Locust-based genetic classifier for abnormality identification in brain

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ABSTRACT

This study investigates the loctus-based genetic classifier for abnormality identification in the brain. In medical care, clinical professionals have to spend a lot of time extracting, identifying, and segmenting the afflicted region from magnetic resonance brain images. Utilizing computer-aided approaches is crucial to overcome this restriction. Henceforth, this paper proposes an efficient classifier for diagnosing abnormalities in human brain using magnetic resonance images (MRI). The focus is on improving the accuracy and efficiency of medical image segmentation, specifically for brain tumours, to assist clinical professionals in early disease detection. In order to improve the image's quality through noise reduction, the Gaussian filter is employed during the pre-processing stage. The proposed tumour segmentation is based on the Otsu algorithm, and the gray-level co-occurrence matrix (GLCM) is used to extract the relevant features. In this work, the locust-based genetic classifier plays a crucial role in early brain disease identification and pinpointing the precise location of the damaged area. Accuracy, sensitivity, and specificity have been used to analyze and validate the outcomes of the proposed technique. The current study's findings indicate accurate prediction of brain abnormality and have a 98.9% accuracy rate, 97.2% specificity, and 96% sensitivity. The study presents a reliable and efficient method for diagnosing brain abnormalities using MRI. The combination of the proposed approaches significantly enhances the segmentation and classification processes, leading to high diagnostic accuracy. This approach offers practical benefits for clinical professionals by reducing the time and effort required for diagnosing brain abnormalities.

Contribution/Originality: This study introduces a novel approach by integrating a locust-based genetic classifier with OTSU algorithm for tumour classification and GLCM for feature extraction. This unique combination significantly enhances accuracy, efficiency, and early detection of brain abnormalities in MRI, achieving a 98.9% accuracy rate.

1. INTRODUCTION

Brain tumours are developed by abnormal cell growth in the brain and can practically afflict people of any age. Brain tumours can appear anywhere and in a range of picture intensities [1] and they can be of any size and shape. The categorization of brain tumours is an important step in the medical process. The clinician must verify the pictures

obtained from several imaging modalities, such as Computed Tomography (CT) and Magnetic Resonance (MR), in order to proceed with treatment. However, manually classifying MR images is a difficult and time-consuming operation [2]. To differentiate between different tumour types, automatic or semiautomatic methods for classification are required since human inspection can lead to classification mistakes. It is discovered that there are numerous classification methods available for identifying the type of tumour from the provided MR images. The development of automatic tumour identification has significantly changed how patients with tumours are treated, perhaps saving their lives [3]. It is important to use image processing techniques such as filtering, segmenting, feature extraction, and neural network training in order to automate the classification of cancer cells. The image's noise is removed using pre-processing techniques, and the Region of Interest is located using segmentation techniques [4].

Median filtering, according to authors in Devkota, et al. [5] is the ideal filtering method for pre-processing images. However, there are some restrictions on how well the very low-frequency components can be preserved. According to authors in Raja [6] low frequency components can be preserved by using mean filtering. However, the generated values vary depending on the type of dataset. As a result, the Gaussian filter is utilized in this paper for image pre-processing.

Challenges may arise during the collection stage of medical image recording, potentially causing the captured image recording, potentially causing the captured image to deteriorate. As a result, the system may not be able to examine the original image. Image segmentation is the division or segmentation of a digital image into comparable sections with the primary goal of making the image under review more relevant and simpler to visually evaluate. Image segmentation is a crucial step in the majority of medical image analyses. Thresholding, region-based, supervised, and unsupervised classification methods are several types of image segmentation approaches [7-10]. The identification of brain tumours has been studied using a variety of methods. To find tumours, morphological processes, thresholding, high-pass filtering, histogram equalization, linked component labelling, and segmentation are used. The volume of the tumour is determined along with the reconstruction of the two-dimensional retrieved tumour images into three dimensions. A method for medical picture segmentation comprises the segmentation method and clustering, in addition to the Fuzzy C Means (FCM) clustering and the separate marker-controlled watershed segmentation algorithms. In this methodology, the input image is initially segmented using clustering, and then the final segmented image is created by applying the segmentation algorithm to the primary segmentation [11]. This study presents the Otsu segmentation methodology as a solution to these significant limitations.

A feature method for extraction is required in order to obtain the features. For testing reasons, feature extraction is used to supply the neural network's input [12, 13]. In this study, we extracted textural features from GLCM data. It is critical and clinically significant to accurately identify retinal defacement and investigate its connections to diabetic risk factor. The proposed work employs a variety of approaches and algorithms to precisely identify and diagnose retinal defacement. They have used techniques like Random Forest [14] Convolutional Neural Network (CNN) [15] and Support Vector Machine (SVM)[16] in the current study. Since none of these methods possess a built-in ability to diagnose, they all generate predictions based on images. Graph theoretical techniques were utilised in the previous study. The evaluation of multiple species presents challenges. In references Huang, et al. [17] and Manogaran, et al. [18] the concept of consistent structures in multi-layer brain systems: applicability to epileptic diagnosis is presented forth. This strategy outperforms several cutting-edge techniques in the classification of brain diseases. But for diagnosing brain disorders, it is ineffective. In references Alhassan and Zainon [19] and Wu, et al. [20] it has been proposed to use a machine learning approach-based gamma dispersion for data collection, imbalance assessment, and brain tumour identification. The proposed approach guarantees the adequate representation and detection of minority class instances, such as rare brain tumour cases. However, to improve accuracy, optimization techniques must be used.

Therefore, this work proposes an effective locust genetic classifier for human brain disorders with high accuracy. Gaussian filter and Otsu algorithm are used for image pre-processing and segmentation, respectively. For feature

extraction, GLCM is utilized. Employing a locust-based genetic classifier, the collected features are classified. Here, a genetic algorithm based on locusts helps to identify the damaged regions by measuring their thickness, size, and area.

2. PROPOSED SYSTEM

An automated technique employed for identifying brain tumours and segmentation is the major contribution of the proposed work. The proposed algorithm, which is employed for image augmentation and segmentation, is based on a locust-based genetic classifier. Figure 1 depicts the block diagram of the brain tumour identification architecture.

The gaussian filter is used to pre-process the image in beginning stage, forecasting an unknown signal through an identical signal as input before filtering to produce an approximate value. The distortion-free image is subsequently segmented by an Otsu technique that chooses an optimum threshold inevitably according to the arrangement of observed pixel values.
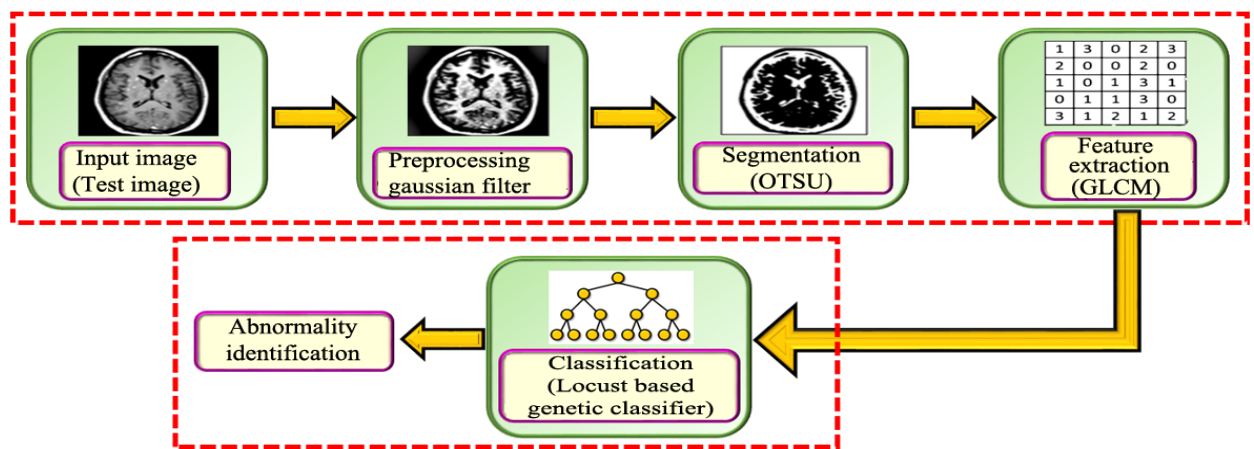

Figure 1. Proposed model.

In order to acquire second-order statistical features of texture for calculating image motion, GLCM implements feature extraction. The image is finally recognised by applying a locust-based genetic classifier that uses little pre-processing and convolution operations, which effectively identifies abnormalities in the human brain.

2.1. Preprocessing By Gaussian Filter

Pre-processing is employed to remove undesired noises in the captured image. It is also utilised to remove the undesirable part of a picture and extract the necessary part from a captured image. Enhancing an image's characteristics is the fundamental goal of preprocessing. Preprocessing is required for medical image interpretation due to imaging device noise that may be added to MR pictures. The Gaussian filter enhances the image quality by reducing noise, contracting enhancement, equalizing intensity, and removing outliers. The 1-D Gaussian distribution has the following shape:

$$G(x) = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{x^2}{2\sigma^2}} \qquad (1)$$

In two dimensions, Gaussian takes the form,

$$G(x,y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2+y^2}{2\sigma^2}} \qquad (2)$$

Where the average variation of the distribution is σ. It also assumed that the mean of the range would be zero. As a result, the gaussian filter evaluates the input images accurately and produces a noise-free output image.

2.2. Otsu Image Segmentation Technique

The Otsu method divides an image into the foreground and background using a single threshold. Otsu segmentation is ineffective in real-time due to its simplicity and accuracy. The probability P that every pixel point has a specific grayscale value if the total number of pixels in the image is T,

$$P_t = \frac{T_i}{T} \tag{3}$$

Where T_i is the number of pixels and i is the grayvalue. Given that the image needs be divided into sections according to the threshold, the likelihood P_t that pixels in the foreground and background would have values of Ω_0 and Ω_1, respectively, is,

$$\Omega_0 = \sum_{t=0}^{k} P_t = \Omega(k) \tag{4}$$

$$\Omega_1 = \sum_{t=k+1}^{L-1} P_t = 1 - \Omega(k) \tag{5}$$

The interclass variance of the two regions divided by the threshold th is also

$$Y(th) = \Omega_0 (\mu_0 - \mu)^2 + \Omega_1 (\mu_1 - \mu)^2 \tag{6}$$

Where the image's mean value, 0 and 1 is are the mean values of the target and background areas, accordingly, and is the image's mean value. The threshold group $th_1, th_2, \ldots, th_n$ separates the image into t + 1 individual intervals, assuming the image's grey level is S. The total variation across classes is,

$$Y(th_1, th_2, \ldots, th_n) = \sum_{t=0}^{t-1} \sum_{j=t+1}^{t} \Omega_i \Omega_j (\mu_i - \mu_j)^2 \tag{7}$$

Where the probabilities of two areas are Ω_i and Ω_j. The means of two sections are μ_i and μ_j. Hence, the proposed OSTU methodology is better suited to noisy images where it is challenging to distinguish the edges successfully segmenting the pre-processed raw image.

2.3. Feature Extraction by GLCM

Surface texture can be defined by the GLCM statistical feature extraction technique, which relies on the spatial connection between the pixels. By computing the pairs of specified values with the spatial relationship that arises from the image, texture characteristics can be retrieved. Utilizing sum entropy and sum average entropy difference variance, texture characteristics are retrieved. Statistical features are retrieved, some of which are used as input to neural networks. These statistical features include Standard Deviation, Kurtosis, mean, and entropy.

The statistical evaluation of textures considers the spatial relationship between the pixels. The GLCM algorithms determine the frequency of combinations of image pixels having specific values and are arranged in a spatial connection, creating a GLCM, and then gathering statistical data from this array to describe the surface texture of a photo. The Gray co-matrix algorithm in MATLAB creates a GLCM by calculating the number of times a pixel having the intensity value i appears in an exact spatial link to a pixel with a value j. The standard terms for a spatial connection are between the pixel of interest and the pixel directly to its right, but one may establish extra spatial connections between the two components. For every component (i, j), the last GLCM simply adds the number of instances the input image's pixel with frequency i formed the necessary spatial connection to a pixel having value j. The total number of rows and columns in a GLCM matrix equals the total number of gray levels in the image. Where $(|i - j|)$ represents the frequency distribution between pixels divided by a pixel distance $P_x(i), P_y(j)$, which contains the chances of change in gray levels i and j at an angle specified and distance in second order. The GLCM is used to calculate the amount of gray levels used, the average value of P, the standard deviation and mean of P_x and P_y, and other characteristics. The rows of $P(i,j)$ are added to find the ith entry, $P_x(i)$,

$$P_x(i) = \sum_{j=0}^{G-1} P(i, j) \tag{8}$$

$$P_y(j) = \sum_{i=0}^{G-1} P(i, j) \tag{9}$$

$$\mu_x = \sum_{i=0}^{G-1} i P_x(i) \tag{10}$$

$$\mu_y = \sum_{j=0}^{G-1} j P_y(j) \tag{11}$$

$$\sigma_x^2 = \sum_{i=0}^{G-1} (P_x(i) - \mu_x(i))^2 \tag{12}$$

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$$\sigma_y^2 = \sum_{j=0}^{G-1} (P_y(j) - \mu_y(j))^2 \qquad (13)$$

It can determine the various textural features that can be utilized to train the classifier by utilizing the equations below.

$$Homogeneity\ (ASM) = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \{P(i,j)\}^2 \qquad (14)$$

$$Contrast = \sum_{n=0}^{G-1} n^2 \{\sum_{i=1}^{G} \sum_{j=1}^{G} \{P(i,j)\} \qquad (15)$$

$$|i - j| = n \qquad (16)$$

$$Correlation = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \frac{\{i \times j\} \times P(i,j) - \{\mu_x \times \mu_y\}}{\sigma_x \times \sigma_y} \qquad (17)$$

An example of a few of the features that are taken from all classes is shown in the above equations. Therefore, the GLCM technique effectively separates the divided features from the image and feeds them into the classification process.

2.4. Locust Based Genetic Classifier

Using hereditary calculations has recently proven to have a number of advantages for resolving multi-target optimization problems. The first steps in using genetic algorithms to solve a problem are,

- Evaluating fitness function.
- During the reproduction stage, genetic processes like selection, crossing, and coupling alter the creation of springs.
- Genetic algorithms are employed to build variable esteems. Below is a list of the variables used in genetic algorithms.

2.4.1. Initial Populace

In GA Figure 2, the population typically consists of a single, random string, while disordered double strings of varying lengths might be interpreted as the chromosomes of each population.

2.4.2. Evaluation of Fitness Function

The process duplicates each string to display the target work values, with "F" representing the wellness work. There is no requirement for a user interface to carry out the wellness work because it is fully objective. The system replaces inherited material with a collection of bits. A person's health is assessed by adding up the strength of the edges in an improved image; a dark image with optically complex edges has a lot of serious edges. The fitness function is calculated by taking the population's total estimate and determining whether the portrayal is accurate or 0. The act of healthy articulation might be challenging in various situations. Re-enactment is done in this circumstance to gauge the amount of wellness work.

2.4.3. Genetic Operators

Genetic operator use traverse to merge data. To improve the yield string, it combines two data strings known as the parent string. It comes in a variety of forms, including steady traverse and one- and two-point traverse. Person's unique chromosomes, which are matched to their parent persons, are what determine variation.

2.4.4. Parameter Domain

Step 1: population size every time, the number of chromosomes indicates the size of the population and creates a certain number of chromosomes that are present in the population.

Step 2: A breakdown of how many generations are produced throughout the iteration is given.

Step 3: You must provide the probability of randomly incorporating additional information, also known as the transformation rate. The potential of mutation, or mutation rate, is required.

2.4.5. Algorithm

Step 1: Obtaining a picture of the brain as an input.

Step 2: Converting a colour image to a grayscale version.

Step 3: Preprocess the image using the gaussian filter to enhance its quality.

Step 4: After improving the image, divide it into samples and use Otsu segmentation to identify the threshold of each sample to find the part of the image that is infected.

Step 5: Using a GLCM, the diseased section is detected and its features extracted.

Step 6: Collect the results.

Step 7: To classify the images, give the output as input to the genetic classifier based on locutus.

Step 8: Create the genetic algorithm's parameters and train them.

Step 9: Use the locust-based genetic algorithm.
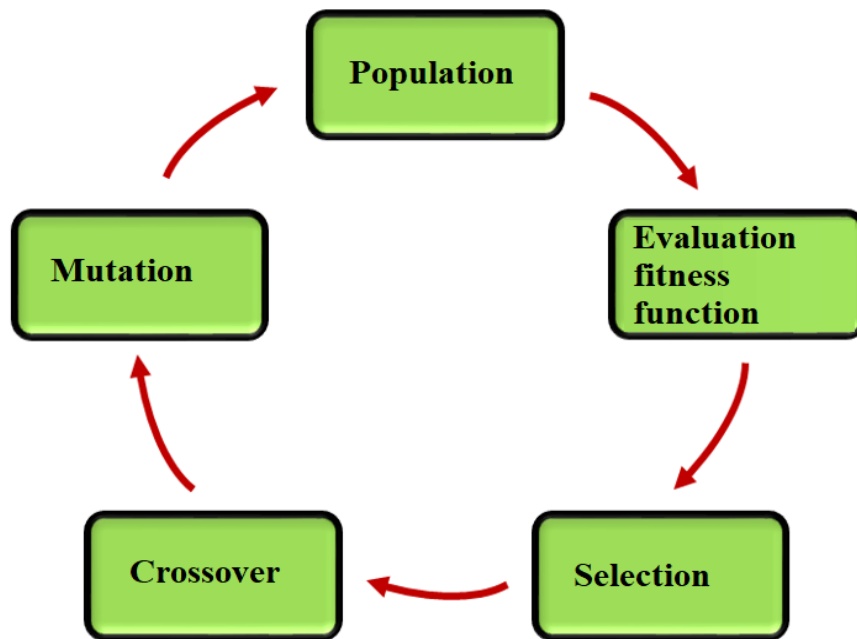
Figure 2. Genetic classifier.

Step 10: Compare the evaluated parameter to the trained parameter.

Step 11: Image is classified by locust-based genetic algorithm.

Step 12: In conclusion, the output image with the classification is shown.

3. RESULTS AND DISCUSSIONS

Since classifying a tumour is a difficult and delicate task, precision and dependability are always valued highly. Therefore, a detailed methodology that opens up new avenues for creating more reliable picture segmentation techniques is highly desired. Images are displayed as an output in these figures, such as a filtered image or a grayscale image. Last but not least, the tumour from the MRI image is removed. Real-time patient data is collected and analyzed for this purpose. It is relatively simple to find the tumour and extract it from an MRI image using Python software since the tumour's intensity in an MRI image is higher than that of its background. Figure 3 provides the input image.
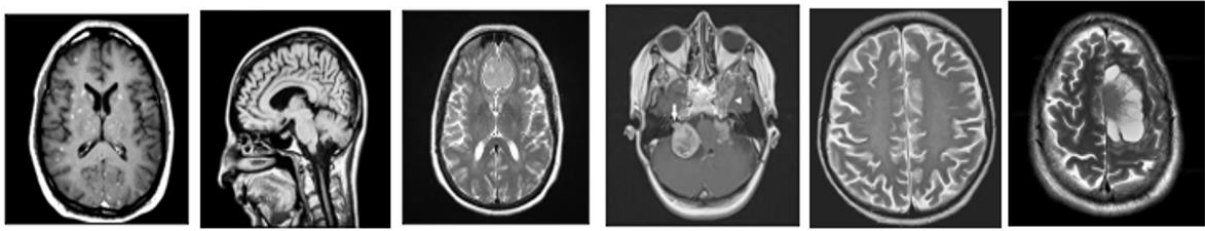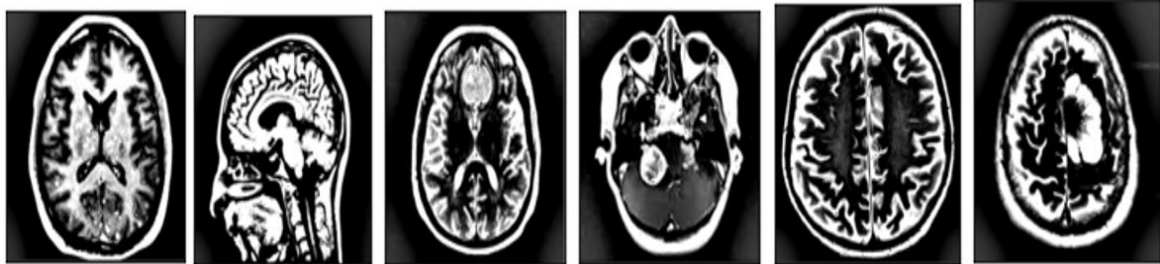
Figure 3. Input image.

Figure 4. Gaussian filter.

Image improvement is the modification of images to make them look better by enhancing visibility and contrast. Gaussian filters are used in image enhancement to reduce noise and improve image quality, as shown in Figure 4. Gaussian a linear filter that predicts white intensity values, is computationally effective and enhances image quality along the image's borders. It greatly aids in reducing noise. High-frequency components like impulse noise, salt noise, and pepper noise are eliminated by the Gaussian filter. Due to the different sounds included in the raw photos, they are not appropriate for direct processing. To remove this noise, this work develops gaussian filter-based picture pre-processing algorithms.

Figure 5. OTSU segmentation.

Segmentation is the process of dividing a digital image into various segments. Simplifying the representation of an image into something more relevant and understandable is the aim of segmentation. One of the most important methods for seeing human tissues is known as image segmentation. It is more likely that faults have been found when segmenting a brain tumour image manually by a professional. The proposed technique is to determine a global threshold value for a specific image in order to automate image segmentation. The Otsu method is employed, which is depicted in Figure 5, to determine the ideal threshold value. Image segmentation is a technique used to extract things from photographs, such as brain tumours. With multiple thresholds, an object can have a specific gray level.

Table 1. Feature extraction.

Images	Extracted feature				
	Homogeneity	Correlation	Dissimilarity	Energy	Contrast
Image.1	0.478	0.990	5.125	0.342	126.459
Image.2	0.412	0.946	14.299	0.333	752.882
Image.3	0.423	0.940	11.386	0.115	0.423
Image.4	0.436	0.962	8.086	0.133	247.478
Image.5	0.362	0.976	6.678	0.206	159.870
Image.6	0.442	0.955	9.838	0.356	395.378

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Table 1 represents the extracted features with their values through the use of GLCM technique. The experimental findings verify the outstanding efficiency of the features extracted using this strategy. For each specific feature, the distance measure of its values within the class is relatively low, whereas it reaches its maximum value between classes. As a result, this work has offered adequate techniques for feature extraction and image pre-processing for MR brain image interpretation. By measuring specific characteristics or features that set apart one input pattern from another pattern, feature extraction aims to decrease the original data set. By taking into account the description of the pertinent aspects of the image into a feature space, the extracted feature should give the classifier the characteristics of the input type. The work utilizes GLCM for image analysis. For classification as well as segmentation applications, however, these features are evaluated in a different way. Image categorization between images approximates the features from the entire image. In contrast, picture segmentation is done within the image, thus each pixel's features are approximated.
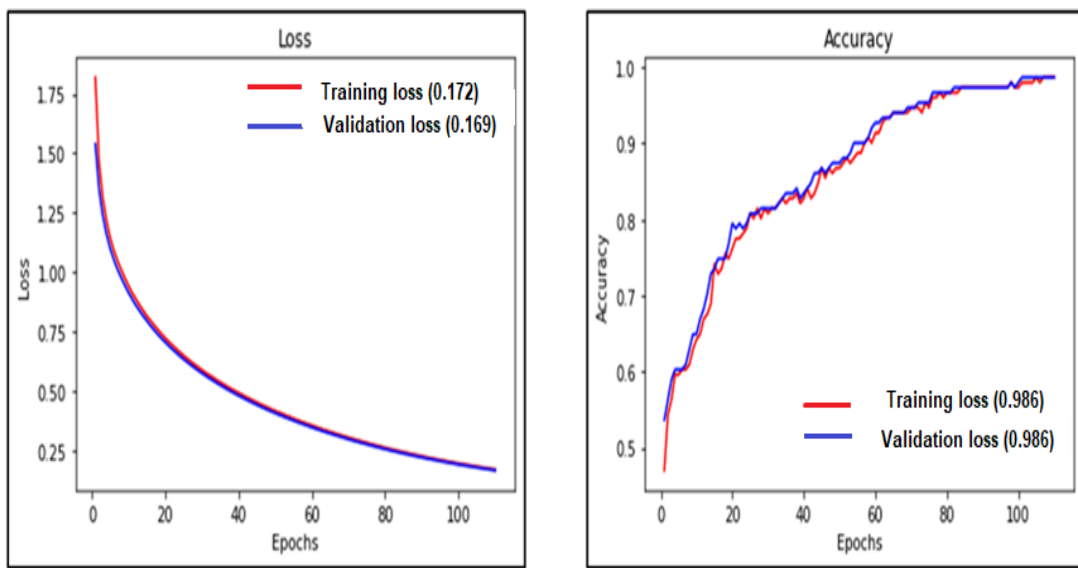

Figure 6. Accuracy & loss of locust based genetic classifier.

Figure 6 displays the classifier's accuracy and loss during its training and testing phases. The graph demonstrates that the proposed classifier has better accuracy with minimal loss during their testing and training period.

Table 2. PSNR, SNR, RMSE, and MSSIM measurements obtained using various noise elimination techniques.

Techniques	SNR (Signal-to-noise ratio)	RMSE (Root mean square error)	PSNR (Peak signal-to-noise ratio)	MSSIM (Multi scale structural similarity)
Median filter	16.270	213.500	16.267	0.648
Wiener filter	15.867	245.500	24.238	0.639
Gaussian filter	20.318	0.005	77.045	0.995

3.1. Comparison Analysis

According to the findings in Table 2, when compared to the wiener and median filters, the proposed Gaussian technique gives improved MSSIM, SNR, and PSNR values, as well as lower RMSE values. This indicates that the filtering step retains the picture features.
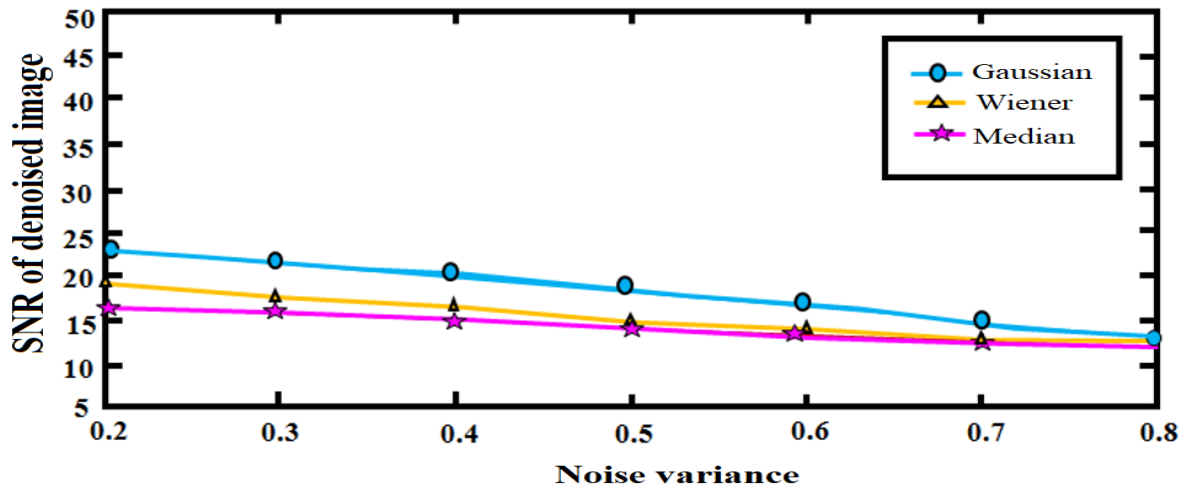
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Figure 7. Enhancing image efficiency under noise SNR determined in relation to several noise values.
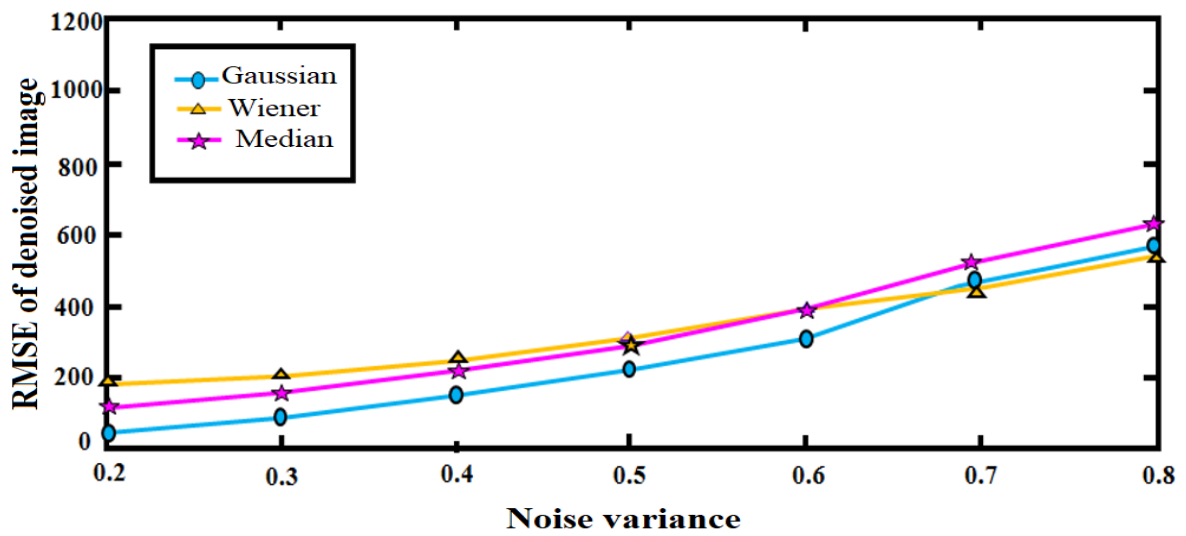
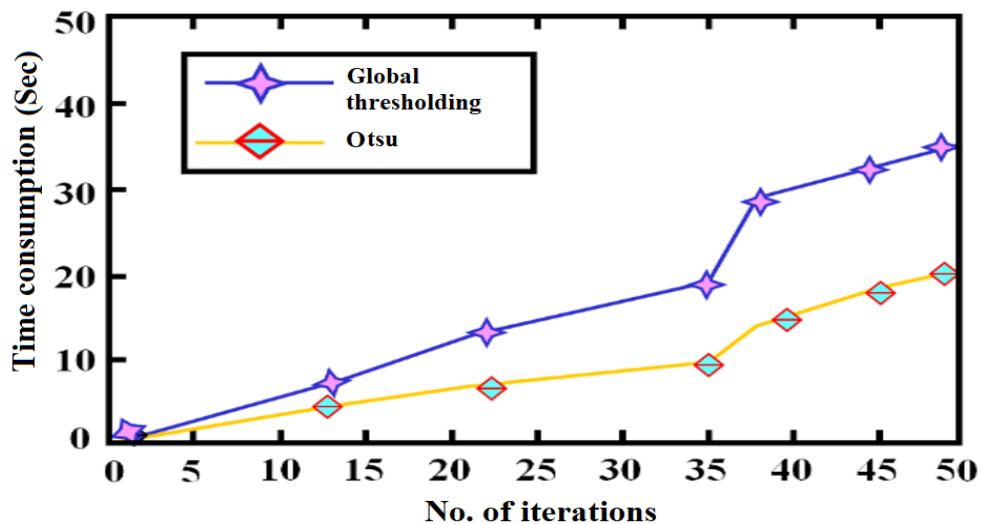**Figure 8.** Image sharpening efficiency under noise RMSE measured in relation to several noise values.

Figure 9. Time consumption comparison.

Figure 7 illustrates that the gaussian filter approach causes a significant SNR gap when contrasted with other noise mitigation strategies. In terms of RMSE, Figure 8 shows that the gaussian filter technique likewise produces

the lowest RMSE value. Figure 9 depicts a comparative assessment of segmentation methods, demonstrating that the proposed Ostu consumes less time than the global thresholding technique.

Table 3. Comparison evaluation of performance metrices.

Methods	Accuracy	Specificity	Sensitivity
Decision tree	89.9	90.4	89.7
Random forest	91.2	91.8	90.2
Support vector machines	93.6	95.6	94.1
Proposed classifier	98.6	97.2	96
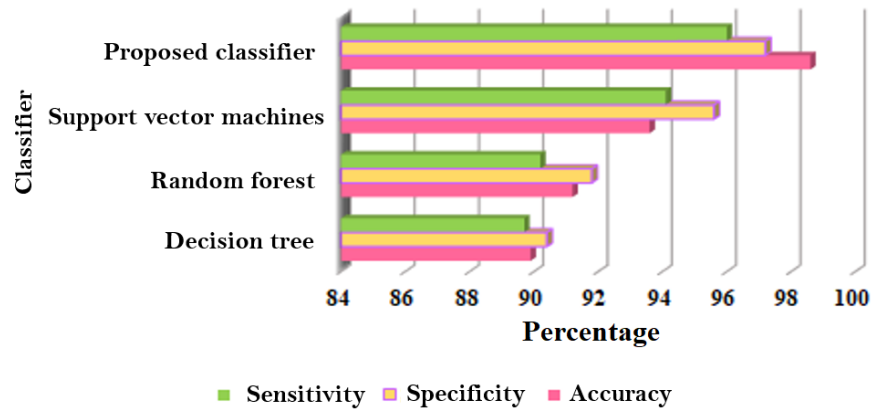
Figure 10. Comparison of performance metrices.

According to the Table 3, the proposed locust genetic classifier performs better than other existing approaches in terms of accuracy, specificity, and sensitivity. The proposed classifier achieves a high accuracy value compared to decision tree, random forest, and SVM techniques, which is illustrated in Figure 10.

4. CONCLUSION

This research thus proposes an effective classifier for identifying brain abnormalities. The Gaussian filter is used during the pre-processing step to enhance the image's quality through noise reduction, contrast improvement, intensity equalising, and outlier elimination. In order to improve accuracy and efficiency in the medical segmentation process, the recommended tumour segmentation adopts Otsu algorithm and employs the GLCM to extract the features. The locust-based genetic classifier employed in this work is crucial for early diagnosis of brain illnesses and localization of the affected region. The results of the suggested technique have been examined and validated using accuracy, sensitivity, and specificity. The results of the presented research provide precise brain abnormality prediction with a 98.9% accuracy rate, 97.2% specificity, and 96% sensitivity.

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