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Fuzzy C-Means Fitness Function of Genetic Algorithm to Extract Brain Tumor from MR Images

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Abstract

The Fitness function in GA (Genetic Algorithm) based FCM (Fuzzy C-Means) clump and Morphological operation is used to extract tumor from MRI. Computer simulations offer a substantial improvement over the existing techniques. Tumor is an abnormal growth of cells in the body. A brain tumor is tough to diagnose at the initial stage. It is now being diagnosed by magnetic resonance imaging (MRI) as it distinguishes different grades of severity by tumors square measure. This paper presents an improved methodology to locate tumor from the whole pictures.

Index Terms: FCM, Fitness Function of Genetic Algorithm, Threshold, Image Segmentation, Morphological Operation.

1. INTRODUCTION

Image Segmentation is an important of Digital image processing. Image segmentation will provide an outcome that streamlines the presentation of a picture and makes image investigation less complicated. Within the division, a reputation is assign to every component that's having comparable qualities, like shading,surface or force,whichis able to facilitate to partitioned off the locales and distinguish the things and their limits. In any case, the difficulty whereas handling is that the chance of over-lapping and boundary displacement.

The preponderance of the tumor is of two types namely benign and malignant. Malignance is referred as cancer, but a abnormal growth of cell within brain is named tumor. Primary tumor originates in elsewhere and migrates to the brain. Secondary tumors area has a lot of common than primary tumors. The causative factors to chemical vinyl chloride, Epstein-Barr virus and selective radiation. The use of mobile phone is considered to be a factor. However conclusive evidence is yet to emerge. Although Meningioma (usually benign), Oligodendrogliomas and astrocytoma such as Glioblastomas are primary growth ordinarily recorded in adults and Medulloblastoma in youngsters. Designation is sometimes done by medical exam with elevation tomography; diagnostic assay is needed for confirmation. Tumors are divided into different grades based on severity. In grade 1, the cells appear to be normal in the initial stage. Abnormality commences, slowly, and steadily tillthere is perceptible change. The growth is very active near the vicinity of the effected tissue and it has a tendency to ramify.[1].

Huge literature exist on brain tumor diagnoses and extraction on MR Imaging of brain [1]. Logeswari and Karnan [2] have projected to use two methods for segmentation. They are ACO hybrid with Fuzzy and HSOM hybrid with Fuzzy. Though the detection procedure is satisfactory, the noise appears to remaining within the image. Behzadfar and Soltanian-Zadeh[5] used low pass filtering, Ridler's technique, morphological operation with thresholding and region growing strategies to extract the brain tumor. However, the dimension of the growth could not be known accurately. Ghanavati etal.[7] used multi-modality framework and AdaBoost classifier to detect the abnormal growth. Even if the growth is detected, it still has noise and therefore the accuracy of the detected growth isn't sensible. It's not like that gift in the ground image.

The present work is planned to locate and extract tumor from MR images exploitation dynamic Fitness Function of the GA primarily based image segmentation and Morphological operation. This can facilitate in the simple detection of tumor and additionally observe the expansion and magnitude of the tumor. The FCM is primarily employed to section the image into F number of clusters [9,10]. Then the centre's of the indidual cluster are identified. The FCM is employed due to it's noise removal capability. Then the threshold is applied on divided pictures so as to detect the region containing the tumor. Finally the morphological operation is employed thereby to enable the extraction of tumor from the full image while keeping the position, the scale and also the space intact. The remaining part of the article is organized as:

II. PROPOSED METHOD

The aim of this paper is to detect and extract tumors from different types of tumor images by following the strategies as shown here under:

- FCM based clustering and centralizing of the image
- FF(Fitness Function) of the GA
- Thresholding
- Morphological operations

A. FCM based Clustering and centralizing of the image

Fuzzy C-Means (FCM) is a methodology is cluster which permits to unities an information from two or many clusters[11,12]. This methodology (developed by Dunn in 1973 and improved y Bezdex in 1981) is often employed in pattern recognition. It has the following objective function:

$$J_m = \sum_{i-1}^{N} \sum_{j-1}^{C} \mu_{ij}^{m} \|x_i - c_j\|^2 \quad ,1 \leq m < \infty \qquad (1)$$

where,

m is any real number bigger than one,

μ_{ij} is the degree of membership of xi within the cluster j,

x_i is the i^{th} of d-dimensional measured data,

c_j isthe d-dimension center of the cluster, and ||*|| is any norm expressing the similarity between any measured data and therefore the center.

Fuzzy partitioning is applied through an iterative optimization of the target function shown higher than, with the update of membership u_{ij} and therefore the cluster centers c_j by:

$$\mu_{ij} = 1 / \sum_{k-1}^{c} \lceil \|x_i - c_j\| / \|x_i - c_k\| \rceil^{2/m-1} \qquad (2)$$

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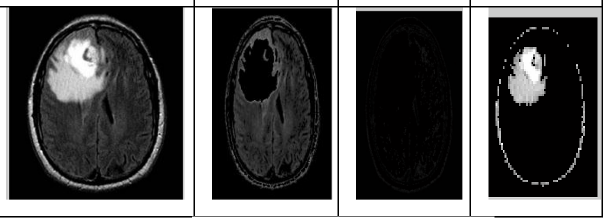
$$C_j = \sum_{I=1}^{N} \mu^m_{ij} x_i / \Sigma \mu_{ij}^m \qquad (3)$$

This iteration can stop once , wherever $\max_{ij} \{|\mu_{ij}^{(k+1)} - \mu_{ij}^{(k)}|\} < \delta$, where δ may be a termination criterion between zero and one, whereas k are the iterations steps. This process converges to a local bare minimum or a saddle purpose of J_m. The clusters of the original images are shown below in the fig.1.

Original Image	**Cluster 1**	**Cluster 2**	**Clusete r3**



(a) (b) (c) (d)

Figure.1.(a)Original Image(b)Cluster 1(c)Cluster2 (d)Cluster3

B. Fitness function of GA.

Fitness function (Evaluation Function) refers how a given solution is closer to the ultimate solution of the desired problem. It determines how *fit* or how *good* the solution is with reference to the problem under consideration[13,14].Calculation of the fitness assessment is ended frequently in a GA and consequently it need to be sufficiently rapid and the graph of Fitness function of GA is as shown in the below fig 2. Here the best fitness function is added to centre of an image and thus form as an average of threshold value. The black dots symbolize the best fitness value and the blue dots stand for mean fitness value.

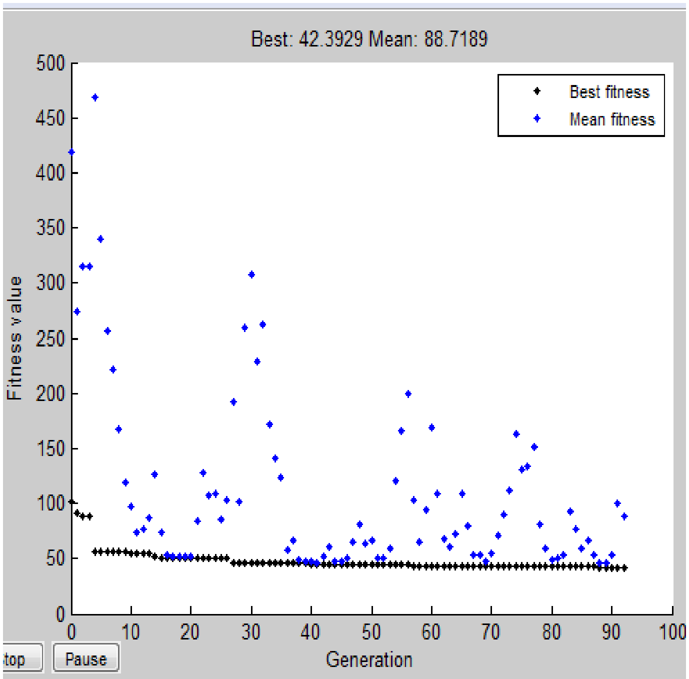


Figure.2. Generation of Best Fitness value

C. Thresholding

The most effective chromosomes set obtained at the center points of the cluster is the final segmental image. At the moment the thresholding is applied on the segmental image so as to come up with a binary image having two values (zero and 255). A value γ is chosen and each pixel that has an intensity value is smaller than γ is created [15]. This operation helps in distinguishing the region that contains tumor and conjointly helps in extracting it.

Hence, a binary image I is constructed

where g is the original image and γ is the threshold value.

$$I(n)=\{0 \text{ if } g(n) \le \gamma \mid 1 \text{ if } g(n) > \gamma\} \qquad (4)$$

The unwanted, non-tumor parts of the MR imaging pictures areremoved by morphological operations[16,17]. For this purpose morphological aperture operation is applied. Dilation and erosion are combined to create the aperture operations, dilation, erosion and gap operation are given by the following formula:

$$\mathit{Dilation}{:}D(f,g)=f\ominus\bigcup_{\alpha\in g}(f-\alpha) \qquad (5)$$

$$\mathit{Erosion}{:}E(f,g)=f\ominus g=\bigcup_{\alpha\in g}(f-\alpha) \qquad (6)$$

$$Opening{:}O(f,g)=f^{\circ}\ominus g=D(E(f,g)g) \qquad (7)$$

In the above equation, f is the image and g is the structuring element.

After performing all the above two alternative steps are involved. They are working on the connected parts by computing the area of every part and then by removing the small objects. The summary of the orderly disposition is given in fig.3.

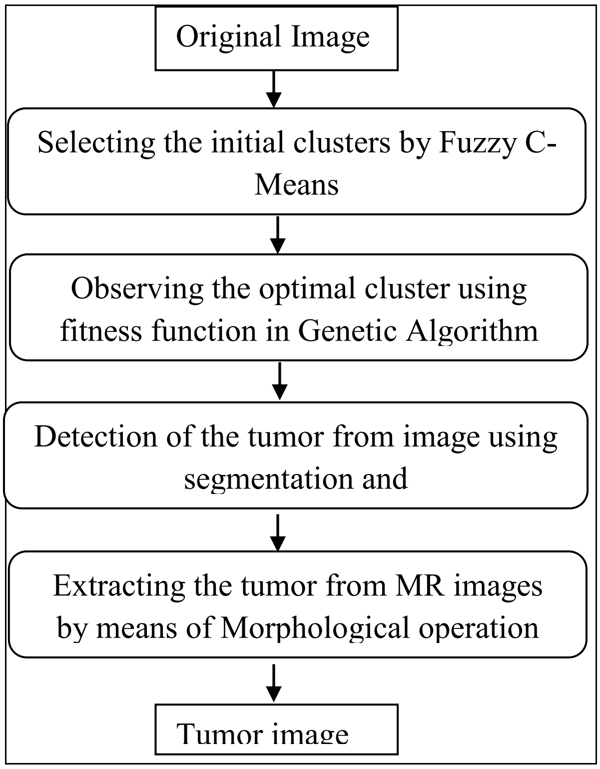


Figure. 3. Flow diagram of the proposed method

III. RESULT ANALYSIS AND VALIDATION

A well-known recital measure of brain tumor segmentations is desirable to ensure enhanced end result in the analysis of MR Images of brain tumor. They are as described as below *Accuracy* is the excellence of the result is being true.

$$\text{Accuracy}=\frac{(TP+TN)}{(TP+TN+FN+FP}\times 100 \qquad (8)$$

where,

- TP=True Positive is one that identify the condition as true.

- TN=True Negative is one that doesn't identify the condition as not true.
- FP= False Positive is one that identify the condition as not true.
- FN= False Negative is one that doesn't identify the condition as true

Mean absolute error (MAE) is a evaluate of a dissimiarity among two constant variables. Suppose X and Y are variables of paired notes that communicate the identical phenomenon.

Dice overlapping Segmentation performs disjoint segment in the low false alarm rate to concentrate on the boundary of the segments.

$$2*\text{Jaccard Index}/1+\text{Jaccard index} \qquad (9)$$

Jaccard Index measures the resemblance between finite sample sets. It is defined as the size of the <u>intersection</u> divided by the size of the <u>union</u> of the sample sets

$$J(A,B)=|A\cap B|/|A\cup B|=|A\cap B|/|A|+|B|-|A\cap B| \qquad (10)$$

(If both *A* and *B* are empty, *J*(*A*,*B*) are considered 1.)

$0\leq J(A,B)\leq 1$

The *Jaccard distance* is a premeditated dissimilarity among expected as well as observed images. It is complementary to the *Jaccard coefficient* and is acquired by subtracting the Jaccard coefficient from one. If x $(x1, x2, \ldots. xn)$ and y $(y1,2, \ldots.)$ are two vectors when, $yi \geq 0$, then their

Jaccard similarity coefficient is as

$$J(x,y)=\Sigma i\min(xi,yi)/\Sigma i\max(xi,yi) \qquad (11)$$

Jaccard distance

$$dJ(x, y) = 1-J(x, y) \qquad (12)$$

If x and y are empty, J(X, Y) = 1. 0 ≤ J x, y ≤ 1. *Jaccard coefficient* is used to measure similarity [16]. It calculates the similarity between segmented and ground truth images. Jaccard's distance values lie between 0 and 1. Jaccard distance reaches its best value at 1 and worst value at 0. The objects having a 0 value along with their variables show a lower similarity.

Mean square error(MSE) is a measure of signal fidelity or image fidelity. The rationale of signal or image reliability measure is to assess the similarity or fidelity between two images by assigning a quantitative achieve. When MSE is premeditated, it is assumed that one of the images is spotlessly unique, at the similar time as the further is indistinct or processed by some means and it is defined as

$$MSE=1/M\times N\Sigma\Sigma(f(x,y)-f^{R}(x,y))^{2} \quad (13)$$

Root Mean Square Error (RMSE) is considered determined as the quantity of the inconsistency among two dissimilar values is in the middle of the rationale of being evaluated. Lower the value of RMSE better will be the result.

$$RMSE=\sqrt{(A-B)}^{2} \quad (14)$$

Peak Signal-to-Noise Ratio is a database. It is a gauge used to assess the quality of reconstruction of processed image and it's formula is given below

$$PSNR=20\log 10(2n-1)/MSE \quad (15)$$

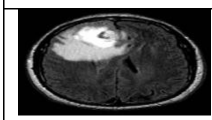
Lower value of MSE and higher value of PSNR refers a good signal-to-noise ratio.

Boundary Displacement Error compute the distance of the pixels in boundary with the nearest pixel in boundary and then sum up both the pixel values.

IV. EXPERIMENTAL RESULTS AND DISCUSSION

4.1 Results

The present work on segmentation is based on the FCM Fitness Function in Genetic Algorithm. The outcome of the different MRI images using proposed method is shown in fig.4. (a) original images, (b) shows the result of FCM Segmentation (c) the result of FCMT, (d) shows the result of PBFCM(e) shows the result of PBFCM&AC and (f) shows the extracted tumor from the original images by FCM FF in GA. The present work indicates better accuracy than the previously mentioned algorithms for nearly 750 original images obtained by Scan centres.

Original Image


(a)

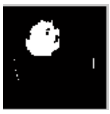
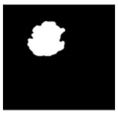
FCM	FCMT	PBFCM	PBFCM&AC	FCM FF IN GA
				
(b)	(c)	(d)	(e)	(f)

Figure 4. Segmentation results of (b) FCM,(c) FCMT,(d) PBFCM,(e) PBFCM&AC and (f) FCM FF in GA

4.2 Discussion

Table 1. Comparison of the Accuracy of Various Segmentation Technique

Algorms.	**Imgs.**	**Acc.**
FCM	Img1	90.4
TFCM	Img1	91.4
PFCM	Img1	91.5
IPBFC	Img1	97.3
FCM FF in GA	Img1	98.0

In Table 1 describes the comparison of four algorithms of the present work where the accuracy improved by 98 percent in FCM FF in GA.whereas in FCM it is only 90.4 percent in all the rest it is between 91.4 to 97.3 percent and The values of accuracy near to 98.0 percent is taken as best result as graphically represented and constructed in bar chart in fig.6

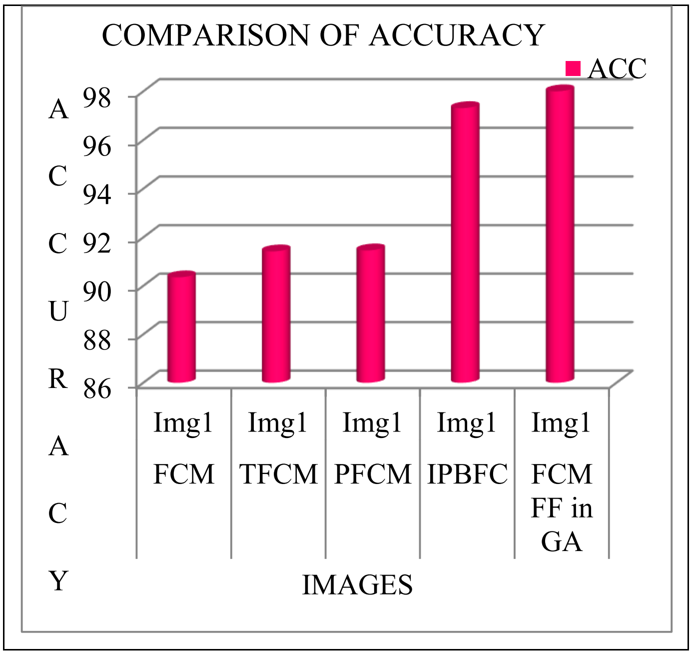


Figure. 6. Performance of various seg. of accuracy

Table 2. Comparison of the PSNR of Various Segmentation Technique

Algorms.	Imgs.	PSNR
FCM	Img1	44.32
TFCM	Img1	44.32
PFCM	Img1	44.31
IPBFC	Img1	55.04
FCM FF in GA	Img1	58.73

Table 2 explains the combined features of FCM FF in GA which works better than the other four combinations of techniques. Based on PSNR values near 59 are highlighted the quality analysis is determined and its corresponding graphical representation of line chart as shown in the below fig.7

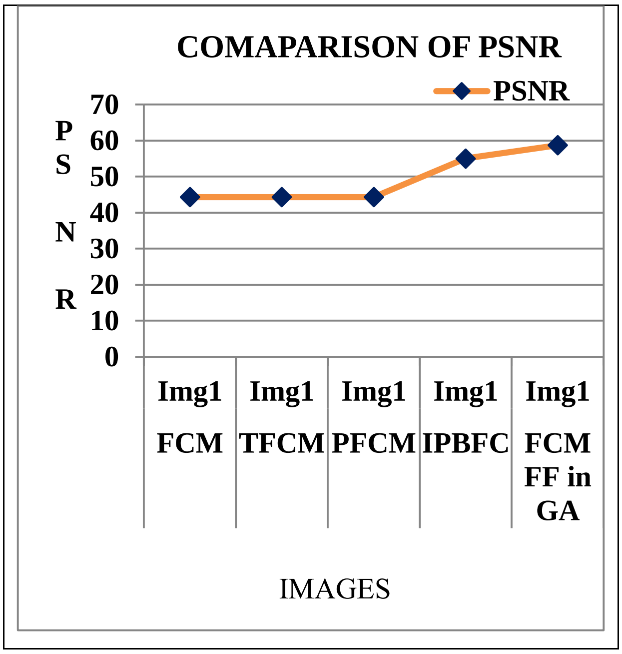


Figure .7. Performance of various seg.of PSNR

Table 3. Comparison of the MSE, MAE & RMSE of Various Segmentation Technique

Algorms.	MSE	MAE	RMSE
FCM	2.42	0.40	1.54
TFCM	2.42	0.41	1.56
PFCM	2.43	0.42	1.56
IPBFC	0.21	0.22	0.45
FCM FF in GA	0.09	0.12	0.30

Table 3 describes the MSE,MAE and RMSE determined the lowest value shows that the FCM FF in GA works well then the other four algorithms. The values of error rate near to zero is taken as best result as graphical representation of Table3 is described in fig,8

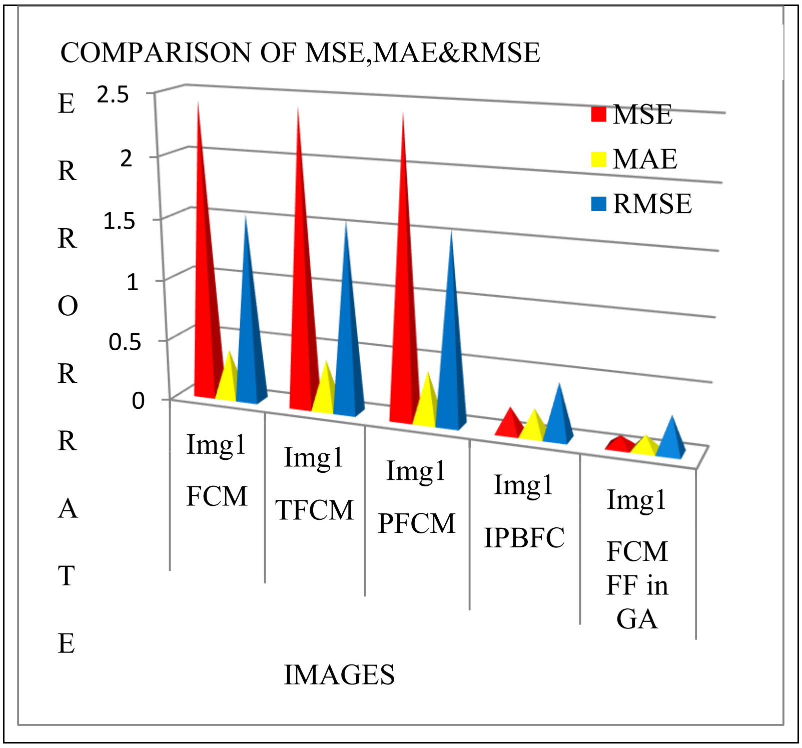


Figure 8. Performance of various seg. of MSE,MAE&RMSE

Table 4. Comparison of the Dicolap,JI,JD,BDE of Various Segmentation Technique

Algorms.	Imgs.	Dicolap	JI	JD	BDE
FCM	Img1	0.87	0.78	0.22	0.40
TFCM	Img1	0.83	0.76	0.30	0.36
PFCM	Img1	0.72	0.57	0.44	0.36
IPBFC	Img1	0.93	0.86	0.14	0.03
FCM FF in GA	Img1	0.94	0.88	0.12	0.02

Table 4 illustrate the valuations of the Fuzzy C-Means fitness function in Genetic algorithm with other four techniques and is determined by the highest values of Jaccard Index and the lowest value of the Jaccard distance. Among the techniques, Fuzzy C-Means fitness function in Genetic algorithm works well for the reason that it consist uppermost similarity among the techniques and lowest distance in Jaccard distance. The values of diceoverlap near to 0.9, JI values near to 0.8, JD values near to 0.1 and BDE values near to zero are taken as best result. The graphical representation of Table 4 is described ina fig. 9

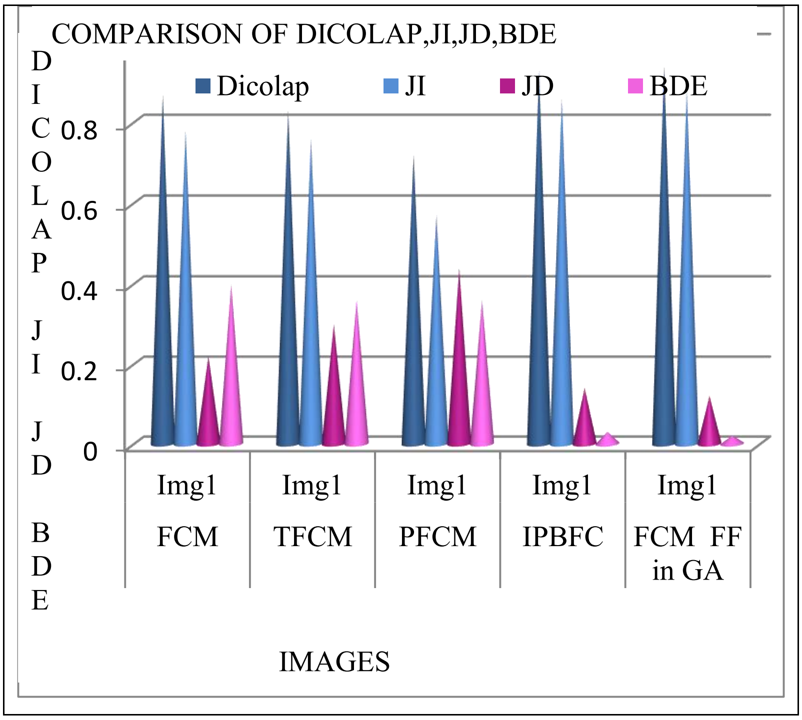


Figure. 9. Performance of various seg. of dicolap,JI,JD&BDE

V. CONCLUSION

Segmenting an ideal abnormal area in MR brain images plays a critical role in medical imaging applications. A diversity of segmentation algorithms is used to extend the accuracy and its performance is evaluated for MR brain medical images. The new FCMFF in GA is applied on few images additionally to experiment results of recital are compared along by means of analysis of the ground truth image. In this work a comparative study of a variety of performance metrics are made. This paper evaluates the performance of Fuzzy c-means, Threshold-based Fuzzy C-Means segmentation, Probability-based Fuzzy C-Means and FCMFF in GA The accuracy, MAE ,Dice overlap, JI,JD,MSE,RMSE,PSNR,BDE of various segmentation techniques are reported. The FCMFF in GA segmentation gives a better result on considering the whole performance. The extension of this work is needed to improve the FCMFF in GA segmentation with some other algorithms, without actually altering the original nature of the MR medical images.

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