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COMPARATIVE ANALYSIS OF GENETIC ALGORITHM - SUPPORT VECTOR MACHINE AND DEEP LEARNING WITH CONVOLUTIONAL NEURAL NETWORK FOR BRAIN TUMOR DETECTION AND CLASSIFICATION

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Abstract

A brain tumor occurs when abnormal cells form within the brain. Many people suffer from brain tumor, and it is a serious and dangerous disease. The detection and classification of brain tumor is an important and difficult task in the medical field. The brain tumor detection technique in the MRI images is very significant in many symptomatic and cure applications. But, as the data in MRI images are of high-quality, tumor detection and classification are very hard in this process. Medical imaging plays a major role in properly diagnosing the disease, wherein an essential part in detecting the tumor is image segmentation. The segmentation provides an automatic brain tumor detection technique in order to increase the precision of the yields while also decreasing the diagnosis time. The goal is to detect the tumor from the MRI images and extract the features from the segmented tumor and finally classify it. The image detection and classification process includes image acquisition, image pre-processing, denoising, image segmentation, feature extraction and classification. The input image is pre-processed using Weiner and median filtering and the noise is removed using Edge Adaptive Total Variation Denoising (EATVD) technique. Once the noise is removed from the image, it is used for segmentation process, where Mean Shift Clustering is used. The segmented tumor undergoes features extraction stage, where Gray Level Co-occurrence Matrix (GLCM) features are used. In the last stage, images are classified either as tumorous or non-tumorous. Classification is done using Genetic Algorithm Support Vector Machine (GA-SVM), Deep Learning with Convolutional Neural Network (CNN). Early detection of the tumor region can be achieved without much time lapse in the calculation by using this efficient classifier model. This system presents a prototype for detecting objects based on GA-SVM that classifies images and assesses whether the image is cancerous. While comparing the accuracy and computational time of these classifiers, CNN would provide high accuracy and GA-SVM with lesser simulation time. The simulation results obtained for brain tumor detection and analysis are done with minimum computational time and with reasonable accuracy. This proposed system is tested using SPL dataset, which consists of 20 cases with 40 image samples of T2 FLAIR weighted MRI image and implemented using MATLAB software.

Keywords:

Wiener filter, Edge Adaptive Total Variation Denoising, Gray Level Co-occurrence Matrix, Genetic Algorithm Support Vector Machine, Convolutional Neural Network

1. INTRODUCTION

Diagnostic imaging has become an indispensable tool in the advanced imaging technology of modern day medicine. X-Ray Angiography (XRA), Magnetic Resonance Angiography (MRA), Magnetic Resonance Imaging (MRI), Computed Tomography (CT) and other imaging modalities are heavily used in clinical practice. Such images provide complementary information about the patient. Due to increase in the complexity in the medical field, it requires latest advances in computer technology in order to reduce the cost and make development of automation possible [1].

Brain tumor occurs when abnormal cells form within the brain. Nowadays brain tumor is a common disease found in the human body. Some of the ways for diagnosing brain tumor are MRI scan, CT scan and biopsy of the head etc. In CT scan technique, the image of the brain is taken from several angles and is studied altogether. In the magnetic imaging techniques, the radio waves are utilized to locate as well as to obtain a digital image of tissues present in the brain. The manual analysis of such images requires training and experience and will often lead to wrong diagnostics. In fact, the traditional MRI method is a very difficult task and time-consuming even for a skilled person, which will also depend on the expert experience on the expected results. So, it is essential to obtain a method that would provide doctors with an accurate and fully automatic technique.

The growth of the tumor occupies space within the skull and affects with normal brain activity. Brain tumor is classified into two type as normal brain and abnormal brain [3]. There are two types of tumors: malignant or cancerous tumor and benign tumors. Cancerous tumor can be divided into primary tumor that start within the brain and secondary tumor that have spread from somewhere else, known as brain metastasis tumor. Brain tumor detection in medical images forms an essential step in solving several practical applications such as diagnosis of the tumor and registration of patient images obtained at different times.

This paper introduces a method for detecting and classifying brain tumors that is performed by focusing on major challenges and problems in medical imaging such as image detection and classification. The detection of tumors consists of image acquisition, pre-processing, denoising, segmentation, extraction and classification of features. Image segmentation is one of the most important tasks in tumor detection. Initially, the MRI image input is pre-processed using wiener filter, followed by denoising where the technique of Edge Adaptive Total Variation is used. Following denoising is a segmentation task consisting of mean shift clustering and content-based active contour techniques that would extract the tumor from the MRI images. The next stage in the proposed system is feature extraction, where GLCM features from the segmented image.

Finally, the classification is done using Genetic Algorithm Support Vector Machine (GA-SVM), Deep Learning with Convolutional Neural Network (CNN). In image processing it is usually necessary to perform high degree of noise reduction in an image before performing higher-level processing steps, such as edge detection [3], smoothing filters is used to remove noise from an image. Each pixel is represented by three scalar values representing the red, green and blue chromatic intensities. At each pixel studied, smoothing filter takes into account the surrounding pixels to design an accurate version of this pixel. By taking neighbouring pixels into considerations, extreme ‘noisy’ pixels can be represented. In research and technology such as geographic information systems, digital images play an important role and it is also the most vital part in the field of medical science such as ultrasound imaging, X-ray imaging, computed tomography and MRI. A very large portion of digital image processing involves restoring images. Specific segmentation method is not found to extract vasculature from every medical images modality. While techniques like clustering, segmentation etc., employ pure intensity-based pattern recognition techniques such as thresholding followed by connected component analysis, edge detection methods are applied explicitly in the tumor models to extract the tumor contours [2].

Based on the image quality, different pre-processing methods are used for segmentation, while methods like low pass filtering, unsharp masking techniques are applied in the post-processing to overcome the problems arising over segmentation. There are six main categories by which medical image segmentation algorithms and techniques can be divided. They are: pattern recognition techniques, model-based approaches, tracking-based approaches, artificial intelligence-based approaches, neural network-based approaches and object detection approaches.

In this paper, mean shift clustering is used for segmenting the tumor from the brain. Extraction of the feature is a process of attribute reduction. Contrary to the selection of features classifying existing attributes by prediction, the removal of features transforms the attributes [8]. Feature extraction projects a data set to a smaller number of dimensions with higher dimensionality. In this paper GLCM features are extracted which is used for training the network [4] [7].

The purpose of the classification process is to categorize all pixels in a digital image into one of several classes or themes of land coverage [20]. Then, this categorized data can be used to produce thematic maps of the land cover in an image. Multispectral data are normally used to perform classification and the spectral pattern present in the data for each pixel is used as the numerical basis for categorization. The aim of image classification is to identify and portray the characteristics that occur in an image in terms of the object or type of land that these characteristics represent on the ground as a unique gray level (or colour).

The main aim of this paper is to automatically detect the position, boundary and the type of tumours based on the symmetry information of MRI. Clinical diagnostics can be aided as the key reason for brain tumors to be detected. The goal is to develop a tumor- proof algorithm that provides a method for tumor detection in MRI brain images by combining various procedures. The scope of this work is to bring some useful information to the users in a simpler way, particularly for the patient's medical staff.

2. LITERATURE REVIEW

There are a lot of research that has been done on brain tumor segmentation and some of the recent research methods are discussed in this section. The paper outlines lab work using artificial neural network for brain tumor detection using MRI images [12]. This paper detects tumor area by darkening tumor portion and enhances the images for detection of brain tumor. The methods used are Image acquisition, pre-processing, image enhancement, thresholding and morphological operation. Median filter is used in pre- processing to remove noise. A high pass filter is applied to digitized MRI image to get Enhanced image. The threshold segmentation is based on threshold value which converts Gray scale image into binary image. The purpose of morphological operator is to separate the tumor part of the image. In the areas of image analysis and computer vision, Active Contour models have been widely used. The contours are driven to reach the boundary of the object by minimizing the fitting energy for contour-based image segmentation. There are two types of active contours: Active parametric contours and Active geometric contours [10]. In terms of curve function, parametric active contours are formulated and highly dependent on curve parameters. Geometric active contours do not involve curve parameterization and can naturally and effectively handle contour topological changes [9].

The Image segmentation is the process of partitioning a digital image into multiple segments. The goal of segmentation is to simplify or change the representation of an image into a more meaningful information, which would be easier to analyse. Segmentation plays an important role in the analysis of medical images for computer-aided diagnosis and therapy. Segmentation is the challenging and complex task in medical imaging due to the imprecise nature of images [1]. For neurological pathology clinical study and research fully automatic brain tissue classification from Magnetic Resonance Images (MRI) is very important. The important task is to segment the MR images into different classes especially Gray Matter (GM), White Matter (WM) and Cerebrospinal Fluid (CSF) accurately. The useful diagnostic information can be known from regional volume calculation [6]. In neurodegenerative disorders such as Alzheimer disease, in movement disorders such as Parkinson or Parkinson related syndrome, in white matter metabolic or inflammatory disease, in congenital brain malformations or perinatal brain damage, or in post-traumatic syndrome, quantization of gray and white matter volumes are considered for calculations.

A multi stage approach using random forest for brain tumour classification and segmenting them using fast bounding box was proposed [18] [5]. The combined approach of GLCM and Gray Level Run Length Matrix (GLRLM) texture feature extraction methodologies used in this work for the classification of tumour. In this proposed system, a comparison is done for classifying the accuracy for the dataset which contains 120 cases of MRI images. The results show that multi stage approach outperforms the reference methods and achieves better accuracy in classifying glioma or meningioma and segmenting the tumour. An important observation in this work is that multi stage approach uses hierarchical classification method which boosts performance significantly. Decisions obtained by applying a hierarchical classification for every single classification task is better than the best individual classification algorithm [5].

These system brain MRI methods have been verified as a significant way to find the brain tumor [14]. The hybrid methodology of gathering support vector machine and fuzzy c-means clustering for classification gives precise result for identifying the brain tumor. For future work, a hybrid SVM algorithm should be proposed to achieve a better accuracy rate and less error rate [16]. A prototype for object detection with

SVMs was presented in [15], which can achieve real-time performance while maintaining high detection accuracy. The 82% of accuracy is achieved and 81.48% of the Positive Predictive Values (PPV) are calculated. The True Positive Cases are 22; True Negative 5 is 22; False Positive 5 is 22. The same prototype can also be used for different applications regardless of the size of the window, the number of support vectors and the size of the image. Many researches were done to automate the segmentation and diagnosis of brain tumors using Deep Learning networks. In the research [17], multiple convolutional networks are used to segment the brain tumors for diagnosis process. The MRI image modalities like T1-weighted, T2-weighted are given more consideration in the segmentation process. In this method, the 3D image voxels are fed into a 2D CNN model. Four CNNs are developed with different block sizes to compare the performance of each model. The accuracy is reasonable compared to the algorithm of Bauer and Menze. The output of the said method is a segmentation of brain tumor out of the whole brain MRI image. It does not predict whether the tumor is either benign or malignant or which tumor type it is.

Automation of detection and segmentation of brain tumors in MRI images is a very challenging task due to occurrence of high degree of gray-level similarity in the image. There is a fully automated two-step segmentation process of brain MRI images [11]. In the first step, skull stripping is performed by generating a skull mask from the MRI image and in the second step, an advanced K-means algorithm improvised by two-level granularity-oriented grid-based localization process based on standard local deviation is used to segment the image into gray matter, white matter and tumor region and then length and breadth of the tumor is assessed.

This research paper presents a method based on image characteristics and automatic detection of abnormalities to automatically classify medical images in two classes Normal and Abnormal [13]. Statistical texture functionality is derived from normal and abnormal pictures. We used the KNN classifier to classify the image [19]. The calculated confusion matrix and result shows that KNN receives an 80 percent classification rate higher than the SVM classification rate. A hybrid GA-SVM based classification model which overcomes these limitations was developed [21]. Post contrast T1 MRIs are used to extract texture and intensity information. The implementation is carried out by using GA-SVM approach on 428 images to classify the five classes of brain tumors, namely, Primary tumors- AS, GBM, MEN, child tumor-MED and secondary tumor-MET. A CAD system is developed to assist radiologists in multiclass brain tumor classification.

A hybrid approach was proposed to classify brain tissue in MRI based on GA and Support Vector Machine (SVM) [22] [23]. A set of texture based on wavelets is derived. Using the Spatial Gray Level Dependence Method (SGLDM), the optimal texture characteristics are extracted from normal and tumor regions. These characteristics are given to the SVM classifier as input. The choice of features, which in classification techniques poses a major problem, is solved through the use of GA. Using these optimal features, brain tissues are classified into normal, benign or malignant tumors. The algorithm performance is evaluated on a series of images of brain tumors.

3. PROPOSED SYSTEM

The proposed system is to detect and classify the brain tumor, which involves pre-processing, denoising, segmentation, feature extraction and classification stages. The software and device that are used for implementing this proposed system is MATLAB R2017b with Intel core i5 processor and 16GB RAM capability. Specimen images collected from SPL [2] which consists of 20 cases with 40 image samples of T2 FLAIR weighted MRI image which is used for training and testing the proposed system. The first stage classifies a normal and abnormal image into 2 classes. Two metrics were calculated to evaluate the classification efficiency: (a) the training performance (i.e. the proportion of cases properly classified in the training process) and (b) the test performance (i.e. the proportion of cases properly classified in the testing process).

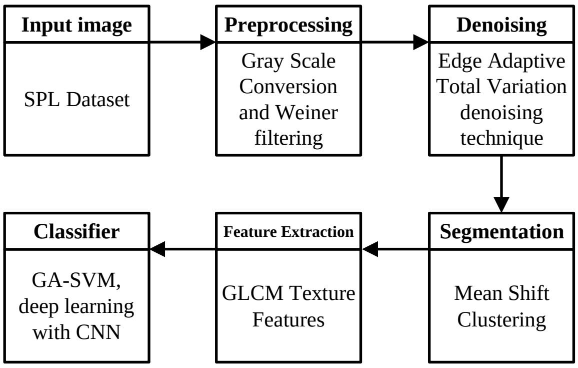


Fig.1. Overview of the proposed system

Initially the MRI image is taken as the input and it is pre-processed using wiener filter and median filter. The wiener and median filter would remove the noise present in the image, and it would blur the image. The pre-processing stage is followed by denoising, where edge adaptive total variation technique is used. The main objective of the denoising is to eliminate the unwanted signal present in the input image. The denoised image is further taken to the Segmentation process in which Mean Shift Clustering is used to cluster the pixel that are of similar properties. Finally, the clustered output is used for extracting the features which is done in Feature Extraction phase and the extracted features are used for classification of tumor. In the classification stage GA-SVM, CNN are used. These are used for classifying the MRI images into tumorous or non-tumours. The overview of the proposed system is given in Fig.1.

3.1 PRE-PROCESSING

Pre-processing is a common name for image operations at the lowest abstraction level-both input and output are intensity images. The aim of the pre-processing is to improve the image data that suppresses unwanted distortion or improves certain image features important for further processing. The different categories of image pre-processing methods depending on the size of the pixel neighborhood used to calculate the new pixel brightness are as follows:

1. Transformations of pixel brightness
2. Transformations of geometry

3. Pre-processing methods that use the processed pixel's local neighborhood
4. Image recovery requiring knowledge of the entire image
5. Other pre-processing image classifications exist

Images obtained from various MRI modalities are influenced by ancient rarities, for example, movement and field inhomogeneity. An MRI can be utilized to assess cerebrum, neck, and spinal string issues. It can likewise enable parental figures to take a gander at issues with the chest, heart, mid-region, joints, or veins. The filtering of Wiener makes an optimal compromise between inverse and noise smoothing filters. It removes the added noise and simultaneously reverses the blurring. In the case of window sizes 3×3, 5×5, 7×7, 13×13 and 23×23 and the like, the quality of the filtered image differs. Median filtering is very widely used in digital image processing because, under certain conditions, it preserves edges while removing noise, also having applications in signal processing. The median filter is to run through the signal entry by entry, replacing each entry with the median of neighbouring entries. Median filtering is one kind of smoothing technique, as linear Gaussian filtering. All smoothing techniques are effective at removing noise in smooth patches or smooth regions of a signal, but undesirably affect edges. Often, at the same time as reducing the noise in a signal, it is important to preserve the edges. Edges are of critical importance to the visual appearance of images. For small to moderate levels of Gaussian noise, the median filter is demonstrably better than Gaussian blur at removing noise whilst preserving edges for a given, fixed window size. However, its performance is not that much better than Gaussian blur for high levels of noise, whereas, for speckle noise and salt-and-pepper noise (impulsive noise), it is particularly effective.

3.2 DENOISING

Digital images, for example geographic information systems, play an important role in research and technology and are key to medical science such as ultrasound imaging, X-rays, computed tomography and MRI. The restoration of images includes a very large part of digital image processing. Restoration of images is a degradation method that takes place during the capture of the image. Degradation due to electronic and photometric sources is caused by sound and blurring. Blurring represents a bandwidth reduction of images caused by an imperfect image formation process, such as relative motion among the camera and the original scene or a distorted optical system. Noise is the undesirable signal that impairs the original signal and degrades the visual quality of digital images. Principal sources of noise in digital images are imperfect instruments, problems with process of data acquisition, natural interference, transmission and compression. The denoising of images is the pre-processing step in photography, research, technologies and the medical science in which the image has been degraded in some way and needs to be restored before further processing. Edge Adaptive Total Variation Denoising is one of the techniques of noise removal that this proposed system employs.

3.3 SEGMENTATION

Segmentation partitions an image into different regions that contain similar attributes for each pixel. The regions should be strongly linked to the described objects or features of interest, which are meaningful and useful for image analysis and interpretation. The segmentation is the first step from low-level image processing to convert a gray or color image into one or more other images to high - level image description in terms of features, objects and scenes. The success of the image analysis depends on the reliability of the segmentation, but an accurate image partitioning is usually a very difficult problem. The techniques of segmentation are either contextual or non-contextual thresholds. In this proposed system two different types of segmentation techniques such as Mean Shift Clustering and Content based Active Contour model are used for the analysis and results are compared.

3.4 FEATURE EXTRACTION

The component extraction includes improving the measure of assets required to depict an extensive arrangement of information precisely. When performing examination of complex information one of the real issues originates from the quantity of factors included. Examination with a substantial number of factors for the most part requires a lot of memory and calculation control or an order calculation which over fits the preparation test and sums up inadequately to new examples. This is a strategy for catching visual substance of pictures for ordering and recovery. Crude or low dimension picture highlights can be either broad highlights, for example, extraction of shading, surface and shape or area explicit highlights. In this proposed methodology, GLCMM algorithm is used to extract the true surface feature for the advancement in the estimation of image. The four highlights specifically, Energy, Contrast, Correlation and Homogeneity are figured utilizing matlab.

3.5 CLASSIFICATION

Classification between objects is an easy task for humans, but for machines it has proven complex. Higher- capacity computing and high-end and cheap video cameras have created an interest in algorithms for the classification of objects, along with the growing need for automated video analyses. A simple grading system consists of a camera that is mounted high above the zone in which images are recorded and thus processed. Classification includes image sensors, pre-processing, detection and division of objects, extraction of functions and classification of objects. Classification systems are a database containing predefined patterns which is to be classified into the proper category compared to detected objects. Classifying images is an important and demanding task in different fields of application such as biomedical imagery, biometry, widespread surveillance, vehicle navigation, industrial visual inspection, robot navigation and remote sensing. This proposed system is used for classifying the brain tumor by the GA-SVM and deep learning using the Convolution Neural Networks.

4. SIMULATION RESULTS AND DISCUSSIONS

The Fig.2 shows the input image with tumor is given as the MATLAB input. This image is then pre-processed using wiener filter by adding speckle noise.

Fig.2. Input image with tumor

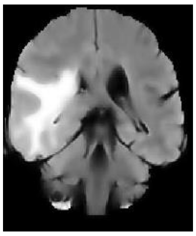


Fig.3. Weiner filtered image

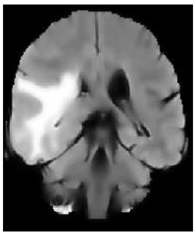


Fig.4. Denoised image

In the pre-processing stage very few amounts of noise are removed, and it is blurred using wiener filter, as shown in Fig.3. The process of the wiener filter is analysed by varying the window size of the filter as 3×3, 5×5, 7×7, 13×13, 15×15, 23×23. When the size of the window is high then the resolution would be minimum while restoring the image. Hence, the 3×3 window size is considered in the pre-processing stage. By comparing the results obtained from the pre-processing stage, it is inferred that median filter would result much better than the wiener filter. The peak signal-to-noise ratio and similarity index are relatively high in the median filter. Hence, the amount of noise removed, and the quality of image is high in terms of median filter. The comparison results for SPL data is tabulated in Table.1.

Table.1. Error metrics obtained by varying the window size of the Wiener filter for SPL dataset

Window Size	Peak-SNR	SNR	MSE	SSIM
3×3	27.7697	8.8576	72.2942	0.7614
5×5	25.9420	16.9580	72.1230	0.7617
7×7	25.0591	16.0897	71.2220	0.7647
13×13	23.5605	14.4160	68.9973	0.7667
23×23	21.6948	12.2987	66.5119	0.7627

The second process is denoising followed by pre- processing, where EATVD technique is used to eliminate the noise content in the image. The result is shown in the Fig.4. The denoised output is used to calculate the peak signal to noise ratio (PSNR) value, signal to noise ratio (SNR) value, structural similarity (SSIM) value and mean squared error (MSE) value. Although a higher PSNR generally indicates that the reconstruction is of higher quality. Higher SNR value means that more amount of noise is removed.

However, as a least squares results, it is slightly biased towards blur. SSIM has been developed to have a quality reconstruction metric that also considers the similarity of the edges (high frequency content) between the denoised image and the input image. These values are compared by varying the window size of the filter as 3×3, 5×5, 7×7, 13×13, 15×15, 23×23 etc. The error metrics obtained by varying the window size of the wiener filter for the SPL dataset is shown in the Table.2 and their EDTV plots are given in Fig.5.

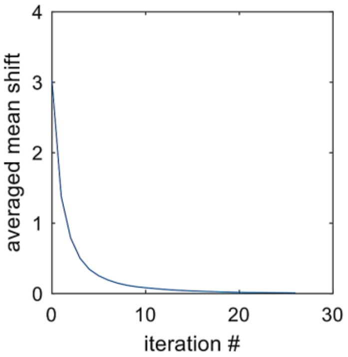


Fig.5. EDTV plot (Averaged mean shift value = 0.0091619)

Table.2. Comparison of Median filter and Weiner filter for SPL dataset

Image	Median filter			
	PSNR	SNR	MSE	SSIM
1	11.2771	24.1840	46.3726	0.9608
2	12.8862	23.3971	50.8637	0.9544
3	14.5966	22.7012	57.4882	0.9670
4	10.8346	25.0751	49.6556	0.9620
5	11.0053	23.3330	36.1042	0.9827
6	11.6307	24.7662	52.0606	0.9582

The segmentation is done using Mean Shift Clustering (MSC) algorithm. The outcome of the MSC algorithm returns the average mean shift value. As detailed by Fig.6, if the value of the average mean shift is high, it implies that the segmentation would have more coverage. The segmentation is also based on the number of iterations that it must undergo for segmenting the tumor. By default, the iteration is taken as 100. When the number of iterations exceeds the limit it may lead to loss in the information. For the given input image, the average mean shift value is maximum as the number of iterations increases. This model is used to extract the boundary region of the tumour and extract it separately from the MRI image. Furthermore, the initial image does not need to be smoothed, even though it is noisy and thus the boundary locations are very well detected and preserved. The mean-shift algorithm with colour and spatial information in the colour image segmentation is generally successful for few cases. However, in some cases, the colour and spatial information are not enough for superior segmentation. Mean Shift is a non-parametric clustering approach that does not take the form of the distribution and the number of clusters into consideration. The GLCM features like contrast, Correlation, energy, Homogeneity, Mean, standard deviation, Entropy, RMS, Variance, Smoothness, Kurtosis, Skewness are extracted from the segmented results. Based on the features extracted, the boundary of the tumor can be identified. The features extracted are stored as database that is used for training and testing the network. The sample features of SPL dataset are given in the Table.3.

Fig.6. Mean shift clustering image

Table.3. Feature extraction for various image sets for SPL dataset

Image set	Image sample 1	Image sample 2	Image sample 3
Mean	0.006309	0.0042661	0.003650
Standard Deviation	0.089592	0.0897133	0.089740
Entropy	3.20515	3.60044	3.37095
RMS	0.089802	0.0898027	0.089802
Variance	0.008017	0.00805059	0.008059
Smoothness	0.959133	0.940723	0.931415
Kurtosis	12.2408	6.01365	7.35059
Skewness	1.10481	0.526678	0.635044
IDM	1.2156	0.380124	0.137806
Contrast	0.305895	0.225528	0.243326
Correlation	0.142097	0.134499	0.093278
Energy	0.786231	0.746563	0.761293
Homogeneity	0.937931	0.929853	0.932884

The Table.4 gives the performance measurements of SVM classifier. For training this network, datasets are taken with 10 cases which consist of 40 image sets; and for testing the network, 20 image sets are taken. The MRI image is classified as No tumor or MRI with tumor (Benign and Malignant). The number of iterations taken for classifying the tumor is 700 and four different types of kernel like RBF, linear, polygonal and quadratic are used. Performance criteria that are measured from this classifier are computational time, classification rate, error rate, sensitivity, specificity, positive predicted value, negative predicted value, and accuracy for different kernels. By varying the kernel function and number of iterations, maximum accuracy can be attained. When the iterations are minimum, the accuracy is also minimum and the time taken for classifying is low. Similarly, when the number of iterations is increased, maximum accuracy is attained, and computational time is high. The comparison plot for the iterations taken and the computational time is specified in the Fig.7.

GA is hybridized with SVM classifier in order to attain more precise results. The outcomes of the GASVM hybrid are given in the Table.5. Based on the accuracy and the type of the tumor, the computational time also varies. In this method, four kernel functions (Linear, RBF, Polynomial, Quadratic) are used for classification. The accuracy can be increased by varying the number of iterations and the kernel type. The time taken for classifying the tumor is comparatively lower than the other classifiers.

Table.4. Output performance measurement of SVM classifier for SPL dataset

Dataset Size	Dataset Images
Training size (with normal MRI images)	10 cases with 40 image set, Benign - 20 images, Malignant - 20 images
Testing size (with normal MRI images)	20 images Benign - 10 images Malignant - 10 images

Image Set	Test image 1	Test image 2	Test image 3
Computational time in seconds	10.806	11.576	11.12
Classification rate	0.55	0.5	0.6
Error rate	0.45	0.5	0.4
Sensitivity	0.6	0.7	0.6
Specificity	0.5	0.3	0.6
Positive Predictive Value	0.5455	0.5	0.456
Negative Predictive Value	0.5556	0.5	0.652
RBF accuracy in %	90	80	80
Linear accuracy in %	100	90	90
Polygonal accuracy in %	80	80	80
Quadratic accuracy in %	80	90	80
Accuracy among kernel (%)	100	90	90
Overall accuracy in %	87.5	85	82.5
Tumor type	No tumor	Benign	Malignant

Table.5. Classification results for GA-SVM for SPL dataset

Parameters	Image sample 1	Image sample 2	Image sample 3
RBF accuracy in %	95.6	98.1	93.3
Polynomial accuracy in %	87.8	94.38	93
Linear accuracy in %	100	95.70	94.7
Quadratic accuracy in %	96.88	96.5	94
Overall accuracy in %	95.07	96.17	93.75
Computational time (s)	10.12	8.489	8.12
Type of tumor	Malignant	Benign	No tumor

The CNN would classify the MRI images into two classes, and 20 image-sets are taken and trained as the data size of the classifier. The neural network has 19 hidden layers and 1 output layer. The data division is considered as random and the training method used is scaled conjugate gradient. This network has 1000 neurons and it would be computed for 7000 epochs. The output data that are taken for training and the performance measures are given in the Table.6.

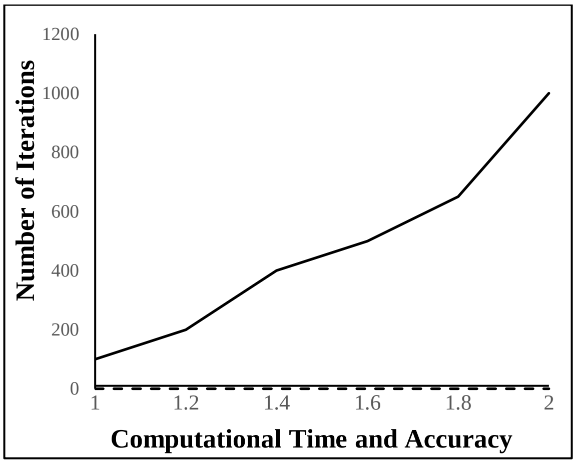


Fig.7. Performance plot of SVM classifier

Table.6. CNN training parameters and outcomes for SPL dataset

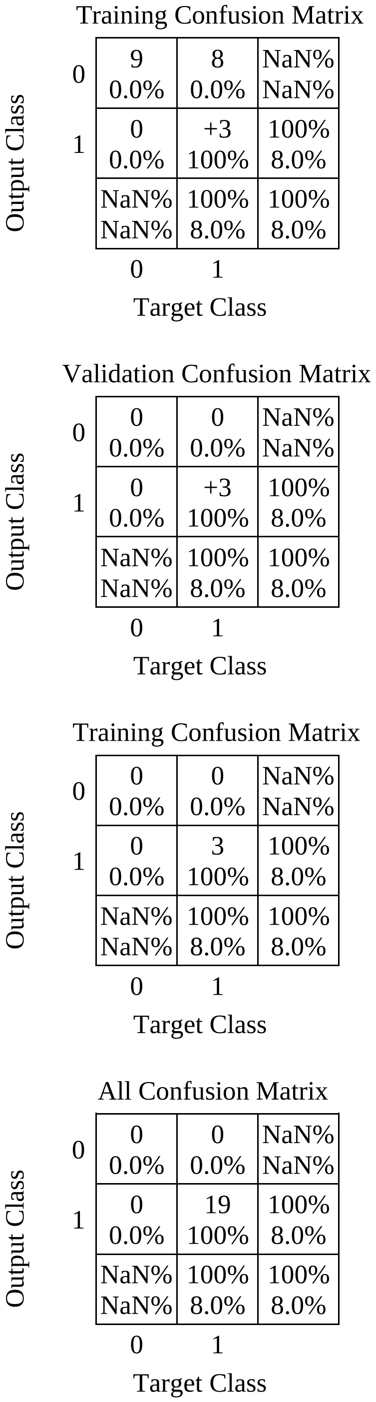
Parameters	Value
Number of classes	2
Size of the dataset	40
MSE	0.132964
Number of hidden layers	19
Data division	Random
Training method	Scaled Conjugate Gradient
Number of epochs	7000
Number of neurons	1000
Training time	0.2996 seconds
Gradient	0.1444
Number of output layer	1
CNN training accuracy in %	89.2105

This network would return the performance of training network, confusion matrix of the training and testing network, the training state plot of the CNN, and the entropy plot of the network. The Fig.8 gives the confusion matrix which is obtained using the predicted label and actual label. The validation performance of the training network is shown in Fig.9. The best validation is obtained at the epoch 0 and the best validation performance value is 2.2204e^{-16}. This validation performance is taken for the cross entropy and the total number of epochs.

The network is tested with 20 sample images of SPL datasets. The network would be tested for 7000 epochs for each image samples, the best performance validation can be attained in different epochs based on the type of the tumor it classifies. This network returns the tumor type, area or size it occupies in the brain, testing time, classification accuracy etc.

The performance measurements of CNN testing is specified in the Table.7 for SPL datasets correspondingly. The Convolutional neural network consists of various layers such as average pooling layer, classification output layer for a neural network, 2D convolutional layer, dropout layer, fully connected layer, rectified linear unit layer etc.

The Fig.10 shows the training performance of the neural network where the X-axis is used for number of epoch and Y-axis is for mean square error, the blue line indicates the training performance at 129 epochs, the best performance is attained.



Training Confusion Matrix

Output Class \ Target Class	0	1	
0	9 0.0%	8 0.0%	NaN% NaN%
1	0 0.0%	+3 100%	100% 8.0%
	NaN% NaN%	100% 8.0%	100% 8.0%

Validation Confusion Matrix

Output Class \ Target Class	0	1	
0	0 0.0%	0 0.0%	NaN% NaN%
1	0 0.0%	+3 100%	100% 8.0%
	NaN% NaN%	100% 8.0%	100% 8.0%

Training Confusion Matrix

Output Class \ Target Class	0	1	
0	0 0.0%	0 0.0%	NaN% NaN%
1	0 0.0%	3 100%	100% 8.0%
	NaN% NaN%	100% 8.0%	100% 8.0%

All Confusion Matrix

Output Class \ Target Class	0	1	
0	0 0.0%	0 0.0%	NaN% NaN%
1	0 0.0%	19 100%	100% 8.0%
	NaN% NaN%	100% 8.0%	100% 8.0%

Fig.8. Confusion matrix for training and testing

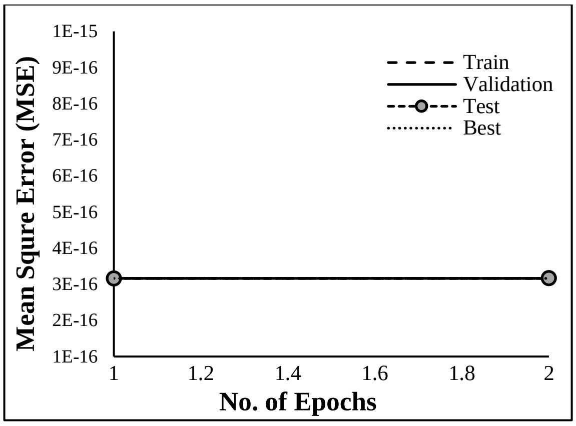


Fig.9. Cross Entropy plot of the training network (Best Training Performance is 8.754e^{-6} at epoch - 69)

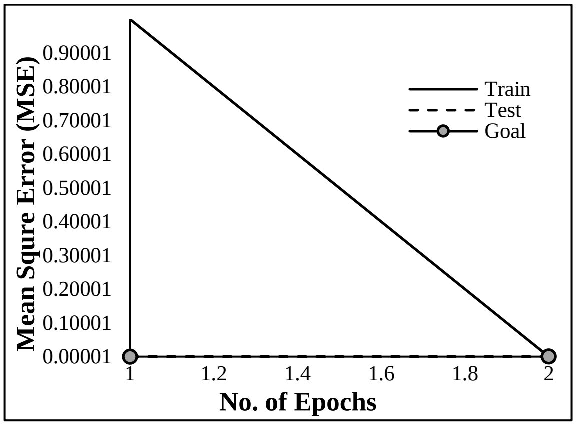


Fig.10. Training performance of the network with respect to Mean square error (Best Training Performance is 8.754e^{-6} at epoch - 69)

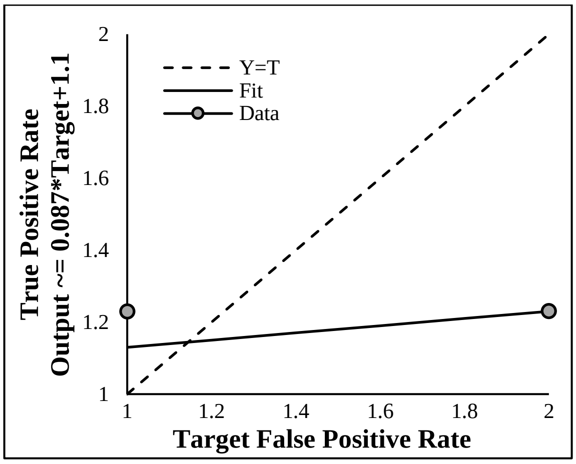


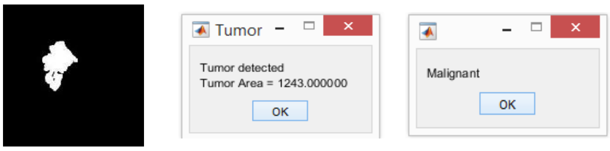
Fig.11. Regression plot (Training R = 0.29417)

Table.7. CNN testing outcomes for SPL dataset

Parameters	**Image sample 1**	**Image sample 2**	**Image sample 3**
Epoch	208	129	184
Testing time (s)	12.36	13.22	10.21
Gradient	9.78 e-06	8.67 e-06	4.75 e-06

Tumor type	Malignant	Benign	No tumor
Tumor area (mm)	3897	2360	Nil
Regression point	0.29471	0.63738	0.6731
Accuracy	0.09187	0.0989	0.0942
Sensitivity	0.65	0.7	0.6
Specificity	0.35	0.3	0.6

Based on the number of iterations or the number of epochs the performance of each image set would vary.



Tumor detected
Tumor Area = 1243.000000

Malignant

(a) (b) (c)

Fig.12. Results of (a) Tumor detected image, (b) Tumor area and (c) classification result

Table.8. Performance measurement comparison of classifiers by SPL dataset

Selected parameters	**Accuracy in %**		
Classifier	**SVM**	**DCNN**	**GA-SVM**
Image sample 1	87.5	91.87	95.07
Image sample 2	85	98.9	96.17
Image sample 3	82.5	94.2	93.75
Selected parameters	**Computational time (s)**		
Classifier	**SVM**	**DCNN**	**GA-SVM**
Image sample 1	10.805	12.36	10.12
Image sample 2	11.576	13.22	8.489
Image sample 3	11.12	10.21	8.12
Selected parameters	**Type of tumor**		
Classifier	**SVM**	**DCNN**	**GA-SVM**
Image sample 1	Malignant	Malignant	Malignant
Image sample 2	Benign	Benign	Benign
Image sample 3	No tumor	No tumor	No tumor

The regression plot shows how the input and the target output matches, and blue line indicates the fit ratio and the dotted line represents the output or target. The R plot for the image set is given in the Fig.11. The final tumor detected image is given in the Fig.12. The Fig.13 represents the histogram computed for the sample image.

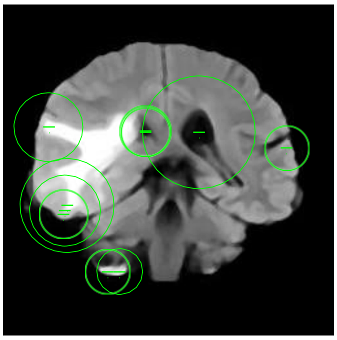


Fig.13. Histogram Computed image for SPL Dataset

CNNs are designed to work with image data, whereas SVM is a more generic classifier. CNNs extract features while SVM simply maps its input to a certain high- dimensional space where variations in class can be revealed. Learning objectives of SVM and CNN are different: SVMs seek to maximize their margin while CNNs do not maximize their margin. On comparing the computation time for both the network Deep learning with CNN is quite faster and the accuracy is better when compared with the support vector machine.

A 94.2% accuracy is obtained by using Deep Learning with CNN classifier while SVM classifier has attained 87.5% accuracy. The number of iterations is fixed for all image sets and kernel type, but for CNN the maximum number of epochs is assumed, and the minimum number of epochs is required automatically to classify the MRI during classification. The comparison between the various parameters of SVM, CNN classifiers are specified in the Table.7.

On comparing the results of the classifiers Deep Learning with CNN would result better when compared with the other classifiers with respect to accuracy and computational time. GASVM has been proposed and tested for gene selection on four real microarray data. This is because GASVM can reduce the cycle-based dimensionality of the data automatically. It is therefore necessary to select genes using GASVM to produce a near-optimal (smaller) subset of informative genes for better cancer classification. On comparing the computational time of the classifiers, it is observed that GA-SVM classifies in a shorter duration.

5. CONCLUSION

Towards accomplishing the purpose of this study, MRI image is fed as input, a speckle noise is added, and pre-processed using wiener and median filter. The parameters used in the wiener filter include the noisy image, the type of noise used, the mean and the image variance. The pre-processed image is then denoised using EDTV technique, wherein the resultant SNR value is inferred to be high, implying that the image resolution would also be high when reconstructed.

In the segmentation of color images, the mean shift algorithm with color and space data is generally successful, but in some cases, color and space information are not sufficient for superior segmentation. Mean Shift is a non-parametric clustering approach that does not consider the distribution form and the number of clusters. Consequently, Mean Shift can deliver better results of segmentation than model-based clustering systems, when used to segment historical images. The extracted characteristics are used to classify the image as the input. To improve classification accuracy, the multiple features of the image and selection of appropriate classification methods are effectively used. CNNs are intended to work with image data, while SVM is an increasingly nonexclusive classifier. The individual features of CNNs while SVM essentially maps its contribution to a specific high-dimensional space where contrasts in class can be uncovered.

There are diverse learning destinations: SVMs are endeavoring to boost the edge, while CNNs are not doing as such. On contrasting the ideal opportunity for both systems, registering Deep learning with CNN is quicker and increasingly exact contrasted to the Support vector machine. The 94.2% exactness is accomplished by utilizing Deep Learning CNN classifier, while SVM classifier accomplished 87.5% precision. On looking at the computational time of the classifier, SVM is characterized in a brief timeframe contrasted with different classifiers. By comparing various parameters of SVM and Deep Learning with CNN, the results of the CNN classifier are better with respect to computational time and accuracy.

GASVM has also been proposed and tried for genes selection on four real microarray information. The reason is that GASVM can naturally diminish the cycle-based component of the information. Iteratively, the mix of genes can likewise automatically decline when the dimensionality is reduced. This iterative procedure is done in higher-dimensional information to produce potential quality subsets and eventually make an ideal subset of enlightening genes. It is therefore necessary to select genes using GASVM to produce a near-optimal (smaller) subset of informative genes for better cancer classification. By comparing various parameters of SVM, Deep Learning with CNN and GA-SVM classifiers, the results of the CNN classifier are better in terms of accuracy and GA-SVM classifier is found to be better in terms of computational time.

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