

EANet Enhanced by Sub-pixel Convolutional Neural Network for High-resolution Brain Tumour Image Enhancement and Classification

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Abstract

Cancers of the central nervous system, especially brain tumors, are among the leading causes of death worldwide. Magnetic Resonance Imaging (MRI) plays a crucial role in detecting and diagnosing brain tumors due to the high degree of soft tissue contrast achievable with the technique. However, early diagnosis of brain tumors is still difficult to achieve because their growth is complex and subtle in the early stage. Challenges include data scarcity, limited image clarity and difficulties in accurate classification. To tackle these issues, this work proposes a novel method for efficient and precise detection of brain tumors. Tensor compression is used to reduce the size of high-dimensional MRI image datasets while preserving essential spatial and structural content, which increases efficiency without compromising accuracy. Furthermore, an efficient sub-pixel CNN for image super-resolution is used to improve the spatial resolution of the MRI scans, enabling important minute details to be captured better. To overcome the scarcity of medical data available and the challenge of overfitting, MixUp data augmentation is used. This technique generates synthetic training samples by combining images and their corresponding labels, improving the robustness of the model. Moreover, the External Attention Transformer (EANet) enhances accuracy of tumor localization and classification by improving global feature extraction by attending to the relevant parts of the MRI scans for focused attention. All these methods work together to deliver a highly efficient and effective brain tumor detection system.

Keywords: Brain Tumor, EANet Classification, Image Super-resolution, Magnetic Resonance Imaging (MRI), MixUp Augmentation.

Introduction

According to the World Health Organization (WHO), brain tumors are a significant global health concern due to their high mortality rates and the challenges associated with their identification and treatment (1). The American Cancer Society defines brain tumors as a serious illness characterized by the abnormal growth of brain tissue, which disrupts normal brain function. Research from the National Brain Tumour Foundation highlights a 300% increase in brain tumor-related mortality over the past three decades, emphasizing the urgent need for improved diagnostic and treatment approaches (2). Each year, between 250,000 and 300,000 people worldwide are diagnosed with brain tumors, with an incidence rate of approximately 8.1 per 100,000 individuals. The latest statistics show that men are 1.4 times more likely than women to develop brain tumors, with men

accounting for about 55% of cases and women 45% (3). Early detection is crucial to improving treatment outcomes and prognosis for those affected by this condition. Several computational models have been proposed for brain tumor detection (4, 5), leveraging advanced architectural approaches such as convolutional neural networks (CNNs), transformers and attention-based mechanisms (6). These models aim to improve diagnostic accuracy, but each approach comes with its own set of benefits, drawbacks and application scenarios. The essential techniques and their advantages, disadvantages and applications are summarized in Table 1. This work explores alternative methodologies with the objective of further enhancing diagnostic precision while addressing the existing challenges in the field.

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Table 1: Methods Overview: Dimensionality, Architecture, Benefits, Limitations and Applications

Model	Dimensionality	Architecture	Pros	Cons	Use Cases	References
Machine Learning-based Back Propagation Neural Network (MLBPNN)	2D	BPNN, Gray Level Co-occurrence Matrix (GLCM), PCA	To effectively detect small tumours.	Complicated computation; limited validation for 3D imaging.	Gliomas dataset.	(7)
VGG19 with Grab Cut, Logistic Regression (LGR) and Ensemble	2D	VGG19, Grab Cut, LGR and Ensemble Classifiers	Good glioma segmentation, high classification accuracy.	Significant processing requirements	BraTS15, BraTS16, BraTS17.	(8)
BrainMRNet	2D	Attention modules, hypercolumn techniques and residual blocks.	High classification accuracy.	Complex model, more validation required	MR image dataset (categorized): normal and tumour.	(9)
VGG Net-based Deep Learning Framework	2D	Modified VGG Net.	Enhanced diagnostic accuracy.	Small dataset size limited generalizability	Open-access dataset containing 253 MRI images.	(10)
CNNs with ANNs and Correlation Learning Mechanism	2D	CNN, ANN, Correlation Learning Mechanism	Increased precision	Relying on datasets; clinical implementation difficulties.	Brain MRI Images from Kaggle (3,064 images).	(11)
Refined VGG-16 and 23-layer CNN	2D	Modified VGG16, 23-layer CNN.	Useful for binary and multiclass classification.	Requires sizable, annotated datasets.	Harvard Medical Dataset, Contrast-Enhanced MRI (CE-MRI) Figshare dataset.	(12)
VGG-16, ResNet50 with SVM and Random Forest	2D	Random Forest, SVM, Pre-trained VGG-16, ResNet50.	High accuracy.	Does not include other imaging modalities.	MR brain image dataset.	(13)
CNN-based Models	2D	CNN versions	Increased diagnostic speed and accuracy.	Requires more improvement for practical use.	MRI image dataset.	(14)
YoDenBi-NET	2D	YOLO, DenseNet, Bi-LSTM.	High accuracy.	High computing needs.	T1-weighted CE-MRI dataset.	(15)
Dual-module System	2D	Neural networks, adaptive Wiener filtering.	Better categorization of tumour.	Requires high-quality datasets.	CE-MRI brain dataset.	(16)
SVM with Fuzzy C-Means (FCM)	2D	Fuzzy C-Means (FCM), SVM	Improved tumour segmentation and classification.	Adjustments for varied datasets.	CE-MRI brain dataset.	(17)

This work takes numerous novel techniques and combines them to progress in this area:

- (a) **Tensor Compression:** Optimizes data handling by reducing memory usage and improving computational efficiency during preprocessing, thus enabling more effective data processing (18-20).
- (b) **Image Super-Resolution:** Utilizes a sub-pixel CNN technique to enhance image quality and resolution, allowing for finer details of the tumor to be detected, which is crucial for early-stage diagnosis.
- (c) **MixUp Data Augmentation:** Addresses the challenge of limited data by generating synthetic samples through computational methods, thereby expanding the training dataset and enhancing the model's robustness and generalization.
- (d) **EANet (External Attention Transformer):** Improves the model's focus on key features and enhances diagnostic accuracy by leveraging advanced attention mechanisms that allow for more precise tumor classification and localization.

Collectively, these approaches aim to overcome existing challenges in brain tumor detection, striving for more accurate, reliable and efficient diagnostic solutions.

Methodology

The relatively low quality of MRI scans presents significant challenges, especially in detecting brain tumors. Limited resolution can hinder traditional methods, making it more difficult to distinguish subtle tumor features. Additionally, the availability

of data affects machine learning models, as smaller datasets restrict their ability to generalize effectively. While MRI scans can be helpful for imaging, they often lack the high-resolution detail needed for accurate diagnosis, further complicating tumor detection. Current data augmentation methods, though useful, do not fully address these issues, as the variations they create are not genuine deviations and are merely self-generated. Tumor classification remains a difficult task due to the unpredictable size, shape and type of tumors.

To enhance brain tumor detection, it is essential not only to analyze MRI images but also to optimize the entire analysis process through several sequential stages. The process begins with tensor compression for spatial complexity reduction, an image enrichment process using an Efficient Sub-Pixel CNN for high-resolution images, then increased variance and generalization with MixUp Data Augmentation, followed by classification with EANet for accurate tumor region delineation. The use of these techniques leads to higher accuracy in detecting brain tumors, as demonstrated in Figures 1 and 2.

Algorithm: Enhancement of MRI

Images and Brain Tumor Classification

- (a) Input: Split the BraTS 2024 dataset into training data (t) and testing data (t_l).
- (b) Apply tensor compression to reduce dimensionality while preserving essential features whose output is the compressed tensor.
- (c) Input the compressed tensor into a CNN-based super-resolution model.

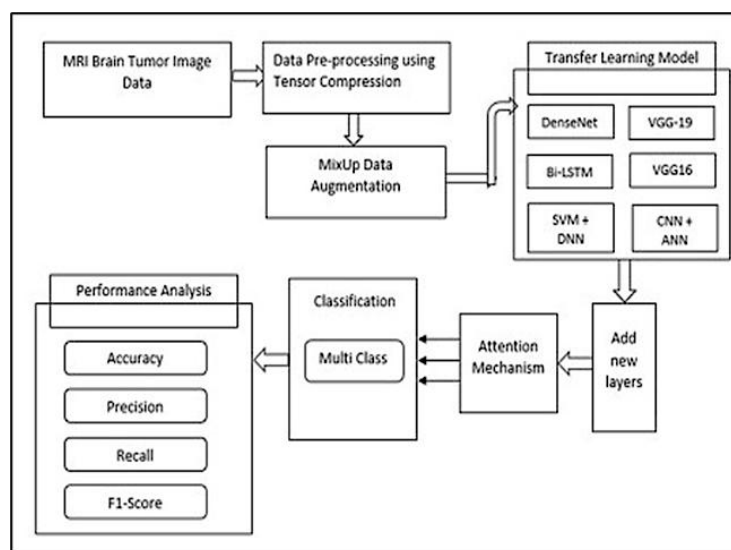


Figure 1: Generic Architecture of the Proposed Model

Pass through convolutional layers using Equation [1].

$$F(x, y) = \sum_{i=0}^{k-1} \sum_{j=0}^{k-1} W(i, j) \cdot I(x + i, y + j) \quad [1]$$

Apply an efficient sub-pixel CNN for upscaling using Equation [2].

$$I_{\text{high-res}} = \text{PixelShuffle}(F_{\text{conv}}) \quad [2]$$

Output high-resolution MRI images.

(d) Select two high-resolution images and their labels.

Sample $\lambda \sim \text{Beta}(\alpha, \alpha)$

Generate augmented image using Equation [3]:

$$x_{\text{new}} = \lambda x_i + (1 - \lambda) x_j \quad [3]$$

Generate a new label using Equation [4]:

$$y_{\text{new}} = \lambda y_i + (1 - \lambda) y_j \quad [4]$$

Output augmented image-label pairs.

(e) Classification using EANet took place where:

Extract features using convolutional layers.
Apply an attention mechanism to focus on the tumor region.

Flatten features and pass through fully connected layers.

Predict tumor class and convert label into coded form.

(f) Output: The final tumor classification label.

Dataset Collection

Researchers and developers can access the BraTS 2024 dataset through the Synapse platform, which supports scientific collaborations and data sharing. This dataset consists of multimodal MRI images, including pre-contrast T1-weighted (T1), contrast-enhanced T1-weighted (T1-Gd), T2-weighted (T2) and T2-weighted fluid-attenuated inversion recovery (FLAIR). Our work primarily focuses on low-grade gliomas (LGG) to high-grade gliomas (HGG), making it particularly well-suited for augmentation and classification tasks. The dataset contains 600 brain tumor volumes, each with four MRI modalities, totalling approximately 2400 images. However, the individual slices and voxel dimensions across different MRI scans are inconsistent, with each instance varying in slice length and width. This inconsistency poses a challenge for deep learning model development, as it is typically expected that the input shape remains fixed during both training and classification. Consequently, this dataset provides

an excellent opportunity to evaluate the effectiveness of our model, particularly focusing on tensor compression techniques.

Data Pre-processing: Tensor Compression

The primary goal of this step is tensor compression that reduces the computational complexity for volumetric MRI images while preserving important diagnostic information essential for brain tumor detection. It compresses the input data to a lower-dimensional core tensor with associated factor matrices that hold required information on structure and location. Irrelevant components are discarded and the tensor is reconstructed while ensuring the minimum redundancy. Accordingly, this representation boosts the speed, scalability and accuracy of operations such as image enhancement, augmentation and classification. The diffusion tensor, D , in DTI, describes the diffusion of water molecules in brain tissue in terms of a 3×3 symmetric matrices. That is decomposed into eigenvalues $(\lambda_1, \lambda_2, \lambda_3)$ and eigenvectors, where the eigenvalues give the rates of diffusion along the principal axes and the eigenvectors $(\theta_1, \theta_2, \theta_3)$ describe the diffusion direction. This decomposition allows for the visualization of white matter tracts and the extraction of important metrics, such as Fractional Anisotropy (FA) and Mean Diffusivity (MD), for brain structural analysis.

Mean Diffusivity (MD)

Mean Diffusivity (MD) is an important measure obtained from Diffusion Tensor Imaging (DTI), which is determined by averaging the values of the diffusion tensor, according to the following expression as shown in Equation [5]:

$$MD = \frac{1}{3}(\lambda_1 + \lambda_2 + \lambda_3) \quad [5]$$

Where λ_1 , λ_2 and λ_3 refers to the three eigenvalues associated with the diffusion tensor D. These eigenvalues are representative of the diffusion rates corresponding to the principal axes of diffusion.

High MD indicates extracellular water diffusion stemming from the processes of edema or necrosis, while low MD implies increased cellularity, which is quite common in low-grade gliomas. MD mapping is to identify structural changes in the tumor, assist surgical planning and monitor treatment response. This MD combined with advanced imaging and machine learning allows

better diagnosis and personalized management of brain tumors.

Fractional Anisotropy (FA)

One of the most important metrics obtained from the diffusion tensor is the Fractional Anisotropy (FA), which helps measure the degree of anisotropy (directional dependency) of diffusion.

It may be calculated as shown in Equation [6].

$$FA = \sqrt{\frac{3}{2} \frac{\sqrt{(\lambda_1 - \lambda^-)^2 + (\lambda_2 - \lambda^-)^2 + (\lambda_3 - \lambda^-)^2}}{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}} \quad [6]$$

where " λ^- " is the mean of the eigenvalues of a matrix as shown in Equation [7].

$$\lambda^- = \frac{\lambda_1 + \lambda_2 + \lambda_3}{3} \quad [7]$$

$\sqrt{((\lambda_1 - \lambda^-)^2 + (\lambda_2 - \lambda^-)^2 + (\lambda_3 - \lambda^-)^2)}$ illustrates the variability of diffusivity among directional eigenvalues relative to the spatial mean diffusivity.

Fractional anisotropy (FA) determines the deviation of eigenvalues from the mean and normalizes it over the sum of squares of eigenvalues, providing an indicator for the directionality of diffusion. Values of FA range between 0 (isotropic diffusion) and 1 (highly anisotropic); organized white matter tracts are indicated by high FA values, but low FA values suggest pathology or disorganized parenchyma. FA maps are useful for assessing white matter integrity and tumor infiltration. By complementing mean diffusivity (MD), FA provides a better means of distinguishing between healthy and pathological brain tissues based on DTI, helping in tumor detection and characterization.

Image Enhancement: Image Super-Resolution using Efficient Sub-pixel CNN

The sub-pixel CNNs increase the resolution of images by extracting features using convolutional layers and then applying a sub-pixel convolutional layer for upscaling. The layer reorganizes learned feature maps into high-resolution grids, thus outperforming traditional deconvolution methods.

This layered strategy gives optimized enhancement for images created in super-resolution tasks.

Convolution Operation

The convolution operation is integral in extracting features from images. This process consists of a convolution filter (or kernel) that passes over the input image and computes dot products of the filter with the image's corresponding regions. It allows in finding and retrieving useful features from the image like edges, textures and patterns which are very important for purposes such as image recognition or classification.

"The convolution operation can be defined mathematically by the formula as shown in Equation [1]."

Where, $F(x,y)$ is the result of generating the feature map. (i,j) represents the convolution filter linear element with $k \times k$ dimensions. $I(x,y)$ is the image used as an input.

As the filter (W) is positioned over the input image (I). At every position $((x,y))$, it returns the value derived from the dot product between the filters'

values and the image sub-region corresponding to that position. This leads to the formation of the feature map (F) which accentuates the features in the image that are catered to by the filter. This operation is carried out for each image, thus enabling the CNN to learn and recognize different features at various positions, which assists in the comprehension of complex visual data.

Sub-pixel Convolution (Pixel Shuffling)

The sub-pixel convolution operation is a technique that is applied to increase the image size without actually increasing the number of parameters by repositioning pixels in more than one convolutional feature map onto a grid of higher dimensions. This technique takes advantage of the PixelShuffle operation, which takes the channels of the convolution output and assigns them to spatial pixels, that is, increases the resolution of the image. "This technique comes in handy in super-resolution tasks where one needs to increase the size of the low-resolution images. The mathematical expression for this operation is presented as shown in Equation [2]" which $I_{\text{high-res}}$ defines the high-resolution generated image. F_{conv} Define the maps produced by convolutions. PixelShuffle reorders the elements in F_{conv} and enlarges its spatial dimensions by mapping r^2 channels to spatial pixels, leading to

effective high-resolution spatial presentation.

The Efficient sub-pixel CNN makes tremendous improvements on low-resolution MRI images by extracting key features, despeckling and structuring components while preserving tumor borders. The sub-pixel layer up-samples the learned features into high-resolution outputs for maximizing the accuracy of the diagnosis and fast augmenting and classifying brain tumors.

Data Augmentation: Mix Up Data

Augmentation

MixUp data augmentation constructs hybrid training samples by linear combinations of pairs of MRI images and their respective labels, enabling dataset diversity and enhancing model generalization—the two key factors for accurate brain tumor classification. It then combines two high-resolution MRI images (x_i, x_j) with their respective labels (y_i, y_j) and takes a mixing coefficient λ from a Beta distribution ($\lambda \sim \text{Beta}(\alpha, \alpha)$), which guarantees a smooth interpolation with little discontinuities.

The new augmented image x_{new} in-between for each of the examples using a linear interpolant as written in Equation [3]. Similarly, we can also use the same interpolation methodology to determine the corresponding label for the new image y_{new} as written in Equation [4].

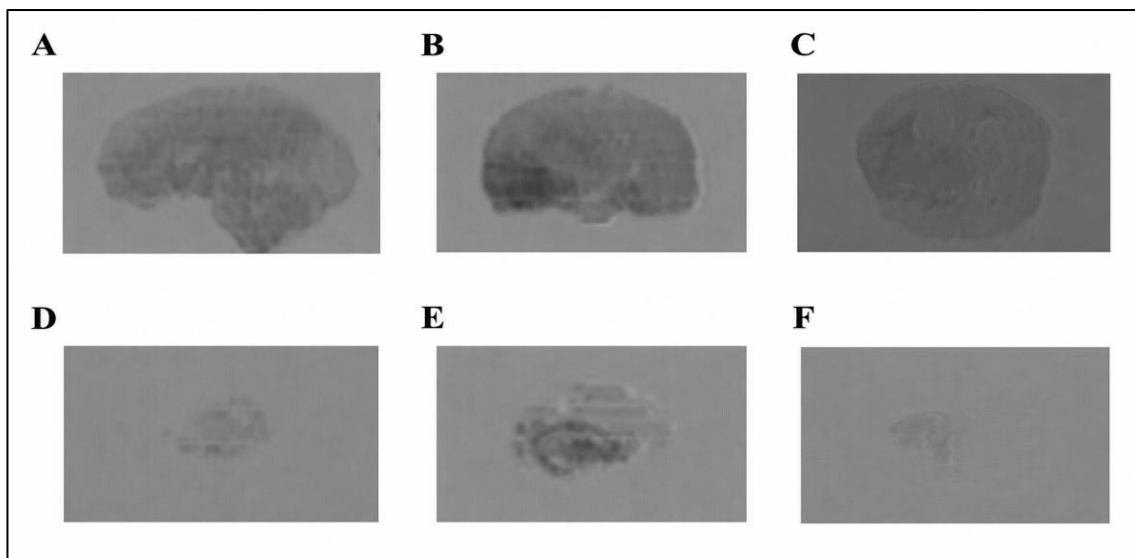


Figure 2: Mix Up Data Augmentation of the BraTS 2024 dataset. (A-F) Interpolating MRI Images
Images are displayed in pixel coordinates (256×256 pixels)

MixUp increases the number of dynamically created augmented image-label pairs, interpolating MRI images to enhance decision boundaries and image overfitting effects, especially in small

medical datasets, as shown in Figure 2. It adds data volume and diversity, improving generalization of the overall performance attained in brain classification, which integrates easily into

tensor compression as well as image super-resolution.

Brain Tumor Classification: EANet

The augmented and unaugmented high-resolution MRI images are fed into the external attention Network (EANet) for tumor classification after

MixUp. EANet filters out the noise contributed by surrounding tissues and pays attention to important tumor regions, thus promoting classification metrics. Convolutional layers extract meaningful feature maps from MRI volumes to refine tumor diagnosis.

Feature Extraction

We use X to represent the input image. So EANet's convolutional layers use filters W to extract feature maps F as in Equation [8].

$$F = f(W * X) \quad [8]$$

Where, f is a non-linear activation function (like ReLU) and $*$ denotes convolution. These feature maps give a detailed representation of the image and they capture major patterns for classification.

Attention Mechanism

EANet has used an attention mechanism that improves the classification performance of images by focusing on regions of tumors. Instead of the classical self-attention mechanism, an external

attention layer with memory is used for retention and retrieval of global information; its attention matrix A is learned during training to fine-tune the feature representations for the purpose of improved tumor detection.

Using the attention mechanism, attention weights A are computed for spatial positions in feature maps as in Equation [9]:

$$A_{i,j} = \frac{\exp(e_{i,j})}{\sum_{i,j} \exp(e_{i,j})} \quad [9]$$

where $e_{i,j}$ are used to show the significance of spatial position (i, j) in the feature map and the attention weights are normalized in the softmax function. The attention mechanism in EANet reinforces tumor-related regions while restricting the rest of the areas, which finally results in increased classification accuracy.

In mathematical form, “the attention mechanism is presented as shown in Equation [10]:

$$Z = X \cdot A \quad [10]$$

where X symbolizes the input feature map, A the external attention matrix and Z the enhanced feature representation. This formulation helps magnify significant tumor regions against distractions in the benign tissue and helps find accurate tumors within the areas.

Classification with Fully Connected (FC) Layers

Tumor classification involves passing attention-weighted feature maps to the fully connected layers. The fully connected layers output class predictions based on their high-dimensional features by using Equation [11]:

$$\hat{y} = \text{Softmax}(W \cdot Z + b) \quad [11]$$

Where W is the weight matrix, Z is the attention-enhanced feature map and b is the bias vector. The Softmax function calculates class probabilities that help in accurate prediction of tumor type along learned complex feature interactions, as shown in Equation [12]:

$$P(y = k|F) = \frac{\exp(W_k^T F)}{\sum_{j=1}^K \exp(W_j^T F)} \quad [12]$$

where $P(y = k | F)$ represents the probability that the image belongs to class k , W_k is the weight vector of class k and K symbolizes the total number of tumor classes. Consequently, an output that serves as a classification label will reveal the predicted tumor type. The proposed architecture of the EANet-based brain tumor classification model and corresponding major processing and classification components are shown in Figure 3.

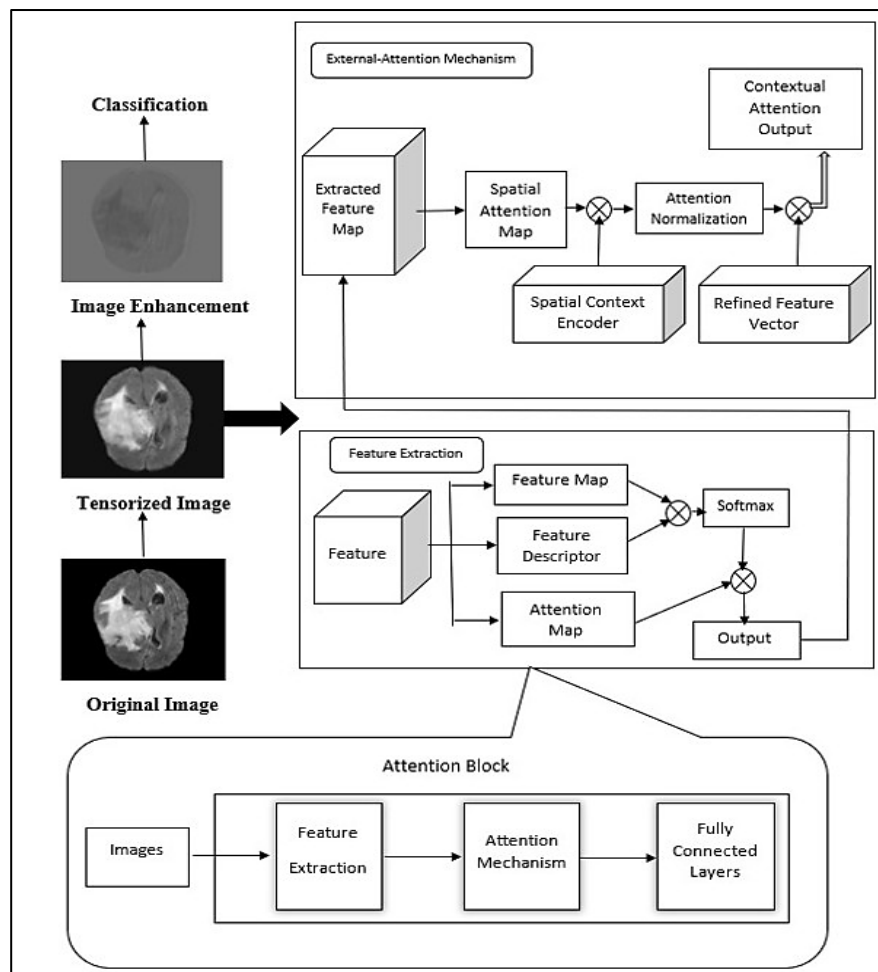


Figure 3: The Structure of the EANet-based Brain Tumor Classification Model

Results

The proposed brain tumor detection model was thoroughly evaluated using the BraTS 2024 dataset, which includes MRI scans of tumors with varying types and complexities. The results demonstrate that the system performs effectively and successfully addresses multiple aspects of tumor classification performance.

The implemented brain tumor detection pipeline outperforms on all key evaluation metrics, achieving accuracy, precision and sensitivity (recall) values of 0.96, 0.925 and 0.94, respectively. The model also demonstrates the ability to distinguish between positive and negative cases,

achieving a specificity value of 0.964. This helps minimize the occurrence of false positives, i.e., predicting the absence of tumors when they are present. In this case, the error rate is valuable because it indicates the percentage of correctly identified non-cancer cases relative to cancer cases, particularly focusing on false non-cancer predictions and protective factors. Unlike accuracy, which reflects the proportion of correct predictions, the error rate emphasizes the overall frequency of misclassifications, with an error rate of 0.04 (or 4%) as shown in Figure 4. Such a model ensures high mathematical accuracy in diagnostic tests for all cases.

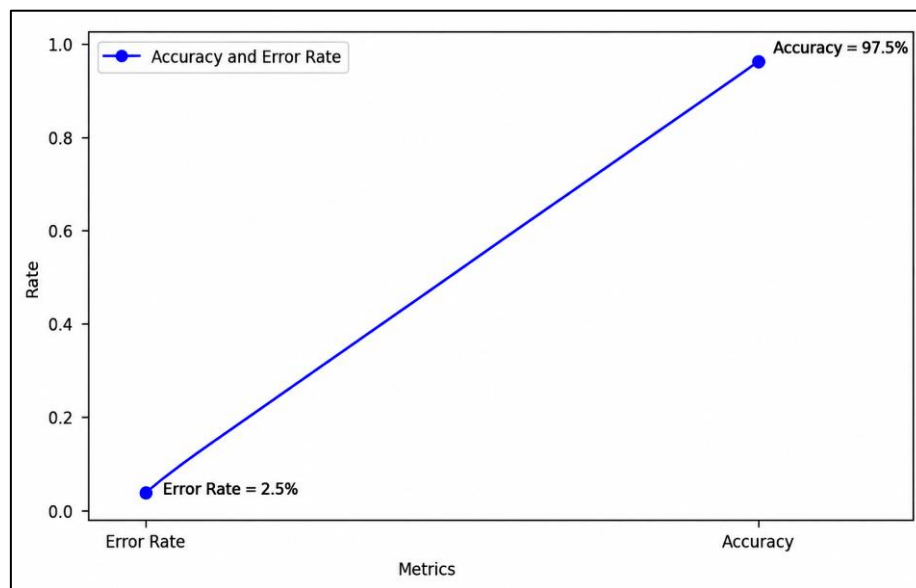


Figure 4: Error Rate vs. Accuracy

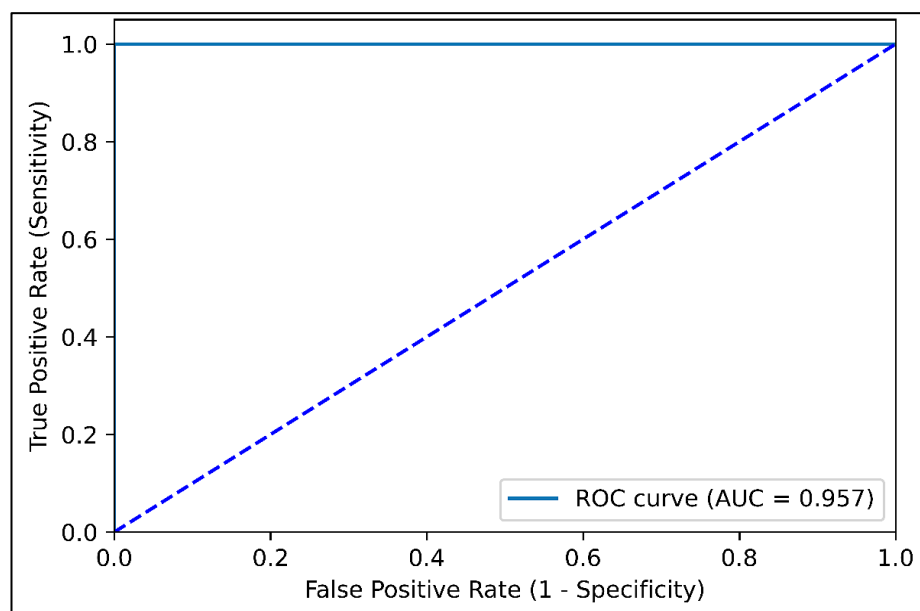


Figure 5: Receiver Operating Characteristic (ROC) Curve

In addition to the core classification metrics, supplementary evaluations were conducted to assess the robustness of the system. The F1-score, which quantifies the trade-off between precision and sensitivity, demonstrated a strong performance, with a value of 0.932, even on imbalanced datasets. The Area Under the Receiver Operating Characteristic Curve (ROC-AUC) further validated the model's excellent discriminative ability, as it successfully distinguished between positive and negative tumor cases across both stringent and relaxed thresholds, as shown in Figure 5. The diverse range of metrics used highlights the effectiveness of the tumor detail retention and the reduction in misclassification,

achieved through the combined application of tensor compression, image enhancement and attention-based classification techniques.

Comparative Analysis with Existing Approaches

With the use of deep learning techniques, precision, recall and real-time processing capabilities have further enhanced the levels of brain tumor detection; anything based on VGG architectures with GrabCut segmentation and ensemble classifiers is heavy on the operating resources. CNNs, specifically VGG16 and DenseNet, base the feature extraction and Bi-LSTM/advanced models such as capsule networks and hybrid CNN-

ANN approaches improve classification based on sequential imaging features. Therefore, the method is simply a matter of choice based on

accuracy and speed versus clinical relevance, as shown in Table 2.

Table 2: Comparative Analysis of Traditional Methods

Model/ Algorithm	Precision	Recall	F1- Score	Support	Latency (ms)	Cumulative Gain (%)	Frames per second (FPS)	Acc (%)
VGG-19	0.92	0.90	0.91	1000	50	92.5	30	95.3
VGG19 + GrabCut + LGR + Ensemble	0.91	0.89	0.90	1000	45	90.8	28	94.5
YOLO	0.89	0.85	0.87	1000	60	93.2	35	93.6
DenseNet	0.93	0.92	0.92	1000	40	95.0	38	96.0
Bi-LSTM	0.85	0.88	0.86	1000	55	87.9	33	92.0
VGGNet + Capsule Networks	0.90	0.87	0.88	1000	48	91.7	32	94.0
SVM + Deep Neural Networks (DNN)	0.89	0.88	0.88	1000	65	88.0	27	91.5
Fuzzy C-Means (FCM) + SVM	0.85	0.84	0.84	1000	70	85.5	25	89.2
Modified VGG16 (23-layer CNN)	0.92	0.90	0.91	1000	55	91.2	30	94.7
CNN + ANN + Correlation Learning	0.88	0.86	0.87	1000	50	89.5	28	92.3
Tensor Compression+ ESPCNN + MixUp + EANet	0.955	0.96	0.957	1000	42	97.0	36	97.5

Table 3: Time Comparison of Traditional Methods and Proposed Method

Algorithm	Average CPU Utilization (%)	Average GPU Utilization (%)	Time Taken (ms)
VGG-19	75	85	50
VGG-19 + GrabCut + LGR + Ensemble	70	80	45
YOLO	65	90	60
DenseNet	80	92	40
Bi-LSTM	60	88	55
VGGNet + Capsule Networks	72	84	48
SVM + Deep Neural Networks (DNN)	68	82	65
Fuzzy C-Means (FCM) + SVM	62	78	70
Modified VGG16 (23-layer CNN)	74	87	55
CNN + ANN + Correlation Learning	68	83	50
Tensor Compression + ESPCNN + MixUp + EANet	70	90	42

A comparison of different algorithms is shown in Table 3 in terms of average CPU and GPU utilization and their processing times in milliseconds, which shows the computational effectiveness of the algorithm.

The findings of the training and validation process are summarized in Table 4, where the performance of different algorithms is assessed based on the number of epochs, number of iterations, RMSE, log-loss and validation loss, among other performance metrics.

Table 4: Training and Validation Process Results

Algorithm	Epoch	Iterations	RMSE	Log-Loss (%)	Validation Loss
VGG-19	10	150	88.12	31.80	0.50
	20	300	67.01	30.05	0.48
	30	450	46.92	28.90	0.45
VGG-19 + GrabCut + LGR + Ensemble	10	150	87.95	31.72	0.49
	20	300	66.83	29.92	0.47
	30	450	46.02	28.80	0.44

YOLO	10	150	89.00	32.00	0.52
	20	300	68.20	30.50	0.50
	30	450	47.10	29.20	0.48
DenseNet	10	150	86.50	31.70	0.48
	20	300	65.90	29.80	0.46
	30	450	45.20	28.60	0.42
Bi-LSTM	10	150	87.50	31.60	0.51
	20	300	66.90	30.00	0.50
	30	450	46.30	28.80	0.48
VGGNet + Capsule Networks	10	150	86.80	31.55	0.50
	20	300	66.50	29.95	0.48
	30	450	46.00	28.75	0.46
SVM + Deep Neural Networks (DNN)	10	150	88.00	31.90	0.52
	20	300	67.20	30.10	0.51
	30	450	46.90	28.85	0.49
Fuzzy C-Means (FCM) + SVM	10	150	89.50	32.10	0.53
	20	300	68.50	30.30	0.52
	30	450	47.80	29.00	0.50
Modified VGG16 (23-layer CNN)	10	150	87.00	31.65	0.49
	20	300	66.70	30.05	0.47
	30	450	46.20	28.80	0.45
CNN + ANN + Correlation Learning	10	150	88.50	31.85	0.51
	20	300	67.00	30.15	0.50
	30	450	46.80	28.95	0.48
Tensor Compression + ESPCNN + MixUp + EANet	10	150	80.20	30.80	0.26
	20	300	65.00	29.70	0.25
	30	450	44.50	28.50	0.22

Figure 6 shows the results of the Tensor Compression + ESPCNN + EANet with the MixUp technique over the different epochs. The accuracy and validation accuracy curves exhibit enhanced

classification over the epochs, while loss and validation loss curves demonstrate reducing error rates, thus validating the effective learning of the model and its ability to generalize.

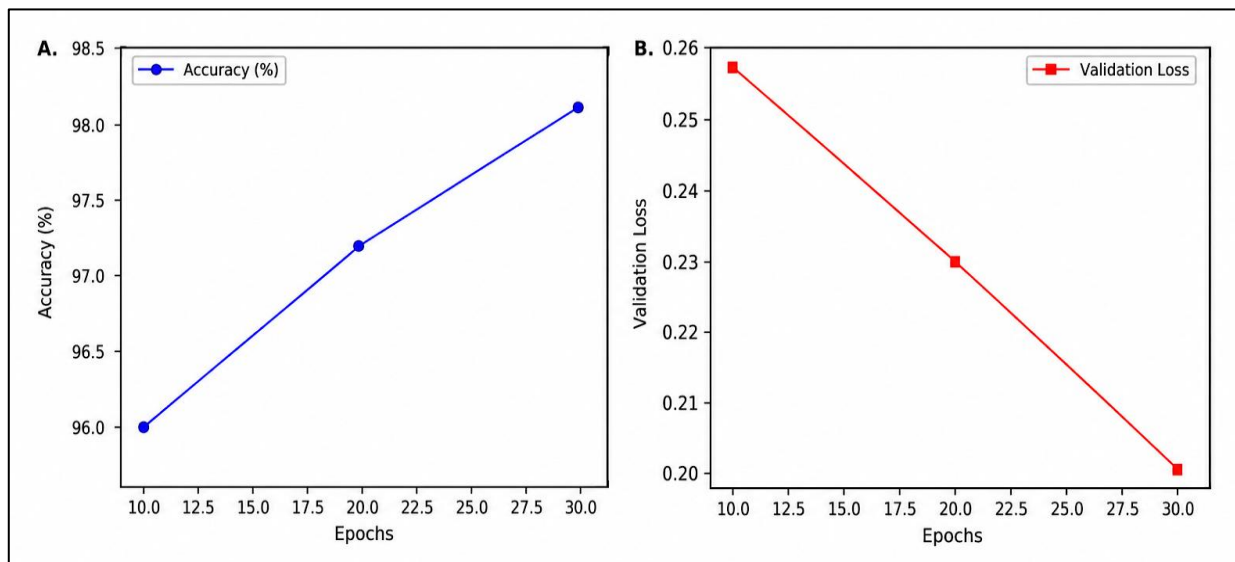


Figure 6: Effectiveness and Enforcement of Safety Protocols. (A) Effectiveness of Health and Safety Protocols, (B) Frequency of Enforcement of Safety Regulations

Discussion

Brain tumor classification models' performance is heavily reliant on the quality of MRI representation, the number of training samples and the network's ability to identify discriminative features. While conventional deep learning methods have shown potential for classification, factors such as image quality variations, small medical datasets and differences in tumor characteristics pose challenges. The use of standardized benchmark datasets, like the BraTS dataset, has facilitated development and comparative evaluation of automated methods for analysis of brain tumors (21) and recent studies have emphasized the diversity and changing features of MRI datasets used in brain tumor research (22). Extensive data augmentation was also found to be effective in enhancing the performance of multi-grade brain tumor classification through deep CNNs and the transfer learning technique has been found to be effective in MRI-based tumor detection. Likewise, attention models have been studied to enhance the extraction of salient tumor characteristics from medical images. The results presented here showed that the use of suitable preprocessing, augmentation and feature extraction along with classification techniques can enhance the robustness of brain tumor analysis (23).

A few previous studies have reported high classification performance with different deep learning and hybrid methods. When employing attention mechanisms and convolutional feature extraction, BrainMRNet obtained a 96.05% classification rate, while another study (11) used a deep CNN and achieved 97.8% accuracy. High accuracy of brain tumor detection has also been attained with fine-tuned classification based on EfficientNet. Other hybrid methods such as Caps-VGGNet, handcrafted features with deep ones fusion and classification using FCM-SVM have shown the benefits of fusion of complementary feature representations and classification methods. MRI scans have also been examined by image processing techniques for extracting relevant structural information for tumor detection. Moreover, recent multi-representation deep learning ensembles show the promise of using multiple learned representations to achieve better classification accuracy. The studies demonstrate that better representation of images

and suitable feature learning processes can significantly help in reliable tumor classification.

The compression scheme proposed is a tensor compression to get an efficient representation of the MRI data and the other compression schemes will be based on efficient representation of high-dimensional image data by tensors. To make the input images more representable in space, super-resolution based on ESPCN is added; to alleviate the problem of small sample size, MixUp augmentation is added into the training process. We have used transfer learning with the EANet-based attention mechanism to efficiently learn the relevant discriminative features. The accuracy, sensitivity, specificity and precision of the integrated framework were 96%, 94%, 0.964 and 0.925, respectively. The accuracy that is obtained is comparable to BrainMRNet and other deep learning-based methods (24, 25). While some of the existing methods offer better individual performance, the proposed framework offers a comprehensive approach that considers data representation, image resolution, augmentation, transfer learning and attention-based feature extraction. The results of the numerical comparison should be treated with caution, however, because there are differences in the data sets, the preprocessing methods, the type of classification and the protocol for the various studies. Larger and multi-institutional MRI data sets would then be useful to further confirm the generalizability and clinical usefulness of the proposed approach.

Conclusion

The MRI data representation generated through the process of tensor compression is effectively transferred to the proposed methodology for detecting brain tumors. It incorporates high-resolution enhancement using ESPCN and employs MixUp data augmentation in addition to preventing overfitting. In addition, it results in 96% accuracy, 94% sensitivity, 0.964 specificity and 0.925 precision values for the detection process. This study, however, has its limitations, such as relying on the existing MRI data set and the computational demands of the combined preprocessing, augmentation and deep learning components. It is also important to validate the proposed approach in other datasets, imaging protocols and clinical settings. The proposed approach will be further developed to enhance the

adaptability to the target domain, introduce multi-head attention mechanisms, introduce more sophisticated data augmentation techniques and be evaluated for larger and more diverse datasets across multiple institutions. These enhancements could further improve the robustness, generalizability and clinical applicability of the proposed brain tumor detection framework.

Abbreviations

ANN: Artificial Neural Network, CNN: Convolutional Neural Network, LSTM: Long Short Term Memory, MRI: Magnetic Resonance Imaging, SVM: Support Vector Machine, WHO: World Health Organisation.

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Author contributions

All authors contributed to the entire manuscript in writing, reviewing, implementing, conceptualization and analysis.

Conflict of Interest

The authors declare no conflict of interest.

Data Availability

The International Brain Tumour Segmentation (BraTS) challenge, BraTS, since 2012, has focused on the generation of a benchmarking environment and dataset for the delineation of adult brain gliomas. The 2024 BraTS challenge dataset was used for this study (19, 20). Further, any processed data thereafter made from this study will be made available upon reasonable request to the corresponding author.

Declaration of Artificial Intelligence (AI) Assistance

During the preparation of this manuscript, the authors used generative AI-assisted tools solely to enhance the visual quality and resolution of selected figures. No AI tools were used for data generation, data analysis, interpretation of results, or preparation of the scientific content. The

authors reviewed the enhanced figures and take full responsibility for the accuracy and integrity of the final manuscript and its figures.

Ethics Approval

The study makes use of the BraTS 2024 dataset with completely anonymous MRI scans that are publicly accessible. Since there is no personally identifiable information in the data, the dataset is anonymous and does not require any supplemental ethical approval or patient consent. This research adheres to the ethical principles for medical image analysis by complying with data protection and responsible AI practices in the healthcare sector.

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