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Research Article,

Advanced Deep Learning Framework for Brain Tumor Segmentation and Classification

Usama Aslam[1, *], Muntaha[1], Shan Zahra[2]

[1]Times University, Multan, 60000, Pakistan

[2]Department of Information Technology, The Women University, Multan, 60000, Pakistan

[*]Corresponding Author: Usama Aslam. Email: usamaaslam9t5@gmail.com

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Abstract: Magnetic Resonance Imaging (MRI) of the brain determines which brain tumors are necessary to be accurately segmented and classified to be effectively diagnosed and treated. Analysis by hand is tedious and subject to inter-observer error. This paper will present a multi-stage deep learning architecture, which utilizes the Convolutional Neural Networks (CNNs) model and implements denoising, image enhancement, skull stripping, and feature optimization to increase robustness and generalization. It tested itself on publicly available MRI datasets by 10-fold cross-validation. The experimental findings indicate that, the CNN attained an accuracy of 84.5, true positive percentage of 0.845 and ROC of 0.897 which is higher than that of the LSTM model at 83.71%. In addition, a hybrid CNNLSTM model (CABGD) based on a combination of spatial and sequential features achieved an 85 percent accuracy and illustrated improved classification performance. Reliability to the proposed approach was demonstrated based on misclassification analysis. These results represent the possibilities of deep learning, especially hybrid systems, as a clinical decision support system to detect and classify brain tumors automatically.

Keywords: Brain Tumor Detection; Deep Learning (DL); Convolutional Neural Network (CNN); Magnetic Resonance Imaging (MRI); Medical Imaging;

1. Introduction

Brain tumors are severe neurological diseases where the brain cells experience abnormal growth that may be benign or malignant tumors [1], [2]. Malignant lesions can either be intrinsic to the brain or can be the result of metastasis of tumors in other organs (e.g., the lungs or the breast) and tend to result in neurological impairments, which depend on the size, growth rate, and location of the lesion [3-5]. Effective treatment planning requires accurate diagnosis at an early stage, to enable it be carried out surgically, through radiotherapy, and through targeted therapies [2], [4].

The gold standard in the assessment of brain tumors is MRI medical scans. These scans have high soft tissue contrast together with high spatial resolution [5], [6]. Manual interpretation of MRI scan however is very laborious, time-consuming, and subject to inter-observer variability [6], [7]. Machine learning techniques, including Support Vector Machines (SVM), Artificial Neural Networks (ANN) as well as Naive

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Bayes, have been used in tumor classification. These methods are based on manual design, must include domain knowledge and tend to be poor with noisy or heterogeneous MRI data [8], [9].

The analysis of medical images has been revolutionized by the concept of deep learning and more specifically through Convolutional Neural Networks (CNNs), where hierarchical features are automatically learned without the need to create additional features or biases [10], [11]. CNN-based systems have shown a better level of capability in terms of tumor segmentation, detection and classification, and they provide better accuracy, robustness and computationalism in comparison to conventional algorithms [11-13]. In the recent research, the advantages of multi-stage architectures, attention mechanisms, and feature optimization to improve the classification performance are also noted [10], [11], [14].

These developments inspired this research, which suggests an efficient multi-stage CNN framework, which classifies brain tumors automatically. The model combines initial processing stages (denoising, image enhancement, skull stripping) and CNN-based feature extraction to enhance robustness and generalization. The main contributions of this work are:

1. Making a multi-stage CNN model that properly classifies brain tumors as either benign or malignant.
2. Detailed analysis of publicly available MRI datasets, which have better accuracy and strength than current techniques.
3. Model stability and computational efficiency based quantitative analysis, with emphasis on possible clinical applicability.

The rest of the paper is structured in the following way: Section 2 presents related literature review; Section 3 is the description of the methodology; Section 4 displays experimental results and discussion; Section 5 presents conclusions with the key findings and future research directions.

2. Literature Review

The development of machine learning, Image processing, and deep learning has advanced in the last decades to create methods of detecting and identifying brain tumors through MRI. Initial methods mostly employed Artificial Neural Networks (ANNs) with texture-based features mining methods (including the Gray Level Co-occurrence Matrix (GLCM)) with moderate performance (~81 percent) at the cost of handcrafted features, thus limiting their robustness and generalization [15], [16]. Other researchers added the steps of preprocessing and segmentation, as in the case of Discrete Wavelet Transform (DWT), Support Vector Machines (SVMs) and Principal Component Analysis (PCA) and were augmented with thresholding and watershed to increase the accuracy (approximately 85 percent) [17], [18]. Hybrid approaches combining ANN with DWT, PCA, or Rough Set Theory (RST), and optimized versions of SVM such as Least-Squares SVM, and more were used to improve the classification process by defining discriminative features and minimizing redundancy [19]. Correct tumor delineation has been identified to be an important factor, and such methods as thresholding, edge detection, region growing, Sobel operator, and hybrid texture descriptors (GLRLM + CSLBP) have proven to be more effective than conventional single-feature methods [20-23]. Irrespective of these advancements, classical approaches are constrained by small data sets, manually designed feature dependency, noise sensitivity and computational inefficiently.

As a result, various deep learning models, notably Convolutional Neural Networks (CNNs), have been embraced that define hierarchical characteristics in raw MRI images; hence, enhancing accuracy, robustness, and scalability. Most recent works have pointed out that multi-stage architecture, hybrid CNN-LSTM, attention, and feature optimization can further improve tumor classification results [14].

Research Gap: Previous research has shown that deep learning models have taken the place of traditional feature-based models, including ANNs and SVMs, and allow the extraction of features automatically and enhance their generalization [15]. However, there are a considerable number of studies which are constrained by small datasets, insufficient assessment of preprocessing and hybrid architectures and inefficient computational efficiency [13], [14], [19]. The lack of comparative studies of CNN, LSTM, and hybrid models, on the same datasets, demonstrates the necessity of an optimized multi-stage paradigm of brain tumor identification and classification utilizing MRI scans preprocessing, feature selection and hybrid deep learning structures in search of the accurate, robust, and efficient brain tumor identification and classification.

Table 1: Summary of Key Studies on Brain Tumor Classification Using MRI

Author(s)	Model	Dataset	Technique	Accuracy
[24]	ANN	50 MRI scans	GLCM texture features	81.4%
[25]	ANN + Image Processing	65 MRI scans	Preprocessing, Segmentation, DWT, PCA	83%
[26]	SVM + Segmentation	100 MRI scans	Thresholding, Watershed	85.32%
[27]	Naive Bayes	60 MRI scans	Statistical features	81.2%
[28]	ANN (Breast Tumor)	184 images	Back-propagation	82.04%

3. Materials and Methods

This paper suggests a machine learning driven model to detect and classify brain tumors in MRI in an automated manner. The entire process is typical of knowledge discovery processes, which involve data procurement, pre-processing, feature extraction and optimization, and classification. Fine-tuning of tumor regions to achieve ground truth was performed by expert radiologists. Gray Level Co-occurrence Matrix (GLCM) was used to extract texture features which were optimized by fused optimization scheme. The machine learning classifiers were then used to classify tumors. [8],[11], [15]

Figure1 depicts the entire pipeline.

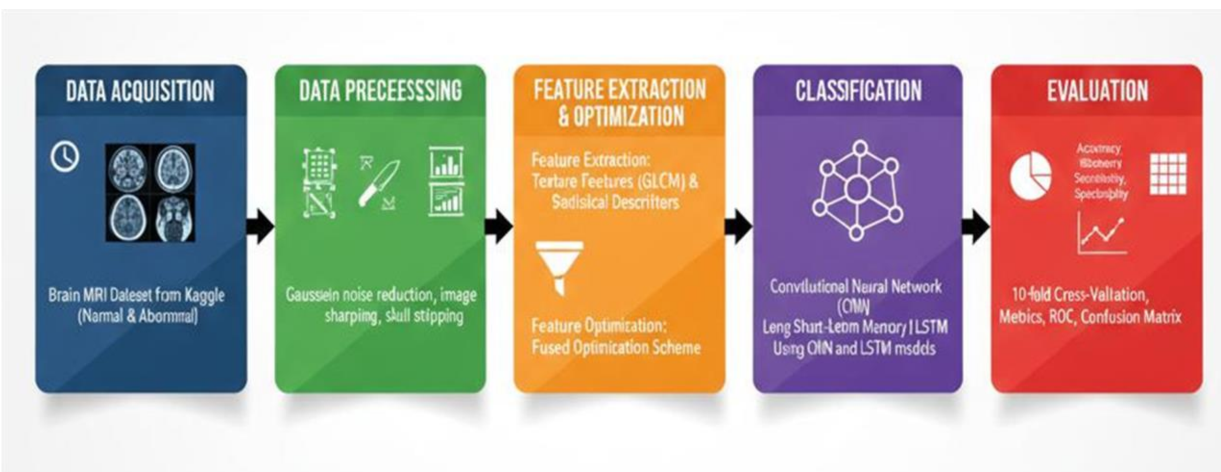

Figure 1: Methodology Pipeline

3.1. Dataset Description

The analysis used publicly available Brain Tumor MRI Dataset on Kaggle that included T1-weighted MRI scans that exist in four categories such as glioma, meningioma, pituitary tumors as well as normal ones. In binary classification, all the different types of tumors were categorized into one group of abnormality, and the healthy brains were the normal group. The data was 3,264 images (1,728 normal, 1,536 abnormal), in class-specific folders. To promote solid evaluation and reduce overfitting, a 10-fold cross-validation strategy was used [11].

Table 2: Overview of Brain Tumor MRI Dataset

Class	Number of Images	Description
Normal	1,728	Healthy brain scans
Abnormal	1,536	Glioma, Meningioma, Pituitary tumors combined
Total	3,264	All MRI scans

3.2. Data Preprocessing

Preprocessing of MRI images was done for the elevation of accuracy of tumor segmentation and classification. Gaussian noise reduction was, first, used to reduce random noise due to acquisition artifacts and patient movement without removal of critical tumor structures and enhance the clarity of the boundaries [7], [14]. Because in some cases the denoising may blur edges, image sharpening was also done to achieve a better contrast and highlight structure representing areas of tumor boundaries, hence improving the capability of the model to distinguish between normal and cancerous tissues [11], [14]. Lastly, skull stripping was implemented to isolate the brain region by removing the other non-brain tissues such as the skull and the background which allowed standardization of the input, shrinkage of computation complexities [6], [7].

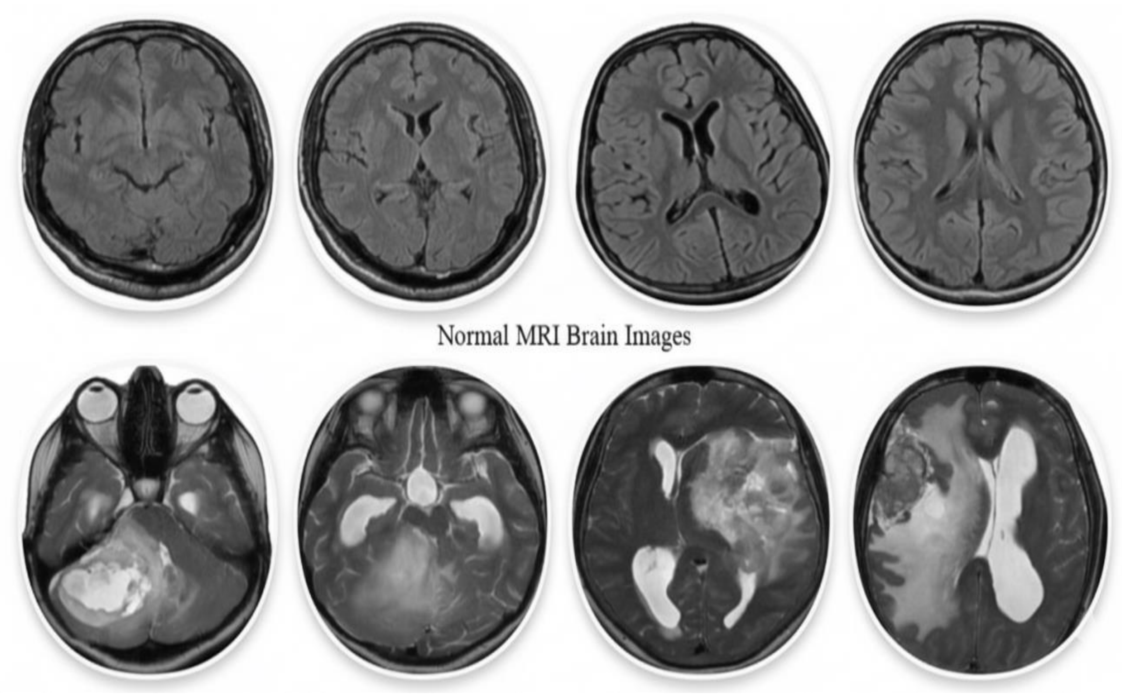

Figure 2: Sample MRI Brain Scans of normal location and tumor location

3.3. Extraction and Optimization of features

Preprocessed MRI images were further processed into optimized features to see variations indicative of the existence of normal and abnormal brain tissues. These were GLCM based texture characteristics (e.g., sum variance, correlation), statistical features (e.g., skewness, angular second moment) and other characteristics of texture (e.g., entropy, contrast) [8-10], [15], [16], [20]. A fused selection scheme was also used to further refine features to preserve discriminative features and eliminate redundancy, improving the performance and resilience of both CNN and LSTM classifiers [11], [19].

Table 3: Optimized Feature Set

Feature Type	Description / Purpose	Count
GLCM-based features	Sum variance, correlation, inverse difference momentum, etc.	20
Statistical features	Skewness, percent 0.01%, angle second moment	3
Other texture descriptors	Entropy, contrast	5

3.4. Train-Test Split

To provide sound assessment and reduce overfitting, a 10-fold cross-validation approach was used [8], [11]. The data were randomly split into training and testing subsets with each fold containing 90 percent of the images of a dataset; the rest (10 percent) were allocated to the testing set. This helped ensure that a given image was only tested once giving a complete view of the classifier generalization and performance [6], [7].

3.5. Model Architecture

In the case of the current research, two deep learning systems were used in automated classification of brain tumors, namely, Convolutional Neural Network (CNN) and Long Short-Term Memory (LSTM) networks. The two models worked to further process the preprocessed MRI image to extract discriminative features in order to classify accurately due to binary classification patterns (normal and abnormal) [10], [11].

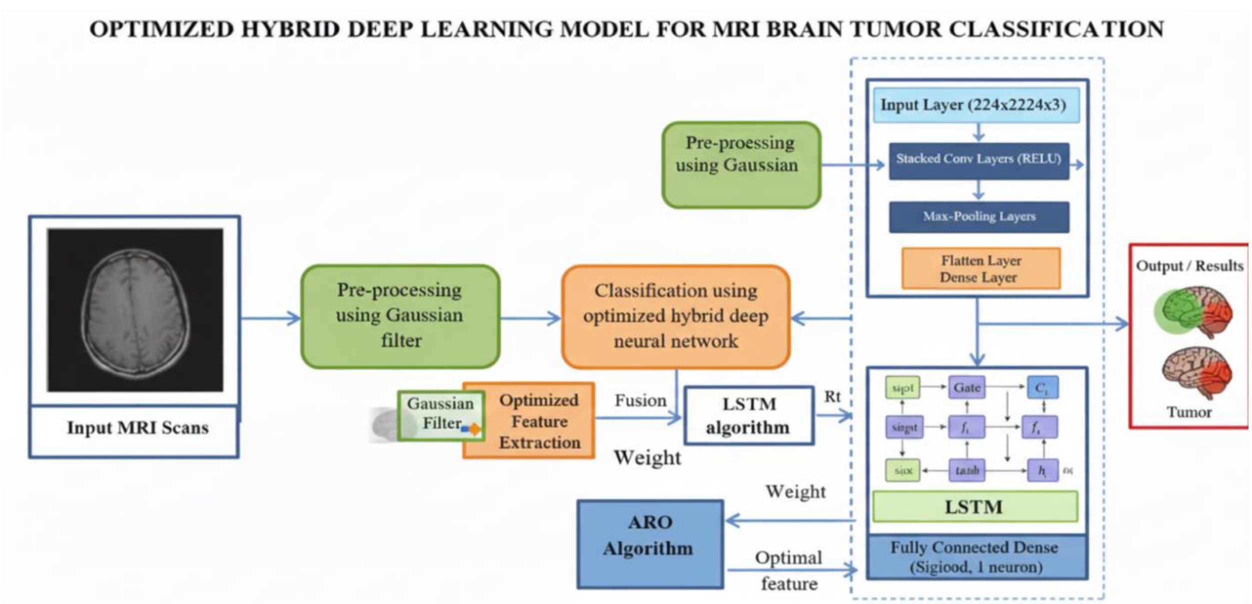

Figure 3: CNN-LSTM hybrid architecture to classify brain tumors

The CNN architecture takes input of MRI images 224 (width) 224 (height) 3 in size through various layers. The layers of convolutional with ReLU activation are stacked to extract hierarchies, which are then down sampled by max-pooling layers to keep the necessary information and decrease spatial dimensions.

The resulting 2D feature maps are flattened into a 1D feature manually, and sent through fully connected dense layers to learn the high-level representations. The binary classification output [11], [13] is a final single neuron whose activation is of the sigmoid type.

The LSTM network gets the sequential dependencies by the extracted features. Input MRI images are transformed into a series of feature vectors that can be passed through LSTM. The LSTM layers with hidden units are either one or multiple layers that represent the time or space-like relationships and then the fully connected dense layer to decode the learned representations. The network ends with one neuron that uses the sigmoid activation to do a binary classification [10], [11].

Training Information: CNN and LSTM models were trained based on binary cross-entropy loss and approaches with Adam optimizer and a learning rate of 0.001 [13]. A batch of 32 was used and 50 epochs were run to carry out the training and the test of the model was conducted on 10-fold cross-validation to guarantee strong generalization [8]. The overall architecture is illustrated in figure 3, and features are first extracted, after which sequential modeling (in the case of LSTM), and binary classification (at the end) is performed using preprocessed MRI images [10], [11].

4. Performance Evaluation

To determine the efficiency of the proposed CNN and LSTM classifiers in a comprehensive manner, several evaluation measurements have been used, some of them are the kappa statistics (K 2 information), receiver operating characteristic (ROC) curves, confusion matrices, and sensitivity, specificity, overall accuracy, and computational time [6], [8], [10], [11], [15], [16]. The measures give complementary approaches to classifier reliability, robustness, and discriminative ability to differentiate between tumor and non-tumor cases.

Kappa measures the correspondence between predicted and actual labels taking into consideration chance correspondence, and is useful when one wishes to have a measure of the predictor consistency of the classifier [20]. The ROC curves present the sensitivity-specificity trade off at different levels of decision threshold, providing a measure of how the model can discriminate [10], [11]. Sensitivity (true positive rate) indicates the percentage of tumor cases identified correctly and specificity (true negative rate) indicates the percentage of correctly identified normal cases. Confusion matrix provides a clear overview of the true positives, true negatives, false positives, and false negatives the pattern of misclassification can be accurately assessed [15], [16].

Combining all these measures of statistical and graphical evaluation, the study can produce a solid and multi-dimensional assessment of classifier performance, with an understanding of its strengths, limitations, and clinical implications of both CNN and LSTM models to detect and classify brain tumor automatically.

5. Results and Discussion

To examine the proportion of false positives (normal images which are mistakenly pronounced abnormal) and false negatives (abnormal images which are mistakenly pronounced normal) the misclassification analysis was conducted, and the total misclassifications were used as an overall measure of the error in the classification [6], [8], [10], [11], [15], [16]. CNN, LSTM and hybrid CNN-LSTM (CABGD) were evaluated based on the following measures of performance: accuracy, kappa statistics, sensitivity, specificity, ROC, false positive rate, computing time, and the number of misclassifications, which provide a detailed indication of their performance.

5.1. Comparative Performance

Table 4 presents the list of CNN and LSTM classifiers performance, including the key metrics of misclassification to make it clearer.

Table 4: CNN and LSTM classifier performance summary

Classifier	Accuracy	Kappa(K)	TP	TN	FP	ROC	Classifier

CNN	84.5%	0.69	0.845	0.868	0.155	0.897	CNN
LSTM	83.71%	0.65	0.825	0.825	0.175	0.887	LSTM

The findings establish that CNN classifier performed slightly better than LSTM model on all metrics of evaluation. CNN had greater accuracy (84.5), and kappa (0.69) which means that it is more consistent with ground truth and more reliable [6], [11]. Moreover, CNN had a better sensitivity (0.845) and specificity (0.868), less false positive (0.155), and higher ROC value (0.897) which demonstrates a high level of discriminative ability to distinguish between tumor and normal brain tissue. Though the LSTM model had similar performance, the CNN was more useful in the classification of MRI brain tumor in terms of overall, robust, and clinical utility [10], [11].

6. Conclusion and Future work.

The proposed paper offered the optimized multi-stage deep learning architecture of the automatic brain tumor detection and classification MRI scans preprocessing, feature extraction, and classification with CNN, LSTM, and a hybrid CNNLSTM (CABGD) model. Experiments showed that CNN offered a classification accuracy of 84.5 percent (TPR = 0.845 ROC = 0.897) and the hybrid CABGD higher classification accuracy of 85 percent validating the strengths of the methodology in differentiating normal and abnormal brain tissues.

These results emphasize the promise of deep learning, and especially hybrid models, to enable fast and precise automated tumor localization, which can aid radiologists by shortening their diagnosis process and facilitate the development of a tailored treatment plan.

The directions of future work will be to consider integrating multimodal imaging (e.g., MRI and CT), combine explainable AI methods like Grad-CAM, which might allow for better interpretability, and to scale the framework to bigger and more diverse datasets to improve further clinical applicability.

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Conflicts of Interest: The authors declare no conflict of interest.

Data Availability: The dataset used in this study is publicly available from Kaggle.

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