Quantitative Analysis of Metastasis Brain Tumor and its Area Estimation in MR Images

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ABSTRACT

Metastasis brain tumor develops multiple tumors at asymmetrical location of the human brain. MRI Imaging is one of the prudent mechanisms to extract the tumor regions and to map the brain for diagnosing. For the better diagnosis, one must detect the tumor accurately and need to calculate the area and volume of the tumor exactly. Here in this letter, we proposed a novel resolution enhancement technique to improve the quality of MR brain image and optimized hybrid clustering 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.

Keywords

Metastasis brain tumor, DWT, SWT, Interpolation, Image Segmentation, FCM, K-means, Optimized pillar algorithm

1. INTRODUCTION

The cells in a human brain progress in a controlled manner. The old and flawed cells recovered with new cells. The cell division grows in capricious style and form as aberrant tissue labeled as Tumor. 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. Secondary tumors are habitually evolving multiple tumors. Secondary brain tumors arise in the lung, breast, kidney, or from melanomas in the skin. Metastatic brain tumors can develop expeditiously, congregate or spoiling nearby brain tissue. Consistently, a patient may have multiple metastatic tumors in distinct areas of the brain. It is well known by all of us that the 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). Most Researchers from the developed countries has 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 produce the complete brain images, we will use CT scan or MRI, which is directed into intracranial cavity of brain. After then, for detection & diagnosis of brain tumor, the scanned brain image will be visually examined by the physician. However this method of detection resists the accurate determination of stage & size of tumor. To avoid the conventional drawbacks such as low resolution images, inaccurate detection of tumor and its size, this thesis work proposed a 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 applying the well known transformation techniques named as discrete wavelet transform (DWT) [2], [3], [7] and stationary wavelet transform (SWT) [4], [5], [6] to resolve the problem of low resolution and to increase the contrast and sharpness of the image. Then after, we had applied proposed optimized hybrid clustering with region split and merge 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.

2. RELEVANT 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 is will be segmented automatically. But, we know that the manual segmentation will consume more time, which in results 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 in accurate 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. In [3] and [4], author developed a discrete wavelet based enhancement techniques to enhance the low resolution MR image. However, DWT is a decimated approach, in which the input image will be decimated with a factor of 2 i.e., the size of DWT sub bands will be reduced to half of the input image. Hence, it is not suitable for lossless enhancement. To overcome this, authors in [5], [6] and [7] proposed an extension version for DWT which does not use decimation factor of 2 named as stationary wavelet transform (SWT), by using the combination of both DWT and SWT original low resoluted image will be enhanced more effectively and will produce the better performance than the DWT approaches. However, due to the lack of number of original pixels all of them were fail to produce a high resoluted 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 oversegmentation 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, pillar algorithm will be merged with k-means clustering, which is proposed in [17] and also proposed feature extraction with approximate reasoning to calculate the area of tumor based on the number of white pixels in the segmented MR brain image. The number of clusters will be selected optimally and also the centroid updation for number of iteration will also be solved in pillar k-means by considering the maximum pixel value instead of calculating the mean of group of clustered pixel values [17]. All the above mentioned algorithms have been developed and tested for primary tumor 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. Here in this letter, we proposed super resolution enhancement using DWT and SWT with Bi-cubic interpolation to enhance the MR image quality and optimized hybrid clustering with region split and merge algorithm to detect the exact tumor location and to calculate the individual areas of multiple tumors from the MR images.

PROPOSED METHADOLOGY Super Resolution Image Enhancement

Discrete wavelet transform and Stationary wavelet transform are used to resolute 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. The high frequency components of the image labeled as sub bands LH, HL, HH. For interpolating data points on a two dimensional regular grid, Bi cubic interpolation is used in order to obtain smooth surface. A growth factor of '2' for Bi cubic interpolation is enforced to high frequency sub band images. Stationary wavelet transform (SWT) is adapted to negotiate the information loss in the Sub bands due to down sampling. The MRI Brain tumor image disintegrates into different sub band images by using Stationary wavelet transform, Low-low (LL)), low-high (LH), high-low (HL), and high-high (HH). The SWT High frequency sub bands and interpolated high frequency sub bands are combined each other. Further intensification is achieved by interpolating the estimated High frequency sub bands. The authentic high resolution input image is having admirable information than low frequency sub bands. Hence the interpolation is again applied on the input MRI image Low frequency sub bands.

3.2 Proposed OHC 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.

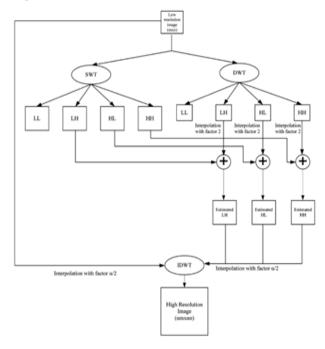


Fig.1 Block Diagram of Super resolution Image enhancement

Step4. Calculate the distance (D) between C_v and 'K' for each pixel to cluster point

Step5. Find number of C_{ν} which are neighboring to the 'K'.

Step6. Select the 'K' with minimum distance and then move

the C_{ν} to the closest relevant centroids

Step8. Re estimate the centroids by selecting the maximum pixel value from the set of relevant centroid data points.

Step9. 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 Fuzzy C-means 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 Split and Merge (SM) 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

3.3 Split and Merge 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. Quardtree 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 pillar K-Means, K-Means, Fuzzy C-Means, methods.

3.4 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.

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

Pixels= Width * Height = 256*256

$$f(0) = black pixel '0$$

f(1) = White pixel '1'

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

 W_p = number of white pixels

1 Pixel width = 0.264 mm

The equation to estimate the tumor area is

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

4. RESULTS AND 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. The combination of DWT and SWT 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. By considering fig 2(a), fig 3(a) and fig4 (a) introducing the SWT information loss due to down sampling in DWT considerably reduced. DWT 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 LSME 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 and merge approaches. 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 consist 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 mm², 2.8434mm2, and tumor3 2.6135mm² 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.

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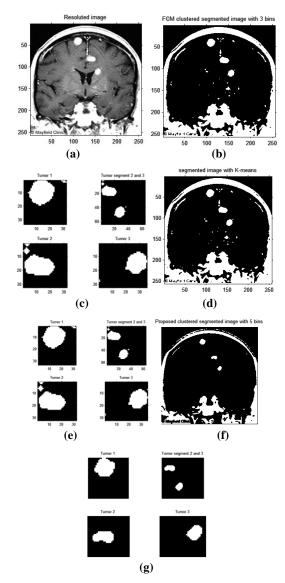
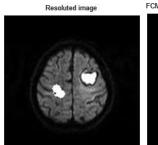


Fig2 (a) Resolute image (b) Segmented image using FCM (c) Tumors separation using SM for FCM (d) Segmentation using K-Means (e) separation of tumors using SM for k-means (f) Segmentation using Proposed OHC and (g) SM for proposed



(a)

FCM clustered segmented image with 3 bins



(b)

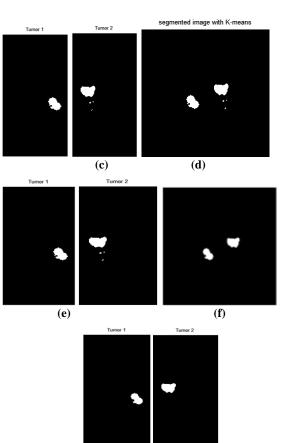


Fig3 (a) Resoluted image (b) Segmented image using FCM (c) Tumors separation using SM for FCM (d) Segmentation using K-Means (e) separation of tumors using SM for k-means (f) Segmentation using Proposed OHC and (g) SM for proposed

(g)

	Area of the tumor(mm ²)					
Tumor No	FCM	K-Means	Proposed			
	Sample 1					
Tumor 1	4.3540	4.3700	3.5222			
Tumor 2	4.2976	4.3057	2.8434			
Tumor 3	3.5518	3.5811	2.6135			
Sample 2						
Tumor 1	5.5251	5.5251	5.0987			
Tumor 2	6.0259	6.0375	5.6990			
Sample 3						
Tumor 1	11.7591	11.8330	6.2641			
Tumor 2	5.6990	5.7416	3.1899			
Sample 4						
Tumor 1	11.0439	10.9520	10.4639			
Tumor 2	8.1327	8.1156	7.8181			

Sample

64.7594

0.09110

3.90684

0.49853

0.00000

1.09528

0.00000

4

Table2. Quality Analysis Comparison for Various Sample **Resolute Images** Quality Sample 1 Sample2 Sample parameter 3 PSNR(db) 58.4795 67.9731 66.0692 0.225881 0.045542 0.07362 AD SC 3.996330 3.906995 3.90690 NCC 0.475903 0.495715 0.49895 MD 0.500000 0.000000 0.00196 1.21422 LMSE 1.220969 1.066670 NAE 0.000000 0.000000 0.00000

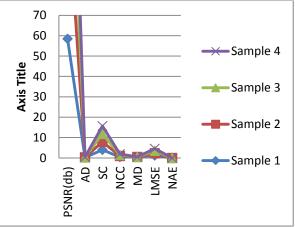


Fig 6. Comparison of Quality parameters for resolute sample images



Volume								
Tumor No	Radius (cm)	Volume (m ³)	Number of tumor	Uni- dimensional				
		、 <i>,</i>	cells	diameter				
			(N)*	(2r)				
			10^{11}	(21)				
			10					
Sample 1								
Tumor 1	0.10590	4.9732	21.18	0.2118				
Tumor 2	0.03030	0.11652	6.06	0.0606				
Tumor 3	0.02905	0.3533	5.81	0.0581				
Sample 2								
Tumor 1	0.0405	0.2797	8.116	0.08116				

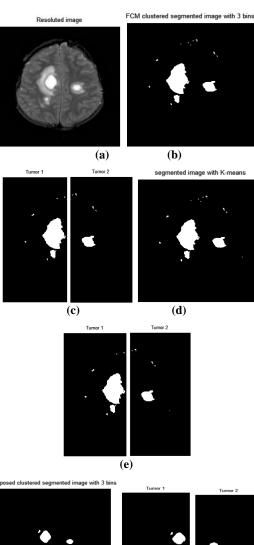




Fig4 (a) Resoluted image (b) Segmented image using FCM (c) Tumors separation using SM for FCM (d) Segmentation

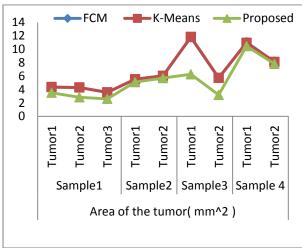
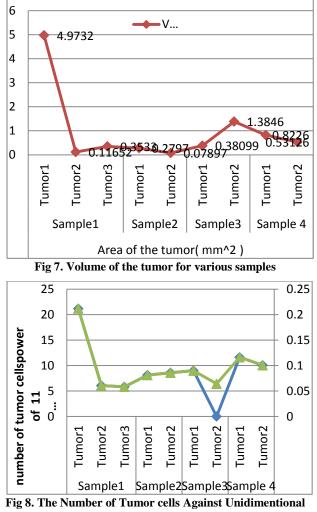


Fig 5. Comparison of Area of the tumors with various approaches

Tumor 2	0.04290	0.07897	8.58	0.0858			
Sample3							
Tumor 1	0.0449	0.38099	8.98	0.0898			
Tumor 2	0.0320	1.3846	6.4 10	0.0641			
Sample 4							
Tumor1	0.0581	0.8226	11.62	0.1162			
Tumor2	0.0502	0.5312	10.05	0.1005			



Diameter

5. CONCLUSION

The experiments were conducted on metastasis multiple tumor images. The tumors are located at various locations. Split and merge approach is favorably considered for estimating the tumor area. The combination of DWT-SWT in conjunction with bi-cubic interpolation approach results intensified low contrast pixel levels image for better analysis. The valued information at the edges are safeguarded and intensified while evaluating the tumor size. The "Optimized hybrid 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 20 numbers 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. The Number of aberrant cell has been quantified by considering one centimeter uni dimensional diameter tumor contains 10^9 tumor cells. Estimating the area and Volume and number of the tumor cells will support for better therapy.

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