Brain Image Segmentation using Conditional Random Field based on Modified Artificial Bee Colony Optimization Algorithm

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Abstract – Tumor is an uncontrolled growth of tissues in any part of the body. Tumors are of different types and they have different characteristics and treatments. Brain tumor is inherently serious and life-threatening because of its character in the limited space of the intracranial cavity (space formed inside the skull). Locating the tumor within MR (magnetic resonance) image of brain is integral part of the treatment of brain tumor. This segmentation task requires classification of each voxel as either tumor or non-tumor, based on the description of the voxel under consideration. Many studies are going on in the medical field using Markov Random Fields (MRF) in segmentation of MR images. Even though the segmentation process is better, computing the probability and estimation of parameters is difficult. In order to overcome the aforementioned issues, Conditional Random Field (CRF) is used in this paper for segmentation, along with the modified artificial bee colony optimization and fuzzy possibility c-means algorithm. This research work is focused to reduce the computational complexity and achieving higher accuracy. The performance of this work is evaluated using region non-uniformity, correlation and computation time. The experimental results are compared with the existing approaches such as MRF with improved Genetic Algorithm (GA) and MRF-Artificial Bee Colony (MRF-ABC) algorithm.

Keywords: Conditional random field, Magnetic resonance, Markov random field, modified artificial bee colony

1. Introduction

Medical image segmentation is an essential step in many image analysis tasks. The process of partitioning a digital image into multiple regions or sets of pixels is called image segmentation. In principle, partitions are different objects in image, which have same texture or colour. The result of image segmentation is a set of regions that collectively cover the entire image or a set of contours extracted from the image [1, 2]. All the pixels in a particular region are similar with respect to some characteristic feature or a computed property, such as colour, intensity or texture. Adjacent regions are significantly different with respect to same characteristics. The segmentation of anatomic structure of the brain plays a crucial role in neuro-image analysis. Efficient numerical algorithms help the researchers, physicians and neurosurgeons to investigate and diagnose the structure and functions of the brain, when it is healthy or affected by tumor. There is a need for segmentation techniques that are robust and use a broad range of anatomic structures, tumor affected images and different image types [3, 4].

Nomenclature

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$x$</td>
<td>Set of vowels</td>
</tr>
<tr>
<td>$y$</td>
<td>Set of labels</td>
</tr>
<tr>
<td>$C_1, C_2, C_3, C_4, \ldots, C_{nm}$</td>
<td>Set of clique</td>
</tr>
<tr>
<td>$\alpha$</td>
<td>Membership matrix</td>
</tr>
<tr>
<td>$\beta$</td>
<td>Possibilistic matrix</td>
</tr>
<tr>
<td>$\gamma$</td>
<td>Resultant cluster center</td>
</tr>
<tr>
<td>$\zeta$ and $\lambda$</td>
<td>Cluster number and data point</td>
</tr>
<tr>
<td>$u_{ik}$ and $t_{ik}$</td>
<td>Membership function</td>
</tr>
<tr>
<td>$p$</td>
<td>No-of white pixels</td>
</tr>
<tr>
<td>$W$</td>
<td>Width</td>
</tr>
<tr>
<td>$H$</td>
<td>Height</td>
</tr>
<tr>
<td>$\sigma^2$</td>
<td>Variance of the whole image</td>
</tr>
<tr>
<td>$\sigma_f^2$</td>
<td>Foreground variance</td>
</tr>
<tr>
<td>$F_T$ and $B_T$</td>
<td>Foreground and background area pixels for the test image</td>
</tr>
<tr>
<td>$D(K)$</td>
<td>Dice Index</td>
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</table>
Magnetic Resonance Imaging (MRI) is an advanced medical imaging technique providing rich information on the soft tissue anatomy of the human brain. It has several advantages over the other imaging techniques enabling it to provide three-dimensional (3D) data with a high contrast between soft tissues. However, the amount of data available is far too much for manual analysis/interpretation and this has been one of the biggest obstacles in the efficiency of MRI. For this reason, automatic or semi-automatic techniques of computer aided image analysis have become essential. Segmentation of the MR images into different tissue classes, namely, gray matter (GM), white matter (WM) and tumor is an important task in the entire process.

A wide variety of approaches have been proposed and used for segmentation of MR image of human brain. Statistical approaches, especially parametric ones, are widely employed in the segmentation of brain [5, 6]. These methods label the pixels according to their probability values, which are determined based on the intensity distribution of the image. After making suitable assumption about the distribution, statistical approaches attempt to solve the problem of estimating the associated class label, given the intensity for each pixel. Such estimation is necessarily formulated from an established criterion. Maximum a posteriori (MAP) or maximum likelihood (ML) principles are examples for such criteria. Before these criteria can be assessed, the formula for the density function of the pixel intensity has to be chosen carefully [7]. Finite Mixture (FM) models, in particular, the Finite Gaussian Mixture (FGM) model when the Gaussian likelihood distribution is assumed [8, 9], is one of the most widely used models in segmentation. FM models have a number of elegant features and are mathematically simple. However, being a histogram-based model, the FM has an intrinsic limitation that the spatial information is not taken into account since all the data points are considered to be independent samples drawn from a given population. Such a limitation causes the FM model to work only on well-defined images with low levels of noise. Unfortunately, this is often not the case with MR images due to artifacts such as the partial volume effect and bias field distortion. Under these conditions, FM model-based methods produce unreliable results.

Brain tumor segmentation in multimodal image data plays a major role in different clinical areas such as radiology, radiotherapy and longitudinal studies. Fully automated segmentation methods facilitate the otherwise cumbersome and time consuming manual segmentation process. There are a number of techniques to segment an image into regions that are homogeneous. Not all the techniques are suitable for medical image analysis due to the complexity and inaccuracy. There is no standard image segmentation technique that can produce satisfactory results for all the imaging applications such as brain MRI, brain tumor diagnosis, etc. Optimal selection of features, tissues, brain and non-brain elements are considered to be the key obstacles for brain image segmentation. Accurate segmentation over full field of view is another hindrance.

2. Related Works

Li et al used knowledge-based thresholding in multimodal MRI data to classify the voxels into multiple intensity categories [10]. In each axial slice, they computed the centroid of voxels categorized as brain. Four points defining a quadrangle were found at the edge of the brain by tracing left, right, up and down from the centroid to a transition in tissue categories. All voxels outside the quadrangle that are not categorized as brain tissues are then masked to define the intracranial contour. This method works only in slices, where the brain constitutes a fairly homogeneous region.

The Ant Colony Optimization (ACO) based image edge detection approach, proposed by Jing Tian et al. aims to utilize the number of ants to move on a 2D image for constructing a pheromone matrix. Each entry of the matrix represents the edge information at each pixel location of the image [2]. Furthermore, the movements of the ants are steered by the local variation of the intensity values of the images. The proposed approach starts from the initialization process and then runs for ‘n’ iterations to construct the pheromone matrix, by iteratively performing both construction and update processes. Finally, the decision process is performed to determine the edge.
The significant part of research in the area of edge detection in the medical images uses specially tailored algorithms. While these algorithms perform efficiently for detecting edges in a certain modality or a certain anatomical structure, they are brittle, in the sense that they cannot be generalized to other modalities or anatomic structures. A robust algorithm is thus essential to overcome this brittleness. GA’s are robust in that they are not affected by spurious local optima in the solution space. This robustness is backed up by a strong mathematical foundation. Many advanced GA operators have been designed for performing effective search of the solution space and speeding up the convergence of solutions. GAs have been previously used in different areas of image processing such as edge detection, image interpretation, image segmentation and contour matching [2].

Most interesting genetic application in edge detection is by Gudmundsson et al and is described in this section. Edges are represented in a binary image, where each pixel takes on either the value 0 (off) for a non-edge pixel or 1 (on) for an edge pixel. Each pixel in the binary map corresponds to an underlying pixel in the original image. This edge representation is simple, which allows direct illustration of results, location of edge points that map directly onto the original image. The adjacency and orientation are preserved during the process. By using the edge map as a solution space for the GA, no special mappings are required. A small neighbourhood window can be overlaid, and edge structures and pixels can be modified on a local, intuitive basis. Furthermore, this representation allows for an easy transition into an extended type of chromosome for the GA, the bit array. A bit array as an array of bits, instead of the conventional bit vector, or string, is used in traditional GAs. A bit array is highly compact, leading to a compact memory usage, which is essential when running a simulation with a large population, or a large image.

Brummer et al. used histogram analysis and morphology to generate a 3D brain mask [11]. Using the model of background noise, they first generated a mask of the head automatically and performed intensity correction on the masked volume. Next, an initial brain mask was created using an automatic threshold based on a pre-supposed brain voxel intensity distribution. Then the regions in the brain mask that were too close to the edge of the head were eliminated. Finally, novel morphological operations were used to clean up the resulting mask. The method relies on a priori intensity correction to deal with RF in homogeneity, hence cannot be used retroactively.

Neural networks have been applied in many image segmentation problems such as edge detection. There are many image-based edge detection algorithms using neural networks, the most successful system was introduced by Rowley et al. The neural network technique presented in this section is such an approach and functions just like a pattern classifier, which collects the input features and outputs the decisions [12].

Although MRF modeling and its application in image segmentation have been investigated by many other researchers [13-15], only in recent years, has MRF theory has become popular in MR image segmentation. However, most of the available methods use MRF only as a general prior in an FM model-based parametric approach to build the MAP estimation. They either lack in proper parameter estimation step to fit the FM model [16, 17] or the parameter estimation procedure they use, such as ML or EM [18-20]. In general, although an MRF prior can improve the performance, the FM assumption is still a big limitation.

2.1. EXISTING METHODOLOGY

MRF based image segmentation using ABC

A. Markov random field

In medical image processing, MRF technique is mostly used for segmentation and with the labels of the neighbouring elements, the images are classified. The traditional image segmentation methods are classified based on the data identity only and not on the labels of the other elements. The image features such as set of vowels $x = \{x_1, \ldots, x_n\}$ and labels $y: p(x|y) = p(x|y)$ are joint probability, modeled by generative approach of MRF and it is calculated by assumptions of the system. The system deduces the likelihood factorized form such as $p(x|y) = \prod_i p(x_i|y_i)$ and it has some restrictions such as independence assumptions and modeling of complex dependencies that are not allowed between features and labels. Usually the set of sites used for segmentation are defined as clique but in MRF model, a clique is defined by a set of sites ‘s’, and the clique in neighborhood system is defined as $\{C_1, C_2, C_3, \ldots, C_m\}$. p(x|y) = \frac{1}{Z} \exp \{\sum_{i \in S} \log(p(x_i|y_i) + \sum_{e \in C} \nu_c(y_e))\}, \quad (1)$

where, $C$ is a set of cliques in the neighborhood (defined here as a set of $k$ planar neighbors). $\nu_c(y_e)$ is a clique potential function of labels for the clique $c \in C$.
and z normalizes over all possible labeling. The Gaussian assumption allows us to use ML parameter estimation.

Each employee bee is moved onto her food source area for influencing an alternative food source within the neighbourhood of the current one and then its nectar amount is evaluated. If the nectar amount of the new one is higher, then the bees forget the preceding one and remember the new one. When the employed bees complete their search, they are back to the hive and share their data about the nectar amounts of their food sources with the onlooker bees waiting in the hive. If the nectar quantity of a food source is higher on comparing with other food sources, then the probability of choosing this source by the onlooker will be more. This method is comparable to the natural selection process in evolutionary algorithms. Each onlooker bee determines a neighbour food source surrounded by the neighbourhood of the one to which she has been allocated and its nectar amount is evaluated.

**Limitations**

- The main disadvantage of MRF-based methods is that, the objective function associated with most non-trivial MRF problems is extremely non-convex and as such the minimization problem is computationally very taxing. Computing the probability and the parameter estimation are difficult tasks in MRF.
- The fundamental ABC algorithm is simple, robust, and can be easily controlled. But, as a random optimization technique, ABC has slow convergence features and easily gets stuck on local solutions.

### 3. Methodology

#### 3.1. Preprocessing and Enhancement Process

**A. Image Acquisition**

To access and use the real medical images for carrying out research is a very difficult due to various technical problems. The MRI data for the research is obtained from the Brain Web Database at the McConnell Brain Imaging Center of the Montreal Neurological Institute (MNI), McGill University. Sample T1-weighted images of size 181x217x36 were taken and used for enhancement and segmentation purpose. T1-weighted images show the water content of the brain, darker and the fat content of the brain, brighter. The images were acquired in MINC format, which are then converted to JPEG format before the processing. Figure 3 shows the MR image immediately after acquisition.
The acquired MR image of the brain consists of lot of film artifacts and labels, which include patient’s name, age and marks for identification on the MRI. These film artifacts were removed using tracking algorithm. The tracking algorithm starts from the first row and first column of the image. The intensity values of the pixels were analyzed using the threshold value of the film artifacts. If the pixel intensity value is greater than that of the threshold value then that pixel intensity was made to zero and removed from MRI. The high intensity values of film artifacts were removed from MR image of the brain. Separate threshold values were set for the labels and the skull region so that the unwanted parts of the MR image of the brain can be removed. Figure 4 shows the image after removing the artifacts.

The CWM filter is a type of weighted median filter, which gives more weight only to the central pixel of each window. This filter can preserve the fine image details while suppressing additive white and impulsive-type noise. When comparing the properties of the CWM filter with other median filters, it is very clear that the CWM filter along with the HE can outperform other median filters.

### 3.2. Image Segmentation

#### A. Conditional Random field

Conditional Random Fields (CRFs) are undirected graphical models that encode a conditional probability distribution using a given set of features [23]. CRFs are defined as follows.

Let \( G \) be an undirected model over sets of random variables \( y \) and \( x \). As a typical special case, \( y = \{y_t\} \) and \( x = \{x_t\} \) for \( t = 1, \ldots, T \), so that \( y \) is a labeling of an observed sequence \( x \). If \( C = \{y_t, x_c\} \) is the set of cliques in \( G \), then CRFs define the conditional probability of a state sequence given the observed sequence as:

\[
p_{\lambda}(y|x) = \frac{1}{Z(x)} \prod_{c \in C} \Phi(y_c, x_c),
\]

(2)

where \( \Phi \) is a potential function and the partition function \( Z(x) = \sum_{y} \prod_{c \in C} \Phi(y_c, x_c) \) is a normalization factor over all state sequences for the sequence \( x \). It is assumed that the potentials factorize according to a set of features \( \{f_k\} \), which are given and fixed, so that

\[
\Phi(y_c, x_c) = \exp \left( \sum_{k} \lambda_k f_k(y_c, x_c) \right),
\]

(3)

The model parameters are a set of real weights \( \Lambda = \{\lambda_k\} \), one weight for each feature.

**Maximum a Posteriori**
The training data is fully observed, i.e., \( D = \{(x,y)\} \), and for each state sequence, an output sequence pair is independently and identically distributed (IID). Maximum a posteriori (MAP) estimation is used to maximize the equation. The prior, \( p(\lambda) \), encodes some prior knowledge that one might have known about the distribution over parameter values. The prior is used for smoothing (regularisation), such that over-fitting of the training sample is minimized and therefore generalization accuracy is not compromised. When the parameter \( \lambda_k \) is zero, the corresponding feature \( f_k \), is ignored. When all the parameters are zero, the distribution \( p(y|x) \) is uniform. Making an a priori assumption of uniformity is a reasonable one and is consistent in nature with the maximum entropy principle, which also maximizes uniformity. The Gaussian probability density function is:

\[
p(\lambda_k) = \frac{1}{\sigma_k \sqrt{2\pi}} \exp \left( -\frac{(\lambda_k - \mu_k)^2}{2\sigma_k^2} \right),
\]

where, \( \mu_k \) is the mean for parameter \( \lambda_k \) and \( \sigma_k \) are the standard deviations. The MAP based on log-likelihood, after excluding constant terms is given in the equation 5.

\[
L^{\text{MAP}} = L - \frac{1}{2} \sum_k \left( \frac{\lambda_k - \mu_k}{\sigma_k} \right)^2,
\]

**B. Minimizing the Maximum a Posteriori using Modified ABC and FPCM**

**Modified Artificial Bee Colony optimization**

Artificial Bee Colony (ABC) algorithm was proposed by Karaboga for optimizing numerical problems. The algorithm simulates the intelligent foraging behavior of honey bee swarms. The artificial bee colony algorithm is a population-based stochastic optimization algorithm and it is very simple and robust. Compared with those of other well-known modern heuristic algorithms such as genetic algorithm, differential evolution, particle swarm optimization, the performance of artificial bee colony algorithm is better or similar with the advantage of employing fewer control parameters.

In artificial bee colony algorithm, each cycle of the search consists of three steps: first, sending the employee bees onto their food sources and evaluating their nectar amounts; second, after sharing the nectar information of food sources, the selection of food source regions by the onlooker and evaluating the nectar amount of the food sources; third, determining the scout bees and sending them randomly onto possible new food sources.

Based on the above descriptions, an improved artificial bee colony algorithm is proposed to maximize the effective coverage of area: max \( \{ R_{\text{area}}(S) \} \). The fitness value function is defined as \( f = R_{\text{area}}(S) \). At the first step, the algorithm generates a randomly distributed initial population \( P \) of \( Q \) solutions, where \( Q \) denotes the size of employed bees or onlooker bees. Each solution is a \( 2N \)-dimensional vector: \( v_i = (x_i^1, y_i^1, x_i^2, y_i^2, ..., x_i^N, y_i^N) \), \( i = 1, 2, ..., Q \), where \( N \) is the number of sensor nodes, and we define \( v_{ij} = (x_{ij}^1, y_{ij}^1) \) as the position of node \( j \). After initialization, the population of the positions is subject to repeated cycles of the search processes of the employee bees, the onlooker bees and the scout bees.

An employee bee produces a modification on the position in her memory depending on the local information. In order to produce a candidate position from the old one in memory, the proposed algorithm uses the equation 6.

\[
v_{ij} = v_{ij} + \phi_{ij} (v_{ij} - v_{kj}),
\]

Where, \( k \in \{1,2,...,Q\} \) and \( j \in \{1,2,...,N\} \) are randomly chosen indexes and \( k \neq j \). \( \phi_{ij} \) is a random number between -1 and 1.

An artificial onlooker bee chooses the position (solution) depending on the probability value associated with it and it will do local search near the position. The probability value \( p_i \) of each position is calculated using the equation 7.

\[
p_i = \frac{f_i}{\sum_{n=1}^{Q} f_n},
\]

In the proposed algorithm, each onlooker bee prefers the position with bigger \( p_i \), so it chooses the position \( v_j \) based on the pseudo-random proportional rule given by the equation 8.

\[
j = \left\{ \begin{array}{ll}
\arg \max \{f_i\}, & q \leq q_0 \\
\arg \max \{f_i\}, & i \in \{1,2,...,Q\} \\
J, & \text{Otherwise}
\end{array} \right.
\]

Where, \( q \) is a random variable uniformly distributing between the region 0 and 1; \( q_0 (0 \leq q_0 \leq 1) \) is parameter and \( J \) is a random variable. The pseudo-random proportional rule can assure that the onlooker bee selects the position with bigger \( p_i \) with larger possibility and can avoid precocious.

In the proposed algorithm, if a position cannot be improved further through a predetermined number of cycles, then it is assumed to be abandoned. The value of predetermined number of cycles is an important control
parameter of the algorithm, which is called “LimitCycle” for abandonment. Assume that the abandoned position is $v_i$ and the scout discovers a new position to be replaced with $v_i$. This operation can be defined as in equation 9.

$$v_i = v_{lb} + \text{rand}[0,1](v_{up} - v_{lb}). \quad (9)$$

Where, $v_{lb}$ is the lower boundary of the position and $v_{up}$ is the upper boundary of the position. In the proposed algorithm, besides abandoning the position with repeat cycles bigger than the LimitCycle, the worst position $v_{\text{worst}}$ with minimal fitness value in each cycle will be abandoned. The operation is same as in equation 9 and given in equation 10.

$$v_{\text{worst}} = v_{lb} + \text{rand}[0,1](v_{up} - v_{lb}). \quad (10)$$

After updating $v_{\text{worst}}$, the proposed algorithm can avoid local optimization and speed convergence. Based on the above description, the detailed pseudo-code of improved ABC algorithm is given below:

1: Initialize the population of solution, $v_i$, $i=1,2,...,Q$
2: Evaluate the population.
3: cycle=1.
4: repeat.
5: produce new solutions for the employee bees by using equation 6 and evaluate them.
6: calculate the probability values $p_i$ by equation 7.
7: apply pseudo-random proportional rule for each onlooker bee selecting solution and produce the new solutions with equation 6.
8: abandon the worst solution $v_{\text{worst}}$ and replace it with a new randomly produced solution by equation 10.
9: if a solution cannot be improved further through LimitCycle, replace it with a new randomly produced solution by equation 9.
10: memorize the best solution achieved so far.
11: cycle=cycle+1.
12: until cycle=MaxCycle.

Figure 5 Flow chart for Modified artificial bee colony optimization
**Fuzzy Possibilistic c-Means Algorithm (FPCM)**

Fuzzy possibility c-means algorithm was first mentioned by Pal et al in 1997 [24]. The algorithm comprises of possibility and membership values of both fuzzy logic and possibility c-means.

\[
\min_{(\alpha, \beta, \gamma)} \{ J_{m, \eta}(\alpha, \beta, \gamma, X) \} = \sum_{i=1}^{\eta} \sum_{k=1}^{\eta} (u_{ik}^m + t_{ik}^n)D_{ikA}, \tag{11}
\]

belongs to

\[
m > 1, \eta > 1, 0 \leq u_{ik}, t_{ik} \leq 1,
\]

and

\[
\sum_{i=1}^{\eta} u_{ik} = 1 \forall k, i.e., U \in M_{\eta \times c},
\tag{12}
\]

and

\[
\sum_{k=1}^{c} t_{ik} = 1 \forall i, i.e., T^i \in M_{c \times \eta},
\tag{13}
\]

where

- \( \alpha \): Membership matrix
- \( \beta \): Possibility matrix
- \( \gamma \): Resultant cluster center
- \( \varsigma \) and \( \lambda \): Cluster number and data point

The conditions for \( J_{m, \eta} \) are:

If \( D_{ikA} = \|x_k - v_i\|_A > 0 \) for all \( i \) and \( k, m, \eta > 1 \)

\( X \) contains at least \( c \) distinct data points

\( (\alpha, \beta, \gamma) \in M_{c \times \eta} \times M_{\eta \times c} \times \mathbb{R}^p, \tag{14} \)

may minimize \( J_{m, \eta} \) only if

\[
u_{ik} = \left( \sum_{i=1}^{\eta} \left( \frac{D_{ikA}}{D_{i,kA}} \right)^{\frac{1}{2/(m-1)}} \right)^{-1}, \quad 1 \leq i \leq c; 1 \leq k,
\tag{15}
\]

\[
t_{ik} = \left( \sum_{i=1}^{\eta} \left( \frac{D_{ikA}}{D_{i,kA}} \right)^{\frac{1}{2/(n-1)}} \right)^{-1}, \quad 1 \leq i \leq c; 1 \leq k,
\tag{16}
\]

\[
v_i = \frac{\sum_{k=1}^{c} (u_{ik}^m + t_{ik}^n)x_k}{\sum_{k=1}^{c} (u_{ik}^m + t_{ik}^n)}, \quad 1 \leq i \leq c,
\tag{17}
\]

The membership functions such as \( u_{ik} \) and \( t_{ik} \) are affected by cluster centers and mainly \( u_{ik} \) is affected by all \( c \) cluster centers while \( t_{ik} \) is affected by \( i \)-th cluster center \( c_i \) in the FPCM equations. The membership function is called as ‘relative typicality’, because \( t_{ik} \) is distributed by possibility term based on ‘\( n \)’ data points that are not on the cluster center. The degree points of the clusters are measured and the data point is also regulated by using the membership functions. The combination of fuzzy logic membership functions and possibility functions of PCM shows the good results when it is compared with traditional methods.

**Algorithm for CRF based MABC-FPCM**

Step 1: Read the human brain MRI images.

Step 2: Label the pixels with same gray value with same number.

Step 3: For each kernel in the image, calculate the posterior \( L_{MAP} \) value using conditional random field formula.

Step 4: The posterior values of all the kernels are stored in a separate matrix.

Step 5: Modified Artificial bee colony optimization is used to minimize the Maximum a posterior function.

6. Initialize number of iterations \( (\mu) \), number of bees \( (\phi) \), initial food position value \( (v_i) \), a constant value for food position update \( (\rho) \). Store the energy function values in \( S \). Initialize all the food position values with \( T_0 = 0.001 \).

For \( N \) times

For each pixel in the image

Calculate the probability value using

\[
\pi_i = \frac{f_i}{\sum_{n=1}^{Q} f_n},
\tag{18}
\]

For each bee update food position values using the modified equation of artificial bee colony

\[
v_{ij} = v_{ij} + \Phi_i (v_{ij} - v_{kj}),
\tag{19}
\]

then new position is updated

\[
v_{new} = (1 - \rho) v_{ij} + \rho v_{ij} + \rho v_{ij}
\tag{20}
\]

End

End

If the slave value is less than the master value, then the value is discarded, else, interchanged.

7. Select a random pixel for each bee, which was not selected previously.

8. Update the food position values for the selected pixels by all the bees.

The optimal value of MABC is used to select the initial cluster point \([33]\).

Calculate the cluster center \( C \)
\[ C = \left( \frac{N}{2} \right)^{1/2}, \]  \hspace{1cm} (21)

Compute the Euclidean distance
\[ D_{ij} = C_{cp} - C_{ni}, \]  \hspace{1cm} (22)

Update the partition matrix
\[ \sum_{i=1}^{c} u_{ij} = 1, \forall \{1, \ldots, n\}, \]  \hspace{1cm} (23)

\[ u_{ij} = \frac{1}{1 + \left[ \frac{d^2(x_i, v_j)}{\eta_i} \right]^{\gamma}}, \]  \hspace{1cm} (24)

\[ v_i = \frac{\sum_{k=1}^{n}(u_{ik}^m + t_{ik}^n)x_k}{\sum_{k=1}^{n}(u_{ik}^m + t_{ik}^n)}, \quad 1 \leq i \leq c, \]  \hspace{1cm} (25)

is the possibilistic typicality value of the training sample \( x_j \) belonging to the cluster ‘\( i \)’. \( m \in [1, \infty] \) is a weighting factor called the possibilistic parameter.

Compute the adaptive threshold using
\[ \text{Adaptive threshold} = \max(\text{Adaptive threshold}, C_i) \quad \text{for } i = 1 \ldots n \]

In the MRI image, the pixels having lower intensity values than the adaptive threshold value are changed to zero. The entire procedure is repeated for any number of times in order to obtain the more approximate value.

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**Figure 6: Proposed CRF-MABC based Algorithm**

- Read the MRI Image
- Pixels with same gray value are labeled with same number
- Calculation of Posterior Value using CRF
- Posterior Energy Values Stored in Matrix
- Random Search by Employee Bees
- Sharing the obtained information by employed bees with onlooker bees
- Apply pseudo random proportional rule for onlooker bee selecting solution
- Checking the stop criteria
- Achieving the Modified Intensity Matrix
- Performing the FPCM algorithm for achieving Modified Intensity Matrix
- Select the scout bees by onlooker bees and performing the recruitment process
- Random search by some silly employee bees
- Searching with guidance of scout bees

No

Yes

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Detection of the Shape of Brain Tumor

In the approximate reasoning step, the tumor area is calculated using the binarization method. In this method, the image has only two values either black or white (1 or 0). Here the JPEG images have a maximum image size (256x256). The binary image can be represented as a summation of total number of black and white pixels.

\[
\text{Image I} = \sum_{W=0}^{255} \sum_{H=0}^{255} [f(0) + f(1)],
\]

where,

\[
P = \text{number of white pixels (width \times height)}
\]

\[
W = 0.264 \text{ mm}
\]

The area calculation formula is

\[
\text{Size of tumour, } S = [(\sqrt{P}) \times 0.264] \text{ mm}^2,
\]

where,

\[
P = \text{no-of white pixels}
\]

\[
W = \text{width}
\]

\[
H = \text{height}
\]

The edge of the gray scale image

\[
\text{Edge strength} = \frac{\sum_{\text{p} \in \text{edge}} P}{N},
\]

where (p) represents edge points gradient values which come from the image step for all pixels (p) on the edge between every two regions, and N are the number of edge pixels.

Algorithm

The steps involved for finding the shape of the brain tumor are as follows:

Step 1: Start the process.
Step 2: Get the segmented MR image of human brain obtained from the CRF-MABC given as an input.
Step 3: Check whether the input image is in required format and move to step 4 if no error messages is displayed.
Step 4: Find the edge of the gray scale image.

\[
\text{Edge strength} = \frac{\sum_{\text{p} \in \text{edge}} P}{N}
\]

Step 5: Calculate the number of white points in the image.

\[
\text{No. of white pixel } P \sum_{W=0}^{255} \sum_{H=0}^{255} f(0)
\]

Step 6: Calculate the size of the tumor using the formula.

\[
\text{Size of tumour, } S = [(\sqrt{P}) \times 0.264] \text{ mm}^2
\]

Step 7: Display the size and stage of tumor.
Step 8: Stop the process.

4. Experimental Results

Data Set

For the purpose of study, the details from ten tumor patients were collected. The scanned images were recorded as DICOM and then converted to JPEG format. For segmentation, a total of 100 images (10 images per patient) were taken. The performance of the algorithm was evaluated based on the region non-uniformity, correlation and computation time. The results of this work were compared with the existing algorithms and the efficiency has been measured.

The test images were also taken from the following databases:

- http://overcode.yak.net/15
- http://www.nanmic.org/Wiki/index.php/Downloads#Data

This work is done in MATLAB 7.0. Environment

Performance Evaluation

Various techniques are available to estimate the performance of the segmentation algorithms and their results. In this paper, region non-uniformity and correlations of segmented images are the main parameters that were used to evaluate the performance of the algorithm proposed.

Region Non-Uniformity

To assess the performance of the segmentation algorithm, the region non-uniformity is defined as,

\[
\text{NU} = \frac{[|F_T| / |F_T + B_T|] \times \sigma^2}{\sigma^2}
\]

where,

\[
\sigma^2 \text{-variance of the whole image}
\]

\[
\sigma_T^2 \text{-foreground variance}
\]

\[
F_T \text{ and } B_T \text{-foreground and background area pixels for the test image}
\]

Non-uniformity close to 0 and the worst case corresponds to NU=1
Correlation

A correlation is used to evaluate the performance of image segmentation algorithm and it is done between the segmented image and the ground truth image.

F-measure

The F-measure is defined as the combination and harmonic mean of precision and recall. The F-measure is given by the equation (31).

\[
F - \text{measure} = \frac{2pr}{r + p}
\]

(31)

Where, 
\(p\) and \(r\) denote precision and recall, respectively.

The F-measure is also an important parameter for evaluating the performance.

Similarity Index

The quantitative evaluation of the performance of the segmentation process is measured using the similarity index between ground truth and result of the segmentation, as given by the equation

\[
D(K) = \frac{2 \cdot V_{\text{prg}}(k)}{V_p(k) + V_g(k)}
\]

(32)

where, 
\(2 \cdot V_{\text{prg}}(k)\) is the number of classified pixels in class \(k\) with two images (a segmented image and a ground truth image)

\(D(K)\) is the Dice Index.

Figure 7: Average Region of Non-uniformity Comparison

Figure 7 shows the average region of non-uniformity for the existing and the proposed approaches. From this graph, it is observed that the proposed segmentation approach has lesser region of non-uniformity when compared with the existing approaches.

Figure 8: Average Correlation Comparison

The figure 8 represents graphically of average correlation value. It is observed from figure 8 that the proposed CRF-MABC based segmentation approach provides better results when compared with the existing approach such as MRF –HPACO, MRF-ABC and CRF-MABC.

Figure 9: Dice similarity index for simulated datasets for existing and proposed approach.

The graphical representation of the dice index is shown in the figure 9. From this graph, it is observed that the similarity index of the proposed approach CRF-
MABC is better index than the other existing approach such as MRF-HPACO and MRF-ABC.

Table 1 shows the comparison of the proposed algorithm with existing algorithm based on the parameters such as correlation, computation time and region of non-uniformity.

**Table 1 Performance Evaluation Results for Medical Images**

<table>
<thead>
<tr>
<th>Images</th>
<th>Region non uniformity</th>
<th>Correlation</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>MRF-HPACO</td>
<td>MRF-ABC</td>
</tr>
<tr>
<td>1</td>
<td>0.17</td>
<td>0.04</td>
</tr>
<tr>
<td>2</td>
<td>0.18</td>
<td>0.05</td>
</tr>
<tr>
<td>3</td>
<td>0.15</td>
<td>0.04</td>
</tr>
<tr>
<td>4</td>
<td>0.24</td>
<td>0.05</td>
</tr>
</tbody>
</table>

For All Images

<table>
<thead>
<tr>
<th>MRF-HPACO</th>
<th>MRF-ABC</th>
<th>CRF-MABC</th>
</tr>
</thead>
<tbody>
<tr>
<td>115</td>
<td>105</td>
<td>85</td>
</tr>
</tbody>
</table>

The sample images are given in Figure 10 (a), (b), (c) and (d) along with the statistics.

The statistical parameters of the segmented images in Figure 10 (a), (b), (c) and (d) are presented in the tables 2 and 3.

**Table 2 Statistical parameters of the Segmented Images**

<table>
<thead>
<tr>
<th>Image</th>
<th>Correlation</th>
<th>NU</th>
<th>Area</th>
<th>Centroid</th>
<th>Eccentricity</th>
</tr>
</thead>
<tbody>
<tr>
<td>10 (a)</td>
<td>1</td>
<td>0.0279</td>
<td>421</td>
<td>71.7577</td>
<td>0.5305</td>
</tr>
</tbody>
</table>
Table 3 Statistical parameters of the Segmented Images

<table>
<thead>
<tr>
<th>Image</th>
<th>Orientation</th>
<th>Solidity</th>
<th>Extent</th>
<th>Perimeter</th>
<th>Max. Intensity</th>
<th>Min. Intensity</th>
</tr>
</thead>
<tbody>
<tr>
<td>10 (a)</td>
<td>-77.8275</td>
<td>0.5759</td>
<td>0.4422</td>
<td>117.7401</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>10 (b)</td>
<td>79.0683</td>
<td>0.9007</td>
<td>0.7262</td>
<td>123.3970</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>10 (c)</td>
<td>-60.6783</td>
<td>0.9042</td>
<td>0.6009</td>
<td>86.0833</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>10 (d)</td>
<td>31.4245</td>
<td>0.7495</td>
<td>0.5173</td>
<td>168.2670</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

5. Discussion

The statistical parameters of the segmented images in the figure 10 are represented in the table 2 and table 3. The main reason for adopting the conditional random field is computation probability and statistical parameter estimation is easy when compared to the existing Markov random field process. The segmented image of proposed method is evaluated using the metrics such as correlation, non uniformity, similarity measure. The performance evaluation of the proposed method is better than the existing methods. The graphical representation of the performance evaluation is shown in the figure 7, 8 and 9. The comparison results of existing and proposed methods are shown in the table 1.

6. Conclusion

Brain tumor is inherently serious and life-threatening because of its character in the limited space of the intracranial cavity (space formed inside the skull). A novel algorithm based on the combination of conditional random field and modified artificial bee colony optimization with fuzzy possibility c-means is proposed in this research. Conditional random field is a widely used method for image segmentation. The combination of Modified ABC optimization algorithm with FPCM is used to find out the optimal label that minimizes the posterior energy function to segment the image. The performance of this proposed algorithm has been evaluated by using the methods such as correlation, similarity measure and computational complexity. It is clearly observed from the results that the proposed approach provides significant results for the statistical parameters taken for consideration and it outperforms the existing approaches such as MRF-HPACO and MRF-ABC.

Acknowledgement

The authors would like to thank the moral and monetary research support provided by the Management, Sur University College, Sur, Oman.

References:

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