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HSO Based FCM with Active Contours for Glioblastoma Multiform Tumor Segmentation

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Abstract: Image segmentation refers to the process of partitioning an image into mutually exclusive regions. Automatic brain tumor segmentation has become a key component for the future of brain tumor treatment. Gliomas are the most common primary brain tumors, evolving from the cerebral supportive cells. Despite intensive research, automatic segmentation remains a challenging problem due to the diverse image content, cluttered objects, occlusion, image noise, non-uniform object texture and other factors. There are many techniques have been proposed in the literature for automatic brain tumor segmentation, those approaches arise from the supervised learning standpoint which requires a labelled training dataset from which to infer the models of the classes whose retrieval becomes a tedious and time-consuming task. On the other hand, unsupervised approaches avoid these limitations but often do not reach comparable results than the supervised methods. In this sense, we propose an automated unsupervised method for brain tumor segmentation based on Magnetic Resonance (MR) images. This study presents a novel unsupervised image clustering based on Harmonic Search Optimization (HSO) and Fuzzy C-Means (FCM) for Glioblastoma Multiform (GBM) Tumor segmentation. The performance of FCM algorithm to obtain an optimal solution depends on the initial positions of the centroids of the clusters. In the existing FCM, the centroids are initialized randomly. This leads to increase in time to reach the optimal solution. In order to accelerate the segmentation process a new method called HSO based FCM is proposed. The proposed algorithms exploits an initial step derived from the HSO, considering Otsu Method as the objective function. After finding the cluster centers using HSO, FCM algorithm is initialized with these cluster centers. Finally, active contours are used for GBM tumor segmentation and boundary tracking. The experimental results confirms that the proposed method as a viable alternative for GBM tumor segmentation.

Key words: Glioblastoma Multiforme (GBM), MRI, FCM, HSO, segmentation

INTRODUCTION

Image segmentation is the procedure in which the original image is partitioned into homogeneous regions. It has been widely used in many application fields such as medical image analysis to characterize and detect anatomical structures, Magnetic Resonance (MR) imaging is a non-invasive medical imaging technique that provides excellent soft tissue contrast and has become the standard imaging technique for brain tumor diagnosis (Angelis, 2001). As the imaging mechanism and the tissues of medical images are different, medical images are easily affected by noise, field migration effect and tissue movement. Compared with the common images, medical images have more non-uniformity and fuzziness. The early identification and delineation of the different tissues related to the tumor becomes crucial to make decisions that can improve the patient survivability. The manual analysis and segmentation of these tissues involves a complex, time-consuming and biased task which caught the attention of the Pattern Recognition (PR) and Machine Learning (ML) community (Bauer *et al*., 2013). Particularly, Glioblastoma Multiforme (GBM) tumor has received most of this attention, as it is the most common and aggressive malignant tumor of the central nervous system (Dolecek *et al*., 2012; Deimling, 2009). GBM's are heterogeneous lesions that present different areas of active tumor, necrosis and edema, all of them exhibiting a high variability related to the aggressiveness of the tumor. Hence, the automated segmentation of these lesions becomes a desired solution from the clinical standpoint.

Most of the recent reviews on brain tumor segmentation is on supervised learning approach (Verma *et al*., 2008; Ruan *et al*., 2011). Support Vector Machines (SVM) were applied to multiparametric MR datasets to segment health and pathological tissues and additionally sub compartments inside these areas (Jensen and Schmainda, 2009) applied several neural networks to detect brain tumor invasion (Lee *et al*., 2008) used a combination of Conditional Random Fields (CRF)

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and SVM to perform tumor segmentation (Bauer *et al.*, 2011). Baur also used SVM and hierarchical CRF to segment both healthy and tumor tissues including sub compartments. Recently, Random Forest (RF) (Breiman, 2001), techniques have shown high success in the supervised brain tumor segmentation task (Meier *et al.*, 2013; Festa *et al.*, 2013; Reza and Iftekharuddin, 2013). In several approaches based on variants of the RF algorithm were proposed for the Image Segmentation Challenge of Medical Image Computing and Computer-Assisted Intervention (MICCAI) 2013 Conference, reaching the first positions in the competition. However, supervised learning requires an expensive, time-consuming and biased task to retrieve a sufficiently large set of labelled samples from which to learn discriminant functions for the posterior segmentation (Schmidt, 2005). Furthermore, the supervised approaches are limited to the size and quality of the dataset, among other limitations such as the over-fitting to the training corpus (Wagstaff, 2002). Moreover, spatio-temporal changes in clinical environment such as new MR machines, protocols or centres may distort the data and hence, could affect the performance of the supervised models (Richard, 2000). Unsupervised learning tackles these limitations in a more straightforward way.

The unsupervised segmentation methods that use image-based features, rather than dividing the image along anatomically meaningful distinctions, divide the images into homogeneous regions using image-based features such as intensities and or textures. These methods can handle more complicated cases, example producing an accurate segmentation of the different regions present in a heterogeneous tumor. In the case of brain tumor segmentation, the lack of shape or intensity priors on the tumors makes unsupervised segmentation more challenging.

Unsupervised learning does not require a training dataset from which to learn the models of the classes but directly uses the patient specific data to find natural groupings of observations called clusters. Hence, unsupervised learning builds an intra-patient segmentation model which is independent from the differences between other patient's data. By the opposite, the absence of a previous manual segmentations to guide the learning process makes the segmentation more challenging and often lead to a worse performance with respect to supervised approaches. Three major disadvantages when using unsupervised segmentation methods using image-based features: the number of regions often needs to be pre-specified, tumors can be divided into multiple regions and tumors may not have clearly defined intensity or textural boundaries. Some attempts for brain tissue segmentation have been made under the unsupervised paradigm proposed an approach based on fuzzy clustering and domain knowledge for multi-parametric non-enhancing tumor segmentation (Fletcher *et al.*, 2001). Domain knowledge and parenchymal tissue detection is based on heuristics related to geometric shapes and locations which may not be robust when high deformation is presented. Moreover, several assumptions such as prior knowledge about the number of existing tumors or the minimum required thickness of the slices introduces several limitations to the method.

On the other hand, the Harmony Search Algorithm (HSA) introduced by Geem *et al.* (2001) is an evolutionary optimization algorithm which is based on the metaphor of the improvisation process that occurs when a musician searches for a better state of harmony. The HSA generates a new candidate solution from all existing solutions. The solution vector is analogous to the harmony in music while the local and global search schemes are analogous to musician's improvisations. In comparison to other metaheuristics methods in the literature, HSA imposes fewer mathematical requirements as it can be easily adapted for solving several sorts of engineering optimization challenges (Mahdavi *et al.*, 2007). Furthermore, numerical comparisons have demonstrated that the convergence for the HSA is faster than GA (Lee and Geem, 2005) which attracts further attention. It has been successfully applied to solve a wide range of practical optimization problems such as discrete and continuous structural optimization (Lee *et al.*, 2005), parameter estimation of the non-linear Muskingum Model (Kim *et al.*, 2001), design optimization of water distribution networks (Geem, 2006), vehicle routing (Geem *et al.*, 2005) combined heat and power economic dispatch (Vasebi *et al.*, 2007) design of steel frames (Degertekin, 2008) and image processing (Cuevas *et al.*, 2012). Although, the standard HSA presents good search characteristics, several modifications to the original HSA have been proposed in the literature in order to enhance its own features (Alia and Mandava, 2011).

MATERIALS AND METHODS

Harmony search algorithm: The harmony search is based on the harmony memory which consists of solutions called harmony. The harmonies are generated by the random selection of vectors. After the generation of the HM a new candidate is generated for each of the harmony. It consists of the worst and the best solution. Then, the HM is updated by comparing the newly generated value with the worst solution of the memory, if the better solution is found then the values should be swapped. It consists of three steps:

- Harmony memory initialization
- New harmony vectors
- Updating the harmony memory

Harmony memory initialization: The memory initialization consists objective function which is used to optimize the problem and it is described by the following function:

$$\begin{aligned}&\text{minimize}\, f(x),\ x = (x(1),\, x(2),\, x(3),\, x(4), \ldots,\, x(n)) \in R^n\\ &\text{subject to: } x(j) \in [l(j), u(j)]\ \ j = 1,\, 2,\, 3,\, \ldots,\, n\end{aligned} \tag{1}$$

Here, f(x) is an objective function which consists of a set of design variables and n is the number of design variables. l(j) and u(j) are the lower bound and upper bound values of x(j), respectively. We have different parameters to be initialized such as Harmony Memory (HM), Harmony Memory Consideration Rate (HMCR) and Number of Improvisations (NI) these represent the total number of iterations. The performance of HSA also depends on the values assigned to these parameters. which in turn, depend on the application domain (Lobo *et al*., 2007).

The initial vector components at HM, that is, HMS vectors are configured. Here, the $x_i = \{x_i(1), x_i(2), \ldots, x_i(n)\}$ these represent the ith randomly generated harmony vector by $x_i(j) = l(j)+(u(j)-l(j)).\text{rand}(0,1)$ for j = 1, 2, 3, ..., n and i = 1, 2, 3, ..., HMS. Where the rand (0, 1) generates a random number between 0 and 1. Then the Harmon memory matrix will be filled with the HMS vectors as follows:

$$HM = [x_1, x_2, x_3, \ldots, x_{HMS}] \tag{2}$$

Improvisation of new harmony vectors: Generation of new harmony is known as improvisation. The new harmony vector x_{new} is built by considering the parameters memory consideration, random re initialization and pitch adjustment. The value of the first decision variable $x_{new}(1)$ for the new vector is chosen randomly form the harmony memory and then compared with the HMCR if the $r_1(0, 1)$ is less than the HMCR then the decision variable $x_{new}(1)$ is generated. Otherwise it is obtained from the l(j) and the u(j). Values of the other variables $x_{new}(2), x_{new}(3), \ldots, x_{new}(n)$ are also chosen accordingly. The operations are carried out as follows:

$$x_{new} = \begin{cases} x_i(j) \in \{x_i(j), \ldots x_{HMS}(j)\}\ \text{with probability} HMCR\\ l(j) + u(j)\text{-}l(j).\text{rand}(0,\ 1) \text{with probability} 1\text{-}HMCR\end{cases} \tag{3}$$

Every component obtained in the HM is examined to determine whether it should be pitch adjusted. For this the Pitch Adjusting Rate (PAR) is defined as to assign the frequency of the adjustment and to control the local search around the elements of the HM. The pitch adjusting decision is calculated as follows:

$$x_{new}(j) = \begin{cases} x_{new}(j) = x_{new}(j) +/- \text{rand}(0,1).\\ BW \text{withprobability} PAR\\ x_{new}(j) \text{ with probability}(1 - PAR)\end{cases} \tag{4}$$

Pitch adjusting is responsible for the generation of the new harmonies as they modify the original variable positions. The decision variable is either perturbed by a random number between 0 and BW or left unaltered. In order to protect the pitch adjusting operation, it is important to assure that points lying outside the feasible range [l, u] must be reassigned.

Updating the harmony memory: After the generation of the new harmony the then it is compared with the worst harmony vector in the HM. If the newly generated harmony is better than the worst then it is replaced with the worst and then it becomes the new worst so after some iterations the HM contains the best vectors.

Algorithm 1 for generation of the best vector:

1) The parameters HMS, HMCR, PAR, BW, NI are initialized
2) The value of the each vector in the harmony memory is calculated using the objective function
3) To improve the new harmony value x_{new}
   The random value generated should be less than the HMCR then $x_{new}(j) = x_{new}(j)$ where a = 1,2,3,...,HMS. Then it should be verified with the PAR value if r_2 is less than the PAR value then $x_{new}(j) = x_{new}(j)$ +/- r_3.BW. Here, r_1, r_2, r_3 are generated by the operation rand (0,1) which selects a value between 0 and 1
   The newly generate harmony is then compared with the lower bound value if it is <l(j) then the new harmony is assigned l(j)
   If the value is greater than the u(j) then the new harmony is assigned with the u(j)
   If every condition as stated as above does not satisfied then the value is calculated according to the $x_w = x_{new}$ if $f(x_{new}) < f(x_w)$
4) Then the worst harmony in the harmony memory is updated with the newly generated harmony
5) If NI (Number of Iterations) are completed then the best harmony vector x_b in the HM is returned else return to step 3

Algorithm 2 for thresholding according to the generated vector:

1 Read an image I, Store it into I_{Gr} and c =1
2 Using the imhist function generate the histogram h^{Gr}
3 The probability is calculated using the distribution obtained in the histograms
4 Initialize a HM $x^c{}_i$ of HMS random particles with k dimensions
5 Initialize HSA parameters: HMS, k, HMCR, PAR, BW, NI and the limits of l and u
6 The values w_i^c of $u^c{}_I$ and are calculated using the objective function in Otsu

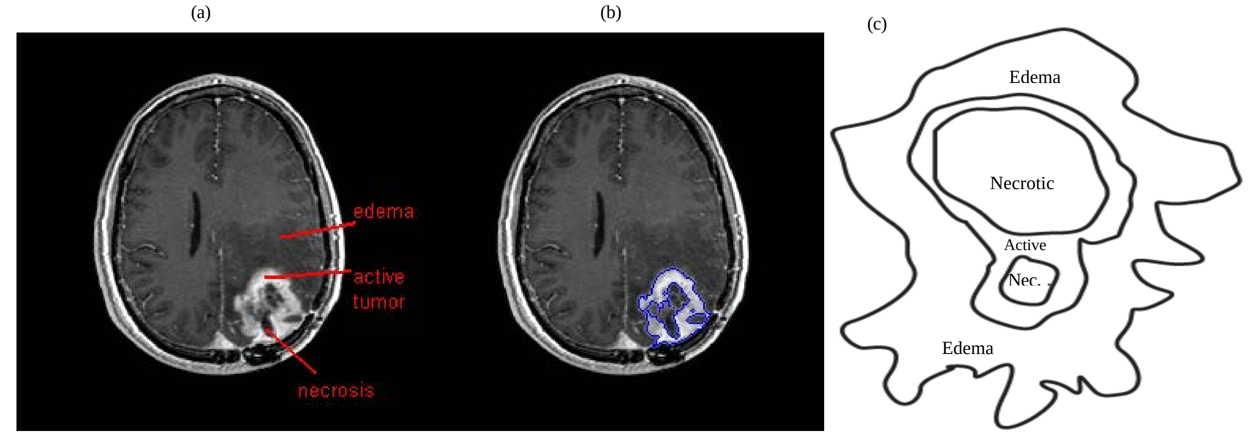

Fig. 1: a, b) Example of the a GBM brain tumor on a T1w post contrast MR image slice and the corresponding tumor contour and c) different heterogeneous regions of the brain tumor and label them as edema, active or necrotic

7. The improvisation of the new harmony is performed as follows:
   The random value generated should be less than the HMCR then
   $x^c_{new}(j) = x_I^c$ where a = 1,2,3,...,HMS
   Then it should be verified with the PAR value if r_2 is less than the PAR value then $x^c_{new}(j) = x^c_a(j)+/-r_3.BW$. Here, r_1, r_2, r_3 are generated by the operation rand (0,1) which selects a value between 0 and 1
   The newly generate harmony is then compared with the lower bound value if it is <l(j) then the new harmony is assigned l(j)
   If the value is greater than the u(j) then the new harmony is assigned with the u(j)
   If every condition as stated as above does not satisfied then the value is calculated as follows:

   $x^c_{new}(j) = 1(j)+r.u(j)-1(j)$ where $r \in$ rand (0,1)

8. Update the HM as $x^c_{worst} = x^c_{new} =$ if $f(x^c_{new})>f)(x^c_{worst})$
9. If NI is completed, then go to next step. Otherwise go to step 6
10. Select the harmony that has the best x^c_{best} objective function value
11. Apply the thresholds values contained x^c_{best} in to the image

Computational procedure: The computational procedure of a basic HSA can be summarized as in Algorithm 1. This procedure is implemented for minimization. If the intention is to maximize the objective function, a sign modification of step 4 ($x_w = x_{new}$ if $f(x_{new} > f(x_w)$) is required. In this HSA is used for maximization process (Fig. 1a-c).

The proposed GBM tumor segmentation system: The proposed medical image segmentation system consists of four stages: pre-processing, finding cluster centers using HSO, segmentation using FCM, tumor extraction using active contours and validation stages. The main idea of HSO is to reduce the number of iterations done by initializing the right cluster centers to fuzzy c-means clustering techniques that, of course, minimizes execution time and give qualitative results. The results of our experiments clarified that our Hybrid Clustering Method (HSOFCM) can detect a tumor that cannot be detected by Fuzzy C-means with less execution time. The main stages of the proposed system will be discussed in more detail in the subsequent sections.

De-noising: MRI preprocessing is an active field of research that attempts to enhance and correct MR images for posterior analysis. In an unsupervised approach there is no reference or manual labeling from which to learn the models of the tissues so common artefacts such as noise. MRI images are usually corrupted by disturbances like Gaussian and Poisson noise (Rodrigues *et al*., 2008). The vast majority of the de-noising algorithms assume additive white Gaussian noise. There are some algorithms that designed for Gaussian noise elimination such as edge preserving bilateral filter, total variation and non-local means. In this research we used median filter (Arias-Castro and Donoho, 2009). Median filtering is a nonlinear filter that is used as an effective method for removing noise while preserving edges. It works by moving pixel by pixel through the image, replacing each value with the median value of neighboring pixels. The pattern of neighbors is called the “window” which slides pixel by pixel over the entire image. The median is calculated by first sorting all the pixel values from the window into numerical order and then replacing the pixel being considered with the middle (median) pixel value.

HSO for cluster center initialization:

Step 1 (Harmony representation): Each harmony (candidate solution) uses k different elements as decision variables within the optimization algorithm. Such decision variables represent a different threshold point th that is used for centre selection. Therefore, the complete population is represented as:

$$\begin{aligned} HM &= [x_1^c x_2^c, \ldots. x_{HMS}^c, HMS] \\ x_i^c &= [th_1^c, th_2^c, \ldots, th_k^c] \end{aligned} \quad (5)$$

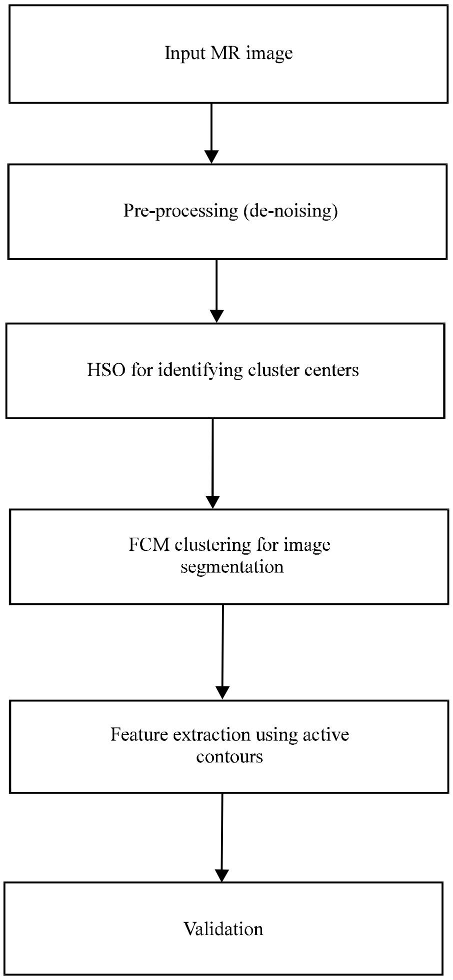

Fig. 2: Block diagram of the proposed GBM tumor segmentation approach

Where:

T = Refers to the transpose operato
HMS = The size of the harmony memory
x_i = The ith element of HM and c = 1 is chosen

For this problem, the boundaries of the search space are set to i = 0 and u = 255 which correspond to image intensity levels (Fig. 2).

Step 2 (HMA implementation): The proposed algorithm has been implemented considering Otsu method (Mahdavi *et al*., 2007) as objective function:

$$J(TH)=\max(\sigma^{2c}(TH)), 0 \le th_i \le L-1, i = 1, 2, 3, \ldots, k \quad (6)$$

where, TH = $\{th_1, th_2, th_3, \ldots, th_{k-1}\}$ is a vector containing multiple thresholds and the variances are computed through:

$$\sigma^{2c} = \Sigma_{i=1}^{k} \sigma_i^c = \Sigma_{i=1}^{k} w_i^c \, (u_i^c - u_T^c)^2 \quad (7)$$

Here, i represents the i class, w_i^c and u_j^c are respectively, the probability of occurrence and the mean of a class. In MT such values are obtained as:

$$w_i^c(th) = \Sigma_{i=1}^{th_i} ph_i^c \text{ and } u_i^c = \Sigma_{i=1}^{th_i} \frac{iph_i^c}{w_i^c(th_i)}$$

Step 3 (Parameter setting): The performance of HSA is strongly influenced by values assigned to parameters HM, HMCR, PAR, BW and NI. Determining the most appropriate parameter values for an arbitrary problem is a complex issue, since such parameters interact to each other in a highly nonlinear manner and no mathematical models of such interaction currently exist. The common method to find the best set of parameter values is to fix each parameter value to a random number within the parameter limits and then HAS is executed. If the final result is not satisfactory; then a new set of parameter values is defined and the evolutionary algorithm is executed again. In order to reduce the number of experiments in this study, it has used the factorial design method proposed by Costa *et al*. (2005) and Khadwilard *et al*. (2012) to systematically identify the best parameters of HSA. The factorial design method (Hunterand Hunter, 1978) is a statistical technique that evaluates at the same time all process variables in order to determine which ones really exert significant influence on the final response. All variables are called factors and the different values chosen to study the factors are called levels. The factors to be considered in the factorial design are the HSA parameters, the Harmony Memory (HM), the Harmony Memory Consideration Rate (HMCR), the Pitch Adjusting Rate (PAR), the Distance Bandwidth (BW) and the number of Improvisations (NI) whereas the response is the best fitness value obtained as a consequence of the HSA execution.

Step 4: With the best possible configuration of HSA using image histograms and the Otsu functions cluster centers are generated (Otsu, 1979).

Fuzzy C-Means (FCM) algorithm: The fuzzy c-means (Zhang *et al*., 2010) is an unsupervised clustering algorithm. The main idea of introducing fuzzy concept in the fuzzy c-means algorithm is that an object can belong simultaneously to more than one class and does so by varying degrees called memberships. It distributes the membership values in a normalized fashion. It does not require prior knowledge about the data to be segmented. It can be used with any number of features and number of classes. The fuzzy c-means is an iterative method which tries to separate the set of data into a number of compact clusters. The fuzzy c-means algorithm is summarized as follows.

Algorithm fuzzy c-means(x, n, c, m)

Input: n = Number of pixels to be clustered

$x = \{x_1, x_2, ..., x_n\}$: pixels of real time image

c = Number of clusters and centroids are estimated by HSO

m = 2: The fuzziness parameter

Output: u: Membership values of pixels and segmented image

Begin:

Step_1: Initialize the membership matrix u_{ij} is a value in (0, 1) and the fuzziness parameter m (m = 2). The sum of all membership values of a pixel belonging to clusters should satisfy the constraint expressed in the following.

$$\sum_{j=1}^{c} u_{ij} = 1 \tag{8}$$

for all i = 1, 2,……., n where (c = 2) is the number of clusters and n is the number of pixels in the image

Step_2: Compute the centroid values for each cluster c_j. Each pixel should have a degree of membership to those designated clusters. So, the goal is to find the membership values of pixels belonging to each cluster. The algorithm is an iterative optimization that minimizes the cost function defined as follows:

$$F = \sum_{j=1}^{N} \sum_{i=1}^{c} u_{ij}^{m} \left\| x_j - c_i \right\|^2 \tag{9}$$

where u_{ij} represents the membership of pixel x_j in the ith cluster and m is the fuzziness parameter.

Step_3: Compute the updated membership values u_{ij} belonging to clusters for each pixel and cluster centroids according to the given formula. If x_j is noisy pixel get the pixel from R(i, j):

$$u_{ij} = \frac{1}{\sum_{K=1}^{c} \left(\left(\frac{\left\| x_j - v_i \right\|}{x_j - v_k} \right)^{2/(m-1)} \right)} \text{ and } \qquad v_i = \frac{\sum_{j=1}^{N} u_{ij}^{m} x}{\sum_{j=1}^{N} u_{ij}^{m}} \tag{10}$$

Step_4: Repeat steps 2-3 until the cost function is minimized.

Feature extraction using active contours: Chan-Vese model for active contours (Chan and Vese, 2001). is a powerful and flexible method which is able to segment many types of images including some that would be quite difficult to segment in means of classical segmentation, i.e., using thresholding or gradient based methods. This model is based on the Mumford-Shah functional (Mumford and Shah, 1989) for segmentation and is used widely in the medical imaging field, especially for the segmentation of the brain, heart and trachea (Rousseau and Bourgault, 2008). The model is based on an energy minimization problem which can be reformulated in the level set formulation, leading to an easier way to solve the problem.

RESULTS AND DISCUSSION

In this study, The performance of the HSOFCM is compared with k-means (Bandhyopadhyay and Paul, 2013), conventional FCM (Zang *et al*., 2010), FFCM (Kalaiselvi and Somasundaram, 2011). We present the experimental results on The Brain Tumor Image Segmentation (BRATS) Benchmark dataset (Menze *et al*., 2014) is used. In this experiment The BRATS dataset is publicly available through the annual Medical Image Computing and Computer Assisted Intervention (MICCAI) Society brain tumor segmentation challenge (Menze *et al*., 2014). The dataset consists of 30 fully anonymized multi-contrast MR scans of glioma patients along with expert annotations, i.e., ground truth manual segmentations. We use 22 images of the FLAIR MRI (axial plane) modality. Figure 3-6 are DS1(Dataset1), DS2, DS3 and DS4, respectively. The experiments were performed on a 2.99 GHz Intel Core 2 Duo processor, Windows XP with 3.21 GB RAM, using Matlab R2012a.

Segmentation results on BRATS data set are shown in Fig. 3. The algorithms k-means (Fig. 3b), FCM (Fig. 3c), FFCM (Fig. 3d) and HSOFCM (Fig. 3e). From these results it is obvious that K-Means, FCM, are very sensitive to the noise while the result and efficiency of FFCM are not satisfied. Though FFCM provide better segmentation there exist obvious misclassification pixels. Visually, the proposed method achieves the better result, over k-means, FCM, FFCM. Similarly Fig. 7 and 8 achieves betters results.

Quantitative results: Performance of different image segmentation algorithm can be compared with following parameters:

- True Positive (TP): both proposed segmentation algorithm and Ground Truth (GT) are positive
- True Negative (TN): both proposed segmentation algorithm and Ground Truth (GT) are negative
- False Positive (FP): proposed segmentation algorithm result is positive and Ground Truth (GT) are negative
- False Negative (FN): proposed segmentation algorithm result is negative and Ground Truth (GT) is positive

$$\text{Sensitivity} = TP/(TP+FN)\times 100\%$$

$$\text{Specificity} = TN/(TN+FP)\times 100\%$$

$$\text{Accuracy} = (TP+TN)/(TP+TN+FP+FN)\times 100\%$$

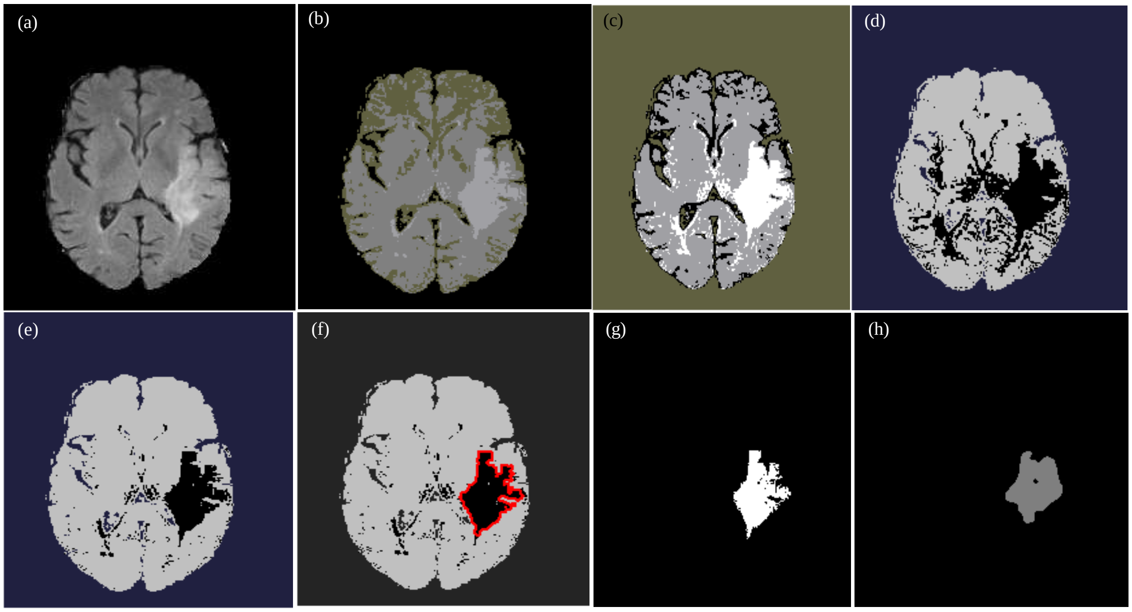

Fig. 3: DS1 image; a) Original image; b) k-means; c) FCM; d) FFCM; e) HSOFCM; f) HSOFCM with active contours; g) extracted feature thresholding on Fig. 3e; h) Ground truth

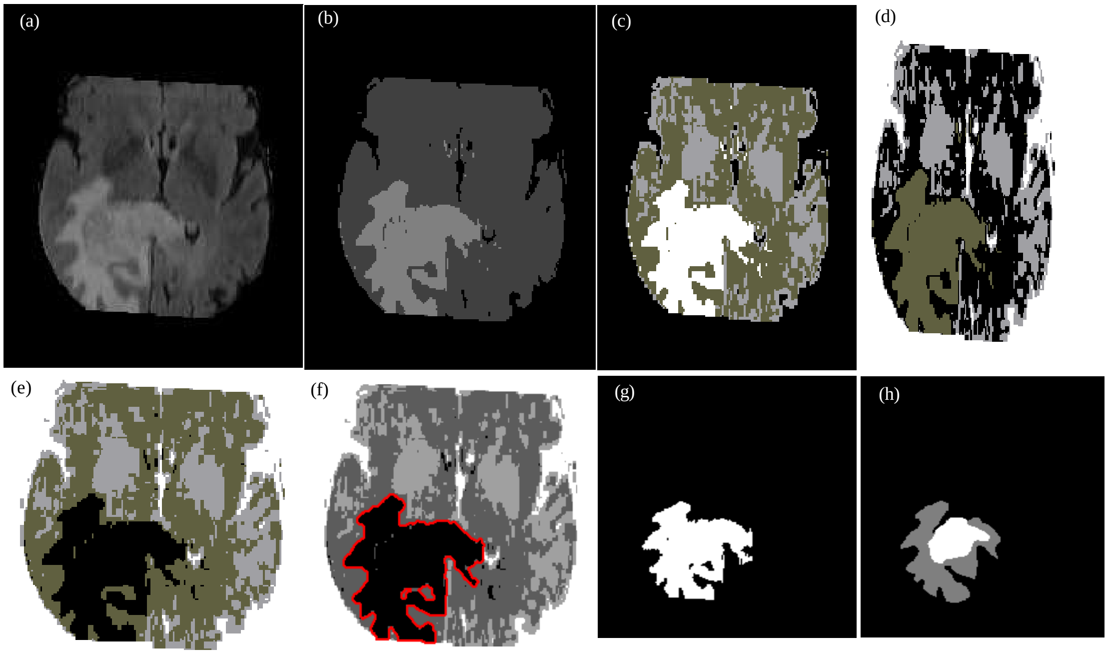

Fig. 4: DS2 image; a) Original image; b) k-means; c) FCM; d) FFCM; e) HSOFCM; f) HSOFCM with active contours; g) Extracted feature (Thresholding on Fig. 4e); h) Ground truth

Computational cost: In terms of computational cost, the objective function of FCM algorithm in its original form (Schmidt, 2005) contains only the difference between the grayscale of the current pixel i and the cluster centers V_j. This is basically to cluster grayscales as there is no spatial information so, it less computational cost. The enhancement of original FCM, (Verma *et al.*, 2008) modified the objective function by adding a term for the spatial information of neighboring pixels. The FFCM algorithm is computationally low as it initializes the cluster

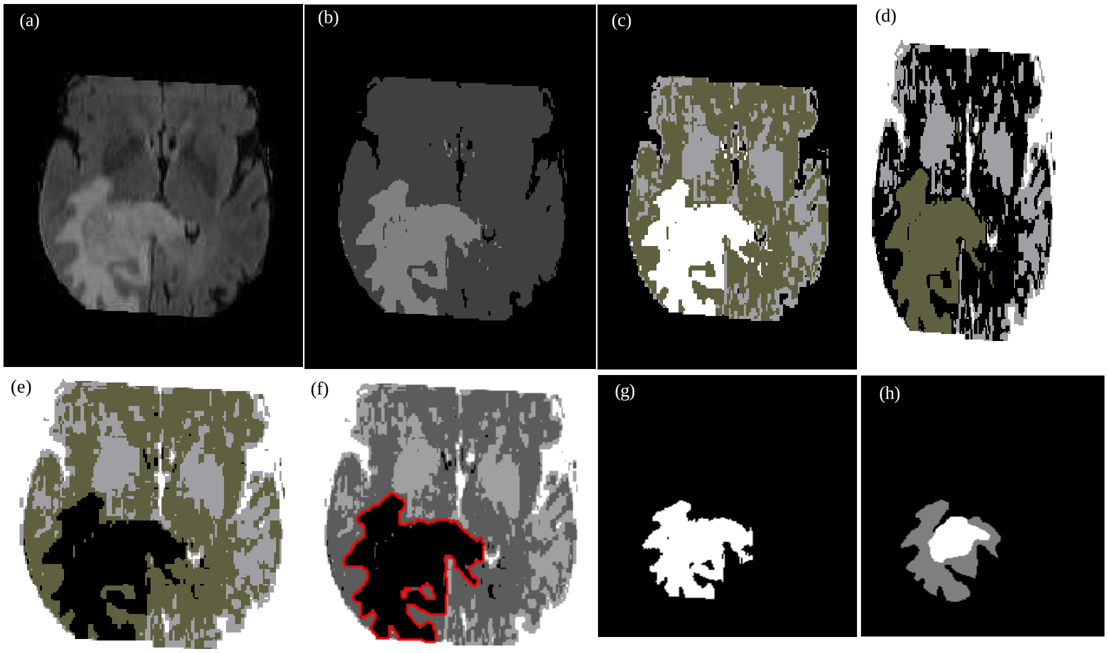

Fig. 5: DS3 image; a) Original image; b) k-means; c) FCM; d) FFCM; e) HSOFCM; f) HSOFCM with active contours; g) Extracted feature (Thresholding on Fig. 5e); h) Ground truth

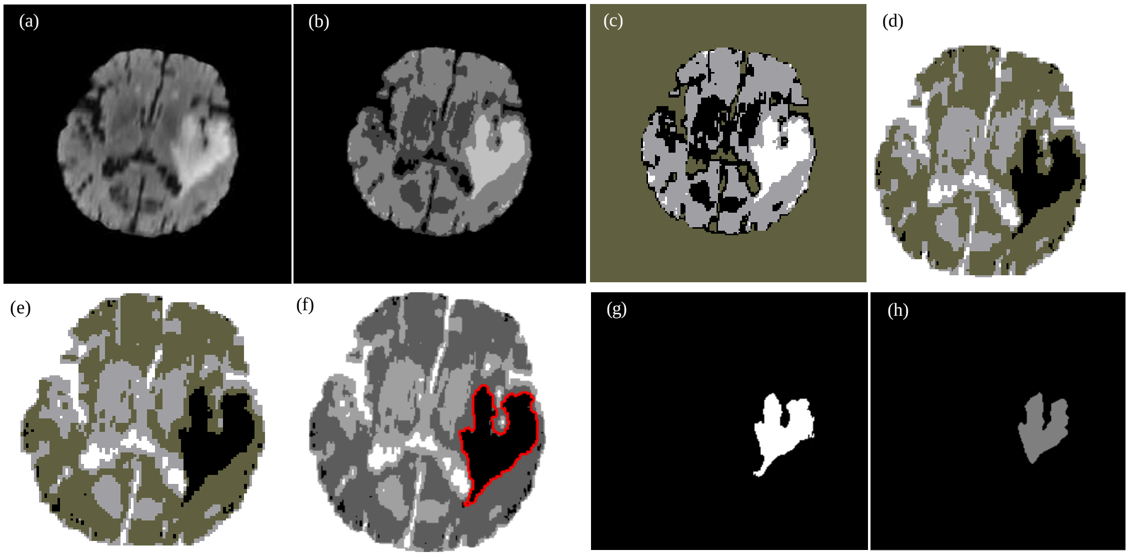

Fig. 6: DS4 image; a) Original image; b) k-means; c) FCM; d) FFCM; e) HSOFCM; f) HSOFCM with active contours; g) Extracted feature (Thresholding on Fig. 6b); h) Ground truth

Table 1: Comparison of average classification performance for the proposed technique and other methods

Variables	FCM (%)	FFCM (%)	Proposed method (%)
Sensitivity	91.4	92.8	96.1
Specificity	88.3	90.2	94.7
Accuracy	92.6	93.5	97.3

Table 2: Comparison in number of iterations

Variables	FCM (%)	FFCM (%)	Proposed method (%)
DS1	81	67	45
DS2	48	44	22
DS3	62	53	34
DS4	56	39	21

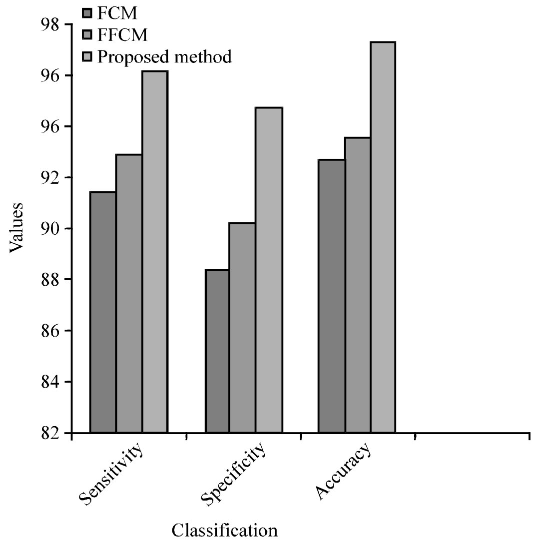

Fig. 7: Comparison of average classification performance for the proposed technique and other methods

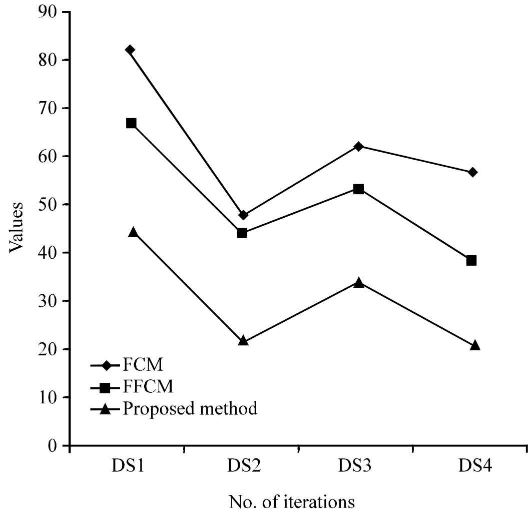

Fig. 8: Comparison in number of iterations

center with local maxima. The proposed algorithm having the lowest computational cost 45, 22, 34 and 21 iterations for DS1-DS4, respectively (Table 1and 2).

CONCLUSION

Image segmentation plays a significant role in medical image processing. In this study, we proposed a new FCM algorithm with harmony search optimization technique for cluster center initialization. Fuzzy c-means can predict tumor cells. In order to improve the performance of traditional FCM we developed a new approach that integrates the HSO and fuzzy c-means algorithm to detect GBM tumor accurately and in minimal execution time. Our framework consists of four stages: pre-processing (de- noising), clustering (HSO based Fuzzy c-means), extraction of tumor using active contours and validation stages. From the experimental results, we proved the effectiveness of our approach in GBM tumor segmentation by comparing it with traditional FCM and FFCM algorithms. The proposed system determines the initial cluster centers from HSO to minimize the execution time and gets the optimal solution in 45 iterations for DS1 where as FCM takes 81 iterations. The performance of the proposed technique, its minimization time strategy and its quality has been demonstrated qualitatively and quantitatively.

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