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A Deep Learning Approach Focusing on Diagnostic Sensitivity to Enhance Clinical Differentiation of Brain Tumors via Sequential ADC-MRI Analysis

Muhammad Fuad Alharis[1,*], Heni Fatmawati[2]

[1] Banyuwangi State Polytechnic, Banyuwangi, Indonesia; f_haris@poliwangi.ac.id
[2] Jember University, Jember, Indonesia; fatmawatiheni@unej.ac.id

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Correspondence:
f_haris@poliwangi.ac.id

Highlights

This study demonstrates a CNN-LSTM model that utilizes ADC-MRI images in distinguishing brain tumors, with perfect sensitivity and no false negatives.

What are the main findings?

- The CNN-LSTM model has a perfect sensitivity and accuracy of 98.05% in distinguishing between malignant and benign brain tumors, with no false negative results in a series of ADC-MRI images.
- The utilization of seven images in a sequence is important in viewing the overall image and how densely cells are packed, including signs of cancer that might be easily overlooked in a single image during regular checks.
- The model is a simulation of how a radiologist might view images in a sequence and comes to a conclusion, with a score of 0.9993 in the AUC-ROC by viewing restricted water diffusion in the overall tumor area.

What are the implications of the main findings?

- The perfect diagnostic sensitivity eliminates the possibility of false negatives, thus preventing delays in life-saving procedures such as the surgical removal of tumors or the application of radiotherapy in the treatment of malignant brain tumors.
- This form of deep learning creates a safe alternative to the dangerous stereotactic biopsies, particularly in tumors in vital areas of the brain that are hard to reach.
- The application of the decision-support tool ensures the standardization of diagnoses, eliminating human error resulting from radiologist fatigue as well as the complexity of the tumor shape, thus providing consistent results irrespective of the hospital's resources.

Abstract

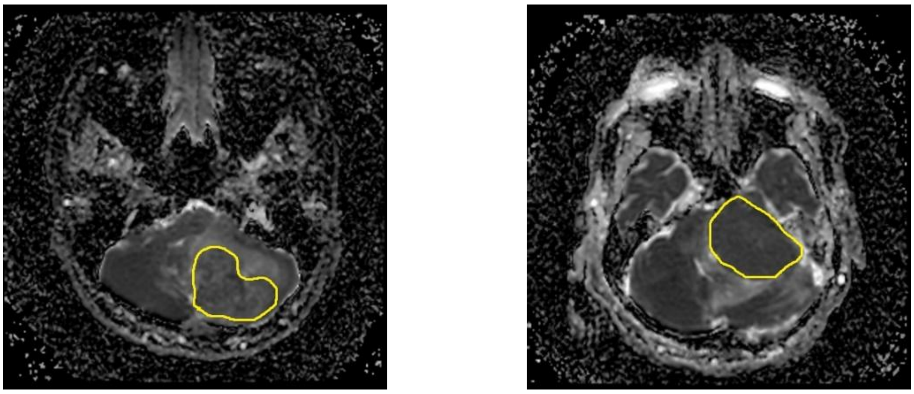
The differentiation of benign and malignant brain tumors using Apparent Diffusion Coefficient (ADC) MRI scans remains a challenge for clinicians, owing to the high variability of morphological features and the subtle signs of tissue densities. The present study proposes a simple yet highly effective deep learning-based framework for the classification of brain tumors as benign or malignant. The proposed framework incorporates a combination of Convolutional Neural Network and Long Short-Term Memory (CNN-LSTM). The major advantage of the proposed framework is the use of seven consecutive image slices for brain tumor classification, unlike the conventional methods where a single individual image slice is considered. The use of seven consecutive image slices by the proposed framework actually attempts to capture the volumetric features of brain tumors, thus creating a more comprehensive picture of the brain tumor. The accuracy of the proposed framework for brain tumor classification is 98.05%, with a sensitivity of 100%, thus making the framework more reliable for the identification of malignant brain tumors and their safe elimination.

Keywords: Apparent diffusion coefficient-diffusion weighted imaging (ADC-MRI), brain tumor, clinical sensitivity, convolutional neural networks (CNN), deep learning, diagnostic accuracy, long short-term memory (LSTM).

1. Introduction

Brain tumor management represents a clinical challenge in the field of neuro-oncology, with high morbidity and mortality rates. The success of patient management and the accuracy of prognostic outcomes are critically dependent on the early and accurate differentiation between benign and malignant brain tumors. Any error in the early classification of brain tumors may lead to the development of inappropriate management strategies, delayed surgical interventions, and a direct negative impact on the survival of the patient. In the modern clinical setting, Apparent Diffusion Coefficient (ADC), obtained from Magnetic Resonance Imaging (MRI), has emerged as an important imaging technique for the evaluation of brain tumors. The quantification of the diffusion of water molecules within the brain tissue is an important functional imaging technique, as it often exceeds the capabilities of structural MRI. However, the interpretation of these images has its own limitations. The interpretation of brain tumor images may vary due to the morphological variability of the tumor, ill-defined borders, and the fatigue of the radiologist. Moreover, the human observer may face difficulty in observing the subtle microscopic patterns at the pixel level, differentiating between the early stages of malignancy and benign tissue.

The progression of Deep Learning offers a promising route to overcoming diagnostic issues in this field. Convolutional Neural Networks have been found to exhibit high success rates in detecting complex visual patterns in medical imaging. Nevertheless, it is not possible to capture all aspects of a tumor by simply analyzing a single slice of a medical image. Hence, a sequential analysis is necessary to capture a tumor as a volumetric object. This is possible by incorporating LSTM networks to enable analysis of consecutive slices of a medical image. This is analogous to a radiologist performing a sequential analysis to examine a complete MRI scan. Fig. 1 emphasizes the importance of sequential analysis in interpreting ADC-MRI scans by presenting examples of benign and malignant tumors, where regions corresponding to lesions exhibit characteristics in terms of diffusion.



(a) (b)

Fig. 1. (a) Benign brain tumor. (b) Malignant brain tumor.

Several studies have also explored various computational techniques that can lead to improved accuracy in brain tumor classification in the past. And for example, [1] have suggested the optimized deep random graph dilated diffusion convolutional attention network, which has resulted in enhanced accuracy using a variety of complex optimization techniques. In another clinically focused work, [2] presented a simple 2D Convolutional Neural Network (CNN), which is designed to ensure that latency is kept low in the classification process. [3] also presented a sequential and stage-based approach that focuses on distinguishing between the detection of neoplastic tissue and the classification of tumors using Nesterov momentum. Apart from deep learning techniques, other approaches such as the combination of edge-refined segmentation and multiple classifiers have also shown significant potential in brain tumor classification and differentiation [4]. With respect to ADC values, traditional machine learning approaches such as the use of texture features such as Grey Level Co-occurrence Matrix have also been applied to classify between malignant and benign brain tumors [5]. However, the majority of these approaches are focused on single-slice analysis and lack the application of sequential analysis, which is essential in brain tumor classification and differentiation.

Recent advancements have also presented multi-modal segmentation approaches that rely on attention mechanisms to reduce the computational burden in brain tumor segmentation and classification [6]. To deal with the inherent uncertainty of tumor properties, parallel architectures that incorporate both Transformer and self-attention mechanisms have been proposed for local and global patterns [7]. In addition, the focus on non-contrast MRI sequences, which involve the combination of T1-weighted and T2-weighted imaging, indicates that there is a growing interest in diagnostic efficiency without the need for contrast agents [8]. Although models like TumorDetNet have reported 100% accuracy in distinguishing between benign and malignant tumors using deep architectures with 48 layers or more [9], there is still a need for more streamlined models that focus on high sensitivity using sequences like ADC.

The present study aims to propose a new diagnostic framework using a CNN-LSTM model for the analysis of ADC-MRI images. The main objective of the study is to improve the sensitivity of the diagnostic system so that no cancerous cases are left out during the screening process. The proposed system will analyze seven successive image slices, thereby taking into account the spatial-temporal continuity of the tumor mass. The study aims to provide a reliable clinical decision support system with minimum room for error in the diagnostic process.

The organization of this paper is as follows: Section II discusses the methodology, including the data set used and the construction of the sequential CNN-LSTM network. The results will be explained in detail in Section III, along with a clinical discussion of the system's performance. In the final section, the results will be summarized and the potential for the use of this system in the clinical environment will be explained.

2. Materials and Methods

2.1. Dataset and Clinical Justification

This paper utilizes an Apparent Diffusion Coefficient (ADC) MRI dataset that is obtained from patients suffering from brain tumors. The dataset contains 41 samples of brain tumors, out of which 14 are malignant and 27 are benign, making up a total of 1,202 image slices. In terms of clinical relevance, the ADC modality is significant since it is able to capture tissue cellularity using the water diffusion property. Malignant tissues have higher cell density, which limits the water diffusion and results in lower ADC values. The focus of this system is to utilize this particular property and obtain a more objective evaluation of the nature of the tumor than is possible using structural MRI techniques, as established in previous works [5], [8].

From a clinical point of view, it is critical to accurately preoperatively distinguish between benign and malignant brain tumors since it is directly linked to their management and postoperative care. In clinical neuro-oncology practice, histopathological examination is currently accepted as the most accurate method to establish malignancy in brain tumors; nevertheless, it is also recognized as being invasive and not always feasible. In particular, there is a considerable risk involved in stereotactic biopsies if tumors are located in eloquent areas of the brain and/or are anatomically difficult to access. In addition, it is also possible that such a biopsy could not identify the highest-grade component of a heterogeneous tumor. In such a context, a diagnostic marker is urgently called for to offer a faster and less risky alternative to early malignancy prediction [3], [10].

Furthermore, the imaging characteristics of the conventional MRI sequences have been found to be non-specific in many tumor types, thereby making the differentiation of malignant from benign tumors difficult. Diffusion imaging is considered promising for tumor characterization, with the apparent diffusion coefficient maps obtained in diffusion-weighted imaging considered promising for this purpose. This is because this imaging technique can provide information on the density of the cells within the tumor. In clinical practice, malignant tumors are usually characterized by a high cellular density, thereby making the ADC values of the tumors relatively low. On the other hand, the ADC values of the benign tumors are relatively high.

2.2. Sequential Volumetric Analysis

The preprocessing phase involves pixel intensity normalization to ensure standardization of the input data. This is often accompanied by specific filters to improve the visibility of features in the input images [1], [11]. Unlike other conventional approaches that involve single-slice analysis of the input images [2], the present study has adopted a sequential approach in processing the input images. Specifically, seven consecutive image slices of each input image have been processed in the present study. This is to ensure that the input image is analyzed as an entire volume to identify features of continuity that often represent invasive tumors, mimicking the entire analysis that is carried out by a consultant radiologist. The approach is in line with the TimeDistributed paradigm in which multiple consecutive image slices are analyzed as a single input to ensure that all the crucial features of the input images are maintained [12].

From a clinical standpoint, radiologists do not use a solitary ADC image for the characterization of tumors since the diffusion patterns of the tumor may vary in adjacent image slices due to the heterogeneous cell densities, necrotic tissues, cysts, and other factors. In actual use, the evaluation of the malignancy of a tumor will be performed by examining a number of sequential image slices to create a mental image of the tumor as a three-dimensional object. In this regard, the sequential evaluation of the image becomes critical to reduce the level of uncertainty that may be experienced by the model when exposed to a two-dimensional image of the tumor [10], [13].

Besides the sensitivity and specificity of the framework, the overall ability of the framework to distinguish between different image classes can be seen in the result of an almost perfect AUC-ROC. This attribute of the proposed framework assumes clinical significance since the thresholds for the hospital screening process may vary. The thresholds may be influenced by a number of factors, including the availability of hospital resources and the acceptable level of false positives or false negatives. The use of a framework with a consistent area under the curve and a well-balanced F1-score becomes important since the framework will be more reliable in the support of the diagnosis of malignant tissues, regardless of the conditions.

Moreover, volumetric evaluation has special importance in ADC imaging because the quantitative diffusion characteristics can change substantially in the same tumor depending on the specific area of interest in the particular plane of interest. In detail, the presence of mixed regions within the tumor with very high cellular densities can cause the ADC values to decrease substantially, and the presence of edema regions can cause the ADC values to increase. Thus, in ADC imaging, there is a risk of sampling bias in the results obtained from processing a single plane of interest. Therefore, processing seven consecutive planes of interest can increase the chances of obtaining results that can be more appropriate for making safer clinical screening decisions about tumors by obtaining a more consistent set of diffusion characteristics related to malignancy. This is achieved in a reproducible computational manner as depicted in Fig 2.

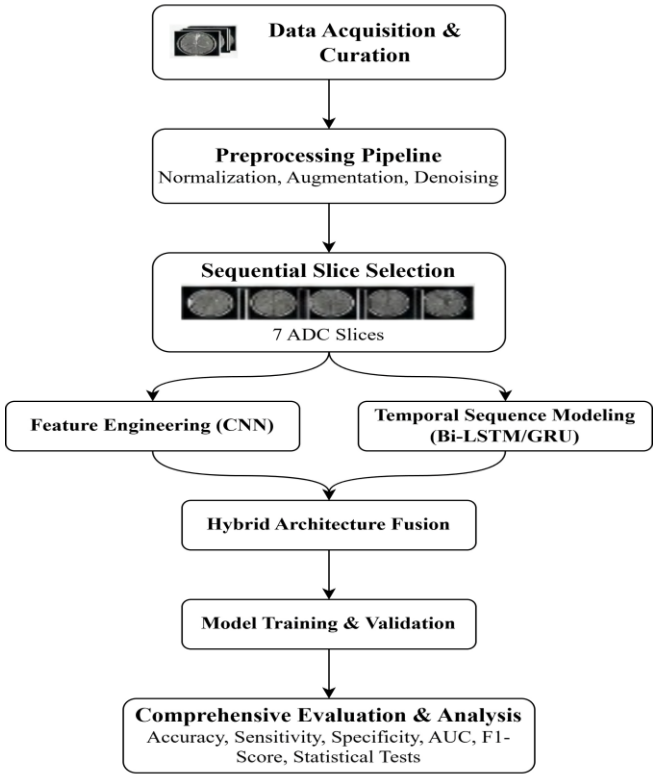


Fig. 2. Flowchart of the proposed sequential ADC-MRI classification pipeline.

2.3. CNN-LSTM Model Architecture

The classification framework can be assembled by using a Convolutional Neural Network (CNN) and a Long Short-Term Memory (LSTM). The CNN component acts as a feature extractor, allowing the system to recognize morphological and textural features at the pixel level [14]. The features are then used by the LSTM component to determine the spatial relationships between the slices in an image sequence. The integration of the two networks helps to eliminate the limitations of the convolutional networks, as the CNN component can use the temporal-like relationships between the image data to perform the classification task [13].

In terms of the diagnostic process, the CNN-LSTM hybrid architecture can be used to mimic the diagnostic process used by a radiologist in the interpretation of brain MRI scans in clinical practice. In the interpretation of the ADC MRI scan, the clinical diagnostic process usually involves the evaluation of the diffusion restriction patterns in the image, not only in one slice but by sequentially scanning the adjacent slices to ensure the continuity of the lesion, the heterogeneity within the lesion, and the invasion-related characteristics. The system can use the CNN component to ensure the extraction of spatial features from each slice, and then the LSTM component can be used to mimic the sequential diagnostic process.

This design is clinically relevant because there is a strong correlation between the ADC value and the cellularity of the tumor, as well as its likelihood of being malignant. However, these characteristics may vary in a heterogeneous manner throughout the tumor due to the presence of heterogeneous regions within the tumor, including solid, necrotic, and edematous regions. In accordance with the tumor evaluation using the ADC technique in clinical practice, the evaluation of the tumor in an unbiased manner, without the need to specify the region of interest (ROI) and without relying on single-slice analysis, can be achieved using the proposed CNN-LSTM integration to ensure the safe pre-operative differentiation between malignant and benign tumors as an imaging-based decision-support technique. Mathematically, each patient case can be represented as follows:

$$X = \{x_1, x_2, \dots, x_T\}, T = 7 \tag{1}$$

Where $x_t \in \mathbb{R}^{H\times W}$ denotes the ADC image at slice t [12] . Each slice is independently processed by the CNN feature extractor to produce a compact embedding:

$$f_t = \phi_{\text{CNN}}(x_t) \tag{2}$$

Where $f_t \in \mathbb{R}^d$ drepresents the learned spatial feature vector [14]. The sequence of extracted features is then fed into the LSTM module to capture inter-slice dependency:

$$h_t = \phi_{\text{LSTM}}(f_t, h_{t-1}) \tag{3}$$

Where $h_t \in \mathbb{R}^k$ denotes the temporal representation at time step t. Finally, the tumor class prediction is obtained using a softmax classifier applied to the final hidden representation:

$$\hat{y} = \text{Softmax}(W h_T + b) \tag{4}$$

Where $\hat{y} \in \mathbb{R}^2$ represents the probability distribution of the benign and malignant tumor classes. The description highlights the role of the convolutional neural network (CNN), which acts as a spatial feature extractor on each slice, and the long short-term memory network (LSTM), which integrates the features from sequential slices to capture the continuity in the tumor volume. The sequential learning process is clinically relevant in the interpretation of ADC-MRI, as the presence of malignancy-related diffusion restriction may show inconsistency in the tumor volume. The CNN-LSTM mechanism provides a mathematical basis to combine the spatial and sequential information from the ADC images to generate a consistent diagnostic prediction.

This expression clearly indicates that the convolutional neural network (CNN) acts as a spatial feature extractor at the slice level, and the long short-term memory network (LSTM) integrates these features from the adjacent slices to capture the continuity in the volumetric data. The sequential learning process has clinical importance in the interpretation of apparent diffusion coefficient-weighted MRI (ADC-MRI), as the malignancy-related diffusion restriction may appear in an inconsistent manner within the tumor volume. The CNN-LSTM mechanism provides a mathematical basis to combine the spatial and sequential ADC data to generate a reliable diagnostic prediction [10], [14].

2.4. Performance Evaluation and Safety Standards

The present study makes use of the Unified Focal Loss function to address the problem of class imbalance between the two classes, i.e., benign and malignant samples. This is extremely important to improve the sensitivity of the model to the subtle signs of malignancy, especially when the malignant samples are scarce in the database [4], [9]. In order to validate the proposed model, the following will be used: accuracy, sensitivity, specificity, and Area Under the Curve (AUC). The major aim is to achieve 100 percent sensitivity to ensure the safety of patients, thereby avoiding the possibility of missing malignant cases during the screening process.

Considering the clinical safety aspect, the sensitivity is the most critical factor in brain tumor screening, where missing the diagnosis may result in the delay of life-saving interventions. This is also in line with the emphasis on the clinical safety of the proposed model, which is similar to the unified models that aim to achieve near-perfect accuracy while maintaining the clinical interpretability of the results [2], [9], [10]. The imposition of higher penalty on the misclassification of malignant samples is expected to improve the discriminative power of the network to capture the subtle signs related to the diffusion patterns.

Moreover, there is an inherent class imbalance in the dataset with the malignant class numerically underrepresented compared to the benign class. This can cause deep learning models to be biased toward the numerically dominant class, leading to decreased performance in detecting malignant patterns. This is not acceptable in the context of deep learning in medicine because the malignant class represents the high-risk group. Therefore, focal loss optimization is used to emphasize the difficult-to-classify malignant patterns while reducing the influence of easily classified patterns of the benign class during training [4], [9]. This is in line with the goal of maintaining high sensitivity while ensuring the stability of the classifier performance in realistic distributions of clinical data. Mathematically, the focal loss function can be defined for binary classification problems as follows:

$$\mathcal{L}_{\text{focal}} = -\alpha(1 - p_t)^{\gamma}\log(p_t) \tag{5}$$

Where p_t is the predicted probability of the actual class for each sample in the training set, α is the balancing factor of the classes, and γ is the focusing parameter that reduces the weight of easily classified patterns. Focal loss imposes a larger penalty on misclassified patterns of the malignant class, which encourages the model to learn more discriminative patterns of diffusion-related features to improve robustness to the inherent class imbalance in the data [9]. Evaluation of the model is based on appropriate performance metrics such as accuracy, sensitivity, specificity, and AUC-ROC curves in the context of clinical safety in malignancy detection, with sensitivity defined as the safety metric of interest [11].

3. Results

Experimental evaluation demonstrates high precision in the classification of intracranial lesion typologies via functional Apparent Diffusion Coefficient (ADC) MRI techniques. Based on empirical quantitative assessment, the computational architecture achieves a global diagnostic accuracy rate of 98.05% coupled with a diagnostic sensitivity rate of 100%. Within the operational parameters of clinical neuro-oncological triage, this absolute sensitivity metric signifies the complete eradication of false-negative classifications between malignant and benign tumor masses. The systematic realization of zero false negatives is critical for time-sensitive, high-stakes medical interventions, including macro-surgical cytoreduction or stereotactic radiotherapy.

Beyond the detection of malignant transformations, the system maintains high fidelity in the identification of benign lesions, registering a specificity rate of 95.52%. While a nominal false-positive margin is observed, this directional variance complies with conservative oncology screening risk-management models, where a false positive prompts secondary non-invasive diagnostic confirmation rather than risking an overlooked malignancy. The capacity of the network to differentiate biophysical tissue characteristics based on water diffusion restriction is further quantified by an Area Under the Receiver Operating Characteristic Curve (AUC-ROC) score of 0.9993, indicating near-perfect discrimination between dense hypercellular malignant formations and permissive benign growths.

The structural stability and stochastic convergence of the framework during the iterative training phase are delineated by the objective performance tracking curves depicted in Fig. 3. The precise alignment and steady trajectory of core metrics, specifically validation accuracy, validation AUC-ROC, and validation F1-score, confirm optimal model convergence without structural oscillations or signs of overfitting.

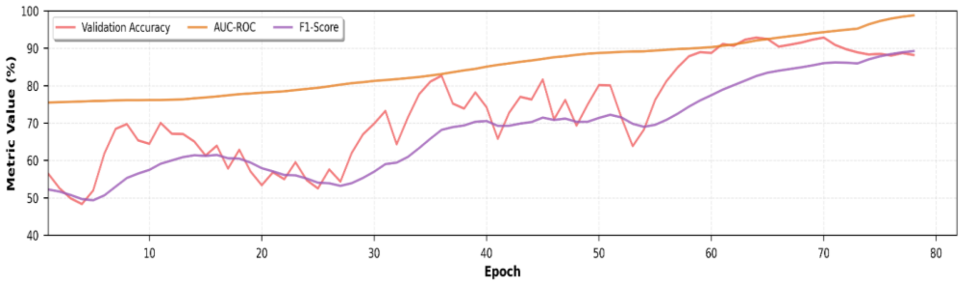


Fig. 3. Validation performance curves of the proposed sequential CNN–LSTM model

To establish the academic positioning of these empirical results within the contemporary state-of-the-art landscape, a rigorous quantitative comparison is executed against diverse baseline and complex deep learning architectures from recent literature, as systematically detailed in TABLE I.

TABLE I

Performance Comparison on Brain Tumor Classification Tasks.

Study	Methodology/ Architecture	MRI Modality/ Sequence	Classification Task (Subject)	Accuracy (%)
Singh et.al [1]	Optimised DR2DCAN	T1, T2, FLAIR	Multi-class (Glioma, Meningioma, Pituitary)	98.70
Saeedi et al. [2]	2D CNN	T1, T2, FLAIR	Multi-class & Healthy Brain	96.47
Simo et al. [3]	Sequential Stage CNN	T1, T2, FLAIR	Neoplastic vs Non-neoplastic	98.00
Ali et al. [4]	ER-BHS + Hybrid ML	DICOM (Multi-sequence)	Malignant vs Benign (6 subtypes)	98.61
Vijithananda et al. [5]	GLCM + Random Forest	ADC-MRI	Malignant vs Benign	90.41
Ranjbarzadeh et al. [6]	Cascade CNN + DWA	Multi-modality	Brain Tumor Segmentation/ Localiz	92.30
Tabatabae et al. [7]	Transformer + iResNet	T1, T2, FLAIR	Multi-class (Figshare Dataset)	99.30
Lu et al. [8]	Darknet53 (Fusion)	T1w + T2w (Non-contrast)	13 Distinct Brain Tumor Types	98.30

Study	Methodology/ Architecture	MRI Modality/ Sequence	Classification Task (Subject)	Accuracy (%)
Ullah et al. [9]	TumorDetNet (48-layer)	Multi-sequence MRI	Malignant vs Benign	99.83
Mehta and Kundra [10]	Hybrid CNN-LSTM	Multimodal (BraTs)	Specific Brain Tumor Classes	97.80
Awate et al. [11]	CNNLST Model	MRI Scans	Malignant vs Benign	94.81
Montaha et al. [12]	TD-CNN-LSTM	3D MRI (BraTs)	Brain Tumor (2 Classes)	98.90
Maheswari et al. [13]	Hybrid CNN-LSTM	MRI (Glioma, etc.)	Multi-class & Normal Samples	97.80
Rajeev et al. [14]	AlexNet + CNN-LSTM	MRI (Skull-stripped)	Multi-class (4 Types)	97.94
Proposed Method	Sequential CNN-LSTM	Sequential ADC-MRI	Malignant vs Benign	98.05

As clearly depicted in Table I, the clinical strength of this study is based on the use of sequential volumetric analysis. The model processes seven consecutive slices to evaluate the tumor as a 3D mass, as opposed to a 2D image. This is analogous to a consulting radiologist's workflow, where the entire volume is used to identify invasive characteristics and continuity. The implementation of this sequential analysis was found to be more effective than traditional single-slice analysis typically used in most literature.

4. Discussion

A The clinical efficacy of the proposed computational framework is fundamentally established by the realization of a 100% diagnostic sensitivity rate. Within the high-stakes domain of neuro-oncological triage, the absolute eradication of false-negative trajectories is paramount. Initial misclassifications that erroneously relegate malignant lesions to benign typologies invariably precipitate catastrophic delays in initiating urgent, time-sensitive interventions such as macro-surgical cytoreduction or stereotactic radiotherapy. Through the achievement of a zero false-negative paradigm, the sequential model provides a robust diagnostic layer ensuring that high-risk malignancies are immediately routed into aggressive therapeutic pipelines, thereby directly addressing the core safety imperative of clinical oncology.

While the model yields a robust specificity of 95.52%, it introduces a nominal margin for false-positive outcomes. In rigorous clinical screening protocols, a false positive is universally recognized as a manageable diagnostic diversion, which is inherently preferable to the fatal consequence of an overlooked malignancy. Such occurrences merely trigger secondary, non-invasive confirmatory diagnostic pathways, an approach that fully aligns with standard defensive medicine and patient-first safety mandates. From a biophysical perspective, the capacity of the model to distinguish distinct tissue microenvironments is mathematically validated by an Area Under the Curve (AUC-ROC) of 0.9993. This exceptional metric signifies near-perfect discrimination between the highly restricted water diffusion patterns characteristic of dense, hypercellular malignant formations and the unhindered, permissive diffusion profiles native to low-grade, benign tissue structures.

The definitive structural strength of this framework lies in the mathematical execution of sequential volumetric analysis. By transitioning from traditional single-slice evaluation to the synchronous processing of seven consecutive cross-sectional images, the network successfully interprets the lesion as a coherent three-dimensional mass rather than a disconnected series of 2D planes. This algorithmic design directly recapitulates the empirical workflow of a consulting neuroradiologist, who relies on spatial continuity across sequential imaging planes to map infiltrative margins and mitigate localized sampling biases caused by internal tumor heterogeneity, such as focal necrosis, cystic components, or surrounding vasogenic edema. The empirical data highlights that integrating this sequential spatial context yields superior diagnostic robustness compared to the isolated single-slice methodologies prevalent in current literature.

This technological superiority becomes distinctly evident when contrasted with the baseline systems outlined in TABLE I. The proposed architecture significantly outperforms the traditional feature extraction framework developed by Vijithananda et al., which was limited to a 90.41% accuracy rate [5], due to its reliance on single-slice Apparent Diffusion Coefficient (ADC) maps processed via Grey Level Co-occurrence Matrix (GLCM) and Random Forest classifiers. It similarly demonstrates enhanced robustness over basic standalone 2D CNN configurations such as the one implemented by Saeedi et al. [2]. While several multi-sequence models operating across T1, T2, and FLAIR modalities, including the optimized graph networks by Singh et al. [1] the hybrid machine learning classifiers by Ali et al. [4], or the complex 48-layer TumorDetNet by Ullah et al. [9], report marginally higher global accuracy scores, the proposed architecture achieves comparable clinical utility through a streamlined, highly focused architecture. Rather than demanding resource-intensive multimodal fusion pipelines [6], parallel hybrid transformers [7], or non-contrast anatomical image alignment [8], this system leverages purely quantitative physiological data from a single functional sequence (ADC-MRI).

Furthermore, while deep architectures like TumorDetNet [9] rely on extreme parameter depth to achieve high binary performance, this model matches that clinical safety standard by optimizing sensitivity to a perfect 100% using a computationally lightweight CNN-LSTM sequence. Implementing this non-invasive system within institutional hospital infrastructures establishes a reliable framework for diagnostic standardization. Operating as an objective clinical decision support system, the model provides an automated, reliable second opinion that reduces the cognitive friction experienced by clinicians during high-throughput screenings, standardizes tumor evaluation across variable institutional resources, and substantially mitigates human errors driven by diagnostic fatigue.

5. Conclusions

The present study proposes a simplified deep learning framework for the classification of brain tumors, utilizing sequential apparent diffusion coefficient (ADC) magnetic resonance imaging (MRI) data. The proposed model, based on the convolutional neural network (CNN) and long short-term memory (LSTM) architectures, attained 98.05% accuracy and 100% sensitivity. From the clinical perspective, the achievement of 100% sensitivity is the most critical factor, as it guarantees the detection of all malignant cases during the initial stage of the screening process. This, in turn, creates a high level of diagnostic security, reducing the possibility of malignant cases remaining undetected, thereby facilitating timely therapeutic interventions.

The implementation of the proposed seven-slice sequential analysis clearly demonstrated the superiority of the proposed method over the conventional single-slice technique, which provides the volumetric context of the brain tumor. This effectively captures the biological heterogeneity of the tumor, providing a more stable assessment. From the results, it is evident that the proposed model, based on the physiological information provided by the ADC values, is capable of providing a robust tool for the diagnosis of brain tumors.

The proposed system has a high potential for integration in the clinical environment. The system can assist radiologists in reducing the diagnostic burden by providing objective and sensitive analysis. This can help in reducing the risks of human fatigue or subjective analysis. The application of the system in the clinical environment will help in the standardization of diagnostic accuracy, thereby enhancing the prognosis of patients with brain tumors.

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