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# TUMOUR DETECTION IN MRI SCAN BY MSFLA-BFO

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**Abstract:** Our work is based on the automatic segmentation of tumour area in MRI scan images of human brain. Automatic detection of tumour is a motive to make our machines smarter so that they can understand the problems by themselves and diagnose them. After analysis of previous work we noted that optimisation algorithms are best for automatic segmentation of tumour which performs well for unsupervised learning algorithms. So we used a hybrid algorithm which is a combination of modified shuffle leap frog algorithm (MSFLA) and bacterial foraging optimisation (BFO) algorithm. We have targeted the segmentation of T2 type tumour segmentation from MRI images which are fetched from the BRATS 2015 (multimodal brain tumour segmentation) database. The whole database is of 2.2 GB and consists of a lot of tumour MRI images with ground truth.

**Keywords:** Image Segmentation, MRI scan, Tumour detection, MSFLA, Optimisation, BFO.

## I. INTRODUCTION

There are diverse motivations for the development of methods for automatic medical image segmentation. Accurate segmentations are needed or would be useful in clinical and scientific applications, but the need for manualintervention is both time consuming and subject to manual variation. This section will first examine applications of segmentation, and proceed to discuss the two drawbacks of manual segmentation. This section will conclude by exploring the properties of this problem that make it an excellent research challenge in the fields of Machine Learning and Pattern Recognition. Many of the current and potential applications of segmentation are discussed in detail in Chapter 1 of [O'Donnell, 2001]. These include enhanced visualizations, high-throughput and consistent volume measurements, research into structural shape and variations, image-guided surgery, and change detection in images acquired at different times. With respect to brain tumors, change detection and volume measurements are often used to evaluate tumor growth or treatment response, but this problematic since current standard methods of tumor volume measurement consist of simple heuristics [Miller et al., 1981, Therasse et al., 2000], that are inaccurate compared to manual segmentations, and where only large changes can be deemed statistically significant. Change detection is also important with respect to evaluating the effectiveness of treatments, since tumors will have varied responses to different types of treatment. Change detection can be relevant over long periods of time, or can be used to detect small changes over short periods of time to assess the immediate patient and tumor-specific effectiveness of different treatment methods. Another motivation for pursuing automatic tumor segmentation methods is alleviating the manual work and reducing the variability associated with defining radiation therapy target areas. This is especially important with respect to new technologies such as radiosurgery and intensity-modulated radiation therapy that allow more precise treatment options than traditional technology [Pirzkall et al., 2001]. Accurate automatic segmentation methods could also lead to new applications, including effective content based image retrieval in large medical databases. This could allow clinicians to find similar images in historical data based on tumour location, grade, size, enhancement, and extent of edema, similar patterns of growth, or a variety of other factors.

In this paper we have proposed a new hybrid method for unsupervised segmentation of brain tumor from MRI dataset. In next section we have explained our proposed work and in section 3 results of proposed work are discussed.

## II. PROPSOED WORK

Our work is based on automatic segmentation of cancerous part with unsupervised learning algorithm which means there is no training of system with prior known cancerous images. Algorithm will extract the desired area direct form test image. The shuffled frog leaping algorithm is modified first which is further hybridised with bacterial foraging optimisation.The major contribution of this work is the proposition of the new fitness function.

A value$Pi\ j$, is calculated for each frog $x(i,j)$of the memplex$i$ as (1). Then we calculate the sum $SP_i$for each memplex.

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$P_{i,j} = 2^{p-i}.x(i,j)$ … (1)

$SP_i = \sum_{j=1}^{j=p} P_{i,j} = 2^{p-1}.x(i,1) + 2^{p-2}.x(i,2) + \cdots .+x(i,p)$ … (2)

After this, an attempt threshold *N*(i) is determined for each memplex using (3).

$N(i) = \frac{255.SP_i}{2^{(p-1)}}$ … (3)

Each *N*(i)is compared with the intensities of pixels of the original image in order to find the sum of pixel intensities above and below *N*(i)(*hsum*and *lsum*respectively), and the total number of pixels above and below *N*(i)(*hnum*and *lnum*respectively). The fitness function is given by (4)

$$fitness(i) = lnum.hnum.(w1 - w2)^2 \quad \ldots (4)$$

With

W1=lnum/lsum

W2= hnum/hsum

The threshold characterizing the tumor region is the rounded value of the coefficient *N*(i)of the best memplex.

**MSFLA**

In MSFLA, the optimal thresholds characterizing the tumor area are selected by a discriminate criterion to maximize the fitness function of each memplex. The main steps of MSFLA are briefly explained as below:

• Initial population of frogs:

The initial population *initpop*contains *F* frogs divided into *m* memplexes, each memplex is formed by *p* frogs (i.e. *F=m*p)*. The initial population is created randomly as indicated in (5).

$$initpop = \begin{pmatrix} x_{11} & \cdots & x_{1m} \\ \vdots & \ddots & \vdots \\ x_{p1} & \cdots & x_{pm} \end{pmatrix} \quad \ldots (5)$$

To reduce the computational time, the frogs having intensities lower or equal to 0.5 are replaced by 0 and the ones having intensities upper than 0.5 are replaced by 1.

• Sorting and distribution

The memplexes are evaluated using the fitness function. Then, they are ranked in descending order. Best and worst memplexes are called *Mb* and *Mw* respectively.

• Memplexes evolution

To improve the worst solution, we use (6). It is an attempt to make the worst solution better than the best one.

$$S_1 = rand(1,p)(M_b - M_w) \quad \ldots (6)$$

Where, $rand(1,p)$, is a random vector which elements are between 0 and 1.

The amelioration of the worst solution is given in (6). If this solution is better than the previous, it will be memorized. Else (6) is repeated for a predefined number of times.

$$IM_W = M_W + S_1 \quad \ldots (7)$$

If these equations do not improve the worst solution, then a new solution is generated randomly.

• Shuffling

After improving the worst solution, memplexes are sorted in descending order again. Then the stage iii is repeated. The shuffling stage is repeated until reaching a terminal condition.

• Terminal condition

If a predefined solution is reached, the algorithm stops.

**Hybridisation of MSFLA with BFO**

In this work we have changed the step of MSFLA by BFO tuned technique. Complete BFO algorithm is not used here rather than we have picked the randomness of bacteria movement in BFO for frog's worst position updation. Equation above updates the position of worst frog by adding the difference of positions of worst and best frog. This updation is position is now handled by BFO's property. We have changed (7) as (8).

$$IM_W = M_W + 0.05 \times delta \quad \ldots (8)$$

Here $delta$ is the direction of bacteria's in BFO. This we here combine the randomness in direction of BFO with position updates of frog in MSFLA. Further it is also checked that updated position by equation is less than 0.5 or not to keep the worst memplex at either 0 or1.

## III. RESULTS & DISCUSSION

Our proposed work is implemented in MATLAB R2013a with many user defined functions and image processing toolbox of MATLAB. The data available for tumour segmentation was downloaded from BRATS website which conducts competition for multimodal brain tumour segmentation every year and for training and testing provides its dataset to participants.We have plotted the graph for our case and compared with the

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SMFLA algorithm for the same test image and same objective function and shown in figure 1. Though the minimum value settled for both algorithms is same yet the peak value for our proposed case is very less than MSFLA optimisation curve. So the analysis of figure 1 shows that proposed hybrid optimisation is better than single MSFLA and it also assures the better performance ahead.

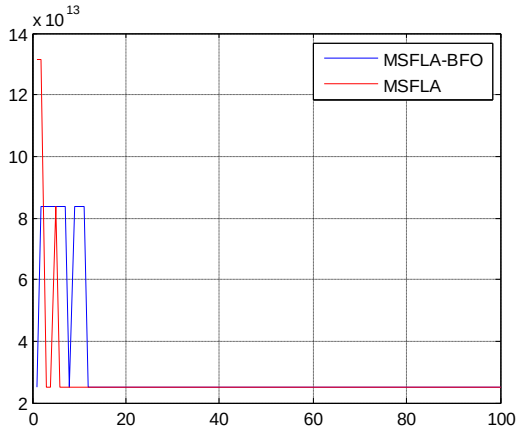


Figure 1: objective function value vs iteration plot

Results of proposed algorithm have been shown in figure 2 (a) and (b). A rectangle is drawn around the cancer detected part after some final morphological operations. As per visualisation, exact cancer part is surrounded by the rectangle which is more clearly shown in figure 3 (a) and (b) with only segmented cancer part and ground truth image of cancerous part.

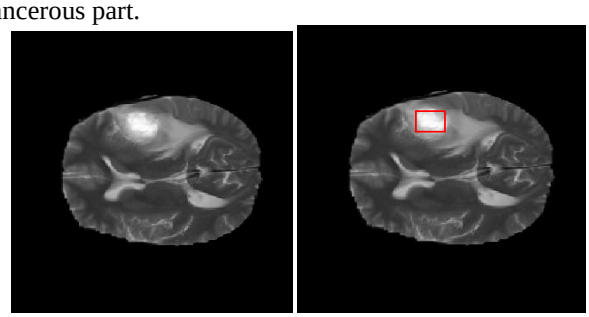

Figure 2: (a) original test image (b) cancer part detected in original image by proposed

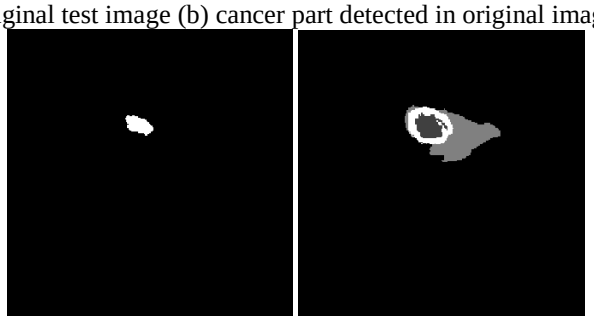

Figure 3: (a) segmented cancer part form the test image (b) ground truth image with 5 differ rent labels

We have evaluated the results on the basis of precision, accuracy and sensitivity. Figure 4 shows that all three evaluation parameters values are higher than MSFLA. So our proposed hybrid optimisation is better than MSFLA. An improvement of 0.43% in accuracy is achieved by our method. This is because MSFLA has already gained a good accuracy level and beyond that the improvement takes place in very small steps.

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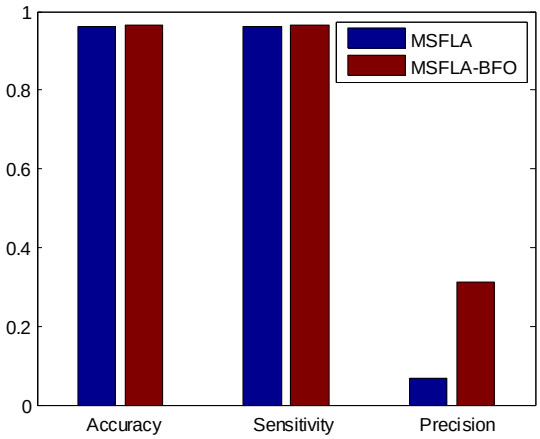


Figure 4: comparison of evaluation parameters for MSFLA+BFO and MSFLA

## III. CONCLUSION

The proposed work is based upon the automatic segmentation of brain tumour form the MHA images for database taken from BRATS 2015. We have hybridised two methods i.e. MSFLA and BFO in which MSFLA is the backbone in which the worst frog's position is updated by the randomness property of BFO. The proposed fitness function assists to quickly discover the adequate position of the tumour in the brain. The new paradigm has demonstrated its adaptability to converge rapidly and to give accurate results. Results have been compared with single MSFLA algorithm in terms of accuracy, precision and specificity. The values of these parameters should be high and close to 1. More closer to 1 is the value, better is the result. The solution is optimal but sometimes its randomness nature may limit its effectiveness.

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