Osteosarcoma Segmentation in MRI using Dynamic Harmony Search Based Clustering

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Abstract

In this paper, the automatic segmentation of Osteosarcoma in MRI images is formed as a clustering problem. Subsequently, a new dynamic clustering algorithm based on the Harmony Search (HS) hybridized with Fuzzy C-means (FCM) called DCHS is proposed to automatically segment the Osteosarcoma MRI images in an intelligent manner. The concept of variable length in each harmony memory vector is applied to encode variable numbers of candidate cluster centers at each iteration. Furthermore, a new HS operator, called the ‘empty operator’ is introduced to support the selection of empty decision variables in the harmony memory vector. FCM is incorporated in DCHS to fine tune the segmentation results. Our approach uses multi-spectral information from STIR (Short Tau Inversion Recovery) and T2-weighted MRI sequences. We used a subset of Haralick texture features and pixel intensity values as a feature space to DCHS to delineate the tumour volume. The segmentation results were statistically evaluated against manually delineated data for four patients. Promising results were obtained with average of 0.72 of Dice measurement.

1. Introduction

Osteosarcoma is the second most prevalent type of malignant bone tumour (after myeloma) which typically affects individuals between the ages of 5 and 25 years. The most common bones affected are the distal femur, proximal tibia and the proximal humerus as can be seen in Fig 1. It may also less commonly affect the cranium, jaw or hip bones. Traditionally, limb amputation was the most reliable way of preventing metastasis. With the advent of new improved drugs, the current standard practice in the management of Osteosarcoma is a combination of neoadjuvant chemotherapy regime and wide resection of the primary tumour. A 5-year survival rate with no detectable metastasis has increased from 20% from surgery alone to about 60-70% with the use of pre-operative neoadjuvant chemotherapy [1], indicating neoadjuvant chemotherapy is an important prognosis factor. Generally, a higher degree of drug-induced tumour necrosis indicates a higher chance of survival in patients [2]. Therefore, it becomes critical to be able to accurately determine the progression of tumour tissue necrosis during the neoadjuvant chemotherapy.

Histopathological analysis is the accepted gold standard in determining the rate of tumour tissue necrosis. However, this procedure is laborious, time consuming and is affected by inter- and intra-observer variations. It is also impossible to perform response monitoring during the course of chemotherapy using this method because the analysis can only be performed on resected tumour specimens [3]. Correspondingly, non-invasive imaging techniques such as CT, MRI and more recently, PET imaging modalities have been used for quantitative analyses in response monitoring and surgical planning for Osteosarcoma.

Generally, the quantitative analysis of medical images is a challenging problem, in which, the segmentation of the structure of interest is the prerequisite to quantification. Manual segmentation of the tumour tissue from each image slice by a trained radiologist, while remaining the most accepted practice, is again a laborious and time consuming process. It is also affected by inter- and intra-observer variations. Automated approaches, on the other hand, are generally considered to be faster, objective measures and provide accurate tumour quantification and/or tissue classification.

Although automated image segmentation is a widely researched problem, there has been only a limited number of reported approaches that address the problem of Osteosarcoma segmentation. These include neural network-based ap-
proaches [4], fuzzy connectedness [5], similarity matching based on normalized cross-correlation of regions [6]. There are however numerous clinical research papers on Osteosarcoma, which cover clinical trials of new imaging modalities, treatment protocol and prognosis factors [1]–[3].

We propose an automated Osteosarcoma segmentation framework which aims to (i) accurately delineate the tumour region from MRI sequences, and in doing so, (ii) perform differentiation between viable and non-viable (necrotic) tissue within the tumour. The significance of the former is to quantify the total tumour volume and the latter, to enable oncologists to monitor patients’ response to chemotherapy by measuring the percentage of drug-induced necrosis of the tumour tissue. Our proposed framework exploits multi spectral information provided by T2-weighted, STIR (Short Tau Inversion Recovery) MRI sequences.

In this paper, we hypothesize that the number of clusters within the tumour region may not be known a priori and we believe that the proposed automatic determination of the number of clusters may help in this respect. Instead of using only the pixel intensity values, we used a set of texture descriptors as feature vectors to significantly improve the segmentation of the Osteosarcoma tumour.

Consequently, we propose a new method called Dynamic Clustering (DCHS) using the Harmony Search algorithm [9] that can automatically segment the tumour tissues as well as necrosis tissues from Osteosarcoma in MRI images. DCHS is able to automatically determine the appropriate number of clusters, as well as the appropriate locations of cluster centers. DCHS works in an iterative manner until the near optimal number of clusters is found and then at every iteration the given dataset with promising results. This algorithm was briefly introduced in our previous works [7] as general purpose image segmentation algorithm. However, in this paper we extend this previous work initially by improving the performance of the algorithm by adding two factors: 1) Introduce a new operator called ‘empty operator’ and 2) Hybridized DCHS with FCM algorithm.

Our segmentation framework is described in detail in the following sections.

### 2. Fundamentals of Fuzzy Clustering

Clustering algorithm classically is performed on a set of \( n \) patterns or objects \( X = \{x_1, x_2, \ldots, x_n\} \), each of which, \( x_i \in \mathbb{R}^d \), is a feature vector consisting of \( d \) real-valued measurements describing the features of the object represented by \( x_i \). Two types of clustering algorithms are available i.e. hard and fuzzy. In hard clustering, the goal would be to partition the dataset \( X \) into non-overlapping non-empty partitions \( G_1, \cdots, G_n \). Whereas in fuzzy clustering algorithms the goal would be to partition the dataset \( X \) into partitions that allows the data object to belong in a particular (possibly null) degree to every fuzzy cluster. The clustering output is a membership matrix called a fuzzy partition matrix \( U = [u_{ij}]_{i \times n} \) as in Eq (1). Where \( u_{ij} \in [0, 1] \) represents the fuzzy membership of the \( ith \) object to the \( jth \) fuzzy cluster.

\[
M_{\text{fcm}} = \left\{ U \in \mathbb{R}^{c \times n} | \sum_{j=1}^{c} U_{ij} = 1, 0 < \sum_{i=1}^{n} U_{ij} < n \right\} \quad (1)
\]

Fuzzy C-means algorithm (FCM) [8] is considered as one of the most popular fuzzy partitioning algorithms. FCM is an iterative procedure which is able to locally minimize the following objective function:

\[
J = \sum_{i=1}^{c} \sum_{j=1}^{n} u_{ij}^m ||x_i - v_j||^2 \quad (2)
\]

where \( \{v_j\}_{j=1}^{c} \) are the centroids of the clusters \( c \) and \( ||.|| \) denotes an inner-product norm (e.g. Euclidean distance) from the data point \( x_i \) to the \( jth \) cluster center, and the parameter \( m \in [1, \infty) \), is a weighting exponent on each fuzzy membership that determines the amount of fuzziness of the resulting classification.

FCM algorithm starts with random initial \( c \) cluster centers, and then at every iteration it finds the fuzzy membership of each data point to every cluster using the following equation:

\[
u_{ij} = \frac{1}{\sum_{k=1}^{c} \frac{||x_i - v_k||^2}{||x_i - v_j||^2}} \quad (3)
\]

Based on the membership values, the cluster centers are recomputed using the following equation:

\[
v_j = \frac{\sum_{i=1}^{n} u_{ij}^m \cdot x_i}{\sum_{i=1}^{n} u_{ij}^m} \quad (4)
\]

The algorithm terminates when there is no further change in the cluster centers.

### 3. Harmony Search-based Fuzzy Clustering - DCHS algorithm

Harmony Search (HS) is a relatively new stochastic meta-heuristic algorithm, which was developed by Geem et al. in 2001 [9] and successfully applied to different optimization problems (see [10] and references therein). HS is a very successful metaheuristic algorithm that can explore the search space of a given data in parallel optimization environment, where each solution (harmony) vector is generated by intelligently exploring and exploiting a search space. The HS mechanism starts with a population of randomly generated solutions stored in 'Harmony Memory (HM)’. At each iteration, a new harmony solution is generated based on three improvisation rules named as: (i) ‘Memory Consideration’ which is responsible for the selection of the new decision variable in harmony vector from historical values stored in HM; (ii) ‘Random Consideration’ which is responsible for exploring unvisited regions in the search space (i.e. diversify the new harmony), and (iii) ‘Pitch Adjustment’, which is responsible for local improvement. A new harmony is then evaluated based on objective function evaluation and surrogated with the worst harmony stored in HM. This process is repeated until an optimal solution is reached. In the following sections we describe a model of HS that represents our proposed algorithm DCHS.
3.1. Initialization of DCHS Parameters

The DCHS algorithm parameters are same as the standard HS parameters except the new operator ‘empty operator’ that will be describing later. These parameters are the harmony memory size (HMS), harmony memory consideration rate (HMCR), pitch adjustment rate (PAR) and the total number of improvisations (NI).

3.2. Initialization of Harmony Memory

Each harmony memory vector encodes the cluster centers of the given dataset. Since the number of these clusters is unknown a priori, a possible range of number of clusters that the given dataset may possess is tested. Consequently, each harmony memory vector can vary in length according to the randomly generated number of clusters for each vector. To initialize the HM with feasible solutions, each harmony memory vector initially encodes a number of cluster centers, denoted by ‘ClustNo’, such that:

\[ \text{clustNo} = (\text{rand}) \times (\text{clustMaxNo} - \text{clustMinNo}) + \text{clustMinNo} \]  

(5)

The number of clusters ‘clustNo’ is picked at random between ‘clustMinNo’ and ‘clustMaxNo’, where ‘clustMaxNo’ is an estimate of the maximum number of clusters (upper bound), while ‘clustMinNo’ is the minimum number of clusters (lower bound). The values of the upper and lower bounds are set depending on the datasets used.

Even though the number of clusters is allowed to vary (i.e the vector length is varying), for a matrix representation, each vector length in HM must be made equal to the maximum number of clusters (upper bound), while ‘clustMinNo’ is the minimum number of clusters (lower bound). The values of the upper and lower bounds are set depending on the datasets used.

In case of encoding a vector with a number of clusters less than the ‘clustMaxNo’, the vector is occupied by these cluster centers in random positions, while the remaining unused vector elements (referred to as ‘don’t care’ as in [11]) are represented with ‘#’ sign. To illustrate the idea, let \( d = 2 \) and \( \text{clustMaxNo} = 6 \), i.e. the feature space is 2-dimensional and the maximum number of clusters is equal to 6. Now let one of the HM vector has only 3-candidate cluster centers such as: \{25.1, 13.2, 14.6, 3.1\}

Then these 3 centers will be set in the vector in arbitrary order while the rest of the vector’s elements are set to “don’t care” with the ‘#’ sign as illustrated in Eq. (6)

\[ HM = \{25.1 \ 13.2 \ # \ # \ # \ 14 \ 6.3 \ # \ # \ 3.8 \} \]  

(6)

The last step in harmony memory initialization process is to calculate the fitness function for each harmony vector and saved in harmony memory as explained in section (3.6).

3.3. Improvisation of a New Harmony Vector

In each iteration of HS, a new harmony vector is generated based on the HS’s improvisation rules mentioned in [9]. These rules are memory consideration; pitch adjustment; or random consideration. In memory consideration, the value of the component (i.e. decision variable) of the new vector is inherited from the possible range of the harmony memory vectors stored in HM. This is the case when a random number \( \epsilon \in [0,1] \) is within the probability of HMCR; otherwise, the value of the component of the new vector is selected from the possible data range with a probability of (1-HMCR).

Furthermore, the new vector components which are selected out of memory consideration operator are examined to be pitch adjusted with the probability of (PAR). If it is, then the value of this component becomes:

\[ (a_{i}^{NEW}) = (a_{i}^{NEW}) \pm \text{rand()} \times \text{bw} \]  

(7)

here, bw is an arbitrary distance bandwidth used to improve the performance of HS and its value is set to \( \text{bw}=0.001 \times \text{maxValue(n)} \). The other important issue worth mentioning is when the inherited components of the new vector have don’t care values ‘#’. In this case, no pitch adjustment will take place.

3.4. Empty Operator

To further enhance the concept of variable-length of the harmony memory vectors, a new HS operator called the ‘empty operator’ is proposed. This new operator is introduced mainly to add the empty (‘don’t care’) decision variables in the newly generated harmony vector with a particular rate, namely Empty Operator Rate (EOR) \( \in [0,1] \). The main rationale behind the new operator is so that DCHS works in a more stable manner. In other words, the new operator is introduced to minimize the variation of the results (i.e. number of clusters) that may be obtained from DCHS in case of multiple runs. The inconsistent results from multiple runs can be due to the dominating effect of a number of solution vectors of the HM through the improvisation process (premature convergence problem). Therefore, the ability of generating of a new vector with various number of clusters is poor. For that, the new operator is introduced to add a new method of having empty ‘don’t care’ decision variables in the newly generated harmony vector. This is done in parallel with the normal way (i.e. inherited from HM) of having the empty components in the new vector. The empty operator works as follows:

1) If the generated random number is within the probability of HMCR, the value of the new decision variable is randomly inherited from the historical values which are stored in the HM.

2) Otherwise, if the generated random number is within the probability of (1-HMCR), a new random number between 0 and 1 is generated. If this random number within the probability of EOR, then the new decision variable is assigned a random number within the possible
Otherwise, a don’t care (‘#’) value is assigned to the new decision variable.

If the value of this rate is too low, only a few random values from the visible data range are selected and it may converge too slowly. If this rate is extremely high (approaching 1), the addition of don’t care elements into the new harmony vector rarely happens which may lead to an unstable clustering results. The value of this operator is indeed subject to the given dataset. According to this added operator, the DCHS algorithm still has the ability to generate a new harmony vector with varying numbers of clusters, even in the final stages of the DCHS algorithm search process. In other words, this new operator increases the diversity of don’t care components in DCHS.

3.5. Update the Harmony Memory

Once the new harmony vector is generated, a count is done on the generated number of cluster centers in the new vector. If it is less than the minimum number of cluster centers (clustMinNo), the new vector will be rejected. Otherwise, the new vector will be accepted and a fitness function is computed using a cluster validity measurement described in Section (3.6). Then, the new vector is compared with the worst harmony memory solution in terms of the fitness function. If it is better, the new vector is included in the harmony memory and the worst harmony is excluded.

3.6. Evaluation of Solutions

The evaluation (fitness value) of each harmony memory vector indicates the degree of goodness of the solution it represents. In order to evaluate the goodness of each harmony memory vector, the empty components that may appear in the harmony vector are removed and the remaining components which represent the cluster centers are used to cluster the given dataset (e.g. image). DCHS performs clustering based on pixels of an image in the gray-scale intensity space, where each data point (e.g. pixel) in the given dataset (image) is assigned to one or more clusters (regions) with a membership grade. The membership value for each data point is calculated based on Eq.(3).

After that, the goodness of the clustering result (i.e. $U$ matrix) is measured using a cluster validity index. Therefore, the validity index measurement is used as the fitness function in this study. In this paper, a recently developed index, which exhibits a good trade-off between efficacy and computational concern, is used. This index is named PBMF-index which is the fuzzy version of PBM-index [12]. PBMF-index is defined as follows:

$$PBMF(c) = \left( \frac{1}{c} \times \frac{E_1}{E_2} \times D_c \right)^p$$

where $c$ is the number of clusters. Here

$$E_c = \sum_{j=1}^{n} \sum_{i=1}^{m} u_{ij}^m \| x_i - v_j \|$$  \hspace{1cm} (9)

and

$$D_c = max_{i,d} \| v_i - v_j \|$$ \hspace{1cm} (10)

where the power $p$ is used to control the contrast between the different cluster configurations and it is set to be 2. $E_1$ is a constant term for a particular dataset and it is used to avoid the index value from approaching zero. The value of $m$, which is the fuzziness weighting exponent, is experimentally set to 1. $D_c$ measures the maximum separation between two clusters over all possible pairs of clusters, while $E_c$ measures the sum of $c$ within-cluster distances (i.e., compactness). The maximization of PBMF-index indicates accurate clustering results and consequently, accurate number of clusters could be achieved.

3.7. Check the Stopping Criterion

This process is repeated until the maximum number of iterations (NI) is reached. In the end, the best solution among the maximum value of fitness function of each HM solution vectors is selected to be the best solution vector.

3.8. Hybridization with FCM

A hybridizing step with FCM is introduced to increase the quality of the DCHS clustering results. This step is introduced to DCHS by calling the FCM algorithm just one time to fine tuning the best solution that have been optimized by DCHS. The solution vector with highest fitness value is selected from harmony memory and considered as initial values for FCM’s cluster centers. In this case, FCM through its mechanism modifies the cluster centers values until the variance of the clusters are minimum, thus yielding more compact clusters.

4. Osteosarcoma Framework

Our proposed framework consists of two phases; the first phase aims to extract the tumour region from MRI images while the second phase involves the determination of the necrotic tissue from the tumour regions. Before proceeding to describe our proposed tumour segmentation algorithm, we first attempt to model the expert knowledge of various MRI modalities which we later use to assist our segmentation framework, particularly in selecting the appropriate clusters belonging to different tissues.

4.1. Modelling Expert Knowledge

An overview of the radiologist experts’ knowledge, that the proposed system will be built based on it, is presented. In fact, the daily routine of radiologist’s to quantitatively analyze the osteosarcoma MR images is based on analysis of the variation of intensity levels that MRI exhibit for different tissue types in different MRI sequences. In other words, the tumor tissue that contains viable tumor cells and necrotic tumor cells (dead cells) may exhibit different intensity level.
in each MRI sequence (T1, T2, STIR and T1 post contrast). Furthermore, surrounding normal tissues in the vicinity of the tumour may be edematous due to inflammation or tumour infiltration. These edematous tissue may also exhibit different intensity ranges in different MRI modalities. For instance, in STIR sequence as in Fig. 2-(a), the viable tumor cells within the tumor tissue exhibit bright intensity level (HYPER), while the necrotic cells exhibit brighter intensity level than viable tumor (VERY HYPER). In the same image the fat tissue is suppressed (HYPO/ NO SIGNAL) and the muscle is less dark than fat tissue (INTERMEDIATE).

![Figure 2. MRI Osteosarcoma images. (a) STIR image. (b) T2-Weighted image](image)

Through consultation with expert radiologists, various relationships between the presentation of intensities in MRI modalities to the corresponding tissue types are summarised and shown in Tables 1 and 2. This knowledge is presented using relative descriptions of intensity differences since there is no fixed range of intensities for each tissue type.

The term ‘HYPER’ represents very high voxel intensity (bright regions), while the term ‘HYPO’ represents low voxel intensity (dark regions). The term ‘INTERMEDIATE’ represents voxel intensities which are higher than hypo-signal, but lesser than hyper-signal, while the term ‘VERY HYPER’ represents voxel intensities which are higher than hyper-signal (very bright regions). The term ‘HYPO-NO SIGNAL’ represents regions that lack any signals. These terms used to describe the intensity levels in T1-weighted, T2-weighted and STIR modalities. While in the T1 post-contrast modality, the term ‘MILD ENHANCEMENT’ denotes tissue that absorbs the contrast agent producing a slightly brighter signal response in the MRI. Finally, the term ‘NO ENHANCEMENT’ denotes tissue that is not affected by the contrast agent producing a dark signal response in the MRI. The last term is ‘ENHANCEMENT’ denotes that the tissue is significantly affected by the contrast agent producing a much higher intensity response in the MRI.

### 4.2. Tumour Region Segmentation

In T2-weighted images (e.g. Fig.2-(b)), tumour tissues are not distinguishable from other tissues (e.g. Fat) since the intensity levels are almost similar. Therefore, we believe that using the STIR images (e.g. Fig.2-(a)) is more appropriate since tumour tissues have very different intensity values (i.e. being ‘HYPER’ or ‘VERY HYPER’) than other tissues. A consequence of that, we apply our proposed algorithm, DCHS, on the STIR sequences by fixing the number of clusters to 2. The image features used in the clustering process are a subset of 9 texture features derived from a compact representation of Gray Level Co-Occurrence Matrices (GLCM) as proposed by Cooper [13] which was originally used for aeromagnetic data. These features include Entropy, Energy, Contrast, Sum Average, Variance, Inverse Difference Moment, Cluster Tendency, Maximum Probability and the voxel intensity. In our method, we compute the GLCM using a 5x5 window. We compare the resultant regions in the segmented image in intensity level with a threshold \( \gamma \), where if this value is exceeded, then we classify this image as a tumour image.

After the initial clustering is completed for each STIR image, the resultant Region of Interest (ROI) which belongs to the tumor is used to perform pixel-wise multiplication with the corresponding T2-weighted image.

The results of the clustering process for Osteosarcoma segmentation and the corresponding ROI extracted from the T2-weighted images are shown in Fig 3.

### 4.3. Necrotic Tissue Identification

As mentioned earlier, there is a need to accurately segment and quantify necrotic tissue within the tumour from the MRI sequences. This is due to the fact that neoadjuvant chemotherapy has been proven [1] to drastically improve the 5-year survival rate for Osteosarcoma patients. A non-invasive procedure is favourable since chemotherapy drug response, and hence the drug-induced necrosis of tumour tissue can be measured during the chemotherapy procedure. It is known that patients who respond well (90% drug-induced necrosis) to chemotherapy eventually live longer.

As an extension to the presented clustering approach to

### Table 1. Relative Signal Response for Various Abnormal Tissues in MRI

<table>
<thead>
<tr>
<th>Tissue Type</th>
<th>T1 Weighted</th>
<th>T2 Weighted</th>
<th>STIR</th>
<th>T1 Post Contrast</th>
</tr>
</thead>
<tbody>
<tr>
<td>Edema</td>
<td>INT</td>
<td>HPR</td>
<td>HPR</td>
<td>Mild E</td>
</tr>
<tr>
<td>Necrotic</td>
<td>INT</td>
<td>VHPR</td>
<td>VHPR</td>
<td>NE</td>
</tr>
<tr>
<td>Viable Tumour</td>
<td>INT</td>
<td>HPR</td>
<td>HPR</td>
<td>E</td>
</tr>
</tbody>
</table>

### Table 2. Relative Signal Response for Various Normal Tissues in MRI

<table>
<thead>
<tr>
<th>Tissue Type</th>
<th>T1 Weighted</th>
<th>T2 Weighted</th>
<th>STIR</th>
<th>T1 Post Contrast</th>
</tr>
</thead>
<tbody>
<tr>
<td>Muscle</td>
<td>INT</td>
<td>LS</td>
<td>INT</td>
<td>NE</td>
</tr>
<tr>
<td>Bone Marrow</td>
<td>HPR</td>
<td>HPR</td>
<td>HNS</td>
<td>NE</td>
</tr>
<tr>
<td>Bone and Tendon</td>
<td>HNS</td>
<td>HNS</td>
<td>HNS</td>
<td>NE</td>
</tr>
<tr>
<td>Fat</td>
<td>HPR</td>
<td>HPR</td>
<td>HNS</td>
<td>NE</td>
</tr>
<tr>
<td>Blood Vessels</td>
<td>HNS</td>
<td>HNS</td>
<td>HNS</td>
<td>E</td>
</tr>
<tr>
<td>Intramuscular Fat</td>
<td>HPR</td>
<td>INT</td>
<td>HNS</td>
<td>NE</td>
</tr>
</tbody>
</table>
Osteosarcoma segmentation, we propose a method to segment various abnormal tissue structures within the tumour itself, with the aim of specifically determining the necrotic and viable tumour tissues. In order to perform this, we propose to use the T2-weighted MRI sequences obtained from the previous segmentation step and apply the DCHS clustering algorithm on the segmented tumour ROI.

The main difference as compared to the tumour segmentation step described in Section 4.2 is that instead of fixing the number of clusters to 2, we now allow the DCHS algorithm to automatically determine the optimal number of clusters for any given image. Based on our prior knowledge of the image intensity ranges, we can experimentally set the number of clusters to range between 2 and 8.

The result of this clustering step would be a set of images, each of which represents a particular pixel cluster corresponding to a particular tissue type. The next step would be to determine which of these resultant clusters (images) belong to the necrotic tissue. In order to perform this, we propose to use a simple pattern classifier approach which is described next:

1) A training set for manually segmented necrotic tissue regions is first built
2) Texture features are calculated for the entire training dataset
3) Mean, μ and Co-variance, Σ statistics are then computed for this training dataset
4) During testing, for each resultant subimage, compute the texture features and compute cluster μ and Σ
5) The normal probability distribution for the cluster is defined as \( p(\mu_c) = N(\mu_c; \mu, \Sigma) \)

6) Based on a predefined threshold, \( \epsilon \), if \( p(\mu_c) \geq \epsilon \), then the respective cluster is classified as necrotic tissue.

While we are still working on the automated implementation of the necrotic tissue identification, we have however visually validated the output of the dynamic clustering approach presented in this section with an experienced radiologist. The following sample image presents the identified necrotic regions which are highlighted in black.

5. Results and Discussion

We have tested our Osteosarcoma segmentation approach on 4 patients data obtained from our university hospital. This data is 3D volumes with total 268 MRI images. These images were obtained from 1.0-Tesla GE/Signa MR scanner.

The parameters of the DCHS algorithm are experimentally set as follows: HM size\(=30 \), HMC\( \alpha\)=0.90, PAR\(=0.30 \), EOR\(=0.85 \) and the maximum number of iteration NI=30000. Furthermore, and as mentioned earlier, for phase one experiment (Tumour delineation) the minimum value for the number of clusters (lower bound) and the maximum number of clusters (upper bound) are both set to 2, while in phase two (Necrotic delineation) the minimum value for the number of clusters (lower bound) is set to 2 and the maximum number of clusters (upper bound) is set to 8. All the experiments are performed on an Intel Core2Duo 2.66 GHz machine, with 2GB of RAM; while the codes are written using Matlab 2008a.

For validation, our approach was compared against the manual delineations from an experienced radiologist. In order to evaluate the spatial agreement between the manual delineation by clinical expert and the automatic segmentation, we chose to use the DICE coefficient or Similarity Index (SI). In addition, the true positive fraction (TPF) or sensitivity, false positive fraction (FPF) and extra fraction (EF) are used to evaluate our approach. The similarity index is defined as follows:

\[
SI = \frac{2(ED \cap Auto)}{ED + Auto}
\]

where \( ED \) and \( Auto \) refer to the expert delineation and automatic segmentation respectively, while \((ED \cap Auto)\) refers
to the overlap of ED and Auto.

\[
TPF = \frac{TP}{TP + FN}. \quad (12)
\]

\[
FPF = \frac{FP}{FP + TN}. \quad (13)
\]

\[
EF = \frac{FP}{TP + FN}. \quad (14)
\]

by false positives (FP), true positives (TP) and false negatives (FN). The true positive fraction is a measure of sensitivity and false positive fraction is measure of (1-specificity). Extra fraction is used to measure the over-segmentation between expert delineations and the automatic segmentation. As can be observed from the Table 3, the segmentation results obtained are very encouraging. There is positive correlation and high similarity between our automated segmentation and the expert segmentation provided which is reflected by SI values ranging from 0.627 (worst case) to 0.807 (best case). Oversegmentation is at an acceptable level between 0.23 (worst case) to (0.170) best case.

### Table 3. Validation Results of Osteosarcoma Segmentation

<table>
<thead>
<tr>
<th>SI</th>
<th>TPF</th>
<th>FPP</th>
<th>EF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patient 1</td>
<td>0.746</td>
<td>0.723</td>
<td>0.241</td>
</tr>
<tr>
<td>Patient 2</td>
<td>0.627</td>
<td>0.520</td>
<td>0.288</td>
</tr>
<tr>
<td>Patient 3</td>
<td>0.807</td>
<td>0.799</td>
<td>0.201</td>
</tr>
<tr>
<td>Patient 4</td>
<td>0.741</td>
<td>0.669</td>
<td>0.202</td>
</tr>
</tbody>
</table>

### 6. Conclusion

We proposed a segmentation approach to delineate osteosarcoma tumour from multi-modal MRI sequences. Our approach which uses texture features coupled with an innovative Dynamic Clustering algorithm using Harmony Search which can reliably segment the tumour region. In addition, we have also proposed a methodology to detect necrotic tissue within the tumour, for which preliminary visual validation is providing encouraging results. We hope to extend this work by implementing an automated method for viable and necrotic tissue identifications which would have significant impact on surgical planning and chemotherapy response monitoring.

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