

# Segmentation of Metastasis Brain Images Using Wavelet Transform Based Hybrid Mean Shift Clustering and Region Split Algorithm

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**Abstract:** Segmentation of multiple tumors is highly challenging task in medical field. MRI Imaging is one of the prudent mechanisms to extract the tumor regions and to map the brain for diagnosing. One must need to detect the tumor accurately for the diagnosis; one must detect the tumor accurately and need to calculate the area and volume of the tumor exactly. Here in this paper, we proposed a novel resolution enhancement technique to improve the quality of MR brain image and optimized hybrid mean shift clustering (OHMSC) with region split and merge algorithm to detect the tumor cells from the original MR images and to estimate the tumors from different locations. Simulation results show that the proposed algorithm has performed superior to conventional clustering algorithms such as Fuzzy C-means (FCM), K- Means and even optimized pillar algorithm.

**Key words:** Metastasis brain tumor, DWT, SWT, Interpolation, Image Segmentation, FCM, K-means, Optimized pillar algorithm.

## I. INTRODUCTION

In radiology, magnetic resonance imaging (MRI) [1] is used to investigate the human body processes and functions of organisms. These images can be formed by using the magnetic fields and radio waves. In hospitals, this technique has been using widely for medical diagnosis, to find the disease stage and follow-up without exposure to ionizing radiation. MRI has a broad range of applications in medical diagnosis and in all over world there are over 25,000 scanners to be in use. It has an impact on diagnosis and treatment in many specialties although the effect on improved health outcomes is uncertain. MRT is more preferable over computed tomography (CT) since it does not use any ionizing radiation, when either modality could yield the same information. The sustained increase in demand for MRI within the healthcare industry has led to concerns about effectiveness of cost and over diagnosis.

Segmenting an image is an effort to group similar colors or elements of an image into a cluster or group. This can be achieved by clustering, which clusters the number of colors or elements into several clusters based on the similarity of color intensities and gray intensities of an image. Main objective of clustering an image is dominant colors extraction from the images. By extracting the information from images such as texture, color, shape and structure, the image segmentation can be very important to simplify. Because of the information extraction in any images, the segmentation has been used in many fields such as Enhancing the image, compression, retrieval systems i.e., search engines, object detection, and medical image processing [2]. Tumors are classified as primary and secondary tumors. The origins of primary tumors

develop with in the brain. When cells split from the primary tumor and shipment through the blood system to another fragment of the body called Secondary tumors or metastases. Metastatic brain tumors can develop efficiently, assemble or spoiling nearby brain tissue. Consistently, a patient may have multiple metastatic tumors in distinct areas of the brain. We all know that the brain tumor is inherently serious and life-threatening.

Most Researchers proven that number of people who have brain tumors were died due to the fact of inaccurate tumor detection and estimation of its size. To avoid the drawbacks of conventional schemes such as low resolution, inaccurate detection of tumor and its size, this work proposed computer aided method for MR brain image segmentation [1]for detecting the tumor cells from different locations of image i.e., from metastasis brain image. In the proposed approach the low resolution MR image is enhanced by using Non-decimated wavelet transform (N-WT). Then after, we had applied proposed OHMSC with region split algorithm to detect the tumor cells from the high resolute MR image. This process includes a new and novel mechanism for clustering the elements of high-resolution images in order to improve the precision and reduce computation time.

## II.RELATED WORK

From the past decades many researchers have developed the MR brain image segmentation algorithms by applying the segmentation algorithms and clustering techniques to detect the tumor cells from the MR images [1]. The author in [2] proposed An Automated 3D Segmented and

DWT Enhanced Model for Brain MRI. In this context, the author used DWT to enhance the MR image from its low resolution image and then by using manual segmentation it will be segmented automatically. But, we know that the manual segmentation will consume more time, which results in the increment in computational time. This will help us that this approach is not suitable for MR image segmentation and by considering the results progression, significant number of miss detected and false detected pixels causes to produce an inaccurate tumor area and also will not detect the tumor cells accurately. The authors from [3], [4], [5], [6] and [7] had proposed image enhancement techniques using transformation approaches such as DWT and SWT decomposition. However, due to the lack of number of original pixels all of them were fail to produce a high resolute image without losing its original content information from the MR images. Manisha et. al. in [8] proposed an improved watershed segmentation algorithm, which provides better results than the manually segmented algorithms but it includes few drawbacks like over-segmentation and sensitivity to false edges. Recent years, Fazel in [9] proposed a fuzzy expert approach for segmenting the tumor cells from the MR brain images. However, that the fuzzy approach has produced good segmented results but it suffers from determining the membership function, which is used to cluster the similar pixels in MR image. Fuzzy will be worked with allocation of membership function to the pixels based on the initial centroids selected from the pixels of input image, which is to be segmented. Specifically, determining the number of the cluster is a considerable limitation with FCM. Since the regions are spatially discontinuous grey level similarity is only verified. Considering the experimental study FCM is converging to local minima of the squared error criterion [9]. Then after, Mohammed et. al. in [10] proposed an efficient brain tumor detection scheme based on the combination of spatial information with fuzzy c-means which overcomes the drawback found in [9], but it takes much time to segment the tumor and will suffer from false edges. To overcome, the drawbacks of manually segmented, watershed and FCM [7], [8], [9], and [10] clustering algorithms, Mary Praveena in [11] proposed a fusion based image segmentation using k-means clustering, which is an extension to the above mentioned algorithms and will provide the best results within less computational time. Later years, there are so many algorithms such as histogram based approach, anisotropic diffusion and FCM have been merged with the k-means and given the best performance over conventional techniques [12], [13], [14] and [15]. However, this k-Means is limited to produce only hyper spherical clusters.

It depends on initial centroids. To update the new centroids the mean of the pixel values of the respective clusters need to be estimated. The floating values obtained in some iteration are not favorable. Significantly, positive integers or scalars are required to replace the new centroids. Hence with K-means algorithm the optimal solution is difficult to achieve. In order to overcome the drawbacks of k-means, Barakbah et. al. in [16] proposed a

pillar algorithm to solve the initial centroid designation problem, by considering the pixel maximization i.e., select maximum pixel value for centroid. To improve the performance of segmentation and detecting the accurate tumor cell from the MR image, iterative mean shifting algorithm will be merged with k-means clustering, which is proposed in [17]. The number of clusters will be selected optimally and also the centroid updation for number of iteration will also be solved in k-means by considering the maximum pixel value instead of calculating the mean of group of clustered pixel values. In [18] Naik et. al. proposed a mean shift clustering scheme to improve the clustering accuracy and number clusters selection. It provides a good accuracy and superior segmented results for unlabeled data. However, the scheme proposed by Naik in [18] will not be able to find the good segmented results with all type of images such as MR and CT, since the number of clusters were not optimized i.e., it doesn't give the optimal solution to extract the regions from the images. And also unable to improve the quality of image before going to segment unlabeled images. All the above mentioned algorithms have been developed and tested for standard images, in which the MR images have only single tumor cell, and will not mention the medical parameters such as accuracy, sensitivity of the tumor.

### III. PROPOSED METHODOLOGY

#### A. Super Resolution Image Enhancement

Non-decimated wavelet transform (N-WT) is used to resolve the Low resolution MR input image. The information loss on its edges i.e., high frequency components may arise by applying the interpolation for image intensification. Safeguard the edges is imperative. DWT has been hired to safeguard the high frequency components of the image. In-order to obtain the redundancy and shift invariance the discrete wavelet transform coefficients are essentially interpolated. Hence DWT is used to disintegrate the MRI Image into sub band images.

First, the LR image is given as an input to the DWT to decompose it into four sub bands LL, LH, HL and HH, which known as approximation, horizontal, vertical and diagonal coefficients and last three sub bands are also called as detail coefficients. These sub bands size will be half of the LR image due to that the DWT has a decimation property. Hence we need to interpolate it to further operate it with the LR image. Now, the LL sub band will be interpolated to subtract from the original image i.e., LR image, after this operation a difference image will be obtained. This difference image will be added to the high frequency sub bands LH, HL and HH to improve the high frequency sub bands information. In order to perform addition for these sub bands, we need interpolation to increase the size of decimated sub bands because, the size of difference image equals to the LR image which is an original image. After performing this operation, the estimated or modified LH, HL and HH will be obtained. The after do the interpolation for LR image

with a factor of  $\alpha/2$ , where the parameter  $\alpha$  is a interpolation factor, and do the same for even estimated LH, HL and HH also. Finally, apply inverse DWT to these four sub bands to get the super resolute image i.e., HR image.

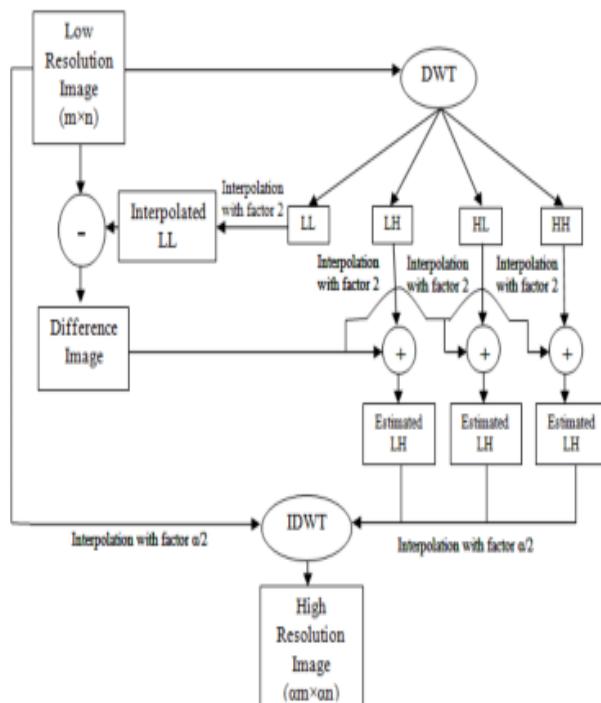


Fig1. Proposed Super resolution flow chart

#### B. Proposed OHMSC Scheme

The proposed Algorithm substantiates the implication of MRI Brain tumor image segmentation and clustering to estimate the tumor area. The proposed approach endorsed optimized results.

##### Algorithm1:

Input image = I  
Output image = O

- Step1. Select and read the input metastasis brain image 'I'
- Step2. Reshape 'I' into data sets of column vector ( $C_v$ ) for segmentation.
- Step3. Determine the number of clusters (K) i.e. centroids.
- Step4. Calculate the distance (D) between  $C_v$  and 'K' for each pixel to cluster point
- Step5. Find number of  $C_v$  which are neighboring to the 'K'.
- Step6. Select the 'K' with minimum distance and then move the  $C_v$  to the closest relevant centroids
- Step7. Re estimate the centroids by selecting the maximum pixel value from the set of relevant centroid data points.
- Step8. Repeat the process until the new centroids and the previous centroids are symmetrical.

##### Algorithm 2:

Input image = O  
Output image = S

Step1: Read the output image 'O', which has been obtained from algorithm1

Step2: Apply optimized algorithm to the image 'O'

Step3: Display the segmented metastasis brain image in which we had multiple tumors

Step4: To calculate the tumor areas individually, first divide the segmented image by using Region Split (RM) algorithm (described in below section)

Step5: After separating the tumors, calculate the area of the tumors by using approximate reasoning method, in which the area of the tumor will be calculated by considering the number of white pixels

Step6: And also compute the CPU time in seconds for the comparison of proposed and existing techniques

##### Algorithm 3:

The optimized algorithm is described as follows. Let  $M=\{m_i|i=1,\dots,n\}$  be the input data,  $k$  be number of clusters,  $C=\{c_i|i=1,\dots,k\}$  be initial centroids,  $D_M=\{m_i|i=1,\dots,n\}$  be accumulated distance metric,  $SM \subseteq M$  be an identification for  $M$  which are already selected in the sequence of process,  $D=\{m_i|i=1,\dots,n\}$  be distance metric for each iteration, and  $\mu$  be the grand mean of  $M$ . The following steps describe the shaft algorithm: $[cluster_{idx}, Center]=shaft(M, k)$

1. Initialize  $C=[ ]$ ,  $SM=[ ]$ , and  $D_M=[ ]$  and set  $k=3$
2. Calculate the value of  $\mu$  (i.e., by taking the mean of  $M$ )
3. Calculate the size of data  $M$ i.e.,  $[r_s, c_n]=size(M)$  where  $r$ =number of rows and  $c$ =number of columns
4. Assign zeros to  $D_M$ i.e.,  $D_M=zeros(1, c_n)$
5. Calculate the distance between  $M$  and  $\mu$  i.e.,  $D \leftarrow dis(M, \mu)$
6. Assign  $d_{max} \leftarrow arg_{max}(D)$
7. Set  $i=1$  as counter to determine the  $i_{th}$  initial centroids
8. if  $i \leq k$  then  $D_M = D_M + D$
9. Select  $\mathfrak{Y} \leftarrow arg_{max}(D_M)$  as the candidate for  $i_{th}$  initial centroids, set  $SM = Union(SM, \mathfrak{Y})$  and  $D_D$  as the distance metric between  $M$ to  $\mathfrak{Y}$ .
10. Set  $no \leftarrow$  number of data points fulfilling  $D \leq d_{max}$ ,  $C=[C \ \mathfrak{Y}]$ ,  $D(SM)=0$ ;  $D_M(no)=0$ ;
11.  $i = i + 1$  and  $[D_{min}, index]=min(D_D)$ ;  $c=index$ ;  $move=d = sum(index \sim c)$ ;
12. assign  $Cluster_{idx} = c$ ; and  $Center = C$ ;

##### C. Region Split (RS) algorithm

For estimating the tumor area, the image should be portioned into regions. A set of pixels associated with analogous properties is labeled as a region. Each region is a segment analogous to the input image. Based on the similarity and spatial proximity the pixels corresponding to region are grouped together. Grey value differences and grey value variance is used to achieve similarity. Euclidian distance and compactness of a region is used to achieve spatial proximity. Region splitting and merging approach is used to divide the multiple tumor MRI image into segments. 256\*256 MRI image is considered as a single region. The similarity condition is to be tested to split the single region image into subsidiary regions. Quadtree

method is adopted for splitting the MRI image. 256\*256 MRI image is divided into four 128\*128 sub regions, each 128\*128 region is further split into four 64\*64 sub regions. This process continues until the region fulfills the similarity (homogeneous) condition. The homogeneous two adjacent regions are merged as a single one. This merging process continues until no two regions fulfill homogeneous condition. Since the multiple tumors located at different portions of the image, Split and merge approach is adopted to segment the MRI image. Algorithm1 and 2 is applied to estimate the area of the tumor. And the estimated value is compared with the existing iterative mean shift clustering, K-Means, Fuzzy C-Means, methods.

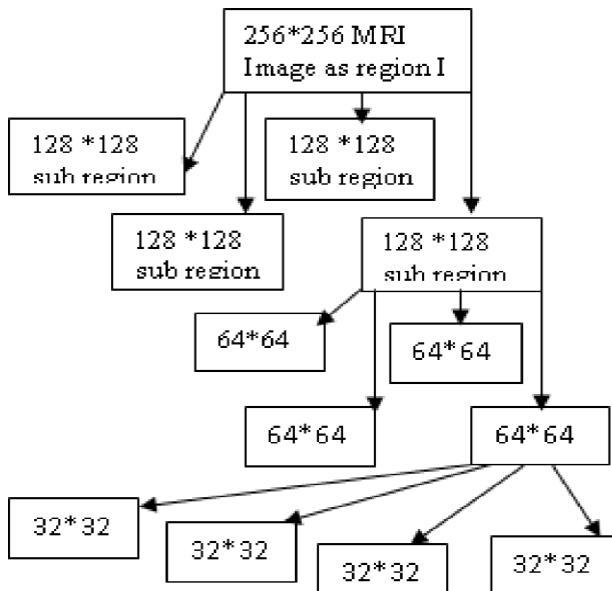


Fig2. Region Split diagram

#### D. Approximate Reasoning

Linearization method is adopted to estimate the area of the tumor. The MRI image comprises of two pixel values either gray or white i.e., 0 or 1. Where '0' is for black and '1' is for white pixel value representation. The size of the image is considered to be 256x256.

$$I = \sum_{x=0}^{255} \sum_{y=0}^{255} [f(0) + f(1)]$$

$$\text{Pixels} = \text{Width} * \text{Height} = 256 * 256$$

$$f(0) = \text{black pixel '0'}$$

$$f(1) = \text{White pixel '1'}$$

$$\text{Total White Pixels } (W_p) = \sum_{x=0}^{255} \sum_{y=0}^{255} f(1)$$

$$W_p = \text{number of white pixels}$$

$$1 \text{ Pixel width} = 0.264 \text{ mm}$$

The equation to estimate the tumor area is

$$\text{Tumor Size } (S) = \left( \sqrt{W_p} * 0.264 \right)$$

## IV. RESULTS & ANALYSIS

The multiple tumors were located asymmetrically in the region of the brain. Estimating the area of the single tumor is not a complex task. But multiple tumors at different locations are a great challenge to the physician. The metastasis MRI image may consist of low resolution pixel levels. N-WT augmenting with the bi-cubic interpolation is enforced to enhance the de-noised tumor image. The major loss of an MRI image after being resolution enhanced by applying interpolation is on its high frequency components, which is by virtue of the smoothing caused by interpolation consequently to increase the quality of the enhanced image.

Preserving the edges is imperative. N-WT has been selected to preserve the high frequency components of the MRI image. The LMSE for sample 2 and sample 4 lies within the value "1" and for sample 1 and sample 3 the LMSE shows "1.2". The small value of LMSE results fine quality. All "MD" values for all the samples lies Less than '1' that shows the quality parameters for the resolute images exhibits good quality.

The image size of 256\*256 is used for enhancement with an interpolation factor of '2'. The resolute image is considered for testing using Region based split approach. Split and merge approach is tested on MR image Samples.

The Fig 3 (b), (c), (d), (e), (f) and (g) represents the experimental results of the sample '1'. The Resolute MR image is considered as a single region and consists of three tumors. The image is split into four sub regions. Region 1 consists of single tumor; whereas region 2 consists of two tumors.

Hence region 2 is again split into 2 sub regions. The area of the tumor 1, 2, 3 is estimated using the existing segmentation and clustering approaches and also with the proposed method i.e. optimized hybrid clustering algorithm.

For sample 1 K-Means and FCM methods produced approximately similar results. Whereas the proposed method exhibits optimum results for tumor1, 2, and 3 is tabulated with 3.5222 mm<sup>2</sup>, 2.8434mm<sup>2</sup>, and tumor3 2.6135mm<sup>2</sup> respectively. The estimated tumor area will be favorable to the Physician for both therapeutic and surgical applications.

The proposed approach is handful support to the physician with no damage to the healthy tissue while treating the tumor region. Considering sample 2 and sample 3, the K-means and FCM approaches grouped neighborhood non tumor pixel values into tumor cluster due to grey level similarity. The FCM approach results significantly weaker results. FCM is more depending on the initial centroids of clusters and difficult to determine the membership functions. Hence the results are significantly higher than the proposed method.

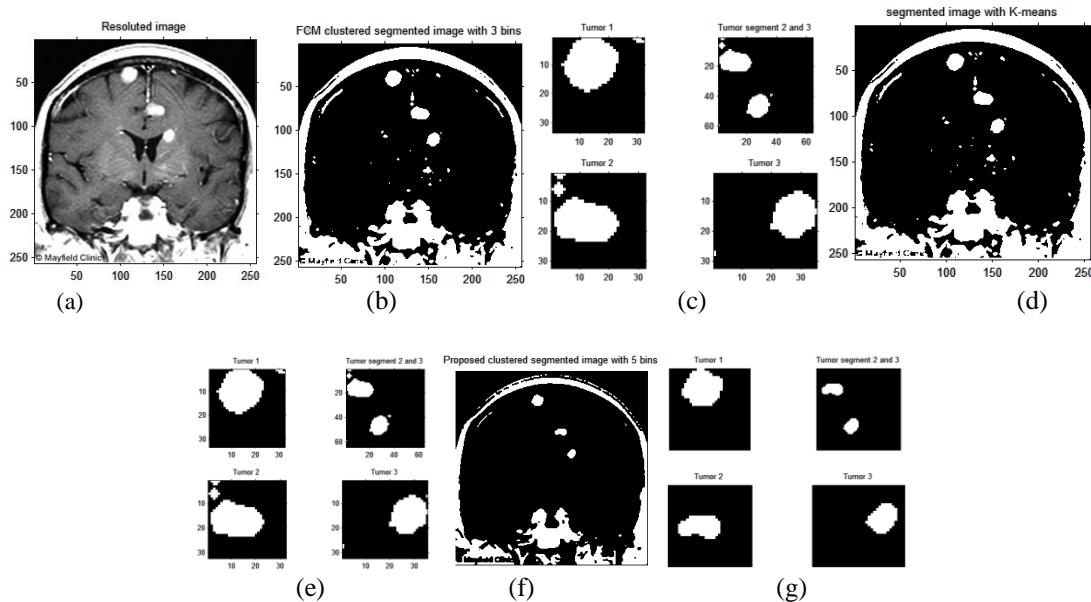


Fig3 (a) Resolute image (b) Segmented image using FCM (c) Tumors separation using RS for FCM (d) Segmentation using K-Means (e) separation of tumors using RS for k-means (f) Segmentation using Proposed and (g) RS for proposed

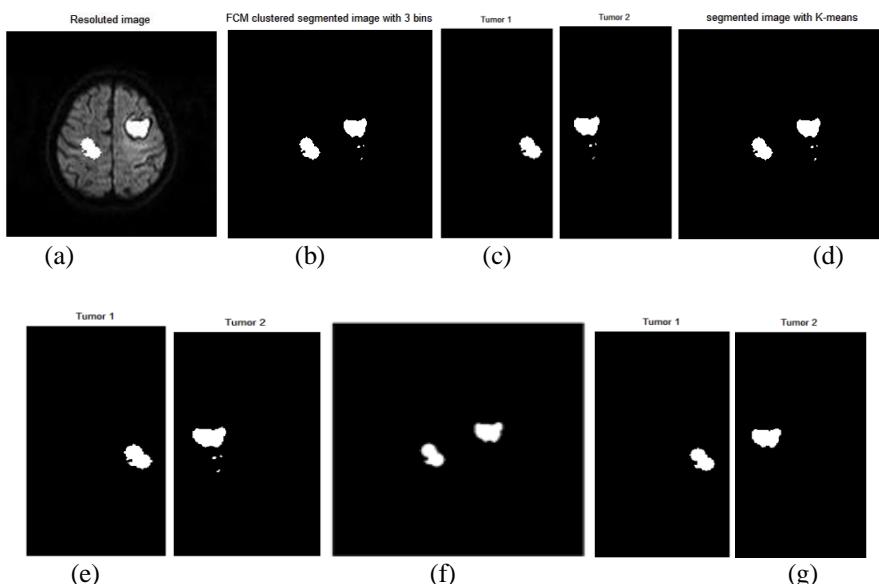
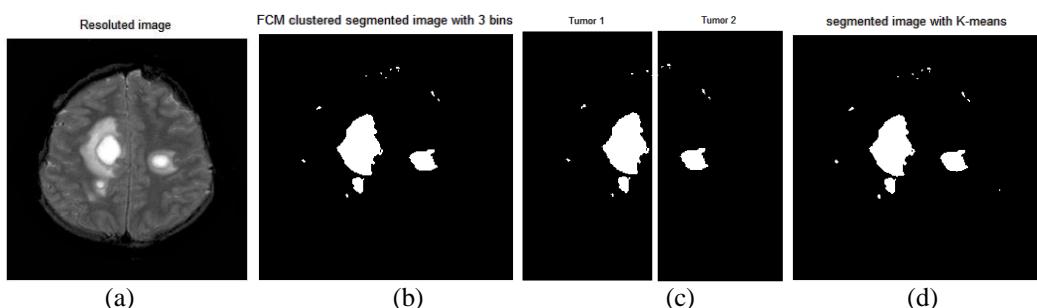


Fig4 (a) Resolated image (b) Segmented image using FCM (c) Tumors separation using RS for FCM (d) Segmentation using K-Means (e) separation of tumors using RS for k-means (f) Segmentation using Proposed and (g) RS for proposed



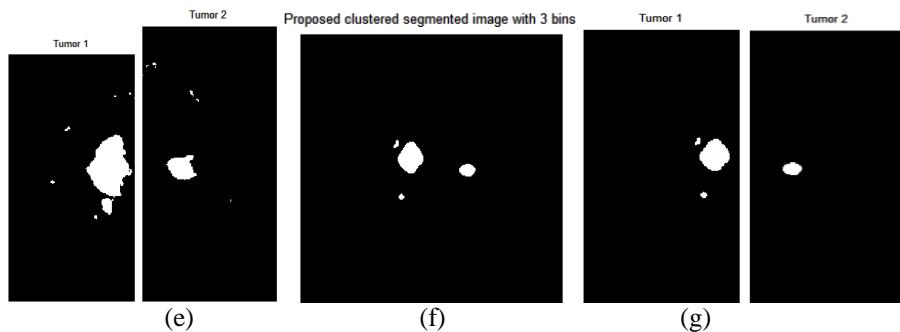


Fig5 (a) Resolved image (b) Segmented image using FCM (c) Tumors separation using RS for FCM (d) Segmentation using K-Means (e) separation of tumors using RS for k-means (f) Segmentation using Proposed OHC and (g) RS for proposed

Table1. Comparison of tumor areas for various methods

Algorithm	Area of the tumor( mm^2 )									
	Sample1			Sample2		Sample3		Sample 4		
	Tumor1	Tumor2	Tumor3	Tumor1	Tumor2	Tumor1	Tumor2	Tumor1	Tumor2	
FCM	4.3540	4.2976	3.5518	5.5251	6.0259	11.7591	5.6990	11.0439	8.1327	
K-Means	4.3700	4.3057	3.5811	5.5251	6.0375	11.8330	5.7416	10.9520	8.1156	
Proposed	3.5222	2.8434	2.6135	5.0987	5.6990	6.2641	3.1899	10.4639	7.8181	

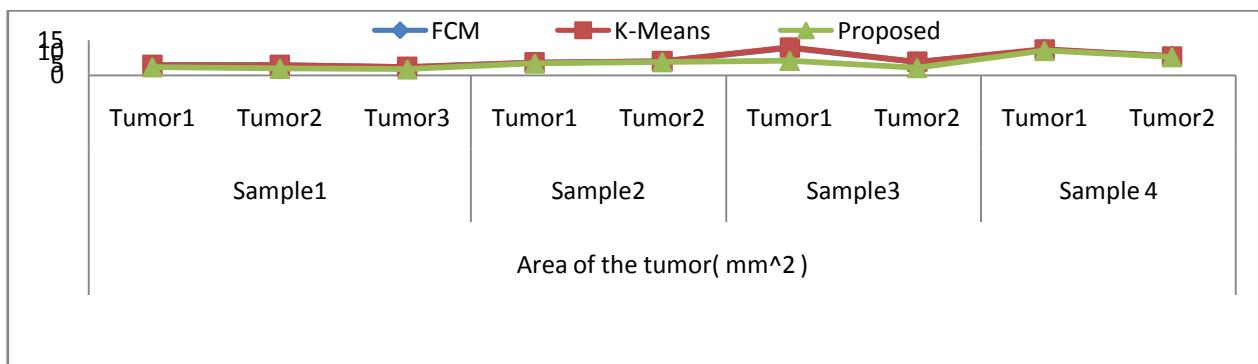


Fig6. Comparison of Area of the tumors with various approaches

Table2. Quality analysis comparison for various sample resolute images

Sample No	PSNR(db)	AD	SC	NCC	MD	LMSE	NAE
Sample 1	58.4795	0.2258812	3.9963302	0.4759032	0.5000002	1.2209692	0.0000002
Sample 2	67.9731	0.0455422	3.9069952	0.4957152	0.0000002	1.0666702	0.0000002
Sample 3	66.0692	0.0736202	3.9069032	0.4989582	0.0019612	1.2142242	0.0000002
Sample 4	64.7594	0.0911032	3.9068482	0.4985392	0.0000002	1.0952882	0.0000002

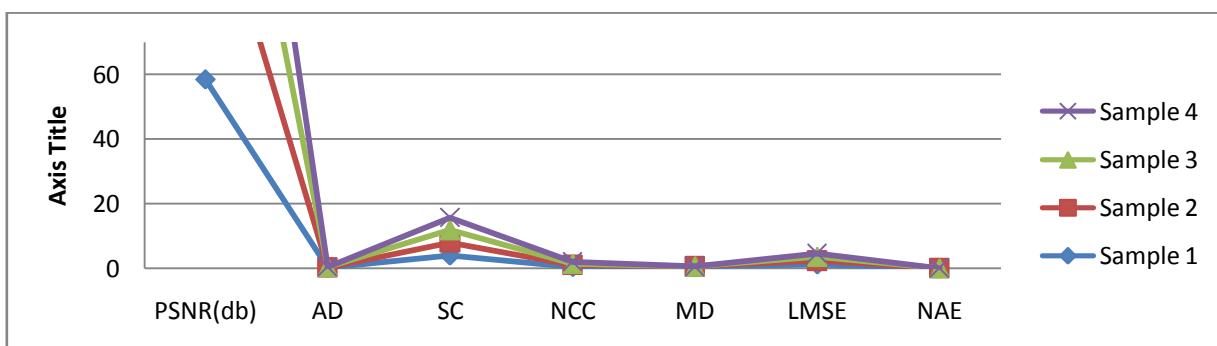


Fig7.Comparison of Quality parameters for resolute sample images

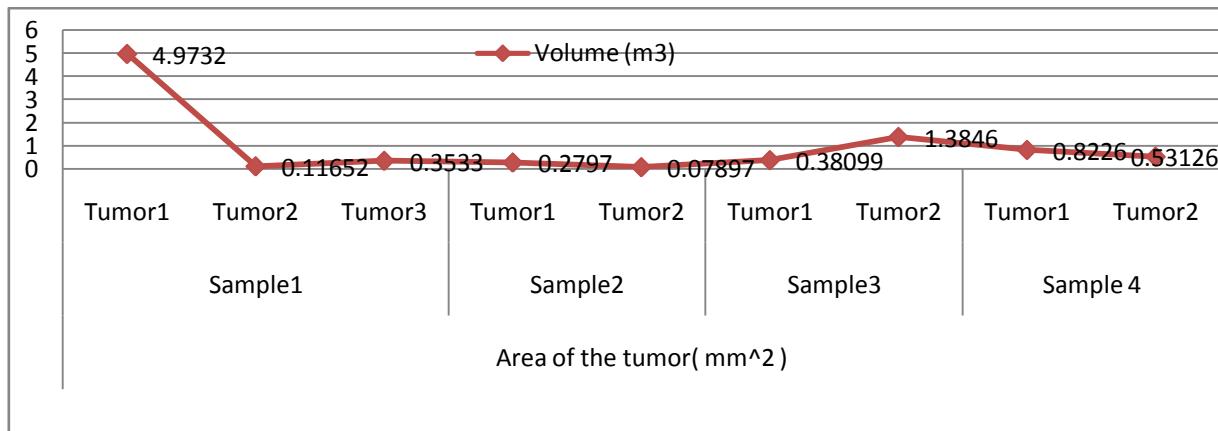


Fig8. Volume of the tumor for various samples

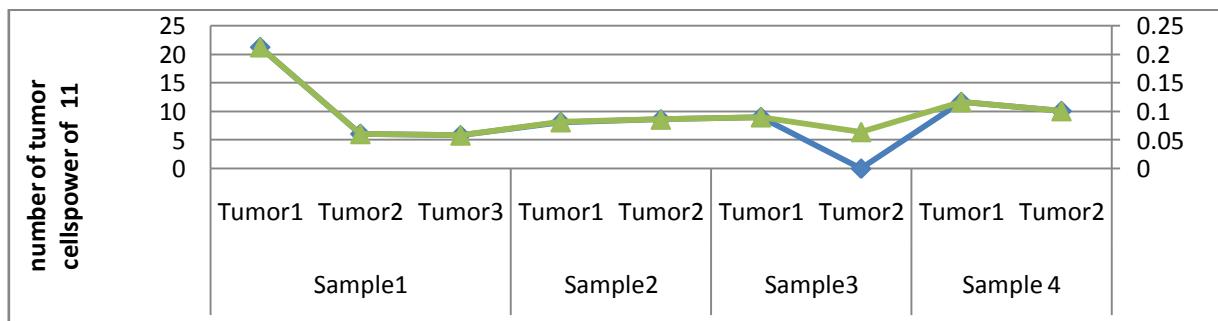


Fig9. The Number of tumor cells against unidimentional diameter

## V.CONCLUSION

The experiments were conducted on metastasis multiple tumor images. The tumors are located at various locations. RS approach is favorably considered for estimating the tumor areas individually. The N-WT in conjunction with bi-cubic interpolation approach results intensified low contrast pixel levels image for better analysis. The "Optimized hybrid Mean Shift Clustering Algorithm" proved as a refined and respectable method to estimate the actual area of the tumor. In future the location of the tumor may be determined in addition with the size i.e. area of the tumor. The developed algorithm has been tested on 15 samples of metastasis tumor MR Images. The split and merge mechanism applied on Optimized hybrid clustering algorithm exhibits some limitation to the MRI samples where a tumor lies between the two segments. Some portion of the tumor lies in one segment and the rest of the tumor portion lies in another segment. Even though, this method proved itself as a refined method for metastasis Brain tumor images.

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### BIOGRAPHIES



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