

Liver Tumor Segmentation using Superpixel based Fast Fuzzy C Means Clustering

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Abstract—In computer aided diagnosis of liver tumor detection, tumor segmentation from the CT image is an important step. The majority of methods are not able to give an integrated structure for finding fast and effective tumor segmentation. Hence segmentation of tumor is most difficult task in diagnosing. In this paper, CT abdominal image is segmented using Superpixel-based fast Fuzzy C Means clustering algorithm to decrease the time needed for computation and eradicate the manual interface. In this algorithm, a superpixel image with perfect contour can be obtained using a Multiscale morphological gradient reconstruction operation. Superpixel is pre-segmentation algorithm and is employed to obtain segmentation accuracy. FCM with modified object is used to obtain the color segmentation. This method is examined on 20 CT images gathered from liveratlas database, results shows that this approach is fast and accurate compared to most of segmentation algorithms. Statistical parameters which include accuracy, precision, sensitivity, specificity, dice, rfn and rfp are calculated for segmented image. The results shows that this algorithm gives high accuracy of 99.58% and improved rfn value of 8.34% compared with methods discussed in the literature.

Keywords—CT scan image; image segmentation; fuzzy c mean clustering; liver mask; superpixel image

I. INTRODUCTION

Liver cancer causes third most deaths in world-wide [1]. Computed tomography is commonly used modality for liver cancer diagnosis. The cancer is treated effectively providing it's detected in early stage. In order to diagnose liver tumors, such as hepatocellular carcinoma and metastatic carcinomas, computer aided diagnosis (CAD) is used. Importance of Segmentation algorithms are to separate cancerous portion which is essential for medical diagnosis of cancer [2]. Structure of liver changes with age, sex, body shape, hence the tumor detection is complicated using CAD system.

There are two sorts of segmentation algorithms that are supervised and unsupervised. Unsupervised does not depend on training data samples and labeling of data, these include GraphCut [3], watershed transform (WT) [4], fuzzy entropy [5], clustering [6], etc. Training data and labelling images are required for supervised segmentation, and these include neural networks [7-8]. In these methods, features are used for learning and to achieve segmentation.

In unsupervised segmentation, clustering is the common form of segmentation utilized for color and grayscale images

[9]. In this method, Segmentation depends on Fuzzy c mean clustering (FCM) with minimized objective function.

II. RELATED WORK

Deepesh Edwin et al used fuzzy logic based thresholding and Shannon's entropy function for tumor segmentation [10]. Amita Das et al utilized adaptive thresholding and FCM for segmentation. The tumor is classified using Multi-Layer Perceptron (MLP) and C4.5 decision tree classifiers [11]. Ramin Ranjbarzadeh et al used the Kirsch filter for extracting organ edges, then calculated the concave and convex points, the mean shift is implemented to obtain uniform images, and eventually FCM is carried out to segment the liver [12].

Muthuswamy J suggested a method in which pre-processing is carried out using median filter and neutrosophic (NS) domain with FCM thresholding for segmentation, then liver contour is obtained using morphological operations, The classifier of support vector machines is used to categorize the tumor [13]. Munipraveena Rela et al used region growing algorithm for tumor segmentation. The tumor is categorized by the area and perimeter of the tumor as benign or malignant. [14].

Jing Zhao et al mentioned a technique to reduce image noise. Here, initially neutrosophic image is obtained, then FCM and particle swarm optimization is utilized to improve the global search [15]. Souhil Larbi Boulanouar et al proposed an algorithm based on the FCM and Modified Fuzzy Bat Algorithm (MFBA) to get better initial cluster centers [16]. Xiaofeng Zhang et al discussed a segmentation method using patch-weighted distance and FCM. Initially patch weighted distance is used to find the correlation between adjacent pixels, and then the influence of neighboring information in fuzzy algorithms is replaced with the pixel correlation, hence this method enhances segmentation[17].

FCM based segmentation algorithms discussed in the literature are sensitive to noise and requires more computation time. These methods require to select the cluster which has liver region, then liver portion is extracted using morphological operations.

Since Superpixel is used in computer vision to enrich the information extracted from an image and group pixels with similar visual properties. Also, a convenient image representation that is reason for computationally efficient. A superpixel picture can give better neighborhood spatial data

than a neighboring window of fixed size and shape, mean shift [18], Simple Linear Iterative Clustering (SLIC) [19] and WT [20], usually regarded as a pre-segmentation algorithm used to improve the segmentation results generated by clustering Algorithm.

Hence, the Superpixel based Fast fuzzy c mean clustering (SFFCM) method of segmentation is performed at low computational complexity, with high accuracy, and fully automatic.

A. Research Problem

The segmentation of Liver Tumor is important step in CAD system, and this is a difficult task due to following reasons:

- Liver region is overlapped with other organs and intensity difference between other organ and liver is very less.
- Only FCM does not segment the tumor accurately, FCM should be used with the pre segmentation algorithms.
- Some algorithms require prior information of region of interest.

Hence the SFFCM clustering is proposed for efficient segmentation, and can portion liver, tumor, and other organ effectively. In this method, a pre-segmentation algorithm called superpixel image is used along with the FCM for accurate segmentation. Hence, Multiscale morphological gradient recon-struction operation and WT (MMGR-WT) is utilized to acquire superpixel image. This algorithm is executed in less time compare to other superpixel algorithms. The performance of algorithm is not sensitive to parameters.

B. Contribution

Majority of the segmentation algorithms mentioned in the literature are noise sensitive and additionally also requires more computation time and human interference. This paper discusses the SFFCM clustering algorithm for tumor segmentation, and is fully automatic segmentation method and additionally shows that this technique offers high accuracy in comparison to the strategies discussed in the literature.

III. RESEARCH METHOD

In this paper, the tumor is segmented from CT liver image utilizing distinctive segmentation methods such as connected component labelling (CCL), K-means clustering (KMC), FCM clustering, SFFCM. Tumor segmentation using the SFFCM method is computed in less time and with less human interaction. In this method, The CT liver image is divided into various regions, then tumor region is extracted based on intensity value selected from the histogram of segmented image. The general block diagram representation of tumor segmentation is shown in Fig. 1.

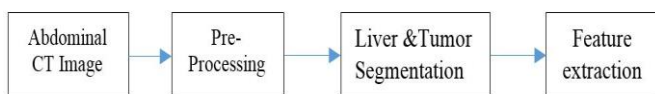


Fig. 1. Block Diagram of CT Liver Tumor Segmentation.

- Abdominal CT image

The CT image containing liver is obtained from liveratlas database. The SFFCM algorithm is implemented on 20 abdomen CT images. These images are converted to JPEG format. Usually CT liver images are low contrast, and liver is overlapped with other organ. So it is important to segment the liver and therefore tumor region.

- Pre-processing

In this step, the noise in the image will be eliminated by using filters such as wiener filter, median filter, and bilateral filters etc. contrast of the image is increased in this process.

- Liver and tumor segmentation

The segmentation of liver is very important step for tumor identification and classification. Segmentation means divide an image into its foreground and background. There are different techniques are available for segmentation. But these techniques don't give any fruitful result. In this paper, the SFFCM clustering method is applied for tumor segmentation. The result obtained using this methodology is compared with other strategies such as CCL, KMC, and FCM clustering.

- Feature Extraction

The ground truth images of tumor are utilized to compare with tumor regions obtained from the different segmentation methods and measured the parameters such as Accuracy, Sensitivity, Fmeasure, Precision, MCC, Dice, Jaccard, Specificity, rfp, rfn. These parameters are important to measure efficiency of tumor segmentation methods.

A. CCL

In CCL, pixel connectivity is used to group the pixels into components in the given input image. After grouping, a gray level is used to assign the pixel in the corresponding component. CCL examines the pixel by pixel so as to identify adjacent pixels with the same intensity values in the region of the image. CCL can be implemented on binary or gray level images and it uses 4- or 8-connectivity. Label connected components can be obtain using the keyword bwlabel in MATLAB.

Fig. 2 shows the block diagram representing the method to segment the tumor region. CT image is given as input. All connected components are identified using CCL. Liver region is selected from connected components, then this region is used as mask to extract only liver area. Again CCL is used to obtain connected components in the liver region, then extracted tumor mask. Tumor mask is used to extract the tumor region from original image.

B. KMC

KMC distribute the data among K number of clusters. If K=2, then two centers will be selected randomly. The data points are allocated to one of the cluster depending upon the distance between the data point and cluster center. Then cluster center will be updated by taking mean of the distance between data points and the center in the cluster.

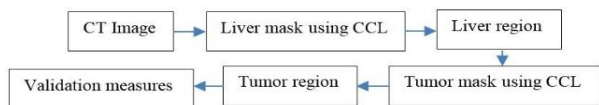


Fig. 2. The Tumor Segmentation from CT Image of Liver using CCL.

Fig. 3 shows tumor segmentation using KMC. The CT image is clustered using $K=4$, selected the cluster which has liver region. Liver is the largest connected component in that cluster and it very well may be extracted by utilizing CCL and also tumor region from liver.

C. Contrast Limited Adaptive Histogram Equalization (CLAHE)

Adaptive histogram equalization (AHE) causes noise amplification, whereas CLAHE is different from AHE. In CLAHE, The noise amplification can be reduced by clipping limit, i.e., the histogram is clipped at predefined value before calculating cumulative distributed function [21]. Block Size (BS) and Clip Limit (CL) are two main parameters in CLAHE. BS is important to divide the input image into non overlapping sections called blocks. If CL increases, the histogram becomes flatter so that it increases brightness of input image. When BS increases, the dynamic range of pixel intensity becomes larger. In CLAHE, histogram equalization is applied to each non overlapping block separately. The CL is employed to clip the original histogram and clipped intensity values are redistributed. The redistributed histogram is dissimilar from original histogram, because CL is utilized to restrict the pixel intensity [22]. Generally Medical images are low contrast, CLAHE is applied for enhancing medical images [23-25].

Syntax: $J = \text{adaphstetq}(I, \text{param1}, \text{val1}, \text{param2}, \text{val2} \dots)$, J is contrast enhanced grayscale image of I . In CLAHE, the image is divided into tiles. The 'Distribution' parameter is utilized to specify the histogram shape, so that histogram of output region should match with it to obtain enhanced contrast of each tile. The artificially boundaries are induced while combining neighboring tiles, the tiles are combined by using bilinear interpolation to eliminate these boundaries. Noise amplification in homogeneous region can be avoided by contrast limiting.

Fig. 4 shows the tumor segmentation using KMC and CLAHE. Here CT image is enhanced by using CLAHE. This gives better results compared to KMC method of segmentation.

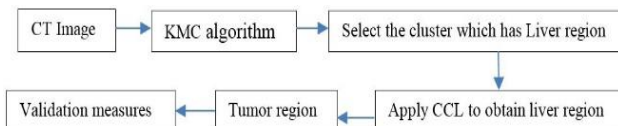


Fig. 3. Tumor Segmentation using KMC.

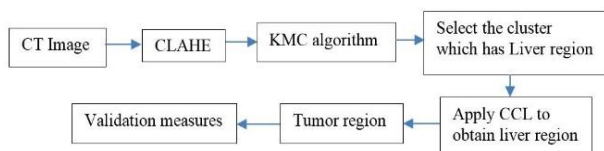


Fig. 4. Tumor Segmentation using KMC and CLAHE.

D. FCM Clustering [9]

Clustering analysis refers to subdivide data set X into c subsets which are called clusters, these clusters are dissimilar, and nonempty. These clusters on combining produce data set X . This is called nonfuzzy clustering. According to Zadeh's, membership function is used to denote the similarity among data point and cluster, it has some value called membership which ranges between $[0,1]$. Each data point has some similarity, called membership in every cluster. If membership is one, then there is high similarity between data point and the cluster. If membership is near to zero, then there is very low similarity between data point and the cluster. A fuzzy c -partition of X describes the membership function to denote the membership of a data point with all clusters. The sum of memberships for any data point must be one [26, 27].

Let $X = \{x_1, x_2, \dots, x_n\}$ be a sample of N observations in 2-dimensional Euclidean space; x_k is the k -th feature vector; x_{kj} the j -th feature of x_k . If c is an integer, $2 \leq c \leq n$, A conventional c -partition of X is a c -tuple (X_1, X_2, \dots, X_c) , subsets of X that satisfies three conditions as shown in (1), (2), and (3):

$$X_i \neq \phi; 1 \leq i \leq c; \tag{1}$$

$$X_i \cap X_j = \phi; i \neq j; \tag{2}$$

$$\bigcup_{i=1}^c X_i = X \tag{3}$$

The FCM algorithms is represented by modifying conditions in matrix-form as shown in Eq. (1). Let U be a real $c \times N$ matrix, $U = [u_{ik}]$. U is the matrix representation of the partition $\{X_i\}$ in (1), it is denoted as in (4), (5), and (6).

$$u_i(x_k) = u_{ik} = \begin{cases} 1; & x_k \in X_i \\ 0; & \text{otherwise} \end{cases} \tag{4}$$

$$\sum_{i=1}^c u_{ik} > 0 \quad \text{for all } i; \tag{5}$$

$$\sum_{i=1}^c u_{ik} = 1 \quad \text{for all } k \tag{6}$$

The generalized least-squared errors method is proposed for detecting fuzzy c -partitions in X . The least squared errors is given in (7).

$$J_m(U, v) = \sum_{k=1}^N \sum_{i=1}^c (u_{ik})^m \|x_k - v_i\|_A^2 \tag{7}$$

Where $X = \{x_1, x_2, \dots, x_n\} \subset R^n$ = the data, c = the number of clusters in Y ; $2 \leq c < n$, m = weighting exponent; $1 \leq m < \infty$, U = fuzzy c-partition of X ; $v = (v_1, v_2, \dots, v_c)$ = vectors of centers; $v_i = (v_{i1}, v_{i2}, \dots, v_{in})$ = centers of cluster i ,

A = positive-definite $(n \times n)$ weight matrix, $\| \cdot \|_A$ = induced A -norm on R^n , d_{ik}^2 is the squared distance between x_k and v_i as given in (8).

$$d_{ik}^2 = \|x_k - v_i\|_A^2 = (x_k - v_i)^T A (x_k - v_i) \quad (8)$$

(U, \hat{v}) Pairs are used to define optimal fuzzy clustering of X that locally minimize J_m . For $m > 1$, if $x_k \neq v_j$ for all j and k , (U, \hat{v}) may be locally optimal for J_m only if v_i and u_{ik} are as shown in (9) and (10).

$$v_i = \sum_{k=1}^N (u_{ik})^m x_k / \sum_{k=1}^N (u_{ik})^m; 1 \leq i \leq c; \quad (9)$$

$$u_{ik} = \left(\sum_{j=1}^c \left(\frac{d_{ik}}{d_{jk}} \right)^{2/(m-1)} \right)^{-1}; 1 \leq k \leq N; 1 \leq i \leq c; \quad (10)$$

Fig. 5 represents tumor segmentation using FCM. Here input image is grouped into four cluster. A cluster which has liver region is selected, then CCL is implemented to that cluster to attain liver and tumor regions.

E. SFFCM Clustering

Majority of image segmentation algorithms based on improved FCM clustering require more execution time and incapable to give desired results because of two reasons [28]. The primary reason is that the immoderate computational complexity within a local neighboring window is due to the repeated distance calculation between clustering centers and pixels. Second reason is that these techniques aren't able to offer preferred results due to constant size and shape of neighboring window. Hence, A SFFCM clustering algorithm requires less execution time and accurate for color image segmentation [29].

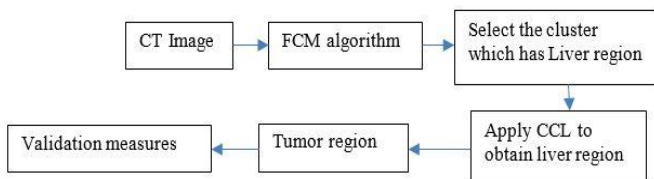


Fig. 5. Tumor Segmentation using FCM.

Local spatial information in a superpixel image is obtained by using MMGR operation. The adaptive local spatial neighborhoods that's helpful for segmentation is provided by superpixel image. The histogram of superpixel picture can be obtained without any problem. Lastly, Segmentation result can be obtained by implementing FCM with histogram parameters on the superpixel image. Improved segmentation results can be obtain by combining MMGR-WT and FCM, since MMGR-WT is utilize to accomplish the local feature of an image whereas global features can be obtained using FCM. A SFFCM algorithm is developed by means of considering adaptive local spatial information into the objective function of FCM [30].

SFFCM's objective function is defined using the MMGR-WT based superpixel image as shown in (11).

$$J_m = \sum_{l=1}^q \sum_{k=1}^c S_l u_{kl}^m \left\| \left(\frac{1}{S_l} \sum_{p \in R_l} x_p \right) - v_k \right\|^2 \quad (11)$$

where l is the color level, $1 \leq l \leq q$, q is the number of regions of the superpixel image, $l, q \in N^+$, S_l is the number of pixels in the l th region R_l , and x_p is the color pixel within the l th region of the superpixel image obtained by MMGR-WT. In this process, to substitute of color pixel in the original picture, the mean value of the color pixels within the corresponding region of the superpixel picture is used, so the number of regions within the superpixel image is same as the number of color levels. Thus, the complexity of this algorithm is efficiently decreased due to $l \ll N$.

The cluster center and fuzzy c partition is obtained using following (12) and (13):

$$v_k = \frac{\sum_{l=1}^q u_{kl}^m \sum_{p \in R_l} x_p}{\sum_{l=1}^q S_l u_{kl}^m} \quad (12)$$

$$u_{kl} = \frac{\left\| \left(\frac{1}{S_l} \sum_{p \in R_l} x_p \right) - v_k \right\|^{-2/(m-1)}}{\sum_{j=1}^c \left\| \left(\frac{1}{S_l} \sum_{p \in R_l} x_p \right) - v_j \right\|^{-2/(m-1)}} \quad (13)$$

The algorithm of SFFCM is shown in Fig. 6.

Fig. 7 shows tumor segmentation using the SFFCM. CT image is converted to Superpixel image using MMGR-WT, then FCM with proposed objective function is utilized to acquire segmented image. Histogram of segmented image is obtained to select the gray level of tumor region. Finally, gray level thresholding is implemented to obtain tumor region.

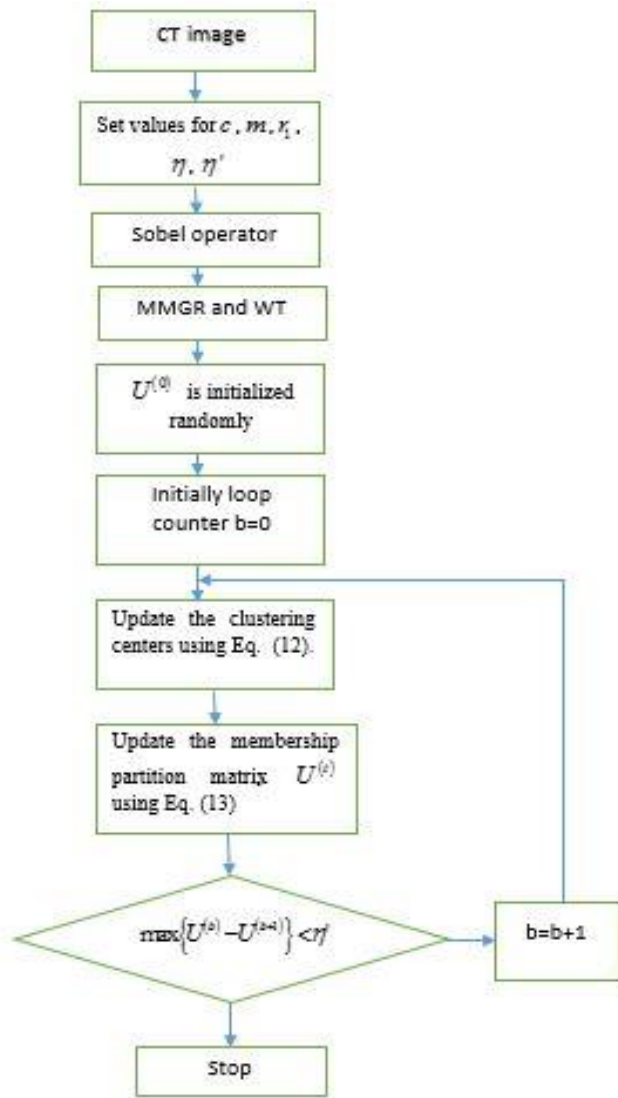


Fig. 6. Algorithm of SFFMC.

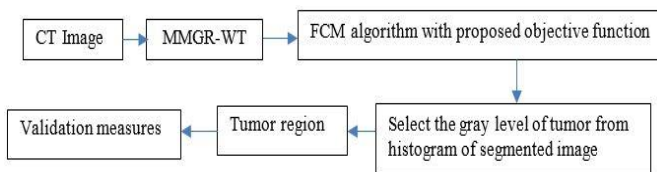


Fig. 7. Tumor Segmentation using the SFFCM.

IV. RESULTS AND DISCUSSIONS

Here 20 CT abdominal images from liveratlas database are considered for analysis. The proposed work carried out using Intel CORE i5 processor and MATLAB R2015a version. In this section, the tumor segmentation obtained by applying different segmentation methods are discussed.

A. Validation Measures

The following parameters are used to compare ground truth and segmented image. These parameters are defined by (14) – (22).

Accuracy (14) is the measure of correctly predicted observations with reference to the total observations.

$$Accuracy = \frac{TP + TN}{FN + FP + TP + TN}; \quad (14)$$

Sensitivity as given in (15), measures which frequently a diagnostic test is positive, given that the person has the disease.

$$Sensitivity = \frac{TP}{TP + FN}; \quad (15)$$

Precision is the quantitative relation of properly expected positive observations to the full expected positive observations, as shown in (16).

$$Precision = \frac{TP}{TP + FP}; \quad (16)$$

Matthews Correlation Coefficient (17).

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{((TP + FP) \times (TP + FN) \times (TN + FP) \times (TN + FN))}}; \quad (17)$$

Dice Coefficient (18) is the proportion of overlap between the two sets, which is a number between 0 and 1.

$$Dice = \frac{2 \times TP}{2 \times TP + FP + FN}; \quad (18)$$

The Jaccard Index (19) is utilized in understanding the similarities between sample sets.

$$Jaccard = \frac{Dice}{2 - Dice}; \quad (19)$$

Specificity (20) is the chance that a diagnostic check is negative, provided that the individual doesn't has the illness.

$$Specificity = \frac{TN}{TN + FP}; \quad (20)$$

The false positive rate (rfp) (21) is defined as the likelihood of falsely rejecting the null hypothesis

$$rfp = \frac{FP}{FP + TN}; \quad (21)$$

The false negative rate (rfn) (22) is the proportion of the individuals with a known positive condition for which the test outcome is negative.

$$rfn = \frac{FN}{FN + TP}; \quad (22)$$

TP - true positive, *FP* - false positive, *TN* - true negative, *FN* - false negative

B. Segmented Images

The input image is color image, hence it is converted to grayscale image. Grayscale image is enhanced by using histogram equalization. Thresholding is utilized to get binary image. bwlabel is employed to label the connected components in binary image. Liver mark is extracted from connected components. Using liver mark, liver is obtained. From liver region, Tumor region is extracted using morphological operations.

C. Parameter Setting

In CCL, histogram equalization is used in preprocessing stage, threshold with level=0.67 is used to obtain binary image, total number of connected components are 116, the largest connected component is 11 which is liver, then morphological operations are used to extract the liver region, thresholding with level 0.5 is used to obtain tumor region.

In FCM, median filter is used as preprocessing. Divided the image into four clusters, selected the cluster which has liver region, then used morphological operations to extract the tumor.

In SFFCM, No. of clusters=8, structuring element for MMGR=3, exponent for the partition matrix U=2, max. Number of iteration=50, min. amount of improvement=1e-5.

D. Results

Fig. 8(a) shows the output of KMC. Fig. 8(b) shows clustering using FCM. From these clustering, the cluster which contains liver region is selected, that is in Fig. 8(a), cluster3 is selected, whereas in Fig. 8(b) cluster4 is selected. Then CCL is applied to this cluster to obtain largest connected component, which is nothing but liver. Then the tumor is identified using morphological operation.

Fig. 9(a), 9(b), 9(c), 9(d), and 9(e) show tumor segmentation using CCL, KMC, and CLAHE enhanced KMC, FCM and SFFCM. Fig. 10 shows the tumor segmentation using SFFCM clustering for different CT images. The SFFCM gives color segmented image. From the color segmented image, pixel value of tumor region is utilized in gray level slicing to get the tumor mask. Then tumor region is extracted by multiplying tumor mask with original image.

Table I lists the comparison of statistical parameters measured for tumor segmented images of CT1, CT2 and CT3 with ground truth images. Fig. 11 shows the plot of statistical parameters for tumor segmented images. Table II gives the comparison of rfp, rfn values with reference to different methods of segmentation. It is observed that segmentation using SFFCM has improved rfn. SFFCM is used to acquire segmented image directly, it is additionally less tedious and fully automatic. The SFFCM method of segmentation gives accuracy of 99.58%, sensitivity of 87.77%, Precision of 96.37%, MCC of 91.61%, Specificity of 99.93%, Jaccard of 84.64%, and Dice of 91.54%.

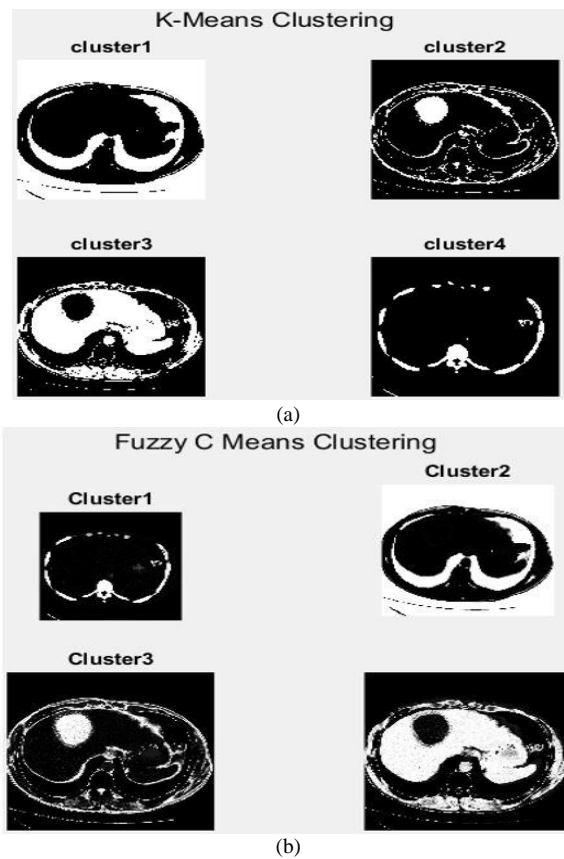


Fig. 8. Results of Clustering using (a) KMC (b) FCM.

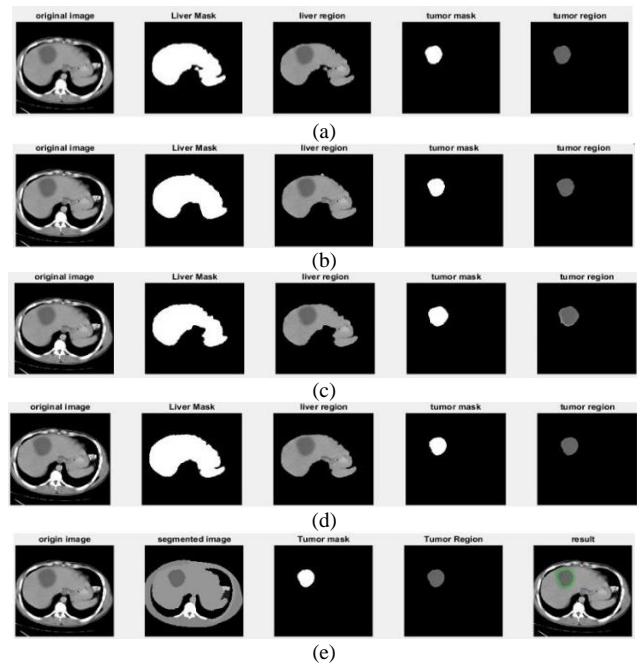


Fig. 9. Tumor Segmentation (a).CCL, (b).KMC, (c). CLAHE and KMC, (d). FCM, (e).SFFCM.

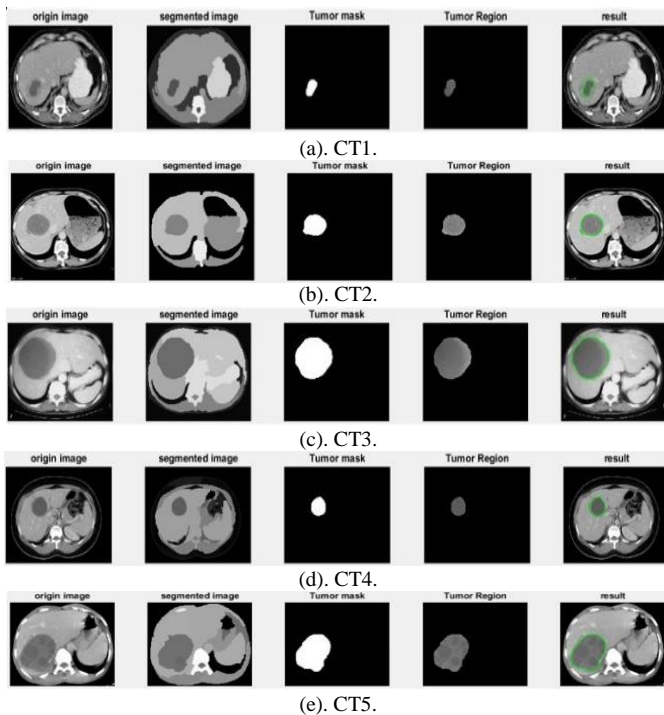


Fig. 10. Tumor Segmentation using SFFCM.

TABLE I. STATISTICAL PARAMETERS FOR IMAGE SEGMENTATION USING SFFCM

| INPUT | CT1 | CT2 | CT3 | CT4 | CT5 | Avg |
|---------|-------|--------|--------|---------|---------|--------|
| Accu | 0.998 | 0.992 | 0.997 | 0.999 | 0.993 | 0.9958 |
| Sens | 0.918 | 0.765 | 0.9504 | 0.97764 | 0.97217 | 0.917 |
| Prec | 0.920 | 1 | 0.9713 | 0.9898 | 0.97096 | 0.970 |
| MCC | 0.918 | 0.8713 | 0.9593 | 0.98334 | 0.96791 | 0.940 |
| Spec | 0.999 | 1 | 0.9989 | 0.99978 | 0.99626 | 0.9988 |
| Jaccard | 0.850 | 0.765 | 0.9244 | 0.96789 | 0.9447 | 0.8904 |
| Dice | 0.919 | 0.867 | 0.9607 | 0.98368 | 0.97157 | 0.9403 |
| rfp | 0.08 | 0 | 0.0281 | 0.0101 | 0.029 | 0.0294 |
| rfn | 0.082 | 0.235 | 0.0496 | 0.0224 | 0.0278 | 0.0834 |

Comparison of accuracy for SFFCM against the methods in literature is listed in Table III. It is shown that, compared with the methods in the literature, the SFFCM provides high accuracy.

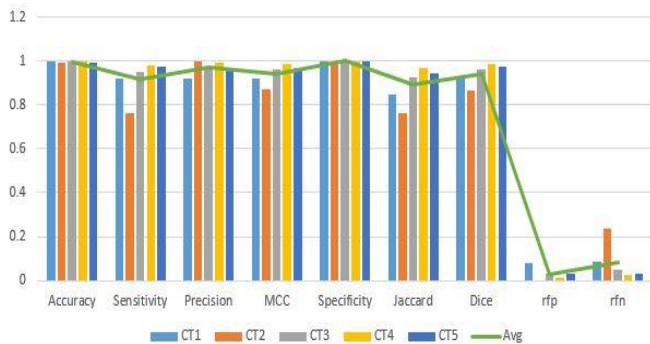


Fig. 11. Statistical Parameter of SFFCM for different Input Images

TABLE II. COMPARISON OF SEGMENTATION METHODS USING *rfp* AND *rfn*

| Segmentation method | rfp | rfn |
|---------------------|---------|---------|
| CCL | 0 | 0.19596 |
| KMC | 0 | 0.21861 |
| CLAHE-KMC | 0.47912 | 0.05777 |
| HPF-KMC | 0 | 0.22631 |
| FCM | 0.05377 | 0.06594 |
| SFFCM | 0 | 0.0834 |

TABLE III. COMPARISON ON ACCURACY FOR SFFCM AGAINST THE METHODS IN LITERATURE

| S.No. | Author | Accuracy |
|-------|----------------------|----------|
| 1 | Grzegorz Chlebus[32] | 90% |
| 2 | Dong Yang[31] | 95% |
| 3 | Sultan Almotairi[28] | 98.8% |
| 4 | Lamia N. Mahdy[33] | 96.86% |
| 5 | SFFCM | 99.58% |

Comparison of computational time of various methods used to obtain superpixel image is shown in Table IV. The results shows that MMGR-WT requires less execution time compare to the methods discussed.

TABLE IV. COMPARISON OF COMPUTATIONAL TIME(IN SECONDS) OF METHODS USED TO OBTAIN SUPERPIXEL IMAGES

| Algorithms | Execution time(in seconds) |
|-------------|----------------------------|
| SLIC | 3.86 |
| mean-shift1 | 1.02 |
| mean-shift2 | 2.66 |
| MMGR-WT | 0.32 |

V. CONCLUSION

In this paper, a SFFCM clustering algorithm is employed for liver tumor segmentation. In order to obtain a good superpixel image, the MMGR operation is presented and the color histogram is integrated into the objective function to achieve fast image segmentation. The experimental findings show that the SFFCM is superior to state-of-the-art clustering algorithms because it offers the best results for segmentation and has the shortest runtime.

The SFFCM-based Liver tumor segmentation is automatic. Therefore, relative to other unsupervised segmentation approaches, human intervention is less. This method has achieved accuracy of 99.5%, Precision of 96.37%, Specificity of 99.93% for tumor segmentation. The results shows that the SFFCM method of segmentation gives high accuracy and improved compared to the methods in literature.

For color image segmentation, our algorithm is very fast because pre-segmentation method called superpixel image is used before segmentation, but it has limitations in realistic applications, similar to other k-means clustering algorithms,

because the number of clusters must be set before-hand. We will combine frequency domain approach and deep learning approach to explore fast clustering algorithms in future work, which automatically estimate the number of clusters.

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