also be studied with different distance classifier technique. The change of growth rate of the tumor of the same patient analyse may also be undertaken.

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