

# Brain Tumor Segmentation from 3D Brain MRI Using 3D Convolutional Neural Network

Hiren Patel, Mehul C Parikh, Mahesh Pipalia

**Abstract:** *Magnetic Resonance Imaging (MRI) is one of the medical imaging modality that widely used by the doctors to represent the internal brain structure information digitally. There are plenty of methods available for the classification and segmentation of tumor from the brain MRI study. Brain tumor detection in the initial stage is very important for accurate and better treatment. Patient survival chances can be increased if the accurate tumor is segmented from the brain which can help doctors to treat the patient accordingly. There are a number of existing emerging machine learning algorithms contributed to this problem area. Convolutional Neural Network (CNN) is a widely used method for this type of image segmentation problems. 3D CNN is already achieving better results in this work but it takes lots of data and the time to train such very high accurate model. In this research, 3D CNN is used along with the biological structural information of the brain i.e. the brain has a symmetric structure which can be divided into two nearly equal half, information from each half can help CNN model to differentiate the abnormal tissues from the normal tissues. Using the biological information the results are improved by 10.27%. The fractal search algorithm is implemented to reduce the time complexity of the tumor segmentation process. The segmentation processing time has been reduced by 41.75% on GPU while 23.69% on CPU and improves the segmentation result by 2.76%.*

**Index Terms:** *Brain tumor segmentation, CNN, Fractal Search,*

## I. INTRODUCTION

In the medical field, brain tumor treatment is very difficult. Brain tumors are the abnormal mass of the tissues spread in 3-dimensional space inside the brain. Its size and the location inside the brain defined the type and level of the tumor. Magnetic Resonance Imaging (MRI) is one of the medical imaging modality that widely used by the doctors to represent the internal brain structure information digitally. Gliomas are one of the brain tumor types which grows in the glial cell. It can be divided into two types, Low Grade (Slow-growing) and High Grade (Fast-growing). LGG generally covers II and III grade of the brain tumor. Treatment for the Brain tumor is decided on the basis of the grade of the tumor, higher the grade represent more treatment required. Brain tumor detection is a very time-consuming task for the radiologist. It needs more time and effort for a single brain MRI study. There are plenty of methods which reduces this tedious task of physicians by using the different classification and

segmentation techniques. Emerging machine learning has also lots of contribution to this problem area. In most of the machine learning methods, Convolutional Neural Network (CNN) is a widely used method for this type of segmentation problems. CNN can be used in 2D and 3D space of the brain structure. 3D CNN is already achieving better results in this work but it takes lots of training data and the time to train such very high accurate model. All these available machine learning algorithms are based on the information of pixel values of the MRI. In this research, 3D CNN is used along with the biological structural information of the brain i.e. the brain has a symmetric structure which can be divided into two nearly equal half, information from each half can help CNN model to differentiate the abnormal tissues from the normal tissues. By using the 3D architecture sufficient amount of search time to find the tumor inside the brain can be reduced.

## LITERATURE SURVEY

Research in medical imaging is a favorite topic in the healthcare domain. There are much research has been done in this problem area and many are ongoing. Work has been done in both machine learning and naïve techniques. Few techniques, architectures, results, findings are listed below.

A. Comparative study of Supervised and Unsupervised Classification has been done on brain tumor segmentation. Supervised methods like KNN, SVM, and ANN are compared with unsupervised techniques like K-means and Fuzzy C-Means. These methods are tested with the BRATS-2015 data set. Results of this study state that the ANN has outperformed the other classification methods, also it states that KNN and SVM performed lower than the unsupervised methods [6].

B. Convolutional Neural Networks (CNN) with small  $3 * 3$  kernel with the intensity normalization methods as a preprocessing step is used in the recent studies. This research has been tested on the BRATS-2013 data sets. Two different models have been designed for the HGG and LGG for tumor segmentation. With LLU activation function taking the Dropout of 0.5 in HGG and 0.1 in LGG dataset in the FC layers is used to reduce the overfitting of the model. Achieved a 0.88 dice score value for the HGG and 0.65 for LGG [7][9].

C. 3D CNN is also used in the recent study because of the 3D structure of the brain. With the help of GMU fusion technique information from the multiple modalities is feed to the CNN network. The research was performed on the BRATS-2015 Dataset which concludes that the GMU fusion technique gives better results than the simple fusions [8].

D. Auto Encoder is also used in the process of brain tumor segmentation. In this research, the author fits the slices of 3D brain MRI

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**Hiren Patel**, Information Technology, L D College of Engineering, Ahmedabad, India.

**Mehul C Parikh**, Information Technology, L D College of Engineering, Ahmedabad, India.

**Mahesh Pipalia**, CEO and Founder, Script All DNA Technology, Ahmedabad, India.



studies as input and collect the same size output. Relu activation function is used along with the L2 regularization. 0.83 dice score value is achieved in this research. Although it is getting better results autoencoder is a very time-consuming technique [10].

E. Biological information of the brain i.e. the symmetrical structure of the brain is used with the fast bounding box technique to segment the brain tumor. By finding the difference between two portions of the brain. The used technique is very fast compared to the machine learning technique. Also, different sets of morphological operations are used in the brain tumor segmentation process. Results obtained by this method are lower than the machine learning methods [13][14].

## II. PROPOSED METHODOLOGY

### A. Datasets

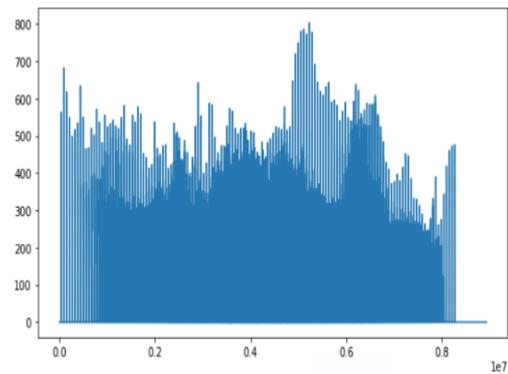
The datasets were collected from the Brain Tumor Segmentation (BraTS) challenge by the Medical Image Computing and Computer-Assisted Intervention (MICCAI) society. It is an international Multimodal brain tumor segmentation challenge. The dataset includes the HGG and LGG tumors. It covers the data from the four different modalities of MRI scan a) T1- weighted b) T1CE c) T2-weighted and d) FLAIR. All the images have been segmented manually by the experienced neuro-radiologists. Provided data is already pre-processed, i.e. interpolated to the same resolution and skull-stripped [1][2][3][4].

### B. Data Preprocessing

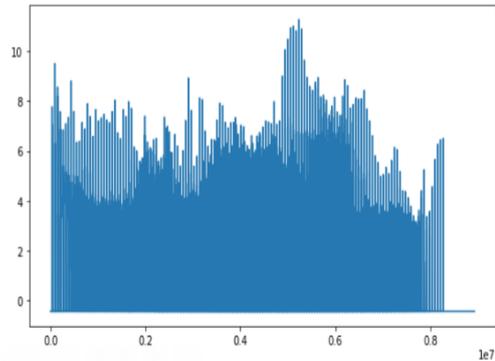
The intensity variation of the MRI images is very high. To balance this nonuniform intensity variation of the MRI images N3 technique is used. The problem of correcting for intensity nonuniformity is greatly simplified if it is modeled as a smooth multiplicative field. Nonparametric data are not required to fit a normal distribution. Nonparametric statistics uses data that is often ordinal, meaning it does not rely on numbers, but rather a ranking or order of sorts. For this purpose, N4ITK Library is used [11][12].

### C. Data Normalization

There are plenty of techniques available for the intensity normalization like histogram equalization, normalize by dividing each value by the max value of the given set, logarithmic normalization. To downgrade the pixel value range to a small amount, Image is subtracted by mean and divided by the standard deviation. By applying this the range of MRI of Sample Brats18\_CBICA\_BFP\_1 if decrease from [0, 803] to [-0.4256, 11.2722], It has been reduced without losing the information from the image. Corresponding histogram plots are shown in Fig 1 which shows that there is no loss in the information but reduces the range of pixel value for a given image [9].



(a)



(b)

Fig 1. (a) Actual Data Distribution. (b) Normalized data Distribution.

### D. Sampling of Data

The brain has an almost symmetric structure. It is human's nature that to compare the objects by referencing it to some other objects. This phenomenon of human's brain nature is applied.

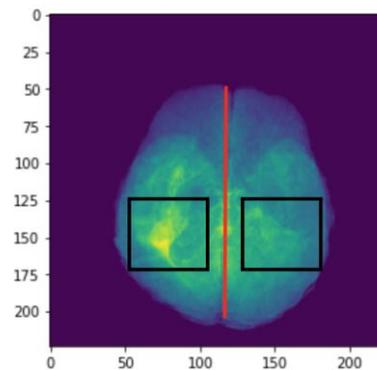


Fig 2. Data Sampling Process.

The dataset contains images of size 155 \* 240 \* 240. For training, the model with this size requires very high computational power and it will take more time in training as well. To do the efficient training with the small size, the 3D samples of windows size 16 has been taken from each MRI image. The sample was taken from both the left and right part of the brain with the same origin point, keeping an equal number of infected and non-infected samples as shown in Fig 2.

E. Model Architecture

Proposed model architecture is shown in Fig 3 and corresponding layer information is listed in Table 1 for a single modality. The same architecture is used for both left CNN and right CNN. Finally, the fusion of the two CNN model will be merged into the fully connected layer as listed in Table II. The binary cross entropy will be used as the loss function to classify the normal and abnormal brain tissue.

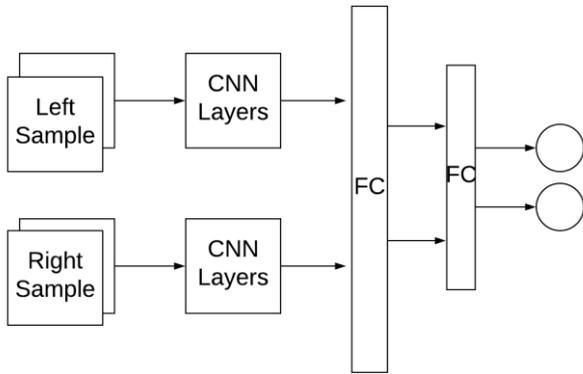


Fig 3. General model Architecture.

	Filter Size	Filter Numbers	Activation
Conv3D	(3, 3, 2)	32	Relu
Conv3D	(3, 3, 2)	32	Relu
Average Pooling	(2, 2, 2)	-	-
Conv3D	(3, 3, 2)	16	Relu
Conv3D	(3, 3, 2)	16	Relu
Average Pooling	(2, 2, 2)	-	-
Conv3D	(3, 3, 2)	8	Relu
Conv3D	(3, 3, 2)	8	Sigmoid
Average Pooling	(2, 2, 2)	-	-

(I)

	Size	Activation
FC	1024	Sigmoid
FC	512	Sigmoid
FC	2	sigmoid

(II)

F. 3D Fractal Search Algorithm

To search tumor region inside the 3D MRI images is very time and space consuming with the small box size. It is reduced by using the basic fractal search technique. Fractal search technique works as digging the region of interest to get a more precise result. In terms of segmentation, it will use the low-resolution segmented tumor to get the high-resolution segmented tumor. As low-resolution segment can be easily calculated by the increasing the stride size. Flow chart for the fractal search algorithm is shown in Fig 4.

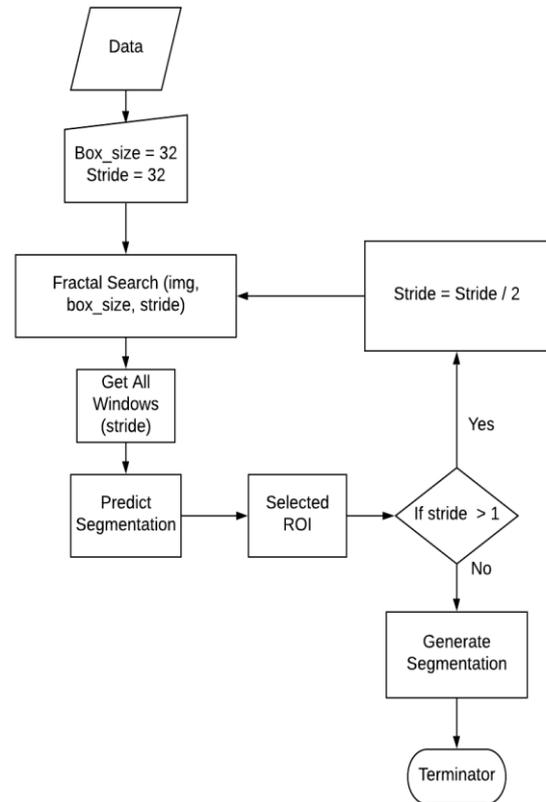


Fig 4. Flow chart for the Fractal Search Technique.

G. Evaluation Methods

1) Dice Coefficient

It is used to find the similarity between two sets. For given set A and B the formula for the dice coefficient is given below [15].

$$DSC = \frac{2 * (A \cap B)}{|A| + |B|}$$

2) Sensitivity and Specificity

Sensitivity measures the proportion of actual positives that are correctly identified and Specificity measures the proportion of actual negatives that are correctly identified. Equations for both given below [5].

$$Sensitivity = \frac{TP}{TP + FN}$$

$$Specificity = \frac{TN}{TN + FP}$$

III. IMPLEMENTATION

The proposed method is implemented using the Keras tensor flow library on python environment. Jupyter notebook and python script are used. Training Data was generated by taking 200 random samples from each brain MRI study.



Data is duplicated by applying rotation and flipping operation to make it unbiased. The final count of the data sample used for the training is listed in the table (III). Model is then trained for 10 epoch with the batch size of 64. The binary cross entropy loss function is used with Adam optimizer. It takes nearly 15 minutes to train the model using the GPU. The current implemented model has 5.15% training loss while 5.96% testing loss which can be improved by changing the model parameters.

Location of Tumor	No of Samples
No Tumor	25653
Left Side	21136
Right Side	24132
Both Side	4776

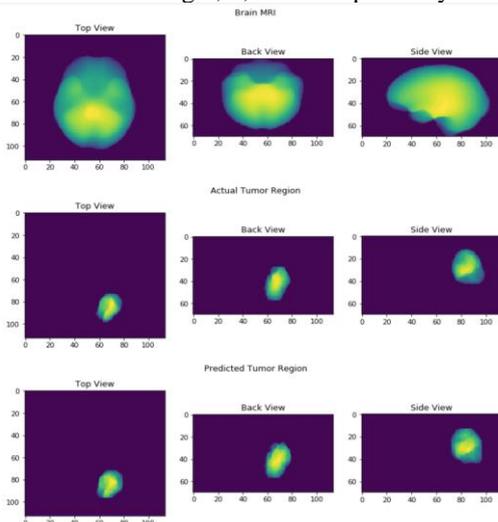
(III)

### IV. RESULTS

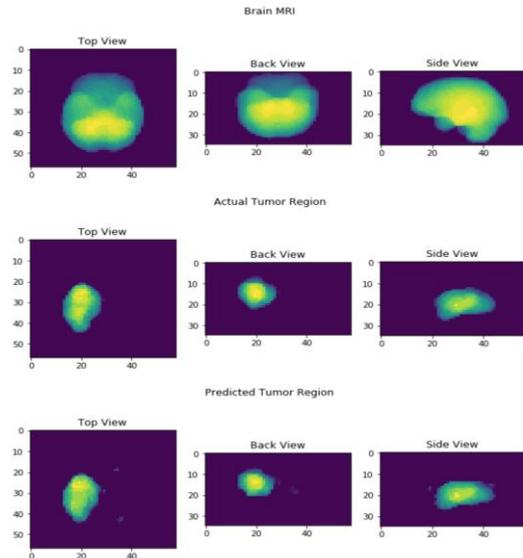
Results of the proposed method are calculated as the dice coefficient. The segmented 3D brain is plotted in 2D view by taking the average in each direction which gives the three different view of the 3D brain model. The first row shows the actual MRI image, the second row shows the manually segmented tumor region and the third row shows the predicted segmented region by the proposed method. Tumors are varying in the shape and size at a different level according to that the model is tested with the differently sized tumor located at a different position inside the brain.

#### A. Based on the Location of the Tumor

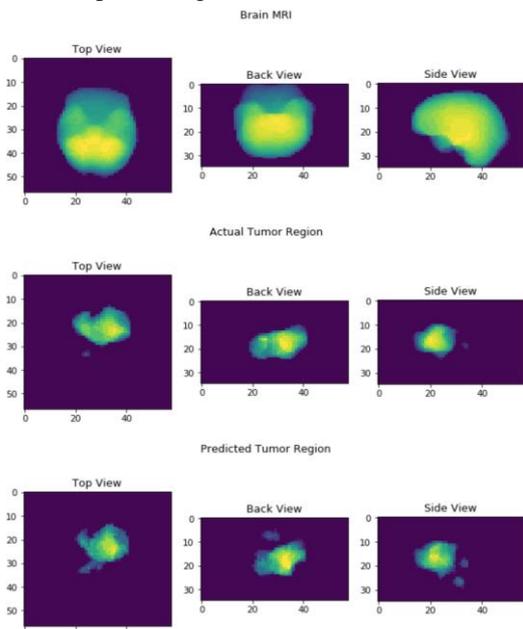
Examples of the brain segmentation using the proposed method varying in the different location of the brain are shown below. A tumor present in the right left and center of the brain is shown in Fig 5, 6, and 7 respectively.



**Fig 5. A sample having a tumor on the right side of the brain.**



**Fig 6. A sample having a tumor on the left side of the brain.**



**Fig 7. A sample having a tumor at the center of the brain.**

#### B. Based on Size of Tumor

The proposed methodology is also tested with the brain study having the tumor of different size. Dataset has a brain study having a tumor with an average of 1.12% of brain size. Actual Brain size is of 155 \* 240 \* 240 pixels. Tumor region is calculated by taking the sum of all the tumor pixels available in the manually segmented sample. Tumor with the tumor region area 0.23% (small tumor) is shown in Fig 8, the tumor with the tumor region area of 2.19% (large tumor) is shown in Fig 9.

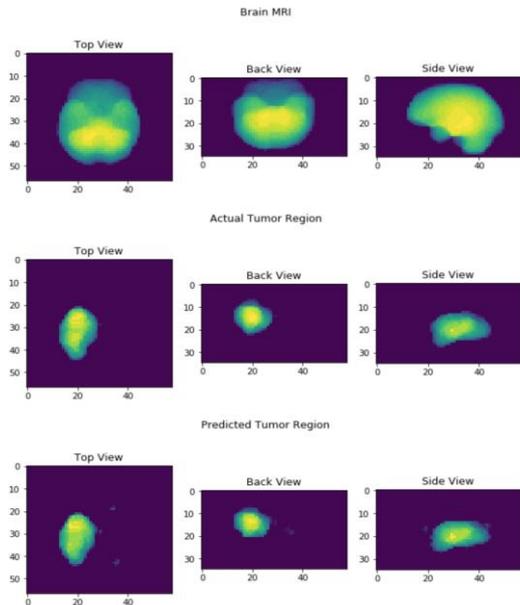


Fig 8. A sample having a small-sized tumor

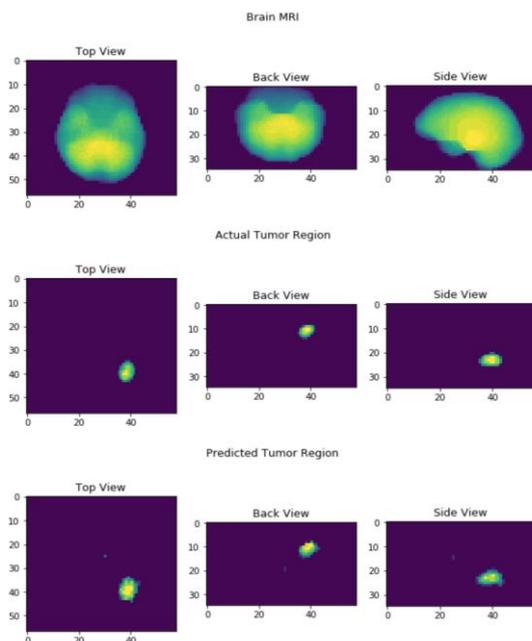


Fig 9. A sample having a large-sized tumor

## V. COMPARISONS

The proposed model is compared with the naive approach with the same size 3D CNN architecture for the same set of the test sample. The different set of sample is taken and segmented using both models and the results are compared as dice coefficient value. Along with the proposed model, the proposed fractal search algorithm is also compared with the direct search technique on both CPU and GPU processors. All the results are taken by keeping the 4-pixel stride. For the comparison purpose, 12 different samples are chosen varying in location and size of the tumor region.

### A. Fractal Search vs Direct Search

#### 1) Time Difference in GPU

The time taken by the direct search method is higher for every sample than the fractal search method. On an average fractal search method is 41.75% faster on GPU and 23.69% faster on CPU than the direct search method with a slight change in the

dice score value. Time taken to segment each sample on GPU and CPU are shown in table IV and table V respectively.

Sample	Direct Search (In Seconds)	Fractal Search (In Seconds)	Improvement (In %)
TCIA10_644_1	21.8781	10.4033	47.5509
TCIA02_368_1	20.3798	7.4878	36.7412
TCIA02_455_1	20.6699	6.1933	29.9627
TCIA10_175_1	20.6941	8.1226	39.2508
TCIA13_618_1	20.5074	8.6384	42.1234
TCIA02_118_1	20.2793	9.9479	49.0546
TCIA02_374_1	20.1932	7.2147	35.7284
CBICA_APR_1	20.1789	6.3191	31.3152
CBICA_AVV_1	20.1415	7.0827	35.1646
TCIA08_242_1	20.6286	10.9696	53.1767
TCIA12_466_1	20.1505	9.5206	47.2475
CBICA_AWH_1	20.2194	10.8225	53.5255

(IV) Time is taken to segment the tumor on GPU

Sample	Direct Search (In Seconds)	Fractal Search (In Seconds)	Improvement (In %)
TCIA10_644_1	217.0490	67.1032	30.9162
TCIA02_368_1	226.5082	41.6174	18.3735
TCIA02_455_1	228.6530	28.8280	12.6077
TCIA10_175_1	228.6044	47.6985	20.8651
TCIA13_618_1	227.5983	53.9294	23.6950
TCIA02_118_1	228.5186	70.4659	30.8359
TCIA02_374_1	227.2234	41.4829	18.2564
CBICA_APR_1	227.7457	29.6955	13.0389
CBICA_AVV_1	227.6137	38.2548	16.8069
TCIA08_242_1	227.2919	81.0595	35.6632
TCIA12_466_1	228.0244	63.6875	27.9301
CBICA_AWH_1	227.0785	81.1253	35.7257

(V) Time is taken to segment the tumor on CPU

#### 2) Performance Difference

The very small performance difference is found between the direct search and fractal search method. The performance was improved by 2.76% using fractal search over direct search. Results are shown in Table VI.

Sample	Direct Search Dice Score	Fractal Search Dice Score	Performance Difference
TCIA10_644_1	0.8243	0.8420	2.1021
TCIA02_368_1	0.9431	0.9343	-0.9419
TCIA02_455_1	0.8386	0.8406	0.2379
TCIA10_175_1	0.9304	0.9104	-2.1968

TCIA13_618_1	0.7965	0.8675	8.1844
TCIA02_118_1	0.8908	0.9008	1.1101
TCIA02_374_1	0.9181	0.9228	0.5093
CBICA_APR_1	0.8406	0.8331	-0.9003
CBICA_AVV_1	0.9440	0.9369	-0.7578
TCIA08_242_1	0.9370	0.9256	-1.2316
TCIA12_466_1	0.6742	0.8455	20.2602
CBICA_AWH_1	0.7229	0.7759	6.8308

(VI)

**B. Normal segmentation vs Symmetric Segmentation**

The Base method is compared with the proposed method by taking a different set of small and large size tumor located at the different side of the brain. Most of the cases, the proposed method gave a better result than the base method. There is 10.27% improvement for the all test dataset available. Results are shown in Table VII.

Sample	Location	Tumor Area %	Base Model Dice Score	Symmetric Model Dice Score	Improvement in %
CBICA_AWH_1	CENTER	1.79	0.5831	0.7759	24.8486
CBICA_APR_1	CENTER	0.82	0.6566	0.8331	21.1859
CBICA_AVV_1	RIGHT	1.46	0.8091	0.9369	13.6407
TCIA13_618_1	LEFT	0.76	0.7573	0.8675	12.7032
TCIA12_466_1	CENTER	0.73	0.7441	0.8455	11.9929
TCIA02_374_1	LEFT	1.47	0.8215	0.9228	10.9775
TCIA02_455_1	LEFT	1.09	0.7666	0.8406	8.8032
TCIA02_368_1	RIGHT	1.96	0.8657	0.9343	7.3424
TCIA02_118_1	LEFT	1.69	0.8407	0.9008	6.6718
TCIA10_175_1	LEFT	2.15	0.8581	0.9104	5.7447
TCIA08_242_1	RIGHT	1.75	0.9043	0.9256	2.3012
TCIA10_644_1	CENTER	1.78	0.8668	0.842	-2.9454

(VII)

**VI. CONCLUSION**

The proposed method has been tested on the 12 different test samples varying in the size and location of the tumor inside the brain. Using the Biological information i.e. symmetric structure of the brain the results are improved by 10.27% compared to 3D CNN technique used earlier by the researcher [1]. Further improvement in the acquired result can be possible by changing the model parameter. The proposed fractal search technique is also tested on the same set of test samples.

The proposed method improves the segmentation processing time by 41.75% on GPU devices while 23.69% on CPU device compare to basic window based image segmentation technique. Fractal search method affects the performance of the tumor segmentation. The fractal search method improves the segmentation result by 2.76%. The fractal search technique still can be improved by using better thresholding techniques.

**VII. FUTURE SCOPE**

1. The results are based on the single modality FLAIR of the MRI images. As different type of modalities used in the different type of tumor visualization, a fusion of the different modalities can be used to get a better accurate result for all types of tumor.
2. The more efficient algorithm can be designed to improve the time complexity to segment the tumor.

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## AUTHORS PROFILE



learning in healthcare.

**Hiren Patel** is Pursuing ME in Information Technology from L D College of engineering, Ahmedabad – 380015. He published a paper in ICRASET Dec-2018 on “Comparative Analysis for Moving Object Detection in Vibrant Background using SVM, LS-SVM, and Random Forest Classifier”. His research domain is in machine



segmentation of moving objects and in medical image processing. He is a life member of CSI, ISTE, and IETE.

**Mehul C. Parikh** is presently working as an associate professor in the Department of Information technology, L.D. College of Engineering, Ahmedabad. He received his M.Tech degree from Nirma University and Ph.D. from Charotar University of Science and Technology, Changa, Gujarat. His research focus in the area of Image processing, especially in



Medicine).

**Mr. Maheshkumar Pipalia** is an engineering graduate in Computer Science from Ganpat University. He is one of the founding members at Script All DNA Technologies. He is having more than 14 Years of experience in developing Healthcare IT solutions. Currently, he is an active member of SIIM (Society for Imaging Informatics in