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Research Article

Hybrid SVD Based Hilbert Huang Transform (HSHHT) Technique for Abnormality Detection in Brain MRI Images

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Abstract: Medical images are widely used by the physicians to find abnormalities in human bodies. However the images sometimes are corrupted with a noise which normally exist or occurs during storage, or while transfer the image and sometimes while handling the devices. Therefore the need to enhance the image is crucial in order to improve the image quality. Segmentation technique for Magnetic Resonance Imaging (MRI) of the brain is one of the method used by radiographer to detect any abnormality happened specifically for brain. In this study we have proposed a method for segment the normal and abnormal tissues in the MRI images. At first we select the input image from the BMRI database. Then apply the skull stripping method to the input brain image. After that the proposed method perform the segmentation technique with the help of improved artificial neural networks here the weights are optimized by means of adaptive genetic algorithm. After the classification, the normal tissues like White Matter (WM), Grey Matter (GM) and Cerebrospinal Fluid (CSF) are segmented from the normal BMRI image. Abnormal tissues like Tumor and Edema are segmented from the abnormal BMRI images. The abnormal tissue segmentation will be carried out by optimal SVD and HHT based segmentation in which optimization can be done by Binary cuckoo search algorithm. Both the classification and the segmentation performance of the proposed technique are evaluated in terms of accuracy, sensitivity and specificity. The implementation of the proposed method is done in the working platform of MATLAB.

Keywords: Adaptive genetic algorithm, artificial neural network, binary cuckoo search, Hilbert Huang transform, singular value decomposition

INTRODUCTION

Computational neuroanatomy is a new growing field of powerful applications in neuroscience. It promises an automated methodology to characterize neuroanatomical configuration of structural Magnetic Resonance Imaging (MRI) brain scans (Schwarz *et al*., 2007). Medical images build essential portions for distinguishing and investigating dissimilar body structures and the diseases offensive them (Zuo *et al*., 2004). Several type of images are generated like ultrasound images, Magnetic Resonance Images (MRI), X-rays which can be again classified in radiographs, computed tomography commonly termed as CT scan, fluoroscopy, mammography (Sharma and Aggarwal, 2010). Researchers in MRI analysis have been intensively working for last few decades to improve the performance of existing data mining techniques using multispectral approaches. But it remains as a challenge because classification accuracy highly depends upon the input data characteristics and feature analysis methods. Pre-processing, feature extraction and classification are the main steps involved in a typical multispectral analysis system (Sindhumol *et al*., 2013).

Brain tissue and tumor segmentation in MR images have been an active research area. Extraction of good features is fundamental to successful image segmentation. Due to complex structures of different tissues such as the Gray Matter (GM), White Matter (WM) and Cerebrospinal Fluid (CSF) in the MR brain images, extraction of useful features is a challenging task. Variability in tumor location, shape, size and texture properties further complicates the search for robust features (Ahmed *et al*., 2011). Image segmentation, do a major role in biomedical imaging applications such as the enumeration of tissue volumes

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diagnosis, confinement of pathology analysis of anatomical structure, treatment planning, partial volume improvement of practical imaging data and computer incorporated surgery (Jabbar and Mehrotra, 2008). With the fast advancement of MRI, which provides high resolution images, the detection of infarct lesion is becoming increasingly more feasible. However, due to their arbitrary shapes and locations, segmentation of lesions is a complex and challenging task (Shen *et al*., 2008).

Tumor is an uncontrolled growth of cancer cells in any part of the body. Tumors are of different types and have different characteristics and different treatments. At present, brain tumors are classified as primary brain tumors and metastatic brain tumors. The former begin in the brain and tend to stay in the brain, the latter begin as a cancer elsewhere in the body and spreading to the brain (Liu *et al*., 2014). The occurrence of brain tumors is mounting quickly, predominantly in the grown-up population weighed against younger population. Brain tumor is a collection of abnormal cells that nurture within the brain or around the brain (Iscan *et al*., 2010). Tumors can straightforwardly wipe out all fit brain cells. It can also obliquely damage strong cells by crowding further parts of the brain and bringing about inflammation, brain swelling and pressure inside the skull (Jaya *et al*., 2009).

In the study, the brain image is efficiently segmented by applying the classification and optimization technique. Here, an improved Artificial Neural Network (ANN) and adaptive genetic algorithm is used. The objective of the paper is segmenting the brain image by utilizing Hybrid SVD based Hilbert Huang Transform (HSHHT). Initially, we select the input image from the BMRI database. Then apply the skull stripping method to the input brain image. After that the proposed method perform the classification with the help of improved artificial neural networks here the weights are optimized by means of adaptive genetic algorithm. After the classification, the normal tissues like White Matter (WM), Grey Matter (GM) and Cerebrospinal Fluid (CSF) are segmented from the normal BMRI image. Abnormal tissues like Tumor and Edema are segmented from the abnormal BMRI images. The abnormal tissue segmentation will be carried out by optimal SVD and HHT based segmentation in which optimization can be done by Binary cuckoo search algorithm.

LITERATURE REVIEW

Literature presents a handful of researches for segmentation and classification of MRI images for abnormality detection and has been a hot topic due to its significant applications. Here, we present a brief review of some of the techniques for medical image segmentation and classification.

Bianchi *et al*. (2014) have proposed an approach that was able to detect mTBI lesions by combining both the high-level context and low-level visual information. The contextual model estimates the progression of the disease using subject information, such as the time since injury and the knowledge about the location of mTBI. The visual model utilizes texture features in MRI along with a probabilistic support vector machine to maximize the discrimination in unimodal MR images. These two models are fused to obtain a final estimate of the locations of the mTBI lesion. The models are tested using a rodent model of repeated mTBI dataset. The experimental results demonstrated that the fusion of both contextual and visual textural features outperforms other state-of-the-art approaches. Clinically, their approach has the potential to benefit both clinicians by speeding diagnosis and patients by improving clinical care.

Kwon *et al*. (2014) have proposed a method for deformable registration of pre-operative and post-recurrence brain MR scans of glioma patients. Performing this type of intra-subject registration was challenging as tumor, resection, recurrence and edema cause large deformations, missing correspondences and inconsistent intensity profiles between the scans. To address this challenging task PORTR a method that explicitly accounts for pathological information was proposed. It segments tumor, resection cavity and recurrence based on models specific to each scan. PORTR then uses the resulting maps to exclude pathological regions from the image-based correspondence term while simultaneously measuring the overlap between the aligned tumor and resection cavity. Embedded into a symmetric registration framework, they determined the optimal solution by taking advantage of both discrete and continuous search methods.

Medical imaging was expensive and very much sophisticated because of proprietary software and expert personalities. Anwar and Iqbal (2013) have proposed an inexpensive, user friendly general-purpose image processing tool and visualization program specifically designed in MATLAB to detect much of the brain disorders as early as possible. The application provides clinical and quantitative analysis of medical images. Minute structural difference of brain gradually results in major disorders such as schizophrenia, Epilepsy, inherited speech and language disorder, Alzheimer's dementia etc. Here the main focusing was given to diagnose the disease related to the brain and its psychic nature (Alzheimer’s disease).

A stochastic model for characterizing tumor texture in brain MR images was proposed by Islam *et al*. (2013). The efficacy of the model was demonstrated in patient-independent brain tumor texture feature extraction and tumor segmentation in Magnetic Resonance Images (MRIs). Due to complex appearance

in MRI, brain tumor texture was formulated using a multiresolution-fractal model known as multi-fractional Brownian motion (mBm). Detailed mathematical derivation for mBm model and corresponding novel algorithm to extract spatially-varying multi-fractal features are proposed. A multifractal feature-based brain tumor segmentation method was developed next. To evaluate efficacy, tumor segmentation performance using proposed multi-fractal feature was compared with that using Gabor like multi-scale texton feature. Furthermore, patient-independent tumor segmentation scheme was proposed by extending the well-known AdaBoost algorithm. The modification of AdaBoost algorithm involves assigning weights to component classifiers based on their ability to classify difficult samples and confidence in such classification. Experimental results for fourteen patients with over three-hundred MRIs showed the efficacy of the proposed technique in automatic segmentation of tumors in brain MRIs.

Zacharaki and Bezerianos (2012) have introduced a semi supervised scheme for abnormality detection and segmentation in medical images. Semi supervised learning does not require pathology modeling and, thus, allows high degree of automation. In abnormality detection, a vector was characterized as anomalous if it does not comply with the probability distribution obtained from normal data. The estimation of the probability density function, however, was usually not feasible due to large data dimensionality. In order to overcome this challenge, they treated every image as a network of locally coherent image partitions (overlapping blocks). They formulated and maximized a strictly concave likelihood function estimating abnormality for each partition and fuse the local estimates into a globally optimal estimate that satisfies the consistency constraints, based on a distributed estimation algorithm. The likelihood function consists of a model and a data term and was formulated as a quadratic programming problem. The method was applied for automatically segmenting brain pathologies, such as simulated brain infarction and dysplasia, as well as real lesions in diabetes patients.

Damianou *et al*. (2009) have investigated Magnetic Resonance Imaging (MRI) for monitoring small and large lesions created by High-Intensity Focused Ultrasound (HIFU) in freshly excised lamb brain and in rabbit brain in vivo. A single-element spherically focused transducer of 5 cm diameter, focusing at 10 cm and operating at 1 MHz was used. A prototype MRI-compatible positioning device that was used to navigate the transducer was described. The effects of HIFU were investigated using T1-W and T2-W fast spin echo (FSE) and fluid-attenuated inversion recovery (FLAIR). T2-W FSE and FLAIR show better anatomical details within the brain than T1-W FSE, but with T1-W FSE, the contrast between lesion and brain was higher for both thermal and bubbly lesions.

Proposed methodology for abnormality detection from brain MRI image: An innovative technique is kick-started to classify the Brain Magnetic Resonance

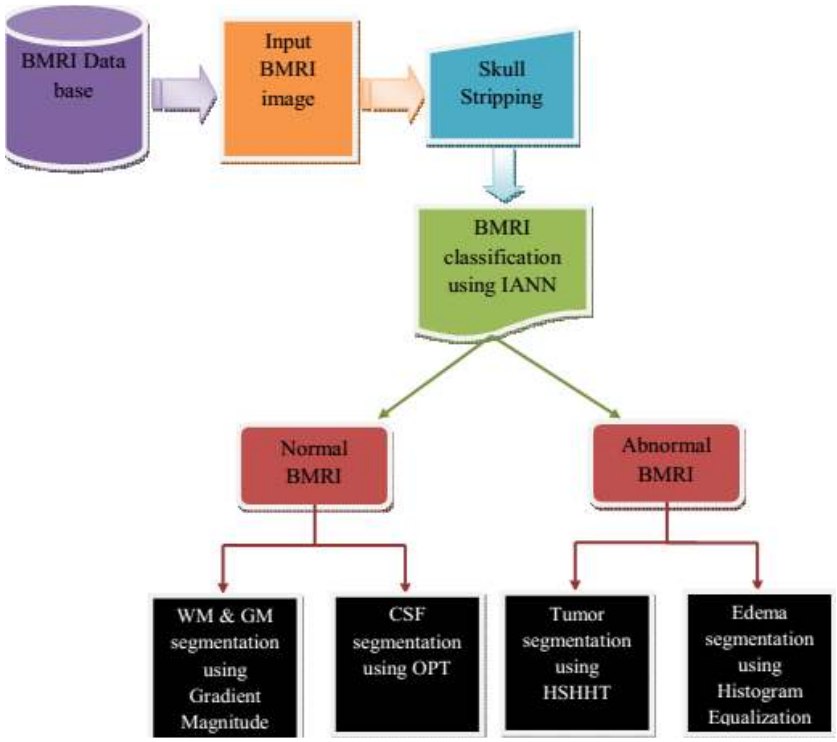


Fig. 1: The block diagram of proposed tissue segmentation

Images and carry out the tissue segmentation. At the outset, the features are extorted from the input images (BI) which are gathered from the BMRI database which include the correlation, covariance and Scale Invariant Feature Transform (SIFT). Thereafter they are furnished to the input of improved artificial neural networks. In our document, the conventional artificial neural network is enhanced by means of adaptive genetic algorithm for weight calculation. The improved neural network is employed to classify the BMRI. Subsequently, the classified abnormal BMRI is initiated on the Hybrid SVD and Hilbert Huang Transform (HSHHT) for segmenting the abnormal tissues like the Tumor and Edema, whereas the normal BMRI tissues like the White Matter (WM), Gray Matter (GM) and Cerebrospinal Fluid (CF) are segmented from the normal BMRI. The structural design of the novel Brain MR Image tissues segmentation method is colorfully illustrated in Fig. 1.

The innovative technique flows through the following three stages:

- Feature extraction
- Classification using IANN with AGA
- Segmentation using HSHHT

Skull stripping: The skull stripping is deployed for the segmentation of brain tissues. The skull, in essence, represents the outer part of the brain surrounding it i.e., after the segregation of its non-cerebral tissues. The stages by which the skull is removed are detailed as follows:

- At first, the size of the image is located and the number of rows and columns are stored in separate variables.
- Thereafter iteration is performed for half of the columns and all the rows.
- Process half of the image to change the white pixels into the black pixels by fixing their gray value as zero.
- The identical steps are performed again for the residual columns and rows.
- In the case of the skull stripping, at first the specified MRI brain image is transformed into gray scale image, followed by a morphological function on in the gray scale image. Thereafter, the brain cortex in the gray scale image is stripped by employing region based binary mask extortion. The preprocessing procedure is carried out in both ordinary images and abnormal images. The consequent image achieved after the skull stripping is labeled as BI_{SS} and is employed for feature extraction.

Feature extraction: The evaluation of the covariance (C_V), correlation (C_R) and SIFT are carried out as per Eq. (1) and (2) furnished below:

$$c_V = \frac{1}{rc}\sum\left(BI(a,b) - \left(\frac{1}{rc}\sum_{a=1}^{r}\sum_{b=1}^{c} BI(a,b)\right)\right) \quad (1)$$

$$c_R = \frac{c_V}{\sqrt{\left(\frac{1}{rc}\sum_{a=1}^{r}\sum_{b=1}^{c}\left(BI(a,b) - \left(\frac{1}{rc}\sum_{a=1}^{r}\sum_{b=1}^{c} BI(a,b)\right)\right)\right)}} \quad (2)$$

where,

r : Number of rows in the given input image
c : Number of column in the given input image

Scale-Invariant Feature Transform (or SIFT) represents a technique in computer vision to identify and depict the local features in images. It is effectively used for extorting the distinctive invariant features from images which can be invariant to image scale and rotation. It comprises the following four phases:

- Scale-space detection
- Key point localization
- Orientation assignment
- Key point descriptor

o In the initial phases i.e., scale-space detection, the Difference-of-Gaussian (DOG) function is effectively employed to locate the potential interest points, which are invariant to scale and orientation. Here, DOG is utilized rather than the Gaussian so as to augment the computation momentum.

o In the subsequent stage i.e., the key point localization phase, the low contrast points are rejected and the edge responses are removed. The Hessian matrix is employed to estimate the principal curvatures and get rid of the key points having a ratio between the principal curvatures exceeding the ratio.

o An orientation histogram was created from the gradient orientations of sample points within an area around the key point with the intention of achieving an orientation assignment.

o In the final stage which is the key point descriptor phase, the local image gradients are evaluated at the preferred scale in the region around each key point. They are then converted into an illustration which permits the noteworthy levels of local shape twist and variation in lighting.

The evaluated correlation, covariance and SIFT features are then furnished to the IANN with AGA classifier to classify the BMRI.

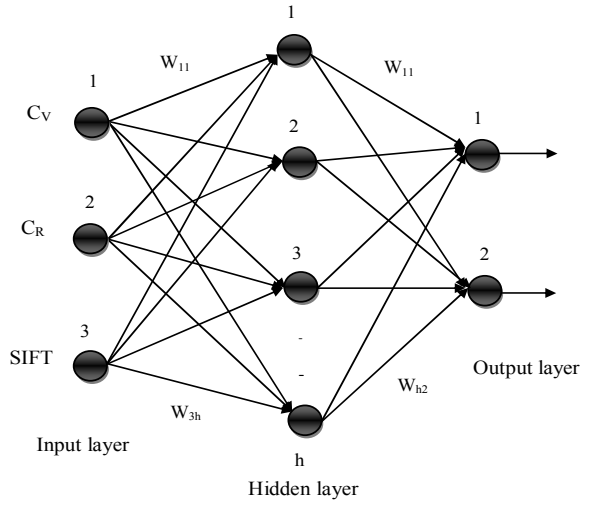


Fig. 2: Structure of artificial neural network

Classification using IANN with AGA: The Improved Artificial Neural Network is utilized to ascertain whether the specified BMRI is abnormal or normal. IANN is trained employing the features like the covariance, correlation and SIFT, which are extracted from each and every image in the BMRI database. The improved artificial neural network is well trained by means of the extorted features. The innovative IANN is home to three input units, n hidden units and one output unit. In our document, the weights are optimized with the help of the adaptive genetic algorithm. The structure of artificial neural network is shown in Fig. 2.

Weight optimization using adaptive genetic algorithm: The innovative Adaptive genetic algorithm is employed to optimize the weights. The conventional genetic algorithm is enhanced with the help of the mutation operator. In this technique, at the outset, the population is generated arbitrarily and two individuals are thereafter chosen in accordance with the fitness. Suppose A possesses fitness higher than that of B, then A will be selected and B ignored. However, they will reproduce to generate one or more offspring. Subsequently, the offspring is mutated arbitrarily. The procedure is carried on till an appropriate solution is arrived at or a specified number of generations have passed, in accordance with the requirements of the user.

Generation of chromosomes: The initial solutions are created arbitrarily and each solution is known as the gene. The individual genes are integrated as chromosomes and it is known as the solution set. The numbers of genes are integrated with the chromosomes and the solution set for the population is generated. The population of genetic algorithm consists of chromosomes and the population size is initialized as permanent. The numbers of solutions are initialized ohm accordance with the standard genetic algorithm. In this case, the initial solutions are known as the weight.

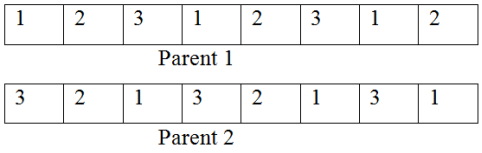


Fig. 3: The parent chromosomes

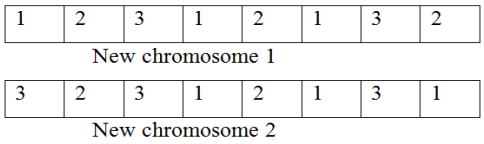


Fig. 4: After the crossover

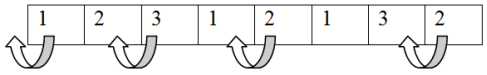


Fig. 5: After the shift the changes within the off-spring

Fitness function: The fitness function is calculated by means of Formula 3 given below:

$$Fitness = \min(sum\ of\ weights) \quad (3)$$

It is evaluated for the initial solution sets of the chromosomes. After the evaluation of the solutions, the cross over and mutation function are applied on the chromosomes of the solutions sets.

Cross over: In cross over, the two parent chromosomes are selected so as to exchange their genes between them. The example given below shows Fig. 3 the parent chromosomes parent 1 and parent 2.

In parent 1 and 2 chromosomes, the bold lettered are kept unchanged in their positions and the residual gene of the chromosomes is swapped between the parent chromosomes. After the crossover, the chromosome appears as shown in Fig. 4.

Mutation: After the crossover, the new chromosome is mutated for enhancing the efficiency of the solution and the bold illustrates the mutated gene of the chromosome. In the innovative mutation, the identical order is chosen within the offspring and it is swapped from its position to other place for yield the most excellent optimal solution. The shift changing mutation technique is employed in the mutation operation and the orders of each chromosome are shifted to left one step and substituted by the new order. After the shift the changes within the off-spring is illustrated as Fig. 5:

Mutation process: From the above the gene of the off spring is shifted one step left and the optimized new solution is getting by the mutation process. The optimal solution is obtained after the mutation function and it shows the final output of the result with their minimal

optimized time and it gives the minimum make span time.

Optimal solution: After the mutation function is over, the new chromosomes are produced for the new solution sets. Subsequently, the fitness value is arrived at for the new solutions. The solution which furnishes the best value is chosen and is treated as the optimal solution. Or else, the above-mentioned steps are repeated for the new solution sets.

Segmentation of tissues: The classified images are utilized to segment the normal and abnormal tissues. In this regard, various techniques are employed to segment the WM, GM, CSF, edema and tumor tissues.

Normal tissue segmentation: The segmentation of normal tissues like the WM, GM and CSF are carried out from the normal BMRI images. Here, the segmentation procedure is carried on in two methods such as the:

- Segmentation of WM and GM using Gradient Technique
- Segmentation of CSF by means of OPT

Segmentation of WM and GM using gradient technique: The gradient technique is employed for segmenting the white matters and gray matters. Here the normal image BI is smoothed with the help of Gaussian convolution filter BI_{SG}. Subsequently, the smoothed image BI_{SG} is subjected to the gradient operation. The gradient of two variables a and b are shown in Eq. (4) below:

$$\nabla BI_{SG}(a,b) = \frac{\partial BI_{SG}}{\partial a}\hat{i} + \frac{\partial BI_{SG}}{\partial b}\hat{j} \quad (4)$$

The gradient values are helpful to mark the current edges in the image which are shown in the following equations:

$$SG = a_{(i)}^2 + b_{(j)}^2 \quad (5)$$

$$E_m = \frac{1}{(1+SG)} \quad (6)$$

Subsequently, the binarization is performed on the edge marked image E_m. In the Binarization process, the value of gray level of every pixel in E_m image is evaluated with the help of a global threshold value. The consequential binarized image after the Binarization procedure is represented as BI_B.

By employing the Morphological Opening and Closing operation, the tiny holes and objects from the image BI_B is eradicated. The WM and GM normal tissues of normal BMRI images are segmented with the help of the intensity values:

$$Intensity = \begin{cases} WM, & if\ BI_{B_i} = 1 \\ GM, & if\ BI_{B_i} = 0 \end{cases} \quad (7)$$

The exacting portion is segmented into White Matter, if the intensity value of the image part is one and then it is deemed as Gray Matter part, if the intensity value is zero and thereafter the images are segmented as per Eq. (7).

Segmentation of CSF by means of OPT: The CSF tissue from the image BI_B is segmented by Orthogonal Polynomial Transform (OPT) by means of Eq. (8) shown below:

$$BI_{CSF} = Sin\left(\frac{BI_{SS(i)}^3}{100}\right)^2 + \left(0.05 * rand\left(|BI_{SS}|\right)\right) \quad (8)$$

Now, the CSF tissue BI_{CSF} from the normal image is segmented effectively. Hence, the normal tissues WM, GM and CSF are segmented from the skull stripped image BI_{ss}.

Abnormal tissue segmentation: The abnormal tissues such as the tumor and edema are segmented by employing HSHHT. In our case, the HSHHT represents the blend of SVD and HHT with binary cuckoo search.

Singular Value Decomposition (SVD): To enhance the image we employ the singular value decomposition in our innovative technique. At the outset, the classified tissue image is furnished to the singular value decomposition. With a view to augment the strength of the image, the Singular Value Decomposition (SVD) is applied in our epoch-making technique, which decays a matrix in three matrices P, Q, R. The equation of the matrices is shown below by means of formula 9:

$$O_m = PQR^T \quad (9)$$

where, O_m represents the original matrix, Q symbolizes the diagonal matrix of the eigenvalues of O_m. The captioned diagonal values are also known as the singular values. P signifies the orthogonal matrices and the transpose of an orthogonal matrix R. P columns are known as the left singular vector and the Q columns are labeled as the right singular vectors of O_m.

Hilbert Huang transform: The vital segment of the HHT is the Empirical Mode Decomposition (EMD) technique, which is highly essential to transform any specified data into a compilation of Intrinsic Mode Functions (IMF). The two criteria will fulfill the IMFs,

as modes; in order that that they will be identical to a generalized Fourier decomposition:

- Isn the entire data set, the number of extrema and the number of zero crossings have to be equivalent or have a maximum divergence of one
- At any point of time, the mean value of the envelope defined by the local maxima and the envelope defined by the local minima has to be zero. The following algorithm furnishes the modus operandi for the extortion of IMF from the signal.

Step 1: Locate all extrema
Step 2: With a view to ascertain the upper and lower envelope, interpolate between the maxima and link them by a cupic sp line curve. So is the case with the minima.
Step 3: Estimate the average of upper and lower envelope
Step 4: Locate the divergence from their mean value

The stopping criteria are very significant for the evaluation of IMFs, which are capable of affecting the number of IMFs components. The normalized squared difference between two successive sifting iterates $sd_{pre}(t)$ and $sd_{cur}(t)$, that is:

$$SD = \sum_{t=0}^{T}\left[\frac{\left|\left(sd_{pre}(t) - sd_{cur}(t)\right)\right|^2}{sd_{pre}(t)}\right] \quad (10)$$

where, T characterizes the total number of samples in the original series and the empirical value of SD employs a set within the range (0.2-0.3). The procedure is repeated till the entire IMFs are extorted and no oscillations whatsoever are carried in the residual signal, as demonstrated by a deficient number of extrema. In accordance with the SD, at last the tumor part is segmented from the abnormal BMRI. The physical choice of the SD range is likely to result in improper segmentation and therefore the Binary Cuckoo Search (BCS) is employed to forecast the SD range which paves the way for attaining amazing accuracy while segmenting the tumor tissues.

Selecting SD range with the help of BCS: In this document the binary cuckoo search algorithm is employed to optimally choose the SD range, which is furnished as input to the BCS algorithm. The overall processes of the binary cuckoo search are detailed as follows.

Steps of binary cuckoo search:
Initialization: The SD range represents the input of BCS algorithm. At the outset, the population of host nest is arbitrarily initialized.

Fitness evaluation: The cuckoo is estimated by means of the objective function for locating the quality of the solutions. In accordance with Eq. (11) shown below, the fitness function is estimated and thereafter the best one is chosen:

$$fitness = \max\ po\ \text{int} \quad (11)$$

From the abnormal BMRI, a region is selected and while applying the SD range, the number of points in that region is counted. The SD range at which maximum points attained are selected as the final SD range.

Updation: Improve the initial solution by means of the levy flights. The supremacy of the new solution is assessed and a nest is chosen randomly. If the chosen nest is superior to the old solutions, it is substituted by the new solution (Cuckoo). Or else, the prior solution is deemed as the best solution. The levy flights used for the cuckoo search algorithm are given by Eq. (12) shown below:

$$N_i^* = N_i^{(t+1)} = N_i^{(t)} + \alpha \oplus Levy\,(n) \quad (12)$$

In the binary cuckoo search the search space is shaped as a d dimensional Boolean lattice, in which the solutions are rationalized across the corners of hypercube. This is performed as per the following Eq. (13):

$$S\left(N_i^{(t+1)}\right) = \frac{1}{1+e^{-N_i^{(t+1)}}} \quad (13)$$

$$N_i^{t+1} = \begin{cases} 1 & if\ S(N_i^{t+1}) > \delta \\ 0 & otherwise \end{cases} \quad (14)$$

Reject worst nest: The worst nests are discarded here. Subsequently in accordance with their fitness function the best solutions are ranked. Thereafter the best solutions are identified and treated as optimal solutions.

Stopping criterion: Until the maximum iteration accomplishes this process is replicated. The SD range achieved at last is used to segment the tumor part separately from the abnormal image. When the segmentation is completed, the segmented tumor part (s_t(a, b)) is employed to segment the edema tissues along with the abnormal image.

Segmenting edema tissues: It is from the abnormal image that the edema tissues are segmented. At the outset, histogram equalization procedure is performed

in the abnormal image in which the quality of the abnormal image is improved. Subsequently the improved image is changed into indexed image by means of the multilevel thresholding. Later on, the indexed image is transformed into HSV (Hue, Saturation and Value) color model. Thereafter, the threshold procedure is carried out. Now we define distinct threshold value for the HSV. To choose the pixel each pixel in the image is assessed and contrasted with the threshold value. Then, the distance is decided between the coordinates of center pixels of the regions. Subsequently, the resulting value is checked with the threshold value and based on these edema regions coordinate values are attained. Thereafter, the morphological dilation and closing operations are carried out in the edema region image.

EXPERIMENTAL RESULTS AND DISCUSSION

The suggested brain MRI image classification has been executed in the working platform of MATLAB. The suggested system has been evaluated with different query images and suitable images are classified from the image database. The image database enclosed number of MRI images accumulated in the JPEG format. The suggested method is based on the feature extraction and next further classification technique applying the neural network integrated with the adaptive genetic algorithm.

The query image are subjected to classification from the images in the image database, to accurate the intensity levels of the input image with the intensity levels of the images in the database. The output objects extracted from the input query image is specified in the beneath figures.

The input image that is given to the proposed method is first subjected to feature extraction and then classified into normal or abnormal images based on the trained data. Once the classification is completed the further process of segmenting the corresponding normal and abnormal images into various brain matters and diseases respectively are performed. The various segmentation algorithms carried out in the process are gradient based technique for normal tissue segmentation and optimal SVD-HHT for abnormal tissue classification like edema and tumor. Table 1 given below shows the classification of the images into normal and abnormal images.

Once the images are being classified into normal and abnormal images, the respective images are then subjected to segmentation process for segmenting the normal and abnormal tissues. The normal tissues like White Matter (WM), Grey Matter (GM) and Cerebrospinal Fluid (CSF) are segmented from the normal Brain MRI image. Abnormal tissues like Tumor and Edema are segmented from the abnormal Brain

Table 1: Adaptive neural network classifier output

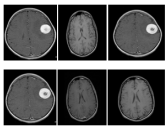
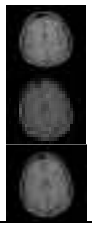
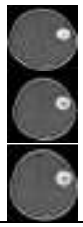
Input MRI images	Modified neural network classifier outcome	
	Normal image	Abnormal image
		

Table 2: Segmented White Matter (WM), Grey Matter (GM) and Cerebrospinal Fluid (CSF) from normal brain MRI images

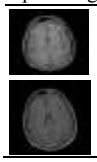
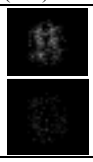
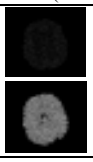
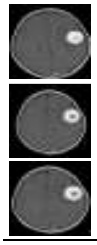
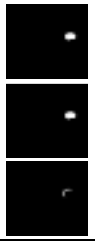
Input images	White matter (WF)	Grey Matter (GM)	Cerebrospinal Fluid (CSF)
			

Table 3: Segmented abnormal tissues like tumor and edema from abnormal images

Input images	Edema	Tumor
		

MRI images. The abnormal tissue segmentation will be carried out by optimal SVD and HHT based segmentation in which optimization can be done by Binary cuckoo search algorithm.

Table 2 shows the normal tissue segmentation from normal brain MRI images like White Matter (WM), Grey Matter (GM) and Cerebrospinal Fluid (CSF).

Table 3 shows the tumor and edema tissues segmented from the abnormal brain MRI images. The segmentation is performed in the abnormal MRI images in order to find the disorders that are present in the abnormal images.

Performance evaluation: The performance evaluation of the proposed methodology is calculated by measuring the accuracy, sensitivity and specificity of the method. The sensitivity, specificity and accuracy values are calculated using the expression given below:

$$Sensitivity = (TP/(TP+FN)) \quad (15)$$

$$Specificity = (TN/(FP+TN)) \quad (16)$$

$$Accuracy = (TP+TN/(TP+FN+FP+TN)) \quad (17)$$

Table 4: Sensitivity, specificity and accuracy for number of input images

Evaluation metrics		Proposed adaptive neural network classifier	Neural network classifier
Input Brain MRI dataset	TP	3	2
	TN	5	5
	FP	0	0
	FN	0	1
	Specificity	1	0.666667
	Sensitivity	1	1
	Accuracy	1	0.875

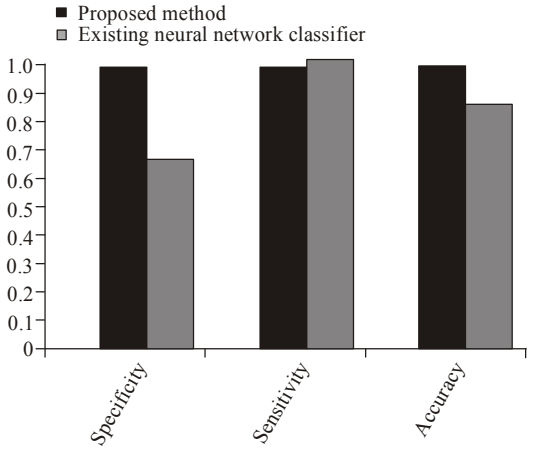


Fig. 6: Graphical representation for comparison of proposed and existing Brain MRI abnormality classification method

where,

True Positive (TP) : The number of images that are correctly classified

True Negative (TN) : The number of irrelevant images that are correctly classified

False Positive (FP) : The number of relevant images that are incorrectly classified as irrelevant images

False Negative (FN) : The number of irrelevant images that are incorrectly classified as relevant image

Table 4 given shows the accuracy, sensitivity and specificity values obtained using the proposed method of adaptive neural network classifier and existing normal neural network classifier.

From the Table 4 it is clear that our proposed method of Brain MRI image classification and segmentation of tissues are more efficient that the existing method of abnormality classification.

Figure 6 given shows the comparison graph of proposed and the existing techniques of MRI abnormality detection.

CONCLUSION

Brain MRI image classification and tissue segmentation technique is proposed in this study. Improved artificial neural network classifier is used to classify the brain MRI images. To segment the normal and abnormal tissues various techniques used here WM and GM by Gradient Magnitude; CSF by OPT; tumor and edema by HSHHT and HE. HSHHT is the combination of singular value decomposition and Hilbert huang transform with binary cuckoo search algorithm. The performance of the proposed technique is evaluated in terms of accuracy, sensitivity and specificity. The implementation result shows that the efficiency of proposed tissue segmentation technique is better when compared with other related techniques.

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