International Journal of Engineering Sciences & Research Technology

(A Peer Reviewed Online Journal)
Impact Factor: 5.164

➕**IJESRT**

Chief Editor

Executive Editor

Dr. J.B. Helonde

Mr. Somil Mayur Shah

IJESRT
INTERNATIONAL JOURNAL OF ENGINEERING SCIENCES & RESEARCH TECHNOLOGY
AN ENHANCED BRAIN TUMOR SEGMENTATION AND CLASSIFICATION USING IMPROVED K-MEANS WITH SWARM-BASED FIREFLY ALGORITHM

Shallu Dogra[*1] & Sandeep Kumar Rawat[2]
[*1&2]Sri Sai University Palampur, India

ABSTRACT
The number of medical cases connected to brain tumors has increased significantly in recent years, making it the 10th most prevalent type of tumor affecting both children and adults. However, if tumor identified in early stage, it is one of the most treatable types of cancer. As a result, scientists and researchers have been attempting to create advanced tools and procedures for determining such kind of tumor with their exact stage condition. Magnetic Resonance Imaging (MRI) and Computer Tomography (CT) are two commonly used procedures for sectioning and evaluating anomalies in the form, size, or location of brain tissues, which can aid in the detection of malignancies. The objective of this paper is to design and apply an Enhanced Brain Tumor Segmentation and Classification (EBSTC) model from MRI using with K-means with Swarm-based Firefly Algorithm (SFA) as a heuristic algorithm and here, Convolutional Neural Network (CNN) is used as a machine learning approach. A novel fitness function of SFA is introduced, which enhances the segmentation accuracy during Region of Tumor segmentation from MRI data. Experimental evaluation is performed against Brain Tumor Segmentation (BraTS) dataset and shown the effectiveness of improved K-means over k-means in terms of segmentation accuracy. We achieved an improvement of 4.54% in segmentation accuracy and 99.55% classification accuracy using CNN.

Keywords: *Magnetic Resonance Imaging (MRI), K-means, Improved K-means, Swarm-based Firefly Algorithm (SFA), Machine Learning, Convolutional Neural Network (CNN).*

1. INTRODUCTION
In medical science, segmentation of medical image is one of the most difficult areas of image processing, and it's employed in a variety of applications such as brain, skin, lungs, leukemia, breast etc. A medical image is segmented into its constituent sections or objects using a segmentation process and one of the most important uses of image segmentation is the isolation of tumors from Magnetic Resonance Imaging (MRI) [1]. The manual identification of tumors in MRI requires skilled radiologists, which is a time-consuming and error-prone approach. Manual identification and segmentation of such huge data is extremely time consuming due to the enormous number of patients and images. As a result, there is a pressing need to automate this process, and segmentation approaches can help [2]. Brain MRI is used to provide delicate information about muscles, ligaments, tendons, nerve injury, hemorrhaged, blood clots, and other soft tissues, and it has the ability to discern between them [3]. Multiple applications in neurology rely on MRI segmentation methodologies, including exact assessment of tumor size, location, volume, lesions, blood cell demarcation, medication, and surgical planning. White Matter (WM), which is the primary component of the nervous system and contains neuropil, glial cells, synapses, and capillaries, makes up the majority of the brain. Gray Matter (GM) differs from white matter (WM) in that it is made up of a large number of cell bodies with a limited number of myelinated axons. The grey color in healthy tissues is quite vivid in MRI data and GM in the brain allows you to see, hear, memories, speak, make decisions, and maintain control. Another component of the brain is the Cerebrospinal Fluid (CSF)-filled cavity. This fluid is exploited to fill the cerebral ventricles and the subarachnoid and spinal cord-covered portion of the brain. Fig. 1 illustrates the visual view of MRI of human brain [4].
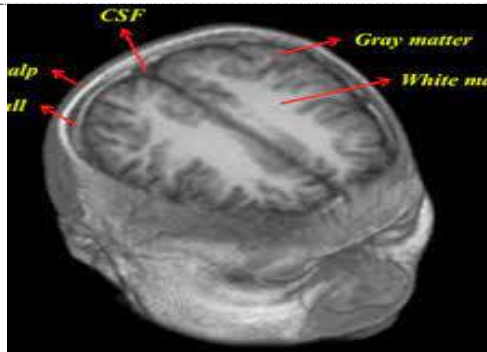
Fig. 1: MRI of Human Brain

The areas of research for automated brain tumor segmentation and classification include Computer Vision (CV) techniques and the creation of computer-aided tools. Some of these procedures have positive outcomes, but there is no clear winner because these tactics are rarely employed in hospitals. Convolutional Neural Networks (CNN) have recently emerged as the approach of choice for state-of-the-art implementations in a variety of image segmentation applications [5]. In this research, we focus to develop an Enhanced Brain Tumour Segmentation and Classification (EBTSC) model using Improved K-means with Swarm-based Firefly Algorithm (SFA). Major contribution of this research is listed as:

→ We presents a brief survey of existing brain tumour segmentation and detection techniques for MRI data.
→ A novel segmentation algorithm for brain tumour segmentation in the pre-processing of EBTSC module using K-means with Swarm-based Firefly Algorithm (SFA) technique is developed.
→ To extract key features from segmented Region of Tumour (ROT), Maximally Stable Extremal Regions (MSER) descriptor is used along with SFA as a feature selection approach based on their fitness criteria.
→ Here, the concept of CNN as an artificial intelligence technique is used to detect and classify the cancer types from MRI.
→ To validate the EBTSC model, a quantities comparison with existing state of arts is done on the basis of the parameters such as Precision, Sensitivity, F-measure, Accuracy, Error, Matthew Correlation Coefficient (MCC), Dice Coefficient (DC), Jaccard Coefficient (JC), Specificity and Execution Time.

Here, the concept of SFA is using along with the K-means technique because, when the brain tumour is segmented using the K-means, the background (GM) and foreground (WM) pixels of images are mixed and reduce the segmentation accuracy. As a result, we applied a swarm-based Meta heuristic optimization strategy to tackle this problem by selecting a pixel threshold level for background and foreground data separation. The following is a breakdown of the paper's structure. The following are the portions of the paper: The state-of-the-art is described in Section 2. The proposed technique is covered in Section 3 as materials and procedures and In Section 4, results and discussion are summarised. Section 5 brings the paper to a final conclusion with future possibilities.

2. RELATED WORK

There are lots of approaches already used to solve segmentation and detection of brain tumors from MRI by focusing on the segmentation failures issues but in this chapter, focus to identify the problem regarding the proposed EBTSC model from MRI using CNN as a Deep Learning. This section of paper illustrates the state-of-art of the current and interrelated work of brain tumor segmentation and detection. This highlights the survey, mechanism, working, benefits and limitations of the related work in the field of brain tumor segmentation and detection using their feature analysis from the MRI. In 2020, *S Nema et al.* [6] had conducted a research for brain tumor segmentation and named as residual cyclic unpaired encoder-decoder network (Rescue-Net). In this research, authors designed a network architecture named as Rescue-Net using the concept of a residual and mirroring principles. This technique utilized the unpaired adversarial training for brain tumor region segmentation followed by core and enhance regions in a brain MRI scan. There are lots of approaches already proposed for an automatic brain tumor analysis but they faced problem of preparing large scale labelled data for training of deep networks. The data labelling is a time consuming process and to eliminate this, authors used unpaired training approach to train the system using Rescue-Net. To validate the system, they evaluated some

specific performance parameters such as Dice and Sensitivity and the experimental results are tested on BraTS 2015 and BraTS 2017 dataset and the result outperforms the existing methods for brain tumor segmentation. They not used the concept of any external segmentation optimization approach that would be better option to make an efficient model for tumor segmentation from MRI images. ***Hao Dong et al.*** [7] presents an automatic brain tumor detection and segmentation using u-net based fully convolutional networks. They proposed a fully automatic method for brain tumor segmentation, which is developed using U-Net based deep convolutional networks. Proposed method was evaluated on BRATS 2015 datasets and cross validation has shown that proposed method can obtain promising segmentation efficiently. The proposed work is only applicable for linear image during the classification process and need to improvement in the pre-processing steps for further usages of non-linear images. ***M. J. Khan et al.*** [8] discussed about non-invasive hybrid brain computer interface methods for enhancing classification accuracy. In hybridization two techniques have been combined to modify the brain images and getting better results. Mainly the aim of hybridization is to enhance the number of control commands, get better classification accuracy and lessen the signal discovery time. ***Astina Minz*** [9] Brain tumor has been recognized by using Magnetic resonance imaging (MRI) technique. In this technique tumor has been analyzed by passing strong magnetic field into the brain of the patient body. Analyzing brain tumor by using MRI method is complex but it provides better accuracy. Author used Adaboost machine learning algorithm for improving the accuracy of the MRI image. Three processes comprises of three steps named as pre-processing, Feature extraction and classifications. Pre-processing has been used for removing the noise in the recorded data. Gray Level Co- occurrence Matrix (GLCM) has been used as feature extraction technique and for classification Adaboost technique has been used. ***C Hemasundara Rao and Dr. PV Naganjaneyulu*** [10] presented an automated scheme to detect and segment the brain tumor area. The proposed system comprises of three steps named as initial segmentation, modelling of energy function and optimizes the energy function. For making the system more reliable author used to present the information in the T1 and FLAIR MRI image. ***R Anita Jasmine and Dr. P Arockia Jansi Rani*** [11] used T1 axial MRI images and the algorithms have been simulated in MATLAB 2010a environment. The parameters that have been measured are true positive (TP), false positive (FP), true negative (TN), false negative (FN). In this research work, only T1 images have been considered. ***M Gupta et al.*** [12] presented a new method used for detecting brain tumor on the basis of grade on the basis of Kurtosis and skewness in conjunction with morphological features. The features have been extracted by using T2 weighted brain MR system for separating the high brain tumor from low brain tumor. Support vector machine has been used as a classifier along with K-fold cross validation. It has been concluded that the accuracy rate obtained by using SVM classifier is 100 %. ***G. Singh and M. A. Ansari*** [13] studied numerous methods used for de-noising the image signal obtained from MRI image. Different filters named as Median filter, Adaptive filter, Averaging filter, Un-sharp masking filter and Gaussian filter have been used for removing the additive noise present in the MRI image. Segmentation of the brain image has been done by using K-mean clustering algorithm. For classification Naive Bayes and Support vector machine (SVM) have been used and hence the accuracy of the system increased. By using SVM obtained accuracy value is 91.49% whereas with Naïve Bayes accuracy rate is 87.23 %. Thus, it has been concluded that SVM performs better than Naive Bayes classifier. ***Shereen A Taie and Wafaa Ghonaim*** [14] proposed a method that has been used for detecting brain tumor from the MR images. The proposed technique measured the growth of the brain tumor in patient's brain by using four steps named as Segmentation, feature extraction, feature reduction and classification. The optimization algorithm that has been used is Chicken Swarm Optimization (CSO) and PSO optimizers to maximize the classification accuracy. ***Lubna Farhi and Adeel Yusuf*** [15] surveyed different machine learning techniques used to detect brain tumor in MRI images. GLCM have been used for differentiating the damaged and undamaged cell. For reducing the extracted features PCA Principle component analysis has been used. The accuracy of the system has been increased from 10% to 27%. ***Kailash D Kharat et al.*** [16] proposed feature extraction techniques named as Principal Component Analysis (PCA), spatial gray level dependence matrix technique for extracting the features of brain MRI images. SVM has been used as a classifier. Genetic algorithm has been used as a classifier. Inclusive technique is better option to find out the better technique for automated segmentation and detection of tumor region from the MR brain images. The comparative analysis of results based on the accuracy is given in Table 1.

Table 1: Comparison of accuracy in existing work

Authors	Accuracy (%)
S Nema et al. [6]	**94.63**
Hao Dong et al. [7]	**90.00**

M. J. Khan et al. [8]	89.30
Astina Minz [9]	87.40
R Anita Jasmine [11]	76.30
G. Singh and M. A. Ansari [13]	71.90
Shereen A Taie and Wafaa Ghonaim [14]	86.11

Though the usage of Swarm Intelligence is not new in the contrast of image segmentation and its optimization, this paper adds up a novel fitness function and updates the behavior of the algorithms for the tumor segmentation. In the most of existing work, segmentation of white matter (foreground) and grey matter (background) was done on the basis of traditional segmentation techniques but they do not cover the error minimization during the segmentation of MRI image foreground and background. The classification accuracy of a brain tumor detection model is depends on the segmentation accuracy, if segmentation is proposer, then the classification becomes more accurate. So, this article introduces the concept of improvisation of K-means based segmentation using the SFA. To evaluate the impact of SFA, we presented a comparative analysis for MRI brain tumor segmentation.

3. MATERIALS AND METHOD

The methodology of proposed EBTSC model takes the raw data as input and applies image quality enrichment based on their contrast and the apply K-means for the segmentation of the image into two part known as background and foreground. It is observed that the original uploaded image requires a little filter to be applied in order to be processed further. As shown in Fig. 2, the original image is enhanced first to label it further. After that, we apply pre-processing on the uploaded MRI images to segment the Region of Tumor (ROT) using the K-means clustering technique with SFA. Before the ROT segmentation, pre-processing is applied to remove various type of noise and image quality improvement that are inherited in the images for proposed model. To extract the key feature from ROT, develop a code for feature extraction from the segmented ROT from MRI images using the MSER descriptor technique. For the relevant feature selection from the extracted MSER feature sets, again SFA will be used as a feature selection or optimization algorithm along with the novel fitness function. At last, Initialize CNN for classification purpose using two phases, namely, training and testing with CNN as classifier. After the training of system, save the trained structure which is used in the classification section to classify the lung cancer from the MRI images. In testing phase, test MRI is uploaded and repeats the steps from 3 to 6. In the classification section, test MRI image feature is matched with trained CNN structure and return result type.
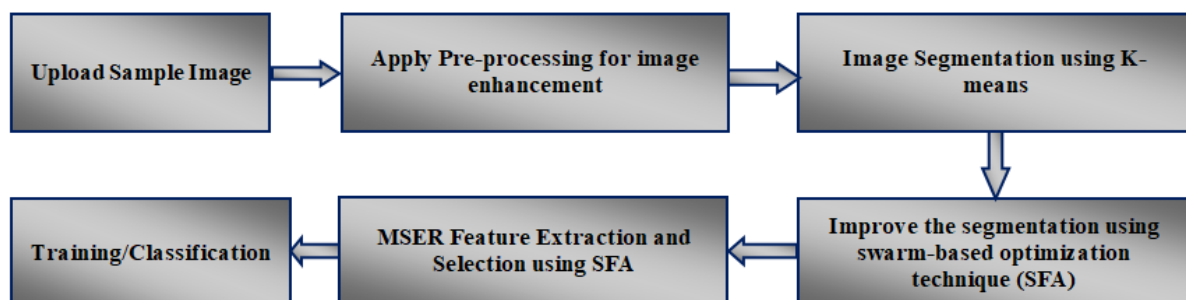

Fig. 2: EBTSC Model Flow Diagram

Dataset: The Brain Tumor Segmentation (BraTS) standard dataset comprises multimodal Magnetic Resonance Imaging (MRI) images that give full data for the experimental analysis. In order to assess the suggested design, 50 DICOM files containing multi-frame overlaid brain pictures that were taken from the dataset were studied by Menze and Kistler in 2014. http://braintumorsegmentation.org/ has the dataset.

Image Pre- processing
This is the foremost step applied after uploading the test tumor image. Here, intensity-based image enhancement technique and contrast enhancement has been performed through limiting. Limiting means that the intensity and contrast of the pixels are increased up to some limit extends. Image pre-processing technique helps to enhance

the quality of the MRI image based on their bands (Red, Green and Blue) so that tumor region segmentation becomes simple and easy to differentiate. Now, we can easily see the exact region of the tumor in the enhanced MRI data with white matter.

Image Segmentation
The segmentation techniques that are used in this work are performed using two techniques (i) K-means, and (ii) K-means with SFA.

Segmentation of ROT using K-means
The clustering issues could be successfully solved with the help of the K-means clustering approach that was proposed by Hartigan and Wong. The algorithm of K-means-based segmentation is written as:

Algorithm 1: K-means-based ROT Segmentation
Input: MRI // Brain pre-processed MRI scan image
Output: ROT // Segmented region of tumor
Calculate: [Row, Col] = size (MRI) // Calculating the size of the image
For in range (Row)
For in range (Col)
Check: if Pixel ε Foreground // Checking whether the pixel size is equal to the foreground
Assign: ROT 1 = Foreground (MRI)
Else:
ROT 2 = Background (MRI)
End – If
End – For
End – For
ROT = minimum ([ROT 1, ROT 2])
Return: ROT // Segmented region of tumor
End – Algorithm

With brain tumor MRI images as input, the K-means method determines the size of the image matrix and divides all pixels into two groups, such as ROI 1 (foreground) and ROI 2 (background) (background). The first goal is to determine whether the MRI image is foreground or background based on the Euclidean distance between centroid C1 and C2, where C1 and C2 are the means of ROI 1 and ROI 2, respectively. Each pixel is classified into two groups based on the C1 and C2 values, which are known as the foreground and background of MRI data. The foreground's ground truth is matched with the C1 based on their distance, therefore if the pixel value is not equal to the backdrop, it is definitely the foreground. The problem with k-means is that it simply divides the picture value into foreground and background. Because it is based on the precise pixel value, the data for the foreground and background may be interchanged, which means that the data may not be true for either the foreground or the background because it is based on the exact pixel value, and a pixel value of some section may be the same. To address this problem, the suggested work model tests a novel behavior for both the PSO and the Firefly algorithms. The segmented results are depicted in Fig. 3.
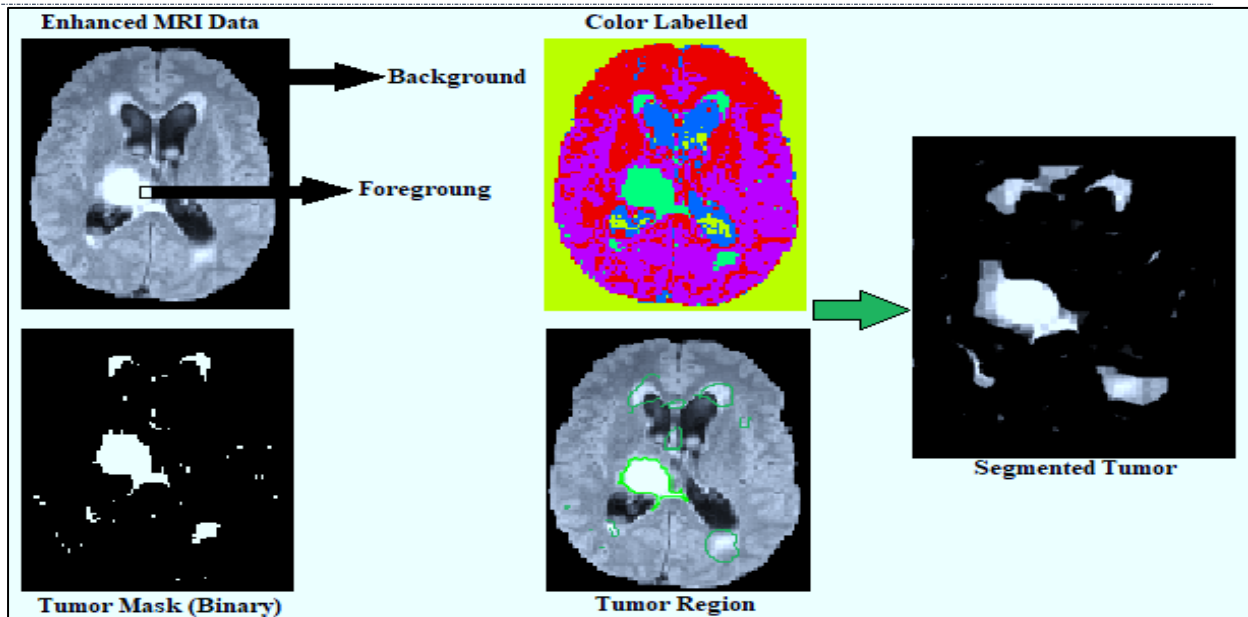
Fig. 3: Segmentation of ROT using K-means

The foreground data is combined with the background data is clearly shown in the above depiction, resulting in an uneven tumor pattern. If we employ this sort of tumor location for feature extraction, we will end up with an irrelevant feature set, making tumor classification difficult. So, to overcome such an issue, we use SFA with K-means as a Meta heuristic techniques.

Segmentation of ROT using K-means with SFA
The SFA is a nature-inspired algorithm similar to the Particle Swarm Optimization (PSO) method. Yang created the programme in 2010 after being inspired by the appealing behaviors of fireflies that is known as SFA. Since 2010, the SFA algorithm has been effectively employed to tackle a variety of optimization issues in a variety of applications. Using SFA, a new solution is developed based on previous outcomes through an iterative process.

The fitness function of SFA, which is represented as below equation:

$$f\,(fit) = \begin{cases} 1 & if\ a\ pixel\ is\ less \\ 0 & otherwise \end{cases}$$

The best solution selection depends upon the movement of flies towards a better solution. Therefore, the attractiveness between the two solutions is calculated using given equation:

$$\beta(d) = \frac{\beta_0}{1+Kd^2}$$

Where, β_0 is the attractiveness distance at distance $d = 0$, K is the constant of proportionality and the algorithm of Improved K-means is written as:

Algorithm 2: Improved K-means for ROT Segmentation

Input: MRI // Brain pre-processed MRI scan image
Output: ROT // Segmented region of tumor
Calculate: [Row, Col] = size (MRI) // Calculating the size of the image
For in range (Row)
   For in range (Col)
      Check: if Pixel ε Foreground // Checking whether the pixel size is equal to the foreground
        Assign: ROT 1 = Foreground (MRI)
     Else:
        ROT 2 = Background (MRI)
     End – If

End – For

End – For

ROT = minimum ([ROT 1, ROT 2])

Data = find (ROT>0)

Initialize SFA parameter – Iterations (T), Population Size (S), Lower Bound (LB), Upper Bound (UB), Fitness function and Number of selection (N)

Calculate T = Size (MR Image)

Fitness function:

$$f(fit) = \begin{cases} 1 & if\ pixel\ is\ less \\ 0 & otherwise \end{cases}$$

For K in range (T)

$$fs = \sum_{i=1}^{P} Data(i)$$

$$ft = \frac{\sum_{i=1}^{P} Data(i)}{Length\ of\ feature}$$

Threshold = SFA (S, T, LB, UB, Data, f (fit))

End – For

While T ~= Maximum

Mask Image = Morphological (ROT, Threshold)

Boundaries = Region (Mask Image)

ROT = MRI × Boundaries

End – While

Return: ROT // Segmented region of tumor

End – Algorithm

SFA provides a better and optimistic result compare to the only K-means, which are also proved by the experimental analysis in the result section.
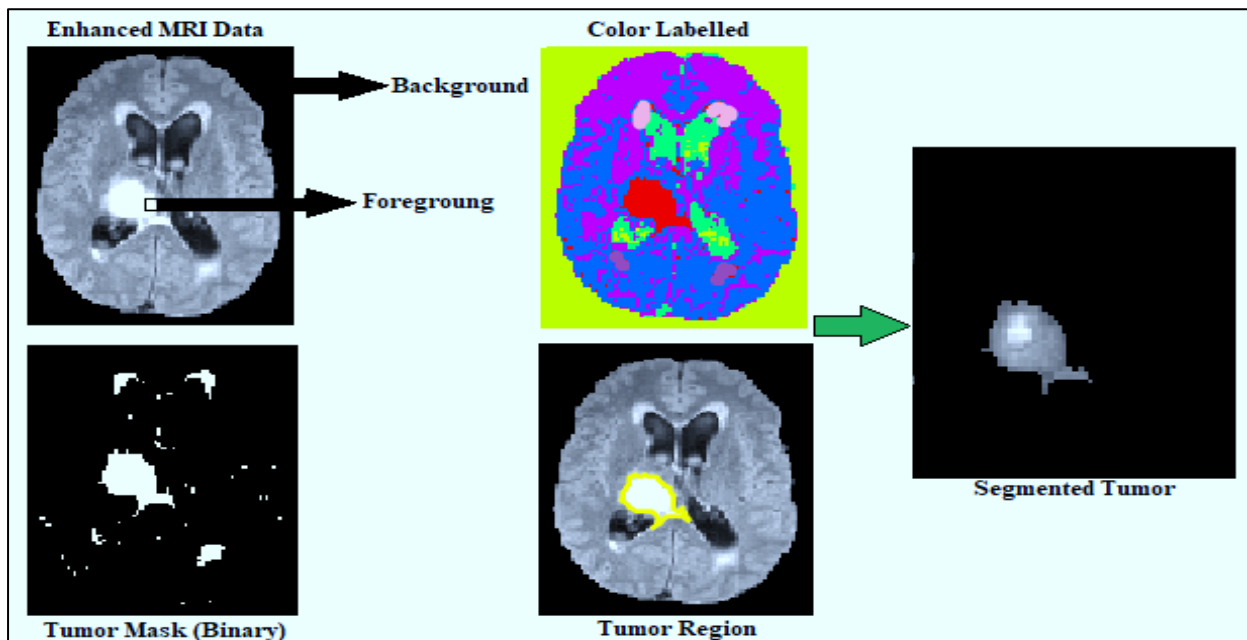

Fig. 4: Segmentation of ROT using Improved K-means

We were able to get a superior segmented outcome by combining the SFA with K-means and some morphological procedures, as seen in the Fig. 4. It is evident that the foreground-background data mix-up

problem has been decreased but not eliminated, thus we are using the notion of SFA as a Meta heuristic technique to handle this problem.

Feature Extraction: Here, we used MSER as a feature descriptor for segmented ROT from MRI using improved K-means. MSER returns a collection of features based on a stable region of the object that contains information about the input MRI data of human brain. The fluctuation in a stable region of an image is minimal. The method seeks out regions that are "maximally stable," that is, they have less volatility than regions one level below or above them. The region below / above may be coincident with the real region due to the discrete character of the image, in which case the region is still regarded maximum. The algorithm of MSER descriptor is written as:

Algorithm 3: MSER Descriptor
Input: ROT // Segmented region of tumor
Output: KF // Key feature points from segmented ROT
Scaling of ROT, Scale = Scaling (ROT, 8×8)
Calculate: Length = Number (scale)
For in range (Length)
Extrema = Extrema (ROT)
Key-point = Key (Extrema)
If localization need orientation
Orientation = (Key-point, Angle)
End – If
KF = Stability (Key-point, Orientation)
End – For
Return: KF as key feature points
End – Algorithm

Using the above mentioned algorithm of MSER descriptor, we extract some key points from the segmented ROT that is depicted in Fig. 5.
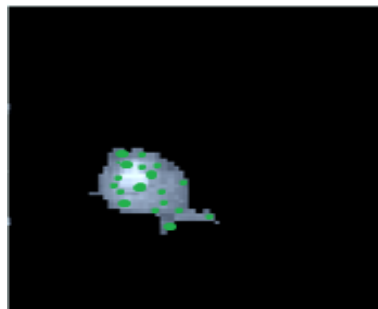

Fig. 5: MSER Features of ROT

Apply swarm intelligence based SFA as a Meta heuristic algorithm as a feature selection technique to select the unique feature from MSER feature sets for each categories based on the objective function (fitness function) of optimization technique. The algorithm of SFA is written as:

Algorithm 4: SFA-based Feature Selection
Input: KF // Key feature points from segmented ROT
Output: SKF // Selected key feature points
Initialize SFA parameter – Iterations (T)
Population Size (S)
Lower Bound (LB)
Upper Bound (UB)
Fitness function
Number of selection (N)

Calculate T = Size (KF)

Fitness function:

$$f(fit) = \begin{cases} 1 & if\ Feature > Threshold \\ 0 & otherwise \end{cases}$$

For K in range (T)

$$fs = \sum_{i=1}^{P} Data(i)$$

$$ft = \frac{\sum_{i=1}^{P} Data(i)}{Length\ of\ feature}$$

Fit Data Index = SFA (S, T, LB, UB, KF, f (fit))

End – For

SKF = KF (Fit Data Index)

Return: Optimized data as set of optimized feature points

End – Algorithm

After feature selection process, we used the concept of Convolutional Neural Network (CNN) as deep learning mechanism to train the proposed EBTSC model. The algorithm of CNN is written as:

Algorithm 5: EBTSC-Net (CNN)

Input: SKF // Selected key feature points
      Target // Class of data available in SKF
Output: EBTSC-Net // Trained Structure of CNN
Initialize CNN parameters: – No. of Epochs (E)
                        – No. of Hidden Layers
                        – Cross entropy
                        – Division: Random
For K in range (Target)
   Group (K) = Class (SKF)
End – For
Call CNN in software using Training data (SKF) and Group
EBTSC-Net = Pattern-Net (T, G, N)
EBTSC-Net = Train (EBTSC-Net, SKF, Group)
Current MRI Feature, CF = KF (MRI)
Output = SIM (EBTSC-Net, CF)
If Output is valid then
   Return class of MRI
Else
   Return Sorry Message
End – If
Return: EBTSC-Net as Trained Structure
End – Algorithm

During testing process, test a MRI data and then proposed EBTSC-Net return classified output based on the trained CNN structure. Here, The CNN mainly comprises of Convolutional layer, pooling layer, input and output layer. Test MRI data features are compared with the data stored into the trained EBTSC-Net structure. If data is matched, then a specific output in terms of class is returned. At last, calculate the performance parameters of the proposed EBTSC model in terms of Precision, Sensitivity, F-measure, Accuracy, Error, MCC, DC, JC, Specificity and Execution Time. The simulation results of proposed an EBTSC model using MRI data with optimized deep learning is described in the below section of paper.

4. RESULT AND DISCUSSION

We created EBTSC-Net that is a very sophisticated neural network for brain tumor classification and segmentation is proposed by improved K-means algorithm in this research. The suggested approach for

segmentation utilizing unpaired medical data has obtained superior accuracy. The proposed network can be trained with a little amount of data from the BraTS database of MRI and has been tested for over 90% of scans from the database. Here, we presents a comparative analysis to select region of tumor from MRI using K-means and SFA as a swarm-based optimization technique. In below Table 2, we presents the comparison of previous work by *S Nema et al.* [6] K-means and K-means with SFA for segmentation.

Table 2: Comparative analysis of Exiting work, K-means and K-means with SFA based on accuracy

Sample	K-means	S Nema et al.	K-means + SFA
10	78.8875	96.7623	99.8295
20	77.5489	96.6756	99.8158
30	77.4211	96.5135	99.7981
40	76.9725	95.3871	99.7972
50	73.9714	95.1935	99.4207
60	72.6569	95.0763	98.8125
70	71.4515	94.0267	98.6649
80	70.6073	93.0077	98.5122
90	70.0263	92.6295	97.8782
100	69.8628	91.1214	97.8405
Average	73.9406	94.6393	99.0369

Based on the obtained segmentation performance in terms of accuracy for 10 to 100 different MRI images or sample, the effectiveness of the proposed K-means with SFA as swarm based optimization technique is far better and helps to solve the pixel mixing problem of K-means and existing work for ROT segmentation. In Fig. 6, the graphical representation of segmentation analysis behalf of accuracy is shown.
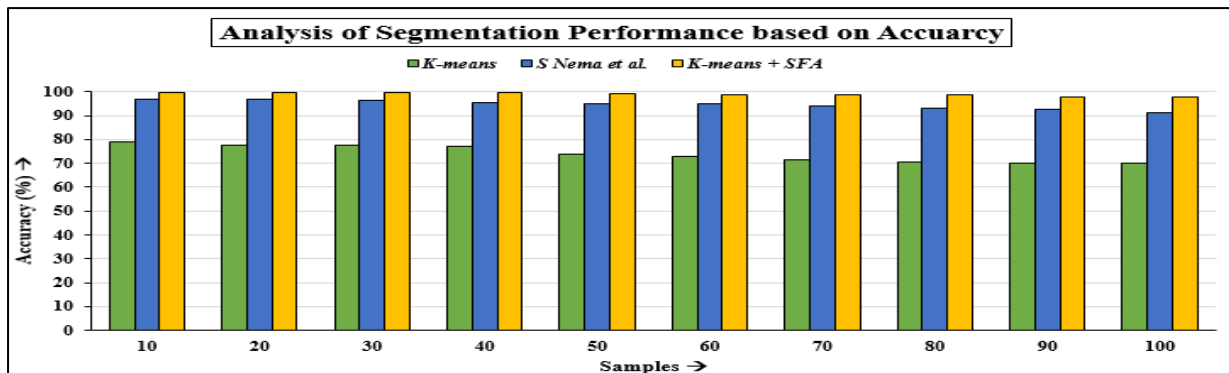

Fig. 6: Analysis of Segmentation Performance

The segmentation of ROT from MRI using K-means with SFA is clearly superior to only K-means and existing work as seen in the above figure. SFA based K-means (Improved K-means) are used to segment the ROT from MRI data, and they are dependent on morphological procedures such as binarization, thinning, filling opening, dilatation, and so on. A morphological operation is a set of non-linear procedures that deal with the form or morphology of picture features. Using some fundamental procedures on segmented ROT, we apply morphological operations to determine the precise ROT from MRI and segmentation is directly proportional to the classification accuracy. After segmentation technique analysis, we presents the simulation results for the proposed EBTSC model during the tumor classification from segmented ROT and the procedural segmentation results of ROT is shown in Fig. 7.
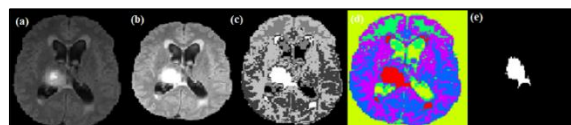

Fig. 7: Segmentation of ROT from MRI (a) Original (b) Enhanced (c) Grey (d) Color Labelled and (e) ROT

The segmentation results obtained for the sample test MRI scans are shown in the above Fig. 7. Segmentation image visualization starting from the original uploaded image to the extracted ROT during the image segmentation performed using k-means with SFA. The classification results of the proposed EBTSC model are calculated in terms of Precision, Recall, F-measure, Accuracy, Error, and Execution Time.

Table 3: Performance evaluation of EBTSC model using BraST Dataset

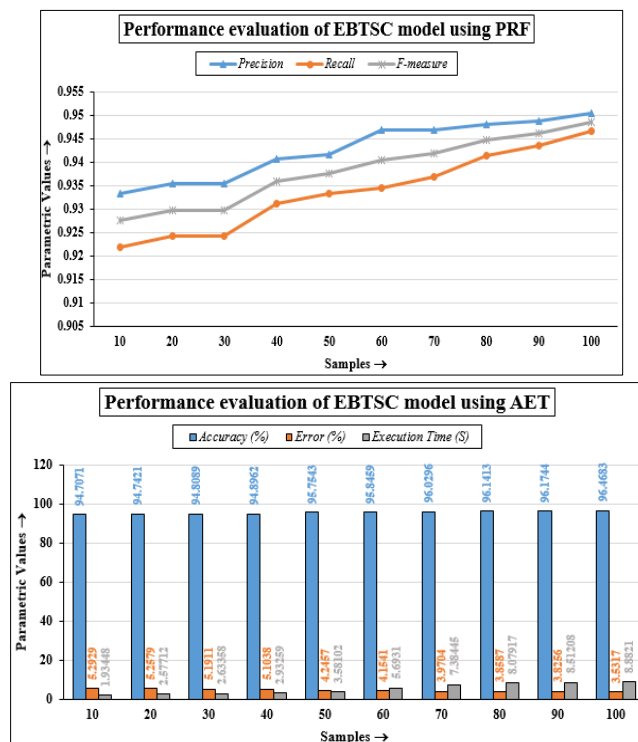| Samples	Precision	Recall	F-measure	Accuracy (%)	Error (%)	Execution Time (S)
10	0.93338	0.921817	0.927562	94.7071	5.2929	1.93448
20	0.935406	0.924111	0.929724	94.7421	5.2579	2.57712
30	0.935415	0.924256	0.929802	94.8089	5.1911	2.63358
40	0.940538	0.931231	0.935861	94.8962	5.1038	2.93259
50	0.941623	0.933317	0.937452	95.7543	4.2457	3.58102
60	0.946732	0.934368	0.940509	95.8459	4.1541	5.6931
70	0.94695	0.936739	0.941817	96.0296	3.9704	7.38445
80	0.947985	0.941472	0.944717	96.1413	3.8587	8.07917
90	0.948726	0.943500	0.946106	96.1744	3.8256	8.51208
100	0.95031	0.946551	0.948427	96.4683	3.5317	8.88210

Fig. 8: Performance evaluation of EBTSC model using BraST Dataset (a) using Precision, Recall and F-measure (PRF) and (b) using Accuracy, Error and Time (AET)

Fig. 8 (a) represents the evaluation of precision, recall and f-measure results for the proposed EBTSC model and in the graph, a number of sample of MRI images is plotted on the x-axis against the obtained parametric values. The average precision, recall and f-measure of proposed EBTSC model is 0.9427, 0.9337, and 0.9381 respectively. Similarly, Fig. 8 (b) represents the evaluation of accuracy, error and execution time for the proposed EBTSC model and the average accuracy, error and execution time of proposed EBTSC model is 95.55%, 4.45%, and 5.22 seconds respectively. So, we can say that the experimental results of proposed EBTSC model is satisfactory in both cases such as segmentation and classification. We discovered that the suggested

training network produces superior visual outcomes than the existing work that is clearly shown in the Tables 2, 3 and Fig. 8 in terms of quantitative parameters.

5. CONCLUSION

In this paper, an EBTSC model is proposed using improved K-means with SFA and for model training the concept of CNN is used as deep learning mechanism. For the segmentation of ROT from MRI, a comparative framework is design using K-means only and improved K-means using SFA. The performance of the proposed EBTSC model is evaluated in terms of Precision, Sensitivity, F-measure, Accuracy, Error, MCC, DC, JC, Specificity and Time for segmentation. Where, for classification, we used Precision, Recall, F-measure, Accuracy, Error, and Time. The average precision, recall and f-measure of proposed EBTSC model is 0.9427, 0.9337, and 0.9381 respectively and average accuracy, error and execution time of EBTSC model is 95.55%, 4.45%, and 5.22 seconds respectively. During, ROT segmentation, we achieved 4.54% improvement in the accuracy by utilizing the concept of SFA along with the K-means algorithm. Overall, it is observed that the ROT has been more precisely and accurately segmented using the combination of K-means with SFA. In future, the work can be extended by including more statistical features, which can help to enhance the detection accuracy and tumor size estimation properly. ROT segmentation accuracy of the proposed EBTSC model is high but segmentation time still high and it should be minimized in the future.

REFERENCES

[1]. M. N. Wu, C. C. Lin and C. C. Chang, "Brain Tumor Detection Using Color-Based K-Means Clustering Segmentation," Third International Conference on Intelligent Information Hiding and Multimedia Signal Processing (IIH-MSP 2007), Kaohsiung, 2007, pp. 245-250.

[2]. Schwartzbaum, J.A., Fisher, J.L., Aldape, K.D., Wrensch, M.: Epidemiology and molecular pathology of glioma. Nat. Clin. Pract. Neurol. 2, 494–503 (2006)

[3]. Smoll, N.R., Schaller, K., Gautschi, O.P.: Long-term survival of patients with glioblastoma multiforme (GBM). J. Clin. Neurosci. 20, 670–675 (2013)

[4]. Ramakrishna, R., Hebb, A., Barber, J., Rostomily, R., Silbergeld, D.: Outcomes in reported low-grade gliomas. Neurosurgery 77, 175–184 (2015)

[5]. Mazzara, G.P., Velthuizen, R.P., Pearlman, J.L., Greenberg, H.M., Wagner, H.: Brain tumor target volume determination for radiation treatment planning through automated MRI segmentation. Int. J. Radiat. Oncol. Biol. Phys. 59, 300–312 (2004)

[6]. Nema, Shubhangi, Akshay Dudhane, Subrahmanyam Murala, and Srivatsava Naidu. "RescueNet: An unpaired GAN for brain tumor segmentation." Biomedical Signal Processing and Control 55 (2020): 101641.

[7]. Dong, Hao, et al. "Automatic brain tumor detection and segmentation using U-Net based fully convolutional networks." annual conference on medical image understanding and analysis. Springer, Cham, 2017.

[8]. Khan, M. Jawad, Melissa Jiyoun Hong, and Keum-Shik Hong. "Decoding of four movement directions using hybrid NIRS-EEG brain-computer interface." Frontiers in human neuroscience 8 (2014): 244.

[9]. Minz, Astina, and Chandrakant Mahobiya. "MR Image classification using adaboost for brain tumor type." Advance Computing Conference (IACC), 2017 IEEE 7th International. IEEE, 2017.

[10]. C. H. Rao, P. V. Naganjaneyulu and K. S. Prasad, "Brain Tumor Detection and Segmentation Using Conditional Random Field," 2017 IEEE 7th International Advance Computing Conference (IACC), Hyderabad, 2017, pp. 807-810.

[11]. Jasmine, R. Anita, and P. Arockia Jansi Rani. "A two phase segmentation algorithm for MRI brain tumor extraction." Control, Instrumentation, Communication and Computational Technologies (ICCICCT), 2016 International Conference on. IEEE, 2016.

[12]. M. Gupta, B. V. V. S. N. P. Rao and V. Rajagopalan, "Brain Tumor Detection in Conventional MR Images Based on Statistical Texture and Morphological Features," 2016 International Conference on Information Technology (ICIT), Bhubaneswar, 2016, pp. 129-133.

[13]. Singh, Garima, and M. A. Ansari. "Efficient detection of brain tumor from MRIs using K-means segmentation and normalized histogram." Information Processing (IICIP), 2016 1st India International Conference on. IEEE, 2016.

[14]. Taie, Shereen A., and Wafaa Ghonaim. "CSO-based algorithm with support vector machine for brain tumor's disease diagnosis." Pervasive Computing and Communications Workshops (PerCom Workshops), 2017 IEEE International Conference on. IEEE, 2017.

[15]. L. Farhi and A. Yusuf, "Comparison of brain tumor MRI classification methods using probabilistic features," 2017 13th IASTED International Conference on Biomedical Engineering (BioMed), Innsbruck, Austria, 2017, pp. 55-62.

[16]. K. D. Kharat, V. J. Pawar and S. R. Pardeshi, "Feature extraction and selection from MRI images for the brain tumor classification," 2016 International Conference on Communication and Electronics Systems (ICCES), Coimbatore, 2016, pp. 1-5.

[17]. B. Beddad and K. Hachemi, "Brain tumor detection by using a modified FCM and Level set algorithms," 2016 4th International Conference on Control Engineering & Information Technology (CEIT), Hammamet, 2016, pp. 1-5.

[18]. Logeswari, T., and M. Karnan, "An improved implementation of brain tumor detection using segmentation based on soft computing," Journal of Cancer

[19]. Mustaqeem, Anam, Ali Javed, and Tehseen Fatima, "An efficient brain tumor detection algorithm using watershed & thresholding based segmentation," International Journal of Image, Graphics and Signal Processing vol.4, 2012, pp. 34-43.

[20]. Dobe, O., Sarkar, A., & Halder, A. (2019). Rough K-means and morphological operation-based brain tumor extraction. In Integrated Intelligent Computing, Communication and Security (pp. 661-667). Springer, Singapore.