Deep learning based enhanced tumor segmentation approach for MR brain images

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HIGHLIGHTS

- A Growing Deep Convolutional Network (GCNN) is proposed for Magnetic Resonance brain image segmentation.
- The proposed approach is different from the conventional deep learning approach.
- Conventional CNN is also implemented for comparative analysis.
- An extensive quantitative analysis is performed in terms of accuracy measures to validate the superior nature of the proposed approach.

ARTICLE INFO

ABSTRACT

Automation in medical industry has become one of the necessities in today's medical scenario. Radiologists/physicians need such automation techniques for accurate diagnosis and treatment planning. Automatic segmentation of tumor portion from Magnetic Resonance (MR) brain images is a challenging task. Several methodologies have been developed with an objective to enhance the segmentation efficiency of the automated system. However, there is always scope for improvement in the segmentation process of medical image analysis. In this work, deep learning-based approach is proposed for brain tumor image segmentation. The proposed method includes the concept of Stationary Wavelet Transform (SWT) and new Growing Convolution Neural Network (GCNN). The significant objective of this work is to enhance the accuracy of the conventional system. A comparative analysis with Support Vector Machine (SVM) and Convolution Neural Network (CNN) is carried out in this work. The experimental results prove that the proposed technique has outperformed SVM and CNN in terms of accuracy, PSNR, MSE and other performance parameters.

1. Introduction

In this era of technology the clinical experts are able to provide more effective health care to the patients by using e-health care systems. There are many problem domains in the medical field where e-health care system are beneficial. In this study we address the issues of brain tumor partition from MRI images. Brian is the utmost complex part of human body that operates with the collaboration of billions of cells [1]. Brain tumor is an uncontrolled condition of brain that leads to the forming of abnormal group of cells in brain or nearby it. These formation of abnormal cells abrupt the normal processing of the brain and have adverse effects on patient's health [2]. To provide the solution of this problem image processing is very beneficial for effective results. To extract the infected region from the brain MRI image the Segmentation is used. To perform segmentation of abnormal cells from normal cells (like; gray matter, white matter and cerebrospinal fluid) many approaches have been used. Brain MRI images are the best resources that researcher used to detect the brain tumor and track its progress of the treatment process. By the use of technology and availability of MRI images the researchers and the experts get huge amount of information to take the decision related to brain tumor [3]. From high resolution MRI images it is easy to find the information related to brain structure and the organization of cells in brain and from where abnormalities in the formation of tissues can be easily detectable [3]. To detect the human brain organization,

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the effective imaging methods are used all over the world such as single model techniques and multi model techniques which provide the vast information related to brain tissues formations. From these images the doctors and experts manually segment the infected region from the non-infected part. The segmentation is the process of separating the image into sections by based on the pixels having similar properties. But the manual segmentation of abnormal brain tissues from the normal tissues consume huge time and can produces inaccurate results. To provide the solution for this and to help the clinical experts for segmentation of brain tumor region from MRI images we produced a new computer aided approach to automate this process with the help of deep learning algorithms. In this paper we have proposed a new approach that solve the issue for the medical image processing to detect the brain tumor with more accuracy. In the previous works for the brain tumor detection manual process is required to some extant for the segmentation but, in this paper a complete automatic approach is proposed. The GCNN will help to process the data in iteration and the growing layers will produced more effective segmentation.

In this paper, an improved and efficient brain tumor segmentation has been performed which also successfully accomplished the following objectives:

- The approach will perform multiple operations as segmentation, feature extraction automatically
- This method has performed better than the others
- This method performed equally effective and large dataset and complex structures

The rest of paper has been organized as follow: Section 2 gives the detail analysis of the planned approach. In Section 3 the result of simulation are given and the performance of proposed approach is evaluated. Section 4 shows the analysis and drawbacks of the study from the comparative analysis and Section 5 gives the conclusion and future scope of the work.

2. Related work

Here, the survey of most widely used techniques for this process by the different researcher is mentioned. Neural network is used in [4] for brain tumor identification and classification. This method claims the 83% accuracy for segmentation. Also, separate quality rates have been generated for WM, GM, CSF and tumor portion. In [5] SVM is used for automatic segmentation of brain tumor from MRI images. In this work Fast Fourier Transform is used for feature extraction and to reduce the size for feature MRMR (Minimal-Redundancy–Maximal-Relevance) is implemented. This approach produced the higher accuracy near to 98%. In brain tumor segmentation the MRI image is subtracted in to two parts. One section consist of normal brain cells and the other have the abnormal (tumor cells) [6,7]. A strategy is planned in [8] to extract brain tumor region by using hybridization of FCM, Seed Region Growing (SRG) and to differentiate the white matter cells from gray matter Jaccard Similarity Coefficient method is used. At the noise level of 3% and 9% the accuracy of segmentation score is achieved by this method is 90%. A new method of segmentation in [9] is given by using neural network and wavelets which produced the more accurate extraction of CSF, gray matter and white matters. [10–12] Address the various protocols related to image processing. They use texture features, wavelet transform and Support vector Machine to handle non-linearity of the dataset and to segment the dynamic contrast enhanced images. As compare to first-order statistical characteristics the approach mentioned in [10] produced more effective predictions and also enhance the clinical factors, tumor volume, and different stages of tumor. Principal Component Analysis (PCA)

and SV with hybridization of Radial Basis Function (RBF) [13] are used to segment the brain tumor. By using this method the accuracy is achieved up to 94% and the error rate is calculated up to 7.5%. Texture-primitive properties are used in [14] for segmentation. In this work the Artificial Neural Network (ANN) is used to automate the process and they claim for highest accuracy. In [15] to create bias region estimation and for accurate classification local fuzzy with spatial information are used, which also help to define the key elements of the segmentation. For performance analysis, Jaccard similarity index is used and the result is calculated which shows that 83% to 95% accuracy can be obtained by using this approach. [16] have conferred a medical image segmentation technique supported active contour model to touch upon the matter of intensity in homogeneities in image segmentation. In [17] a method is planned for automatic feature extraction for neoplasm detection supported Gaussian mixture model (GMM) victimization MRI Images during this technique, victimization principal part analysis (PCA) and ripple primarily based options, the performance of the GMM feature extraction is increased. Associate in Nursing accuracy of 97% for the T1-weighted and T2-weighted and ninety four. 11% for FLAIR-weighted MRI dataset are obtained. [10] Have planned a method of utmost learning machine for classification of neoplasm from MRI dataset. This technique obtained Associate in Nursing accuracy of 93%, the sensitivity of 91%, and specificity of 97%. A multiclass neoplasm classification, segmentation has conferred in [18], and have extraction performed employing a dataset of 428 MRI pictures. During this technique, authors used ANN and so PCA-ANN and discovered the increment in classification accuracy from 77 to 91%. In [19] harmony-Crow Search (HCS) optimization and SVNN are used on BRATS database to classify the brain tumor. In this method for segmentation and feature extraction Bayesian fuzzy is used. Here the level of brain tumor based on the features extracted by Bayesian and the theoretical measures. The accuracy of this method is 93%. An automatic data augmentation [1] approach based on generative adversarial networks is used to train the classifier for the annotated samples. In this method coarse-to-fine generator is used to extract the manifold of the dataset and produced generic augmented data. In [20] three techniques of computer vision have been used for MR image processing to detect the ROI based on texture and HOG features. Based on this dataset of feature ANN has been used to automatically segment the ROI form the whole image. In [21] brain tumor detection is performed in three stages; first feature extraction is done based on texture features from the gray scale images. In second phase K-means is used to mark the ROI and then used ANN for the training and classification process. In [22] a new Analysis of Human Tissue Densities (AHTD) is used to extract the features through human tissue densities from brain images. In Hounsfield sector Radiological densities of human tissues are used to manage the extraction process.

From the above mention review it has been cleared that some methods are design only of segmentation, some for solely for feature extraction and some are for classification only. The techniques that have been used for multi operations as a single unit [23] are not effective for large dataset and complex structures because of SVM and also if SVM is used on large number of classes the computational cost will be increased.

3. Proposed approach

In this section detail discussion of proposed approach has been given and shows how hybridization of different methods segments the MRI images effectively. The previously existing techniques are basically solely perform different operations only and those that perform multiple operation jointly are not effective on large dataset and on complex structured problems.
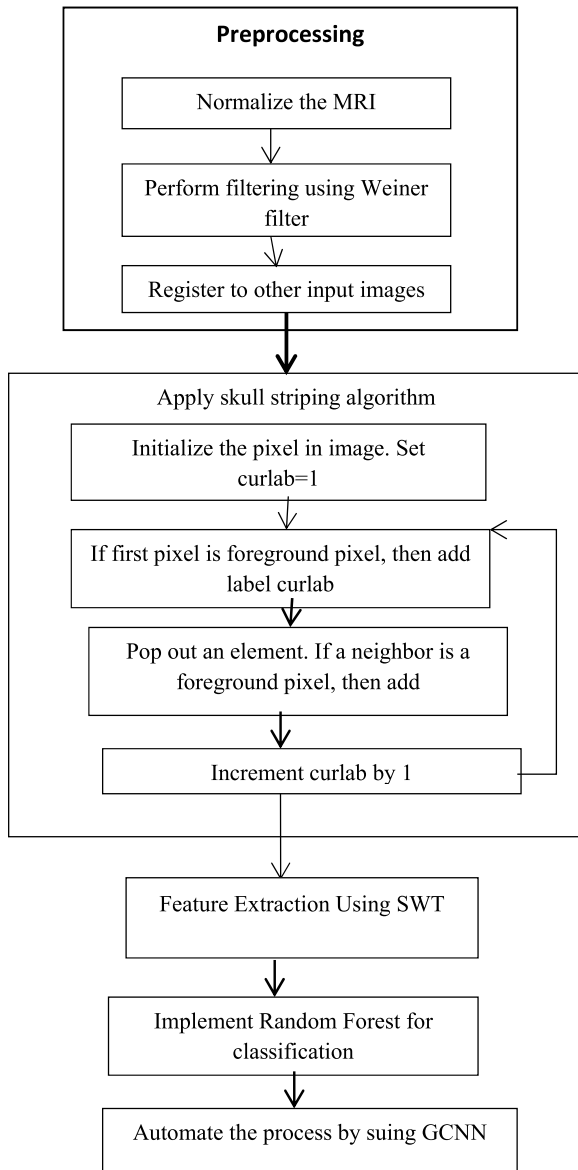
Preprocessing

Normalize the MRI

↓

Perform filtering using Weiner filter

↓

Register to other input images

⬇

Apply skull striping algorithm

Initialize the pixel in image. Set curlab=1

↓

If first pixel is foreground pixel, then add label curlab

↓

Pop out an element. If a neighbor is a foreground pixel, then add

↓

Increment curlab by 1

↓

Feature Extraction Using SWT

↓

Implement Random Forest for classification

↓

Automate the process by suing GCNN

Fig. 3.1. Flow graph of proposed approach.

Therefore, an algorithm that fulfills all requirements has been proposed. In Fig. 3.1 the flow chart of the proposed approach has been shown.

In this proposed methodology, the input image is pre-processed before the actual segmentation. In the first stage, normalization of the input image is carried out to prepare the image for further processing. The wiener filter is applied for noise removal and to process the blurred images. In the second stage, skull striping is performed. A new approach for skull removal from the MRI image is performed using traversal graph method. It is a two-phase approach. After finding the ROI, feature extraction is performed using SWT. SWT perform better than the Fourier methods because wavelets can be used for the data having discontinuities and spikes. After this stage GCNN is used to train and classify the normal and abnormal data.

3.1. Preprocessing

In this research work the input image is first preprocessed to remove the anomalies from image and make it ready for further
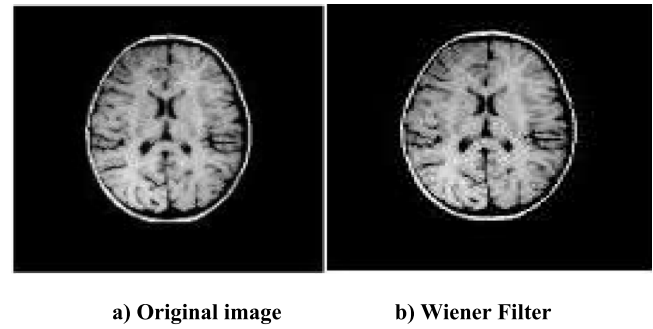

a) **Original image**   b) **Wiener Filter**

Fig. 3.1.1. Output image of wiener filter.

operations. In this preliminary stage there are three steps to be followed as mentioned below:

Step 1: Normalization

Normalization is the first step of this research work. It is basically used normalize the image based on the pixel's intensity values. Normalization of image is the process of removing illumination and the other factors from the MRI images that arrives due to the weather condition at the time of image is being captured. In this approach for normalization selected and estimated background (SEB) method is used [24]. In this to compute the normalize image the best fitting linear line in every neighborhoods. By using least square we compute the best suited line for each pixel based on the SEB values of the neighbors of that pixel. From that linear line related to that pixel the approximated value for that position is computed. If it is not straight line as final approximation of the background then the line portion is go through every point on the curve at the parallel pixel location form at the enclosure of that approximation curve [24].

Step 2: Noise Removal

In this approach Weiner filter is implemented to eliminate noise from the normalized image. Anisotropic filter can also be used [25] but as compare to Weiner filter it proved low PSNR value (as per Figs. 3.1.1 and 3.1.2). Weiner filter smooth the crisp edges and protect the inner details of the image. The reverse sifting is a reclamation procedure for deconvolution, i.e., when the picture is obscured by a realized lowpass channel, it is conceivable to recuperate the picture by backwards separating or summed up converse separating. The methodology of diminishing one corruption at once enables us to build up a rebuilding calculation for each kind of debasement and just consolidate them. The Wiener sifting executes an ideal tradeoff between backwards separating and clamor smoothing. It expels the added substance clamor and alters the obscuring at the same time. The Wiener separating is ideal for the mean square error. The methodology depends on a stochastic structure.

Step 3: Conversion of Gray image to Binary Image

Thresholding is the one of the simplest and important way of pixel-based segmentation. In its simplest case, it is used for gray scale conversion to binary image. A threshold value a is chosen for segmentation. The pixels have the intensity value low then the threshold value a is converted to black and the pixels having intensity value higher than threshold value a are converted to white. For this, Otsu's method is used to choose threshold value and the gray image is converted to binary image. Converted image is achieved as follow:

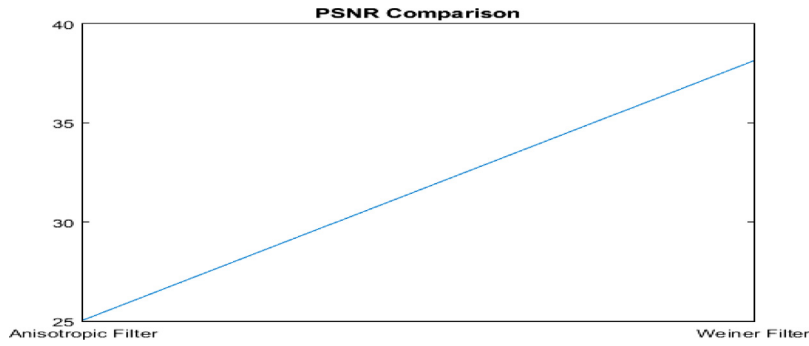$$a_b^2(tv) = b_0(tv)\, a_0^2(tv) + y_1(tv) a_1^2(tv) \qquad (1)$$

Fig. 3.1.2. Performance comparison of Weiner and anisotropic filters based on PSNR values.

Where,

b_0 and b_1 are the probabilities of the two classes that are divided by a threshold value tv

a_0^2 and a_1^2 are the variances of these two classes

Find maximum value of $a_b^2(tv)$ where,

$$b_0(tv) = \sum_{j=0}^{tv-1} x(j) \qquad (2)$$

$$b_1(tv) = \sum_{j=tv}^{L-1} x(j) \qquad (3)$$

Where,

$b_0(tv)$ and $b_1(tv)$ are calculated from L histogram.

3.2. Skull stripping

Skull stripping is a crucial stage in brain tumor segmentation. It separate skull, fat, skin and the section of brain that are not region of interest. It subtracts the additional portion from the brain to simplify and effective the segmentation process. The skull stripping algorithm by using morphological operations [25] that, produced weak skull stripping and more not effective when used for DICOM images. In this paper blob detection and labeling method are used for the purpose of skull striping.

The region in an image in which all the pixels or points have the same or approximately the same properties is known as a blob. In a blob, all the points are considered to be same in some manner and different from the surroundings. The main region of using blob is that, it provides better results and helps to provide information about regions in an image more accurately than edge detector and corner detector. There are many applications of blob detectors in the area of image processing. It includes:

- Region of interest evaluation for further processing.
- Object recognition and object tracking.
- Peak detection with application to segmentation in histogram analysis.
- Texture analysis and texture recognition.
- Stereo matching.
- Ridge detection, etc.

Labeling method is an algorithm that is used in graph theory. It is used to label the connected components (or blobs) on the basis of some parameters. It is used to identify the connected regions in an image. It is used to label the regions in an image that are connected physically. According to this algorithm, each pixel is given some value. The pixels having same value are labeled within the same region.

The algorithm consists of two passes: one component at a time and second pass. These are as follows:

One component at a time

This algorithm is very easy to implement and it is also speedy. The algorithm is based on traversal of graph method. According to this, on finding the very initial pixel of a cohere region, the whole pixels of that cohere region are labeled first before moving forward to the further pixel in an image. For carrying out this task, a linked list is also formed that keeps track of all the pixels and their neighbors. This algorithm assumes image to be a binary image having pixels of foreground and background. The algorithm is as follows:

Algorithm: Skull Stripping

Begin

Step1: Initialize Image I_{ij} and Q[n]

Step2: Set current label to 1   i.e. curlab=1

Step 3: if(I_{ij} == foreground && != labeled)

        {

            for(i=2, i<n, i++)

             labeled= curlab   // labeling of
             pixel after first pixel.

             I_{ij}=Q_{i-1}

        }

        else (I_{ij}== background)

Step 4: for all Q[n]

    Implement breath first search or depth first
    search algorithm (to extract neighbor of Q[n])

    For(k=0, k=n, k++)

      if (Q_{k+1}= foreground&& Q_{k+1}!= labeled)

        Set Q_{k+1}= curlab

      else (Q_k== background)

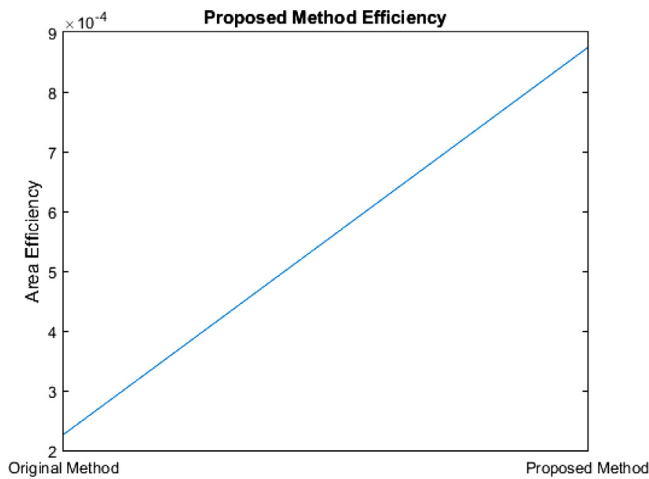Step 4: apply step 3 for all pixels in the Image

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Fig. 3.3. Proposed methods and the existing method compare on the base of efficiency.

The above algorithm only checks the foreground pixels and their neighbors. It does not go for the background pixels.

Two Pass

This algorithm is also simple and easily implementable. As its name suggests, it iterates through two passes. During 1st pass, the provisory tags are assigned to pixels and their parallels are recorded. And during the 2nd pass, provisory tag is restored by the minimal tag of its equivalent class. The labels of the neighboring pixels are checked by carrying connectivity checks. The connectivity is assumed to be 4 or 8. The performance of the existing method is much better than existing method as shown in Fig. 3.3. The following conditions are checked assuming the connectivity of 4:

- Does the pixel to the left (west) have exactly the same value as the running pixel?

  – Yes – we are in the same region. Then the same label is ascribed to the running pixel.
  – No – look forward to the next condition.

- Do the pixels to the north and the west direction of the running pixel have the value identical to the value of the running pixel but they do not have the same label?

  – Yes – the running pixel is ascribed the minimum of the label of the north and west pixel. Then their equivalence association is also recorded.
  – No – look forward to the next condition.

- Does the pixel to the left (west) have a distinguishable value and the pixel to the north have an identical value as that of the running pixel?

  – Yes – the label of the north pixel is ascribed to the running pixel.
  – No – look forward to the next condition.

- Does the pixel to the north and west of the running pixel have the distinguishable values than the value of the running pixel?

  – Yes – new label id is created. This new label id is then ascribed to the running pixel.

3.3. Feature extraction

SWT is implemented to find features from an input image for the purpose of segmentation. Wavelets are used to divide data into different frequency components. They are better than the Fourier methods because wavelets can be used for the data having discontinuities and spikes. Discrete Wavelet Transform (DWT) infected from the scarcity of translation-invariance. SWT surmount the problem of DWT by removing the up and down samplers in the DWT. We calculated the coefficients up-to second order. We also overburdened four features like; energy, entropy, mean absolute deviation and SD (standard deviation). The following features are extracted by the proposed method as shown in Table 3.3.1 Energy:

3.4. Segmentation

After the feature extraction the processed image will be segmented into infected part and non-infected part. In this experiment we use Random Forest classifier for classifying the feature to their respective classes [26]. Random forest is an ensemble classifier that is suits a number of decision trees on different subsamples of the dataset. Random forest will also perform better than other classifiers as there is no need to mention the number of classes in prior it sleek random segment centers. Once the features are classified to automate the process, we use deep learning method Growing Convolution Neural Network (GCNN) [27]. It permits to encode properties from inputs, improve the next function, and reduce the number of parameters for the network with complex domains. Without any change of the organization of the input GCNN trained for different task by using generic features. Beside all the similarities, the difference between other NN and GCNN is the ability of dynamically expansion of their network depends on the rules and instruction used for expansion. First, the count of different layers like, CONV, RELU, &amp, POOL needs to be defined. When network grow to form layers, the growing algorithm will be implemented to define the set of feasible stages and to also mention the action to be performed in the circumstances when these stages are present. After that the network will be expand automatically in interactive manner, with the back propagation available on fixed edges and nodes of different layers. The accentuate hypothesis state that the network will continue to be trained for training dataset and the feedback computed from backpropagation for the further group of filters until it reached to the predefined threshold value for accuracy or if the accuracy is not further improving. Until the overall error of the network focalizes to the minimal value the weights of the edges will be continue to be updated. The training function will be lingered to expand as per the growing algorithm in the case when the error confluence speed turns to less than a threshold value. As the result of this the GCNN network will not be overworked before the segmentation start and it also makes the network topology dynamic in nature. The initial defined layer and architecture when reach to the specific point the next layers are included based on the expansion rules mentioned in the algorithm, until the first-class scores are not evaluated for each image of input matrix the program execution is right. After that for forming of feature map will take place for next stage which will be done by merging of kernel matrices of the previous layers [28].

4. Simulated results

The table 1 shows the algorithmic approach of complete methodology. The database is used of BRAINIX medical images. This methodology is compared with SVM (Support Vector Machine), CNN (Convolution Neural Network), SOM (Self Organizing Map) and Genetic Algorithms through quantitative evaluation performance metrics.

Table 3.3.1
Feature extracted by using the planned approach for some of images.

Image number	Energy	Entropy	Mean	Standard deviation	Homogeneity	Contrast	Correlation
Image_1	12.84	0.74	7.58	42.99	0.9153	0.2714	0.9756
Image_2	15.47	1.93	10.71	48.12	0.8533	0.4732	0.9558
Image_3	55.98	3.12	37.40	76.57	0.9423	0.2856	0.9576
Image_4	9.12	0.52	7.84	37.46	0.8972	0.3669	0.97683
Image_5	31.17	2.19	12.90	36.81	0.8974	0.3241	0.9845

Algorithm: Proposed Algorithm

Step 1: Input MR Image
Step 2: Normalize the MR image(as per equation 4)

$$I_n = \frac{I}{\max(I)}$$

Equation 4

Step 3: Apply thresholding

$$\sigma_w^2(t) = w_0(t)\sigma_0^2(t) + w_1(t)\sigma_0^2(t)$$

Equation 5

Find maximum value of $\sigma_w^2(t)$ (as per equation 5)where,

$$w_0(t) = \sum_{i=0}^{t-1} p(i)$$
$$w_1(t) = \sum_{i=t}^{L-1} p(i)$$

Equation 6

Step 4: Strip the skull and other irrelevant tissues using proposed skull stripping method based on blob detection and labeling method.

```
{
 Initialize pixel;
 Set curlab=1;
 If
  {
  1st pixel=foreground;
  Then
   {label=curlab};
  }
 Pop an element
  {
  If
  {neighbor=foreground};
  Then
   {label=curlab};
  }
Curlab ++;
 }
```
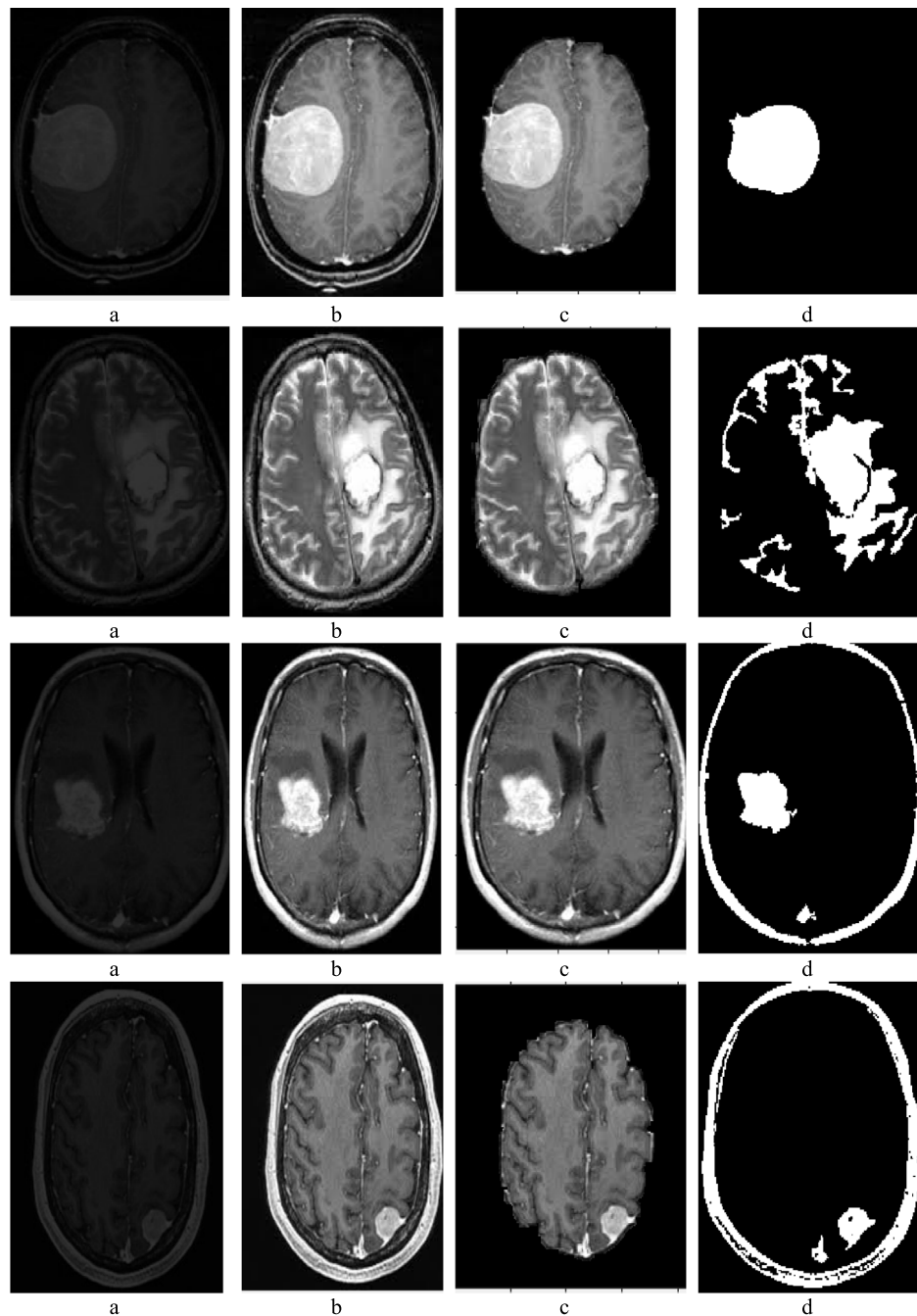
Step 5: Apply filtering using Weiner filter.
Step 6: Apply stationary wavelet transform to extract features from an image.
Step 7: Combine and normalize the obtained features.
Step 8: Train GCNN by using random Forest for Segmentation

Fig. 4.1.1. (a) Input original image, (b) binary conversion of inputted image using threshold, (c) Skull stripping image, (d) Segmented image (the dark white shows the infected area).

4.1. Qualitative analysis

From the survey, it has been founded that K-Nearest Neighbor (K-NN) [29] may have low execution-time performance in case when the training dataset is extensive as long as whole experiment is performed at run-time, k-NN is very receptive to inappropriate or duplicate properties because all properties devote to the similarity and thus to the segmentation and which can be alleviate by attentive selection of features or assigning the weights to them. Despite of the training time of SVM [30] is very high but the issue of patient oriented learning and storage must be caused as the drawback of SVM based approach. The primary drawback of the SOM [28] is that the amount of neural entities in the competitive layer required being relatively equivalent to the count of the groups required in the classified image. One issue of SOM application, mainly to navies' users, would be the selection of various tunable parameters, that may be hinder the potential users from going further SOM applications. One of the drawbacks of the genetic algorithms [31] is that it purely reckon on the fitness function. The planned hypothesis will effectively solve the problems of above mention algorithms and produced results with more accuracy. Fig. 4.1.1 show the results of proposed approach.

4.2. Quantitative analysis

To comparative analysis between the proposed methodology and the techniques mentions above various quantitative performance measures are used. TP (True Positive) is the precise

Table 4.2.1
Performance metrics 1 for comparison.

Methods	TP	FP	TN	FN	Precision	Recall
K-NN [29]	0.876	1.214	0.854	1.344	0.4191	0.3946
SOM [28]	0.912	1.012	0.892	1.121	0.4740	0.4486
SVM [30]	0.891	1.024	0.912	0.97	0.4653	0.4788
Genetic algorithm [31]	0.913	0.184	0.924	0.174	0.8323	0.8399
CNN [32]	0.952	0.144	0.945	0.184	0.8686	0.8380
GCNN	1	0.012	0.984	0.018	0.9881	0.9823
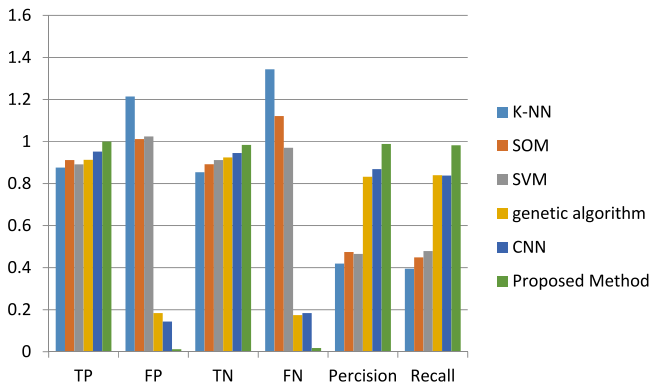
Fig. 4.2.1. Graphical comparison on the basis of parameters mention in Table X1.

Table 4.2.2
Performance metrics 1 for comparison.

Methods	MSE	PSNR	SSIM
K-NN	0.23	72.1	0.87
SOM	0.256	73.5	0.891
SVM	0.021	74.2	0.898
Genetic algorithm	0.045	88.4	0.941
CNN	0.012	94.2	0.961
GCNN	0.001	96.64	0.986

prediction of positive data, TN (True negative) is the precise prognosis of negative values, FP (False Positive) is the inaccurate prediction of positive data and FN (False Negative) is the incorrect prediction of negative data are computed. Based on these four values specificity, sensitivity and accuracy is also calculated. Moreover some other parameters are also used to compare the performance like, PSNR, MSE, SSIM, Disc score.

Table 4.2.1 shows the TP, FP, TN, FN , precision and recall values of different methods.

Fig. 4.2.1 shows the graphical results for the above mention table. It show that designed methodology achieve effective results as compare to above mention methods.

Table 4.2.2 shows the MSE, PSNR and SSIM values of different methods.

Fig. 4.2.2 shows the graphical results for the above mention table. It show that proposed methodology performed better as compare to other methods.

The proposed methodology is compare with the K-NN, SVM, SOM, GN and CNN. The result is computed on 2457 images from BRAINIX MRI images. Fig. 4.2.3 shows the graphical representation of the performance.

The computation time is estimated and compared with other works for validating the superior nature of the proposed approach. Fig. 4.2.4 shows the segmentation time taken by different methods.
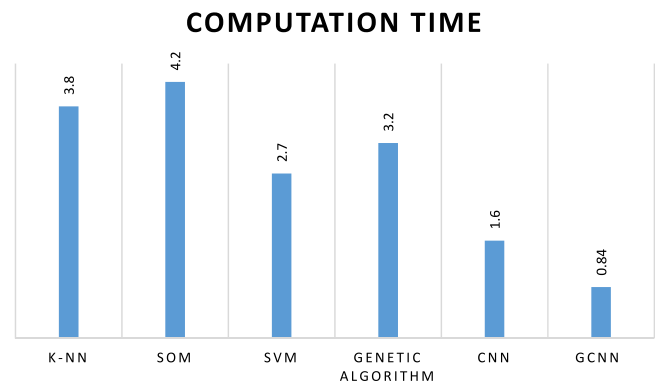
From the above mention data it has been cleared that proposed methodology performed better and more efficient than the other mentioned techniques.
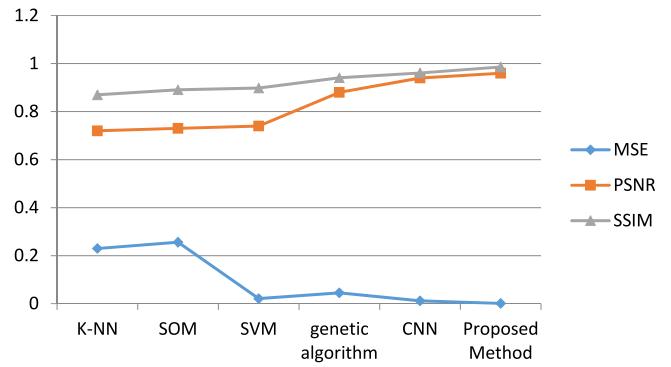
Fig. 4.2.2. Graphical comparison on the basis of parameters mention in Table X2.
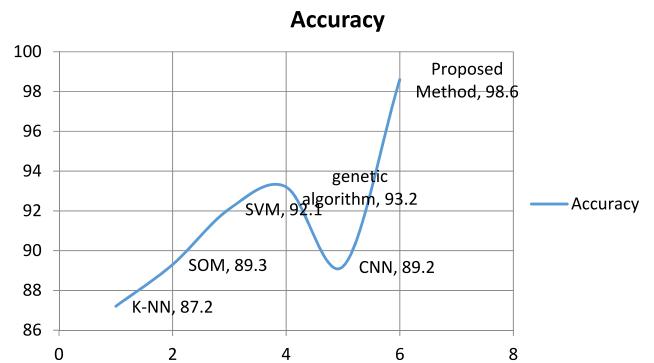
Fig. 4.2.3. Comparison on the basis of accuracy.

Fig. 4.2.4. Computation time in seconds for comparative analysis.

5. Discussion

From the above mention method and results it is very much evitable that the planned methodology achieve more effective results as other mention techniques. Some of the observation obtained from the experiment are:

- The proposed method extracts more features to classify the ROI more accurately
- The outcomes of the proposed method are much better than the other mentioned techniques,
- The proposed method has not degraded the quality of the image.

For future work in the approach can include;

- Database like PASCAL, Berkeley or BRATS can be used

- More combination of different classifiers can be used to improve the performance of the proposed system.

6. Conclusion

In this research work, an effective approach has been proposed to segment abnormal tissue from MRI images of brain using deep learning algorithms. A combination of SWT and GCNN is used in this work to automatically carry out the segmentation process. The proposed combination has proved to be more effective than the individual automation process. An approximate 2% improvement in PSNR and SSIM has been achieved with the proposed method over the conventional CNN approach. The Mean Square Error is significantly reduced in the proposed GCNN approach in comparison to the conventional CNN approach. A similar comparison with other conventional methods has also proved the efficiency of the proposed system. Thus, the proposed approach is suitable for brain tumor segmentation in real-time applications.

References

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