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A Novel Deep Learning Framework for Automated Brain Tumor Classification Based on CNN-BiLSTM Model

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Abstract: Early identification of brain tumors is crucial for effective therapy and improved clinical outcomes. For brain tumor detection, this study presents a novel neural network that combines a three-layer Convolutional Neural Network (CNN) with a Bidirectional LSTM (BiLSTM). The proposed approach can automatically identify complex patterns and features from medical imaging data by using advanced computational techniques, leading to faster and more accurate evaluations. This study contributes to the field of medical image analysis by providing a reliable and accurate computational approach for brain tumor recognition. The BR35H dataset is used in this research, which comprises MRI images of both tumor and non-tumor subjects. The proposed CNN-BiLSTM model showed strong performance in tumor detection, with an accuracy of 98%, a precision of 98.48%, a recall of 97.5%, and an F1-score of 97.99%. The effectiveness of the proposed method is demonstrated through a thorough final evaluation, which includes a confusion matrix, comparison with current algorithms, and experiments using different data sizes. These experimental outcomes show the significance of combining CNN and BiLSTM models for brain tumor recognition.

Keywords: Brain Tumors, Bidirectional LSTM (BiLSTM), Convolutional Neural Network (CNN), Deep Learning, Machine Learning, Magnetic Resonance Imaging (MRI).

1. Introduction

The brain is crucial for human life, yet medical research remains challenging because of its intricate architecture and functionality. Brain tumors are a major problem in the cerebral region and are caused by abnormal tissues growing uncontrollably. They can originate in the brain itself or develop as secondary tumors in other parts of the body, such as the skin, kidneys, lungs, or breasts, before spreading through blood vessels to the brain [1]. These highly dangerous tumors cause many fatalities worldwide and present a significant therapeutic challenge. Although there are more than 120 different types of brain tumors, the more common ones are gliomas, pituitary tumors, and meningiomas, with corresponding recurrence levels of 45%, 15%, and 15% [2]. In the current medical scenario, effective identification of neurological disorders has become crucial. Although many imaging methods are available, MRI stands out as a valuable method because of its non-invasive nature and radiation-free procedure. In contrast to CT scans [3], MRI enables a thorough analysis of brain anatomy, facilitating quicker diagnosis and potentially better outcomes for patients [4]. Deep CNN-based methods can accurately classify brain tumors from MRI data, potentially leading to improved medical diagnosis and treatment planning [5].

Clinical imaging methods are essential diagnostic tools for the accurate detection of several serious health conditions [6-10]. The primary scanning method is magnetic resonance imaging (MRI), which provides an accurate, effective, and non-invasive examination. There are substantial time and labor costs associated with manually identifying and classifying brain tumors in large databases of medical images in standard healthcare facilities. To address this issue, sophisticated computer-aided methods [11, 12] are currently being investigated to improve patient outcomes and evaluate MRI scans efficiently.

Brain tumor identification techniques are categorized into machine learning (ML) and deep learning (DL) approaches. Conventional ML techniques depend on trained professionals to identify significant features and require a laborious feature extraction process. Because of these issues, ML-based approaches become less precise and more susceptible to errors, particularly when larger datasets are used [13]. On the other hand, CNNs and other DL-based techniques [14, 15] are gaining prominence across many fields, particularly in medical imaging. CNNs are considered more effective because they can automatically extract both low-level and high-level features from input data [16–21]. The computational complexity of conventional CNNs for brain tumor identification leads to prolonged training periods and increased computational requirements. To address these issues, lightweight CNNs have become important because they process data quickly and use fewer resources, which makes algorithms better suited for the current evaluation of medical images in resource-limited settings [22–25].

The key objective of this work is to create an efficient model with superior performance while initially emphasizing a low number of variables. As a result, transformer-based structures and more complex hybrid frameworks were not included in this research because of their intrinsically high parameter counts. In order to preserve a fair comparison against our proposed framework, which was designed to be more parameter-efficient, excluding these alternatives was necessary. Therefore, this research proposes a novel framework based on the combination of CNN and BiLSTM models for the detection of brain tumors. The suggested technique has three important phases: data preprocessing, feature extraction, and classification. Initially, the data preprocessing step is used to label the data, resize images, normalize the data, and partition the data. Next, the proposed CNN-BiLSTM hybrid model is utilized to extract features and classify tumor and non-tumor MRI images.

2. Related Work

Brain tumor identification is significant because of its medical complexity. This section analyzes earlier studies and distinguishes techniques across ML- and DL-based methodologies. ML approaches depend on manual feature identification, which limits efficiency because of their reliance on handcrafted features [26]. Biswas *et al.* [27] addressed the problem of effectively categorizing and retrieving medical images. Their method used SPT and LNDP. Although sensitivity to changes in resolution or noise remains a limitation, the researchers showed notable improvements over existing approaches in experiments on different healthcare databases. Singh *et al.* [28] addressed the difficulty of tumor categorization by combining ICA and a K-SVM approach, achieving notable performance. This method is adaptable to various databases, but differences in MRI image properties remain challenging.

Alnaggar *et al.* [29] used Hyper-Layer-CNN for feature extraction along with Hyper-Heuristic-ELM for tumor identification, and this technique produced a remarkable accuracy rate. For tumor classification, Dehkordi *et al.* [30] compared DL and conventional ML approaches. Their enhanced CNN model outperformed previous approaches with a high level of accuracy, using datasets from Harvard Medical School and BRATS 2015. Lu *et al.* [31] improved abnormal brain state identification in MRI by using a modified AlexNet and an ELM tuned with CBA, attaining an excellent accuracy of 96.43%. Nevertheless, the method can identify brain images only as abnormal or normal, and future studies should focus on multi-level categorization. Murthy et al. [32] presented a brain tumor characterization framework incorporating OCNN-EC and AFDF-based classification. Using a Kaggle dataset, the algorithm achieved an accuracy of 85% in brain tumor categorization.

In a study [33], Brain MRNet, an innovative CNN for MRI-based brain tumor identification, outperformed pre-trained CNNs with an accuracy of 96.05%. A CNN-based system for tumor categorization was introduced by Cinar et al. [34]. This approach produced outstanding accuracy, identifying meningioma tumors with 96.53% accuracy and glioma with 99.64% accuracy. Waghmare et al. [35] implemented the VGG16 framework for brain tumor classification. Applying data augmentation and preprocessing methods before feeding the data into the CNN improved accuracy. Mzoughi et al. [36] created a CNN algorithm to discriminate HGG and LGG from the data. Although enormous progress has been made in this area, finding a practical and efficient method for classifying brain MR images remains difficult. A novel CNN approach has been employed for brain tumor identification and has shown acceptable performance [37]. Next, a customized CNN is utilized for the identification of brain tumors [38]. The customization process involves creating a structure that improves the accuracy of feature extraction and classification for medical imaging problems. Then, a unique CNN model is implemented for brain tumor categorization [39] to maintain network effectiveness and prioritize key elements, such as max-pooling stages, which help reduce the amount of information flowing through the network. These investigations focus only on binary tumor categorization, leaving out the important task of multi-class classification for distinguishing tumor types; this is a major limitation. Additional research is needed to close this gap and improve the categorization approach.

3. Materials and Methods

This section presents a brief review of the CNN and Bidirectional LSTM (BiLSTM) that are utilized in the proposed work. The comprehensive details about these models are described below:

3.1 CNN

Over the past few years, CNNs have achieved notable performance on many difficult tasks, and numerous research studies have examined their ability to extract features [40]. The fundamental idea behind CNN is that it uses convolution to extract higher-level features from lower-level features in order to determine structural attributes. In comparison with ML methods, CNN does not require manual feature creation. Unlike traditional models, CNNs usually consist of two distinct stages: feature extraction and classification. They can learn through several neural network layers in a single pass. The CNN module consists of a convolution layer, batch normalization with ReLU activation, and a max-pooling layer. Initially, the convolution layer enables the model to acquire low-level and high-level features from the input at different stages. Let be the input image and be the filter or kernel, and this kernel slides throughout the image. As the kernel moves, the values of the image and kernel are multiplied and then added together, and this process continues throughout the image to produce the feature map. The convolution process is described as:

$$F[c,d] = (X * K)[c,d] \tag{1}$$

$$F[c,d] = \sum_i \sum_j X[i,j]K[c-i,d-j] \tag{2}$$

where X represents the input image or feature matrix, K denotes the convolution kernel (filter), and $F[c,d]$ represents the resulting feature map at spatial location (c,d). i and j represent the spatial indices of the input matrix, and the kernel K slides across the input matrix to compute the weighted sum of the local receptive field.

Next, the output of the convolution is given to a ReLU activation function, which determines how a neuron transforms the input to generate the desired output. Finally, a max-pooling layer is used to downsample the output of the previous layer and reduce the computational load.

3.2 Bidirectional-LSTM (BiLSTM)

BiLSTM is a type of recurrent neural network (RNN) that processes a sequence in both the forward and reverse directions. It is designed using two unidirectional LSTMs, one for forward learning and the other for backward learning. The internal architecture of BiLSTM is shown in Figure 1. The mathematical expression for the hidden state of the BiLSTM is described as follows:

$$H_t = H_t^{p,c} \oplus H_t^{p,d} \tag{3}$$

Where $H_t^{p,c}$ and $H_t^{p,d}$ are p^{th} LSTM element output, which denotes the hidden state of the forward and backward LSTM, respectively. Additionally, the $H_t^{p,c}$ and $H_t^{p,d}$ are assessed utilizing the subsequent formulas:

$$H_t^{p,c} = O_t^{p,c}.\tanh(P_t^{p,c}) \tag{4}$$

$$H_t^{p,d} = O_t^{p,d}.\tanh(\, P_t^{p,d}) \tag{5}$$

Where represents the output gate, denotes the cell state, and is the hyperbolic tangent activation function used to regulate the hidden-state output.

4. Proposed Methodology

This work proposes an innovative model that combines CNN and BiLSTM for the detection of brain tumors. The proposed framework presents a distinctive design and feature-processing technique for brain MRI classification, which is different from existing CNN-RNN-based medical image classification systems.

First, a unique CNN architecture with three convolutional blocks is designed to extract hierarchical spatial features from MRI images. Next, the proposed architecture incorporates a BiLSTM layer to capture dependencies among the deep features extracted by the CNN model. The complete block diagram of the proposed work is shown in Figure 2. The suggested approach has three important stages: data preprocessing, feature extraction, and classification. Initially, the preprocessing step labels the data, resizes images, normalizes the data, and partitions the data. Next, the proposed CNN-BiLSTM hybrid deep learning network extracts features and classifies tumor and non-tumor MRI images. The comprehensive details of each step are discussed in the subsequent sections.

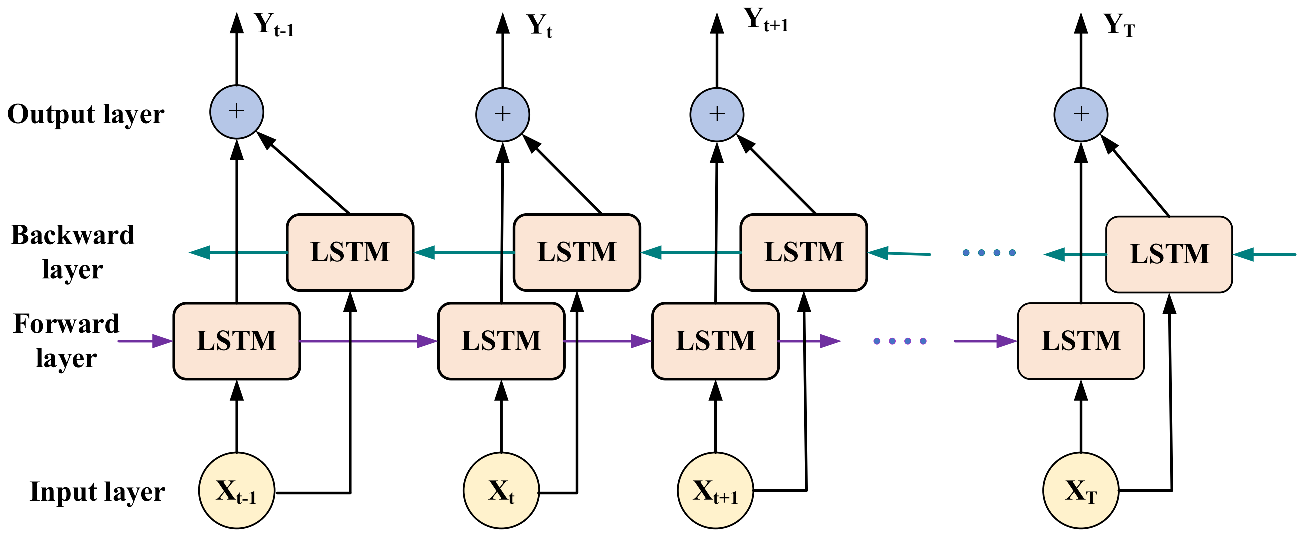

Figure 1. Bidirectional LSTM structure.

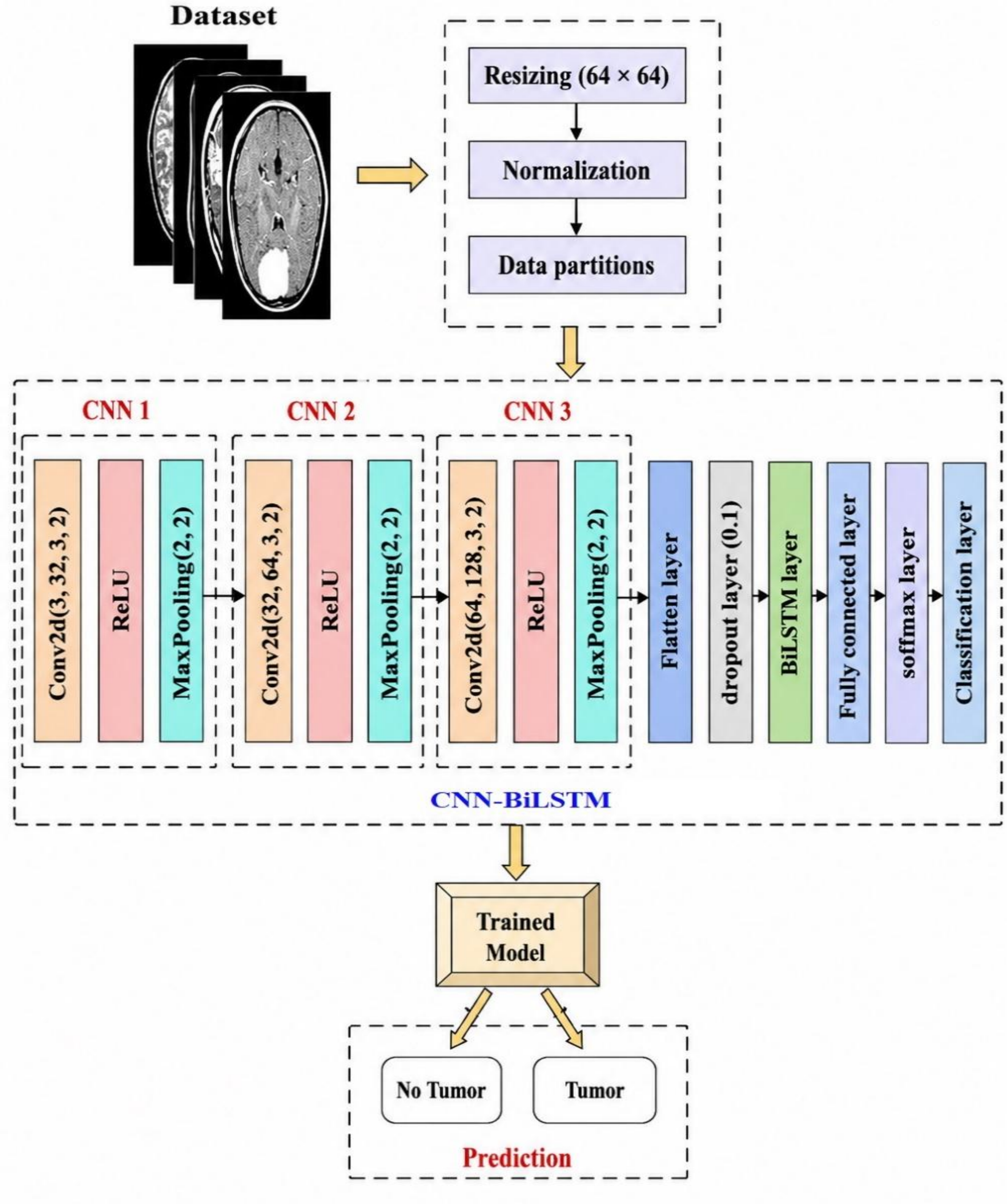

Figure 2. Block diagram of the proposed work.

4.1 Data Preprocessing

The preprocessing stage of the proposed work includes a few crucial phases. First, the images in the dataset are labelled and then resized to ensure uniform specifications. Following that, data normalization is performed, and the dataset is divided for further investigation.

Data preprocessing: In order to maximize the effectiveness of deep learning models, preparing the BR35H dataset is a crucial initial stage. First, every image is assigned a label to organize the dataset. Then, images with tumors are assigned 1, whereas images without tumors are assigned 0. This categorization method enables supervised learning, allowing the algorithms to accurately discriminate between tumor and non-tumor brain MRI images.

Resizing Images: Resizing is the process of altering an image's size without affecting its important content. Next, in order to minimize computational complexity and training time, all input images are resized to 64 × 64 pixels while maintaining the crucial structural characteristics needed for tumor classification. This decision aligns with preprocessing techniques used in previous studies on the BR35H dataset and related MRI classification tasks. Then, to enable smooth incorporation within the DL workflow, the resizing stage is essential for preserving uniformity in the input data size throughout the dataset.

Normalization: This is an important preprocessing phase that rescales the pixel values in the images. The pixel values are adjusted to fall between 0 and 1 using standard normalization. This is accomplished by dividing each pixel value by the maximum RGB pixel value of 255. It provides a more consistent optimization process by keeping all input values on a similar scale.

Data Splitting: Due to the constrained size of the dataset, the data division technique is carefully considered in this work. The image collection is separated into training and testing sets of 90%, 80%, 70%, and 60% for training, and 10%, 20%, 30%, and 40% for testing. The complete details of the data partitioning are presented in the dataset section. This splitting strategy keeps a separate subset for objective testing while ensuring that the algorithms are trained on a sufficiently large amount of data.

4.2 Proposed CNN-BiLSTM Model

This section describes the proposed CNN-BiLSTM hybrid network for brain tumor identification. First, the CNN module consists of three convolutional blocks, in which the first block comprises a convolutional layer with a 3×3 kernel size, 32 filters, and a 1×1 stride. In this case, the convolutional layer can acquire more information from the input images and extract deeper features because of the 3×3 kernel size. The 1×1 stride length preserves detailed spatial information while keeping the computational cost manageable, and the use of 32 filters enhances the depth of the feature maps. Similarly, the convolutional layer in the second block has a 3×3 kernel size, 64 filters, and a 2×2 stride, providing a detailed feature extraction process while maintaining spatial resolution. Likewise, the third convolutional layer contains 128 filters with a kernel size of 3×3 and a 2×2 stride to provide deeper features. Then, a ReLU activation function is applied, allowing the system to learn more complex representations of the data by activating only positive values. Finally, a max-pooling layer is employed to downsample the output of the preceding layer, thus reducing the computational burden. After that, the features obtained from the CNN module are flattened and passed to the BiLSTM layer through a dropout layer. Here, the BiLSTM processes the features extracted by CNN and enables the model to capture dependencies among these features across different regions of the image, which are useful for the detection of brain tumors. Sequential relationships and patterns within the extracted feature sequence can be learned by BiLSTMs, a type of RNN. Because of this capability, the model is better able to understand and categorize complex patterns in brain lesions, which may include subtle changes in texture, intensity, and structure across various brain regions. The final layers are a fully connected layer with softmax and classification layers for brain tumor categorization. The detailed tensor sizes of the proposed work at each stage, after each convolution/pooling operation, flattening, BiLSTM input, and BiLSTM output, are included in Table 1.

The pseudo-code of the proposed CNN-BiLSTM model is described as follows:

Proposed CNN-BiLSTM model Algorithm:

```
Load MRI images from the dataset directory
Assign class labels based on folder names
Shuffle the dataset randomly
Resize all images to $64 \times 64$
Split the dataset into training (80%) and testing (20%)
Construct a CNN with three convolutional blocks
Extract deep features and flatten
Pass features through BiLSTM layer (128 hidden units)
Apply fully connected layer with SoftMax activation
Train the network using Adam optimizer, learning rate of 0.001, L2Regularization of 0.0001, batch size of 32, and 50 Epochs.
Evaluate the model on test set
Compute performance metrics: Accuracy, Precision, Sensitivity, and F1-score.
```

5. Results and Discussion

In this section, the effectiveness of the proposed work is assessed using MRI image data obtained from the Brain Tumor Detection 2020-BR35H dataset. In the subsequent sections, the comprehensive details about the dataset and the different evaluation metrics used in this work are discussed. Moreover, the quantitative evaluation and computational findings demonstrate the effectiveness of the proposed method for brain tumor identification.

5.1 Dataset

The current study conducts numerous evaluations using the publicly accessible Brain Tumor Detection 2020-BR35H dataset. This dataset provides axial MRI images for assessment and supports a binary split between brain tumors and normal brain images. The complete dataset contains 3864 MRI images. However, this research uses a balanced set of 2000 images for experimentation [41], which comprises 1000 tumor images and 1000 normal brain images for binary categorization. In the present study, different train–test ratios (90:10, 80:20, 70:30, and 60:40) were employed to evaluate the robustness of the proposed model under varying training conditions. The test sets were strictly reserved for performance evaluation and were not used during model training or parameter tuning. The complete details of the dataset partitions for training and testing are shown in Table 2.

5.2 Evaluation Metrics

For assessing the effectiveness of tumor categorization approaches, the most commonly used evaluation metrics are Accuracy, Precision, Recall, and F1-score. A confusion matrix is an important source of information for classification outcomes.

Table 1. The layers of the proposed network

Input Layer	Image Input	64 × 64 × 3
Conv Layer 1	Conv2D (3×3, 32 filters, stride=1, padding=0)	62 × 62 × 32
ReLU	Activation	62 × 62 × 32
Max Pooling 1	2×2, stride=2	31 × 31 × 32
Conv Layer 2	Conv2D (3×3, 64 filters, padding=0)	29 × 29 × 64
ReLU	Activation	29 × 29 × 64
Max Pooling 2	2×2, stride=2	14 × 14 × 64
Conv Layer 3	Conv2D (3×3, 128 filters, padding=0)	12 × 12 × 128
ReLU	Activation	12 × 12 × 128
Max Pooling 3	2×2, stride=2	6 × 6 × 128
Flatten Layer	Feature Vector	4608 × 1
BiLSTM Input	Sequence representation	4608 time steps × 1 feature
BiLSTM Output	OutputMode = last, 128 units	256 × 1 (Forward 128 + Backward 128)
Fully Connected	Dense Layer	2 × 1
Softmax	Probability Output	2 × 1
Classification	Final Prediction	2 classes

Table 2. Comprehensive depiction of dataset partitions

Total number of images	Images considered	Data partitions	
		Training set	Testing set
3864	2000	90% (1800 images- 900 Tumor & 900 Normal)	10% (200 images - 100 Tumor & 100 Normal)
		80% (1600 images - 800 Tumor & 800 Normal)	20% (400 images - 200 Tumor & 200 Normal)
		70% (1400 images - 700 Tumor & 700 Normal)	30% (600 images - 300 Tumor & 300 Normal)
		60% (1200 images - 600 Tumor & 600 Normal)	40% (800 images - 400 Tumor & 400 Normal)

In this context, the terms True positive (Trp), True negative (Trn), False positive (Fsp), and False negative (Fsn) are described as follows:

Trp: Brain tumors are correctly classified.

Trn: Normal tissue is correctly classified.

Fsp: A normal image is mistakenly identified as tumor tissue.

Fsn: A tumor image is incorrectly classified as normal.

The mathematical terminologies for the evaluation metrics are defined as:

$$Accuracy = \left(\frac{Tr_p+Tr_n}{Tr_p+Tr_n+Fs_p+Fs_n}\right) \tag{6}$$

$$Precision = \left(\frac{Tr_p}{Tr_p+Fs_p}\right) \tag{7}$$

$$Recall = \left(\frac{Tr_p}{Tr_p+Fs_p}\right) \tag{8}$$

$$F1-score = \left(\frac{Tr_p}{Tr_p+\frac{1}{2}(Fs_p+Fs_n)}\right) \tag{9}$$

5.3 Experimental Results

The present research is carried out through an extensive set of simulations using brain tumor data to analyze the reliability of the CNN-BiLSTM model in brain tumor categorization and demonstrate its effectiveness. The MATLAB 2023b platform is used to conduct all experiments on the BR35H brain tumor dataset. For the experiments, the dataset is first divided into 80% training data and 20% testing data. Next, for training the proposed network, the hyperparameters such as the number of epochs, initial learning rate, and L2 regularization factor are set to 50, 0.001, and 0.0001, respectively. Then, to determine how the number of training samples processed before updating the network parameters affects learning efficiency and performance, batch sizes of 16, 32, and 64 are considered and analyzed in this work. From this analysis, it is observed that a batch size of 32 gives better performance in tumor detection. Further, for iteratively adjusting the weights of the network parameters, the optimizers Adam, SGDM, and RMSprop are considered and examined in this research, and it is observed that the Adam optimizer shows superior performance. The optimizer and batch size were selected based on standard configurations usually adopted in related studies and were determined during the training phase without utilizing the test data. By using these hyperparameters, the proposed CNN-BiLSTM is assessed on the BR35H brain tumor data, and it attained an accuracy of 98%, a precision of 98.48%, a recall of 97.5%, and an F1-score of 97.99%. In addition, to highlight the efficiency of the proposed model, its performance is compared with three recent existing networks: Deep CNN [37], Customized CNN [38], and CNN [39]. The parameters and specifications for evaluating these three existing models are considered as described in the respective works. Next, Table 3 displays the performance comparison between the proposed CNN-BiLSTM and the three existing models. From this comparison, it is found that the proposed work shows improved performance in terms of all evaluation metrics, which reveals the superiority of the proposed CNN-BiLSTM model in the effective identification of brain tumors. For better clarity, Figure 3 shows the metric-wise comparison analysis.

The confusion matrix of the existing and proposed models is displayed in Figure 4, which shows the ability of the proposed CNN-BiLSTM to correctly recognize true positives and true negatives, demonstrating its accuracy in tumor classification. The proposed model showed a good ability to discriminate between the two categories by correctly identifying 195 true positives and 197 true negatives. The number of misclassifications is low, with 5 non-tumor cases wrongly diagnosed as tumors and 3 tumor cases incorrectly recognized as non-tumors. The outcomes presented here validate the effectiveness of the CNN-BiLSTM model in tumor recognition, with a strong capacity to determine the presence as well as the absence of lesions. The achieved performance therefore reflects the capability of the proposed model to effectively learn discriminative features from the dataset. It should also be noted that the BR35H dataset does not provide detailed patient-level metadata, which limits the possibility of performing patient-wise splitting.

Table 3. Performance comparison of the Proposed CNN-BiLSTM model with existing approaches

Authors	Year	Dataset	Model	Accuracy	Precision	Sensitivity	F1-score
Gupta *et al.*, [37]	2024	BR35H	Deep CNN	93.75	91.87	96.00	93.89
Nazir *et al.*, [38]	2024	BR35H	Customized CNN	95.75	95.07	96.50	95.78
Rasool *et al.*, [39]	2025	BR35H	CNN	90.25	84.26	93.65	91.03
		BR35H	CNN-BiLSTM [Proposed]	98.00	98.48	97.50	97.99

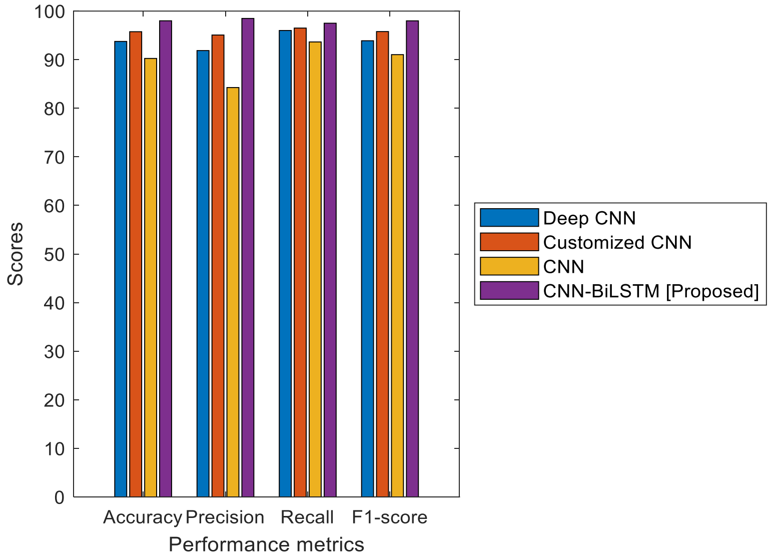

Figure 3. Metric-wise performance comparison.

Table 4. Performance of the Proposed CNN-BiLSTM model against different folds.

Folds	Accuracy	Precision	Sensitivity	F1-score	Specificity	AUC
Fold 1	98.25	98.49	98.00	98.25	98.50	99.72
Fold 2	98.00	97.06	99.00	98.02	97.00	99.84
Fold 3	97.50	97.47	97.50	96.98	97.50	99.78
Fold 4	98.50	97.65	98.50	98.45	98.56	98.44
Fold 5	97.25	97.43	97.00	96.20	97.50	98.91
Mean ± std	**97.90 ± 0.52**	**97.62 ± 0.53**	**98.00 ± 0.79**	**97.58 ± 0.96**	**97.81 ± 0.69**	**0.993 ± 0.006**

Nevertheless, the adopted experimental setup follows the same evaluation strategy commonly reported in related literature using this dataset, allowing fair comparison with existing methods.

In addition, the performance of the proposed method is evaluated using 5-fold cross-validation to ensure robustness and generalization. The model is trained and tested across five different folds, and the performance metrics are averaged to obtain the final results. Table 4 presents the fold-wise performance of the proposed model. It can be observed that the model maintains consistent performance across all folds, with only minor variations, confirming its robustness to data partitioning. Further, the performance of the proposed model is evaluated using the Area under the ROC Curve (AUC). The model achieves an average AUC of 99.3 with a 95% confidence interval of [98.79, 99.89], indicating strong discriminative ability between tumor and non-tumor classes

5.3.1 Performance of the Proposed Model on Different Training and Testing Sizes

This section uses various training and testing sizes of the dataset to assess the effectiveness of the proposed CNN-BiLSTM model. In the present study, different train–test ratios, including 90:10, 80:20, 70:30, and 60:40, were employed to evaluate the robustness of the proposed model under varying training conditions. The proposed CNN-BiLSTM network is trained on 90%, 80%, 70%, and 60% of the training data across 50 epochs, with each epoch representing one complete pass over the training dataset. For every setting, training loss and accuracy are presented. These metrics demonstrate the extent to which the proposed approach can adapt what it has learned from the data to new situations. The corresponding learning and loss curves are depicted in Figure 5. The confusion matrices for varying test set sizes are shown in Figure 6, while Table 5 shows the corresponding results for different partitions. The proposed CNN-BiLSTM technique achieved accuracies of 98.13%, 97.17%, 98%, and 97% for the data splits of 60%, 70%, 80%, and 90%, respectively. From this study, it is evident that the proposed framework exhibits notable performance for all data partitions.

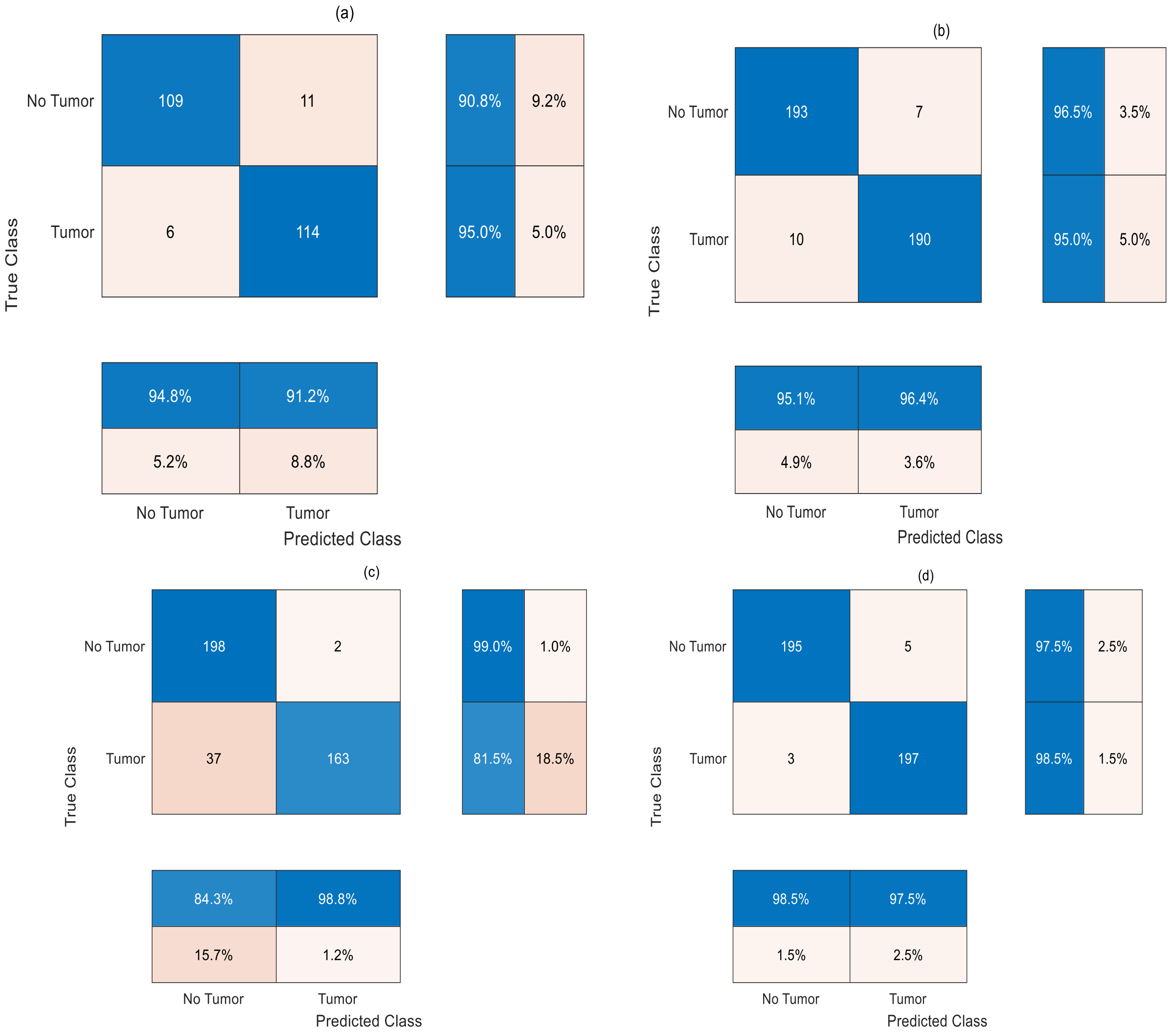

Figure 4. Confusion matrices of the existing **(a)** Deep CNN; **(b)** Customized CNN; **(c)** CNN, and **(d)** Proposed CNN-BiLSTM models.

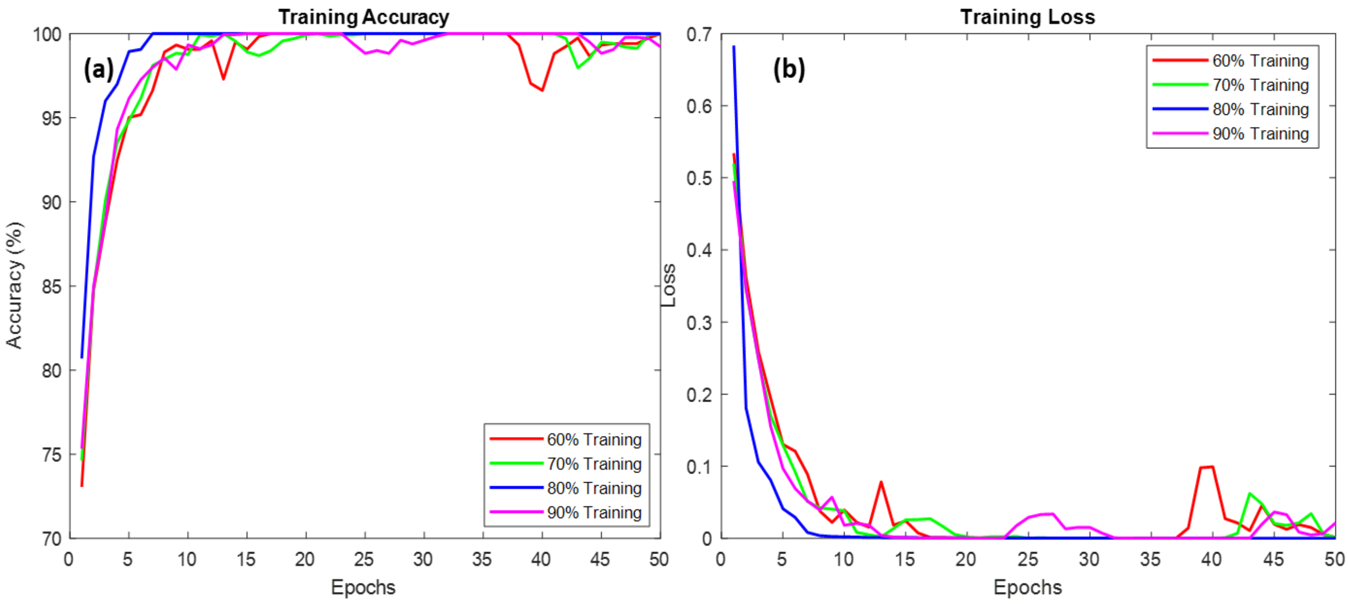

Figure 5. **(a)** Training accuracy, and **(b)** Training loss curves of the proposed CNN-BiLSTM model for different sizes

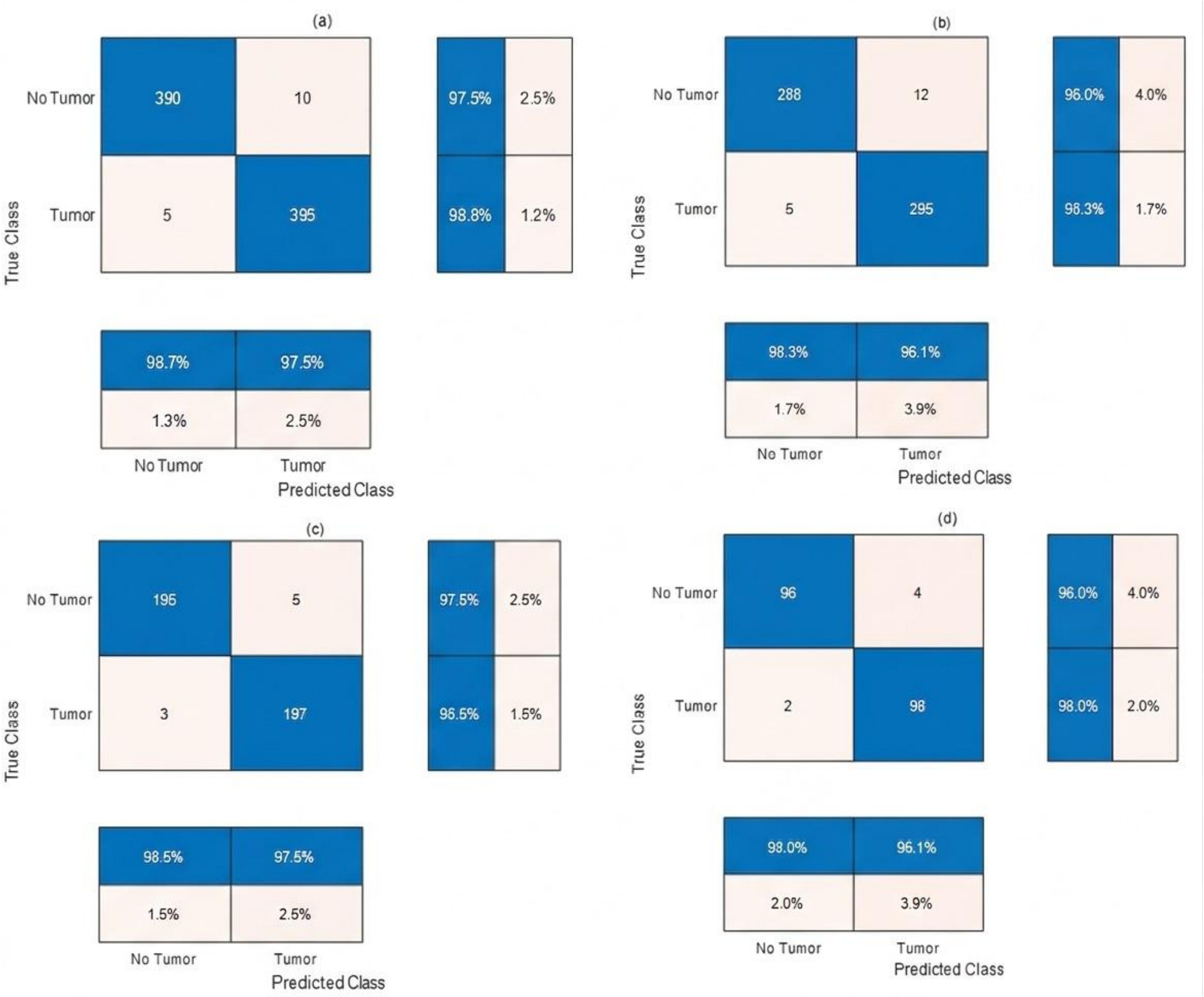

Figure 6. Confusion matrix for different training and testing ratios: **(a)** 60-40; **(b)** 70-30; **(c)** 80-20; **(d)** 90-10.

Table 5. Performance of the proposed model for different sizes of the dataset

Data splitting	Training samples	Testing samples	Accuracy	Precision	Sensitivity	F1-Score
60:40	60% (1200)	40% (800)	98.13	98.73	97.50	98.11
70:30	70% (1400)	30% (600)	97.17	98.29	96.00	97.13
80:20	80% (1600)	20% (400)	98.00	98.48	97.50	97.99
90:10	90% (1800)	10% (200)	97.00	97.96	96.00	96.97

Table 6. Ablation study of the proposed CNN-BiLSTM model

CNN			BiLSTM	SoftMax	Accuracy	Precision	sensitivity	F1-score
Block 1	Block 2	Block 3						
√	×	×	×	√	97.00	96.47	94.50	96.92
√	√	×	×	√	97.75	97.79	97.50	97.74
√	√	√	×	√	97.85	97.54	97.50	97.75
√	√	√	√	√	98.00	98.48	97.50	97.99

5.3.2 Ablation Study

In addition, the ablation study of the proposed CNN-BiLSTM technique is conducted in this work to understand the significance of each component or feature in the final outcome.

The primary components of the proposed model are feature extraction using the CNN module and classification of tumor and normal MRI images using the BiLSTM module. The ablation study examines the impact of each block in the implementation of the proposed CNN-BiLSTM approach, and the corresponding outcomes are displayed in Table 6.

The results of this study provide the following insights: when a single convolution block is used alone in the CNN module to obtain features from the MRI images, the CNN-BiLSTM framework achieved 97% accuracy, 96.47% precision, 94.5% sensitivity, and a 96.92% F1-score. When a second convolution block is included in the CNN module, it strengthens the extracted features and improves model performance by 0.75% in accuracy, 1.32% in precision, 3% in sensitivity, and 0.82% in F1-score. When a third convolution block is added to the convolution module, it produces slight changes in the outcomes of the proposed model. Finally, when the BiLSTM module is added at the classification stage, the model shows superior performance and achieves 98% accuracy, 98.48% precision, 97.5% sensitivity, and 97.99% F1-score. Consequently, these outcomes demonstrate the effectiveness of the combined CNN-BiLSTM framework for tumor identification.

6. Conclusion

The MRI-based brain diagnostic procedure is substantially more sophisticated than earlier techniques, which makes it difficult for existing models to accurately predict the appearance and exact location of brain tumors. Brain-related abnormalities can be fatal and present a serious risk, highlighting the urgent need for prompt brain tumor classification. Hence, it is essential to develop an innovative approach for brain tumor detection. Although current approaches have shown adequate performance in brain tumor detection, there is still scope to further enhance performance. Therefore, the present research marks a significant improvement in the field of brain tumor identification by utilizing a hybrid deep learning network created by combining CNN and BiLSTM techniques. A thorough examination and discussion have demonstrated the capability of the proposed CNN-BiLSTM network to precisely detect brain tumors from MRI data. The proposed CNN-BiLSTM model has demonstrated strong results in tumor identification, with an accuracy of 98%, a precision of 98.48%, a recall of 97.5%, and an F1-score of 97.99%. The effectiveness of the proposed technique is demonstrated through a complete final assessment that includes a confusion matrix, comparison with present algorithms, and experiments on data of various sizes.

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Chembeti Saraswathi: Conceptualization, Methodology, Formal Analysis, Writing – Original Draft. K.S. Chakradhar: Data Curation, Investigation, Validation, Writing – Review & Editing, Supervision. Both the authors have read and agreed to the published version of the manuscript.

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Data Availability

The data supporting the findings of this study can be obtained from the corresponding author upon reasonable request.

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