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Brain Tumor Segmentation from MRI Head Scans through GSO based FCM Clustering and Region Growing Technique

P.Nagaraja[1], T.Kalaiselvi[2*], P.Sriramakrishnan[3]

[1, 2*,3] Department of Computer Science and Applications,
Gandhigram Rural Institute – Deemed University, Gandhigram, Tamil Nadu, India

[*]*Corresponding Author:* kalaiselvi.gri@gmail.com, *Tel.: +91-9486362843*

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***Abstract*—** This proposed work is aimed to develop an automatic method for brain tumor segmentation based on glowworm swarm optimization based fuzzy c-means clustering (GSOFCM) and region growing technique. The proposed method consists of three stages: Stage-1 is accelerating the FCM clustering for tissue segmentation process based on GSO. In Stage-2, is an abnormal detection process that helps to check the results of GSOFCM method by fuzzy symmetric measure (FSM). In Stage-3 is segment the tumor region from abnormal slices by region growing technique. The quantitative analysis of brain tumor segmentation process uses the parameters dice coefficient (DC), positive predictive value (PPV), and processing time. The proposed method is very efficient to segment the tumor region from MRI head scans.

***Keywords*—** Clustering, Fuzzy c-means, Glowwarm Swarm Optimization, Segmentation.

I. INTRODUCTION

Image segmentation is an initial and vital step for most of image analyzing tasks in digital image processing. It is partitioning of an image into different meaningful regions. The segmentation is based on measurements taken from the image and might be gray level, color, texture, depth or motion. Segmentation is most important study of image analysis, which is used to obtain the essential information from the images. It plays an essential role in medical image analysis [1] [2]. The diagnosis of medical imaging techniques such as computed tomography (CT), positron emission tomography (PET), magnetic resonance imaging (MRI) and single photon emission computed tomography (SPECT). MRI provides prosperous information about the human soft tissue anatomy and diagnosing the organs of human body. In recent years, MRI has become an important modality for neurological image diagnosis. Nowadays, brain tumor segmentation for MRI is difficult task for medical applications [3] [4].

Brain tumor is any mass that results from an abnormal and an uncontrolled growth of cells in the brain. Brain tumors are generally classified into three common types: benign (non-cancer), pre-malignant (pre-cancerous stage), malignant tumor (cancer). Benign brain tumors are low grade, non cancerous brain tumors, which, grow slowly and push aside normal tissue but do not invade the surrounding normal tissue. Malignant brain tumor is cancerous brain tumor, which grow rapidly and invade the surrounding normal tissue [5]. Tumors are classified based on the four properties for intra-tumoral regions, namely "edema", "non enhancing (solid) core", "necrotic (or fluid-filled) core," and "active core". The annotating of both high and low grade cases are separated from different structures. Human experts indicate each segmentation map into three classes, namely the "whole" tumor (including all four tumor classes), the tumor "core" (including all tumor classes except "edema"), and the "active" tumor (containing the "active core" only). The perifocal edema and core regions also appear in FLAIR, T2-weighted images and more sensitive to suspect brain pathology [6]

Several image segmentation methods have been developed for brain tumor segmentation. Generally, image segmentation techniques are categorized into four classes: thresholding, clustering, edge detection, and region extraction. Clustering and region based segmentation techniques are most popular for image segmentation. Shin proposed a hybrid clustering and logistic regression for multi-model brain tumor segmentation. This framework used different methods for detecting the edema and tumor regions. The sparse coding is used for simple classification of the edema region. And then logistic regression and k-means clustering are applied for segmenting the tumor region. This method failed to give satisfactory results for both high and low grade glioma images [7]. Geremia et al., proposed a spatial decision forests for glioma segmentation in multi channel MR images. This method is composed of three frameworks: context-rich decision forest, spatial prior and long-range comparisons with 3D regions. This method requires multi-channel images to detect the tumor [8]. Riklin Raviv et al., proposed a spatial

probability map for tumor location and level-set approach to solve joint segmentation problem. Manual initialization, based on a few mouse clicks to determine the approximate tumor center and extent was used. The proposed method was able to give satisfactory results only for high grade glioma images only [9].

Baurer et al., proposed an integrated random forest classification with hierarchical conditional random field regularization in an energy minimization scheme for tumor segmentation [10]. Buendia et al., proposed a GAIN+ (Grouping Artificial Immune Network) was developed for fully automated MRI brain segmentation. It is adopted to input patterns for training multiple images and segmentation of tumors in MRI brain images. This method obtained good results for high grade glioma images when apply pre and post processing [11]. Cordier et al., proposed a fully automated approach by the brain labeling method which is similar to multi atlas label methods. The segmentation process is based on similarities between multi-channel patches [12].

Festa et al., proposed a trained random decision forest to classify the voxels, based on its meaningful features. Three pre-processing steps were performed: bias field correction with N4ITK, histogram matching using ITK and random decision forest that is used to classify each brain voxel based on 404 features used to extract from the training data [13]. Taylor et al., proposed a novel map-reduce enabled extension to hidden markov models to enable high-throughput training and segmentation of brain tumors in MRI images. This method gives better results for high grade glioma images only and attained minimum DC value [14].

The proposed work based on the combination of GSO based FCM for fast segmentation of tissue and tumor regions which overcomes the above said problems and works efficiently for FLAIR images. The proposed method uses GSO for selecting the initial centroids for the FCM method and segments the brain tissues such as background, gray matter (GM), white matter (WM), cerebrospinal fluid (CSF). Then abnormal detection process is done by FSM. Finally, the region growing method is applied in abnormal slices to segment the tumor region. The experimental results show that the proposed method gives satisfied results for brain tumor segmentation.

This paper is organized as follows. The materials used in the experiment are given in section 2, the GSO clustering algorithm is explained in section 3, the FCM is explained in section 4, the proposed method is explained in section 5, the results and discussion are given in section 6 and the conclusion is given in section 7.

II. MATERIALS

The proposed method used 25 datasets from FLAIR MRI head scans of high grade (HG) and low grade (LG) glioma images are selected from the BRATS2012 database. The datasets are classified into four categories, namely T1-weighted, T1-weighted contrast-enhancement (Gadolinium) image, T2-weighted and FLAIR. The clinical images required manual clarifications for simulated ground truth information with different tumor structures. The proposed method used FLAIR images for segmenting the complete tumor region only.

III. GSO CLUSTERING ALGORITHM

In GSO, a swarm of glowworms are randomly distributed in the search space of object functions. The agents in the glowworm algorithm carry a luminescence quantity called luciferin along with them. Each glowworm is attracted by the brighter glow of other neighboring glowworms. A glowworm identifies another glowworm as a neighbor, when it is located within its current local decision domain. The higher the intensity of luciferin, the better is the location of glowworm in the search space. In each iteration, all the glowworms position will change, and then the luciferin value also follows updates. Each iteration consists of a luciferin-update phase followed by a movement-phase based on a transition rule [15] [16].

The basic steps in GSO algorithm:

Step 1: The key parameters of GSO algorithm are s, ρ, β, r_0, and r_s.

Step 2: Glowworms' initialization: glowworms are initially distributed randomly, equally dispersed luciferin and sensor range and set the current iteration is set to 1.

Step 3: Luciferin update phase: Each glowworm updates luciferin according to the following equation:

$$l_i(t+1) = (1-\rho) l_i(t) + \gamma J_t(t+1) \quad (1)$$

where $li(t)$ is the luciferin of glowworm i at time t, ρ is the luciferin decay constant ($0<\rho< 1$), γ represents the luciferin enhancement constant, and $Ji(t)$ is the function value.

Step 4: Movement Phase: For each glowworm i, the probability equation of moving toward a neighbor j can be stated as

$$p_{ij}(t) = \frac{(l_j(t) - l_i(t+1))}{\sum_{k \in N(t)} (l_k(t) - l_i(t+1))} \quad (2)$$

Then, the equation of the glowworm movements is given by,

$$x_i(t+1) = x_i(t) + s * \left(\frac{x_j(t) - x_i(t)}{\left\| x_j(t) - x_i(t) \right\|} \right) \quad (3)$$

where $j \in N_i(t) \neq \Phi$, $N_i = \{ j : d_{ij}(t) < r_i^d(t) \text{ and } l_j(t) \}$ is the set of neighbours of glowworm *i*, $r_i^d(t)$ is the variable local-decision domain, and $d_{ij}(t)$ represents the Euclidean distance between glowworms *i* and *j* at time *t*, $x_i(t)$ represents the location of glowworms *i* at time *t*, *s* is the step size, and $\|.\|$ is the Euclidean norm operator.

Step 5: Local-decision domain update function for each glowworm.

$$r_i^d(t+1) = \min\{ r_s, \max\{ 0, r_i^d(t) + \beta(n_t - |N_i(t)|) \} \} \quad (4)$$

where β is a constant parameter and n_t is a threshold parameter used to control the number of neighbours. Table 1 shown the value of important parameters used for GSO clustering.

Table 1. The parameters used in the GSO clustering algorithm

γ	β	ρ	n_t	S	l_0	r_s	n
0.4	0.6	0.08	5	0.03	5	255	4

The proposed GSO clustering algorithm is described as follows:

Input cluster data object;

Set maximum iteration number =*iter* _max ;

Let *s* be the step size;

Let *r* be the local space radius;

Let l_i (0) be the initial luciferin ;

Let (0) be the initial dynamic decision domain radius

Set *t* =1

While (*t* <= *iter_max*) do:

{

for *i* = 1 to *n* do

$$N_r = \{ j : \| x_j(t) - x_i(t) \| < r \}$$

$$d(x_i(t)) = \frac{|N_r x_i(t)|}{g}$$

$$J(x_i(t)) = -\ln\left(\frac{1}{g} \right) + \ln(d(x_i(t)))$$

$$l_i(t+1) = (1-\rho) l_i(t) + \gamma J_t(t+1)$$

for each glowworm *i* do: % Movement-phase

$N_i = \{ j : d_{ij}(t) < r_i^d(t) \text{ and } l_j(t) \}$

where $\|\overline{x}\|$ is the norm of

for each glowworm $j \in N_i(t)$ do:

$$p_{ij}(t) = \frac{(l_j(t) - l_i(t+1))}{\sum_{k \in N(t)} (l_k(t) - l_i(t+1))}$$

j= select_glowworm $\left(\overrightarrow{p} \right)$

where is the maximal element of *p*

$$x_i(t+1) = x_i(t) + s * \left(\frac{x_j(t) - x_i(t)}{\left\| x_j(t) - x_i(t) \right\|} \right)$$

$r_i^d(t+1) = 255;$

}

$t \leftarrow t+1:$

}

Algorithm symbolic description: $x_i(t)$ is the glowworm *i* in *t* iteration location; $l_i(t)$ is the luciferin of the glowworm *i* in *t* iteration; $N_i(t)$ is the neighbourhood set of glowworm *i* in *t* iteration; $r_i^d(t)$ is the dynamic decision domain radius of glowworm *i* in *t* iteration; is the upper bound of the $r_i^d(t)$; $p_{ij}(t)$ is the probability of glowworm *i* selects neighbour *j*.

IV. FUZZY C-MEANS CLUSTERING

This algorithm divides the image space into smaller regions or units called clusters and by definition such regions are to be disjoined [17] [18]. It is based on fuzzy partioning is that makes the data point belongs to all groups with different membership grades between 0 and 1. The aim of FCM clustering is to find the cluster centers that minimize dissimilarity (objective) function.

The objective function is,

$$J_m = \sum_{i=1}^{n} \sum_{j=1}^{c} u_{ij}^m \, d_{ij} \quad (5)$$

where, m [1,∞] is a weighting exponent, u_{ij} [0,1] is the degree of membership x_i in the cluster *j*, x_i is the i^{th} element of d-dimensional measure data, c_j is the d-dimensional enter of the cluster and d_{ij} is the Euclidean distance between i^{th} data point (x_i) and j^{th} centroids (c_j).

The updated membership functions are defined as follows,

$$u_{ij} = \frac{1}{\sum_{k=1}^{c}\left[\frac{d_{ij}}{d_{ik}}\right]^{\frac{2}{m-1}}} \quad (6)$$

$$c_j = \frac{\sum_{i=1}^{n} u_{ij}^{m} x_i}{\sum_{i=1}^{n} u_{ij}^{m}} \quad (7)$$

This iteration will stop if the improvement of the objective function over the previous iteration is below critical value, ε [0,1]. This algorithm is iteratively updating the centers and membership grades for each data point. FCM iteratively moves the cluster centers to the right location within a data set.

V. PROPOSED METHOD

This proposed method is a fully automatic brain tumor segmentation method using FLAIR MRI head scans. The framework of the proposed work is given in Fig.1. The different stages of tumor detection methods are explained in the following sections.

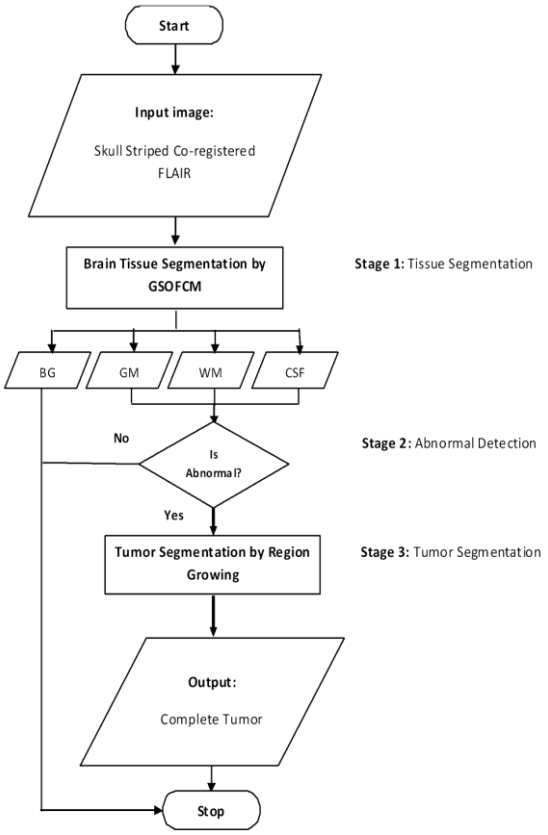

Figure 1. Framework of proposed method

5.1. Stage 2: Tissue Segmentation

In Stage 1, tissue segmentation process is done by GSOFCM clustering. The proposed method is an automatic centroid selection based on GSO for FCM. In the initial stage, the GSO clustering module is executed for a short period for automatic clustering, forming spherical or close to spherical shape data clusters. The result from the GSO clustering technique is used as the initial centroid value of the FCM clustering. Finally, the given input image is classified into four segmented regions: background, WM, GM and CSF. Then abnormal slices are checked from these segmented regions.

5.2. Stage 2: Abnormal Detection

Abnormality in the WM, GM and CSF regions can be detected by measuring the symmetry using FSM. The symmetry property of FLAIR MRI head scans are computed by the FSM [19] [20] and given by,

$$FSM = \frac{1}{1+\left(\frac{n_L - n_R}{100}\right)^2} \quad (8)$$

where n_L and n_R are the number of foreground (white) pixels in the left and right half of the abnormal image present at either side of the central vertical line of slice. The symmetry values calculated from normal images are generally much larger than T_i (T_i =0.1), and the values for abnormal images are much smaller than T_i [21]. The proposed method is used this threshold (T_i) value for abnormal slice detection process.

5.3 Stage 3: Tumor Segmentation

A. Region Growing Method

The region growing method (RG) is used to segment the brain tumor precisely. RG method is a procedure that groups pixels or sub regions into larger regions based on predefined function. RG requires some as additional input values for extracting the objects.

The proposed RG algorithm applied in this study is summarized as follows:

Input : Abnormal slice is given as Input image

Output : The segmented Tumor image

1. *Read the Abnormal Slice: AS(i,j)*
2. *T_o =graythresh(I);*

   where T_i is represent as a Otsu's Threshold value
3. *Apply Region growing Method:*
   - i. *Four (RG4) and Eight (RG8) neighborhood functions*
   - ii. *AS(i,j)> T_o and AS(i,j) <=MAX_i)*
   - iii. *if AS(i,j) ≠ MIN_i*


```
/*RG4 neighborhood*/
        for j=1:1:k
        for i=1:1:r
        if (((j-2) > 1 )&& ((j+2) < k))
           if (((i-2) > 1 )&& ((i+2) < r))
              if a(i,j)==0
                    b(i,j-1)=0;
                    b(i,j)=0;
                    b(i,j+1)=0;
                    b(i+1,j-1)=0;
                    b(i+1,j)=0;
                    b(i+1,j+1)=0;
                    b(i-1,j-1)=0;
                    b(i-1,j)=0;
                    b(i-1,j+1)=0;
```

iv. *if AS(i,j)=MIN_i*

```
/*RG8 neighborhood*/
   if (((j-1) > 1 )&& ((j+1) < k))
    if (((i-1)>1)&& ((i+1) < r))
       if a(i,j)==0
            b(i,j-1)=0;
            b(i,j)=0;
            b(i,j+1)=0;
            b(i+1,j-1)=0;
            b(i+1,j)=0;
            b(i+1,j+1)=0;
            b(i-1,j-1)=0;
            b(i-1,j)=0;
            b(i-1,j+1)=0;
```

where *b* is represent as a grouping the adjacent pixels, MAX_i is represents the maximum intensity value (*MIV=255*), MIN_i represents the minimum intensity value (*MIV=0*),

4. *Extract the tumor portion from abnormal slice.*
5. *Stop*

The proposed RG method used a global threshold value for throughout tumor segmentation process. Initially, abnormal slice (*AS*) is taken as the input image. The Otsu's thresholding technique is used for selecting intial the threshold value (T_o) and this method gives good segmented binary image [22]. Then applied four neighbourhoods (RG4) of the pixels of *AS(i,j)* whose intensity value is greater than T_o and less than or equal to MAX_i are set to MIN_i and otherwise the eight neighbourhoods (RG8) are set to MIN_i. The RG4 or RG8 pixels set to MIN_i constitute the edge region and extracting the tumor region from *AS*.

VI. RESULTS AND DISCUSSION

Our algorithm was implemented in MATLAB2009 on a PC with Intel Pentium Core Duo 1.6GHz processor and 512MB RAM. The performance analysis of the proposed methodology is compared with the corresponding ground truth images from BRATS2012 database. The computation time for tumor segmentation ranged from 1 to 2 minutes depending on the size of the dataset. The qualitative validation in the form of visual inspection is done with some of the sample FLAIR MRI head scans are shown in Fig.2.

In Fig.2, the original FLAIR MRI head scans are given in column 1, the corresponding ground truth images are given in column 2, and the results of proposed method are given in column 3. This proposed work gives good results for both high and low grade FLAIR and FLAIR glioma MRI head scans.

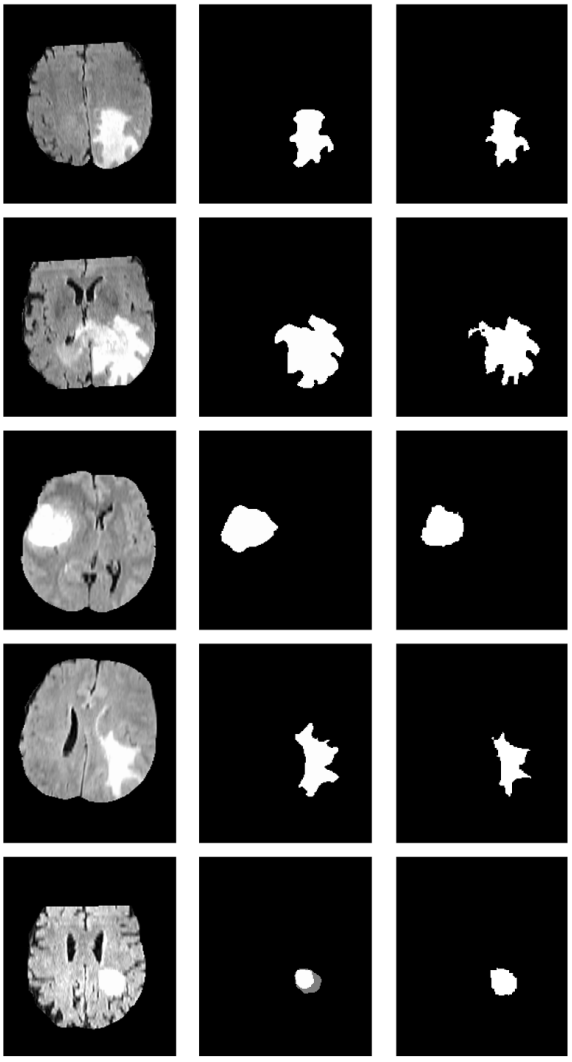

Figure 2. the original FLAIR MRI head scans are in column 1, , corresponding ground truth images are in column 2 and the results of proposed method are in column 3.

The performance analysis of proposed method used the parameters: predictive accuracy (PA), dice coefficient (DC) and processing time.

The PA is given by:

$$PA(\%) = \frac{TP + TN}{TP + TN + FP + FN} * 100 \quad (9)$$

where,

True positive (TP) = the test result is positive in the abnormal cases correctly classified.

True Negative (TN) = the test result is negative in the normal cases correctly classified.

False Positive (FP) = the test result is positive in the normal cases classified abnormal.

False Negative (FN) = the test result is negative in the abnormal cases classified normal.

Table 2. PA and DC values of the proposed method

S. No.	Volume		Ground Truth Range	Proposed method		
	Name	*Slice No.*		*Range*	*PA (%)*	*DC (%)*
1	HG1	1-216	46-119	46-119	99	84
2	HG2	1-216	44-110	44-110	99	71
3	HG3	1-216	62-146	62-146	99	83
4	HG4	1-216	81-150	81-150	99	84
5	HG5	1-216	68-131	68-131	98	71
6	HG6	1-236	87-161	87-161	98	77
7	HG7	1-236	78-137	78-137	97	65
8	HG8	1-216	55-133	55-133	98	79
9	HG9	1-216	75-147	75-147	98	67
10	HG10	1-216	77-117	77-117	97	65
11	HG11	1-216	64-131	64-131	99	84
12	HG12	1-216	94-136	94-136	99	71
13	HG15	1-216	72-151	72-151	98	74
14	HG22	1-240	39-95	39-95	99	79
15	HG24	1-240	115-174	115-174	98	69
16	HG25	1-230	94-165	94-165	97	72
17	HG26	1-230	99-179	99-179	97	67
18	LG1	1-296	65-105	65-105	99	72
19	LG4	1-236	64-117	64-117	95	76
20	LG8	1-236	84-114	84-114	100	83
21	LG11	1-220	118-166	118-166	100	93
22	LG12	1-230	78-119	78-119	98	71
23	LG13	1-220	81-132	81-132	99	77
24	LG14	1-230	94-120	94-120	99	71
25	LG15	1-230	61-101	61-101	99	78
	Mean				**98.3**	**75.3**

The DC is given by:

$$D(A, B) = \frac{2|A \cap B|}{|A| + |B|} \quad (10)$$

where A represents the ground truth image and B represents the proposed result image.

The performance analysis of proposed method is based on the parameters PA and DC values given in Table 2. The PA and DC of proposed method are 98% and 75% in both HG and LG glioma images. The DC value and processing time of proposed method are compared with existing methods values that are given in B.H. Menze et al., 2015. They are tabulated in Table 3 which shows that the proposed method yields better DC value and takes less time for processing, than the existing methods. Our proposed method is faster and has given better results for both HG and LG FLAIR weighted glioma volumes when compared with existing methods.

Table 3. Processing time for the proposed method and existing methods

S.No.	Methods	DC (%) (Complete Tumor)	Processing Time (min)
1	Geremia et al., 2012	62	10
2	Shin, 2012	30	8
3	Riklin Raviv et al., 2012	74*	8
4	Baurer et al., 2012	68	4-12
5	Buendia et al., 2013	57	21** and 20sec
6	Cordier et al., 2013	68	20
7	Festa et al., 2013	62	20-25
8	Taylor et al., 2013	44	1
9	Proposed Method	**75**	**1-2**

*High grade only, **Pre-processing time

VII. CONCLUSION

This paper proposed a combination of GSOFCM and region growing method to segment the brain tumor region efficiently and quickly from FLAIR MRI head scans. The performance analysis of the proposed method is verified in terms of PA, DC and processing time. The experimental results of the proposed methodology depicted with maximum PA and DC value and processed faster than while compared with existing methods. This proves that the proposed work quickly segment the tumor region from FLAIR MRI head scans and thus saves the diagnosis time of the medical specialists.

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Authors Profile

Dr. Nagaraja currently working as a guest faculty in Gandhigram Rural Institute - Deemed University, Dindigul, India. He received his Bachelor of Science (B.Sc) degree in Physics in the year 2008 and Master of Computer Applications (MCA) degree in the year 2011 from The Gandhigram Rural Institute (Deemed to be University). He received his Ph.D (Full-time) degree from The Gandhigram Rural Institute (Deemed to be University) in the year 2017. He has published 16 research articals in reputed international journals including Thomson Reuters (SCI & Web of Science) and conferences including Springer and it's also available online. His Research focuses on Medical Image Processing to enrich the Computer Aided Diagnostic process.

Kalaiselvi T. is currently working as an Assistant Professor in Department of Computer Science and Applications, The Gandhigram Rural Institute, Dindigul, Tamilnadu, India. She received her Bachelor of Science (B.Sc) degree in Mathematics and Physics in 1994 & Master of Computer Applications (M.C.A) degree in 1997 from Avinashilingam University, Coimbatore, Tamilnadu, India. She received her Ph.D degree from The Gandhigram Rural University in February 2010. She has completed a DST sponsored project under Young Scientist Scheme. She was a PDF in the same department during 2010-2011. An Android based application developed based on her research work has won First Position in National Student Research Convention, ANVESHAN-2013, organized by Association of Indian Universities (AUI), New Delhi, under Health Sciences Category. Her research focuses on MRI of human Brain Image Analysis to enrich the Computer Aided Diagnostic process, Telemedicine and Teleradiology Technologies.

Sriramakrishnan P. is a Research Scholar (Full-time) in the Department of Computer Science and Applications, Gandhigram Rural Institute - Deemed University, Dindigul, India. He received his Bachelor of Science (B.Sc.) degree in 2011 from Bharathidasan University, Trichy, Tamilnadu, India. He received Master of Computer Applications (M.C.A) degree in 2014 from The Gandhigram Rural Institute- Deemed University, Dindigul, Tamilnadu, India. He worked as Software Engineer in the Dhvani Research and Development Pvt. Ltd, Indian Institute of Technology Madras Research Park, Chennai during January 2014 – March 2015. He is currently pursuing Ph.D. degree in The Gandhigram Rural Institute - Deemed University. His research focuses on Medical Image Processing and Parallel Computing. He has qualified UGC-NET for lectureship in June 2015.

