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Detection and Classification of MRI Brain Tumors using S3-DRLSTM Based Deep Learning Model

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ABSTRACT- Developing an automated brain tumor diagnosis system is a highly challenging task in current days, due to the complex structure of nervous system. The Magnetic Resonance Imaging (MRIs) are extensively used by the medical experts for earlier disease identification and diagnosis. In the conventional works, the different types of medical image processing techniques are developed for designing an automated tumor detection system. Still, it remains with the problems of reduced learning rate, complexity in mathematical operations, and high time consumption for training. Therefore, the proposed work intends to implement a novel segmentation-based classification system for developing an automated brain tumor detection system. In this framework, a Convoluted Gaussian Filtering (CGF) technique is used for normalizing the medical images by eliminating the noise artifacts. Then, the Sparse Space Segmentation (S3) algorithm is implemented for segmenting the pre-processed image into the non-overlapping regions. Moreover, the multi-feature extraction model is used for extracting the contrast, correlation, mean, and entropy features from the segmented portions. The Deep Recurrent Long-Short Term Memory (DRLSTM) technique is utilized for predicting the classified label as normal of disease affected. During results analysis, the performance of the proposed system is tested and compared by using various evaluation measures.

Keywords: Brain Tumor Detection, Magnetic Resonance Imaging (MRI), Convoluted Gaussian Filtering (CGF), Sparse Space Segmentation (S^3), Multi-Feature Extraction, and Deep Recurrent Long Short-Term Memory (DRLSTM) Classification

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1. INTRODUCTION

In recent times, the accurate identification of brain tumor is highly a challenging process due to the complex structure of brain [1]. Typically, the brain tumor [2] is a growth of abnormal cells in the nervous system that interrupts the normal functions of brain by increasing the inflammation. According to the reports of WHO, it is analyzed that nearly 50% of people can affect by this outrageous disease around the world [3]. Hence, it is more important to identify and diagnose this disease for saving the life of human. The Magnetic Resonance Imaging (MRI) is one of the most popular imaging tool increasingly used by the medical experts for diagnosing the brain tumor [4]. Normally, the brain tumor can be categorized into the types of benign and malignant (i.e. mild and severe). Recently, various research works [5] have developed an automated diagnosis system for identifying and classifying the brain tumors

Moreover, it is more useful for the medical experts to predict the disease at the earlier stages for providing the proper treatments. In the conventional works [6, 7], an automated tumor detection system is developed by using various medical image processing techniques such as preprocessing, feature extraction, optimization, and classification. In which, the classification techniques [8] play a vital role in the disease identification system, because which predicts the label for identifying the brain image as whether normal or disease affected. Due to an accurate detection rate, and increased processing speed, the deep learning techniques are widely used in the medical imaging systems. However, it faced the challenges related to the problems [9, 10] reduced learning rate, more time for training & testing, and high complexity in computational operations. Therefore, the proposed work objects to develop a novel segmentation based deep learning system for an accurate tumor identification and classification. The major research objectives of this work are as follows:

- To remove the noise artifacts and to increase the quality of MRI brain images, a Convoluted Gaussian Filtering (CGF) technique is employed.
- To accurately segment the preprocessed image into non-overlapping regions, a Sparse Space Segmentation (S^3) technique is deployed.
- To improve the learning rate of classifier, a set of multi-level features such as contrast, mean, correlation, and entropy have been extracted.
- To predict the normal and disease affected tissues based on the features of brain image, a novel Deep Recurrent Long Short-Term Memory (DRLSTM) mechanism is implemented.
- To test the validness and performance of the proposed S^3-DRLSTM system, various evaluation indicators have been computed during analysis.

The other portions of this paper are segregated into the followings: the conventional medical image processing techniques are reviewed in *Section II*. The description of the proposed S^3-DRLSTM technique is presented in *Section III*. The results are validated and compared using various measures in Section IV. Finally, the overall paper is concluded with the future work in *Section V*.

2. RELATED WORKS

This section reviews the conventional image processing techniques used for developing the medical disease diagnosis system, where the pros and cons of each technique is discussed according to its operations and features.

Razzak, et al [11] investigated the importance and advantages of using deep learning techniques for medical image processing. Here, the major differences between the conventional machine learning and deep learning techniques have been discussed. This paper investigates the architecture models of various deep learning techniques such as Deep Neural Network (DNN), Convolutional Neural Network (CNN), Recurrent Neural Network (RNN), and Deep Convolution Networks (DCN). According to this analysis, it is observed that the deep learning techniques have the advantages of high accuracy, fast learning, and better detection performance. Mallick, et al [12] employed a deep wavelet auto encoder based DNN technique for MRI brain image segmentation and classification. This paper integrates the functions of Deep Wavelet Auto-encoder (DWA) with DNN technique for improving the image decomposition. Here, the auto-encoding and decoding processes help to increase the detection accuracy and learning rate of classifier. Moreover, it provides better overall accuracy, and similarity coefficients due to the integration of image encoding operations. Jia and Chen [13] implemented a Fully Automatic Heterogeneous Segmentation based Support Vector Machine (FAHS-SVM) classification mechanism for identifying the human brain abnormality with better learning rate. Here, the MRI images have been used to predict the normal and abnormal tissues from the brain. In addition to that, an Extreme Learning Machine (ELM) classifier was used to improve the detection accuracy. Hussain, et al [14] utilized a CNN technique for identifying the alzheimer's disease from the brain MRIs. The work objects to 12-layered CNN architecture for improving the prediction accuracy of disease identification system. Siar, et al [15] employed a CNN mechanism for processing the MRI brain images. Here, the image de-noising and data labeling operations have been performed for improving the quality of image.

According to the review, it is analyzed that the conventional works faced difficulties in complex operations, high time consumption, reduced learning rate, and error rate.

3. PROPOSED METHODOLOGY

This section presents the explanation about the proposed segmentation based classification methodology for identifying the tumor affected portions from the brain MRIs. The contribution of this work is to exactly spot the abnormal tissues from the brain images with the help of novel segmentation based deep learning classification techniques. Here, the MRI brain image dataset is obtained as the input for system implementation, then the consequent image processing operations are performed for tumor detection. At first, the input MRI is preprocessed by using the Convoluted Gaussian Filtering (CGF) technique for quality improvement, contrast enhancement, and noise elimination. After that, the Sparse Space Segmentation (S^3) technique is applied to segment the preprocessed image into non-overlapping regions in the same subspace. Moreover, the Multi-Feature Extraction (MFE) model is employed to extract the contrast, correlation, mean, and entropy features of the segmented regions. Finally, the Deep Recurrent – LSTM (DRLSTM) mechanism is used to predict the normal and abnormal issues of brain. The overall flow and operations involved in the proposed S^3-DRLSTM model is shown in *figure 1*.

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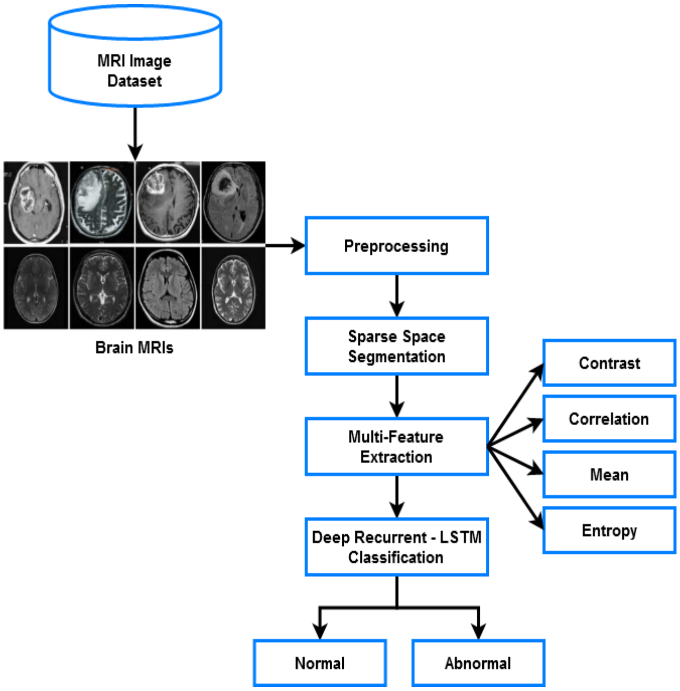

Fig 1. Flow of SSS-DRLSTM based brain tumor detection system

3.1 Preprocessing

After obtaining the input image from the dataset, the Convoluted Gaussian Filtering (CGF) technique is used for noise removal and quality enhancement. The reason of using this filtering is to minimize the effects of artifacts for obtaining the clear texture patterns of image. The key benefit of this technique is, it filters the noisy pixels and improves the edge details with better image quality. Moreover, the classification accuracy and learning rate of classifier is entirely depends on the quality of normalized output image. In this mechanism, the noise K_{ab} is represented as follows:

$$K_{ab} = \begin{cases} D_{ij}, & \text{if}\left(\text{mean}\left(S_{ij}\right) > Im_{ab}\right) \\ 0, & \text{Otherwise} \end{cases} \quad (1)$$

Where, Im_{ab} indicates the image pixels, $a = \{1,2, \dots M\}$, $b = \{1,2, \dots N\}$, M indicates the row size, N is the column size of image, D_{ij} denotes the center pixel, and S_{ij} indicates the image cells. Then, the image is sharpened G_e by using the following model:

$$G_e(a,b) = Img_{in}(a,b) + \partial Hf(a,b) \quad (2)$$

Where, ∂ is the tuning filter parameter, $Img_{in}(a,b)$ is the input image, and $Hf(a,b)$ denotes the high pass filter mask. Consequently, the image separation K_{ij} is performed by using the following model:

$$K_{ij} = G_e(a-1{:}a+1, b-1{:}b+1) \quad (3)$$

Then, the average difference value in K_{ij} is estimated according to the mask matrix P_D and size of filter mask L as shown in Fig 2, where the index of matrix is represented in 3×3 and 5×5 matrices. Moreover, the performance of this technique is improved with reduced noisy pixels.

i-1, j-1	i, j-1	i+1, j-1
i-1, j	i, j	i+1, j
i-1, j+1	i, j+1	i+1, j+1

(a)

i-2, j-2	i-1, j-2	i, j-2	i+1, j-2	i+2, j-2
i-2, j-1	i-1, j-1	i, j-1	i+1, j-1	i+2, j-1
i-2, j	i-1, j	i, j	i+1, j	i+2, j
i-2, j+1	i-1, j+1	i, j+1	i+1, j+1	i+2, j+1
i-2, j+2	i-1, j+2	i, j+2	i+1, j+2	i+2, j+2

(b)

Fig 2. Mask matrix (a). 3 × 3, and (b). 5 × 5

3.2 Sparse Space Segmentation (S3)

After filtering, the segmentation technique is implemented to segment the preprocessed image into the non-overlapping regions. The main purpose of using this technique is to minimize the computational complexity of data operations, and increases the convenience of subsequent processing. During this segmentation, the normalized image is split into super pixels, which are also termed as irregular image blocks of adjacent pixels. It has the similar characteristics of color, brightness, and texture, then it replaces the large number pixels into minimum. In this model, the data matrix is determined at first according to the dimensions of linear subspace as shown in below:

$$DM = \{d_1, d_2, d_3 \dots d_n\} \times P_M \quad (4)$$

Where, DM indicates the data matrix, P_M denotes the permutation matrix, $DM_i \in X^{Di \times N_i}$ defines the matrix of ith subspace data. In subspace, every data in the matrix DM is linearly represented in the same subspace as represented below:

$$d_i = DMs_i, s_{ii=0} \quad (5)$$

Where, $s_i = [s_{i1}, s_{i2} \dots s_{in}]^H$, and the set S can be represented by using the following model:

$$DM = DMS, \; S_{ii} = 0 \quad (6)$$

Where, $S = [s_1, s_2 \dots s_n] \in X^{N \times N}$ is the generated sparse matrix. Consequently, the linear fusion function is computed by using the following model:

$$LI_{ij} = \omega_1 P_1(i,j) + \omega_2 P_2(i,j) + \omega_3 P_3(i,j \quad (7)$$

Where, LI_{ij} is the fused image, $\omega_1, \omega_2, \omega_3$ are the weight values, and P_1, P_2, P_3 are the pixel values at position (i, j). By using this model, the segmented image can be obtained for further operations.

3.3 Multi-Feature Extraction

In this stage, the different types of imaging features such as contrast, correlation, mean, and entropy are extracted from the segmented region. These features are used to train the classifier for accurately predicting the normal and abnormal tissues. Moreover, it helps to improve the precision and accuracy of the tumor detection system. Normally, the accurate detection of tumor is highly crucial due to its complex structures and tissues. Here, the feature extraction helps to obtain the more relevant features used for improving accuracy of classification. Typically, the contrast, entropy, contrast, and mean are considered as the most essential features used for determining the performance of classifier, which are estimated as follows:

$$\mathrm{Mean} = \left(\frac{1}{a,b}\right)\sum_{a=0}^{i-1}\sum_{b=0}^{j-1} f(a,b) \qquad (8)$$

$$\mathrm{Ent} = -\sum_{a=0}^{i-1}\sum_{b=0}^{j-1} f(a,b)\log_2 f(a,b) \qquad (9)$$

$$\mathrm{Corr} = \frac{\sum_{a=0}^{i-1}\sum_{b=0}^{j-1}(a,b)f(a,b) - \mathrm{Mean}_j \mathrm{Mean}_i}{\sigma_j\sigma_i} \qquad (10)$$

$$\mathrm{Cont} = \sum_{a=0}^{i-1}\sum_{b=0}^{j-1}(a-b)^2 f(a,b) \qquad (11)$$

Where, a, b are the histogram elements, i, j are the width and height of image respectively, and σ is the standard deviation. The extracted features are used to train the classifier for detecting the normal and abnormal tissues.

3.4 Deep Recurrent Long Short-Term Memory (DRLSTM) Classification

After extracting the feature extracts, an advanced deep learning classification technique, named as, DRLSTM is utilized to accurately predict the classified label. In this framework, all units exist in the hidden layer are exchanged with the memory blocks, where each memory block comprises minimum of one cell that is activated by the regulating gates. By using these gates, the incoming and outgoing data packets are controlled, in which the forget gate is located among the incoming and outgoing units. These units are also termed as the sigmoid units, where the activation function is ranging from 0 to 1. In DRLSTM model, the optimal parameter tuning is performed, and the logical probabilistic rules have been generated for the data vector. In addition to that, an architecture unit has been used to separate the blocks of DRLSTM. Then, the forward pass could be performed by using the fully connected layer, dropout layer, and LSTM layer. Moreover, the loss functions are estimated based on the Mean Squared Error (MSE). The key benefits of using this technique are high learning rate, accurate prediction results, minimal computational complexity, and less delay. The architecture model of the proposed DRLSTM is shown in *figure 3*.

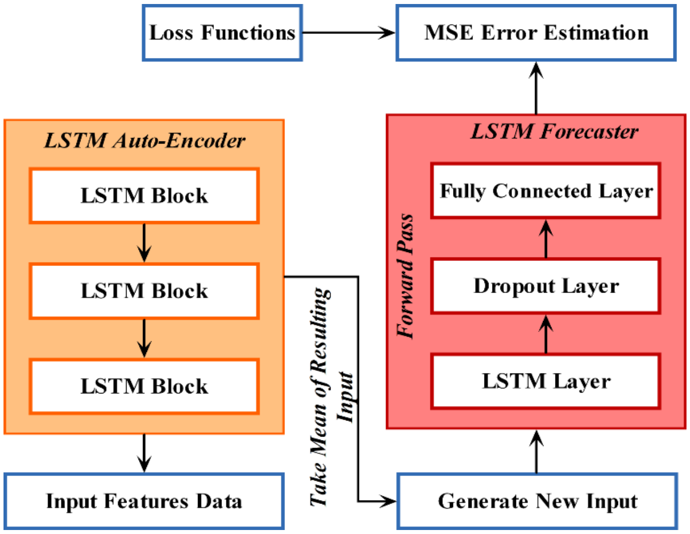

Fig 3. Architecture of DRLSTM

During this operation, the extracted features are used to train the classifier, where the probabilistic rules are generated by estimating the logical relation α. Initially, the logical probabilistic rules $\Delta P_k(t)$ are estimated with respect to the data vector E_D^i and logical facts δ, which is represented as follows:

$$\Delta P_k(t) = f_k'(nt_k(t)(\delta - E_D^k(t))) \qquad (12)$$

Then, the feature map g^k is obtained by performing the mathematical operations between the sets of information as shown in below:

$$g^k = E_D^k(t) + (\Delta P_k(t) + E_D^k(t)) \qquad (13)$$

Moreover, the trail vector is estimated for the R^kth target vector by using the following model:

$$R_{i,j}^k = \begin{cases} g_{i,j}^k & \text{if} \quad D_L == 1 \\ \Delta P_{i,j}^k & \text{else} \end{cases} \qquad (14)$$

Where, D_L indicates the labeled data. According to the weight value of the target vector, the dropout factor is tuned and, the randomly selected neurons are eliminated for enhancing the process of training. Moreover, it helps the network to learn with neurons based on the specialization of training data as illustrated below:

$$T_D(t) = \frac{1}{2}\left(t - \sum_{k=1}^{n} \tau\ \omega_k'\ R^k\right) \qquad (15)$$

Where τ is the dropout factor and ω_k' indicates the weight value of the k^{th} target vector. After that, the memory cells are updated with forward pass as represented below:

$$m^t = T_D(t) \odot v^t + f_k'\big(nt_k(t)\big) \odot m^t \qquad (16)$$

Where, m^t is the memory cells and v^t is the combination of feature map and feedback. After that, the feature vectors are obtained from the output of LSTM layer, which can be passed to the input of fully connected sigmoid layer. It computes the probability distribution for each category of class as represented below:

$$Q_{sig}(C_{lbl}) = \frac{e^{D_L^j}}{1+e^{D_L^j}} \qquad (15)$$

Where, D_L^j is the output value belongs to j^{th}class. Consequently, the disparity w_s among the actual segments are estimated based on the binary cross entropy of the loss function as computed below:

$$w_s = \sum_{i=1}^{k} P(D_L^i) \text{ x } \log(Q_{sig}(D_L^i)) \qquad (16)$$

At last, the output class is obtained as follows:

$$C_{lbl} = D_L(Q_{sig} \leq 1) \qquad (17)$$

Based on this label, the given brain image is detected as whether normal or disease affected.

4. RESULTS AND DISCUSSIONS

In this section, the performance and results of the proposed DRLSTM based brain tumor identification and classification system is validated and compared using different evaluation measures. For this analysis, the BRATS 2015 dataset available in [16] is used, which comprises the training cases of 110, and testing cases of 220. The measures taken for this analysis are accuracy, sensitivity, specificity, precision, f1-score and dice, which are mainly used for validating the detection performance of the disease detection and classification techniques. *Table 1* and *figure 4* validates the accuracy of conventional [17] and proposed classification techniques. Typically, the accuracy is considered as an essential measure used for validating the detection efficiency of classifier, which is estimated by using the following model:

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \times 100\% \qquad (18)$$

Where, TP – True Positives, TN – True Negatives, FP – False Positives, and FN – False Negatives. According to this analysis, it is evaluated that the proposed DRLSTM overwhelms the other conventional classifiers with high accuracy by accurately predicting the classified label.

Table 1. Accuracy analysis

Techniques	**Accuracy (%)**
Regularized Extreme Learning Machine (RELM)	94.23
Deep CNN (DCNN)	95
Deep Neural Networks – Deep Wavelet Auto encoder (DNN-DWA)	96
K-Nearest Neighbor (KNN)	96.6
CNN	97.5
CNN-SVM	98.5
Proposed DRLSMT	99

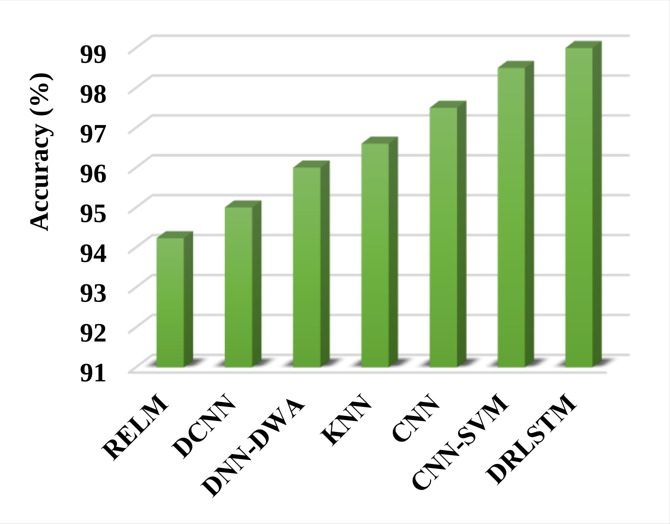

Fig 4. Accuracy

Table 2 validates the accuracy of conventional SVM, CNN, CNN-SVM and the proposed DRLSTM classifiers with respect to the classification stages of benign and malignant. Generally, the abnormal brain tissues are categorized into the types of benign and malignant (*i.e.* mild and severe). Based on the results, it is identified that the proposed DRLSTM provides an increased accuracy by exactly predicting the stages of tumor.

Table 2. Accuracy with respect to the classes of benign and malignant

Techniques	Stages	
	Benign	Malignant
SVM	61.67	67.98
CNN	97.72	97.72
CNN-SVM	98.5	98.6
Proposed DRLSTM	98.8	98.9

Table 3 and figure 5 compares the conventional CNN, RF, GA, FCM and proposed DRLSMT classifiers based on the parameters of sensitivity, specificity, and segmentation accuracy. Typically, the sensitivity, and specificity are considered as the most important parameters used for testing the detection efficiency of classifier, which are estimated by using the following models:

$$\text{Sensitivity} = \frac{TP}{TP+FN} \times 100\% \qquad (19)$$

$$\text{Specificity} = \frac{TN}{TN+FP} \times 100\% \qquad (20)$$

Moreover, the obtained results show that the proposed DRLSTM outperforms the other conventional classifiers with better results.

Table 3. Comparative analysis based on various measures

Techniques	Sensitivity (%)	Specificity (%)	Segmentation accuracy (%)
CNN	97.2	98.9	98.5
Random Forest (RF)	96.1	97.5	98.01
Genetic Algorithm (GA)	91	90	91.7
Fuzzy C-Means (FCM)	90.6	91.7	92.5
Proposed DRLSTM	97.5	99	99

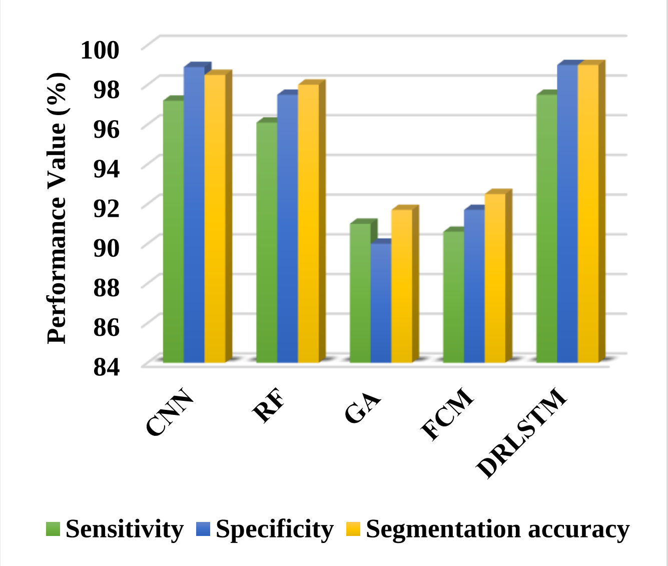

Fig 5. Analysis based on sensitivity, specificity, and segmentation accuracy

Table 4 compares the conventional CNN and proposed DRLSTM techniques based on various evaluation parameters, where the results are taken for before and after segmentation outputs. Similar to the other measures, the precision, f1-score, and dise similarity coefficient are also widely used for testing the validness and exactness of classification approaches, which are computed as follows:

$$\text{Precision} = \frac{\text{TP}}{\text{TP+FP}} \times 100\% \tag{21}$$

$$\text{F1} - \text{score} = \frac{2\times\text{Precision}\times\text{Sensitivity}}{\text{Precision+Sensitivity}} \times 100\% \tag{22}$$

$$\text{Dise} = \frac{2\times\text{TP}}{\text{TP+TN+FP+FN}} \times 100\% \tag{23}$$

Based on the results, it is evident that the proposed DRLSTM technique overwhelms the other techniques with improved values of these measures. Due to the proper noise removal, segmentation, and feature extraction, the DRLSTM technique could exactly predict the classified label with better performance outcomes.

Table 4. Comparative analysis based on before and after segmentation

Parameters	Existing CNN		Proposed DRLSTM	
	Before segmentation	After segmentation	Before segmentation	After segmentation
Sensitivity	94.1	97.2	95.2	97.5
Specificity	95.4	98.9	95.8	99
Accuracy	95.3	98.5	96.2	98.9
Precision	95.9	97.6	96.1	98.5
F-score	95.6	98.1	95.9	98.9
Dise	96.1	98.7	96.5	99

5. CONCLUSION

This paper develops a new segmentation-based classification approach, named as, S^3-DRLSTM technique for the MRI brain tumor disease detection. The contribution of this paper is to obtain an improved tumor prediction rate by implementing a simple and efficient segmentation based classification technique. Here, the CGF technique is used to preprocess the given MRI brain image by eliminating the noise artifacts, increasing the contrast and quality of image. Then, the S^3 algorithm is utilized to segment the non-overlapping regions of the image by constructing the sparse matrix. Moreover, the multi-feature extraction technique is deployed to extract the distinct features like contrast, correlation, entropy and mean for improving the learning rate of classifier. Finally, the DRLSTM technique is used to predict the classified label based on the extracted features, where the optimal parameter tuning is performed that reduces the complexity of computations. The key benefits of using this technique are high learning rate, accurate prediction results, minimal computational complexity, and less delay. For testing the performance of this detection system, various evaluation indicators have been evaluated and compared during results analysis. The estimated results state that the proposed S^3-DRLSTM technique overwhelms the other conventional approaches with better performance results. In future, this work can be further extended by incorporating the meta-heuristic optimization technique for simplifying the classification process.

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